



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:54 AM UTC

PDB ID : 4TN0 / pdb_00004tn0
Title : Crystal Structure of the C-terminal Periplasmic Domain of Phosphoethanolamine Transferase EptC from *Campylobacter jejuni*
Authors : Fage, C.D.; Brown, D.; Boll, J.M.; Keatinge-Clay, A.T.; Trent, M.S.
Deposited on : 2014-06-02
Resolution : 2.40 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	:	9.0.010 (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

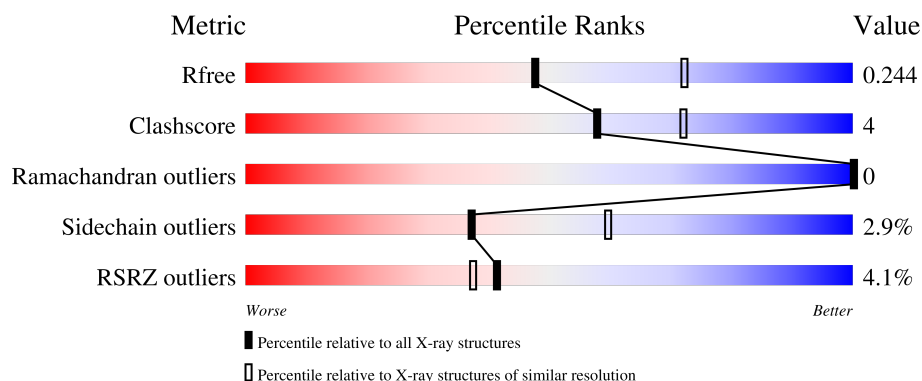
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	325	4% 81% 13% • 5%
1	B	325	4% 82% 12% • 6%
1	C	325	4% 80% 14% • 5%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7411 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 UPF0141 protein yjdB.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	308	Total	C	N	O	P	S	0	0	0
			2467	1574	398	483	1	11			
1	B	307	Total	C	N	O	P	S	0	0	0
			2456	1568	394	482	1	11			
1	C	308	Total	C	N	O	P	S	0	0	0
			2467	1574	398	483	1	11			

There are 45 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	202	MET	-	initiating methionine	UNP A3ZEY5
A	513	GLY	-	expression tag	UNP A3ZEY5
A	514	GLY	-	expression tag	UNP A3ZEY5
A	515	GLY	-	expression tag	UNP A3ZEY5
A	516	GLY	-	expression tag	UNP A3ZEY5
A	517	GLY	-	expression tag	UNP A3ZEY5
A	518	GLY	-	expression tag	UNP A3ZEY5
A	519	HIS	-	expression tag	UNP A3ZEY5
A	520	HIS	-	expression tag	UNP A3ZEY5
A	521	HIS	-	expression tag	UNP A3ZEY5
A	522	HIS	-	expression tag	UNP A3ZEY5
A	523	HIS	-	expression tag	UNP A3ZEY5
A	524	HIS	-	expression tag	UNP A3ZEY5
A	525	HIS	-	expression tag	UNP A3ZEY5
A	526	HIS	-	expression tag	UNP A3ZEY5
B	202	MET	-	initiating methionine	UNP A3ZEY5
B	513	GLY	-	expression tag	UNP A3ZEY5
B	514	GLY	-	expression tag	UNP A3ZEY5
B	515	GLY	-	expression tag	UNP A3ZEY5
B	516	GLY	-	expression tag	UNP A3ZEY5
B	517	GLY	-	expression tag	UNP A3ZEY5
B	518	GLY	-	expression tag	UNP A3ZEY5
B	519	HIS	-	expression tag	UNP A3ZEY5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	520	HIS	-	expression tag	UNP A3ZEY5
B	521	HIS	-	expression tag	UNP A3ZEY5
B	522	HIS	-	expression tag	UNP A3ZEY5
B	523	HIS	-	expression tag	UNP A3ZEY5
B	524	HIS	-	expression tag	UNP A3ZEY5
B	525	HIS	-	expression tag	UNP A3ZEY5
B	526	HIS	-	expression tag	UNP A3ZEY5
C	202	MET	-	initiating methionine	UNP A3ZEY5
C	513	GLY	-	expression tag	UNP A3ZEY5
C	514	GLY	-	expression tag	UNP A3ZEY5
C	515	GLY	-	expression tag	UNP A3ZEY5
C	516	GLY	-	expression tag	UNP A3ZEY5
C	517	GLY	-	expression tag	UNP A3ZEY5
C	518	GLY	-	expression tag	UNP A3ZEY5
C	519	HIS	-	expression tag	UNP A3ZEY5
C	520	HIS	-	expression tag	UNP A3ZEY5
C	521	HIS	-	expression tag	UNP A3ZEY5
C	522	HIS	-	expression tag	UNP A3ZEY5
C	523	HIS	-	expression tag	UNP A3ZEY5
C	524	HIS	-	expression tag	UNP A3ZEY5
C	525	HIS	-	expression tag	UNP A3ZEY5
C	526	HIS	-	expression tag	UNP A3ZEY5

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

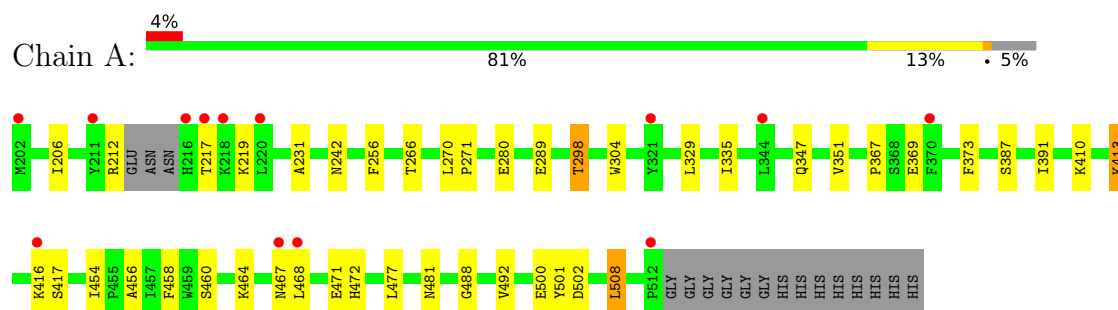
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	7	Total O 7 7	0	0
3	B	10	Total O 10 10	0	0
3	C	1	Total O 1 1	0	0

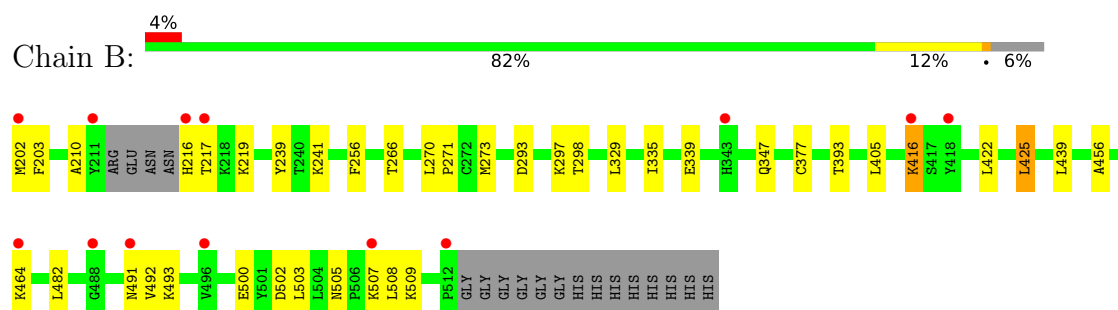
3 Residue-property plots [i](#)

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.

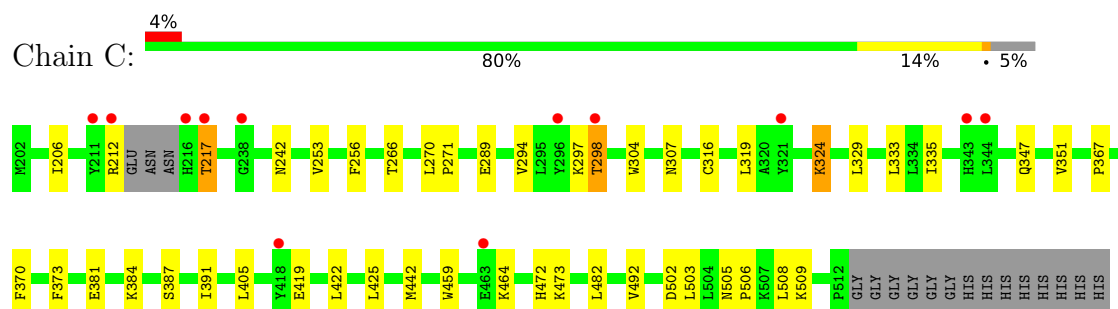
• Molecule 1: UPF0141 protein yjdB



• Molecule 1: UPF0141 protein yjdB



• Molecule 1: UPF0141 protein yjdB



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	121.85Å 183.14Å 121.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.58 – 2.40 54.58 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.7 (54.58-2.40) 99.6 (54.58-2.40)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 2.40Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.215 , 0.256 (Not available) , 0.244	Depositor DCC
R_{free} test set	2703 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	39.4	Xtriage
Anisotropy	0.729	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 31.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7411	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.99% 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: ZN, TPO

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	0.56	0/2512	0.87	4/3396 (0.1%)
1	B	0.57	0/2501	0.86	2/3382 (0.1%)
1	C	0.55	0/2512	0.85	2/3396 (0.1%)
All	All	0.56	0/7525	0.86	8/10174 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	335	ILE	CA-C-N	-5.71	113.80	119.56
1	C	335	ILE	C-N-CA	-5.71	113.80	119.56
1	A	417	SER	N-CA-C	-5.48	106.43	113.01
1	B	335	ILE	CA-C-N	-5.41	114.09	119.56
1	B	335	ILE	C-N-CA	-5.41	114.09	119.56
1	A	464	LYS	N-CA-C	-5.24	107.02	113.41
1	A	335	ILE	CA-C-N	-5.03	114.48	119.56
1	A	335	ILE	C-N-CA	-5.03	114.48	119.56

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	2467	0	2390	20	0
1	B	2456	0	2377	20	0
1	C	2467	0	2390	25	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	7	0	0	0	0
3	B	10	0	0	0	0
3	C	1	0	0	0	0
All	All	7411	0	7157	65	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 (65) 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:413:LYS:HA	1:A:416:LYS:HE3	1.62	0.82
1:B:505:ASN:OD1	1:B:507:LYS:HG3	1.88	0.73
1:A:217:THR:O	1:A:347:GLN:NE2	2.27	0.68
1:C:503:LEU:HA	1:C:508:LEU:HD22	1.80	0.64
1:C:212:ARG:HG3	1:C:298:THR:HG23	1.80	0.63
1:C:217:THR:O	1:C:347:GLN:NE2	2.31	0.63
1:A:212:ARG:HD3	1:A:298:THR:HG22	1.80	0.63
1:B:217:THR:O	1:B:347:GLN:NE2	2.34	0.60
1:B:256:PHE:HB2	1:B:456:ALA:HB3	1.84	0.60
1:C:294:VAL:O	1:C:298:THR:HB	2.02	0.59
1:A:219:LYS:HB2	1:A:347:GLN:HG3	1.86	0.58
1:A:387:SER:O	1:A:391:ILE:HG12	2.05	0.56
1:B:500:GLU:OE1	1:B:500:GLU:N	2.33	0.56
1:C:298:THR:HG21	1:C:492:VAL:HG22	1.88	0.54
1:A:367:PRO:HB2	1:A:369:GLU:OE1	2.09	0.53
1:B:210:ALA:HA	1:B:493:LYS:O	2.08	0.53
1:B:500:GLU:HA	1:B:508:LEU:HA	1.90	0.52
1:B:503:LEU:HA	1:B:508:LEU:HD22	1.93	0.51
1:B:502:ASP:HB3	1:B:505:ASN:HB3	1.93	0.50
1:A:488:GLY:HA3	1:A:502:ASP:OD1	2.11	0.49
1:C:307:ASN:HB2	1:C:333:LEU:HD21	1.95	0.49
1:A:477:LEU:HD21	1:A:508:LEU:HD11	1.95	0.48
1:B:270:LEU:HB3	1:B:271:PRO:HD3	1.95	0.48
1:C:206:ILE:O	1:C:297:LYS:NZ	2.47	0.48
1:C:316:CYS:HA	1:C:319:LEU:HD13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:202:MET:HG2	1:B:203:PHE:N	2.29	0.47
1:A:206:ILE:HG12	1:A:289:GLU:HB2	1.97	0.47
1:C:212:ARG:HD3	1:C:298:THR:O	2.14	0.47
1:A:256:PHE:HB2	1:A:456:ALA:HB3	1.95	0.46
1:B:298:THR:HG21	1:B:492:VAL:HG22	1.97	0.46
1:C:324:LYS:HE2	1:C:324:LYS:HB3	1.75	0.46
1:C:304:TRP:CZ3	1:C:351:VAL:HG11	2.51	0.46
1:C:270:LEU:HB3	1:C:271:PRO:HD3	1.97	0.46
1:C:253:VAL:HG12	1:C:459:TRP:HB2	1.99	0.45
1:C:405:LEU:HD22	1:C:422:LEU:HD21	1.97	0.45
1:A:270:LEU:HB3	1:A:271:PRO:HD3	1.99	0.45
1:A:231:ALA:HB2	1:A:454:ILE:C	2.41	0.45
1:B:405:LEU:HD22	1:B:422:LEU:HD21	2.00	0.44
1:B:464:LYS:O	1:B:464:LYS:HG2	2.16	0.44
1:C:212:ARG:HG3	1:C:298:THR:CG2	2.47	0.44
1:C:387:SER:O	1:C:391:ILE:HG12	2.18	0.44
1:C:212:ARG:NH2	1:C:347:GLN:OE1	2.45	0.44
1:C:256:PHE:CD2	1:C:473:LYS:HA	2.54	0.43
1:A:298:THR:HG21	1:A:492:VAL:HG22	2.00	0.43
1:B:377:CYS:H	1:B:393:THR:HG1	1.65	0.43
1:A:472:HIS:CD2	1:A:508:LEU:HD12	2.54	0.43
1:A:468:LEU:O	1:A:472:HIS:ND1	2.52	0.42
1:C:472:HIS:CG	1:C:508:LEU:HD23	2.54	0.42
1:B:216:HIS:HB2	1:B:347:GLN:HE22	1.84	0.42
1:B:239:TYR:CZ	1:B:241:LYS:HB3	2.54	0.42
1:C:505:ASN:HA	1:C:506:PRO:HD3	1.82	0.42
1:C:381:GLU:OE1	1:C:384:LYS:HD2	2.19	0.42
1:C:367:PRO:HG2	1:C:370:PHE:HD2	1.85	0.42
1:C:502:ASP:HB3	1:C:505:ASN:HB3	2.02	0.42
1:A:458:PHE:CZ	1:A:460:SER:HB2	2.55	0.42
1:B:293:ASP:O	1:B:297:LYS:HG3	2.20	0.41
1:A:467:ASN:O	1:A:471:GLU:HG3	2.20	0.41
1:B:416:LYS:H	1:B:416:LYS:HG3	1.39	0.41
1:A:242:ASN:HB3	1:A:373:PHE:CZ	2.56	0.41
1:B:219:LYS:NZ	1:B:491:ASN:OD1	2.54	0.41
1:C:242:ASN:HB3	1:C:373:PHE:CZ	2.56	0.41
1:C:206:ILE:HG12	1:C:289:GLU:HB2	2.03	0.40
1:A:304:TRP:CZ3	1:A:351:VAL:HG11	2.57	0.40
1:A:481:ASN:ND2	1:A:501:TYR:HD2	2.20	0.40
1:B:273:MET:SD	1:B:425:LEU:HD21	2.62	0.40

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	303/325 (93%)	292 (96%)	11 (4%)	0	100	100
1	B	302/325 (93%)	292 (97%)	10 (3%)	0	100	100
1	C	303/325 (93%)	295 (97%)	8 (3%)	0	100	100
All	All	908/975 (93%)	879 (97%)	29 (3%)	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	A	274/285 (96%)	267 (97%)	7 (3%)	40	63
1	B	273/285 (96%)	266 (97%)	7 (3%)	40	63
1	C	274/285 (96%)	264 (96%)	10 (4%)	31	52
All	All	821/855 (96%)	797 (97%)	24 (3%)	37	60

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

Mol	Chain	Res	Type
1	A	280	GLU
1	A	298	THR
1	A	329	LEU
1	A	410	LYS
1	A	413	LYS

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Mol	Chain	Res	Type
1	A	500	GLU
1	A	508	LEU
1	B	329	LEU
1	B	339	GLU
1	B	416	LYS
1	B	425	LEU
1	B	439	LEU
1	B	482	LEU
1	B	509	LYS
1	C	217	THR
1	C	298	THR
1	C	324	LYS
1	C	329	LEU
1	C	419	GLU
1	C	425	LEU
1	C	442	MET
1	C	464	LYS
1	C	482	LEU
1	C	509	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	208	ASN
1	A	467	ASN
1	B	208	ASN
1	B	347	GLN
1	B	467	ASN
1	B	481	ASN
1	B	511	ASN
1	C	208	ASN
1	C	281	ASN
1	C	323	GLN
1	C	343	HIS
1	C	511	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 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	266	2,1	8,10,11	1.08	1 (12%)	10,14,16	1.19	1 (10%)
1	TPO	B	266	2,1	8,10,11	1.15	1 (12%)	10,14,16	1.50	3 (30%)
1	TPO	C	266	2,1	8,10,11	1.18	1 (12%)	10,14,16	1.44	1 (10%)

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	266	2,1	-	1/9/11/13	-
1	TPO	B	266	2,1	-	4/9/11/13	-
1	TPO	C	266	2,1	-	3/9/11/13	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	266	TPO	P-OG1	2.62	1.64	1.59
1	A	266	TPO	P-OG1	2.53	1.64	1.59
1	C	266	TPO	P-OG1	2.40	1.63	1.59

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	266	TPO	CG2-CB-CA	-2.66	108.08	113.26
1	B	266	TPO	CG2-CB-CA	-2.30	108.77	113.26
1	B	266	TPO	O-C-CA	-2.24	119.00	124.77
1	A	266	TPO	CG2-CB-CA	-2.12	109.13	113.26
1	B	266	TPO	P-OG1-CB	2.04	128.87	123.33

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C	266	TPO	O-C-CA-CB
1	B	266	TPO	C-CA-CB-CG2
1	C	266	TPO	C-CA-CB-CG2
1	B	266	TPO	CB-OG1-P-O3P
1	A	266	TPO	O-C-CA-CB
1	B	266	TPO	O-C-CA-CB
1	B	266	TPO	N-CA-CB-CG2
1	C	266	TPO	N-CA-CB-CG2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	307/325 (94%)	0.37	13 (4%) 40 36	26, 49, 73, 86	0
1	B	306/325 (94%)	0.32	13 (4%) 40 36	26, 45, 76, 83	0
1	C	307/325 (94%)	0.43	12 (3%) 43 39	30, 48, 76, 87	0
All	All	920/975 (94%)	0.37	38 (4%) 41 37	26, 48, 75, 87	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	321	TYR	6.5
1	A	321	TYR	4.6
1	B	211	TYR	4.3
1	C	216	HIS	4.3
1	B	216	HIS	4.0
1	C	212	ARG	3.7
1	A	216	HIS	3.6
1	C	217	THR	3.2
1	C	343	HIS	3.1
1	C	211	TYR	2.9
1	B	343	HIS	2.8
1	B	416	LYS	2.7
1	A	202	MET	2.7
1	A	512	PRO	2.6
1	A	217	THR	2.5
1	B	488	GLY	2.5
1	A	211	TYR	2.5
1	B	217	THR	2.4
1	C	238	GLY	2.3
1	C	418	TYR	2.3
1	A	416	LYS	2.3
1	A	344	LEU	2.2
1	A	370	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	507	LYS	2.2
1	A	220	LEU	2.2
1	B	491	ASN	2.1
1	A	468	LEU	2.1
1	B	464	LYS	2.1
1	B	496	VAL	2.1
1	C	344	LEU	2.1
1	C	296	TYR	2.1
1	B	418	TYR	2.1
1	A	467	ASN	2.0
1	C	463	GLU	2.0
1	A	218	LYS	2.0
1	C	298	THR	2.0
1	B	512	PRO	2.0
1	B	202	MET	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	C	266	11/12	0.92	0.10	41,43,55,57	0
1	TPO	A	266	11/12	0.94	0.09	32,36,41,46	0
1	TPO	B	266	11/12	0.95	0.07	33,40,50,55	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($\text{\AA}^2$)	Q<0.9
2	ZN	B	601	1/1	0.98	0.10	34,34,34,34	1
2	ZN	C	601	1/1	0.98	0.05	38,38,38,38	1
2	ZN	A	601	1/1	0.99	0.09	33,33,33,33	1

6.5 Other polymers [i](#)

There are no such residues in this entry.