



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 12:32 PM UTC

PDB ID : 4BD8 / pdb\_00004bd8  
Title : Bax domain swapped dimer induced by BimBH3 with CHAPS  
Authors : Czabotar, P.E.; Westphal, D.; Adams, J.M.; Colman, P.M.  
Deposited on : 2012-10-05  
Resolution : 2.22 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

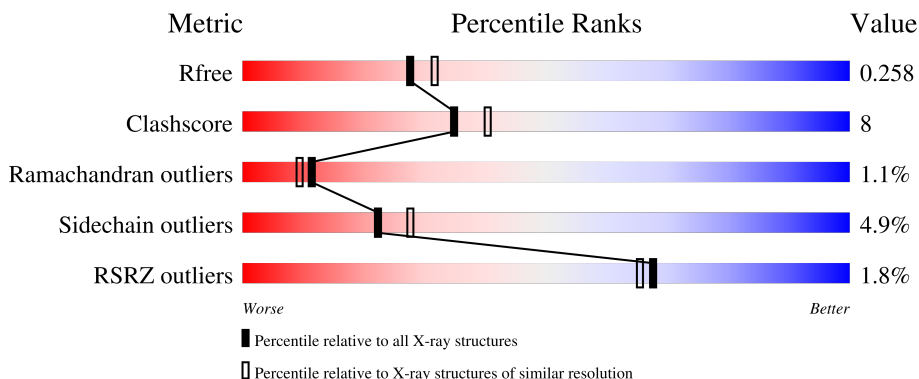
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.22 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))
$R_{free}$	180053	7682 (2.24-2.20)
Clashscore	190562	8402 (2.24-2.20)
Ramachandran outliers	187476	8303 (2.24-2.20)
Sidechain outliers	187428	8304 (2.24-2.20)
RSRZ outliers	180081	7683 (2.24-2.20)

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	174	
1	B	174	
1	C	174	
1	D	174	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4664 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 APOPTOSIS REGULATOR BAX.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	145	1136	728	195	208	5	0	0	0
1	B	152	1179	760	199	215	5	0	0	0
1	C	133	1031	667	177	183	4	0	0	0
1	D	136	1058	682	178	193	5	0	0	0

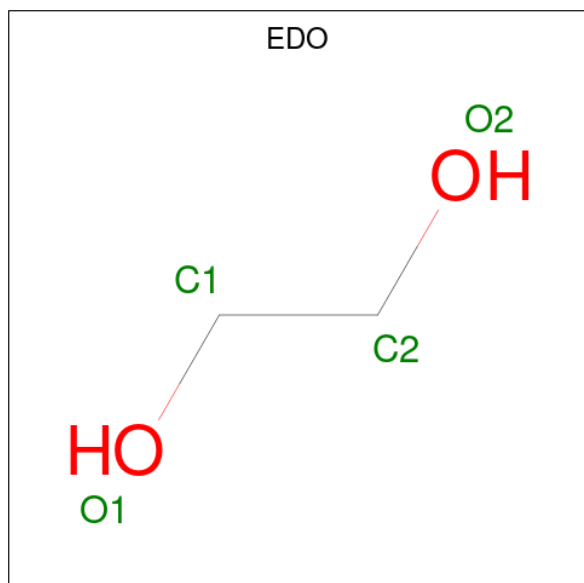
There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	172	GLY	-	expression tag	UNP Q07812
A	173	SER	-	expression tag	UNP Q07812
A	174	SER	-	expression tag	UNP Q07812
A	62	SER	CYS	engineered mutation	UNP Q07812
A	126	SER	CYS	engineered mutation	UNP Q07812
B	172	GLY	-	expression tag	UNP Q07812
B	173	SER	-	expression tag	UNP Q07812
B	174	SER	-	expression tag	UNP Q07812
B	62	SER	CYS	engineered mutation	UNP Q07812
B	126	SER	CYS	engineered mutation	UNP Q07812
C	172	GLY	-	expression tag	UNP Q07812
C	173	SER	-	expression tag	UNP Q07812
C	174	SER	-	expression tag	UNP Q07812
C	62	SER	CYS	engineered mutation	UNP Q07812
C	126	SER	CYS	engineered mutation	UNP Q07812
D	172	GLY	-	expression tag	UNP Q07812
D	173	SER	-	expression tag	UNP Q07812
D	174	SER	-	expression tag	UNP Q07812
D	62	SER	CYS	engineered mutation	UNP Q07812
D	126	SER	CYS	engineered mutation	UNP Q07812

- Molecule 2 is PRASEODYMIUM ION (CCD ID: PR) (formula: Pr).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Pr	0	0
			1	1		
2	B	1	Total	Pr	0	0
			1	1		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: 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	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is water.

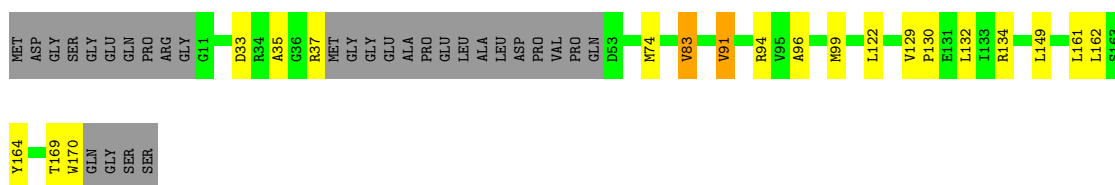
<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
4	A	84	Total 84	O 84	0	0
4	B	60	Total 60	O 60	0	0
4	C	36	Total 36	O 36	0	0
4	D	46	Total 46	O 46	0	0

### 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.

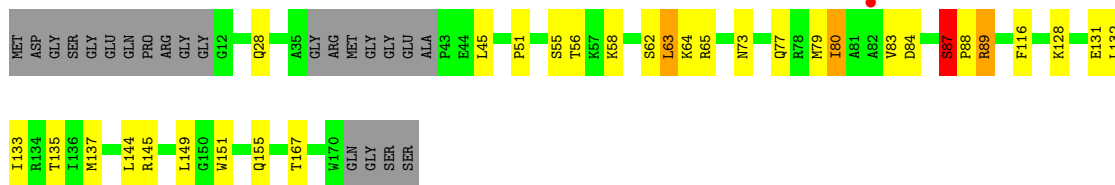
- Molecule 1: APOPTOSIS REGULATOR BAX

Chain A:  72% 10% 17%



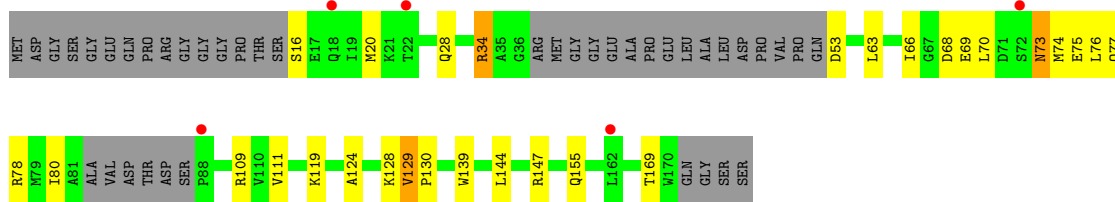
- Molecule 1: APOPTOSIS REGULATOR BAX

Chain B:  69% 16% 13%



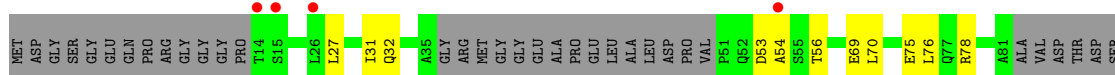
- Molecule 1: APOPTOSIS REGULATOR BAX

Chain C:  3% 60% 15% 24%



- Molecule 1: APOPTOSIS REGULATOR BAX

Chain D:  2% 64% 14% 22%



R88	R89	D102	L132	G138	L141	D142	F143	L144	L148	W151	I152	Q153	D154	Q155	G156	G157	L161	W170	GLN	GLY	SER	SER
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## 4 Data and refinement statistics i

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	142.95Å 142.95Å 86.71Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.82 – 2.22 19.82 – 2.22	Depositor EDS
% Data completeness (in resolution range)	98.5 (19.82-2.22) 98.4 (19.82-2.22)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.09 (at 2.21Å)	Xtrriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.197 , 0.256 0.204 , 0.258	Depositor DCC
$R_{free}$ test set	1607 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	46.2	Xtrriage
Anisotropy	0.036	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 64.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.018 for $-2/3^*h-1/3^*k-4/3^*l,-1/3^*h-2/3^*k+4/3^*l,-1/3^*h+1/3^*k+1/3^*l$ 0.017 for $-h,1/3^*h-1/3^*k-4/3^*l,-1/3^*h-2/3^*k+1/3^*l$ 0.014 for $-1/3^*h+1/3^*k+4/3^*l,-k,2/3^*h+1/3^*k+1/3^*l$ 0.013 for $-h,2/3^*h+1/3^*k+4/3^*l,1/3^*h+2/3^*k-1/3^*l$ 0.024 for $-1/3^*h-2/3^*k+4/3^*l,-2/3^*h-1/3^*k-4/3^*l,1/3^*h-1/3^*k-1/3^*l$ 0.013 for $1/3^*h+2/3^*k-4/3^*l,-k,-2/3^*h-1/3^*k-1/3^*l$ 0.028 for $h,-h-k,-l$	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4664	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	83.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.90% 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: PR, EDO

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	0.59	0/1159	0.87	0/1564
1	B	0.62	0/1205	0.91	2/1633 (0.1%)
1	C	0.44	1/1052 (0.1%)	0.82	0/1422
1	D	0.41	0/1080	0.83	1/1460 (0.1%)
All	All	0.53	1/4496 (0.0%)	0.86	3/6079 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	129	VAL	CA-CB	5.15	1.57	1.54

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	87	SER	CA-C-N	6.38	127.81	119.84
1	B	87	SER	C-N-CA	6.38	127.81	119.84
1	D	155	GLN	N-CA-C	-5.51	106.56	113.72

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	1136	0	1124	17	0
1	B	1179	0	1159	21	0
1	C	1031	0	999	19	0
1	D	1058	0	1018	18	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	20	0	30	3	0
3	B	8	0	12	0	0
3	D	4	0	6	1	0
4	A	84	0	0	5	0
4	B	60	0	0	5	0
4	C	36	0	0	7	0
4	D	46	0	0	3	0
All	All	4664	0	4348	66	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 8.

The worst 5 of 66 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:96:ALA:HA	1:A:99:MET:HE2	1.65	0.76
1:A:161:LEU:HD21	1:B:63:LEU:HD13	1.71	0.73
1:D:157:GLY:O	4:D:2041:HOH:O	2.07	0.71
1:A:134:ARG:NH2	4:A:2066:HOH:O	2.24	0.69
1:C:73:ASN:O	4:C:2010:HOH:O	2.10	0.69

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	141/174 (81%)	138 (98%)	3 (2%)	0	100	100
1	B	148/174 (85%)	141 (95%)	4 (3%)	3 (2%)	6	3
1	C	127/174 (73%)	117 (92%)	7 (6%)	3 (2%)	4	2
1	D	130/174 (75%)	126 (97%)	4 (3%)	0	100	100
All	All	546/696 (78%)	522 (96%)	18 (3%)	6 (1%)	11	9

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	155	GLN
1	B	88	PRO
1	C	73	ASN
1	C	75	GLU
1	B	84	ASP

### 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	118/142 (83%)	115 (98%)	3 (2%)	42	55
1	B	122/142 (86%)	111 (91%)	11 (9%)	9	8
1	C	102/142 (72%)	97 (95%)	5 (5%)	22	27
1	D	107/142 (75%)	104 (97%)	3 (3%)	38	50
All	All	449/568 (79%)	427 (95%)	22 (5%)	22	27

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	28	GLN
1	C	144	LEU
1	C	119	LYS
1	C	169	THR
1	B	83	VAL

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

Mol	Chain	Res	Type
1	D	155	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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	1173	-	3,3,3	0.43	0	2,2,2	0.64	0
3	EDO	A	1174	-	3,3,3	0.43	0	2,2,2	0.26	0
3	EDO	A	1172	-	3,3,3	0.44	0	2,2,2	0.54	0
3	EDO	A	1175	-	3,3,3	0.50	0	2,2,2	0.40	0
3	EDO	B	1172	-	3,3,3	0.42	0	2,2,2	0.37	0
3	EDO	D	1171	-	3,3,3	0.43	0	2,2,2	0.49	0
3	EDO	A	1176	-	3,3,3	0.44	0	2,2,2	0.33	0
3	EDO	B	1173	-	3,3,3	0.43	0	2,2,2	0.39	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	1173	-	-	1/1/1/1	-
3	EDO	A	1174	-	-	0/1/1/1	-
3	EDO	A	1172	-	-	0/1/1/1	-
3	EDO	A	1175	-	-	1/1/1/1	-
3	EDO	B	1172	-	-	0/1/1/1	-
3	EDO	D	1171	-	-	0/1/1/1	-
3	EDO	A	1176	-	-	1/1/1/1	-
3	EDO	B	1173	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1176	EDO	O1-C1-C2-O2
3	A	1173	EDO	O1-C1-C2-O2
3	A	1175	EDO	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1173	EDO	1	0
3	A	1172	EDO	1	0
3	D	1171	EDO	1	0
3	A	1176	EDO	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, 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	145/174 (83%)	-0.31	0 <span style="border: 1px solid blue; padding: 2px;">100</span> <span style="border: 1px solid blue; padding: 2px;">100</span>	41, 64, 95, 114	0
1	B	152/174 (87%)	-0.23	1 (0%) <span style="border: 1px solid blue; padding: 2px;">84</span> <span style="border: 1px solid blue; padding: 2px;">83</span>	40, 62, 99, 162	0
1	C	133/174 (76%)	0.35	5 (3%) <span style="border: 1px solid red; padding: 2px;">44</span> <span style="border: 1px solid red; padding: 2px;">41</span>	49, 96, 164, 236	0
1	D	136/174 (78%)	0.24	4 (2%) <span style="border: 1px solid gray; padding: 2px;">53</span> <span style="border: 1px solid gray; padding: 2px;">51</span>	54, 101, 171, 234	0
All	All	566/696 (81%)	0.00	10 (1%) <span style="border: 1px solid blue; padding: 2px;">67</span> <span style="border: 1px solid blue; padding: 2px;">65</span>	40, 75, 149, 236	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	15	SER	3.8
1	D	14	THR	2.7
1	B	82	ALA	2.5
1	C	22	THR	2.4
1	D	26	LEU	2.3

### 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 oligosaccharides 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( $\text{\AA}^2$ )	Q<0.9
3	EDO	A	1175	4/4	0.69	0.13	74,74,90,91	0
3	EDO	B	1172	4/4	0.70	0.11	90,91,95,100	0
3	EDO	D	1171	4/4	0.75	0.18	90,92,93,93	0
3	EDO	B	1173	4/4	0.81	0.12	85,86,89,90	0
3	EDO	A	1172	4/4	0.86	0.13	73,76,77,81	0
3	EDO	A	1174	4/4	0.91	0.12	84,84,87,90	0
3	EDO	A	1176	4/4	0.93	0.11	73,77,80,83	0
3	EDO	A	1173	4/4	0.94	0.09	63,69,86,101	0
2	PR	A	1171	1/1	1.00	0.04	56,56,56,56	0
2	PR	B	1171	1/1	1.00	0.01	75,75,75,75	0

## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.