



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 7, 2020 – 04:38 AM BST

PDB ID : 5KDS
Title : ZmpB metallopeptidase in complex with an O-glycopeptide (a2,6-sialylated core-3 pentapeptide).
Authors : Noach, I.; Ficko-Blean, E.; Stuart, C.; Boraston, A.B.
Deposited on : 2016-06-08
Resolution : 1.60 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

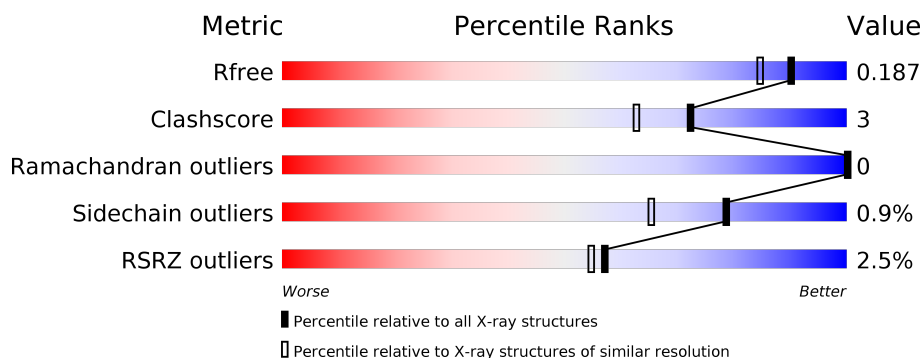
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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 ≥ 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	G	5	<div> <div>60%</div> <div> <div>40%</div> <div>60%</div> </div> </div>
2	A	530	<div> <div>2%</div> <div> <div>91%</div> <div>5%</div> <div>• •</div> </div> </div>
3	B	3	<div> <div>33%</div> <div>67%</div> </div>

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 5044 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 alpha2,6-sialylated core-3 pentapeptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	G	5	Total	C	N	O	0	0	0
			27	16	5	6			

- Molecule 2 is a protein called F5/8 type C domain protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	511	Total	C	N	O	S	0	7	0
			4127	2618	691	807	11			

There are 23 discrepancies between the modelled and reference sequences:

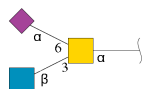
Chain	Residue	Modelled	Actual	Comment	Reference
A	474	MET	-	initiating methionine	UNP A0A0H2YN38
A	475	GLY	-	expression tag	UNP A0A0H2YN38
A	476	SER	-	expression tag	UNP A0A0H2YN38
A	477	SER	-	expression tag	UNP A0A0H2YN38
A	478	HIS	-	expression tag	UNP A0A0H2YN38
A	479	HIS	-	expression tag	UNP A0A0H2YN38
A	480	HIS	-	expression tag	UNP A0A0H2YN38
A	481	HIS	-	expression tag	UNP A0A0H2YN38
A	482	HIS	-	expression tag	UNP A0A0H2YN38
A	483	HIS	-	expression tag	UNP A0A0H2YN38
A	484	SER	-	expression tag	UNP A0A0H2YN38
A	485	SER	-	expression tag	UNP A0A0H2YN38
A	486	GLY	-	expression tag	UNP A0A0H2YN38
A	487	LEU	-	expression tag	UNP A0A0H2YN38
A	488	VAL	-	expression tag	UNP A0A0H2YN38
A	489	PRO	-	expression tag	UNP A0A0H2YN38
A	490	ARG	-	expression tag	UNP A0A0H2YN38
A	491	GLY	-	expression tag	UNP A0A0H2YN38
A	492	SER	-	expression tag	UNP A0A0H2YN38
A	493	HIS	-	expression tag	UNP A0A0H2YN38

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Chain	Residue	Modelled	Actual	Comment	Reference
A	494	MET	-	expression tag	UNP A0A0H2YN38
A	495	ALA	-	expression tag	UNP A0A0H2YN38
A	496	SER	-	expression tag	UNP A0A0H2YN38

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-[N-acetyl-alpha-neuraminic acid-(2-6)]2-acetamido-2-deoxy-alpha-D-galactopyranose.

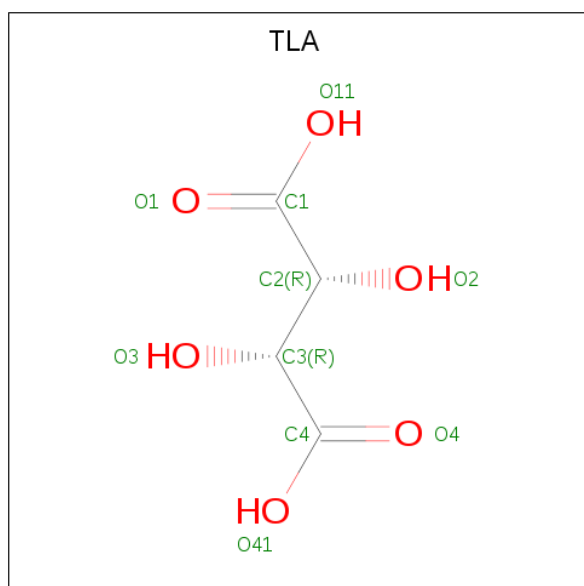


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	B	3	Total	C	N	O	0	0	0
			48	27	3	18			

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

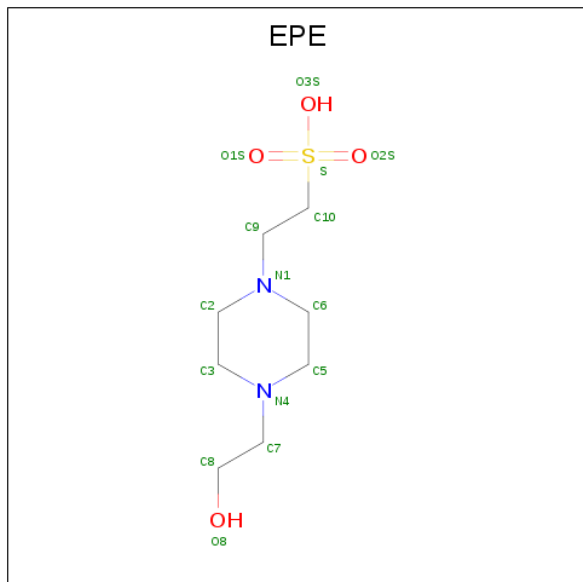
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		

- Molecule 5 is L(+)-TARTARIC ACID (three-letter code: TLA) (formula: C₄H₆O₆).



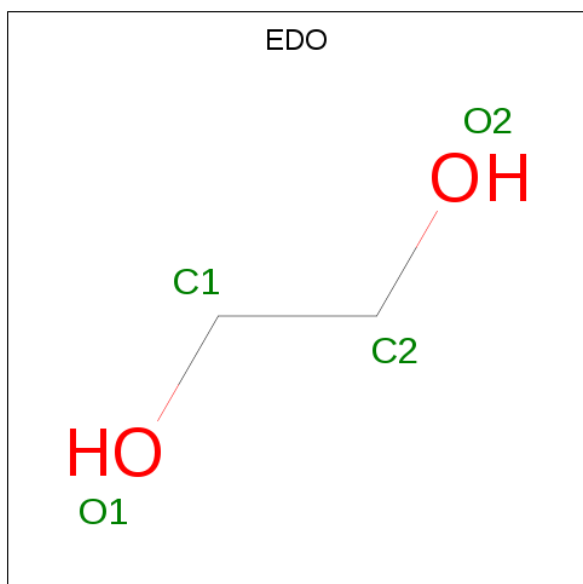
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			10	4	6		

- Molecule 6 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).



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

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

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

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	G	8	Total	O	0	0
			8	8		
8	A	786	Total	O	0	2
			788	788		

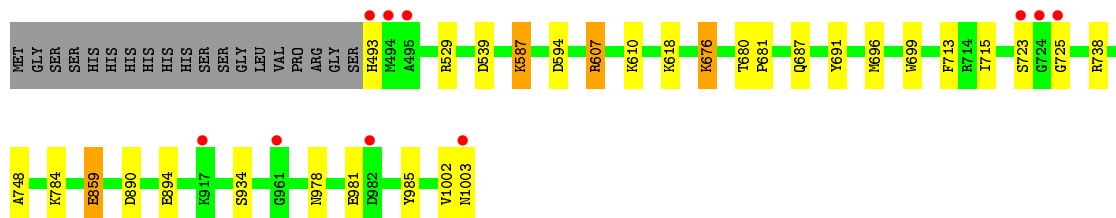
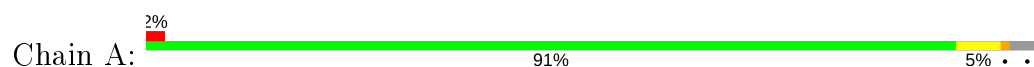
3 Residue-property plots [i](#)

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: alpha2,6-sialylated core-3 pentapeptide



- Molecule 2: F5/8 type C domain protein



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-[N-acetyl-alpha-neuraminic acid-(2-6)]2-acetamido-2-deoxy-alpha-D-galactopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	66.18Å 68.95Å 171.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 1.60 36.65 – 1.60	Depositor EDS
% Data completeness (in resolution range)	95.9 (40.00-1.60) 95.9 (36.65-1.60)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.83 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.158 , 0.185 0.159 , 0.187	Depositor DCC
R_{free} test set	4992 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	18.3	Xtriage
Anisotropy	0.136	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 47.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.015 for k,h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5044	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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, NAG, EDO, SIA, A2G, EPE, TLA

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	G	0.72	0/27	0.59	0/36
2	A	0.76	0/4241	0.86	5/5736 (0.1%)
All	All	0.76	0/4268	0.86	5/5772 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	A	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	529	ARG	NE-CZ-NH2	-7.47	116.57	120.30
2	A	607	ARG	NE-CZ-NH2	-6.43	117.08	120.30
2	A	594	ASP	CB-CG-OD1	6.40	124.06	118.30
2	A	696	MET	CA-CB-CG	-5.85	103.36	113.30
2	A	676	LYS	CD-CE-NZ	5.74	124.91	111.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	934	SER	Peptide

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	G	27	0	23	6	0
2	A	4127	0	4006	20	0
3	B	48	0	40	5	0
4	A	1	0	0	0	0
5	A	10	0	3	2	0
6	A	15	0	18	1	0
7	A	20	0	30	0	0
8	A	788	0	0	3	0
8	G	8	0	0	4	0
All	All	5044	0	4120	28	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 3.

The worst 5 of 28 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)
8:G:202:HOH:O	3:B:2:NAG:H61	1.83	0.78
2:A:784:LYS:HE3	8:A:1799:HOH:O	1.85	0.76
2:A:493:HIS:CE1	2:A:618:LYS:HD2	2.24	0.72
1:G:4:THR:N	5:A:1102:TLA:HB	2.00	0.59
2:A:859:GLU:H	2:A:859:GLU:CD	2.05	0.58

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	G	3/5 (60%)	3 (100%)	0	0	100	100
2	A	516/530 (97%)	506 (98%)	10 (2%)	0	100	100
All	All	519/535 (97%)	509 (98%)	10 (2%)	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	G	2/2 (100%)	2 (100%)	0	100	100
2	A	449/458 (98%)	445 (99%)	4 (1%)	78	65
All	All	451/460 (98%)	447 (99%)	4 (1%)	78	65

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	587	LYS
2	A	691	TYR
2	A	699	TRP
2	A	859	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	493	HIS
2	A	812	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 ⓘ

3 monosaccharides 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	A2G	B	1	1,3	14,14,15	1.19	2 (14%)	17,19,21	1.61	3 (17%)
3	NAG	B	2	3	14,14,15	0.50	0	17,19,21	1.31	3 (17%)
3	SIA	B	3	3	17,20,21	0.67	0	21,28,31	1.09	1 (4%)

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	A2G	B	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	B	2	3	-	2/6/23/26	0/1/1/1
3	SIA	B	3	3	-	0/14/34/38	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1	A2G	C1-C2	2.58	1.56	1.52
3	B	1	A2G	O5-C1	-2.32	1.40	1.43

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1	A2G	O5-C5-C6	-4.93	99.47	107.20
3	B	1	A2G	C2-N2-C7	-2.75	118.99	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	2	NAG	C6-C5-C4	-2.45	107.27	113.00
3	B	2	NAG	O5-C1-C2	-2.39	107.52	111.29
3	B	2	NAG	C3-C4-C5	2.30	114.33	110.24

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	2	NAG	C4-C5-C6-O6
3	B	2	NAG	O5-C5-C6-O6
3	B	1	A2G	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	3	SIA	2	0
3	B	2	NAG	3	0

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 1 is monoatomic - leaving 7 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	$\# Z > 2$
6	EPE	A	1103	-	15,15,15	1.84	2 (13%)	18,20,20	1.61	5 (27%)
7	EDO	A	1106	-	3,3,3	0.47	0	2,2,2	0.36	0
7	EDO	A	1107	-	3,3,3	0.44	0	2,2,2	0.76	0
7	EDO	A	1104	-	3,3,3	0.54	0	2,2,2	0.70	0
5	TLA	A	1102	4	3,9,9	1.09	0	6,12,12	1.13	0
7	EDO	A	1108	-	3,3,3	0.47	0	2,2,2	0.79	0
7	EDO	A	1105	-	3,3,3	0.46	0	2,2,2	0.50	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
6	EPE	A	1103	-	-	4/9/19/19	0/1/1/1
7	EDO	A	1106	-	-	0/1/1/1	-
7	EDO	A	1107	-	-	1/1/1/1	-
7	EDO	A	1104	-	-	0/1/1/1	-
5	TLA	A	1102	4	-	0/4/12/12	-
7	EDO	A	1108	-	-	1/1/1/1	-
7	EDO	A	1105	-	-	0/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1103	EPE	C10-S	-5.99	1.69	1.77
6	A	1103	EPE	O2S-S	2.35	1.52	1.45

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1103	EPE	C6-N1-C2	3.26	116.17	108.83
6	A	1103	EPE	C5-C6-N1	2.87	116.54	110.64
6	A	1103	EPE	O1S-S-C10	2.66	110.12	106.92
6	A	1103	EPE	C3-C2-N1	2.51	115.80	110.64
6	A	1103	EPE	O2S-S-O1S	-2.04	106.89	113.95

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	1103	EPE	C10-C9-N1-C6
6	A	1103	EPE	C8-C7-N4-C5
6	A	1103	EPE	S-C10-C9-N1
7	A	1107	EDO	O1-C1-C2-O2
6	A	1103	EPE	C10-C9-N1-C2

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1103	EPE	1	0
5	A	1102	TLA	2	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, 95th 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 ²)	Q<0.9
1	G	5/5 (100%)	3.88	3 (60%) 0 0	23, 34, 75, 79	0
2	A	511/530 (96%)	-0.35	10 (1%) 65 64	12, 18, 36, 65	0
All	All	516/535 (96%)	-0.31	13 (2%) 57 55	12, 18, 37, 79	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	8	GLY	8.7
2	A	725	GLY	6.6
2	A	724	GLY	6.0
2	A	1003	ASN	5.5
1	G	7	GLY	5.4

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](#)

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, 95th 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 ²)	Q<0.9
3	NAG	B	2	14/15	0.78	0.23	28,41,49,55	0
3	SIA	B	3	20/21	0.92	0.13	19,26,37,37	0
3	A2G	B	1	14/15	0.96	0.07	18,20,22,24	0

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, 95th 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(\AA^2)	Q<0.9
7	EDO	A	1108	4/4	0.84	0.16	37,37,37,43	0
5	TLA	A	1102	10/10	0.90	0.19	26,32,36,37	0
7	EDO	A	1107	4/4	0.90	0.14	34,36,38,43	0
6	EPE	A	1103	15/15	0.93	0.30	25,65,86,86	0
7	EDO	A	1106	4/4	0.94	0.30	35,37,37,40	0
7	EDO	A	1104	4/4	0.95	0.08	22,29,30,38	0
7	EDO	A	1105	4/4	0.98	0.12	24,29,31,32	0
4	ZN	A	1101	1/1	1.00	0.09	25,25,25,25	0

6.5 Other polymers [i](#)

There are no such residues in this entry.