



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 3ZWF / pdb_00003zwf
Title : Crystal structure of Human tRNase Z, short form (ELAC1).
Authors : Allerston, C.K.; Krojer, T.; Berridge, G.; Burgess-Brown, N.; Chaikuad, A.; Chalk, R.; Elkins, J.M.; Gileadi, C.; Latwiel, S.V.A.; Savitsky, P.; Vollmar, M.; Arrowsmith, C.H.; Weigelt, J.; Edwards, A.; Bountra, C.; von Delft, F.; Gileadi, O.
Deposited on : 2011-07-29
Resolution : 1.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

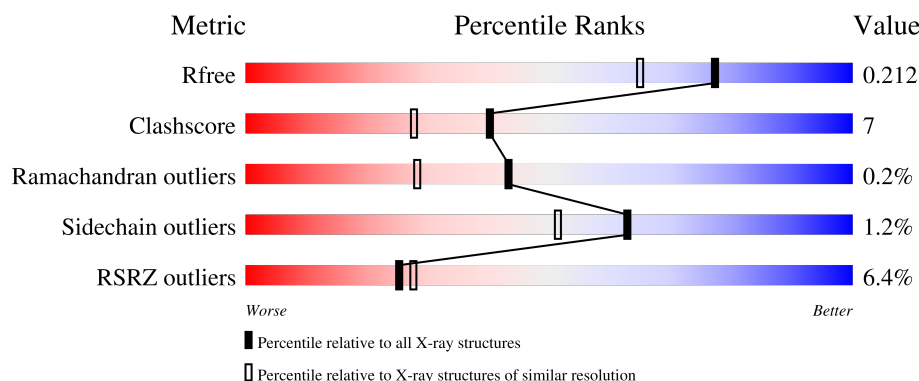
1 Overall quality at a glance

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}	180053	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (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 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	368	5% 63% 7% • 30%
1	B	368	4% 65% 5% 30%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	EDO	A	1369	-	-	X	-
2	EDO	A	1370	-	-	X	-
4	PO4	A	1365	-	X	-	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4292 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 ZINC PHOSPHODIESTERASE ELAC PROTEIN 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	259	Total	C	N	O	S	0	7	0
			1974	1276	323	359	16			
1	B	259	Total	C	N	O	S	0	7	0
			1981	1278	328	359	16			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	364	ALA	-	expression tag	UNP Q9H777
A	365	GLU	-	expression tag	UNP Q9H777
A	366	ASN	-	expression tag	UNP Q9H777
A	367	LEU	-	expression tag	UNP Q9H777
A	368	TYR	-	expression tag	UNP Q9H777
A	369	PHE	-	expression tag	UNP Q9H777
A	370	GLN	-	expression tag	UNP Q9H777
B	364	ALA	-	expression tag	UNP Q9H777
B	365	GLU	-	expression tag	UNP Q9H777
B	366	ASN	-	expression tag	UNP Q9H777
B	367	LEU	-	expression tag	UNP Q9H777
B	368	TYR	-	expression tag	UNP Q9H777
B	369	PHE	-	expression tag	UNP Q9H777
B	370	GLN	-	expression tag	UNP Q9H777

- Molecule 2 is 1,2-ETHANEDIOL (CCD ID: 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	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	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Zn	0	0
			2	2		
3	B	2	Total	Zn	0	0
			2	2		

- Molecule 4 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



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

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Na	0	0
			1	1		

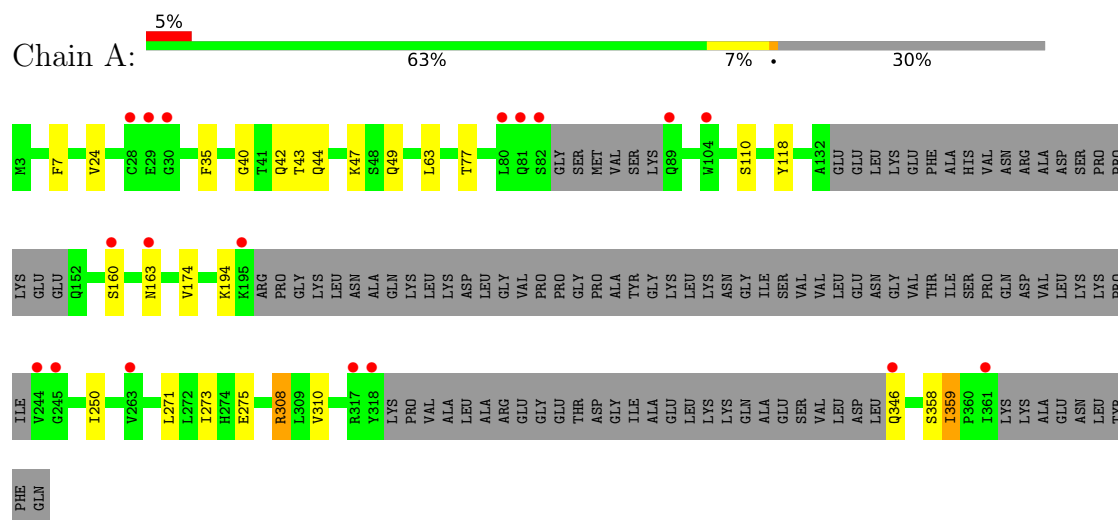
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	156	Total	O	0	0
			156	156		
6	B	126	Total	O	0	0
			126	126		

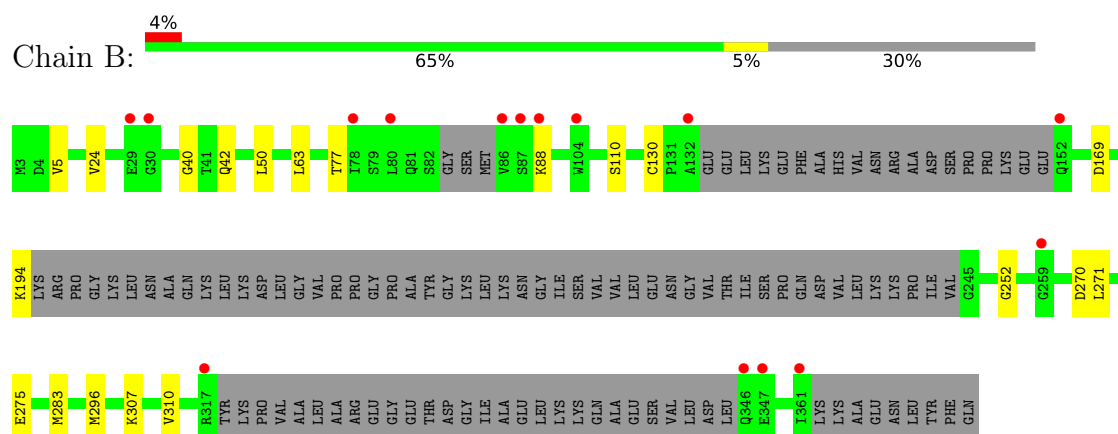
3 Residue-property plots [i](#)

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: ZINC PHOSPHODIESTERASE ELAC PROTEIN 1



• Molecule 1: ZINC PHOSPHODIESTERASE ELAC PROTEIN 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	59.52Å 73.79Å 73.66Å 90.00° 98.69° 90.00°	Depositor
Resolution (Å)	72.81 – 1.70 72.81 – 1.70	Depositor EDS
% Data completeness (in resolution range)	96.7 (72.81-1.70) 96.7 (72.81-1.70)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.16 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.187 , 0.210 0.189 , 0.212	Depositor DCC
R_{free} test set	3400 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	22.7	Xtriage
Anisotropy	0.491	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	4292	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.97% 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, NA, ZN, PO4

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	0.86	0/2036	0.83	0/2761
1	B	0.90	0/2040	0.86	0/2763
All	All	0.88	0/4076	0.85	0/5524

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	1974	0	1923	30	0
1	B	1981	0	1932	19	0
2	A	24	0	36	20	0
2	B	16	0	24	4	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
5	B	1	0	0	0	0
6	A	156	0	0	3	0
6	B	126	0	0	0	0
All	All	4292	0	3915	52	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 7.

All (52) 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:43[B]:THR:HG23	2:A:1370:EDO:O2	1.43	1.18
1:A:42:GLN:OE1	1:A:77[B]:THR:HG21	1.58	1.02
1:B:42:GLN:OE1	1:B:77[B]:THR:HG21	1.63	0.98
2:A:1369:EDO:H21	1:B:40:GLY:HA3	1.47	0.96
1:A:43[B]:THR:CG2	2:A:1370:EDO:O2	2.16	0.92
2:A:1369:EDO:H21	1:B:40:GLY:CA	2.03	0.89
1:B:130:CYS:SG	2:B:1368:EDO:H22	2.17	0.84
1:B:5:VAL:HG13	1:B:24[A]:VAL:HG12	1.63	0.78
1:B:5:VAL:HG13	1:B:24[A]:VAL:CG1	2.13	0.77
1:B:5:VAL:CG1	1:B:24[A]:VAL:CG1	2.73	0.67
1:A:271:LEU:HD12	1:A:308:ARG:HG2	1.76	0.67
1:B:130:CYS:SG	2:B:1368:EDO:C2	2.83	0.66
2:A:1369:EDO:H11	2:A:1370:EDO:H22	1.77	0.65
2:A:1369:EDO:H11	2:A:1370:EDO:C2	2.27	0.64
1:A:271:LEU:CD1	1:A:308:ARG:HG2	2.27	0.64
1:A:359:ILE:HD12	1:A:359:ILE:N	2.13	0.63
2:A:1369:EDO:H11	2:A:1370:EDO:C1	2.29	0.63
1:A:118:TYR:CE2	2:A:1368:EDO:H22	2.34	0.62
1:A:49:GLN:H	2:A:1366:EDO:C1	2.12	0.62
1:A:43[B]:THR:HG21	2:A:1369:EDO:O2	1.99	0.61
1:A:44:GLN:HG2	2:A:1370:EDO:H12	1.84	0.59
1:A:43[B]:THR:HG23	2:A:1370:EDO:HO2	1.67	0.57
1:A:40:GLY:HA2	2:A:1369:EDO:H22	1.88	0.56
2:A:1369:EDO:H21	1:B:40:GLY:HA2	1.86	0.55
1:A:346:GLN:N	6:A:2143:HOH:O	2.41	0.52
1:A:44:GLN:CG	2:A:1370:EDO:H12	2.38	0.52
1:A:174:VAL:HG23	1:A:194:LYS:HE2	1.92	0.51
1:A:49:GLN:H	2:A:1366:EDO:H11	1.75	0.51
1:A:160:SER:HB3	6:A:2110:HOH:O	2.09	0.51
1:A:174:VAL:CG2	1:A:194:LYS:HE2	2.41	0.51
2:A:1369:EDO:H11	2:A:1370:EDO:H11	1.94	0.49
1:B:252:GLY:HA2	2:B:1369:EDO:H21	1.93	0.49
1:A:40:GLY:O	1:A:43[B]:THR:HG22	2.13	0.49
1:A:49:GLN:H	2:A:1366:EDO:H12	1.76	0.48
1:B:5:VAL:CG1	1:B:24[A]:VAL:HG11	2.42	0.48
1:B:283:MET:HE2	1:B:296:MET:HG3	1.96	0.47
1:A:174:VAL:HG23	1:A:194:LYS:CE	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24[B]:VAL:HG23	1:A:35:PHE:HB2	1.96	0.47
1:A:63:LEU:O	1:B:110:SER:HA	2.14	0.47
1:A:110:SER:HA	1:B:63:LEU:O	2.16	0.46
1:A:47:LYS:NZ	6:A:2020:HOH:O	2.47	0.46
1:B:271:LEU:HD11	1:B:310:VAL:HG23	1.99	0.45
1:A:174:VAL:CG2	1:A:194:LYS:CE	2.96	0.44
1:B:270:ASP:HA	1:B:307:LYS:HD2	1.99	0.44
1:A:43[A]:THR:HG21	2:A:1369:EDO:O2	2.18	0.43
1:B:50:LEU:HG	2:B:1367:EDO:H22	2.01	0.43
2:A:1369:EDO:C1	2:A:1370:EDO:H22	2.45	0.43
1:B:169:ASP:OD1	1:B:194:LYS:NZ	2.38	0.42
1:A:7:PHE:CZ	1:A:310:VAL:HG11	2.55	0.42
1:A:250:ILE:HG12	1:A:273:ILE:HD12	2.01	0.42
1:B:271:LEU:HD11	1:B:310:VAL:CG2	2.50	0.41
1:A:358:SER:C	1:A:359:ILE:HD12	2.45	0.41

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	A	256/368 (70%)	248 (97%)	8 (3%)	0	100	100
1	B	256/368 (70%)	247 (96%)	8 (3%)	1 (0%)	30	16
All	All	512/736 (70%)	495 (97%)	16 (3%)	1 (0%)	43	28

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	88	LYS

5.3.2 Protein sidechains [i](#)

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	208/312 (67%)	204 (98%)	4 (2%)	50	34
1	B	208/312 (67%)	207 (100%)	1 (0%)	81	76
All	All	416/624 (67%)	411 (99%)	5 (1%)	63	51

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	163	ASN
1	A	275	GLU
1	A	308	ARG
1	A	359	ILE
1	B	275	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 5 are monoatomic - leaving 12 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	1362	-	3,3,3	0.35	0	2,2,2	0.44	0
4	PO4	B	1364	3	4,4,4	1.72	1 (25%)	6,6,6	1.62	1 (16%)
2	EDO	B	1366	-	3,3,3	0.40	0	2,2,2	0.25	0
2	EDO	B	1368	-	3,3,3	0.39	0	2,2,2	0.06	0
2	EDO	B	1369	-	3,3,3	0.60	0	2,2,2	0.19	0
2	EDO	A	1366	-	3,3,3	0.37	0	2,2,2	0.20	0
2	EDO	A	1369	-	3,3,3	0.40	0	2,2,2	0.23	0
2	EDO	A	1368	-	3,3,3	0.39	0	2,2,2	0.09	0
4	PO4	A	1365	3	4,4,4	2.21	3 (75%)	6,6,6	1.96	2 (33%)
2	EDO	A	1370	-	3,3,3	0.34	0	2,2,2	0.70	0
2	EDO	A	1367	-	3,3,3	0.37	0	2,2,2	0.46	0
2	EDO	B	1367	-	3,3,3	0.35	0	2,2,2	0.32	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	1362	-	-	1/1/1/1	-
2	EDO	B	1366	-	-	0/1/1/1	-
2	EDO	B	1368	-	-	0/1/1/1	-
2	EDO	B	1369	-	-	1/1/1/1	-
2	EDO	A	1366	-	-	0/1/1/1	-
2	EDO	A	1369	-	-	0/1/1/1	-
2	EDO	A	1368	-	-	0/1/1/1	-
2	EDO	A	1370	-	-	0/1/1/1	-
2	EDO	A	1367	-	-	0/1/1/1	-
2	EDO	B	1367	-	-	0/1/1/1	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1364	PO4	P-O3	-2.62	1.47	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1365	PO4	P-O2	2.60	1.62	1.54
4	A	1365	PO4	P-O3	-2.26	1.48	1.54
4	A	1365	PO4	P-O1	2.07	1.55	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1365	PO4	O4-P-O3	4.01	120.38	107.91
4	B	1364	PO4	O4-P-O2	3.41	118.52	107.91
4	A	1365	PO4	O2-P-O1	-2.03	103.79	110.95

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1369	EDO	O1-C1-C2-O2
2	A	1362	EDO	O1-C1-C2-O2

There are no ring outliers.

7 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1368	EDO	2	0
2	B	1369	EDO	1	0
2	A	1366	EDO	3	0
2	A	1369	EDO	11	0
2	A	1368	EDO	1	0
2	A	1370	EDO	10	0
2	B	1367	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	259/368 (70%)	0.21	18 (6%) 23 25	15, 32, 68, 90	7 (2%)
1	B	259/368 (70%)	0.16	15 (5%) 29 32	13, 31, 56, 101	7 (2%)
All	All	518/736 (70%)	0.18	33 (6%) 25 27	13, 32, 61, 101	14 (2%)

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	318	TYR	4.5
1	B	86	VAL	3.9
1	B	30	GLY	3.9
1	B	104	TRP	3.8
1	B	80	LEU	3.7
1	A	81	GLN	3.6
1	A	104	TRP	3.5
1	A	361	ILE	3.4
1	A	346	GLN	3.3
1	A	195	LYS	3.2
1	B	361	ILE	3.1
1	B	87	SER	3.1
1	A	30	GLY	3.1
1	A	244	VAL	3.1
1	B	29	GLU	3.1
1	B	346	GLN	3.0
1	A	163	ASN	3.0
1	B	317	ARG	2.8
1	B	347	GLU	2.6
1	A	28	CYS	2.5
1	B	132	ALA	2.5
1	A	317	ARG	2.4
1	A	160	SER	2.4
1	A	263	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	152	GLN	2.2
1	A	80	LEU	2.2
1	A	245	GLY	2.1
1	A	29	GLU	2.1
1	A	82	SER	2.1
1	B	88	LYS	2.0
1	A	89	GLN	2.0
1	B	259	GLY	2.0
1	B	78	ILE	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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
2	EDO	A	1367	4/4	0.66	0.21	74,75,78,81	0
2	EDO	A	1366	4/4	0.76	0.27	42,42,66,71	0
2	EDO	A	1362	4/4	0.80	0.18	62,69,70,72	0
2	EDO	A	1368	4/4	0.81	0.19	37,54,72,72	0
2	EDO	B	1368	4/4	0.82	0.17	49,52,62,78	0
2	EDO	B	1366	4/4	0.85	0.21	54,60,64,87	0
2	EDO	B	1367	4/4	0.86	0.17	25,32,51,68	0
2	EDO	B	1369	4/4	0.89	0.13	34,48,55,65	0
2	EDO	A	1369	4/4	0.91	0.22	27,32,32,33	0
2	EDO	A	1370	4/4	0.93	0.17	25,28,31,42	0
3	ZN	B	1363	1/1	0.94	0.21	54,54,54,54	0
4	PO4	A	1365	5/5	0.94	0.11	24,26,35,39	0
5	NA	B	1365	1/1	0.94	0.13	31,31,31,31	0
4	PO4	B	1364	5/5	0.96	0.08	26,30,37,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	ZN	A	1364	1/1	1.00	0.01	30,30,30,30	0
3	ZN	B	1362	1/1	1.00	0.05	30,30,30,30	1
3	ZN	A	1363	1/1	1.00	0.02	26,26,26,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.