



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 01:33 PM UTC

PDB ID : 5LR8 / pdb_00005lr8
Title : Structure of plastidial phosphorylase Pho1 from Barley
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Deposited on : 2016-08-18
Resolution : 2.70 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 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

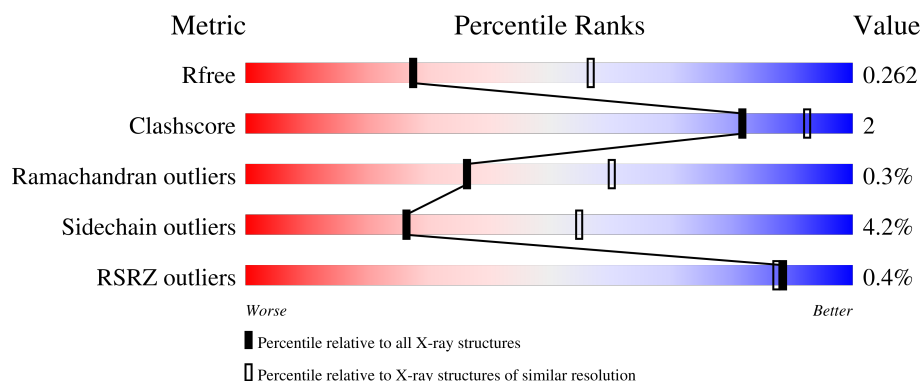
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	938	 82% 7% • 10%
1	B	938	 81% 8% • 10%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13695 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-1,4 glucan phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	844	Total	C	N	O	S	0	5	0
			6753	4301	1148	1274	30			
1	B	843	Total	C	N	O	S	0	7	0
			6751	4302	1145	1273	31			

There are 26 discrepancies between the modelled and reference sequences:

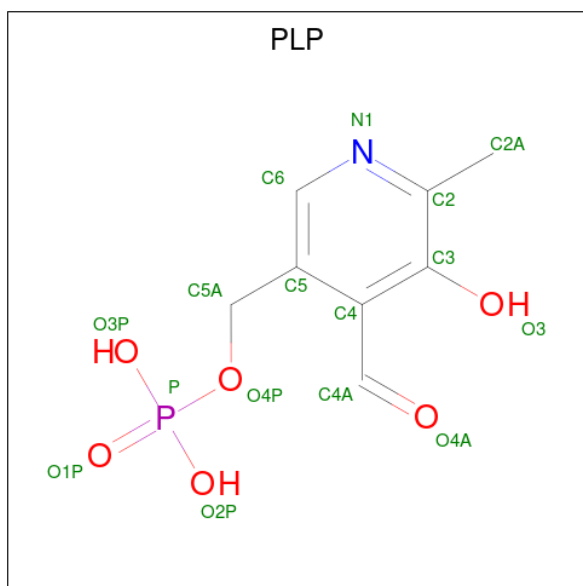
Chain	Residue	Modelled	Actual	Comment	Reference
A	43	MET	-	initiating methionine	UNP F2E0G2
A	969	THR	-	expression tag	UNP F2E0G2
A	970	PHE	-	expression tag	UNP F2E0G2
A	971	PRO	-	expression tag	UNP F2E0G2
A	972	ASP	-	expression tag	UNP F2E0G2
A	973	ILE	-	expression tag	UNP F2E0G2
A	974	GLU	-	expression tag	UNP F2E0G2
A	975	ASN	-	expression tag	UNP F2E0G2
A	976	LEU	-	expression tag	UNP F2E0G2
A	977	TYR	-	expression tag	UNP F2E0G2
A	978	PHE	-	expression tag	UNP F2E0G2
A	979	GLN	-	expression tag	UNP F2E0G2
A	980	GLY	-	expression tag	UNP F2E0G2
B	43	MET	-	initiating methionine	UNP F2E0G2
B	969	THR	-	expression tag	UNP F2E0G2
B	970	PHE	-	expression tag	UNP F2E0G2
B	971	PRO	-	expression tag	UNP F2E0G2
B	972	ASP	-	expression tag	UNP F2E0G2
B	973	ILE	-	expression tag	UNP F2E0G2
B	974	GLU	-	expression tag	UNP F2E0G2
B	975	ASN	-	expression tag	UNP F2E0G2
B	976	LEU	-	expression tag	UNP F2E0G2
B	977	TYR	-	expression tag	UNP F2E0G2
B	978	PHE	-	expression tag	UNP F2E0G2
B	979	GLN	-	expression tag	UNP F2E0G2

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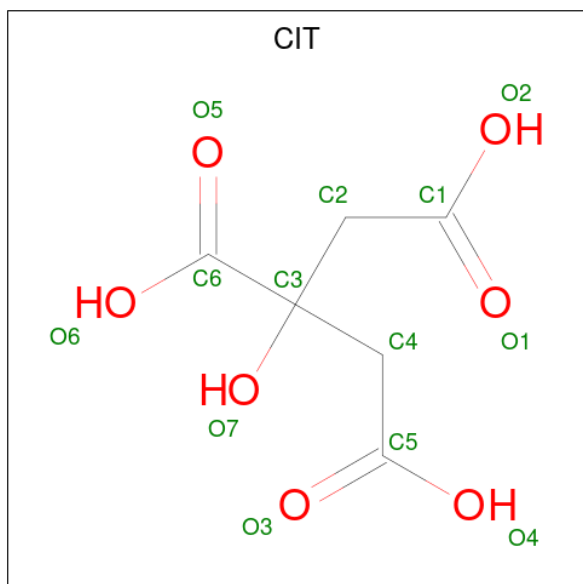
Chain	Residue	Modelled	Actual	Comment	Reference
B	980	GLY	-	expression tag	UNP F2E0G2

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: PLP) (formula: $C_8H_{10}NO_6P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 3 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	69	Total	O	0	0
			69	69		
4	B	79	Total	O	0	0
			79	79		

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.

- [illegible]

- [illegible]

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	229.21Å 63.48Å 148.82Å 90.00° 115.21° 90.00°	Depositor
Resolution (Å)	50.00 – 2.70 50.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.4 (50.00-2.70) 99.4 (50.00-2.70)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.15 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.217 , 0.257 0.223 , 0.262	Depositor DCC
R_{free} test set	1600 reflections (3.00%)	wwPDB-VP
Wilson B-factor (Å ²)	62.1	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 39.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13695	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 52.37 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.9083e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: CIT, PLP

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	0.42	0/6923	0.73	0/9376
1	B	0.41	0/6927	0.73	0/9382
All	All	0.42	0/13850	0.73	0/18758

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	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	257	THR	Peptide

5.2 Too-close contacts [i](#)

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	6753	0	6651	31	0
1	B	6751	0	6650	36	0
2	A	15	0	6	0	0
2	B	15	0	6	1	0
3	A	13	0	5	0	0
4	A	69	0	0	0	0
4	B	79	0	0	0	0
All	All	13695	0	13318	67	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 2.

All (67) 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:455:MET:HE1	1:A:485:LEU:HD22	1.60	0.82
1:B:258:ASP:O	1:B:260:ARG:N	2.16	0.79
1:B:455:MET:HE1	1:B:485:LEU:HD22	1.71	0.71
1:B:926:TYR:O	1:B:929:GLN:NE2	2.24	0.69
1:B:257:THR:O	1:B:258:ASP:HB2	1.92	0.67
1:B:258:ASP:C	1:B:260:ARG:H	2.04	0.65
1:A:455:MET:HE1	1:A:485:LEU:CD2	2.29	0.60
1:A:258:ASP:O	1:A:260:ARG:N	2.36	0.59
1:B:177:ALA:HB1	1:B:211:GLY:HA3	1.85	0.59
1:A:177:ALA:HB1	1:A:211:GLY:HA3	1.85	0.58
1:B:258:ASP:C	1:B:260:ARG:N	2.58	0.58
1:B:467:ILE:O	1:B:470:LEU:N	2.37	0.57
1:A:878:ARG:NH2	1:A:895:GLU:OE2	2.40	0.55
1:B:633:SER:O	1:B:637:GLY:O	2.25	0.55
1:A:636:ILE:HD11	1:A:651:LEU:HD13	1.89	0.54
1:A:69:ILE:HG23	1:A:69:ILE:O	2.08	0.54
1:B:943:SER:N	1:B:944:PRO:CD	2.71	0.53
1:B:146:ILE:CG2	1:B:152:THR:HA	2.39	0.53
1:A:281:TYR:CE2	1:A:282:LYS:HG3	2.45	0.52
1:A:258:ASP:C	1:A:260:ARG:H	2.17	0.52
1:A:697:VAL:HG13	1:A:782:TYR:CZ	2.45	0.51
1:A:943:SER:N	1:A:944:PRO:CD	2.73	0.50
1:B:697:VAL:HG13	1:B:782:TYR:CZ	2.46	0.50
1:B:281:TYR:CE2	1:B:282:LYS:HG3	2.47	0.50
1:A:454:LEU:HD22	1:A:576:VAL:HG21	1.95	0.48
1:B:638:SER:HB3	1:B:640:ASP:H	1.79	0.47
1:B:475:LYS:O	1:B:569:ARG:NH1	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:437:GLN:HG2	1:B:444:VAL:HG11	1.97	0.47
1:A:578:GLY:O	1:A:607:LYS:HE3	2.16	0.46
1:A:146:ILE:CG2	1:A:152:THR:HA	2.46	0.46
1:B:461:LYS:HD3	1:B:603:MET:HE3	1.98	0.46
1:A:802:THR:HB	1:A:805:MET:HG3	1.97	0.46
1:B:455:MET:HE1	1:B:485:LEU:CD2	2.43	0.45
1:B:697:VAL:CG1	1:B:697:VAL:O	2.64	0.45
1:B:257:THR:O	1:B:257:THR:HG23	2.16	0.45
1:A:636:ILE:CD1	1:A:651:LEU:HD13	2.47	0.45
1:A:668:LYS:O	1:A:672:LYS:HG3	2.17	0.45
1:A:752[B]:ARG:NH2	1:A:889:GLU:HG2	2.32	0.45
1:B:694:ASP:OD1	1:B:694:ASP:C	2.59	0.45
1:B:942:GLY:C	1:B:944:PRO:HD2	2.42	0.45
1:B:734:PRO:HA	1:B:773:LEU:O	2.17	0.44
1:B:802:THR:HB	1:B:805:MET:HG3	1.99	0.44
1:A:464:THR:OG1	1:A:465:ALA:N	2.50	0.44
1:B:258:ASP:O	1:B:260:ARG:HG2	2.18	0.44
1:A:258:ASP:C	1:A:260:ARG:N	2.76	0.43
1:A:942:GLY:C	1:A:944:PRO:HD2	2.43	0.43
1:A:812:ASN:OD1	1:A:812:ASN:N	2.52	0.43
1:B:463:GLY:O	1:B:464:THR:HG23	2.19	0.43
1:B:135:GLU:HB3	1:B:184:GLY:HA3	2.01	0.42
1:A:710:ILE:O	1:A:714:VAL:HG23	2.20	0.41
1:A:733:VAL:HG11	1:A:926:TYR:CD2	2.56	0.41
1:B:353:LEU:O	1:B:357:ILE:HG12	2.20	0.41
1:A:694:ASP:OD1	1:A:694:ASP:C	2.62	0.41
1:A:886:ASN:HD22	1:A:886:ASN:H	1.68	0.41
1:B:578:GLY:O	1:B:607:LYS:HE3	2.20	0.41
1:B:691:ALA:HB3	1:B:736:VAL:HG23	2.02	0.41
1:A:876:TYR:O	1:A:879:SER:HB3	2.21	0.41
1:B:92:HIS:HE2	1:B:94:SER:HG	1.67	0.41
1:B:463:GLY:O	1:B:464:THR:OG1	2.33	0.41
1:B:791:ILE:HB	1:B:792:PRO:HD3	2.03	0.41
1:A:697:VAL:HG12	1:A:697:VAL:O	2.21	0.41
1:B:208:TYR:CE2	1:B:328:LEU:HD13	2.57	0.40
1:B:661:GLN:O	1:B:665:ARG:HG3	2.21	0.40
1:B:811:SER:OG	2:B:1001:PLP:O2P	2.31	0.40
1:A:323:LYS:HA	1:A:326:HIS:CG	2.57	0.40
1:A:433:LEU:O	1:A:437:GLN:HB2	2.21	0.40
1:A:697:VAL:O	1:A:697:VAL:CG1	2.69	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	845/938 (90%)	802 (95%)	41 (5%)	2 (0%)	43	68
1	B	846/938 (90%)	807 (95%)	36 (4%)	3 (0%)	30	54
All	All	1691/1876 (90%)	1609 (95%)	77 (5%)	5 (0%)	36	60

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	258	ASP
1	B	259	GLY
1	B	464	THR
1	A	259	GLY
1	A	464	THR

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	731/810 (90%)	696 (95%)	35 (5%)	23	50
1	B	731/810 (90%)	702 (96%)	29 (4%)	28	56
All	All	1462/1620 (90%)	1398 (96%)	64 (4%)	26	53

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	ILE

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Mol	Chain	Res	Type
1	A	72	SER
1	A	87	LEU
1	A	154	GLN
1	A	183	LEU
1	A	209	ARG
1	A	216	ILE
1	A	219	LYS
1	A	222	GLN
1	A	225	VAL
1	A	248	LYS
1	A	260	ARG
1	A	270	LYS
1	A	371	GLU
1	A	388	LEU
1	A	413	GLU
1	A	437	GLN
1	A	459	VAL
1	A	461	LYS
1	A	478	ARG
1	A	559	LYS
1	A	622	ARG
1	A	633	SER
1	A	651	LEU
1	A	697	VAL
1	A	698	LYS
1	A	699[A]	ARG
1	A	699[B]	ARG
1	A	726	LYS
1	A	746	THR
1	A	812	ASN
1	A	840	GLU
1	A	857	GLN
1	A	889	GLU
1	A	930	LYS
1	B	143	THR
1	B	154	GLN
1	B	183	LEU
1	B	209	ARG
1	B	216	ILE
1	B	222	GLN
1	B	248	LYS
1	B	383	ASP

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Mol	Chain	Res	Type
1	B	388	LEU
1	B	413	GLU
1	B	424	LEU
1	B	426	GLU
1	B	459	VAL
1	B	467	ILE
1	B	563	GLN
1	B	622	ARG
1	B	638	SER
1	B	697	VAL
1	B	698	LYS
1	B	699[A]	ARG
1	B	699[B]	ARG
1	B	726	LYS
1	B	746	THR
1	B	790	LEU
1	B	812	ASN
1	B	840	GLU
1	B	857	GLN
1	B	898[A]	GLU
1	B	898[B]	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	138	GLN
1	A	148	ASN
1	A	180	ASN
1	A	268	ASN
1	A	307	ASN
1	A	354	GLN
1	A	610	ASN
1	A	886	ASN
1	B	180	ASN
1	B	268	ASN
1	B	354	GLN

5.3.3 RNA ⓘ

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](#)

3 ligands 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$
2	PLP	B	1001	1	15,15,16	2.96	3 (20%)	21,22,23	1.35	3 (14%)
3	CIT	A	1002	-	12,12,12	1.06	0	17,17,17	1.35	1 (5%)
2	PLP	A	1001	1	15,15,16	2.94	3 (20%)	21,22,23	1.46	2 (9%)

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	PLP	B	1001	1	-	4/6/6/8	0/1/1/1
3	CIT	A	1002	-	-	9/16/16/16	-
2	PLP	A	1001	1	-	1/6/6/8	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	PLP	C5-C4	7.91	1.49	1.40
2	B	1001	PLP	C5-C4	7.60	1.49	1.40
2	B	1001	PLP	C3-C2	7.13	1.48	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	PLP	C3-C2	6.70	1.47	1.41
2	B	1001	PLP	C3-C4	4.01	1.47	1.40
2	A	1001	PLP	C3-C4	3.98	1.47	1.40

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	PLP	C4A-C4-C5	3.39	124.43	120.94
3	A	1002	CIT	O6-C6-C3	3.33	119.53	113.14
2	B	1001	PLP	C4A-C4-C5	2.69	123.71	120.94
2	A	1001	PLP	C6-N1-C2	2.20	123.19	119.20
2	B	1001	PLP	C6-N1-C2	2.10	123.01	119.20
2	B	1001	PLP	C6-C5-C4	2.07	119.79	118.10

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1001	PLP	C4-C5-C5A-O4P
2	B	1001	PLP	C5A-O4P-P-O1P
3	A	1002	CIT	C1-C2-C3-O7
3	A	1002	CIT	O7-C3-C6-O5
3	A	1002	CIT	O7-C3-C6-O6
3	A	1002	CIT	C4-C3-C6-O5
3	A	1002	CIT	C4-C3-C6-O6
3	A	1002	CIT	C1-C2-C3-C6
3	A	1002	CIT	C1-C2-C3-C4
2	B	1001	PLP	C4-C5-C5A-O4P
2	B	1001	PLP	C6-C5-C5A-O4P
3	A	1002	CIT	C3-C4-C5-O4
2	B	1001	PLP	C5A-O4P-P-O2P
3	A	1002	CIT	C3-C4-C5-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1001	PLP	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	844/938 (89%)	-0.09	4 (0%)	87 86	31, 60, 90, 128	5 (0%)
1	B	843/938 (89%)	-0.08	3 (0%)	88 87	27, 61, 91, 121	7 (0%)
All	All	1687/1876 (89%)	-0.08	7 (0%)	88 87	27, 61, 91, 128	12 (0%)

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	68	SER	3.6
1	B	69	ILE	3.1
1	A	69	ILE	2.8
1	B	424	LEU	2.5
1	B	465	ALA	2.4
1	A	968	PRO	2.1
1	A	424	LEU	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 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
3	CIT	A	1002	13/13	0.77	0.17	93,96,98,98	0
2	PLP	B	1001	15/16	0.94	0.08	46,48,58,59	0
2	PLP	A	1001	15/16	0.94	0.09	46,47,59,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.