



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 16, 2017 – 03:14 PM EST

PDB ID : 5UPS  
Title : Acyl-CoA synthetase PtmM4 from *Streptomyces platensis* in complex with SBNP663 ligand  
Authors : Osipiuk, J.; Hatzos-Skintges, C.; Endres, M.; Babnigg, G.; Rudolf, J.D.; Chang, C.-Y.; Ma, M.; Shen, B.; Phillips Jr., G.N.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG); Enzyme Discovery for Natural Product Biosynthesis (NatPro)  
Deposited on : 2017-02-03  
Resolution : 2.05 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	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20028442
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)	:	rb-20028442

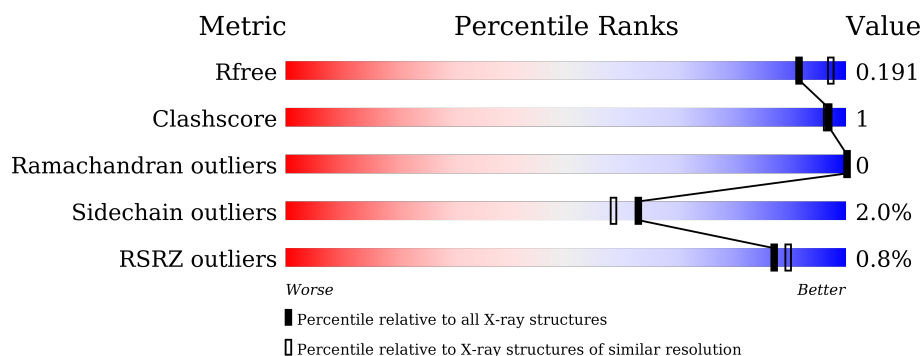
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.05 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	1192 (2.04-2.04)
Clashscore	102246	1269 (2.04-2.04)
Ramachandran outliers	100387	1258 (2.04-2.04)
Sidechain outliers	100360	1258 (2.04-2.04)
RSRZ outliers	91569	1194 (2.04-2.04)

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	525	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 98%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> <span>%</span> <span>94%</span> <span>5% .</span> </div> </div>
1	B	525	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 98%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> <span>%</span> <span>94%</span> <span>5% .</span> </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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	FMT	A	703	-	-	-	X
4	FMT	B	601	-	-	-	X
4	FMT	B	604	-	-	-	X
4	FMT	B	605	-	-	-	X
4	FMT	B	607	-	-	-	X
4	FMT	B	608	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8854 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.

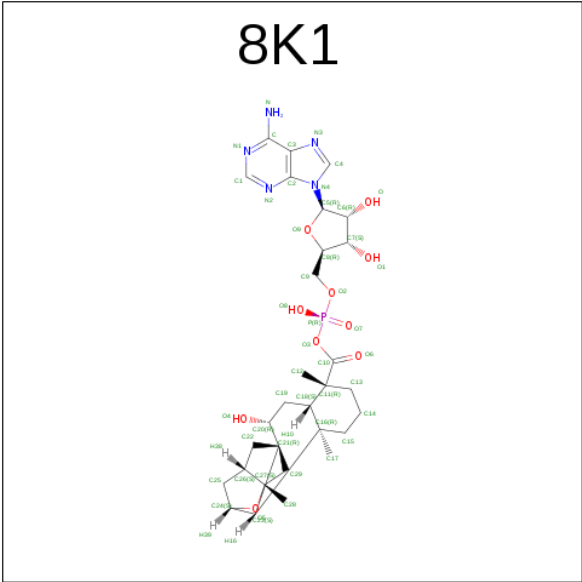
- Molecule 1 is a protein called Acyl-CoA synthetase PtmA2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	520	Total	C	N	O	S	Se	0	7	0
			4015	2507	748	742	7	11			
1	B	520	Total	C	N	O	S	Se	0	4	0
			3993	2493	742	740	7	11			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP A0A0A0V031
A	-1	ASN	-	expression tag	UNP A0A0A0V031
A	0	ALA	-	expression tag	UNP A0A0A0V031
A	1	LEU	-	expression tag	UNP A0A0A0V031
A	141	PRO	ALA	conflict	UNP A0A0A0V031
A	246	ASP	GLY	conflict	UNP A0A0A0V031
B	-2	SER	-	expression tag	UNP A0A0A0V031
B	-1	ASN	-	expression tag	UNP A0A0A0V031
B	0	ALA	-	expression tag	UNP A0A0A0V031
B	1	LEU	-	expression tag	UNP A0A0A0V031
B	141	PRO	ALA	conflict	UNP A0A0A0V031
B	246	ASP	GLY	conflict	UNP A0A0A0V031

- Molecule 2 is 5'-O-[(R)-hydroxy{[(7beta,8alpha,9beta,10alpha,11beta,13alpha)-7-hydroxy-19-oxo-11,16-epoxykauran-19-yl]oxy}phosphoryl]adenosine (three-letter code: 8K1) (formula: C<sub>30</sub>H<sub>42</sub>N<sub>5</sub>O<sub>10</sub>P).

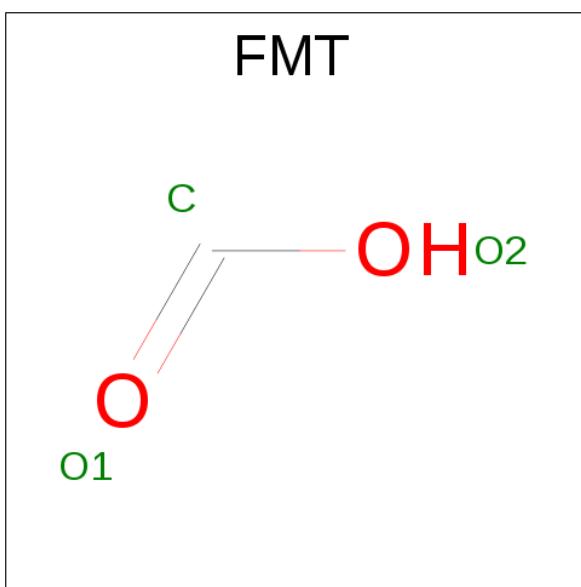


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			46	30	5	10	1		
2	B	1	Total	C	N	O	P	0	0
			46	30	5	10	1		

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Na	0	0
			1	1		
3	A	1	Total	Na	0	0
			1	1		

- Molecule 4 is FORMIC ACID (three-letter code: FMT) (formula: CH<sub>2</sub>O<sub>2</sub>).



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

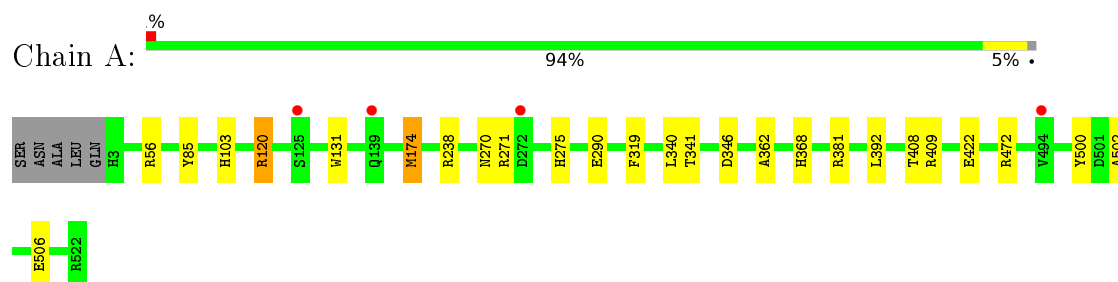
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	361	Total	O	0	0
			361	361		
5	B	361	Total	O	0	0
			361	361		

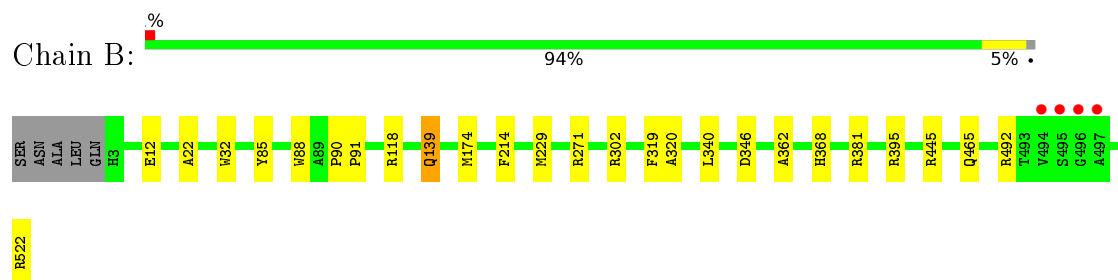
### 3 Residue-property plots [i](#)

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: Acyl-CoA synthetase PtmA2



- Molecule 1: Acyl-CoA synthetase PtmA2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	162.67Å 162.67Å 114.14Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.30 – 2.05 48.25 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.30-2.05) 99.9 (48.25-2.05)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.83 (at 2.05Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.156 , 0.188 0.164 , 0.191	Depositor DCC
$R_{free}$ test set	5381 reflections (5.20%)	DCC
Wilson B-factor (Å <sup>2</sup> )	37.0	Xtriage
Anisotropy	0.049	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 41.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.023 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	8854	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.11% 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: NA, FMT, 8K1

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	0.55	0/4123	0.75	2/5591 (0.0%)
1	B	0.57	0/4093	0.76	6/5554 (0.1%)
All	All	0.56	0/8216	0.75	8/11145 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	445	ARG	NE-CZ-NH2	-6.02	117.29	120.30
1	B	271	ARG	NE-CZ-NH1	5.99	123.29	120.30
1	B	381	ARG	NE-CZ-NH1	5.98	123.29	120.30
1	B	302	ARG	NE-CZ-NH1	5.38	122.99	120.30
1	A	346	ASP	CB-CG-OD1	5.37	123.13	118.30
1	B	346	ASP	CB-CG-OD1	5.29	123.06	118.30
1	A	381	ARG	NE-CZ-NH1	5.27	122.94	120.30
1	B	229	MSE	CG-SE-CE	-5.07	87.75	98.90

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	4015	0	3916	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3993	0	3884	10	0
2	A	46	0	0	0	0
2	B	46	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	12	0	6	0	0
4	B	18	0	9	0	0
5	A	361	0	0	2	0
5	B	361	0	0	0	0
All	All	8854	0	7815	21	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 1.

All (21) 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:340:LEU:HD11	1:A:362:ALA:HB1	1.82	0.61
1:A:502:ALA:O	1:A:506:GLU:HG2	2.03	0.58
1:B:340:LEU:HD11	1:B:362:ALA:HB1	1.86	0.58
1:A:120:ARG:HG3	1:A:131:TRP:CH2	2.41	0.55
1:A:341[B]:THR:HG22	1:B:12:GLU:HB2	1.89	0.55
1:A:422:GLU:OE2	5:A:801:HOH:O	2.20	0.50
1:B:320:ALA:HB1	1:B:340:LEU:HD22	1.95	0.48
1:B:85:TYR:CE2	1:B:214:PHE:CE1	3.03	0.46
1:A:56:ARG:H	1:A:103[A]:HIS:HD2	1.63	0.45
1:B:139:GLN:CD	1:B:139:GLN:H	2.19	0.45
1:A:271:ARG:NH1	1:A:290:GLU:OE1	2.50	0.44
1:A:56:ARG:H	1:A:103[A]:HIS:CD2	2.34	0.44
1:A:409[A]:ARG:CZ	1:A:500:TYR:HB3	2.48	0.43
1:B:22:ALA:HB2	1:B:32:TRP:CD2	2.55	0.42
1:B:85:TYR:HB2	1:B:88:TRP:CD2	2.54	0.42
1:A:270:ASN:OD1	1:A:275:HIS:HB2	2.19	0.42
1:B:85:TYR:HB2	1:B:88:TRP:CE2	2.55	0.41
1:A:174:MSE:HE2	1:A:408:THR:HG21	2.02	0.41
1:A:472:ARG:HD2	5:A:852:HOH:O	2.21	0.40
1:B:85:TYR:HA	1:B:214:PHE:CD2	2.56	0.40
1:B:90:PRO:HB2	1:B:91:PRO:HD3	2.03	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	525/525 (100%)	514 (98%)	11 (2%)	0	100	100
1	B	522/525 (99%)	510 (98%)	12 (2%)	0	100	100
All	All	1047/1050 (100%)	1024 (98%)	23 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	407/393 (104%)	400 (98%)	7 (2%)	68	65
1	B	404/393 (103%)	395 (98%)	9 (2%)	60	53
All	All	811/786 (103%)	795 (98%)	16 (2%)	63	58

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	85	TYR
1	A	120	ARG
1	A	174	MSE
1	A	238	ARG
1	A	319	PHE
1	A	368	HIS
1	A	392	LEU
1	B	118	ARG

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Mol	Chain	Res	Type
1	B	139	GLN
1	B	174	MSE
1	B	319	PHE
1	B	368	HIS
1	B	395	ARG
1	B	465	GLN
1	B	492	ARG
1	B	522	ARG

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

### 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](#)

Of 14 ligands modelled in this entry, 2 are monoatomic - leaving 12 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
2	8K1	A	701	-	49,53,53	1.19	3 (6%)	61,89,89	1.56	6 (9%)
4	FMT	A	703	-	0,2,2	0.00	-	0,1,1	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	FMT	A	704	-	0,2,2	0.00	-	0,1,1	0.00	-
4	FMT	A	705	-	0,2,2	0.00	-	0,1,1	0.00	-
4	FMT	A	706	-	0,2,2	0.00	-	0,1,1	0.00	-
4	FMT	B	601	-	0,2,2	0.00	-	0,1,1	0.00	-
2	8K1	B	602	-	49,53,53	1.69	5 (10%)	61,89,89	1.70	9 (14%)
4	FMT	B	604	-	0,2,2	0.00	-	0,1,1	0.00	-
4	FMT	B	605	-	0,2,2	0.00	-	0,1,1	0.00	-
4	FMT	B	606	-	0,2,2	0.00	-	0,1,1	0.00	-
4	FMT	B	607	-	0,2,2	0.00	-	0,1,1	0.00	-
4	FMT	B	608	-	0,2,2	0.00	-	0,1,1	0.00	-

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	8K1	A	701	-	-	0/15/109/109	0/5/8/8
4	FMT	A	703	-	-	0/0/0/0	0/0/0/0
4	FMT	A	704	-	-	0/0/0/0	0/0/0/0
4	FMT	A	705	-	-	0/0/0/0	0/0/0/0
4	FMT	A	706	-	-	0/0/0/0	0/0/0/0
4	FMT	B	601	-	-	0/0/0/0	0/0/0/0
2	8K1	B	602	-	-	0/15/109/109	0/5/8/8
4	FMT	B	604	-	-	0/0/0/0	0/0/0/0
4	FMT	B	605	-	-	0/0/0/0	0/0/0/0
4	FMT	B	606	-	-	0/0/0/0	0/0/0/0
4	FMT	B	607	-	-	0/0/0/0	0/0/0/0
4	FMT	B	608	-	-	0/0/0/0	0/0/0/0

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	602	8K1	P-O8	-2.30	1.45	1.55
2	B	602	8K1	P-O3	2.22	1.65	1.60
2	B	602	8K1	P-O7	2.27	1.59	1.51
2	B	602	8K1	C3-C2	2.31	1.45	1.40
2	A	701	8K1	C1-N2	2.35	1.36	1.32
2	A	701	8K1	C3-C2	2.80	1.46	1.40
2	A	701	8K1	O3-C10	4.89	1.43	1.37
2	B	602	8K1	O3-C10	9.57	1.50	1.37

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	8K1	N2-C1-N1	-7.41	123.05	128.87
2	B	602	8K1	N2-C1-N1	-6.51	123.75	128.87
2	B	602	8K1	C19-C20-C21	-4.67	109.25	112.27
2	A	701	8K1	C27-C29-C21	-4.53	100.29	106.99
2	A	701	8K1	C5-N4-C2	-3.88	122.47	126.81
2	B	602	8K1	C27-C29-C21	-3.69	101.53	106.99
2	B	602	8K1	O6-C10-C11	-3.12	120.51	125.27
2	B	602	8K1	C5-N4-C2	-3.11	123.33	126.81
2	B	602	8K1	O5-C24-C25	-2.68	97.13	103.98
2	B	602	8K1	C17-C16-C15	-2.39	104.18	108.23
2	A	701	8K1	C12-C11-C10	-2.37	100.95	106.49
2	A	701	8K1	O3-C10-O6	-2.22	120.38	122.10
2	A	701	8K1	C21-C23-C16	2.02	119.17	115.85
2	B	602	8K1	C15-C16-C18	2.32	111.17	108.06
2	B	602	8K1	N-C-N1	2.77	123.17	118.52

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers ⓘ

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	509/525 (96%)	-0.49	4 (0%) 87 90	29, 38, 55, 77	0
1	B	509/525 (96%)	-0.53	4 (0%) 87 90	28, 37, 55, 82	0
All	All	1018/1050 (96%)	-0.51	8 (0%) 87 90	28, 38, 55, 82	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	497	ALA	3.8
1	B	496	GLY	3.1
1	B	494	VAL	2.5
1	B	495	SER	2.5
1	A	272	ASP	2.4
1	A	139	GLN	2.4
1	A	494	VAL	2.0
1	A	125	SER	2.0

### 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, 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
4	FMT	B	604	3/3	0.80	0.16	7.99	51,51,51,53	0
4	FMT	B	607	3/3	0.96	0.14	7.68	51,51,51,53	0
4	FMT	B	605	3/3	0.88	0.22	6.28	56,56,57,58	0
4	FMT	A	703	3/3	0.77	0.24	3.72	51,51,58,61	0
4	FMT	B	601	3/3	0.88	0.25	3.24	50,50,52,56	0
4	FMT	B	608	3/3	0.87	0.16	2.52	51,51,53,56	0
4	FMT	B	606	3/3	0.88	0.11	1.80	42,42,46,50	0
4	FMT	A	706	3/3	0.94	0.14	1.79	31,31,38,43	0
4	FMT	A	705	3/3	0.93	0.18	0.54	59,59,60,61	0
2	8K1	A	701	46/46	0.98	0.11	0.15	28,30,33,34	0
2	8K1	B	602	46/46	0.98	0.10	0.02	28,32,38,41	0
3	NA	B	603	1/1	0.95	0.07	-0.67	43,43,43,43	0
3	NA	A	702	1/1	0.99	0.06	-0.82	41,41,41,41	0
4	FMT	A	704	3/3	0.92	0.16	-	63,63,63,64	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.