



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 8, 2020 – 10:44 AM BST

PDB ID : 6U3U  
Title : Crystal Structure of Shiga Toxin 2K  
Authors : Zhang, Y.Z.; He, X.H.  
Deposited on : 2019-08-22  
Resolution : 2.29 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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
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) : 2.13.1

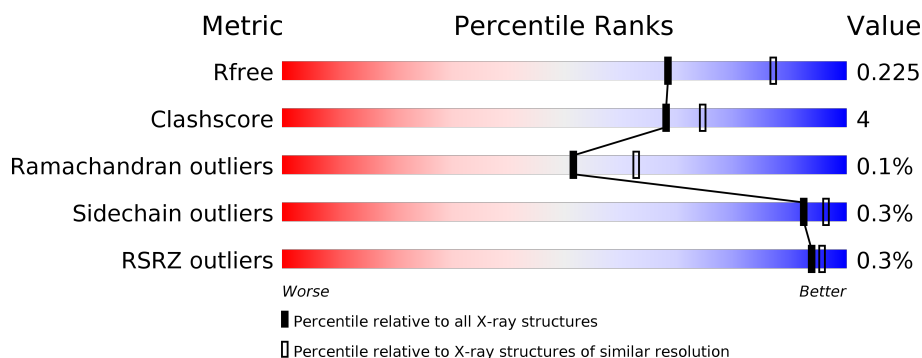
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


The reported resolution of this entry is 2.29 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	6980 (2.30-2.26)
Clashscore	141614	7711 (2.30-2.26)
Ramachandran outliers	138981	7597 (2.30-2.26)
Sidechain outliers	138945	7598 (2.30-2.26)
RSRZ outliers	127900	6849 (2.30-2.26)

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	297	 85% 10% 5%
1	B	297	 87% 8% 5%
2	C	70	 97% •
2	D	70	 94% 6%
2	E	70	 97% •
2	F	70	 94% 6%

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Mol	Chain	Length	Quality of chain
2	G	70	<div><div></div><div>84%16%</div></div>
2	H	70	<div><div></div><div>93%7%</div></div>
2	I	70	<div><div></div><div>89%11%</div></div>
2	J	70	<div><div></div><div>%94%6%</div></div>
2	K	70	<div><div></div><div>%99%. </div></div>
2	L	70	<div><div></div><div>91%9%</div></div>

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 19716 atoms, of which 9662 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 Shiga toxin 2K subunit A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	283	Total	C	H	N	O	S	0	1	0
			4412	1393	2190	391	431	7			
1	A	283	Total	C	H	N	O	S	0	0	0
			4404	1390	2186	393	428	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	167	GLN	GLU	engineered mutation	UNP L0I969
A	167	GLN	GLU	engineered mutation	UNP L0I969

- Molecule 2 is a protein called Shiga toxin 2K subunit B.

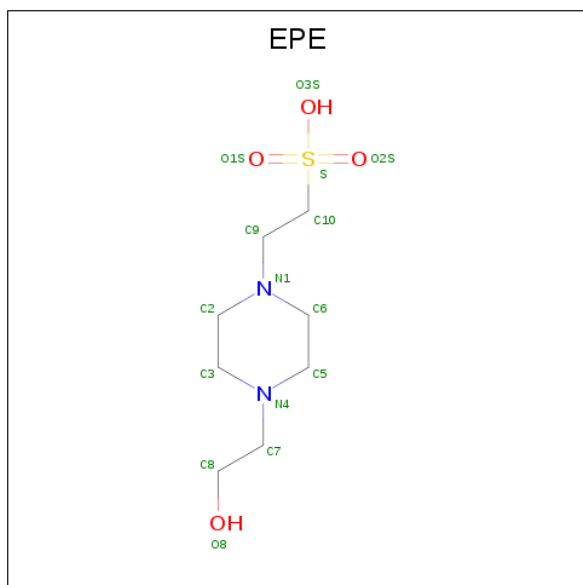
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	70	Total	C	H	N	O	S	0	0	0
			1065	340	521	91	110	3			
2	D	70	Total	C	H	N	O	S	0	0	0
			1065	340	521	91	110	3			
2	E	70	Total	C	H	N	O	S	0	0	0
			1065	340	521	91	110	3			
2	H	70	Total	C	H	N	O	S	0	0	0
			1065	340	521	91	110	3			
2	I	70	Total	C	H	N	O	S	0	0	0
			1065	340	521	91	110	3			
2	F	70	Total	C	H	N	O	S	0	0	0
			1065	340	521	91	110	3			
2	G	70	Total	C	H	N	O	S	0	0	0
			1065	340	521	91	110	3			
2	J	70	Total	C	H	N	O	S	0	0	0
			1065	340	521	91	110	3			
2	K	70	Total	C	H	N	O	S	0	0	0
			1065	340	521	91	110	3			

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	L	70	Total	C	H	N	O	S	0	0	0
			1064	340	521	91	109	3			

- Molecule 3 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
3	B	1	Total	C	H	N	O	S	0	0
			32	8	17	2	4	1		
3	A	1	Total	C	H	N	O	S	0	0
			32	8	17	2	4	1		

- Molecule 4 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
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	C	1	Total	C	H	O	0	0
			10	2	6	2		
4	D	1	Total	C	H	O	0	0
			10	2	6	2		
4	I	1	Total	C	H	O	0	0
			10	2	6	2		
4	J	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Zn	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	33	Total	O	0	0
			33	33		

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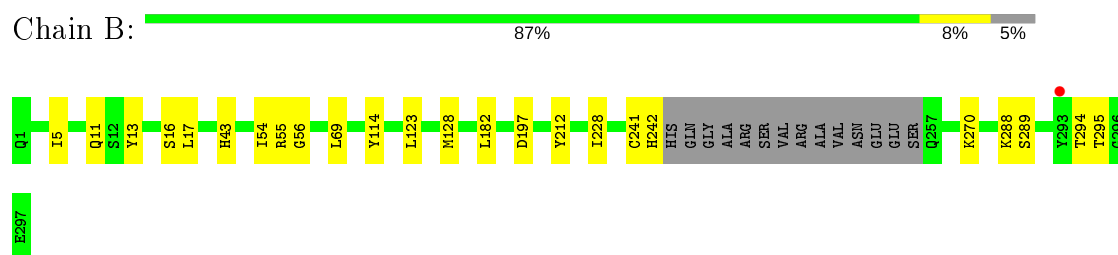
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	C	10	Total O 10 10	0	0
6	D	10	Total O 10 10	0	0
6	E	6	Total O 6 6	0	0
6	H	4	Total O 4 4	0	0
6	I	11	Total O 11 11	0	0
6	A	22	Total O 22 22	0	0
6	F	4	Total O 4 4	0	0
6	G	6	Total O 6 6	0	0
6	J	4	Total O 4 4	0	0
6	K	1	Total O 1 1	0	0
6	L	5	Total O 5 5	0	0

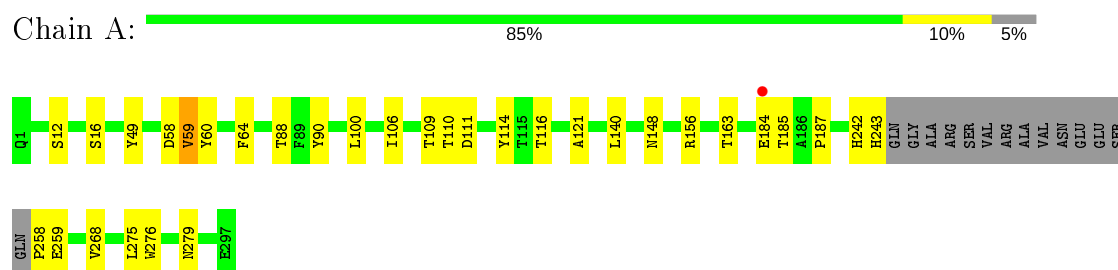
### 3 Residue-property plots [i](#)

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.

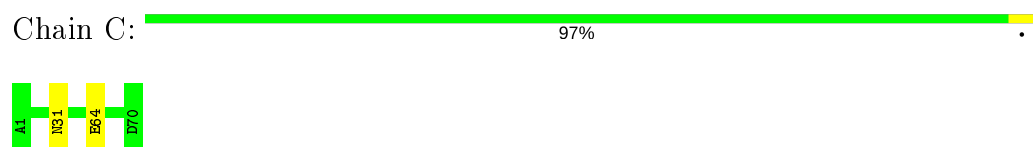
- Molecule 1: Shiga toxin 2K subunit A



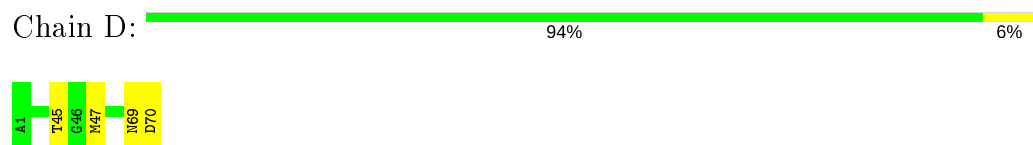
- Molecule 1: Shiga toxin 2K subunit A



- Molecule 2: Shiga toxin 2K subunit B

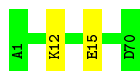


- Molecule 2: Shiga toxin 2K subunit B



- Molecule 2: Shiga toxin 2K subunit B





- Molecule 2: Shiga toxin 2K subunit B

Chain H: 93% 7%



- Molecule 2: Shiga toxin 2K subunit B

Chain I: 89% 11%



- Molecule 2: Shiga toxin 2K subunit B

Chain F: 94% 6%



- Molecule 2: Shiga toxin 2K subunit B

Chain G: 84% 16%



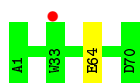
- Molecule 2: Shiga toxin 2K subunit B

Chain J: 94% 6%



- Molecule 2: Shiga toxin 2K subunit B

Chain K: 99% 1%



- Molecule 2: Shiga toxin 2K subunit B

Chain L: 91% 9%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.18Å 157.02Å 107.41Å 90.00° 94.61° 90.00°	Depositor
Resolution (Å)	52.08 – 2.29 107.06 – 2.29	Depositor EDS
% Data completeness (in resolution range)	98.8 (52.08-2.29) 98.8 (107.06-2.29)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.32 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, $R_{free}$	0.197 , 0.225 0.197 , 0.225	Depositor DCC
$R_{free}$ test set	1994 reflections (2.37%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	60.6	Xtriage
Anisotropy	0.127	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 45.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	19716	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% 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: ZN, EPE, 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	0.28	0/2260	0.49	0/3073
1	B	0.28	0/2266	0.47	0/3081
2	C	0.28	0/554	0.46	0/747
2	D	0.27	0/554	0.45	0/747
2	E	0.28	0/554	0.45	0/747
2	F	0.29	0/554	0.46	0/747
2	G	0.35	0/554	0.50	0/747
2	H	0.28	0/554	0.45	0/747
2	I	0.28	0/554	0.50	0/747
2	J	0.29	0/554	0.46	0/747
2	K	0.29	0/554	0.48	0/747
2	L	0.28	0/553	0.46	0/747
All	All	0.29	0/10065	0.47	0/13624

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	2218	2186	2186	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2222	2190	2190	16	0
2	C	544	521	521	2	0
2	D	544	521	521	3	0
2	E	544	521	521	2	0
2	F	544	521	521	3	0
2	G	544	521	521	7	0
2	H	544	521	521	3	0
2	I	544	521	521	7	0
2	J	544	521	521	4	0
2	K	544	521	521	1	0
2	L	543	521	521	5	0
3	A	15	17	17	1	0
3	B	15	17	17	1	0
4	B	12	18	18	3	0
4	C	4	6	6	0	0
4	D	4	6	6	0	0
4	I	4	6	6	0	0
4	J	4	6	6	0	0
5	A	1	0	0	0	0
6	A	22	0	0	2	0
6	B	33	0	0	3	0
6	C	10	0	0	0	0
6	D	10	0	0	0	0
6	E	6	0	0	1	0
6	F	4	0	0	1	0
6	G	6	0	0	2	0
6	H	4	0	0	1	0
6	I	11	0	0	3	0
6	J	4	0	0	1	0
6	K	1	0	0	0	0
6	L	5	0	0	0	0
All	All	10054	9662	9662	75	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 4.

The worst 5 of 75 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)
2:G:2:ASP:OD2	6:G:101:HOH:O	1.85	0.92
2:G:55:THR:OG1	2:G:60:SER:OG	1.78	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:THR:HG23	1:A:116:THR:HG21	1.60	0.83
2:G:68:ASN:OD1	6:G:102:HOH:O	2.02	0.77
1:A:184:GLU:OE2	1:A:184:GLU:N	2.21	0.74

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	279/297 (94%)	269 (96%)	9 (3%)	1 (0%)	34	40
1	B	280/297 (94%)	272 (97%)	8 (3%)	0	100	100
2	C	68/70 (97%)	67 (98%)	1 (2%)	0	100	100
2	D	68/70 (97%)	66 (97%)	2 (3%)	0	100	100
2	E	68/70 (97%)	67 (98%)	1 (2%)	0	100	100
2	F	68/70 (97%)	64 (94%)	4 (6%)	0	100	100
2	G	68/70 (97%)	66 (97%)	2 (3%)	0	100	100
2	H	68/70 (97%)	65 (96%)	3 (4%)	0	100	100
2	I	68/70 (97%)	67 (98%)	1 (2%)	0	100	100
2	J	68/70 (97%)	67 (98%)	1 (2%)	0	100	100
2	K	68/70 (97%)	66 (97%)	2 (3%)	0	100	100
2	L	68/70 (97%)	67 (98%)	1 (2%)	0	100	100
All	All	1239/1294 (96%)	1203 (97%)	35 (3%)	1 (0%)	51	63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	59	VAL

### 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	248/259 (96%)	248 (100%)	0	100	100
1	B	249/259 (96%)	246 (99%)	3 (1%)	71	82
2	C	59/59 (100%)	59 (100%)	0	100	100
2	D	59/59 (100%)	59 (100%)	0	100	100
2	E	59/59 (100%)	59 (100%)	0	100	100
2	F	59/59 (100%)	59 (100%)	0	100	100
2	G	59/59 (100%)	59 (100%)	0	100	100
2	H	59/59 (100%)	59 (100%)	0	100	100
2	I	59/59 (100%)	59 (100%)	0	100	100
2	J	59/59 (100%)	59 (100%)	0	100	100
2	K	59/59 (100%)	59 (100%)	0	100	100
2	L	59/59 (100%)	59 (100%)	0	100	100
All	All	1087/1108 (98%)	1084 (100%)	3 (0%)	92	96

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

Mol	Chain	Res	Type
1	B	43	HIS
1	B	197	ASP
1	B	289	SER

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

Mol	Chain	Res	Type
1	A	226	ASN

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 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	D	101	-	3,3,3	0.47	0	2,2,2	0.32	0
3	EPE	B	301	-	15,15,15	0.79	1 (6%)	18,20,20	1.63	5 (27%)
4	EDO	J	101	-	3,3,3	0.47	0	2,2,2	0.25	0
4	EDO	C	101	-	3,3,3	0.47	0	2,2,2	0.30	0
4	EDO	B	304	-	3,3,3	0.47	0	2,2,2	0.28	0
4	EDO	B	303	-	3,3,3	0.46	0	2,2,2	0.39	0
4	EDO	B	302	-	3,3,3	0.47	0	2,2,2	0.22	0
4	EDO	I	101	-	3,3,3	0.47	0	2,2,2	0.32	0
3	EPE	A	302	-	15,15,15	0.76	1 (6%)	18,20,20	1.90	6 (33%)

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	D	101	-	-	0/1/1/1	-
3	EPE	B	301	-	-	4/9/19/19	0/1/1/1
4	EDO	J	101	-	-	1/1/1/1	-
4	EDO	C	101	-	-	0/1/1/1	-
4	EDO	B	304	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	B	303	-	-	1/1/1/1	-
4	EDO	B	302	-	-	1/1/1/1	-
4	EDO	I	101	-	-	1/1/1/1	-
3	EPE	A	302	-	-	5/9/19/19	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	301	EPE	C10-S	2.59	1.81	1.77
3	A	302	EPE	C10-S	2.46	1.81	1.77

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	302	EPE	C5-N4-C3	4.67	119.33	108.83
3	B	301	EPE	C5-N4-C3	3.27	116.20	108.83
3	A	302	EPE	O2S-S-C10	3.20	110.77	106.92
3	A	302	EPE	C7-N4-C3	3.03	119.00	111.23
3	A	302	EPE	C7-N4-C5	2.91	118.68	111.23

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	302	EPE	C10-C9-N1-C2
4	I	101	EDO	O1-C1-C2-O2
3	B	301	EPE	C9-C10-S-O3S
3	A	302	EPE	N4-C7-C8-O8
3	B	301	EPE	N4-C7-C8-O8

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	301	EPE	1	0
4	B	302	EDO	3	0
3	A	302	EPE	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 ⓘ

### 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, 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	283/297 (95%)	0.35	1 (0%) 92 94	48, 71, 91, 113	0
1	B	283/297 (95%)	0.33	1 (0%) 92 94	45, 66, 85, 116	0
2	C	70/70 (100%)	0.28	0 100 100	46, 62, 83, 90	0
2	D	70/70 (100%)	0.23	0 100 100	46, 65, 83, 94	0
2	E	70/70 (100%)	0.45	0 100 100	48, 67, 80, 88	0
2	F	70/70 (100%)	0.25	0 100 100	50, 71, 93, 99	0
2	G	70/70 (100%)	0.21	0 100 100	53, 69, 88, 91	0
2	H	70/70 (100%)	0.40	0 100 100	52, 74, 92, 101	0
2	I	70/70 (100%)	0.27	0 100 100	47, 61, 76, 82	0
2	J	70/70 (100%)	0.18	1 (1%) 75 79	51, 68, 89, 98	0
2	K	70/70 (100%)	0.32	1 (1%) 75 79	57, 78, 98, 105	0
2	L	70/70 (100%)	0.32	0 100 100	51, 68, 84, 90	0
All	All	1266/1294 (97%)	0.31	4 (0%) 94 95	45, 68, 89, 116	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	293	TYR	3.6
1	A	184	GLU	3.2
2	K	33	TRP	2.7
2	J	1	ALA	2.3

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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, 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
4	EDO	C	101	4/4	0.76	0.19	69,86,99,119	0
3	EPE	A	302	15/15	0.84	0.17	87,105,117,118	0
3	EPE	B	301	15/15	0.85	0.17	78,100,112,117	0
4	EDO	B	302	4/4	0.86	0.15	49,61,74,83	0
4	EDO	B	303	4/4	0.87	0.25	72,86,100,111	0
4	EDO	J	101	4/4	0.88	0.16	71,91,109,121	0
4	EDO	B	304	4/4	0.91	0.22	71,86,90,104	0
4	EDO	I	101	4/4	0.93	0.14	59,81,98,98	0
4	EDO	D	101	4/4	0.93	0.08	72,96,115,127	0
5	ZN	A	301	1/1	0.98	0.19	88,88,88,88	0

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

There are no such residues in this entry.