



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 23, 2022 – 03:16 pm GMT

PDB ID : 7Q84  
Title : Crystal structure of human peroxisomal acyl-Co-A oxidase 1a, apo-form  
Authors : Sonani, R.R.; Blat, A.; Dubin, G.  
Deposited on : 2021-11-10  
Resolution : 2.00 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](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 : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.26  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0267  
CCP4 : 7.1.010 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.26

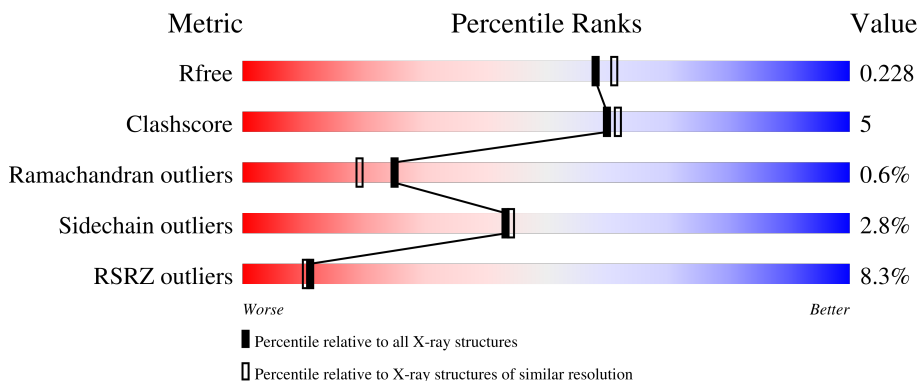
# 1 Overall quality at a glance

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))
$R_{free}$	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (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 of 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	667	 7% 82% 11% • 6%
1	B	667	 9% 83% 10% • 6%

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	PGE	A	701	-	-	X	-
3	EDO	A	708	-	-	-	X

## 2 Entry composition [i](#)

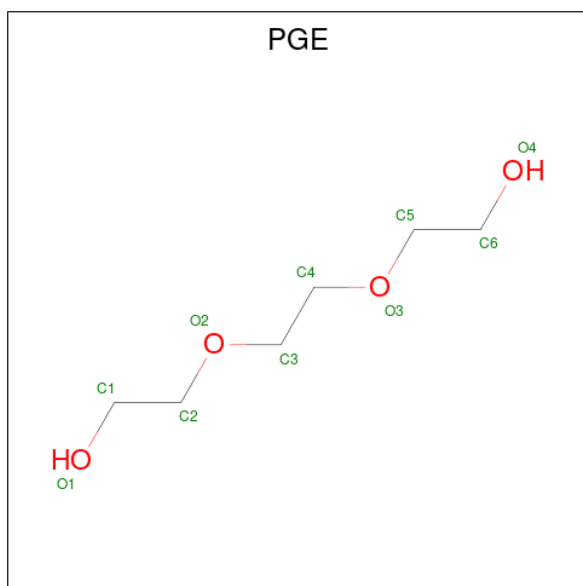
There are 6 unique types of molecules in this entry. The entry contains 10556 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Isoform 2 of Peroxisomal acyl-coenzyme A oxidase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	628	Total	C	N	O	S	0	0	0
			5002	3185	868	920	29			
1	B	625	Total	C	N	O	S	0	0	0
			4977	3169	863	916	29			

- Molecule 2 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	Total	C	O	0	0
			10	6	4		
2	B	1	Total	C	O	0	0
			10	6	4		

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



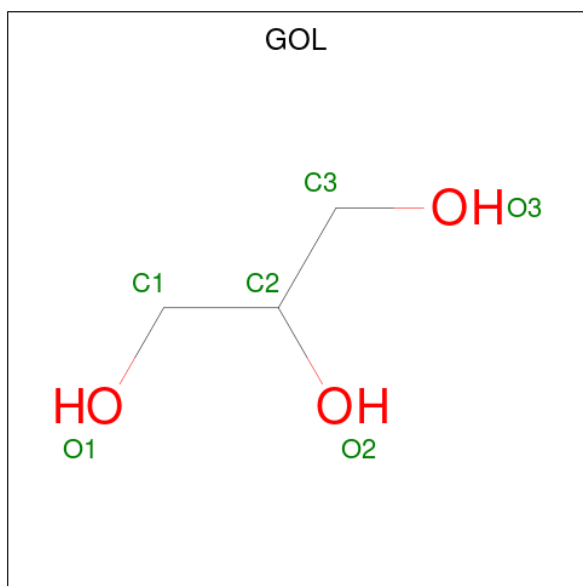
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0

- Molecule 4 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
4	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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

- Molecule 6 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
6	A	221	Total 221	O 221	0	0
6	B	271	Total 271	O 271	0	0





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	87.87Å 133.22Å 139.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.23 – 2.00 48.18 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.1 (48.23-2.00) 99.1 (48.18-2.00)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.92 (at 2.00Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.183 , 0.220 0.192 , 0.228	Depositor DCC
$R_{free}$ test set	5573 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.1	Xtrriage
Anisotropy	0.822	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.006 for -h,l,k	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	10556	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.24% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PGE, EDO, PEG, CSO, 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	0.92	3/5099 (0.1%)	1.00	4/6896 (0.1%)
1	B	0.92	1/5073 (0.0%)	0.99	6/6861 (0.1%)
All	All	0.92	4/10172 (0.0%)	0.99	10/13757 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	350	GLU	CD-OE2	5.83	1.32	1.25
1	A	37	GLU	CD-OE1	-5.63	1.19	1.25
1	B	131	GLU	CD-OE1	5.40	1.31	1.25
1	A	28	GLU	CG-CD	5.10	1.59	1.51

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	623	ARG	CB-CA-C	-6.00	98.41	110.40
1	A	525	ARG	NE-CZ-NH2	-5.95	117.32	120.30
1	A	525	ARG	NE-CZ-NH1	5.91	123.26	120.30
1	B	291	ARG	NE-CZ-NH1	5.83	123.22	120.30
1	A	210	ARG	NE-CZ-NH2	-5.73	117.44	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	5002	0	4972	50	0
1	B	4977	0	4944	44	0
2	A	10	0	14	6	0
2	B	10	0	14	4	0
3	A	24	0	36	3	0
3	B	16	0	24	0	0
4	A	7	0	10	0	0
5	A	6	0	8	2	0
5	B	12	0	16	1	0
6	A	221	0	0	5	0
6	B	271	0	0	4	0
All	All	10556	0	10038	92	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 92 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:348:MET:HE1	1:A:374:THR:HG22	1.60	0.81
1:A:307:ARG:HE	2:A:701:PGE:H12	1.45	0.79
1:A:348:MET:CE	1:A:374:THR:HG22	2.17	0.74
1:A:309:GLN:HG2	2:A:701:PGE:H2	1.73	0.71
1:A:103:HIS:HD2	1:A:134:GLY:H	1.39	0.70

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	618/667 (93%)	593 (96%)	21 (3%)	4 (1%)	25 19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	615/667 (92%)	597 (97%)	15 (2%)	3 (0%)	29 23
All	All	1233/1334 (92%)	1190 (96%)	36 (3%)	7 (1%)	25 19

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	176	TRP
1	A	473	THR
1	B	176	TRP
1	B	473	THR
1	A	365	SER

### 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	539/576 (94%)	522 (97%)	17 (3%)	39 38
1	B	536/576 (93%)	523 (98%)	13 (2%)	49 51
All	All	1075/1152 (93%)	1045 (97%)	30 (3%)	43 44

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	651	LYS
1	B	539	PHE
1	B	56	ARG
1	B	654	LYS
1	B	369	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	627	ASN
1	B	90	ASN

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Mol	Chain	Res	Type
1	B	503	GLN
1	B	48	HIS
1	B	103	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

4 non-standard protein/DNA/RNA residues 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
1	CSO	A	449	1	3,6,7	1.25	0	0,6,8	-	-
1	CSO	A	199	1	3,6,7	1.35	1 (33%)	0,6,8	-	-
1	CSO	B	449	1	3,6,7	1.17	0	0,6,8	-	-
1	CSO	B	199	1	3,6,7	1.16	0	0,6,8	-	-

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
1	CSO	A	449	1	-	0/1/5/7	-
1	CSO	A	199	1	-	0/1/5/7	-
1	CSO	B	449	1	-	0/1/5/7	-
1	CSO	B	199	1	-	0/1/5/7	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	199	CSO	O-C	2.21	1.28	1.19

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

16 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	$\# Z  > 2$
3	EDO	A	703	-	3,3,3	0.77	0	2,2,2	1.00	0
3	EDO	B	702	-	3,3,3	1.37	0	2,2,2	0.96	0
3	EDO	B	703	-	3,3,3	1.12	0	2,2,2	0.61	0
3	EDO	B	704	-	3,3,3	0.81	0	2,2,2	0.59	0
3	EDO	A	708	-	3,3,3	0.61	0	2,2,2	0.35	0
3	EDO	B	706	-	3,3,3	0.16	0	2,2,2	0.31	0
2	PGE	B	701	-	9,9,9	0.85	0	8,8,8	0.94	0
4	PEG	A	704	-	6,6,6	0.76	0	5,5,5	0.42	0
2	PGE	A	701	-	9,9,9	0.61	0	8,8,8	1.09	2 (25%)
3	EDO	A	706	-	3,3,3	0.26	0	2,2,2	0.37	0
3	EDO	A	709	-	3,3,3	0.20	0	2,2,2	0.32	0
5	GOL	B	705	-	5,5,5	0.16	0	5,5,5	0.42	0
5	GOL	A	707	-	5,5,5	0.27	0	5,5,5	0.58	0
5	GOL	B	707	-	5,5,5	0.20	0	5,5,5	0.50	0
3	EDO	A	705	-	3,3,3	0.73	0	2,2,2	0.25	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	EDO	A	702	-	3,3,3	1.31	0	2,2,2	1.10	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
3	EDO	A	703	-	-	0/1/1/1	-
3	EDO	B	702	-	-	1/1/1/1	-
3	EDO	B	703	-	-	1/1/1/1	-
3	EDO	B	704	-	-	1/1/1/1	-
3	EDO	A	708	-	-	1/1/1/1	-
3	EDO	B	706	-	-	1/1/1/1	-
2	PGE	B	701	-	-	4/7/7/7	-
4	PEG	A	704	-	-	3/4/4/4	-
2	PGE	A	701	-	-	3/7/7/7	-
3	EDO	A	706	-	-	0/1/1/1	-
3	EDO	A	709	-	-	1/1/1/1	-
5	GOL	B	705	-	-	4/4/4/4	-
5	GOL	A	707	-	-	0/4/4/4	-
5	GOL	B	707	-	-	0/4/4/4	-
3	EDO	A	705	-	-	1/1/1/1	-
3	EDO	A	702	-	-	1/1/1/1	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	PGE	C3-O2-C2	-2.12	104.10	113.29
2	A	701	PGE	O2-C2-C1	-2.03	101.14	110.07

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	705	GOL	O1-C1-C2-O2
5	B	705	GOL	O1-C1-C2-C3
5	B	705	GOL	C1-C2-C3-O3
4	A	704	PEG	O2-C3-C4-O4

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Mol	Chain	Res	Type	Atoms
2	B	701	PGE	O2-C3-C4-O3

There are no ring outliers.

5 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	701	PGE	4	0
2	A	701	PGE	6	0
5	B	705	GOL	1	0
5	A	707	GOL	2	0
3	A	702	EDO	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 [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	626/667 (93%)	0.28	45 (7%) 15 14	30, 48, 81, 145	0
1	B	623/667 (93%)	0.34	59 (9%) 8 7	29, 45, 79, 125	0
All	All	1249/1334 (93%)	0.31	104 (8%) 11 10	29, 47, 80, 145	0

The worst 5 of 104 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	655	SER	8.7
1	A	472	PRO	6.8
1	B	472	PRO	5.8
1	B	355	ILE	5.6
1	B	653	LEU	5.6

### 6.2 Non-standard residues in protein, DNA, RNA chains [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
1	CSO	A	199	7/8	0.83	0.31	20,20,20,20	0
1	CSO	A	449	7/8	0.85	0.27	20,20,20,20	0
1	CSO	B	449	7/8	0.86	0.39	20,20,20,20	0
1	CSO	B	199	7/8	0.91	0.28	20,20,20,20	0

### 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, 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	708	4/4	0.72	0.49	63,68,70,73	0
5	GOL	A	707	6/6	0.82	0.16	63,65,72,73	0
2	PGE	A	701	10/10	0.85	0.39	43,54,64,70	0
3	EDO	A	709	4/4	0.86	0.25	59,64,67,72	0
2	PGE	B	701	10/10	0.87	0.37	41,64,72,77	0
3	EDO	B	703	4/4	0.89	0.16	52,57,57,61	0
3	EDO	B	704	4/4	0.91	0.17	42,58,62,63	0
3	EDO	A	702	4/4	0.92	0.19	44,52,52,54	0
3	EDO	A	705	4/4	0.92	0.15	53,60,67,69	0
4	PEG	A	704	7/7	0.92	0.21	61,65,72,75	0
3	EDO	B	702	4/4	0.92	0.45	38,50,59,59	0
3	EDO	B	706	4/4	0.93	0.17	49,59,62,65	0
3	EDO	A	703	4/4	0.94	0.28	36,48,50,54	0
3	EDO	A	706	4/4	0.94	0.15	50,53,57,57	0
5	GOL	B	707	6/6	0.94	0.23	54,58,59,64	0
5	GOL	B	705	6/6	0.95	0.14	63,70,75,77	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.