



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 02:22 am GMT

PDB ID : 4O6Z
Title : Crystal structure of serine hydroxymethyltransferase with covalently bound
PLP Schiff-base from Plasmodium falciparum
Authors : Chitnumsub, P.; Jaruwat, A.; Leartsakulpanich, U.
Deposited on : 2013-12-24
Resolution : 2.98 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

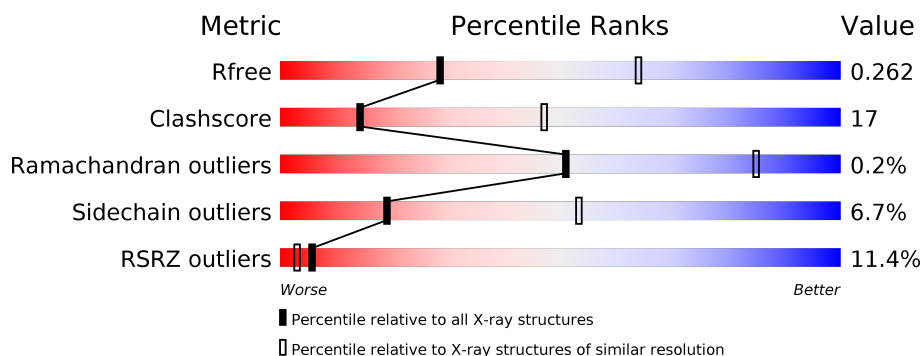
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.98 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}	100719	2168 (3.00-2.96)
Clashscore	112137	2535 (3.00-2.96)
Ramachandran outliers	110173	2451 (3.00-2.96)
Sidechain outliers	110143	2454 (3.00-2.96)
RSRZ outliers	101464	2192 (3.00-2.96)

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	480	<div> <div>0%</div> <div> <div>63%</div> <div>28%</div> <div>7%</div> </div> </div>
1	B	480	<div> <div>0%</div> <div> <div>59%</div> <div>30%</div> <div>7%</div> </div> </div>
1	C	480	<div> <div>5%</div> <div> <div>63%</div> <div>27%</div> <div>8%</div> </div> </div>
1	D	480	<div> <div>36%</div> <div> <div>58%</div> <div>31%</div> <div>7%</div> </div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PLP	B	701	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14254 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 Serine hydroxymethyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	448	Total	C	N	O	S	0	0	0
			3544	2251	603	672	18			
1	B	445	Total	C	N	O	S	0	0	0
			3516	2231	598	669	18			
1	C	441	Total	C	N	O	S	0	0	0
			3490	2215	594	664	17			
1	D	445	Total	C	N	O	S	0	0	0
			3516	2231	598	669	18			

There are 156 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-37	MET	-	EXPRESSION TAG	UNP Q8I566
A	-36	ARG	-	EXPRESSION TAG	UNP Q8I566
A	-35	GLY	-	EXPRESSION TAG	UNP Q8I566
A	-34	SER	-	EXPRESSION TAG	UNP Q8I566
A	-33	HIS	-	EXPRESSION TAG	UNP Q8I566
A	-32	HIS	-	EXPRESSION TAG	UNP Q8I566
A	-31	HIS	-	EXPRESSION TAG	UNP Q8I566
A	-30	HIS	-	EXPRESSION TAG	UNP Q8I566
A	-29	HIS	-	EXPRESSION TAG	UNP Q8I566
A	-28	HIS	-	EXPRESSION TAG	UNP Q8I566
A	-27	GLY	-	EXPRESSION TAG	UNP Q8I566
A	-26	MET	-	EXPRESSION TAG	UNP Q8I566
A	-25	ALA	-	EXPRESSION TAG	UNP Q8I566
A	-24	SER	-	EXPRESSION TAG	UNP Q8I566
A	-23	MET	-	EXPRESSION TAG	UNP Q8I566
A	-22	THR	-	EXPRESSION TAG	UNP Q8I566
A	-21	GLY	-	EXPRESSION TAG	UNP Q8I566
A	-20	GLY	-	EXPRESSION TAG	UNP Q8I566
A	-19	GLN	-	EXPRESSION TAG	UNP Q8I566
A	-18	GLN	-	EXPRESSION TAG	UNP Q8I566
A	-17	MET	-	EXPRESSION TAG	UNP Q8I566

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	GLY	-	EXPRESSION TAG	UNP Q8I566
A	-15	ARG	-	EXPRESSION TAG	UNP Q8I566
A	-14	ASP	-	EXPRESSION TAG	UNP Q8I566
A	-13	LEU	-	EXPRESSION TAG	UNP Q8I566
A	-12	TYR	-	EXPRESSION TAG	UNP Q8I566
A	-11	ASP	-	EXPRESSION TAG	UNP Q8I566
A	-10	ASP	-	EXPRESSION TAG	UNP Q8I566
A	-9	ASP	-	EXPRESSION TAG	UNP Q8I566
A	-8	ASP	-	EXPRESSION TAG	UNP Q8I566
A	-7	LYS	-	EXPRESSION TAG	UNP Q8I566
A	-6	ASP	-	EXPRESSION TAG	UNP Q8I566
A	-5	HIS	-	EXPRESSION TAG	UNP Q8I566
A	-4	PRO	-	EXPRESSION TAG	UNP Q8I566
A	-3	PHE	-	EXPRESSION TAG	UNP Q8I566
A	-2	THR	-	EXPRESSION TAG	UNP Q8I566
A	-1	PRO	-	EXPRESSION TAG	UNP Q8I566
A	0	GLY	-	EXPRESSION TAG	UNP Q8I566
A	292	GLU	PHE	ENGINEERED MUTATION	UNP Q8I566
B	-37	MET	-	EXPRESSION TAG	UNP Q8I566
B	-36	ARG	-	EXPRESSION TAG	UNP Q8I566
B	-35	GLY	-	EXPRESSION TAG	UNP Q8I566
B	-34	SER	-	EXPRESSION TAG	UNP Q8I566
B	-33	HIS	-	EXPRESSION TAG	UNP Q8I566
B	-32	HIS	-	EXPRESSION TAG	UNP Q8I566
B	-31	HIS	-	EXPRESSION TAG	UNP Q8I566
B	-30	HIS	-	EXPRESSION TAG	UNP Q8I566
B	-29	HIS	-	EXPRESSION TAG	UNP Q8I566
B	-28	HIS	-	EXPRESSION TAG	UNP Q8I566
B	-27	GLY	-	EXPRESSION TAG	UNP Q8I566
B	-26	MET	-	EXPRESSION TAG	UNP Q8I566
B	-25	ALA	-	EXPRESSION TAG	UNP Q8I566
B	-24	SER	-	EXPRESSION TAG	UNP Q8I566
B	-23	MET	-	EXPRESSION TAG	UNP Q8I566
B	-22	THR	-	EXPRESSION TAG	UNP Q8I566
B	-21	GLY	-	EXPRESSION TAG	UNP Q8I566
B	-20	GLY	-	EXPRESSION TAG	UNP Q8I566
B	-19	GLN	-	EXPRESSION TAG	UNP Q8I566
B	-18	GLN	-	EXPRESSION TAG	UNP Q8I566
B	-17	MET	-	EXPRESSION TAG	UNP Q8I566
B	-16	GLY	-	EXPRESSION TAG	UNP Q8I566
B	-15	ARG	-	EXPRESSION TAG	UNP Q8I566
B	-14	ASP	-	EXPRESSION TAG	UNP Q8I566

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-13	LEU	-	EXPRESSION TAG	UNP Q8I566
B	-12	TYR	-	EXPRESSION TAG	UNP Q8I566
B	-11	ASP	-	EXPRESSION TAG	UNP Q8I566
B	-10	ASP	-	EXPRESSION TAG	UNP Q8I566
B	-9	ASP	-	EXPRESSION TAG	UNP Q8I566
B	-8	ASP	-	EXPRESSION TAG	UNP Q8I566
B	-7	LYS	-	EXPRESSION TAG	UNP Q8I566
B	-6	ASP	-	EXPRESSION TAG	UNP Q8I566
B	-5	HIS	-	EXPRESSION TAG	UNP Q8I566
B	-4	PRO	-	EXPRESSION TAG	UNP Q8I566
B	-3	PHE	-	EXPRESSION TAG	UNP Q8I566
B	-2	THR	-	EXPRESSION TAG	UNP Q8I566
B	-1	PRO	-	EXPRESSION TAG	UNP Q8I566
B	0	GLY	-	EXPRESSION TAG	UNP Q8I566
B	292	GLU	PHE	ENGINEERED MUTATION	UNP Q8I566
C	-37	MET	-	EXPRESSION TAG	UNP Q8I566
C	-36	ARG	-	EXPRESSION TAG	UNP Q8I566
C	-35	GLY	-	EXPRESSION TAG	UNP Q8I566
C	-34	SER	-	EXPRESSION TAG	UNP Q8I566
C	-33	HIS	-	EXPRESSION TAG	UNP Q8I566
C	-32	HIS	-	EXPRESSION TAG	UNP Q8I566
C	-31	HIS	-	EXPRESSION TAG	UNP Q8I566
C	-30	HIS	-	EXPRESSION TAG	UNP Q8I566
C	-29	HIS	-	EXPRESSION TAG	UNP Q8I566
C	-28	HIS	-	EXPRESSION TAG	UNP Q8I566
C	-27	GLY	-	EXPRESSION TAG	UNP Q8I566
C	-26	MET	-	EXPRESSION TAG	UNP Q8I566
C	-25	ALA	-	EXPRESSION TAG	UNP Q8I566
C	-24	SER	-	EXPRESSION TAG	UNP Q8I566
C	-23	MET	-	EXPRESSION TAG	UNP Q8I566
C	-22	THR	-	EXPRESSION TAG	UNP Q8I566
C	-21	GLY	-	EXPRESSION TAG	UNP Q8I566
C	-20	GLY	-	EXPRESSION TAG	UNP Q8I566
C	-19	GLN	-	EXPRESSION TAG	UNP Q8I566
C	-18	GLN	-	EXPRESSION TAG	UNP Q8I566
C	-17	MET	-	EXPRESSION TAG	UNP Q8I566
C	-16	GLY	-	EXPRESSION TAG	UNP Q8I566
C	-15	ARG	-	EXPRESSION TAG	UNP Q8I566
C	-14	ASP	-	EXPRESSION TAG	UNP Q8I566
C	-13	LEU	-	EXPRESSION TAG	UNP Q8I566
C	-12	TYR	-	EXPRESSION TAG	UNP Q8I566
C	-11	ASP	-	EXPRESSION TAG	UNP Q8I566

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-10	ASP	-	EXPRESSION TAG	UNP Q8I566
C	-9	ASP	-	EXPRESSION TAG	UNP Q8I566
C	-8	ASP	-	EXPRESSION TAG	UNP Q8I566
C	-7	LYS	-	EXPRESSION TAG	UNP Q8I566
C	-6	ASP	-	EXPRESSION TAG	UNP Q8I566
C	-5	HIS	-	EXPRESSION TAG	UNP Q8I566
C	-4	PRO	-	EXPRESSION TAG	UNP Q8I566
C	-3	PHE	-	EXPRESSION TAG	UNP Q8I566
C	-2	THR	-	EXPRESSION TAG	UNP Q8I566
C	-1	PRO	-	EXPRESSION TAG	UNP Q8I566
C	0	GLY	-	EXPRESSION TAG	UNP Q8I566
C	292	GLU	PHE	ENGINEERED MUTATION	UNP Q8I566
D	-37	MET	-	EXPRESSION TAG	UNP Q8I566
D	-36	ARG	-	EXPRESSION TAG	UNP Q8I566
D	-35	GLY	-	EXPRESSION TAG	UNP Q8I566
D	-34	SER	-	EXPRESSION TAG	UNP Q8I566
D	-33	HIS	-	EXPRESSION TAG	UNP Q8I566
D	-32	HIS	-	EXPRESSION TAG	UNP Q8I566
D	-31	HIS	-	EXPRESSION TAG	UNP Q8I566
D	-30	HIS	-	EXPRESSION TAG	UNP Q8I566
D	-29	HIS	-	EXPRESSION TAG	UNP Q8I566
D	-28	HIS	-	EXPRESSION TAG	UNP Q8I566
D	-27	GLY	-	EXPRESSION TAG	UNP Q8I566
D	-26	MET	-	EXPRESSION TAG	UNP Q8I566
D	-25	ALA	-	EXPRESSION TAG	UNP Q8I566
D	-24	SER	-	EXPRESSION TAG	UNP Q8I566
D	-23	MET	-	EXPRESSION TAG	UNP Q8I566
D	-22	THR	-	EXPRESSION TAG	UNP Q8I566
D	-21	GLY	-	EXPRESSION TAG	UNP Q8I566
D	-20	GLY	-	EXPRESSION TAG	UNP Q8I566
D	-19	GLN	-	EXPRESSION TAG	UNP Q8I566
D	-18	GLN	-	EXPRESSION TAG	UNP Q8I566
D	-17	MET	-	EXPRESSION TAG	UNP Q8I566
D	-16	GLY	-	EXPRESSION TAG	UNP Q8I566
D	-15	ARG	-	EXPRESSION TAG	UNP Q8I566
D	-14	ASP	-	EXPRESSION TAG	UNP Q8I566
D	-13	LEU	-	EXPRESSION TAG	UNP Q8I566
D	-12	TYR	-	EXPRESSION TAG	UNP Q8I566
D	-11	ASP	-	EXPRESSION TAG	UNP Q8I566
D	-10	ASP	-	EXPRESSION TAG	UNP Q8I566
D	-9	ASP	-	EXPRESSION TAG	UNP Q8I566
D	-8	ASP	-	EXPRESSION TAG	UNP Q8I566

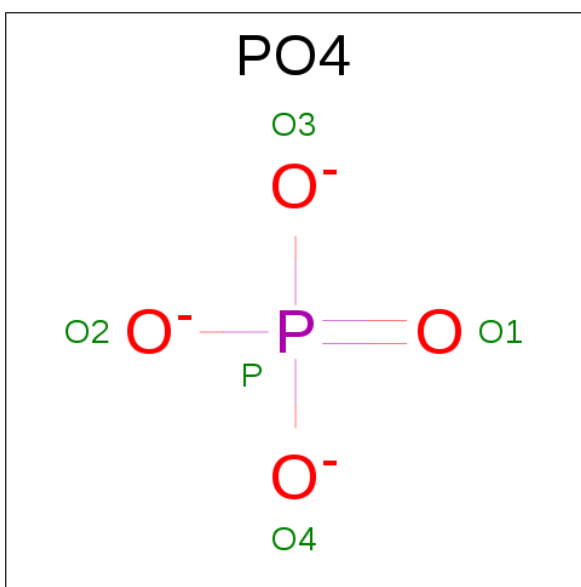
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Chain	Residue	Modelled	Actual	Comment	Reference
D	-7	LYS	-	EXPRESSION TAG	UNP Q8I566
D	-6	ASP	-	EXPRESSION TAG	UNP Q8I566
D	-5	HIS	-	EXPRESSION TAG	UNP Q8I566
D	-4	PRO	-	EXPRESSION TAG	UNP Q8I566
D	-3	PHE	-	EXPRESSION TAG	UNP Q8I566
D	-2	THR	-	EXPRESSION TAG	UNP Q8I566
D	-1	PRO	-	EXPRESSION TAG	UNP Q8I566
D	0	GLY	-	EXPRESSION TAG	UNP Q8I566
D	292	GLU	PHE	ENGINEERED MUTATION	UNP Q8I566

- # PLP
-
- The chemical structure of PLP (Pyridoxal phosphate) is shown. It consists of a pyridine ring substituted with a hydroxyl group at the 3-position and a hydroxymethyl group at the 4-position. The hydroxyl group is labeled with a red 'OH' and a green 'O3'. The hydroxymethyl group is labeled with a green 'C5A' and a red 'O'. The pyridine ring is labeled with a blue 'N1' at the nitrogen atom and green 'C2', 'C3', 'C4', 'C5', and 'C6' at the carbon atoms. The hydroxymethyl group is further substituted with a phosphate group, which is labeled with a green 'O4P' and a red 'O'. The phosphate group is labeled with a green 'P' and green 'O1P', 'O2P', and 'O3P' at the oxygen atoms.

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

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- WORLD WIDE
PDB
PROTEIN DATA BANK

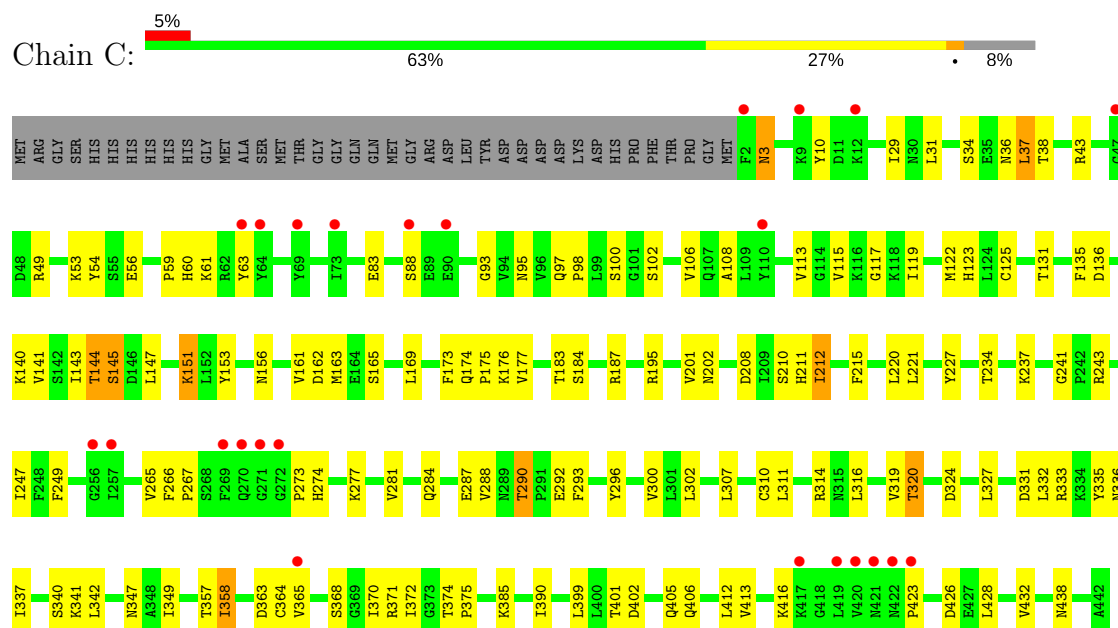


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	56	Total	O	0	0
			56	56		
4	B	55	Total	O	0	0
			55	55		
4	C	20	Total	O	0	0
			20	20		
4	D	7	Total	O	0	0
			7	7		

• Molecule 1: Serine hydroxymethyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	254.95Å 254.95Å 61.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.85 – 2.98 29.85 – 2.98	Depositor EDS
% Data completeness (in resolution range)	99.7 (29.85-2.98) 99.8 (29.85-2.98)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	9.03 (at 3.00Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.224 , 0.270 0.216 , 0.262	Depositor DCC
R_{free} test set	4739 reflections (11.16%)	DCC
Wilson B-factor (Å ²)	63.6	Xtriage
Anisotropy	0.253	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 64.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.021 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	14254	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.09% 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: PO4, 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	0.64	0/3612	0.79	2/4878 (0.0%)
1	B	0.66	0/3581	0.81	2/4835 (0.0%)
1	C	0.56	0/3554	0.74	1/4798 (0.0%)
1	D	0.51	1/3581 (0.0%)	0.69	0/4835
All	All	0.60	1/14328 (0.0%)	0.76	5/19346 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	435	TRP	CD2-CE2	5.54	1.48	1.41

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	353	LEU	CA-CB-CG	6.76	130.85	115.30
1	C	327	LEU	CA-CB-CG	5.90	128.88	115.30
1	B	327	LEU	CB-CG-CD1	-5.30	101.98	111.00
1	A	190	ASP	CB-CG-OD2	-5.29	113.54	118.30
1	A	327	LEU	CA-CB-CG	5.25	127.37	115.30

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	3544	0	3558	131	0
1	B	3516	0	3537	134	0
1	C	3490	0	3508	115	0
1	D	3516	0	3539	136	0
2	A	15	0	6	2	0
2	B	15	0	7	1	0
2	C	15	0	6	2	0
3	D	5	0	0	1	0
4	A	56	0	0	6	0
4	B	55	0	0	2	0
4	C	20	0	0	3	0
4	D	7	0	0	1	0
All	All	14254	0	14161	492	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 17.

The worst 5 of 492 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:D:337:ILE:HD11	1:D:401:THR:HB	1.29	1.14
1:B:337:ILE:HD11	1:B:401:THR:HB	1.22	1.07
1:A:151:LYS:HE3	1:A:173:PHE:CD1	1.90	1.07
1:C:290:THR:HG22	1:C:293:PHE:H	1.20	1.06
1:A:290:THR:HG22	1:A:293:PHE:H	1.17	1.05

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	446/480 (93%)	422 (95%)	23 (5%)	1 (0%)	51 85

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	443/480 (92%)	426 (96%)	17 (4%)	0	100	100
1	C	439/480 (92%)	415 (94%)	22 (5%)	2 (0%)	32	72
1	D	443/480 (92%)	428 (97%)	15 (3%)	0	100	100
All	All	1771/1920 (92%)	1691 (96%)	77 (4%)	3 (0%)	51	85

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	364	CYS
1	C	156	ASN
1	A	374	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	395/421 (94%)	369 (93%)	26 (7%)	19	54
1	B	392/421 (93%)	363 (93%)	29 (7%)	16	48
1	C	389/421 (92%)	368 (95%)	21 (5%)	26	62
1	D	392/421 (93%)	363 (93%)	29 (7%)	16	48
All	All	1568/1684 (93%)	1463 (93%)	105 (7%)	19	53

5 of 105 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	337	ILE
1	C	53	LYS
1	D	321	ASN
1	B	355	LYS
1	B	429	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	356	ASN
1	C	202	ASN
1	D	356	ASN
1	B	405	GLN
1	C	3	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

4 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	A	701	1	15,15,16	0.97	1 (6%)	20,22,23	1.88	7 (35%)
2	PLP	B	701	1	15,15,16	1.55	1 (6%)	20,22,23	1.68	5 (25%)
2	PLP	C	701	1	15,15,16	0.76	0	20,22,23	1.48	4 (20%)
3	PO4	D	501	-	4,4,4	0.54	0	6,6,6	0.92	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	PLP	A	701	1	-	0/6/6/8	0/1/1/1
2	PLP	B	701	1	-	0/6/6/8	0/1/1/1
2	PLP	C	701	1	-	0/6/6/8	0/1/1/1
3	PO4	D	501	-	-	0/0/0/0	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	701	PLP	C3-C2	-5.55	1.36	1.40
2	A	701	PLP	C3-C2	-3.32	1.38	1.40

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	PLP	C4A-C4-C3	-3.10	115.19	120.54
2	C	701	PLP	O2P-P-O4P	-2.99	98.76	106.73
2	B	701	PLP	C5A-C5-C6	-2.68	114.71	119.33
2	B	701	PLP	C4A-C4-C3	-2.27	116.63	120.54
2	A	701	PLP	O2P-P-O4P	-2.26	100.71	106.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	701	PLP	2	0
2	B	701	PLP	1	0
2	C	701	PLP	2	0
3	D	501	PO4	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	448/480 (93%)	-0.35	3 (0%) 87 73	24, 46, 88, 108	0
1	B	445/480 (92%)	-0.44	3 (0%) 87 73	25, 42, 73, 112	0
1	C	441/480 (91%)	0.33	24 (5%) 26 15	31, 77, 119, 120	0
1	D	445/480 (92%)	1.75	172 (38%) 0 0	55, 116, 120, 120	0
All	All	1779/1920 (92%)	0.32	202 (11%) 6 3	24, 63, 120, 120	0

The worst 5 of 202 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	364	CYS	8.0
1	D	441	PHE	6.3
1	D	306	ALA	5.9
1	D	345	THR	5.9
1	D	315	ASN	5.9

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 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
2	PLP	B	701	15/16	0.99	0.26	2.52	26,28,29,29	0
2	PLP	C	701	15/16	0.92	0.24	0.22	73,79,89,90	0
2	PLP	A	701	15/16	0.97	0.19	-0.01	26,31,33,36	0
3	PO4	D	501	5/5	0.91	0.25	-1.16	67,73,88,88	0

6.5 Other polymers [i](#)

There are no such residues in this entry.