



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 1, 2017 – 08:10 PM EDT

PDB ID : 3SSM  
Title : MycE Methyltransferase from the Mycinamycin Biosynthetic Pathway in Complex with Mg and SAH, Crystal form 1  
Authors : Akey, D.L.; Smith, J.L.  
Deposited on : unknown  
Resolution : 2.25 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 : 1.7.2 (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

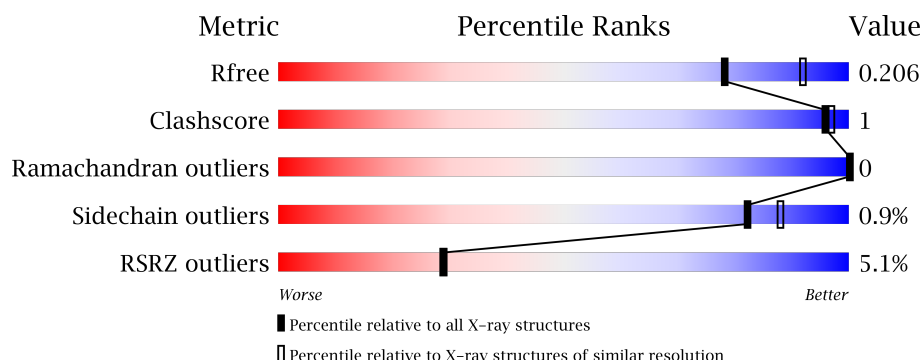
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.25 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	1804 (2.26-2.22)
Clashscore	112137	1957 (2.26-2.22)
Ramachandran outliers	110173	1916 (2.26-2.22)
Sidechain outliers	110143	1917 (2.26-2.22)
RSRZ outliers	101464	1809 (2.26-2.22)

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	419	<div> <div>5%</div> <div> <div></div> <div>90%</div> <div>•</div> <div>8%</div> </div> </div>
1	B	419	<div> <div>7%</div> <div> <div></div> <div>81%</div> <div>•</div> <div>16%</div> </div> </div>
1	C	419	<div> <div>3%</div> <div> <div></div> <div>82%</div> <div>•</div> <div>13%</div> </div> </div>
1	D	419	<div> <div>4%</div> <div> <div></div> <div>91%</div> <div>•</div> <div>6%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12852 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	387	Total	C	N	O	S	0	0	0
			3085	1960	548	569	8			
1	B	354	Total	C	N	O	S	0	0	0
			2805	1768	502	529	6			
1	C	363	Total	C	N	O	S	0	1	0
			2910	1852	517	533	8			
1	D	393	Total	C	N	O	S	0	0	0
			3126	1982	554	582	8			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP Q83WF2
A	-18	GLY	-	EXPRESSION TAG	UNP Q83WF2
A	-17	SER	-	EXPRESSION TAG	UNP Q83WF2
A	-16	SER	-	EXPRESSION TAG	UNP Q83WF2
A	-15	HIS	-	EXPRESSION TAG	UNP Q83WF2
A	-14	HIS	-	EXPRESSION TAG	UNP Q83WF2
A	-13	HIS	-	EXPRESSION TAG	UNP Q83WF2
A	-12	HIS	-	EXPRESSION TAG	UNP Q83WF2
A	-11	HIS	-	EXPRESSION TAG	UNP Q83WF2
A	-10	HIS	-	EXPRESSION TAG	UNP Q83WF2
A	-9	SER	-	EXPRESSION TAG	UNP Q83WF2
A	-8	SER	-	EXPRESSION TAG	UNP Q83WF2
A	-7	GLY	-	EXPRESSION TAG	UNP Q83WF2
A	-6	LEU	-	EXPRESSION TAG	UNP Q83WF2
A	-5	VAL	-	EXPRESSION TAG	UNP Q83WF2
A	-4	PRO	-	EXPRESSION TAG	UNP Q83WF2
A	-3	ARG	-	EXPRESSION TAG	UNP Q83WF2
A	-2	GLY	-	EXPRESSION TAG	UNP Q83WF2
A	-1	SER	-	EXPRESSION TAG	UNP Q83WF2
A	0	HIS	-	EXPRESSION TAG	UNP Q83WF2
B	-19	MET	-	EXPRESSION TAG	UNP Q83WF2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	EXPRESSION TAG	UNP Q83WF2
B	-17	SER	-	EXPRESSION TAG	UNP Q83WF2
B	-16	SER	-	EXPRESSION TAG	UNP Q83WF2
B	-15	HIS	-	EXPRESSION TAG	UNP Q83WF2
B	-14	HIS	-	EXPRESSION TAG	UNP Q83WF2
B	-13	HIS	-	EXPRESSION TAG	UNP Q83WF2
B	-12	HIS	-	EXPRESSION TAG	UNP Q83WF2
B	-11	HIS	-	EXPRESSION TAG	UNP Q83WF2
B	-10	HIS	-	EXPRESSION TAG	UNP Q83WF2
B	-9	SER	-	EXPRESSION TAG	UNP Q83WF2
B	-8	SER	-	EXPRESSION TAG	UNP Q83WF2
B	-7	GLY	-	EXPRESSION TAG	UNP Q83WF2
B	-6	LEU	-	EXPRESSION TAG	UNP Q83WF2
B	-5	VAL	-	EXPRESSION TAG	UNP Q83WF2
B	-4	PRO	-	EXPRESSION TAG	UNP Q83WF2
B	-3	ARG	-	EXPRESSION TAG	UNP Q83WF2
B	-2	GLY	-	EXPRESSION TAG	UNP Q83WF2
B	-1	SER	-	EXPRESSION TAG	UNP Q83WF2
B	0	HIS	-	EXPRESSION TAG	UNP Q83WF2
C	-19	MET	-	EXPRESSION TAG	UNP Q83WF2
C	-18	GLY	-	EXPRESSION TAG	UNP Q83WF2
C	-17	SER	-	EXPRESSION TAG	UNP Q83WF2
C	-16	SER	-	EXPRESSION TAG	UNP Q83WF2
C	-15	HIS	-	EXPRESSION TAG	UNP Q83WF2
C	-14	HIS	-	EXPRESSION TAG	UNP Q83WF2
C	-13	HIS	-	EXPRESSION TAG	UNP Q83WF2
C	-12	HIS	-	EXPRESSION TAG	UNP Q83WF2
C	-11	HIS	-	EXPRESSION TAG	UNP Q83WF2
C	-10	HIS	-	EXPRESSION TAG	UNP Q83WF2
C	-9	SER	-	EXPRESSION TAG	UNP Q83WF2
C	-8	SER	-	EXPRESSION TAG	UNP Q83WF2
C	-7	GLY	-	EXPRESSION TAG	UNP Q83WF2
C	-6	LEU	-	EXPRESSION TAG	UNP Q83WF2
C	-5	VAL	-	EXPRESSION TAG	UNP Q83WF2
C	-4	PRO	-	EXPRESSION TAG	UNP Q83WF2
C	-3	ARG	-	EXPRESSION TAG	UNP Q83WF2
C	-2	GLY	-	EXPRESSION TAG	UNP Q83WF2
C	-1	SER	-	EXPRESSION TAG	UNP Q83WF2
C	0	HIS	-	EXPRESSION TAG	UNP Q83WF2
D	-19	MET	-	EXPRESSION TAG	UNP Q83WF2
D	-18	GLY	-	EXPRESSION TAG	UNP Q83WF2
D	-17	SER	-	EXPRESSION TAG	UNP Q83WF2

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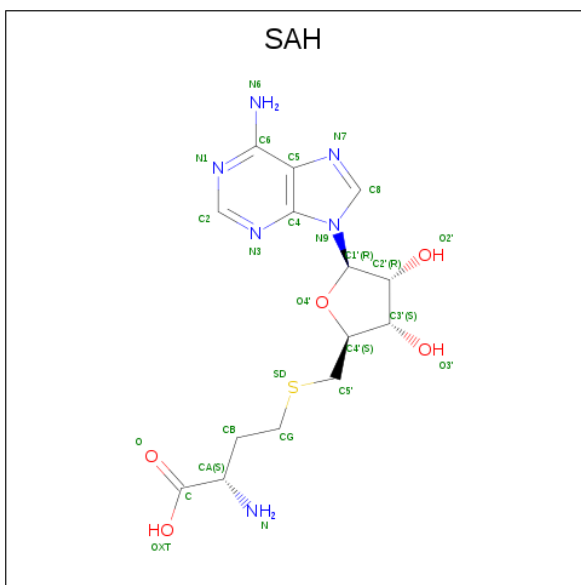
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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	EXPRESSION TAG	UNP Q83WF2
D	-15	HIS	-	EXPRESSION TAG	UNP Q83WF2
D	-14	HIS	-	EXPRESSION TAG	UNP Q83WF2
D	-13	HIS	-	EXPRESSION TAG	UNP Q83WF2
D	-12	HIS	-	EXPRESSION TAG	UNP Q83WF2
D	-11	HIS	-	EXPRESSION TAG	UNP Q83WF2
D	-10	HIS	-	EXPRESSION TAG	UNP Q83WF2
D	-9	SER	-	EXPRESSION TAG	UNP Q83WF2
D	-8	SER	-	EXPRESSION TAG	UNP Q83WF2
D	-7	GLY	-	EXPRESSION TAG	UNP Q83WF2
D	-6	LEU	-	EXPRESSION TAG	UNP Q83WF2
D	-5	VAL	-	EXPRESSION TAG	UNP Q83WF2
D	-4	PRO	-	EXPRESSION TAG	UNP Q83WF2
D	-3	ARG	-	EXPRESSION TAG	UNP Q83WF2
D	-2	GLY	-	EXPRESSION TAG	UNP Q83WF2
D	-1	SER	-	EXPRESSION TAG	UNP Q83WF2
D	0	HIS	-	EXPRESSION TAG	UNP Q83WF2

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0
2	C	1	Total Mg 1 1	0	0

- Molecule 3 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: C<sub>14</sub>H<sub>20</sub>N<sub>6</sub>O<sub>5</sub>S).



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

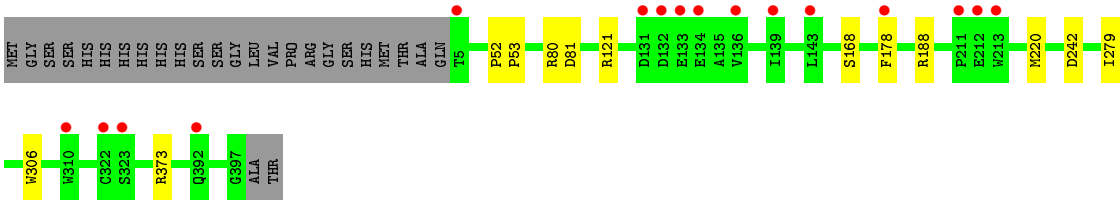
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	242	Total O 242 242	0	0
4	B	207	Total O 207 207	0	0
4	C	197	Total O 197 197	0	0
4	D	199	Total O 199 199	0	0



- Molecule 1: Methyltransferase







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	73.91Å 143.41Å 84.64Å 90.00° 105.60° 90.00°	Depositor
Resolution (Å)	81.52 – 2.25 47.65 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.5 (81.52-2.25) 99.5 (47.65-2.25)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.49 (at 2.24Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.165 , 0.210 0.163 , 0.206	Depositor DCC
$R_{free}$ test set	4019 reflections (5.27%)	DCC
Wilson B-factor (Å <sup>2</sup> )	32.9	Xtriage
Anisotropy	0.314	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 41.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	12852	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.83% 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: MG, SAH

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	0.40	0/3168	0.53	0/4300
1	B	0.39	0/2866	0.52	0/3879
1	C	0.39	0/2986	0.53	0/4047
1	D	0.39	0/3210	0.52	0/4358
All	All	0.39	0/12230	0.52	0/16584

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 [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	3085	0	2983	10	0
1	B	2805	0	2728	9	0
1	C	2910	0	2815	11	0
1	D	3126	0	3013	10	0
2	A	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	26	0	19	0	0
3	C	26	0	19	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	26	0	19	0	0
4	A	242	0	0	2	0
4	B	207	0	0	1	0
4	C	197	0	0	0	0
4	D	199	0	0	1	0
All	All	12852	0	11596	30	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 (30) 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:B:327:LEU:HD21	1:C:338:GLN:HG3	1.73	0.69
1:C:168:SER:HA	1:C:173:THR:HG23	1.89	0.54
1:B:253:GLN:HG2	4:B:515:HOH:O	2.11	0.50
1:A:125:LEU:HB2	1:C:178:PHE:CZ	2.48	0.49
1:A:387:PHE:HB2	1:D:279:ILE:HD11	1.94	0.49
1:C:134:GLU:HB3	1:C:138:GLN:HG2	1.95	0.49
1:A:379:ILE:HG13	1:D:306:TRP:CD2	2.49	0.48
1:B:187:ASP:O	1:B:191:ARG:HD3	2.14	0.47
1:D:168:SER:HB2	1:D:220:MET:HE3	1.97	0.47
1:B:253:GLN:OE1	1:B:282:HIS:CE1	2.68	0.47
1:A:264:ARG:NH1	4:A:563:HOH:O	2.49	0.46
1:A:251:GLY:HA3	1:A:258:PHE:CZ	2.51	0.46
1:C:373:ARG:HD2	1:D:121:ARG:C	2.38	0.44
1:D:188:ARG:NE	4:D:431:HOH:O	2.42	0.44
1:B:282:HIS:C	1:B:282:HIS:ND1	2.71	0.43
1:B:125:LEU:HB2	1:D:178:PHE:CZ	2.53	0.43
1:C:12:VAL:HG22	1:C:41:LEU:HD11	2.00	0.43
1:A:160:ARG:NH2	4:A:877:HOH:O	2.51	0.43
1:B:183:THR:N	1:B:184:PRO:CD	2.82	0.43
1:D:80:ARG:O	1:D:81:ASP:HB2	2.19	0.42
1:B:52:PRO:HA	1:B:53:PRO:HD3	1.88	0.42
1:A:125:LEU:HD21	1:B:380:PRO:HG3	2.01	0.42
1:C:125:LEU:O	1:C:126:PHE:C	2.58	0.42
1:C:336:ALA:HB1	1:C:354:ASP:HA	2.02	0.42
1:C:173:THR:OG1	1:C:175:LYS:HG2	2.20	0.41
1:C:119:GLY:HA2	1:D:373:ARG:O	2.21	0.41
1:D:52:PRO:HA	1:D:53:PRO:HD3	1.96	0.41
1:A:387:PHE:CB	1:D:279:ILE:HD11	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:251:GLY:HA3	1:A:258:PHE:CE2	2.56	0.41
1:A:188:ARG:NE	1:C:117:PRO:HG3	2.37	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	383/419 (91%)	376 (98%)	7 (2%)	0	100	100
1	B	344/419 (82%)	336 (98%)	8 (2%)	0	100	100
1	C	358/419 (85%)	347 (97%)	11 (3%)	0	100	100
1	D	391/419 (93%)	381 (97%)	10 (3%)	0	100	100
All	All	1476/1676 (88%)	1440 (98%)	36 (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	328/353 (93%)	326 (99%)	2 (1%)	89	92
1	B	302/353 (86%)	298 (99%)	4 (1%)	73	82
1	C	306/353 (87%)	301 (98%)	5 (2%)	68	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	332/353 (94%)	331 (100%)	1 (0%)	94	96
All	All	1268/1412 (90%)	1256 (99%)	12 (1%)	82	88

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	173	THR
1	A	242	ASP
1	B	6	GLU
1	B	161	LYS
1	B	242	ASP
1	B	282	HIS
1	C	6	GLU
1	C	133	GLU
1	C	173	THR
1	C	242	ASP
1	C	373	ARG
1	D	242	ASP

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 ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 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	$\# Z  > 2$
3	SAH	A	601	-	20,28,28	1.12	1 (5%)	20,40,40	1.84	3 (15%)
3	SAH	C	601	-	20,28,28	1.15	2 (10%)	20,40,40	1.72	3 (15%)
3	SAH	D	601	-	20,28,28	1.16	1 (5%)	20,40,40	1.79	3 (15%)

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
3	SAH	A	601	-	-	0/7/31/31	0/3/3/3
3	SAH	C	601	-	-	0/7/31/31	0/3/3/3
3	SAH	D	601	-	-	0/7/31/31	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	601	SAH	C2-N3	2.03	1.35	1.32
3	A	601	SAH	C5-C4	3.14	1.47	1.40
3	C	601	SAH	C5-C4	3.16	1.47	1.40
3	D	601	SAH	C5-C4	3.24	1.47	1.40

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	601	SAH	N3-C2-N1	-6.28	123.39	128.86
3	A	601	SAH	N3-C2-N1	-6.18	123.47	128.86
3	C	601	SAH	N3-C2-N1	-5.94	123.68	128.86
3	C	601	SAH	C4-C5-N7	-3.26	106.26	109.41
3	D	601	SAH	C4-C5-N7	-2.92	106.59	109.41
3	A	601	SAH	CB-CG-SD	-2.74	108.30	113.57
3	A	601	SAH	C4-C5-N7	-2.51	106.98	109.41
3	D	601	SAH	CB-CG-SD	-2.10	109.51	113.57
3	C	601	SAH	CB-CG-SD	-2.01	109.69	113.57

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

### 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	387/419 (92%)	-0.20	19 (4%) 30 30	17, 32, 79, 164	0
1	B	354/419 (84%)	0.05	29 (8%) 12 12	18, 41, 93, 166	0
1	C	363/419 (86%)	-0.13	12 (3%) 47 48	19, 35, 70, 146	0
1	D	393/419 (93%)	-0.10	16 (4%) 38 38	20, 39, 76, 109	0
All	All	1497/1676 (89%)	-0.10	76 (5%) 29 29	17, 36, 83, 166	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	381	THR	5.9
1	B	133	GLU	5.9
1	C	134	GLU	5.8
1	B	132	ASP	5.6
1	A	347	ASN	5.5
1	A	346	PRO	5.4
1	B	323	SER	5.2
1	B	172	PHE	5.1
1	A	344	SER	4.5
1	B	139	ILE	4.2
1	B	131	ASP	3.8
1	B	182	PHE	3.7
1	A	390	LEU	3.6
1	B	214	GLY	3.6
1	A	392	GLN	3.5
1	A	384	PRO	3.5
1	B	396	GLY	3.4
1	B	134	GLU	3.3
1	A	381	THR	3.3
1	D	178	PHE	3.2
1	C	137	GLU	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	130	THR	3.1
1	C	133	GLU	3.1
1	A	130	THR	3.1
1	D	5	THR	3.1
1	A	391	VAL	3.0
1	D	213	TRP	3.0
1	D	310	TRP	3.0
1	D	136	VAL	3.0
1	D	134	GLU	2.9
1	B	240	HIS	2.9
1	B	137	GLU	2.9
1	B	346	PRO	2.9
1	C	132	ASP	2.9
1	D	133	GLU	2.9
1	A	382	TRP	2.8
1	C	129	LEU	2.8
1	B	171	TYR	2.8
1	B	277	SER	2.7
1	D	323	SER	2.6
1	A	383	ILE	2.6
1	C	380	PRO	2.6
1	B	83	PRO	2.6
1	D	392	GLN	2.5
1	C	136	VAL	2.5
1	B	90	ASP	2.5
1	D	211	PRO	2.5
1	A	345	ASP	2.5
1	B	135	ALA	2.4
1	B	142	TYR	2.4
1	B	87	VAL	2.4
1	D	143	LEU	2.4
1	B	241	VAL	2.4
1	C	379	ILE	2.4
1	A	387	PHE	2.3
1	D	131	ASP	2.3
1	B	324	GLY	2.3
1	D	139	ILE	2.3
1	A	393	ALA	2.3
1	B	88	GLY	2.3
1	B	56	ASP	2.3
1	A	389	SER	2.3
1	A	394	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	144	LEU	2.2
1	C	90	ASP	2.2
1	B	143	LEU	2.1
1	B	347	ASN	2.1
1	D	212	GLU	2.1
1	C	382	TRP	2.1
1	C	93	PHE	2.1
1	B	136	VAL	2.1
1	D	322	CYS	2.1
1	A	388	GLU	2.0
1	A	348	ARG	2.0
1	A	343	PRO	2.0
1	D	132	ASP	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( $\text{\AA}^2$ )	Q<0.9
3	SAH	C	601	26/26	0.96	0.14	1.41	37,39,41,43	0
2	MG	D	501	1/1	0.92	0.14	1.14	73,73,73,73	0
3	SAH	D	601	26/26	0.95	0.17	0.68	56,57,62,62	0
2	MG	A	501	1/1	0.94	0.12	0.53	52,52,52,52	0
3	SAH	A	601	26/26	0.97	0.09	-0.97	25,28,31,31	0
2	MG	C	501	1/1	0.97	0.05	-2.55	64,64,64,64	0

## 6.5 Other polymers

There are no such residues in this entry.