



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 17, 2026 – 02:25 PM EDT

PDB ID : 36LN / pdb_000036ln
Title : X-ray structure of chicken PLCZ1 with alternate EF-hand conformation, active site blocked by phosphorylated threonine in the XY linker
Authors : Edwards, M.M.; Friberg, A.; Dong, A.; Seitova, A.; Loppnau, P.; Edwards, A.M.; Brauer, N.; Arrowsmith, C.H.; Structural Genomics Consortium (SGC)
Deposited on : 2026-06-16
Resolution : 1.99 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	:	4-5-2 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	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

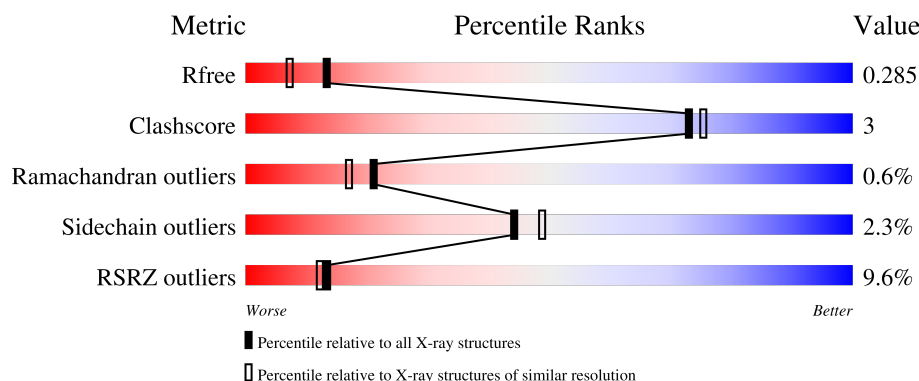
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	638	
1	B	638	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9816 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 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase zeta-1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	595	Total	C	N	O	P	S	0	4	0
			4727	3009	792	900	2	24			
1	B	582	Total	C	N	O	P	S	0	1	0
			4598	2934	778	861	2	23			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q2VRL0
B	0	GLY	-	expression tag	UNP Q2VRL0

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

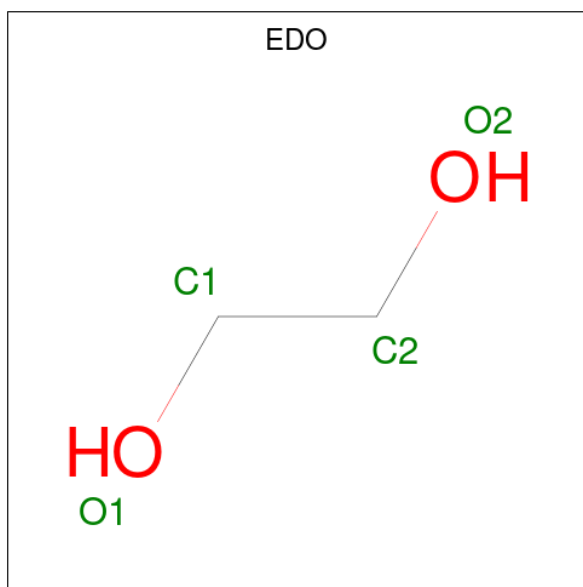
- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 4 is UNKNOWN LIGAND (CCD ID: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total	X	0	0
			3	3		
4	B	1	Total	X	0	0
			1	1		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

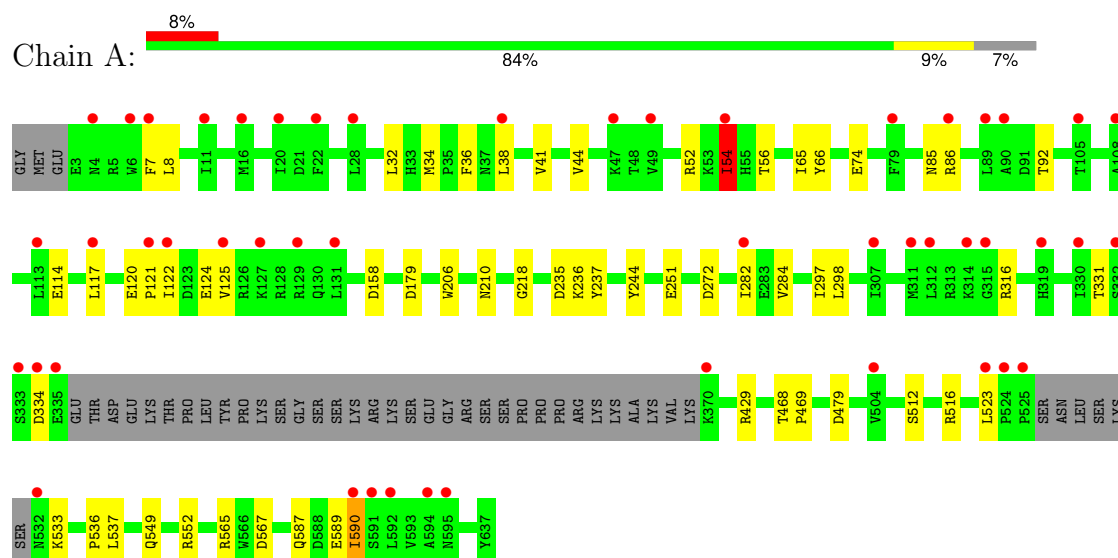
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	238	Total	O	0	1
			239	239		
6	B	232	Total	O	0	1
			233	233		

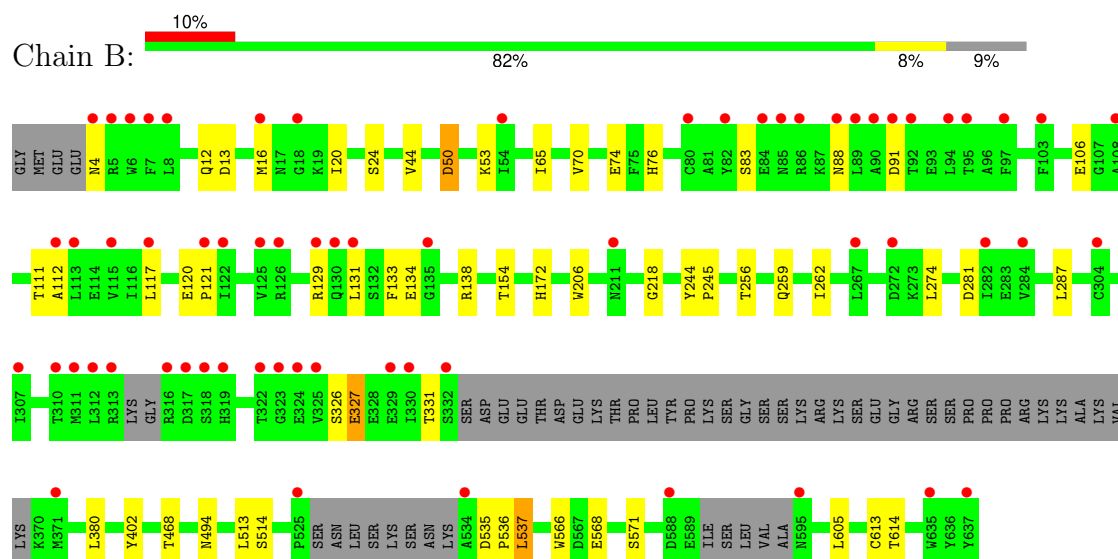
3 Residue-property plots [i](#)

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: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase zeta-1



- Molecule 1: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase zeta-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	92.42Å 134.94Å 138.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	76.95 – 1.99 76.95 – 1.99	Depositor EDS
% Data completeness (in resolution range)	99.7 (76.95-1.99) 99.7 (76.95-1.99)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.02 (at 1.98Å)	Xtriage
Refinement program	REFMAC 8.0	Depositor
R, R_{free}	0.243 , 0.283 0.248 , 0.285	Depositor DCC
R_{free} test set	5960 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	22.3	Xtriage
Anisotropy	0.294	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 63.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.015 for -h,l,k	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9816	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.72% 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: CL, SEP, CA, TPO, UNX, 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	0.57	0/4812	0.95	4/6517 (0.1%)
1	B	0.57	0/4681	0.94	2/6340 (0.0%)
All	All	0.57	0/9493	0.95	6/12857 (0.0%)

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
1	A	0	3
1	B	0	1
All	All	0	4

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	468	THR	CA-CB-OG1	-6.55	99.78	109.60
1	B	256	THR	CA-CB-OG1	-6.28	100.19	109.60
1	A	244	TYR	CB-CA-C	6.21	117.81	108.86
1	A	334	ASP	CA-CB-CG	5.52	118.12	112.60
1	A	158	ASP	CA-CB-CG	5.13	117.73	112.60
1	A	479	ASP	CA-CB-CG	5.01	117.61	112.60

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	429	ARG	Sidechain
1	A	523	LEU	Peptide
1	A	552	ARG	Sidechain
1	B	536	PRO	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	A	4727	0	4551	31	0
1	B	4598	0	4429	27	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	3	0	0	0	0
4	B	1	0	0	0	0
5	A	4	0	6	2	0
5	B	4	0	6	0	0
6	A	239	0	0	5	0
6	B	233	0	0	4	0
All	All	9816	0	8992	58	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.

All (58) 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:83:SER:OG	1:B:88:ASN:O	2.08	0.69
1:B:614:THR:HG23	6:B:861:HOH:O	1.93	0.69
1:A:272:ASP:HB2	6:B:1004:HOH:O	1.94	0.67
1:A:114:GLU:OE1	6:A:801:HOH:O	2.14	0.65
1:B:326:SEP:O	1:B:327:GLU:CB	2.51	0.58
1:A:589:GLU:O	1:A:590:ILE:HB	2.03	0.58
1:B:513:LEU:HD22	1:B:605:LEU:HD11	1.86	0.57
1:B:537:LEU:C	1:B:537:LEU:HD12	2.30	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:ASN:OD1	1:A:85:ASN:C	2.51	0.54
1:B:50:ASP:C	1:B:50:ASP:OD1	2.52	0.53
1:A:516:ARG:NH2	6:A:808:HOH:O	2.42	0.53
1:A:590:ILE:O	1:A:590:ILE:HG23	2.08	0.52
1:B:91:ASP:CB	1:B:129:ARG:HH11	2.23	0.52
1:A:549:GLN:NE2	6:A:803:HOH:O	2.21	0.51
1:A:120:GLU:OE2	1:A:121:PRO:HD2	2.11	0.50
1:A:54:ILE:HG22	1:A:56:THR:HG22	1.93	0.50
1:B:274:LEU:HD21	1:B:380:LEU:HD22	1.93	0.50
1:A:516:ARG:NE	6:A:806:HOH:O	2.39	0.50
1:B:20:ILE:HB	1:B:24:SER:HB2	1.94	0.49
1:B:44:VAL:HG12	1:B:65:ILE:HG12	1.94	0.49
1:B:331:TPO:P	6:B:803:HOH:O	2.70	0.49
1:B:70:VAL:O	1:B:74:GLU:HG3	2.14	0.47
1:B:287:LEU:HD21	1:B:402:TYR:HA	1.96	0.47
1:B:120:GLU:HB2	1:B:131:LEU:HD12	1.96	0.47
1:B:13:ASP:HA	1:B:16:MET:HE2	1.96	0.47
1:A:122:ILE:HG23	1:A:125:VAL:HG23	1.97	0.46
1:A:122:ILE:HG23	1:A:125:VAL:CG2	2.46	0.46
1:A:120:GLU:OE2	1:A:122:ILE:HG22	2.17	0.45
1:A:282:ILE:HD12	1:A:282:ILE:N	2.30	0.45
1:A:536:PRO:HA	1:A:587:GLN:O	2.16	0.45
1:A:236:LYS:HD3	1:A:237:TYR:CE2	2.52	0.44
1:A:251:GLU:OE2	5:A:707:EDO:H11	2.17	0.44
1:A:331:TPO:OG1	5:A:707:EDO:O1	2.31	0.44
1:B:259:GLN:O	1:B:262:ILE:HB	2.18	0.44
1:A:74:GLU:HG2	1:A:565:ARG:NH1	2.33	0.43
1:A:34:MET:HE3	1:A:66:TYR:CZ	2.53	0.43
1:A:117:LEU:C	1:A:117:LEU:HD23	2.44	0.42
1:A:297:ILE:C	1:A:298:LEU:HD12	2.44	0.42
1:B:614:THR:CG2	6:B:1029:HOH:O	2.66	0.42
1:B:537:LEU:C	1:B:537:LEU:CD1	2.92	0.42
1:A:44:VAL:HG12	1:A:65:ILE:HG12	2.01	0.42
1:B:206:TRP:CZ2	1:B:218:GLY:HA3	2.55	0.42
1:B:566:TRP:O	1:B:568:GLU:HG3	2.19	0.42
1:B:134:GLU:OE1	1:B:138:ARG:NH1	2.53	0.41
1:A:565:ARG:HH21	1:A:567:ASP:CG	2.28	0.41
1:A:298:LEU:HD12	1:A:298:LEU:N	2.35	0.41
1:A:589:GLU:O	1:A:590:ILE:CB	2.67	0.41
1:B:120:GLU:OE1	1:B:121:PRO:HD2	2.20	0.41
1:A:7:PHE:CE1	1:A:32:LEU:HD22	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:ASP:OD2	6:A:802:HOH:O	2.21	0.41
1:B:244:TYR:HB3	1:B:245:PRO:HD2	2.03	0.41
1:B:111:THR:O	1:B:112:ALA:C	2.64	0.41
1:A:36:PHE:CD2	1:A:41:VAL:HG21	2.56	0.40
1:B:76:HIS:HA	1:B:133:PHE:CE1	2.56	0.40
1:A:206:TRP:CZ2	1:A:218:GLY:HA3	2.57	0.40
1:B:494:ASN:OD1	1:B:494:ASN:C	2.64	0.40
1:A:468:THR:N	1:A:469:PRO:CD	2.84	0.40
1:B:172:HIS:NE2	1:B:331:TPO:O2P	2.55	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	591/638 (93%)	564 (95%)	23 (4%)	4 (1%)	18	14
1	B	571/638 (90%)	552 (97%)	16 (3%)	3 (0%)	24	21
All	All	1162/1276 (91%)	1116 (96%)	39 (3%)	7 (1%)	21	17

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	590	ILE
1	A	52	ARG
1	A	316	ARG
1	B	106	GLU
1	B	327	GLU
1	B	53	LYS
1	A	54	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	515/573 (90%)	503 (98%)	12 (2%)	44	49
1	B	495/573 (86%)	483 (98%)	12 (2%)	43	47
All	All	1010/1146 (88%)	986 (98%)	24 (2%)	44	47

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	LEU
1	A	38	LEU
1	A	54	ILE
1	A	86	ARG
1	A	92	THR
1	A	124	GLU
1	A	179	ASP
1	A	210	ASN
1	A	284	VAL
1	A	512	SER
1	A	533	LYS
1	A	537	LEU
1	B	4	ASN
1	B	12	GLN
1	B	50	ASP
1	B	117	LEU
1	B	154[A]	THR
1	B	154[B]	THR
1	B	281	ASP
1	B	514	SER
1	B	535	ASP
1	B	537	LEU
1	B	571	SER
1	B	613	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	HIS
1	A	73	ASN
1	A	232	HIS
1	A	473	GLN
1	B	232	HIS
1	B	252	ASN
1	B	398	HIS
1	B	418	HIS
1	B	449	GLN
1	B	575	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	TPO	A	331	3,1	8,10,11	0.70	0	10,14,16	0.86	0
1	TPO	B	331	3,1	8,10,11	0.84	0	10,14,16	0.87	0
1	SEP	A	326	1	8,9,10	0.69	0	7,12,14	0.74	0
1	SEP	B	326	1	8,9,10	0.65	0	7,12,14	0.67	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
1	TPO	A	331	3,1	-	2/9/11/13	-
1	TPO	B	331	3,1	-	1/9/11/13	-
1	SEP	A	326	1	-	2/6/8/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SEP	B	326	1	-	1/6/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	331	TPO	O-C-CA-CB
1	B	326	SEP	C-CA-CB-OG
1	A	331	TPO	CB-OG1-P-O2P
1	A	326	SEP	CB-OG-P-O3P
1	A	326	SEP	CA-CB-OG-P
1	B	331	TPO	C-CA-CB-CG2

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	331	TPO	1	0
1	B	331	TPO	2	0
1	B	326	SEP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 7 are monoatomic and 4 are unknown - leaving 2 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
5	EDO	A	707	-	3,3,3	0.06	0	2,2,2	0.14	0
5	EDO	B	706	-	3,3,3	0.13	0	2,2,2	0.06	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
5	EDO	A	707	-	-	0/1/1/1	-
5	EDO	B	706	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	706	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	707	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	593/638 (92%)	0.39	49 (8%) 17 16	13, 36, 82, 114	4 (0%)
1	B	580/638 (90%)	0.58	64 (11%) 10 9	15, 38, 85, 116	1 (0%)
All	All	1173/1276 (91%)	0.48	113 (9%) 13 12	13, 37, 83, 116	5 (0%)

All (113) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	534	ALA	6.8
1	B	282	ILE	6.4
1	B	635	TRP	6.2
1	B	130	GLN	5.2
1	A	590	ILE	5.1
1	B	6	TRP	4.9
1	A	525	PRO	4.9
1	A	532	ASN	4.7
1	A	524	PRO	4.7
1	B	637	TYR	4.6
1	A	6	TRP	4.6
1	B	307	ILE	4.3
1	B	8	LEU	4.2
1	B	113	LEU	4.2
1	B	122	ILE	4.2
1	B	89	LEU	4.2
1	B	92	THR	4.1
1	A	592	LEU	4.1
1	A	282	ILE	4.0
1	A	117	LEU	4.0
1	B	117	LEU	3.8
1	B	525	PRO	3.7
1	A	54	ILE	3.7
1	B	90	ALA	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	54	ILE	3.6
1	B	332	SER	3.5
1	B	318	SER	3.5
1	B	310	THR	3.5
1	B	312	LEU	3.5
1	B	84	GLU	3.4
1	B	131	LEU	3.4
1	B	304	CYS	3.3
1	B	330	ILE	3.3
1	B	91	ASP	3.3
1	B	7	PHE	3.3
1	A	332	SER	3.3
1	A	122	ILE	3.2
1	A	330	ILE	3.2
1	B	211	ASN	3.2
1	B	80	CYS	3.2
1	B	284	VAL	3.1
1	B	94	LEU	3.0
1	B	5	ARG	3.0
1	B	16	MET	3.0
1	B	125	VAL	3.0
1	A	125	VAL	3.0
1	A	105	THR	3.0
1	B	115	VAL	2.9
1	A	22	PHE	2.9
1	A	16	MET	2.8
1	A	131	LEU	2.8
1	B	322	THR	2.8
1	B	324	GLU	2.8
1	A	90	ALA	2.8
1	B	272	ASP	2.8
1	B	85	ASN	2.7
1	A	38	LEU	2.7
1	A	7	PHE	2.7
1	A	86	ARG	2.7
1	B	319	HIS	2.7
1	A	108	ALA	2.6
1	A	594	ALA	2.6
1	A	311	MET	2.6
1	B	88	ASN	2.6
1	A	307	ILE	2.6
1	B	595	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	313	ARG	2.6
1	A	47	LYS	2.5
1	B	311	MET	2.5
1	B	82	TYR	2.4
1	B	329	GLU	2.4
1	A	335	GLU	2.4
1	B	317	ASP	2.4
1	A	319	HIS	2.4
1	A	315	GLY	2.4
1	A	89	LEU	2.3
1	A	129	ARG	2.3
1	B	95	THR	2.3
1	B	323	GLY	2.3
1	B	325	VAL	2.3
1	A	523	LEU	2.3
1	B	267	LEU	2.3
1	B	97	PHE	2.3
1	B	121	PRO	2.3
1	A	504	VAL	2.2
1	B	371	MET	2.2
1	B	126	ARG	2.2
1	A	11	ILE	2.2
1	A	20	ILE	2.2
1	A	113	LEU	2.2
1	A	334	ASP	2.2
1	A	79	PHE	2.2
1	B	103	PHE	2.2
1	A	4	ASN	2.2
1	B	4	ASN	2.2
1	A	49	VAL	2.2
1	B	588	ASP	2.2
1	B	135	GLY	2.2
1	A	314	LYS	2.1
1	B	86	ARG	2.1
1	B	108	ALA	2.1
1	A	121	PRO	2.1
1	A	312	LEU	2.1
1	B	112	ALA	2.1
1	A	127	LYS	2.1
1	A	370	LYS	2.0
1	B	18	GLY	2.0
1	A	28	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	333	SER	2.0
1	A	591	SER	2.0
1	A	595	ASN	2.0
1	B	129	ARG	2.0
1	B	316	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	TPO	B	331	11/12	0.84	0.20	71,84,92,97	0
1	SEP	B	326	10/11	0.91	0.15	70,80,85,87	0
1	SEP	A	326	10/11	0.92	0.09	47,52,60,67	0
1	TPO	A	331	11/12	0.92	0.11	52,72,75,76	0

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(Å ²)	Q<0.9
5	EDO	B	706	4/4	0.83	0.21	47,56,56,58	0
5	EDO	A	707	4/4	0.91	0.14	37,42,47,48	0
4	UNX	B	705	1/1	0.91	0.18	39,39,39,39	0
4	UNX	A	704	1/1	0.93	0.12	27,27,27,27	0
4	UNX	A	705	1/1	0.95	0.16	34,34,34,34	0
3	CA	B	703	1/1	0.95	0.06	65,65,65,65	0
3	CA	A	702	1/1	0.96	0.06	67,67,67,67	0
4	UNX	A	706	1/1	0.98	0.10	18,18,18,18	0
2	CL	B	702	1/1	0.98	0.07	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CL	B	701	1/1	0.99	0.06	24,24,24,24	0
2	CL	A	701	1/1	0.99	0.04	26,26,26,26	0
3	CA	B	704	1/1	0.99	0.02	29,29,29,29	0
3	CA	A	703	1/1	1.00	0.03	31,31,31,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.