



# Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 05:09 pm BST

PDB ID : 6MTU  
Title : Crystal structure of human Scribble PDZ1:pMCC complex  
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Deposited on : 2018-10-22  
Resolution : 2.14 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

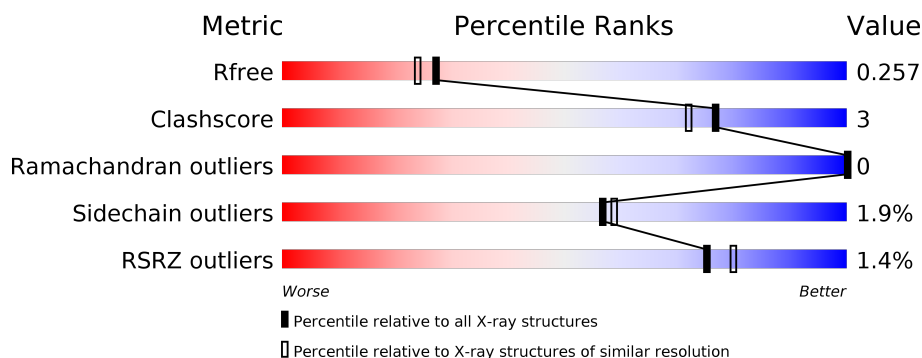
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.14 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	2523 (2.16-2.12)
Clashscore	141614	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)
RSRZ outliers	127900	2485 (2.16-2.12)

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	118	<div> <div>2%</div> <div>81% 6% 14%</div> </div>
1	B	118	<div> <div>71% 10% 19%</div> </div>
2	C	8	<div> <div>88% 13%</div> </div>
2	D	8	<div> <div>13% 88% 13%</div> </div>

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 3425 atoms, of which 1691 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 Protein scribble homolog.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	102	Total	C	H	N	O	S	0	0	0
			1521	468	762	141	148	2			
1	B	96	Total	C	H	N	O	S	0	0	0
			1437	442	719	134	140	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	699	GLY	-	expression tag	UNP Q14160
B	699	GLY	-	expression tag	UNP Q14160

- Molecule 2 is a protein called Colorectal mutant cancer protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	8	Total	C	H	N	O	P	0	0	0
			122	37	55	11	18	1			
2	D	8	Total	C	H	N	O	P	0	0	0
			122	37	55	11	18	1			

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



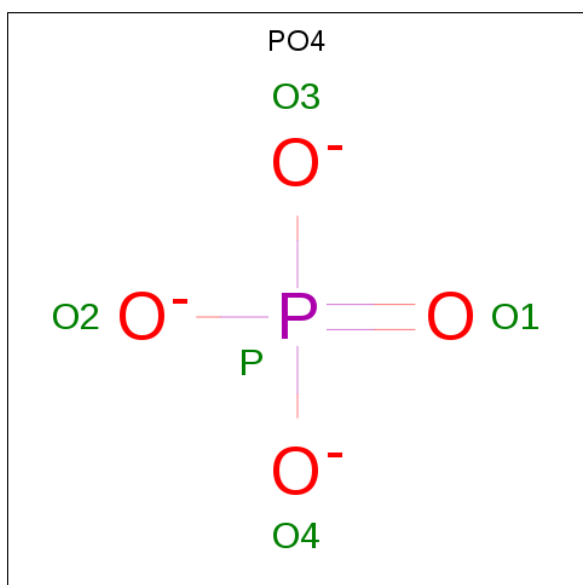
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			17	4	10	3		
3	A	1	Total	C	H	O	0	0
			17	4	10	3		
3	B	1	Total	C	H	O	0	0
			17	4	10	3		
3	B	1	Total	C	H	O	0	0
			17	4	10	3		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



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

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



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

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

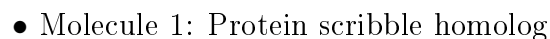
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Cl	0	0
			1	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	28	Total	O	0	0
			28	28		
7	B	13	Total	O	0	0
			13	13		
7	C	2	Total	O	0	0
			2	2		
7	D	1	Total	O	0	0
			1	1		



- Molecule 1: Protein scribble homolog



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	53.60Å 53.60Å 214.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.88 – 2.14 42.88 – 2.14	Depositor EDS
% Data completeness (in resolution range)	53.2 (42.88-2.14) 53.2 (42.88-2.14)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.04 (at 2.14Å)	Xtriage
Refinement program	PHENIX (1.14_3260)	Depositor
R, $R_{free}$	0.197 , 0.255 0.198 , 0.257	Depositor DCC
$R_{free}$ test set	892 reflections (10.12%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	42.2	Xtriage
Anisotropy	0.021	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.43 , 38.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.479 for -h,k,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3425	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.02% 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: PEG, PO4, CL, EDO, SEP

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	0.25	0/767	0.48	0/1032
1	B	0.25	0/725	0.43	0/973
2	C	0.27	0/57	0.41	0/74
2	D	0.19	0/57	0.45	0/74
All	All	0.25	0/1606	0.45	0/2153

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 [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	759	762	761	4	0
1	B	718	719	718	6	1
2	C	67	55	55	1	0
2	D	67	55	55	1	0
3	A	14	20	20	0	0
3	B	14	20	20	0	0
4	A	32	48	48	0	1
4	B	8	12	12	0	0
5	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	5	0	0	0	0
6	A	1	0	0	0	0
7	A	28	0	0	1	1
7	B	13	0	0	0	1
7	C	2	0	0	1	0
7	D	1	0	0	0	0
All	All	1734	1691	1689	10	2

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 3.

All (10) 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:B:766:GLU:O	1:B:771:ARG:NH1	2.29	0.64
1:B:762:ARG:NH2	7:C:901:HOH:O	2.34	0.61
1:A:800:LEU:HD13	2:D:829:LEU:HD13	1.91	0.53
1:B:792:GLU:N	1:B:795:GLU:OE2	2.40	0.52
1:A:806:ALA:O	7:A:1001:HOH:O	2.20	0.49
1:A:722:ILE:O	1:A:815:ARG:HG3	2.13	0.48
1:A:716:LEU:C	1:A:716:LEU:HD12	2.35	0.47
1:B:794:HIS:O	1:B:798:GLU:HG3	2.18	0.44
1:B:741:SER:HA	2:C:828:SEP:HA	2.00	0.43
1:B:780:LEU:HG	1:B:788:LEU:HD12	2.03	0.41

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:772:ALA:O	4:A:905:EDO:O2[3_545]	2.06	0.14
7:A:1019:HOH:O	7:B:1006:HOH:O[6_645]	2.15	0.05

## 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	100/118 (85%)	95 (95%)	5 (5%)	0	100	100
1	B	92/118 (78%)	91 (99%)	1 (1%)	0	100	100
2	C	5/8 (62%)	5 (100%)	0	0	100	100
2	D	5/8 (62%)	5 (100%)	0	0	100	100
All	All	202/252 (80%)	196 (97%)	6 (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	75/88 (85%)	73 (97%)	2 (3%)	44	43
1	B	71/88 (81%)	70 (99%)	1 (1%)	67	70
2	C	7/7 (100%)	7 (100%)	0	100	100
2	D	7/7 (100%)	7 (100%)	0	100	100
All	All	160/190 (84%)	157 (98%)	3 (2%)	57	59

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	718	GLU
1	A	762	ARG
1	B	724	GLU

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 ⓘ

2 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	$\# Z  > 2$
2	SEP	C	828	2	8,9,10	1.55	1 (12%)	8,12,14	1.65	2 (25%)
2	SEP	D	828	2	8,9,10	1.54	1 (12%)	8,12,14	1.67	2 (25%)

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	SEP	C	828	2	-	1/5/8/10	-
2	SEP	D	828	2	-	4/5/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	828	SEP	P-O1P	3.38	1.61	1.50
2	D	828	SEP	P-O1P	3.36	1.61	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	828	SEP	P-OG-CB	-3.55	108.51	118.30
2	D	828	SEP	P-OG-CB	-3.20	109.49	118.30
2	D	828	SEP	OG-CB-CA	2.85	110.92	108.14
2	C	828	SEP	OG-CB-CA	2.52	110.60	108.14

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	828	SEP	N-CA-CB-OG
2	D	828	SEP	CB-OG-P-O1P
2	D	828	SEP	CB-OG-P-O2P
2	D	828	SEP	CB-OG-P-O3P
2	C	828	SEP	N-CA-CB-OG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	828	SEP	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 1 is monoatomic - leaving 16 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	$\# Z  > 2$
4	EDO	A	907	-	3,3,3	0.46	0	2,2,2	0.38	0
5	PO4	A	904	-	4,4,4	0.91	0	6,6,6	0.44	0
4	EDO	A	906	-	3,3,3	0.45	0	2,2,2	0.28	0
4	EDO	A	908	-	3,3,3	0.47	0	2,2,2	0.28	0
4	EDO	A	912	-	3,3,3	0.46	0	2,2,2	0.18	0
4	EDO	A	902	-	3,3,3	0.46	0	2,2,2	0.34	0
3	PEG	B	905	-	6,6,6	0.49	0	5,5,5	0.29	0
3	PEG	B	904	-	6,6,6	0.49	0	5,5,5	0.29	0
4	EDO	A	905	-	3,3,3	0.47	0	2,2,2	0.22	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	PEG	A	901	-	6,6,6	0.49	0	5,5,5	0.31	0
4	EDO	A	910	-	3,3,3	0.46	0	2,2,2	0.30	0
4	EDO	A	909	-	3,3,3	0.46	0	2,2,2	0.30	0
5	PO4	B	901	-	4,4,4	0.92	0	6,6,6	0.44	0
4	EDO	B	902	-	3,3,3	0.46	0	2,2,2	0.34	0
3	PEG	A	903	-	6,6,6	0.49	0	5,5,5	0.45	0
4	EDO	B	903	-	3,3,3	0.46	0	2,2,2	0.30	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	EDO	A	907	-	-	0/1/1/1	-
4	EDO	A	906	-	-	0/1/1/1	-
4	EDO	A	908	-	-	0/1/1/1	-
4	EDO	A	912	-	-	1/1/1/1	-
4	EDO	A	902	-	-	0/1/1/1	-
3	PEG	B	905	-	-	3/4/4/4	-
3	PEG	B	904	-	-	1/4/4/4	-
4	EDO	A	905	-	-	0/1/1/1	-
3	PEG	A	901	-	-	0/4/4/4	-
4	EDO	A	910	-	-	0/1/1/1	-
4	EDO	A	909	-	-	0/1/1/1	-
4	EDO	B	902	-	-	1/1/1/1	-
3	PEG	A	903	-	-	3/4/4/4	-
4	EDO	B	903	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	902	EDO	O1-C1-C2-O2
3	A	903	PEG	O2-C3-C4-O4
3	B	905	PEG	C4-C3-O2-C2
3	A	903	PEG	C4-C3-O2-C2
3	B	905	PEG	O2-C3-C4-O4

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Mol	Chain	Res	Type	Atoms
3	B	904	PEG	O1-C1-C2-O2
3	A	903	PEG	C1-C2-O2-C3
4	A	912	EDO	O1-C1-C2-O2
3	B	905	PEG	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	905	EDO	0	1

## 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	102/118 (86%)	0.22	2 (1%) 65 71	30, 46, 66, 68	0
1	B	96/118 (81%)	0.06	0 100 100	30, 44, 61, 67	0
2	C	7/8 (87%)	0.17	0 100 100	39, 42, 54, 70	0
2	D	7/8 (87%)	0.50	1 (14%) 2 3	38, 52, 62, 67	0
All	All	212/252 (84%)	0.16	3 (1%) 75 80	30, 45, 65, 70	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	803	ALA	2.5
1	A	732	LEU	2.1
2	D	822	PRO	2.1

### 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
2	SEP	C	828	10/11	0.95	0.11	37,51,65,67	0
2	SEP	D	828	10/11	0.95	0.10	37,51,63,69	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.



## 6.4 Ligands ⓘ

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
4	EDO	B	902	4/4	0.68	0.13	57,68,79,79	0
3	PEG	A	903	7/7	0.80	0.16	59,79,95,95	0
3	PEG	B	905	7/7	0.87	0.10	50,65,78,84	0
4	EDO	A	912	4/4	0.89	0.09	48,58,68,68	0
4	EDO	A	905	4/4	0.92	0.14	39,47,70,70	0
4	EDO	A	910	4/4	0.92	0.08	44,58,70,70	0
4	EDO	A	902	4/4	0.93	0.17	27,35,61,73	0
4	EDO	A	907	4/4	0.94	0.09	45,54,58,58	0
4	EDO	A	909	4/4	0.94	0.13	48,65,66,78	0
4	EDO	A	906	4/4	0.96	0.16	28,39,51,51	0
5	PO4	A	904	5/5	0.97	0.14	38,51,60,62	0
4	EDO	A	908	4/4	0.97	0.10	32,53,74,74	0
3	PEG	A	901	7/7	0.98	0.10	33,45,63,68	0
5	PO4	B	901	5/5	0.98	0.14	42,50,58,60	0
6	CL	A	911	1/1	0.98	0.13	49,49,49,49	0
3	PEG	B	904	7/7	0.98	0.07	46,56,59,60	17
4	EDO	B	903	4/4	0.99	0.10	30,53,70,70	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.