



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:21 PM GMT

PDB ID : 4XK1  
Title : Crystal Structure of a Phosphoserine/phosphohydroxythreonine Aminotransferase (PSAT) from *Pseudomonas aeruginosa* with cofactor Pyridoxal Phosphate and bound Glutamate  
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)  
Deposited on : 2015-01-09  
Resolution : 2.15 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](mailto: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.

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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 : 1.7 (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

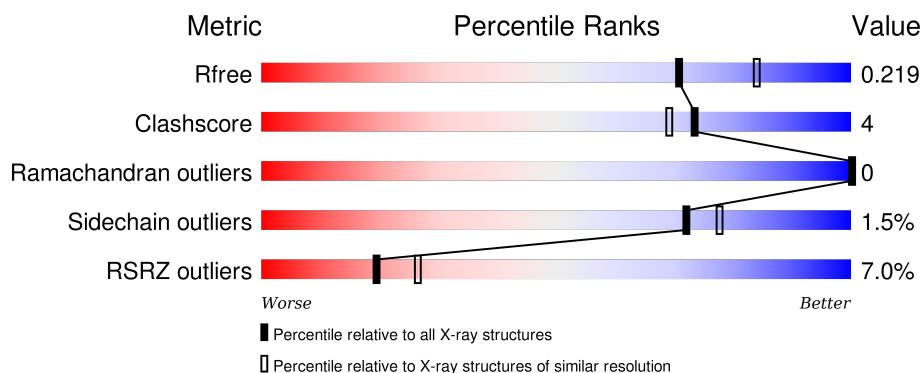
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.15 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	1045 (2.16-2.16)
Clashscore	102246	1152 (2.16-2.16)
Ramachandran outliers	100387	1131 (2.16-2.16)
Sidechain outliers	100360	1131 (2.16-2.16)
RSRZ outliers	91569	1050 (2.16-2.16)

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. 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	369	<div> <div>3%</div> <div>87%</div> <div>9%</div> <div>.</div> </div>
1	B	369	<div> <div>11%</div> <div>84%</div> <div>9%</div> <div>6%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5629 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.

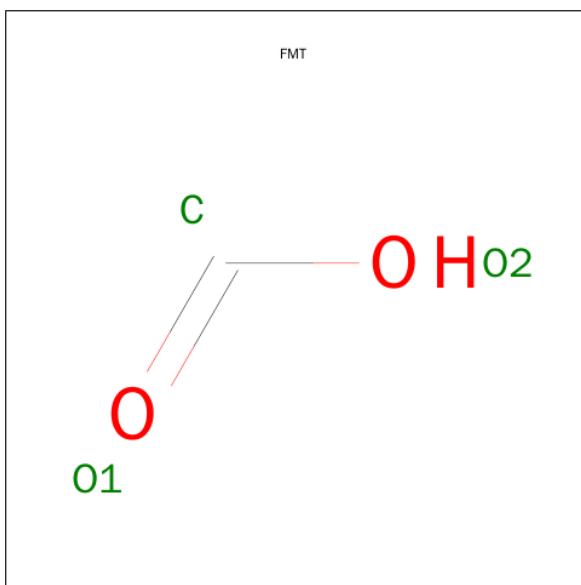
- Molecule 1 is a protein called Phosphoserine aminotransferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	355	Total	C	N	O	P	S	0	1	0
			2748	1745	461	530	1	11			
1	B	347	Total	C	N	O	P	S	0	3	0
			2629	1668	441	509	1	10			

There are 16 discrepancies between the modelled and reference sequences:

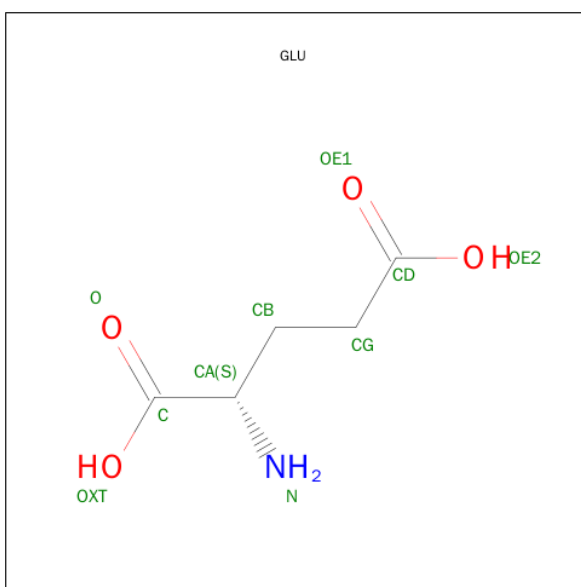
Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	UNP Q9HZ66
A	-6	ALA	-	expression tag	UNP Q9HZ66
A	-5	HIS	-	expression tag	UNP Q9HZ66
A	-4	HIS	-	expression tag	UNP Q9HZ66
A	-3	HIS	-	expression tag	UNP Q9HZ66
A	-2	HIS	-	expression tag	UNP Q9HZ66
A	-1	HIS	-	expression tag	UNP Q9HZ66
A	0	HIS	-	expression tag	UNP Q9HZ66
B	-7	MET	-	initiating methionine	UNP Q9HZ66
B	-6	ALA	-	expression tag	UNP Q9HZ66
B	-5	HIS	-	expression tag	UNP Q9HZ66
B	-4	HIS	-	expression tag	UNP Q9HZ66
B	-3	HIS	-	expression tag	UNP Q9HZ66
B	-2	HIS	-	expression tag	UNP Q9HZ66
B	-1	HIS	-	expression tag	UNP Q9HZ66
B	0	HIS	-	expression tag	UNP Q9HZ66

- Molecule 2 is FORMIC ACID (three-letter code: FMT) (formula: CH<sub>2</sub>O<sub>2</sub>).



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

- Molecule 3 is GLUTAMIC ACID (three-letter code: GLU) (formula:  $C_5H_9NO_4$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			10	5	1	4		

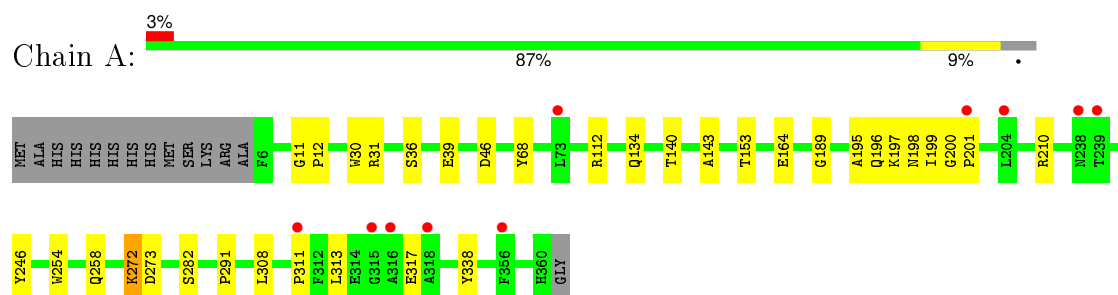
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	159	Total 160	O 160	0	1
4	B	73	Total 73	O 73	0	0

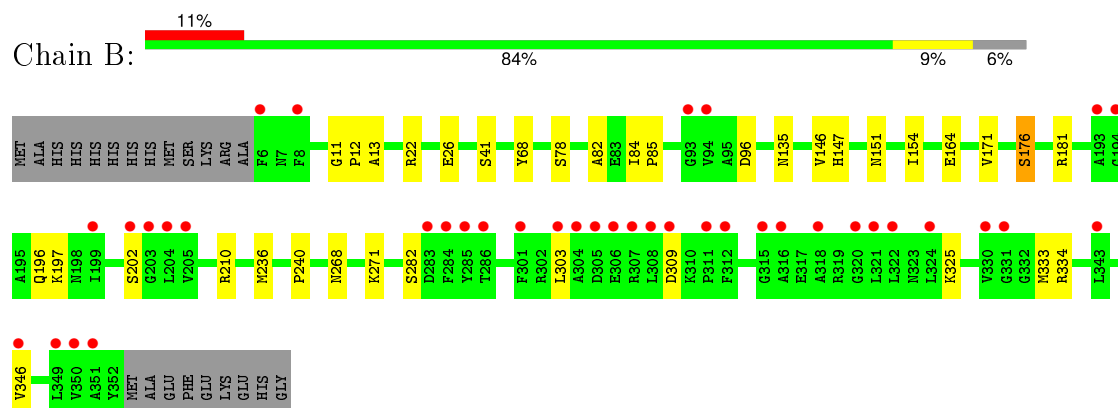
### 3 Residue-property plots [i](#)

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 ( $\text{RSRZ} > 2$ ). 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: Phosphoserine aminotransferase



#### • Molecule 1: Phosphoserine aminotransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	72.22Å 72.22Å 268.48Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.74 – 2.15 40.74 – 2.15	Depositor EDS
% Data completeness (in resolution range)	97.3 (40.74-2.15) 97.3 (40.74-2.15)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.59 (at 2.16Å)	Xtriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.179 , 0.219 0.177 , 0.219	Depositor DCC
$R_{free}$ test set	2200 reflections (4.98%)	DCC
Wilson B-factor (Å <sup>2</sup> )	42.7	Xtriage
Anisotropy	0.015	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 40.0	EDS
Estimated twinning fraction	0.045 for -h,-k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 44183 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5629	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.18% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: FMT, LLP

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	0.46	0/2788	0.62	0/3793
1	B	0.41	0/2671	0.58	0/3643
All	All	0.44	0/5459	0.60	0/7436

There are no bond length outliers.

There are no bond angle outliers.

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	2748	0	2632	22	0
1	B	2629	0	2486	21	0
2	A	6	0	2	1	0
2	B	3	0	1	1	0
3	B	10	0	5	0	0
4	A	160	0	0	3	0
4	B	73	0	0	2	0
All	All	5629	0	5126	43	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 (43) 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:291:PRO:HB3	2:A:402:FMT:H	1.74	0.69
1:A:282:SER:O	4:A:612:HOH:O	2.15	0.64
1:A:68:TYR:CZ	1:A:210:ARG:HG2	2.38	0.58
1:B:282:SER:O	4:B:537:HOH:O	2.17	0.57
1:A:46:ASP:OD2	4:A:610:HOH:O	2.17	0.57
1:B:268:ASN:HA	1:B:271:LYS:HE2	1.88	0.54
1:B:271:LYS:HB3	1:B:346:VAL:HG21	1.90	0.54
2:B:401:FMT:H	4:B:534:HOH:O	2.09	0.52
1:A:272:LYS:HE2	1:A:273:ASP:OD1	2.12	0.50
1:B:151:ASN:HD22	1:B:176:SER:HB2	1.76	0.49
1:A:189:GLY:HA2	1:A:210:ARG:HG3	1.95	0.49
1:B:96:ASP:HB2	1:B:146:VAL:HG22	1.95	0.49
1:A:68:TYR:CE2	1:A:210:ARG:HG2	2.47	0.49
1:A:153:THR:OG1	1:A:197:LLP:O3	2.22	0.48
1:B:82:ALA:O	1:B:85:PRO:HD2	2.12	0.48
1:B:78:SER:HB2	1:B:197:LLP:OP2	2.13	0.47
1:A:12:PRO:HD2	1:B:41:SER:HA	1.97	0.47
1:B:68:TYR:CZ	1:B:210:ARG:HG2	2.50	0.47
1:B:325:LYS:HA	1:B:333:MET:HE2	1.98	0.46
1:A:36:SER:HB3	1:A:39:GLU:HG3	1.97	0.45
1:B:22:ARG:O	1:B:26:GLU:HG2	2.16	0.45
1:B:84:ILE:HB	1:B:85:PRO:HD3	1.98	0.45
1:A:308:LEU:C	1:A:311:PRO:HD2	2.37	0.45
1:A:11:GLY:HA2	1:A:12:PRO:C	2.37	0.44
1:B:196:GLN:HB3	1:B:202:SER:HA	1.99	0.43
1:B:11:GLY:HA2	1:B:12:PRO:HA	1.83	0.43
1:B:197:LLP:HE3	1:B:197:LLP:O3	2.19	0.43
1:A:198:ASN:OD1	1:A:338:TYR:HB3	2.19	0.42
1:B:13:ALA:HB2	1:B:197:LLP:O	2.20	0.42
1:A:200:GLY:HA3	1:A:201:PRO:HD3	1.82	0.42
1:A:30:TRP:CH2	1:A:31:ARG:HD2	2.54	0.42
1:A:254:TRP:O	1:A:258:GLN:HG2	2.19	0.42
1:B:154:ILE:HD13	1:B:334:ARG:HH12	1.85	0.42
1:B:147:HIS:HA	1:B:171:VAL:O	2.20	0.41
1:B:236:MET:HG2	1:B:240:PRO:HG3	2.01	0.41
1:A:196:GLN:HA	1:A:200:GLY:O	2.21	0.41
1:A:140:THR:HB	1:A:143:ALA:HB2	2.02	0.41
1:A:313:LEU:HD23	1:A:313:LEU:HA	1.95	0.41
1:A:195:ALA:HA	1:A:199:ILE:HB	2.03	0.41
1:B:303:LEU:HD12	1:B:309:ASP:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:ARG:NH2	4:A:505:HOH:O	2.46	0.40
1:B:196:GLN:NE2	1:B:197:LLP:OP3	2.53	0.40

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	353/369 (96%)	343 (97%)	10 (3%)	0	100	100
1	B	347/369 (94%)	335 (96%)	12 (4%)	0	100	100
All	All	700/738 (95%)	678 (97%)	22 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	277/298 (93%)	272 (98%)	5 (2%)	66	71
1	B	258/298 (87%)	252 (98%)	6 (2%)	58	62
All	All	535/596 (90%)	524 (98%)	11 (2%)	72	65

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	164[A]	GLU
1	A	164[B]	GLU
1	A	246	TYR
1	A	272	LYS
1	A	317	GLU
1	B	135[A]	ASN
1	B	135[B]	ASN
1	B	164[A]	GLU
1	B	164[B]	GLU
1	B	176	SER
1	B	181	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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	197	1	23,24,25	2.75	9 (39%)	28,32,34	1.55	5 (17%)
1	LLP	B	197	1	23,24,25	2.24	4 (17%)	28,32,34	1.60	7 (25%)

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	197	1	-	0/15/17/19	0/1/1/1
1	LLP	B	197	1	-	0/15/17/19	0/1/1/1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	197	LLP	OP4-C5'	-2.56	1.34	1.44
1	A	197	LLP	C4-C5	-2.46	1.38	1.42
1	A	197	LLP	OP4-C5'	-2.44	1.34	1.44
1	A	197	LLP	CD-CE	2.18	1.58	1.51
1	A	197	LLP	CE-NZ	2.26	1.51	1.46
1	A	197	LLP	C2-N1	2.37	1.39	1.34
1	B	197	LLP	C4-C4'	2.47	1.51	1.46
1	A	197	LLP	C6-C5	3.17	1.44	1.37
1	A	197	LLP	C4-C4'	3.45	1.52	1.46
1	B	197	LLP	P-OP4	5.57	1.78	1.60
1	A	197	LLP	P-OP4	5.93	1.80	1.60
1	B	197	LLP	C4'-NZ	7.55	1.50	1.27
1	A	197	LLP	C4'-NZ	9.25	1.55	1.27

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	197	LLP	C4-C4'-NZ	-3.13	107.62	125.06
1	B	197	LLP	OP3-P-OP4	-3.06	97.75	106.56
1	B	197	LLP	C4-C4'-NZ	-3.03	108.21	125.06
1	A	197	LLP	OP4-P-OP1	-2.95	99.63	107.14
1	A	197	LLP	OP2-P-OP4	-2.85	98.37	106.56
1	B	197	LLP	OP4-P-OP1	-2.79	100.05	107.14
1	B	197	LLP	CE-NZ-C4'	-2.33	112.23	118.97
1	B	197	LLP	O-C-CA	-2.14	119.93	125.49
1	A	197	LLP	O-C-CA	-2.13	119.93	125.49
1	B	197	LLP	OP3-P-OP1	2.08	117.28	110.58
1	B	197	LLP	OP3-P-OP2	2.79	118.00	107.38
1	A	197	LLP	OP3-P-OP2	3.07	119.06	107.38

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	197	LLP	1	0
1	B	197	LLP	4	0

## 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	FMT	A	401	-	0,2,2	0.00	-	0,1,1	0.00	-
2	FMT	A	402	-	0,2,2	0.00	-	0,1,1	0.00	-
2	FMT	B	401	-	0,2,2	0.00	-	0,1,1	0.00	-
3	GLU	B	402	-	3,9,9	0.44	0	2,11,11	0.53	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	FMT	A	401	-	-	0/0/0/0	0/0/0/0
2	FMT	A	402	-	-	0/0/0/0	0/0/0/0
2	FMT	B	401	-	-	0/0/0/0	0/0/0/0
3	GLU	B	402	-	-	0/3/9/9	0/0/0/0

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.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	402	FMT	1	0
2	B	401	FMT	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 ⓘ

### 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, 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	354/369 (95%)	-0.05	10 (2%) 56 66	32, 47, 76, 103	0
1	B	346/369 (93%)	0.43	39 (11%) 7 11	41, 61, 103, 138	0
All	All	700/738 (94%)	0.19	49 (7%) 19 26	32, 55, 92, 138	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	312	PHE	6.2
1	B	320	GLY	6.0
1	B	318	ALA	5.7
1	B	311	PRO	5.2
1	B	304	ALA	5.1
1	B	330	VAL	5.1
1	B	303	LEU	4.7
1	B	321	LEU	4.6
1	B	305	ASP	4.2
1	B	351	ALA	4.0
1	B	284	PHE	3.9
1	B	307	ARG	3.8
1	B	315	GLY	3.6
1	A	356	PHE	3.5
1	B	285	TYR	3.5
1	A	318	ALA	3.2
1	A	73	LEU	3.2
1	B	316	ALA	3.2
1	B	8	PHE	3.2
1	B	199	ILE	3.1
1	B	193	ALA	3.1
1	B	301	PHE	3.1
1	B	346	VAL	3.1
1	B	324	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	204	LEU	2.9
1	B	322	LEU	2.9
1	B	350	VAL	2.9
1	B	308	LEU	2.9
1	B	343	LEU	2.8
1	B	194	GLY	2.7
1	A	239	THR	2.6
1	B	6	PHE	2.6
1	B	306	GLU	2.6
1	B	283	ASP	2.6
1	A	316	ALA	2.5
1	B	203	GLY	2.5
1	B	94	VAL	2.4
1	A	201	PRO	2.3
1	B	205	VAL	2.2
1	A	204	LEU	2.2
1	B	331	GLY	2.2
1	B	349	LEU	2.2
1	B	202	SER	2.1
1	B	309	ASP	2.1
1	B	286	THR	2.1
1	A	311	PRO	2.1
1	A	315	GLY	2.1
1	A	238	ASN	2.0
1	B	93	GLY	2.0

## 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, 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	LLP	B	197	24/25	0.94	0.20	-	51,65,87,92	7
1	LLP	A	197	24/25	0.95	0.20	-	37,49,64,77	8

## 6.3 Carbohydrates ⓘ

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, 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	FMT	B	401	3/3	0.88	0.24	1.78	64,64,65,69	0
3	GLU	B	402	10/10	0.91	0.12	-0.07	62,76,97,102	0
2	FMT	A	401	3/3	0.93	0.09	-0.10	68,68,78,85	0
2	FMT	A	402	3/3	0.83	0.26	-	68,68,70,72	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.