



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 25, 2020 – 06:15 pm BST

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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

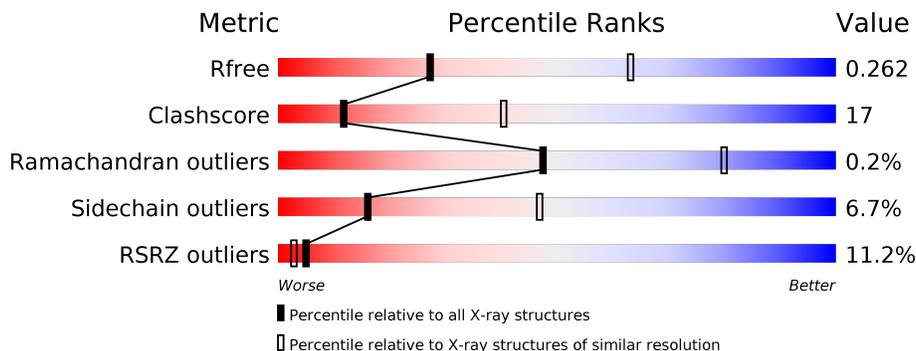
# 1 Overall quality at a glance

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))
$R_{free}$	130704	2754 (3.00-2.96)
Clashscore	141614	3103 (3.00-2.96)
Ramachandran outliers	138981	2993 (3.00-2.96)
Sidechain outliers	138945	2996 (3.00-2.96)
RSRZ outliers	127900	2644 (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  $\geq 3$ , 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	480	 % 63% 28% • 7%
1	B	480	 % 59% 30% • 7%
1	C	480	 5% 63% 27% • 8%
1	D	480	 36% 58% 31% • 7%

## 2 Entry composition [i](#)

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
			Total	C	N	O	S			
1	A	448	3544	2251	603	672	18	0	0	0
1	B	445	3516	2231	598	669	18	0	0	0
1	C	441	3490	2215	594	664	17	0	0	0
1	D	445	3516	2231	598	669	18	0	0	0

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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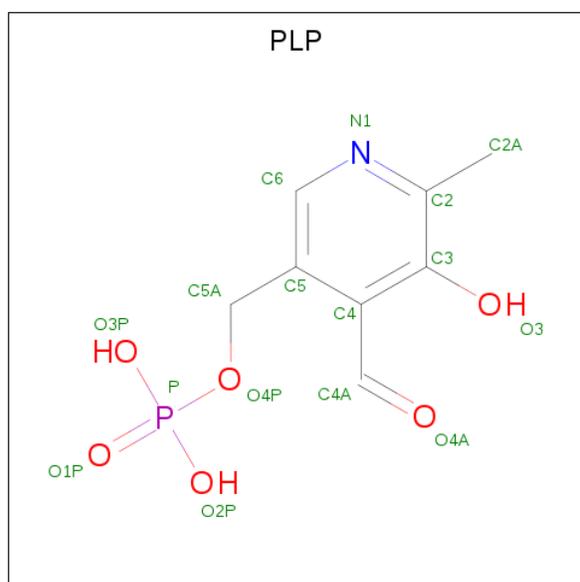
Chain	Residue	Modelled	Actual	Comment	Reference
C	-10	ASP	-	expression tag	UNP Q8I566
C	-9	ASP	-	expression tag	UNP Q8I566
C	-8	ASP	-	expression tag	UNP Q8I566
C	-7	LYS	-	expression tag	UNP Q8I566
C	-6	ASP	-	expression tag	UNP Q8I566
C	-5	HIS	-	expression tag	UNP Q8I566
C	-4	PRO	-	expression tag	UNP 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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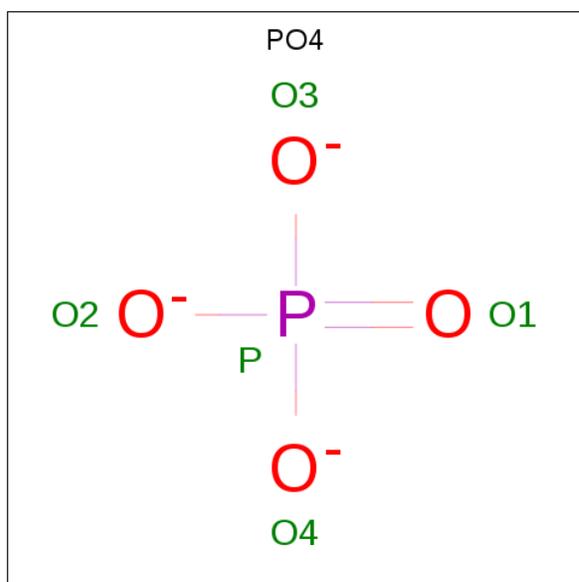
Chain	Residue	Modelled	Actual	Comment	Reference
D	-7	LYS	-	expression tag	UNP Q8I566
D	-6	ASP	-	expression tag	UNP Q8I566
D	-5	HIS	-	expression tag	UNP Q8I566
D	-4	PRO	-	expression tag	UNP Q8I566
D	-3	PHE	-	expression tag	UNP Q8I566
D	-2	THR	-	expression tag	UNP Q8I566
D	-1	PRO	-	expression tag	UNP Q8I566
D	0	GLY	-	expression tag	UNP Q8I566
D	292	GLU	PHE	engineered mutation	UNP Q8I566

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C<sub>8</sub>H<sub>10</sub>NO<sub>6</sub>P).



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

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



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

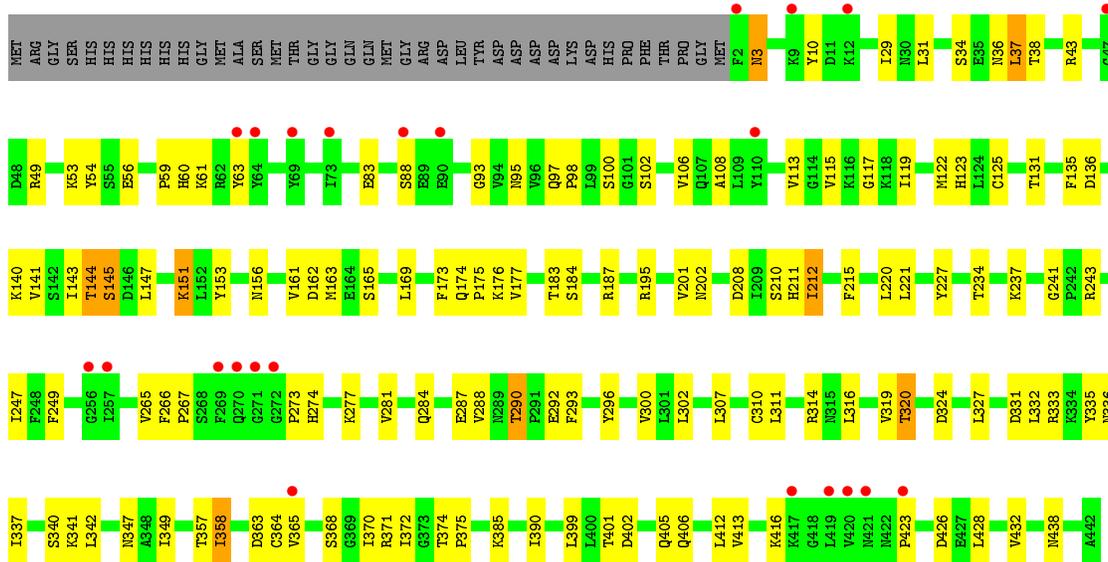
- Molecule 4 is water.

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		

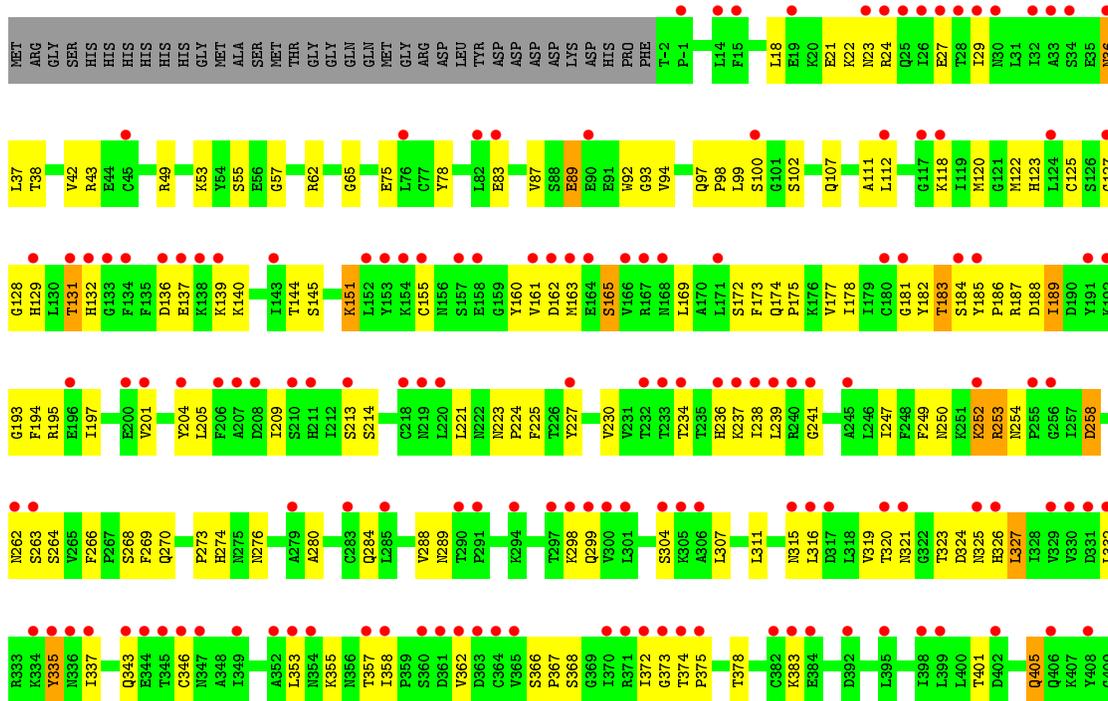




• Molecule 1: Serine hydroxymethyltransferase



• Molecule 1: Serine hydroxymethyltransferase



K410	K411	L412	V413	D414	F415	K416	K417	G418	L419	V420	N421	M422	F423	K424	I425	D426	E427	L428	K429	K430	E431	V432	V433	Q434	M435	A436	K437	N438	L439	P440	F441	A442
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	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
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	9.03 (at 3.00Å)	Xtrriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.224 , 0.270 0.216 , 0.262	Depositor DCC
$R_{free}$ test set	4743 reflections (10.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	63.6	Xtrriage
Anisotropy	0.253	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 64.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.021 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	14254	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	70.0	wwPDB-VP

Xtrriage'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.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [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	446/480 (93%)	422 (95%)	23 (5%)	1 (0%)	47 80

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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%)	29	66
1	D	443/480 (92%)	428 (97%)	15 (3%)	0	100	100
All	All	1771/1920 (92%)	1691 (96%)	77 (4%)	3 (0%)	47	80

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 [i](#)

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%)	16	47
1	B	392/421 (93%)	363 (93%)	29 (7%)	13	42
1	C	389/421 (92%)	368 (95%)	21 (5%)	22	55
1	D	392/421 (93%)	363 (93%)	29 (7%)	13	42
All	All	1568/1684 (93%)	1463 (93%)	105 (7%)	16	47

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	0.80	1 (6%)	20,22,23	1.88	8 (40%)
2	PLP	C	701	1	15,15,16	0.75	0	20,22,23	1.51	5 (25%)
2	PLP	B	701	1	15,15,16	1.21	1 (6%)	20,22,23	1.74	6 (30%)
3	PO4	D	501	-	4,4,4	0.64	0	6,6,6	1.04	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	-	5/6/6/8	0/1/1/1
2	PLP	C	701	1	-	2/6/6/8	0/1/1/1
2	PLP	B	701	1	-	1/6/6/8	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	701	PLP	C3-C2	-4.01	1.36	1.40
2	A	701	PLP	C3-C2	-2.46	1.38	1.40

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	PLP	C4A-C4-C5	4.83	125.91	120.94
2	B	701	PLP	O4P-C5A-C5	4.08	117.12	109.35
2	A	701	PLP	C4A-C4-C3	-3.13	115.19	120.50
2	C	701	PLP	O2P-P-O4P	-2.99	98.76	106.73
2	B	701	PLP	C5A-C5-C6	-2.83	114.71	119.37

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	701	PLP	C4-C5-C5A-O4P
2	A	701	PLP	C6-C5-C5A-O4P
2	A	701	PLP	C5A-O4P-P-O1P
2	A	701	PLP	C5A-O4P-P-O2P
2	A	701	PLP	C5A-O4P-P-O3P

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	C	701	PLP	2	0
2	B	701	PLP	1	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

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	448/480 (93%)	-0.35	3 (0%) 87 74	24, 46, 88, 108	0
1	B	445/480 (92%)	-0.45	3 (0%) 87 74	25, 42, 73, 112	0
1	C	441/480 (91%)	0.33	23 (5%) 27 16	31, 77, 119, 120	0
1	D	445/480 (92%)	1.75	171 (38%) 0 0	55, 116, 120, 120	0
All	All	1779/1920 (92%)	0.32	200 (11%) 5 3	24, 63, 120, 120	0

The worst 5 of 200 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	315	ASN	5.9
1	D	345	THR	5.8

### 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. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	PO4	D	501	5/5	0.91	0.25	67,73,88,88	0
2	PLP	C	701	15/16	0.92	0.24	73,79,89,90	0
2	PLP	A	701	15/16	0.97	0.19	26,31,33,36	0
2	PLP	B	701	15/16	0.99	0.26	26,28,29,29	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.