



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 08:45 PM GMT

PDB ID : 1LW4
Title : X-ray structure of L-Threonine Aldolase (low-specificity) in complex with L-allo-threonine
Authors : Kielkopf, C.L.; Burley, S.K.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2002-05-30
Resolution : 1.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

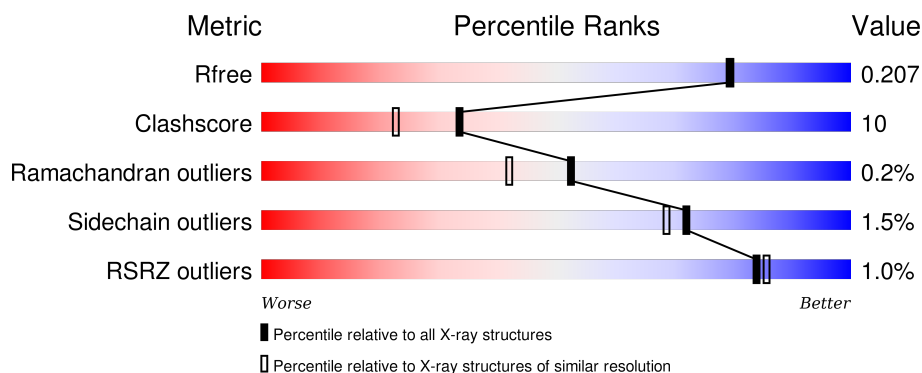
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	91344	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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. 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	347	<div> <div></div> <div>82%16%.</div> </div>
1	B	347	<div> <div></div> <div>81%17%..</div> </div>
1	C	347	<div> <div></div> <div>82%16%.</div> </div>
1	D	347	<div> <div></div> <div>81%17%..</div> </div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 11495 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 L-allo-threonine aldolase.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
1	A	343	Total	C	N	O	P	S	Se	0	0	0
			2599	1626	463	493	1	3	13			
1	B	343	Total	C	N	O	S	Se		0	1	0
			2587	1621	461	489	3	13				
1	C	343	Total	C	N	O	S	Se		0	0	0
			2584	1618	463	487	3	13				
1	D	344	Total	C	N	O	S	Se		0	0	0
			2600	1627	463	493	3	14				

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	CLONING ARTIFACT	UNP Q9X266
A	-2	PRO	-	CLONING ARTIFACT	UNP Q9X266
A	-1	HIS	-	CLONING ARTIFACT	UNP Q9X266
A	0	MSE	-	CLONING ARTIFACT	UNP Q9X266
B	-3	GLY	-	CLONING ARTIFACT	UNP Q9X266
B	-2	PRO	-	CLONING ARTIFACT	UNP Q9X266
B	-1	HIS	-	CLONING ARTIFACT	UNP Q9X266
B	0	MSE	-	CLONING ARTIFACT	UNP Q9X266
C	-3	GLY	-	CLONING ARTIFACT	UNP Q9X266
C	-2	PRO	-	CLONING ARTIFACT	UNP Q9X266
C	-1	HIS	-	CLONING ARTIFACT	UNP Q9X266
D	-3	GLY	-	CLONING ARTIFACT	UNP Q9X266
D	-2	PRO	-	CLONING ARTIFACT	UNP Q9X266
D	-1	HIS	-	CLONING ARTIFACT	UNP Q9X266

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

Continued on next page...

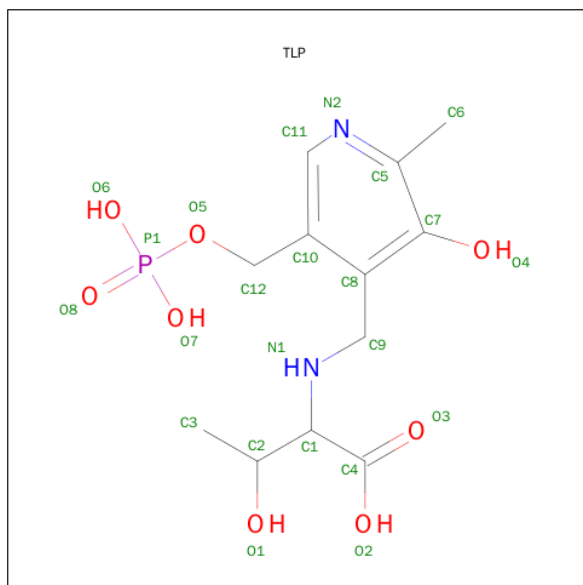
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		
2	D	2	Total	Ca	0	0
			2	2		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 4 is 3-HYDROXY-2-[(3-HYDROXY-2-METHYL-5-PHOSPHONOOXYMETHYL)-PYRIDIN-4-YLMETHYL)-AMINO]-BUTYRIC ACID (three-letter code: TLP) (formula: C₁₂H₁₉N₂O₈P).



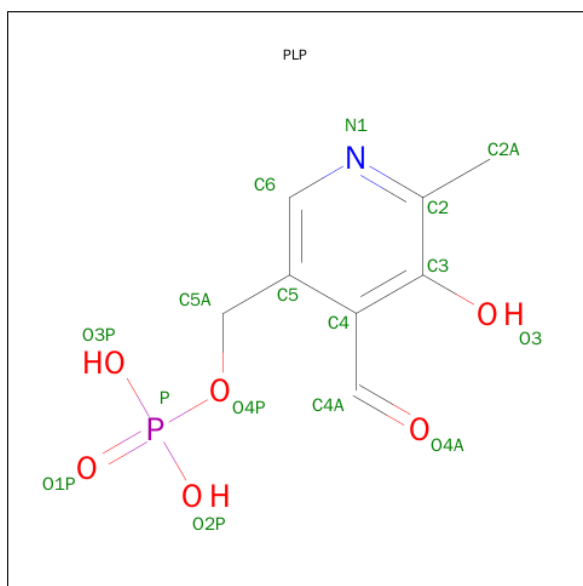
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	P	0	1
			23	12	2	8	1		
4	C	1	Total	C	N	O	P	0	0
			23	12	2	8	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	D	1	Total	C	N	O	P	0	0
			23	12	2	8	1		

- Molecule 5 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: $C_8H_{10}NO_6P$).



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

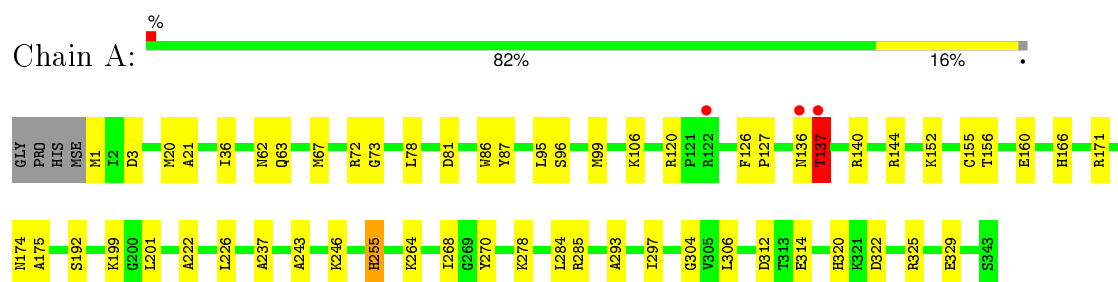
- Molecule 6 is water.

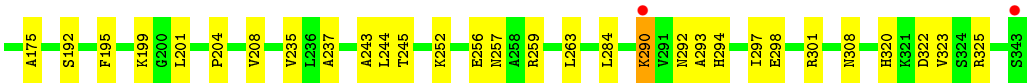
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	255	Total	O	0	0
			255	255		
6	B	234	Total	O	0	0
			234	234		
6	C	266	Total	O	0	0
			266	266		
6	D	274	Total	O	0	0
			274	274		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: L-allo-threonine aldolase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	95.90Å 100.50Å 150.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.90 29.86 – 1.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-1.90) 99.8 (29.86-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.44 (at 1.91Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.183 , 0.206 0.184 , 0.207	Depositor DCC
R_{free} test set	7902 reflections (6.91%)	DCC
Wilson B-factor (Å ²)	19.8	Xtriage
Anisotropy	0.064	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 57.7	EDS
Estimated twinning fraction	0.006 for k,h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 114556 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11495	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.31% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: LLP, CA, TLP, PLP, CL

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	0.31	0/2603	0.63	1/3500 (0.0%)
1	B	0.30	0/2597	0.64	1/3493 (0.0%)
1	C	0.39	1/2603 (0.0%)	0.67	4/3500 (0.1%)
1	D	0.40	2/2618 (0.1%)	0.74	4/3517 (0.1%)
All	All	0.35	3/10421 (0.0%)	0.67	10/14010 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	301	ARG	CZ-NH1	10.15	1.46	1.33
1	C	298	GLU	CB-CG	10.13	1.71	1.52
1	D	301	ARG	CG-CD	6.41	1.68	1.51

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	301	ARG	NE-CZ-NH1	19.79	130.20	120.30
1	B	137	THR	N-CA-C	-10.13	83.65	111.00
1	A	137	THR	N-CA-C	-9.29	85.93	111.00
1	D	137	THR	N-CA-C	-9.26	86.00	111.00
1	C	137	THR	N-CA-C	-8.72	87.44	111.00

There are no chirality outliers.

There are no planarity outliers.

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	2599	0	2578	53	0
1	B	2587	0	2566	64	0
1	C	2584	0	2571	57	0
1	D	2600	0	2586	59	0
2	A	1	0	0	0	0
2	B	3	0	0	0	0
2	D	2	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	B	23	0	15	4	0
4	C	23	0	15	1	0
4	D	23	0	15	2	0
5	B	15	0	6	4	0
6	A	255	0	0	7	0
6	B	234	0	0	6	0
6	C	266	0	0	9	1
6	D	274	0	0	13	1
All	All	11495	0	10352	212	1

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 10.

The worst 5 of 212 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:199[A]:LLP:NZ	4:B:1050[A]:TLP:H13	1.37	1.37
1:A:99:MSE:HE3	1:C:100:PRO:HG3	1.29	1.08
1:C:340:ARG:HG2	6:C:1320:HOH:O	1.53	1.05
1:B:199[A]:LLP:NZ	4:B:1050[A]:TLP:C9	2.20	1.04
1:D:136:ASN:O	1:D:137:THR:HG23	1.58	1.04

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:1316:HOH:O	6:D:1270:HOH:O[2_665]	2.15	0.05

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	340/347 (98%)	333 (98%)	6 (2%)	1 (0%)	46	35
1	B	340/347 (98%)	331 (97%)	8 (2%)	1 (0%)	46	35
1	C	340/347 (98%)	334 (98%)	5 (2%)	1 (0%)	46	35
1	D	341/347 (98%)	333 (98%)	8 (2%)	0	100	100
All	All	1361/1388 (98%)	1331 (98%)	27 (2%)	3 (0%)	52	42

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	137	THR
1	A	137	THR
1	B	137	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	269/269 (100%)	266 (99%)	3 (1%)	80	79
1	B	268/269 (100%)	263 (98%)	5 (2%)	65	59
1	C	269/269 (100%)	267 (99%)	2 (1%)	88	88
1	D	272/269 (101%)	266 (98%)	6 (2%)	60	53
All	All	1078/1076 (100%)	1062 (98%)	16 (2%)	72	69

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	312	ASP
1	C	137	THR
1	D	106	LYS
1	B	287	ASP
1	D	137	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	101	HIS
1	C	166	HIS
1	D	308	ASN
1	C	107	ASN
1	C	257	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

5 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	LLP	A	199	1	23,24,25	3.81	7 (30%)	28,32,34	2.39	12 (42%)
1	LLP	B	199[A]	1	7,8,25	0.45	0	6,8,34	1.18	1 (16%)
1	LLP	B	199[B]	1	7,8,25	0.95	1 (14%)	6,8,34	1.12	0
1	LLP	C	199	1	7,8,25	0.48	0	6,8,34	0.93	1 (16%)
1	LLP	D	199	1	7,8,25	0.45	0	6,8,34	0.94	1 (16%)

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	LLP	A	199	1	-	0/15/17/19	0/1/1/1
1	LLP	B	199[A]	1	-	0/5/7/19	0/0/0/1
1	LLP	B	199[B]	1	-	0/5/7/19	0/0/0/1
1	LLP	C	199	1	-	0/5/7/19	0/0/0/1
1	LLP	D	199	1	-	0/5/7/19	0/0/0/1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	199	LLP	P-OP3	-2.55	1.45	1.54
1	B	199[B]	LLP	CB-CA	-2.25	1.51	1.53
1	A	199	LLP	C4-C3	2.08	1.43	1.40
1	A	199	LLP	C6-N1	3.19	1.41	1.34
1	A	199	LLP	C2-N1	3.38	1.41	1.34

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	199	LLP	C3-C4-C4'	-3.66	115.43	120.16
1	A	199	LLP	C3-C2-N1	-3.16	116.25	120.61
1	A	199	LLP	C5-C6-N1	-2.79	119.02	123.86
1	A	199	LLP	C4-C4'-NZ	-2.78	109.60	125.06
1	A	199	LLP	O3-C3-C2	-2.37	113.53	117.66

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	199	LLP	2	0
1	B	199[A]	LLP	4	0
1	B	199[B]	LLP	3	0
1	C	199	LLP	1	0
1	D	199	LLP	2	0

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 16 ligands modelled in this entry, 12 are monoatomic - leaving 4 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$
4	TLP	B	1050[A]	-	20,23,23	4.44	8 (40%)	25,33,33	3.18	10 (40%)
5	PLP	B	1053[B]	-	15,15,16	5.16	7 (46%)	21,22,23	2.55	9 (42%)
4	TLP	C	1051	-	20,23,23	4.29	8 (40%)	25,33,33	3.10	9 (36%)
4	TLP	D	1052	-	20,23,23	4.29	7 (35%)	25,33,33	3.14	9 (36%)

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
4	TLP	B	1050[A]	-	-	0/15/19/19	0/1/1/1
5	PLP	B	1053[B]	-	-	0/6/6/8	0/1/1/1
4	TLP	C	1051	-	-	0/15/19/19	0/1/1/1
4	TLP	D	1052	-	-	0/15/19/19	0/1/1/1

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1051	TLP	C9-N1	-3.14	1.36	1.46
4	B	1050[A]	TLP	C9-N1	-3.00	1.37	1.46
4	D	1052	TLP	C9-N1	-2.71	1.38	1.46
4	D	1052	TLP	P1-O7	-2.35	1.46	1.54
5	B	1053[B]	PLP	P-O3P	-2.29	1.46	1.54

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
5	B	1053[B]	PLP	C3-C2-N1	-3.24	116.14	120.61
4	B	1050[A]	TLP	C7-C5-N2	-3.15	116.26	120.61
4	C	1051	TLP	C7-C5-N2	-3.15	116.26	120.61
4	D	1052	TLP	C7-C5-N2	-3.11	116.31	120.61
4	C	1051	TLP	C10-C11-N2	-3.09	118.50	123.86

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1050[A]	TLP	4	0
5	B	1053[B]	PLP	4	0
4	C	1051	TLP	1	0
4	D	1052	TLP	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	329/347 (94%)	-0.10	3 (0%) 85 87	13, 20, 30, 41	0
1	B	329/347 (94%)	-0.10	2 (0%) 90 91	11, 18, 32, 41	0
1	C	329/347 (94%)	-0.02	4 (1%) 81 83	10, 21, 33, 42	1 (0%)
1	D	329/347 (94%)	-0.08	4 (1%) 81 83	11, 18, 34, 46	0
All	All	1316/1388 (94%)	-0.07	13 (0%) 84 86	10, 19, 32, 46	1 (0%)

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	137	THR	5.4
1	B	137	THR	5.3
1	D	137	THR	5.0
1	C	137	THR	4.7
1	C	72	ARG	3.4

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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
1	LLP	B	199[A]	9/25	0.95	0.39	-	13,14,19,23	9
1	LLP	D	199	9/25	0.96	0.14	-	12,14,23,29	0
1	LLP	B	199[B]	9/25	0.95	0.39	-	16,17,21,22	9
1	LLP	A	199	24/25	0.91	0.18	-	13,22,27,30	0
1	LLP	C	199	9/25	0.96	0.16	-	12,14,23,25	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
4	TLP	B	1050[A]	23/23	0.91	0.22	1.82	14,19,21,22	23
4	TLP	D	1052	23/23	0.92	0.16	0.76	13,19,28,32	0
5	PLP	B	1053[B]	15/16	0.94	0.16	0.56	18,24,27,27	15
4	TLP	C	1051	23/23	0.96	0.14	0.44	15,18,24,28	0
3	CL	C	1061	1/1	0.99	0.05	-1.08	24,24,24,24	0
3	CL	A	1060	1/1	1.00	0.03	-2.33	19,19,19,19	0
2	CA	B	1054	1/1	1.00	0.04	-2.68	17,17,17,17	0
2	CA	A	1056	1/1	0.99	0.05	-2.74	19,19,19,19	0
2	CA	D	1059	1/1	0.99	0.03	-3.85	18,18,18,18	0
2	CA	B	1057	1/1	1.00	0.04	-4.06	18,18,18,18	0
2	CA	D	1055	1/1	0.99	0.04	-4.08	17,17,17,17	0
3	CL	A	1064	1/1	0.99	0.03	-	31,31,31,31	0
3	CL	B	1063	1/1	0.98	0.04	-	29,29,29,29	0
3	CL	D	1062	1/1	0.96	0.07	-	31,31,31,31	0
3	CL	B	1065	1/1	0.98	0.07	-	28,28,28,28	0
2	CA	B	1058	1/1	0.98	0.12	-	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.