



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 4, 2017 – 05:17 PM EST

PDB ID : 5UFM  
Title : Crystal structure of Burkholderia thailandensis 1,6-didemethyltoxoflavin-N1-methyltransferase with bound 1,6-didemethyltoxoflavin and S-adenosylhomocysteine  
Authors : Fenwick, M.K.; Ealick, S.E.; Almaguer, K.H.; Begley, T.P.; Philmus, B.  
Deposited on : unknown  
Resolution : 1.77 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.

---

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 : rb-20030345  
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) : rb-20030345

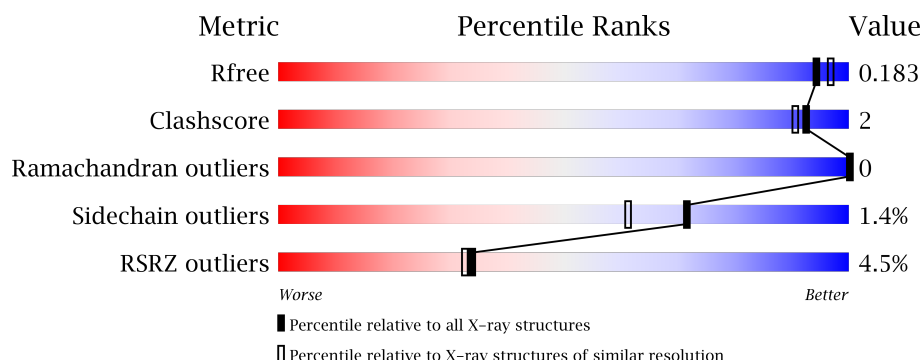
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.77 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	7172 (1.80-1.76)
Clashscore	112137	8247 (1.80-1.76)
Ramachandran outliers	110173	8154 (1.80-1.76)
Sidechain outliers	110143	8153 (1.80-1.76)
RSRZ outliers	101464	7262 (1.80-1.76)

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	238	<div> <div>5%</div> <div> <div></div> <div>88%</div> <div>6%</div> <div>5%</div> </div> </div>
1	B	238	<div> <div>4%</div> <div> <div></div> <div>90%</div> <div>6%</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	EPE	A	308	-	-	-	X
5	EPE	A	309[A]	-	-	-	X
5	EPE	A	309[B]	-	-	-	X

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4232 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.

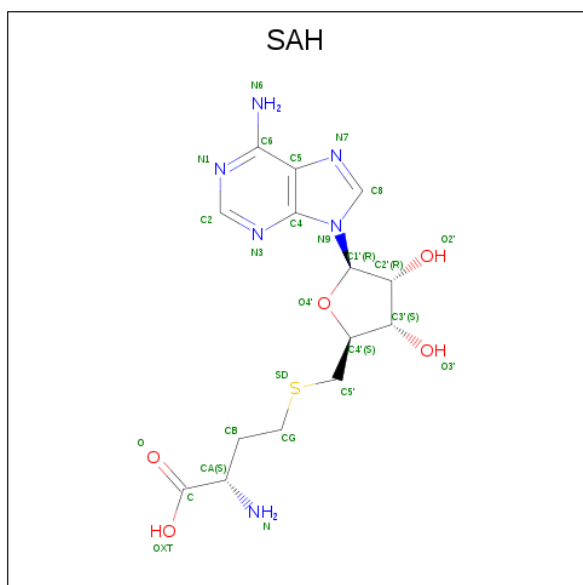
- Molecule 1 is a protein called Methyltransferase domain protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	225	Total	C	N	O	S	0	9	0
			1811	1138	338	331	4			
1	B	223	Total	C	N	O	S	0	4	0
			1783	1121	340	318	4			

There are 4 discrepancies between the modelled and reference sequences:

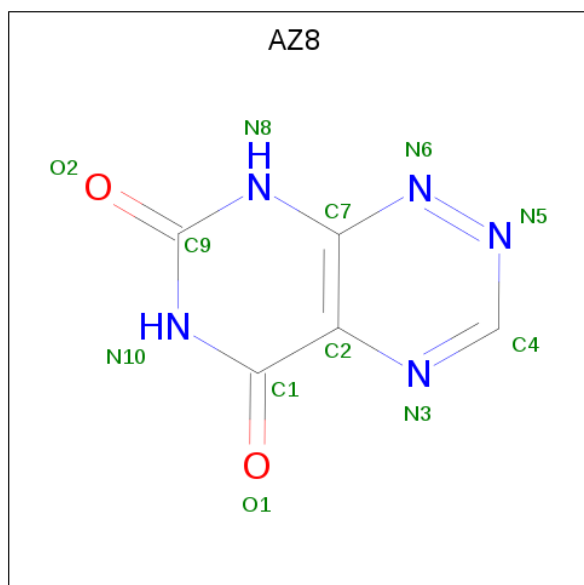
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q2T5S0
A	0	HIS	-	expression tag	UNP Q2T5S0
B	-1	GLY	-	expression tag	UNP Q2T5S0
B	0	HIS	-	expression tag	UNP Q2T5S0

- Molecule 2 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula:  $C_{14}H_{20}N_6O_5S$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	B	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

- Molecule 3 is pyrimido[5,4-e][1,2,4]triazine-5,7(6H,8H)-dione (three-letter code: AZ8) (formula: C<sub>5</sub>H<sub>3</sub>N<sub>5</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			12	5	5	2		
3	B	1	Total	C	N	O	0	0
			12	5	5	2		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C<sub>8</sub>H<sub>18</sub>N<sub>2</sub>O<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
5	A	1	Total	C	N	O	S	0	1
			30	16	4	8	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	221	Total	O	0	6
			221	221		
6	B	241	Total	O	0	1
			241	241		



- Molecule 1: Methyltransferase domain protein



- |     |     |     |     |     |     |     |    |    |     |     |     |     |     |     |     |      |      |      |      |      |      |      |      |      |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|----|----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GLY | HIS | NET | SER | ALA | ALA | GLU | PO | H7 | R13 | V18 | D19 | A20 | F21 | F36 | E98 | E111 | H139 | D171 | G172 | L176 | R183 | E190 | R198 | P228 | SER | THR | ASP | ALA | ALA | SER | GLY | ARG | ARG |
|-----|-----|-----|-----|-----|-----|-----|----|----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	112.70 Å 112.70 Å 78.37 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	23.00 – 1.77 23.03 – 1.77	Depositor EDS
% Data completeness (in resolution range)	98.1 (23.00-1.77) 98.2 (23.03-1.77)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.00 (at 1.77 Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: 000)	Depositor
R, $R_{free}$	0.152 , 0.184 0.151 , 0.183	Depositor DCC
$R_{free}$ test set	2663 reflections (4.92%)	DCC
Wilson B-factor (Å <sup>2</sup> )	19.5	Xtriage
Anisotropy	0.575	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 52.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.040 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	4232	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.06% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: AZ8, SAH, EPE, SO4

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	0.36	0/1864	0.54	0/2543
1	B	0.34	0/1835	0.53	0/2500
All	All	0.35	0/3699	0.53	0/5043

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	1811	0	1718	7	0
1	B	1783	0	1713	5	0
2	A	26	0	19	0	0
2	B	26	0	19	1	0
3	A	12	0	0	0	0
3	B	12	0	0	0	0
4	A	30	0	0	0	0
4	B	25	0	0	0	0
5	A	45	0	54	0	0
6	A	221	0	0	1	0
6	B	241	0	0	3	0
All	All	4232	0	3523	13	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 2.

All (13) 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:94:VAL:HG21	1:A:123:LEU:HD11	1.71	0.71
1:B:98:GLU:OE2	6:B:401:HOH:O	2.13	0.67
1:A:4:ALA:HB2	1:A:175[A]:ARG:HD3	1.76	0.66
1:A:26:HIS:ND1	6:A:403:HOH:O	2.31	0.61
1:A:119:PRO:HD2	1:A:122[B]:GLU:HG3	1.82	0.59
1:B:18:VAL:HG21	1:B:176:LEU:HD23	1.92	0.51
1:B:13:ARG:HD2	6:B:404:HOH:O	2.16	0.46
1:A:99:PRO:HD2	1:A:102:TRP:CE2	2.53	0.43
1:A:190:GLU:HA	1:A:220:LEU:HD21	1.99	0.43
1:A:77:ARG:HA	1:A:99:PRO:HG3	2.01	0.42
2:B:302:SAH:HB1	2:B:302:SAH:H4'	2.02	0.42
1:B:36:PHE:CE2	1:B:183[B]:ARG:HD2	2.55	0.41
1:B:198[A]:ARG:NH2	6:B:405:HOH:O	2.36	0.41

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	229/238 (96%)	225 (98%)	4 (2%)	0	100	100
1	B	224/238 (94%)	221 (99%)	3 (1%)	0	100	100
All	All	453/476 (95%)	446 (98%)	7 (2%)	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	181/185 (98%)	178 (98%)	3 (2%)	66	53
1	B	177/185 (96%)	175 (99%)	2 (1%)	78	70
All	All	358/370 (97%)	353 (99%)	5 (1%)	71	61

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	ASP
1	A	33[A]	ARG
1	A	139	HIS
1	B	139	HIS
1	B	190	GLU

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](#)

18 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	SAH	A	301	-	20,28,28	1.20	2 (10%)	20,40,40	1.95	3 (15%)
3	AZ8	A	302	-	11,13,13	1.81	3 (27%)	10,18,18	4.03	9 (90%)
4	SO4	A	303	-	4,4,4	0.17	0	6,6,6	0.08	0
4	SO4	A	304	-	4,4,4	0.17	0	6,6,6	0.13	0
4	SO4	A	305	-	4,4,4	0.15	0	6,6,6	0.06	0
4	SO4	A	306	-	4,4,4	0.15	0	6,6,6	0.06	0
4	SO4	A	307	-	4,4,4	0.13	0	6,6,6	0.07	0
5	EPE	A	308	-	15,15,15	1.92	1 (6%)	18,20,20	1.34	3 (16%)
5	EPE	A	309[A]	-	15,15,15	1.91	1 (6%)	18,20,20	1.42	3 (16%)
5	EPE	A	309[B]	-	15,15,15	1.92	1 (6%)	18,20,20	1.40	3 (16%)
4	SO4	A	310	-	4,4,4	0.40	0	6,6,6	0.18	0
4	SO4	B	301	-	4,4,4	0.16	0	6,6,6	0.31	0
2	SAH	B	302	-	20,28,28	1.16	2 (10%)	20,40,40	1.82	2 (10%)
3	AZ8	B	303	-	11,13,13	1.89	2 (18%)	10,18,18	3.84	8 (80%)
4	SO4	B	304	-	4,4,4	0.14	0	6,6,6	0.15	0
4	SO4	B	305	-	4,4,4	0.19	0	6,6,6	0.34	0
4	SO4	B	306	-	4,4,4	0.14	0	6,6,6	0.07	0
4	SO4	B	307	-	4,4,4	0.15	0	6,6,6	0.05	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	SAH	A	301	-	-	0/7/31/31	0/3/3/3
3	AZ8	A	302	-	-	0/0/0/0	0/2/2/2
4	SO4	A	303	-	-	0/0/0/0	0/0/0/0
4	SO4	A	304	-	-	0/0/0/0	0/0/0/0
4	SO4	A	305	-	-	0/0/0/0	0/0/0/0
4	SO4	A	306	-	-	0/0/0/0	0/0/0/0
4	SO4	A	307	-	-	0/0/0/0	0/0/0/0
5	EPE	A	308	-	-	0/9/19/19	0/1/1/1

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EPE	A	309[A]	-	-	0/9/19/19	0/1/1/1
5	EPE	A	309[B]	-	-	0/9/19/19	0/1/1/1
4	SO4	A	310	-	-	0/0/0/0	0/0/0/0
4	SO4	B	301	-	-	0/0/0/0	0/0/0/0
2	SAH	B	302	-	-	0/7/31/31	0/3/3/3
3	AZ8	B	303	-	-	0/0/0/0	0/2/2/2
4	SO4	B	304	-	-	0/0/0/0	0/0/0/0
4	SO4	B	305	-	-	0/0/0/0	0/0/0/0
4	SO4	B	306	-	-	0/0/0/0	0/0/0/0
4	SO4	B	307	-	-	0/0/0/0	0/0/0/0

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	308	EPE	C10-S	-7.16	1.66	1.77
5	A	309[B]	EPE	C10-S	-7.15	1.66	1.77
5	A	309[A]	EPE	C10-S	-7.11	1.66	1.77
3	B	303	AZ8	N5-N6	-3.87	1.29	1.34
3	A	302	AZ8	N5-N6	-3.10	1.30	1.34
3	A	302	AZ8	C7-N8	2.19	1.39	1.34
2	A	301	SAH	O4'-C1'	2.37	1.44	1.41
2	B	302	SAH	O4'-C1'	2.68	1.45	1.41
2	B	302	SAH	C5-C4	2.76	1.46	1.40
2	A	301	SAH	C5-C4	3.04	1.47	1.40
3	B	303	AZ8	C1-C2	3.39	1.47	1.41
3	A	302	AZ8	C1-C2	3.41	1.47	1.41

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	SAH	N3-C2-N1	-7.10	122.67	128.86
2	B	302	SAH	N3-C2-N1	-6.46	123.24	128.86
3	A	302	AZ8	N3-C4-N5	-4.98	120.57	128.65
3	B	303	AZ8	N3-C4-N5	-4.75	120.94	128.65
3	B	303	AZ8	C2-C1-N10	-4.08	117.68	123.48
3	A	302	AZ8	C2-C1-N10	-3.51	118.49	123.48
3	A	302	AZ8	C1-C2-C7	-2.86	117.65	119.96
3	A	302	AZ8	C2-C7-N6	-2.80	117.67	122.20
3	B	303	AZ8	C2-C7-N8	-2.21	118.42	122.11
2	A	301	SAH	C4-C5-N7	-2.10	107.38	109.41
2	B	302	SAH	C2-N1-C6	2.23	122.67	118.77
5	A	308	EPE	O2S-S-C10	2.35	108.81	106.79

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	309[A]	EPE	O3S-S-C10	2.47	109.09	106.06
2	A	301	SAH	C2-N1-C6	2.56	123.25	118.77
5	A	309[B]	EPE	O3S-S-C10	2.61	109.26	106.06
3	A	302	AZ8	C1-C2-N3	2.72	121.65	118.23
3	B	303	AZ8	N8-C7-N6	2.75	122.55	116.91
3	B	303	AZ8	C1-C2-N3	2.79	121.73	118.23
5	A	308	EPE	O3S-S-C10	2.92	109.65	106.06
5	A	308	EPE	O1S-S-C10	3.04	109.41	106.79
5	A	309[B]	EPE	O1S-S-C10	3.05	109.41	106.79
3	A	302	AZ8	N8-C7-N6	3.09	123.26	116.91
5	A	309[A]	EPE	O1S-S-C10	3.10	109.45	106.79
3	A	302	AZ8	C4-N3-C2	3.26	118.41	115.47
5	A	309[A]	EPE	O2S-S-C10	3.44	109.75	106.79
5	A	309[B]	EPE	O2S-S-C10	3.74	110.00	106.79
3	B	303	AZ8	C4-N3-C2	3.87	118.96	115.47
3	A	302	AZ8	C4-N5-N6	4.67	122.67	117.11
3	B	303	AZ8	C4-N5-N6	4.78	122.81	117.11
3	B	303	AZ8	C1-N10-C9	6.69	121.01	115.16
3	A	302	AZ8	C1-N10-C9	7.51	121.73	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	302	SAH	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	225/238 (94%)	0.05	11 (4%) 30 29	15, 22, 46, 86	1 (0%)
1	B	223/238 (93%)	-0.04	9 (4%) 39 38	15, 23, 49, 76	0
All	All	448/476 (94%)	0.01	20 (4%) 34 33	15, 22, 49, 86	1 (0%)

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	20	ALA	6.4
1	B	20	ALA	6.3
1	A	21	PRO	5.9
1	B	19	ASP	5.1
1	B	21	PRO	5.1
1	B	6	PRO	4.8
1	A	19	ASP	4.6
1	B	8	TYR	4.4
1	A	4	ALA	3.7
1	A	26	HIS	3.6
1	B	171	ASP	3.5
1	A	22	LEU	3.4
1	A	23	ALA	3.3
1	A	171	ASP	2.6
1	A	124	ASP	2.3
1	B	111	GLU	2.2
1	A	18	VAL	2.2
1	B	228	ASP	2.2
1	B	172	GLY	2.2
1	A	24	ALA	2.2



## 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
5	EPE	A	309[B]	15/15	0.59	0.32	8.36	81,93,112,113	15
5	EPE	A	309[A]	15/15	0.59	0.32	8.13	79,93,112,113	15
5	EPE	A	308	15/15	0.73	0.34	7.51	79,93,95,95	0
2	SAH	A	301	26/26	0.97	0.09	0.22	11,17,21,21	0
4	SO4	B	301	5/5	0.99	0.07	0.01	21,22,25,26	0
4	SO4	B	305	5/5	0.99	0.07	-0.01	29,34,36,37	0
3	AZ8	A	302	12/12	0.95	0.10	-0.17	18,23,39,41	0
4	SO4	A	310	5/5	0.97	0.07	-0.30	21,22,24,24	0
2	SAH	B	302	26/26	0.97	0.07	-0.66	14,17,21,22	0
3	AZ8	B	303	12/12	0.96	0.06	-1.41	20,23,28,28	0
4	SO4	A	304	5/5	0.98	0.11	-	34,41,45,56	0
4	SO4	A	303	5/5	0.99	0.10	-	28,34,36,43	0
4	SO4	B	307	5/5	0.91	0.31	-	100,101,102,103	0
4	SO4	A	305	5/5	0.96	0.17	-	56,58,63,69	0
4	SO4	B	304	5/5	0.96	0.09	-	45,55,60,64	0
4	SO4	B	306	5/5	0.89	0.26	-	85,93,97,98	0
4	SO4	A	306	5/5	0.94	0.31	-	109,111,112,114	0
4	SO4	A	307	5/5	0.90	0.21	-	109,109,109,111	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.