



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 24, 2024 – 08:06 AM EDT

PDB ID : 6OZD
Title : Crystal structure of Putative exported protein (BPSS2145) from Burkholderia pseudomallei K96243
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2019-05-15
Resolution : 1.55 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

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>.

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	:	2.37.1
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)	:	2.37.1

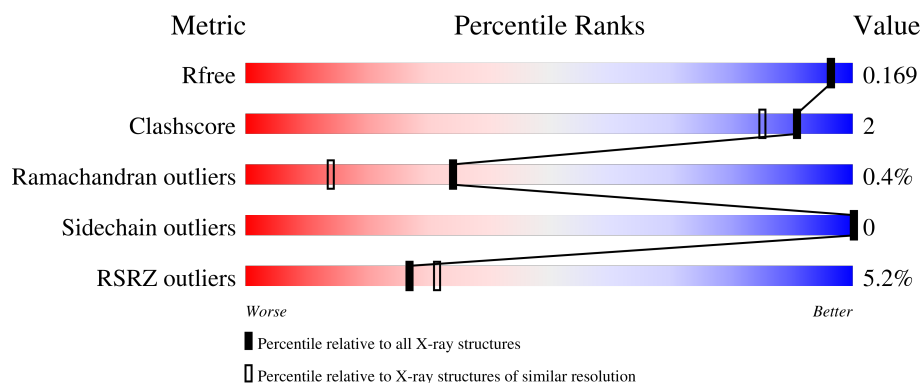
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.55 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	1483 (1.56-1.56)
Clashscore	141614	1529 (1.56-1.56)
Ramachandran outliers	138981	1498 (1.56-1.56)
Sidechain outliers	138945	1495 (1.56-1.56)
RSRZ outliers	127900	1465 (1.56-1.56)

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 ≥ 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	538	<div> <div>8%</div> <div>94%</div> <div>.</div> <div>.</div> </div>
1	B	538	<div> <div>2%</div> <div>93%</div> <div>.</div> <div>.</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9159 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 Putative exported protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	520	Total	C	N	O	S	0	12	0
			3712	2317	673	713	9			
1	B	523	Total	C	N	O	S	0	12	0
			3744	2337	679	719	9			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	26	MET	-	initiating methionine	UNP Q63IC6
A	27	ALA	-	expression tag	UNP Q63IC6
A	28	HIS	-	expression tag	UNP Q63IC6
A	29	HIS	-	expression tag	UNP Q63IC6
A	30	HIS	-	expression tag	UNP Q63IC6
A	31	HIS	-	expression tag	UNP Q63IC6
A	32	HIS	-	expression tag	UNP Q63IC6
A	33	HIS	-	expression tag	UNP Q63IC6
B	26	MET	-	initiating methionine	UNP Q63IC6
B	27	ALA	-	expression tag	UNP Q63IC6
B	28	HIS	-	expression tag	UNP Q63IC6
B	29	HIS	-	expression tag	UNP Q63IC6
B	30	HIS	-	expression tag	UNP Q63IC6
B	31	HIS	-	expression tag	UNP Q63IC6
B	32	HIS	-	expression tag	UNP Q63IC6
B	33	HIS	-	expression tag	UNP Q63IC6

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	1
			8	4	4		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	1
			8	4	4		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 4	C 2	O 2	0	0
2	A	1	Total 4	C 2	O 2	0	0
2	A	1	Total 4	C 2	O 2	0	0
2	A	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 8	C 4	O 4	0	1
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0

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

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Cl 1 1	0	0

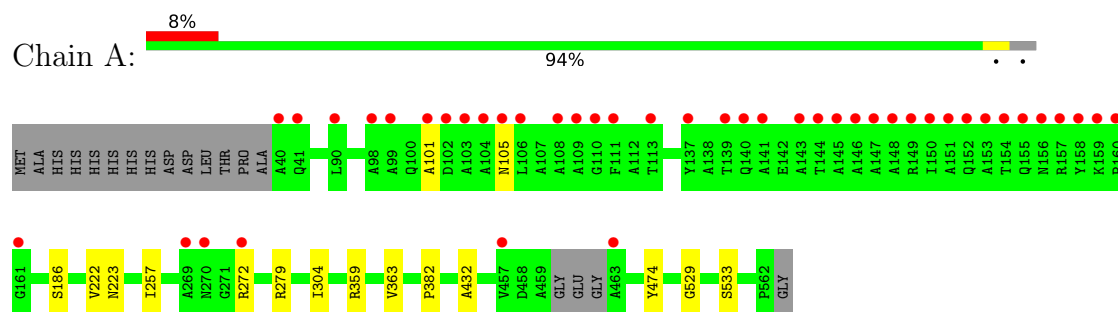
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	711	Total O 729 729	0	19
4	B	779	Total O 797 797	0	18

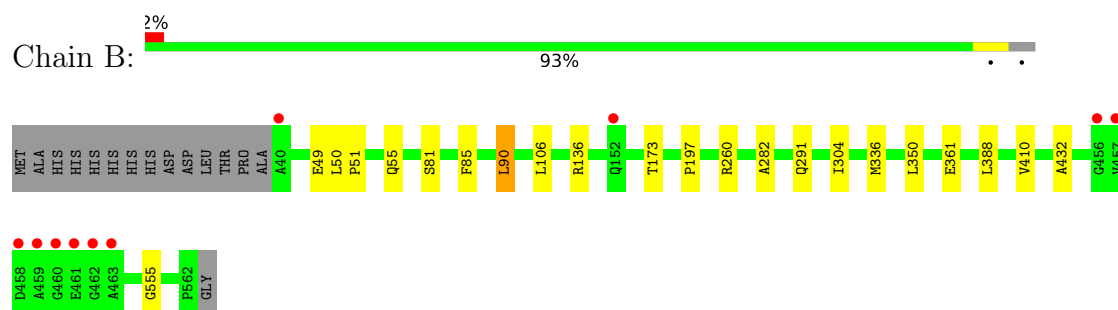
3 Residue-property plots [i](#)

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: Putative exported protein



- Molecule 1: Putative exported protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.95Å 96.36Å 95.93Å 90.00° 91.36° 90.00°	Depositor
Resolution (Å)	47.95 – 1.55 47.95 – 1.55	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.95-1.55) 99.8 (47.95-1.55)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.47 (at 1.55Å)	Xtriage
Refinement program	PHENIX dev_3500	Depositor
R, R_{free}	0.147 , 0.169 0.147 , 0.169	Depositor DCC
R_{free} test set	1944 reflections (1.12%)	wwPDB-VP
Wilson B-factor (Å ²)	14.8	Xtriage
Anisotropy	0.726	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 56.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.010 for -h,-l,-k 0.000 for -h,l,k 0.018 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	9159	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.78% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, CL

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	0.37	0/3816	0.61	0/5227
1	B	0.37	0/3849	0.64	1/5270 (0.0%)
All	All	0.37	0/7665	0.62	1/10497 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	90	LEU	CA-CB-CG	-6.32	100.75	115.30

There are no chirality outliers.

There are no planarity outliers.

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	A	3712	0	3697	11	0
1	B	3744	0	3738	14	0
2	A	80	0	120	3	0
2	B	96	0	144	5	0
3	B	1	0	0	0	0
4	A	729	0	0	3	2
4	B	797	0	0	3	2
All	All	9159	0	7699	26	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 2.

All (26) 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:359[B]:ARG:NH1	4:A:983[B]:HOH:O	2.35	0.59
1:B:336[B]:MET:HE1	1:B:410:VAL:HG11	1.88	0.56
1:B:49:GLU:OE2	1:B:55:GLN:NE2	2.41	0.54
1:A:257[B]:ILE:HD12	4:A:739:HOH:O	2.08	0.53
1:A:101:ALA:O	1:A:105:ASN:HB2	2.08	0.53
1:A:474:TYR:HE2	2:A:604[B]:EDO:H11	1.75	0.52
1:B:85:PHE:CE1	1:B:136:ARG:HG2	2.45	0.51
1:B:260:ARG:HD2	4:B:862[B]:HOH:O	2.11	0.50
1:A:279:ARG:NH1	4:A:712:HOH:O	2.47	0.48
1:B:90:LEU:HD22	1:B:106:LEU:HD11	1.95	0.48
1:B:291:GLN:NE2	4:B:702:HOH:O	2.30	0.46
1:A:222[B]:VAL:HG13	1:A:223:ASN:O	2.16	0.46
1:B:81:SER:HB2	1:B:173:THR:OG1	2.17	0.45
1:B:49:GLU:OE1	2:B:614:EDO:H12	2.16	0.45
1:A:474:TYR:CE2	2:A:604[A]:EDO:H12	2.52	0.45
1:A:363:VAL:HG13	1:A:382:PRO:HD3	1.99	0.45
1:B:361:GLU:HA	1:B:388:LEU:O	2.18	0.44
2:B:618:EDO:H11	4:B:1314:HOH:O	2.19	0.43
1:B:50:LEU:HD12	1:B:51:PRO:HD2	2.00	0.43
1:B:51:PRO:HA	2:B:614:EDO:H22	2.02	0.41
1:A:186:SER:HA	1:A:272:ARG:CD	2.50	0.41
1:B:197:PRO:HD3	1:B:555:GLY:O	2.21	0.41
1:B:282:ALA:HB3	2:B:606:EDO:H11	2.02	0.41
1:B:350:LEU:HG	2:B:602:EDO:H11	2.03	0.41
1:A:474:TYR:HE2	2:A:604[A]:EDO:H12	1.86	0.41
1:A:529:GLY:HA2	1:A:533:SER:OG	2.21	0.40

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)
4:A:743:HOH:O	4:B:968:HOH:O[2_554]	2.00	0.20
4:A:1110:HOH:O	4:B:1347:HOH:O[2_554]	2.17	0.03

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	A	528/538 (98%)	509 (96%)	17 (3%)	2 (0%)	34	14
1	B	533/538 (99%)	517 (97%)	14 (3%)	2 (0%)	34	14
All	All	1061/1076 (99%)	1026 (97%)	31 (3%)	4 (0%)	34	14

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	432	ALA
1	B	432	ALA
1	A	304	ILE
1	B	304	ILE

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	359/367 (98%)	359 (100%)	0	100	100
1	B	362/367 (99%)	362 (100%)	0	100	100
All	All	721/734 (98%)	721 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes 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 ⓘ

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 45 ligands modelled in this entry, 1 is monoatomic - leaving 44 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	$\# Z > 2$
2	EDO	A	609	-	3,3,3	0.44	0	2,2,2	0.57	0
2	EDO	B	618	-	3,3,3	0.48	0	2,2,2	0.42	0
2	EDO	A	606	-	3,3,3	0.37	0	2,2,2	0.59	0
2	EDO	A	613	-	3,3,3	0.44	0	2,2,2	0.42	0
2	EDO	B	603	-	3,3,3	0.46	0	2,2,2	0.34	0
2	EDO	B	622	-	3,3,3	0.45	0	2,2,2	0.38	0
2	EDO	B	608	-	3,3,3	0.43	0	2,2,2	0.42	0
2	EDO	B	602	-	3,3,3	0.44	0	2,2,2	0.47	0
2	EDO	A	603	-	3,3,3	0.37	0	2,2,2	0.67	0
2	EDO	B	604[A]	-	3,3,3	0.49	0	2,2,2	0.32	0
2	EDO	B	611	-	3,3,3	0.45	0	2,2,2	0.27	0
2	EDO	B	623	-	3,3,3	0.46	0	2,2,2	0.35	0
2	EDO	A	608	-	3,3,3	0.60	0	2,2,2	0.39	0
2	EDO	A	618	-	3,3,3	0.45	0	2,2,2	0.38	0
2	EDO	A	610	-	3,3,3	0.44	0	2,2,2	0.61	0
2	EDO	B	605	-	3,3,3	0.48	0	2,2,2	0.28	0
2	EDO	B	617	-	3,3,3	0.47	0	2,2,2	0.32	0
2	EDO	B	615	-	3,3,3	0.42	0	2,2,2	0.45	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	EDO	A	614	-	3,3,3	0.54	0	2,2,2	0.16	0
2	EDO	B	612	-	3,3,3	0.49	0	2,2,2	0.30	0
2	EDO	B	616	-	3,3,3	0.48	0	2,2,2	0.29	0
2	EDO	A	615	-	3,3,3	0.53	0	2,2,2	0.16	0
2	EDO	A	617	-	3,3,3	0.47	0	2,2,2	0.41	0
2	EDO	B	620	-	3,3,3	0.48	0	2,2,2	0.37	0
2	EDO	A	602	-	3,3,3	0.41	0	2,2,2	0.51	0
2	EDO	A	616	-	3,3,3	0.43	0	2,2,2	0.42	0
2	EDO	B	606	-	3,3,3	0.42	0	2,2,2	0.54	0
2	EDO	B	610	-	3,3,3	0.45	0	2,2,2	0.45	0
2	EDO	A	607[B]	-	3,3,3	0.42	0	2,2,2	0.38	0
2	EDO	A	612	-	3,3,3	0.46	0	2,2,2	0.27	0
2	EDO	B	619	-	3,3,3	0.43	0	2,2,2	0.47	0
2	EDO	B	614	-	3,3,3	0.44	0	2,2,2	0.39	0
2	EDO	B	601	-	3,3,3	0.50	0	2,2,2	0.12	0
2	EDO	B	621	-	3,3,3	0.44	0	2,2,2	0.51	0
2	EDO	A	604[B]	-	3,3,3	0.45	0	2,2,2	0.41	0
2	EDO	A	601	-	3,3,3	0.62	0	2,2,2	0.46	0
2	EDO	A	607[A]	-	3,3,3	0.42	0	2,2,2	0.52	0
2	EDO	A	611	-	3,3,3	0.42	0	2,2,2	0.36	0
2	EDO	B	613	-	3,3,3	0.60	0	2,2,2	0.05	0
2	EDO	B	607	-	3,3,3	0.56	0	2,2,2	0.43	0
2	EDO	A	605	-	3,3,3	0.47	0	2,2,2	0.33	0
2	EDO	B	609	-	3,3,3	0.46	0	2,2,2	0.68	0
2	EDO	B	604[B]	-	3,3,3	0.46	0	2,2,2	0.26	0
2	EDO	A	604[A]	-	3,3,3	0.46	0	2,2,2	0.31	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
2	EDO	A	609	-	-	0/1/1/1	-
2	EDO	B	618	-	-	1/1/1/1	-
2	EDO	A	606	-	-	1/1/1/1	-
2	EDO	A	613	-	-	1/1/1/1	-
2	EDO	B	603	-	-	1/1/1/1	-
2	EDO	B	622	-	-	0/1/1/1	-
2	EDO	B	608	-	-	1/1/1/1	-
2	EDO	B	602	-	-	0/1/1/1	-
2	EDO	A	603	-	-	0/1/1/1	-
2	EDO	B	604[A]	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	B	611	-	-	0/1/1/1	-
2	EDO	B	623	-	-	1/1/1/1	-
2	EDO	A	608	-	-	0/1/1/1	-
2	EDO	A	618	-	-	1/1/1/1	-
2	EDO	A	610	-	-	1/1/1/1	-
2	EDO	B	605	-	-	0/1/1/1	-
2	EDO	B	617	-	-	1/1/1/1	-
2	EDO	B	615	-	-	1/1/1/1	-
2	EDO	A	614	-	-	0/1/1/1	-
2	EDO	B	612	-	-	0/1/1/1	-
2	EDO	B	616	-	-	1/1/1/1	-
2	EDO	A	615	-	-	1/1/1/1	-
2	EDO	A	617	-	-	0/1/1/1	-
2	EDO	B	620	-	-	0/1/1/1	-
2	EDO	A	602	-	-	1/1/1/1	-
2	EDO	A	616	-	-	1/1/1/1	-
2	EDO	B	606	-	-	0/1/1/1	-
2	EDO	B	610	-	-	0/1/1/1	-
2	EDO	A	607[B]	-	-	1/1/1/1	-
2	EDO	A	612	-	-	0/1/1/1	-
2	EDO	B	619	-	-	0/1/1/1	-
2	EDO	B	614	-	-	0/1/1/1	-
2	EDO	B	601	-	-	0/1/1/1	-
2	EDO	B	621	-	-	1/1/1/1	-
2	EDO	A	604[B]	-	-	0/1/1/1	-
2	EDO	A	601	-	-	0/1/1/1	-
2	EDO	A	607[A]	-	-	0/1/1/1	-
2	EDO	A	611	-	-	0/1/1/1	-
2	EDO	B	613	-	-	0/1/1/1	-
2	EDO	B	607	-	-	0/1/1/1	-
2	EDO	A	605	-	-	0/1/1/1	-
2	EDO	B	609	-	-	1/1/1/1	-
2	EDO	B	604[B]	-	-	0/1/1/1	-
2	EDO	A	604[A]	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	613	EDO	O1-C1-C2-O2
2	A	606	EDO	O1-C1-C2-O2
2	A	616	EDO	O1-C1-C2-O2
2	B	616	EDO	O1-C1-C2-O2
2	A	618	EDO	O1-C1-C2-O2
2	B	615	EDO	O1-C1-C2-O2
2	B	623	EDO	O1-C1-C2-O2
2	A	602	EDO	O1-C1-C2-O2
2	B	608	EDO	O1-C1-C2-O2
2	B	617	EDO	O1-C1-C2-O2
2	B	603	EDO	O1-C1-C2-O2
2	B	621	EDO	O1-C1-C2-O2
2	A	607[B]	EDO	O1-C1-C2-O2
2	A	610	EDO	O1-C1-C2-O2
2	A	615	EDO	O1-C1-C2-O2
2	B	609	EDO	O1-C1-C2-O2
2	B	618	EDO	O1-C1-C2-O2

There are no ring outliers.

6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	618	EDO	1	0
2	B	602	EDO	1	0
2	B	606	EDO	1	0
2	B	614	EDO	2	0
2	A	604[B]	EDO	1	0
2	A	604[A]	EDO	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

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, 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	A	520/538 (96%)	0.22	44 (8%)	10 12	11, 17, 48, 73	0
1	B	523/538 (97%)	-0.04	10 (1%)	66 73	10, 17, 34, 71	0
All	All	1043/1076 (96%)	0.09	54 (5%)	27 31	10, 17, 40, 73	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	101	ALA	10.3
1	A	40	ALA	8.6
1	B	460	GLY	7.3
1	A	158	TYR	6.6
1	A	151	ALA	6.2
1	A	108	ALA	5.8
1	A	463	ALA	5.8
1	A	104	ALA	5.5
1	B	459	ALA	5.5
1	B	457	VAL	4.9
1	A	155	GLN	4.7
1	A	154	THR	4.7
1	A	111	PHE	4.6
1	A	144	THR	4.5
1	A	105	ASN	4.3
1	A	148	ALA	4.3
1	A	150	ILE	4.1
1	A	103	ALA	4.0
1	A	102	ASP	4.0
1	A	156	ASN	4.0
1	B	40	ALA	4.0
1	B	458	ASP	3.9
1	A	145	ALA	3.8
1	A	159	LYS	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	160	PRO	3.6
1	A	141	ALA	3.5
1	B	462	GLY	3.5
1	A	99	ALA	3.4
1	A	153	ALA	3.3
1	B	463	ALA	3.3
1	B	461	GLU	3.3
1	A	147	ALA	3.3
1	A	109	ALA	3.2
1	A	106	LEU	3.1
1	A	143	ALA	3.1
1	A	269	ALA	3.1
1	A	98	ALA	3.1
1	A	152	GLN	3.1
1	A	149	ARG	2.9
1	A	157	ARG	2.9
1	A	270	ASN	2.9
1	A	272	ARG	2.7
1	A	161	GLY	2.7
1	B	456	GLY	2.6
1	B	152	GLN	2.5
1	A	41	GLN	2.5
1	A	113	THR	2.5
1	A	457	VAL	2.5
1	A	90	LEU	2.3
1	A	137	TYR	2.3
1	A	146	ALA	2.2
1	A	139	THR	2.1
1	A	110	GLY	2.1
1	A	140	GLN	2.0

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 monosaccharides 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, 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
2	EDO	B	612	4/4	0.67	0.18	49,58,58,59	0
2	EDO	A	617	4/4	0.69	0.14	52,57,58,60	0
2	EDO	A	605	4/4	0.78	0.16	39,40,41,42	0
2	EDO	B	616	4/4	0.80	0.15	52,55,55,58	0
2	EDO	B	618	4/4	0.81	0.20	40,47,55,60	0
2	EDO	A	606	4/4	0.83	0.20	45,46,48,50	0
2	EDO	B	619	4/4	0.83	0.18	40,40,42,51	0
2	EDO	B	615	4/4	0.84	0.19	55,57,60,67	0
2	EDO	A	613	4/4	0.85	0.17	55,55,58,65	0
2	EDO	B	603	4/4	0.86	0.12	27,31,35,42	0
2	EDO	A	616	4/4	0.86	0.18	63,63,64,65	0
2	EDO	A	612	4/4	0.87	0.32	61,61,62,62	0
2	EDO	A	618	4/4	0.87	0.10	60,64,65,65	0
2	EDO	A	607[A]	4/4	0.89	0.13	28,30,32,35	4
2	EDO	B	617	4/4	0.89	0.17	66,66,67,67	0
2	EDO	A	607[B]	4/4	0.89	0.13	30,30,31,34	4
2	EDO	A	614	4/4	0.89	0.22	27,38,39,42	0
2	EDO	B	622	4/4	0.89	0.23	34,53,57,59	0
2	EDO	B	605	4/4	0.90	0.14	36,36,50,55	0
2	EDO	B	606	4/4	0.90	0.16	28,37,43,49	0
2	EDO	B	609	4/4	0.90	0.19	25,26,42,53	0
2	EDO	B	611	4/4	0.90	0.12	51,51,53,55	0
2	EDO	A	603	4/4	0.90	0.11	33,38,39,47	0
2	EDO	B	614	4/4	0.90	0.16	42,48,48,57	0
2	EDO	B	623	4/4	0.90	0.11	52,54,54,59	0
2	EDO	A	604[A]	4/4	0.91	0.11	27,29,30,31	4
2	EDO	A	604[B]	4/4	0.91	0.11	27,29,30,31	4
2	EDO	A	610	4/4	0.91	0.16	30,33,39,53	0
2	EDO	A	611	4/4	0.91	0.18	50,50,56,61	0
2	EDO	B	608	4/4	0.92	0.31	38,48,55,64	0
2	EDO	A	608	4/4	0.92	0.08	18,26,28,28	0
2	EDO	B	607	4/4	0.92	0.09	19,28,30,30	0
2	EDO	B	604[B]	4/4	0.93	0.11	29,29,31,32	4
2	EDO	B	604[A]	4/4	0.93	0.11	28,30,30,32	4
2	EDO	A	602	4/4	0.94	0.12	25,28,37,37	0
2	EDO	B	620	4/4	0.94	0.09	34,38,45,50	0
2	EDO	A	601	4/4	0.94	0.09	15,16,18,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	EDO	A	615	4/4	0.94	0.11	26,37,38,40	0
2	EDO	B	602	4/4	0.95	0.13	25,25,38,39	0
2	EDO	B	621	4/4	0.95	0.14	47,54,59,59	0
2	EDO	B	610	4/4	0.95	0.08	22,25,26,33	0
2	EDO	B	613	4/4	0.95	0.13	18,26,34,34	0
2	EDO	A	609	4/4	0.96	0.18	18,30,46,53	0
2	EDO	B	601	4/4	0.97	0.09	14,15,16,23	0
3	CL	B	624	1/1	0.97	0.06	28,28,28,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.