



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 13, 2020 – 10:12 PM BST

PDB ID : 5UOF
Title : Crystal structure of alpha,alpha-trehalose 6-phosphate sythase from Burkholderia multivorans
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2017-01-31
Resolution : 1.70 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 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 : 2.14.4.dev1
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) : 2.14.4.dev1

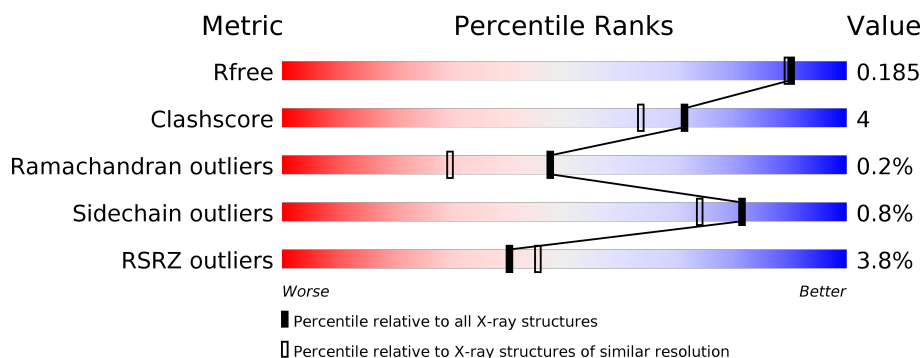
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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	A	481	<div> <div>5%</div> <div> <div></div> <div>91%</div> <div>7%</div> <div></div> </div> </div>
1	B	481	<div> <div>3%</div> <div> <div></div> <div>88%</div> <div>8%</div> <div>5%</div> </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8844 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 Alpha,alpha-trehalose-phosphate synthase (UDP-forming).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	471	Total	C	N	O	S	0	20	0
			3749	2387	668	677	17			
1	B	459	Total	C	N	O	S	0	21	0
			3681	2349	651	664	17			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP A0A0H3KGN3
A	2	ALA	-	expression tag	UNP A0A0H3KGN3
A	3	HIS	-	expression tag	UNP A0A0H3KGN3
A	4	HIS	-	expression tag	UNP A0A0H3KGN3
A	5	HIS	-	expression tag	UNP A0A0H3KGN3
A	6	HIS	-	expression tag	UNP A0A0H3KGN3
A	7	HIS	-	expression tag	UNP A0A0H3KGN3
A	8	HIS	-	expression tag	UNP A0A0H3KGN3
B	1	MET	-	initiating methionine	UNP A0A0H3KGN3
B	2	ALA	-	expression tag	UNP A0A0H3KGN3
B	3	HIS	-	expression tag	UNP A0A0H3KGN3
B	4	HIS	-	expression tag	UNP A0A0H3KGN3
B	5	HIS	-	expression tag	UNP A0A0H3KGN3
B	6	HIS	-	expression tag	UNP A0A0H3KGN3
B	7	HIS	-	expression tag	UNP A0A0H3KGN3
B	8	HIS	-	expression tag	UNP A0A0H3KGN3

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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	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	A	1	Total	C	O	0	0
			4	2	2		

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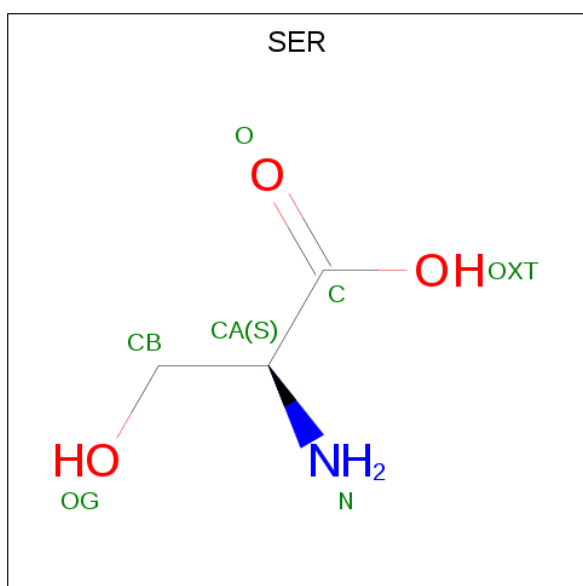
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 4	C 2	O 2	0	0
3	A	1	Total 4	C 2	O 2	0	0
3	A	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0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

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

- Molecule 4 is SERINE (three-letter code: SER) (formula: $C_3H_7NO_3$).

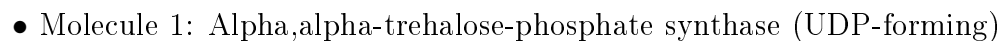


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			7	3	1	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	531	Total	O	0	26
			557	557		
5	B	643	Total	O	0	37
			680	680		

- Molecule 1: Alpha,alpha-trehalose-phosphate synthase (UDP-forming)



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	117.58Å 128.92Å 85.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.70 48.53 – 1.70	Depositor EDS
% Data completeness (in resolution range)	98.8 (50.00-1.70) 98.8 (48.53-1.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.37 (at 1.70Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.158 , 0.185 0.158 , 0.185	Depositor DCC
R_{free} test set	2056 reflections (1.45%)	wwPDB-VP
Wilson B-factor (Å ²)	15.0	Xtriage
Anisotropy	0.831	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 58.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	8844	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 5.39% 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: NA, 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	0.33	0/3894	0.53	0/5291
1	B	0.34	0/3827	0.55	0/5198
All	All	0.34	0/7721	0.54	0/10489

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

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	3749	0	3713	25	0
1	B	3681	0	3677	29	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	64	0	96	5	0
3	B	104	0	156	10	0
4	B	7	0	4	0	0
5	A	557	0	0	4	0
5	B	680	0	0	5	0
All	All	8844	0	7646	54	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.

All (54) 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:281:VAL:H	3:B:523[A]:EDO:H21	1.51	0.76
1:B:80:ARG:NH1	5:B:605:HOH:O	2.25	0.68
1:A:221:LEU:HD22	1:A:230:VAL:HG21	1.79	0.64
1:B:352:ARG:NH1	1:B:380:GLU:OE2	2.25	0.64
1:A:273:ARG:HH12	3:A:508:EDO:H21	1.63	0.63
1:A:233:TYR:HD2	1:A:456[A]:THR:HG23	1.64	0.62
1:B:226[A]:ARG:NH2	5:B:612:HOH:O	2.34	0.60
1:A:67:ASP:HB3	1:A:72:TYR:HE2	1.67	0.59
1:B:452:VAL:O	1:B:456[A]:THR:HG22	2.02	0.58
1:B:233:TYR:HD2	1:B:456[A]:THR:HG23	1.68	0.58
1:A:452:VAL:O	1:A:456[A]:THR:HG22	2.05	0.57
1:B:147:ALA:HB2	1:B:189:TYR:CE1	2.40	0.57
1:B:404[B]:GLU:HG3	3:B:505:EDO:H12	1.88	0.55
3:B:516[B]:EDO:O1	5:B:601:HOH:O	2.16	0.55
1:A:147:ALA:HB2	1:A:189:TYR:CE1	2.42	0.55
1:A:233:TYR:CD2	1:A:456[A]:THR:HG23	2.42	0.54
1:B:164:HIS:CE1	3:B:517:EDO:H21	2.44	0.53
1:A:200:ARG:HG3	1:A:230:VAL:HG12	1.90	0.53
1:B:187:CYS:O	1:B:226[A]:ARG:HD3	2.09	0.53
1:B:273:ARG:HH22	3:B:519:EDO:H22	1.73	0.52
1:B:233:TYR:CD2	1:B:456[A]:THR:HG23	2.46	0.51
1:A:91:ASN:HD21	3:A:514:EDO:H12	1.75	0.51
1:B:442:LEU:HD22	3:B:522:EDO:H22	1.92	0.51
1:A:149:ALA:HB2	3:A:507:EDO:H12	1.94	0.50
1:B:109[B]:ARG:HG3	1:B:109[B]:ARG:HH11	1.76	0.50
1:B:81:ASP:OD1	1:B:117:ARG:NH2	2.28	0.50
1:B:387:PRO:HD3	3:B:522:EDO:H21	1.92	0.50
1:B:50:TRP:HB2	3:B:503:EDO:H11	1.94	0.48
1:B:273:ARG:NH2	1:B:275:ASP:OD2	2.48	0.46
1:B:242:ILE:HG23	1:B:356[B]:MET:CG	2.45	0.46
1:B:147:ALA:O	1:B:151:ARG:HG2	2.15	0.46
1:B:32:LEU:HD12	3:B:516[A]:EDO:H11	1.99	0.45
1:A:147:ALA:O	1:A:151:ARG:HG2	2.17	0.45
1:A:456[A]:THR:HG21	5:A:990:HOH:O	2.17	0.44
1:B:353:ASN:ND2	3:B:515:EDO:O2	2.46	0.44
1:A:171[B]:ASP:OD1	5:A:601:HOH:O	2.21	0.44
1:A:89:PHE:CE2	1:A:94[A]:LEU:HG	2.53	0.44
1:A:244[B]:GLN:NE2	5:A:605:HOH:O	2.40	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:81:ASP:OD2	5:B:602:HOH:O	2.21	0.44
1:A:371[B]:ARG:HD3	1:A:371[B]:ARG:HA	1.66	0.44
1:A:235:ILE:HD13	3:A:509:EDO:H21	2.00	0.43
1:A:110:GLN:HG2	5:A:848:HOH:O	2.19	0.42
1:B:344:GLN:NE2	5:B:621[B]:HOH:O	2.38	0.42
1:B:356[B]:MET:HG3	1:B:384:SER:OG	2.18	0.42
1:A:248[B]:GLN:HG2	1:A:249:TYR:HD1	1.84	0.42
1:A:253:LYS:O	1:A:257[B]:MET:HG2	2.20	0.42
1:A:169:SER:OG	1:B:171[B]:ASP:OD2	2.28	0.42
1:A:467:ALA:O	1:A:471:THR:HG23	2.19	0.42
1:A:371[B]:ARG:HB2	1:A:371[B]:ARG:HH21	1.84	0.41
1:B:385:GLN:HB2	1:B:438:HIS:CE1	2.56	0.41
1:A:385:GLN:HB2	1:A:438:HIS:CE1	2.56	0.41
1:A:300:ARG:HD3	3:A:504:EDO:H21	2.03	0.40
1:B:35:GLY:O	1:B:454:ARG:HD3	2.22	0.40

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	489/481 (102%)	477 (98%)	11 (2%)	1 (0%)	47	30
1	B	475/481 (99%)	466 (98%)	8 (2%)	1 (0%)	47	30
All	All	964/962 (100%)	943 (98%)	19 (2%)	2 (0%)	47	30

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	375	ASN
1	B	375	ASN

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	382/384 (100%)	378 (99%)	4 (1%)	76	67
1	B	381/384 (99%)	379 (100%)	2 (0%)	88	83
All	All	763/768 (99%)	757 (99%)	6 (1%)	81	74

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	HIS
1	A	9	MET
1	A	66	ARG
1	A	471	THR
1	B	175	LEU
1	B	315	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	HIS
1	A	41	GLN
1	B	353	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 [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 45 ligands modelled in this entry, 2 are monoatomic - leaving 43 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	504	-	3,3,3	0.46	0	2,2,2	0.25	0
3	EDO	B	525	-	3,3,3	0.47	0	2,2,2	0.43	0
3	EDO	A	517	-	3,3,3	0.48	0	2,2,2	0.28	0
3	EDO	B	517	-	3,3,3	0.39	0	2,2,2	0.42	0
3	EDO	B	516[B]	-	3,3,3	0.45	0	2,2,2	0.43	0
3	EDO	A	516	-	3,3,3	0.48	0	2,2,2	0.16	0
3	EDO	B	503	-	3,3,3	0.54	0	2,2,2	0.08	0
3	EDO	B	523[B]	-	3,3,3	0.49	0	2,2,2	0.11	0
3	EDO	B	516[A]	-	3,3,3	0.48	0	2,2,2	0.22	0
3	EDO	A	502	-	3,3,3	0.47	0	2,2,2	0.30	0
3	EDO	B	512	-	3,3,3	0.42	0	2,2,2	0.34	0
3	EDO	B	523[A]	-	3,3,3	0.45	0	2,2,2	0.30	0
3	EDO	A	510	-	3,3,3	0.47	0	2,2,2	0.32	0
3	EDO	A	514	-	3,3,3	0.45	0	2,2,2	0.37	0
3	EDO	B	504	-	3,3,3	0.47	0	2,2,2	0.25	0
3	EDO	A	512	-	3,3,3	0.46	0	2,2,2	0.38	0
3	EDO	B	510	-	3,3,3	0.43	0	2,2,2	0.48	0
3	EDO	B	511	-	3,3,3	0.43	0	2,2,2	0.26	0
3	EDO	B	514	-	3,3,3	0.46	0	2,2,2	0.40	0
3	EDO	A	511	-	3,3,3	0.51	0	2,2,2	0.24	0
3	EDO	B	515	-	3,3,3	0.45	0	2,2,2	0.37	0
3	EDO	A	515	-	3,3,3	0.47	0	2,2,2	0.19	0
3	EDO	A	513	-	3,3,3	0.39	0	2,2,2	0.54	0
3	EDO	B	521	-	3,3,3	0.46	0	2,2,2	0.39	0
3	EDO	B	520	-	3,3,3	0.46	0	2,2,2	0.38	0
4	SER	B	501	-	3,6,6	0.33	0	1,7,7	0.32	0
3	EDO	B	519	-	3,3,3	0.44	0	2,2,2	0.51	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	B	505	-	3,3,3	0.47	0	2,2,2	0.42	0
3	EDO	A	507	-	3,3,3	0.40	0	2,2,2	0.27	0
3	EDO	B	522	-	3,3,3	0.52	0	2,2,2	0.28	0
3	EDO	B	513	-	3,3,3	0.45	0	2,2,2	0.33	0
3	EDO	B	508	-	3,3,3	0.49	0	2,2,2	0.30	0
3	EDO	B	524	-	3,3,3	0.45	0	2,2,2	0.39	0
3	EDO	A	503	-	3,3,3	0.44	0	2,2,2	0.56	0
3	EDO	B	518[A]	-	3,3,3	0.47	0	2,2,2	0.30	0
3	EDO	B	506	-	3,3,3	0.44	0	2,2,2	0.43	0
3	EDO	B	518[B]	-	3,3,3	0.46	0	2,2,2	0.37	0
3	EDO	B	509	-	3,3,3	0.56	0	2,2,2	0.12	0
3	EDO	A	506	-	3,3,3	0.44	0	2,2,2	0.39	0
3	EDO	A	509	-	3,3,3	0.48	0	2,2,2	0.35	0
3	EDO	B	507	-	3,3,3	0.58	0	2,2,2	0.05	0
3	EDO	A	505	-	3,3,3	0.53	0	2,2,2	0.23	0
3	EDO	A	508	-	3,3,3	0.42	0	2,2,2	0.43	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	504	-	-	0/1/1/1	-
3	EDO	B	525	-	-	0/1/1/1	-
3	EDO	A	517	-	-	1/1/1/1	-
3	EDO	B	517	-	-	1/1/1/1	-
3	EDO	B	516[B]	-	-	1/1/1/1	-
3	EDO	A	516	-	-	1/1/1/1	-
3	EDO	B	503	-	-	0/1/1/1	-
3	EDO	B	523[B]	-	-	1/1/1/1	-
3	EDO	B	516[A]	-	-	0/1/1/1	-
3	EDO	A	502	-	-	0/1/1/1	-
3	EDO	B	512	-	-	0/1/1/1	-
3	EDO	B	523[A]	-	-	0/1/1/1	-
3	EDO	A	510	-	-	0/1/1/1	-
3	EDO	A	514	-	-	0/1/1/1	-
3	EDO	B	504	-	-	0/1/1/1	-
3	EDO	A	512	-	-	0/1/1/1	-
3	EDO	B	510	-	-	0/1/1/1	-
3	EDO	B	511	-	-	0/1/1/1	-
3	EDO	B	514	-	-	0/1/1/1	-
3	EDO	A	511	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	B	515	-	-	0/1/1/1	-
3	EDO	A	515	-	-	1/1/1/1	-
3	EDO	A	513	-	-	1/1/1/1	-
3	EDO	B	521	-	-	0/1/1/1	-
3	EDO	B	520	-	-	1/1/1/1	-
4	SER	B	501	-	-	1/2/6/6	-
3	EDO	B	519	-	-	0/1/1/1	-
3	EDO	B	505	-	-	0/1/1/1	-
3	EDO	A	507	-	-	0/1/1/1	-
3	EDO	B	522	-	-	1/1/1/1	-
3	EDO	B	513	-	-	0/1/1/1	-
3	EDO	B	508	-	-	0/1/1/1	-
3	EDO	B	524	-	-	1/1/1/1	-
3	EDO	A	503	-	-	0/1/1/1	-
3	EDO	B	518[A]	-	-	0/1/1/1	-
3	EDO	B	506	-	-	0/1/1/1	-
3	EDO	B	518[B]	-	-	0/1/1/1	-
3	EDO	B	509	-	-	0/1/1/1	-
3	EDO	A	506	-	-	0/1/1/1	-
3	EDO	A	509	-	-	1/1/1/1	-
3	EDO	B	507	-	-	0/1/1/1	-
3	EDO	A	505	-	-	0/1/1/1	-
3	EDO	A	508	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	517	EDO	O1-C1-C2-O2
3	B	517	EDO	O1-C1-C2-O2
3	A	516	EDO	O1-C1-C2-O2
3	A	513	EDO	O1-C1-C2-O2
4	B	501	SER	C-CA-CB-OG
3	A	515	EDO	O1-C1-C2-O2
3	B	522	EDO	O1-C1-C2-O2
3	B	524	EDO	O1-C1-C2-O2
3	B	520	EDO	O1-C1-C2-O2
3	B	516[B]	EDO	O1-C1-C2-O2
3	B	523[B]	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
3	A	509	EDO	O1-C1-C2-O2

There are no ring outliers.

14 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	504	EDO	1	0
3	B	517	EDO	1	0
3	B	516[B]	EDO	1	0
3	B	503	EDO	1	0
3	B	516[A]	EDO	1	0
3	B	523[A]	EDO	1	0
3	A	514	EDO	1	0
3	B	515	EDO	1	0
3	B	519	EDO	1	0
3	B	505	EDO	1	0
3	A	507	EDO	1	0
3	B	522	EDO	2	0
3	A	509	EDO	1	0
3	A	508	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 ⓘ

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	471/481 (97%)	-0.15	22 (4%) 31 35	9, 19, 51, 79	0
1	B	459/481 (95%)	-0.35	13 (2%) 53 57	10, 17, 39, 68	0
All	All	930/962 (96%)	-0.25	35 (3%) 40 45	9, 18, 46, 79	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	478	ILE	5.5
1	B	468	ALA	4.9
1	A	475	GLY	4.8
1	A	21	ILE	4.7
1	A	474	ALA	4.6
1	B	467	ALA	4.5
1	A	57	THR	4.4
1	A	219	GLY	4.3
1	A	471	THR	4.2
1	A	473	ARG	4.0
1	A	217	GLU	4.0
1	B	219	GLY	3.8
1	A	470	VAL	3.5
1	A	472	GLN	3.3
1	A	218	ASP	3.3
1	A	55	VAL	3.2
1	A	20	ALA	3.2
1	B	217	GLU	3.1
1	A	22	GLY	3.1
1	B	338	LEU	3.1
1	A	216	SER	3.1
1	A	311	ARG	3.0
1	A	469	SER	3.0
1	B	466	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	310	THR	2.9
1	A	56	GLY	2.9
1	B	315	GLN	2.9
1	A	312	SER	2.8
1	B	216	SER	2.6
1	B	218	ASP	2.6
1	A	54	ILE	2.6
1	B	336	SER	2.5
1	A	467	ALA	2.3
1	B	469	SER	2.3
1	B	215	ALA	2.1

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 [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	EDO	A	515	4/4	0.56	0.20	53,60,62,63	0
4	SER	B	501	7/7	0.67	0.20	55,58,59,62	0
3	EDO	B	523[A]	4/4	0.70	0.29	29,33,34,35	4
3	EDO	A	516	4/4	0.70	0.19	59,60,61,62	0
3	EDO	B	523[B]	4/4	0.70	0.29	27,32,34,34	4
3	EDO	A	502	4/4	0.72	0.32	56,58,61,63	0
3	EDO	B	520	4/4	0.73	0.15	55,57,60,66	0
3	EDO	A	509	4/4	0.75	0.17	46,47,47,48	0
3	EDO	A	514	4/4	0.79	0.22	55,57,58,64	0
3	EDO	B	522	4/4	0.80	0.20	29,39,47,47	0
3	EDO	A	513	4/4	0.82	0.17	38,45,47,51	0
3	EDO	A	517	4/4	0.82	0.15	57,59,60,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	EDO	B	516[A]	4/4	0.83	0.19	31,33,33,34	4
3	EDO	B	516[B]	4/4	0.83	0.19	32,33,34,36	4
3	EDO	B	524	4/4	0.84	0.22	40,42,50,57	0
3	EDO	B	505	4/4	0.84	0.14	35,44,46,49	0
3	EDO	B	515	4/4	0.84	0.15	45,48,48,50	0
3	EDO	B	519	4/4	0.85	0.13	38,43,46,52	0
3	EDO	A	505	4/4	0.86	0.14	23,35,36,41	0
3	EDO	A	511	4/4	0.86	0.13	34,41,47,55	0
3	EDO	B	518[A]	4/4	0.87	0.14	33,40,44,44	4
3	EDO	B	518[B]	4/4	0.87	0.14	44,44,45,45	4
3	EDO	A	503	4/4	0.88	0.15	40,45,50,51	0
3	EDO	A	506	4/4	0.89	0.18	33,39,39,40	0
3	EDO	B	521	4/4	0.89	0.19	49,55,61,66	0
3	EDO	B	504	4/4	0.90	0.17	46,49,53,58	0
3	EDO	A	510	4/4	0.90	0.13	38,39,46,56	0
3	EDO	B	507	4/4	0.91	0.12	23,26,35,35	0
3	EDO	A	508	4/4	0.91	0.15	37,40,40,45	0
3	EDO	B	517	4/4	0.91	0.14	24,27,41,53	0
3	EDO	A	512	4/4	0.91	0.18	40,48,49,49	0
3	EDO	A	507	4/4	0.92	0.12	26,28,30,38	0
3	EDO	A	504	4/4	0.93	0.13	50,51,54,60	0
3	EDO	B	525	4/4	0.93	0.14	20,37,37,42	0
3	EDO	B	514	4/4	0.94	0.09	41,43,43,44	0
3	EDO	B	506	4/4	0.94	0.13	33,34,48,58	0
3	EDO	B	512	4/4	0.95	0.16	41,42,43,43	0
3	EDO	B	503	4/4	0.95	0.12	18,24,30,33	0
3	EDO	B	511	4/4	0.96	0.08	21,25,28,32	0
3	EDO	B	509	4/4	0.96	0.10	16,22,25,26	0
3	EDO	B	513	4/4	0.97	0.08	23,23,28,37	0
3	EDO	B	510	4/4	0.98	0.06	19,21,21,22	0
3	EDO	B	508	4/4	0.98	0.08	15,17,19,22	0
2	NA	B	502	1/1	0.99	0.07	13,13,13,13	0
2	NA	A	501	1/1	1.00	0.04	14,14,14,14	0

6.5 Other polymers ⓘ

There are no such residues in this entry.