



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:42 AM GMT

PDB ID : 3BWC  
Title : Crystal structure of spermidine synthase from Trypanosoma cruzi in complex with SAM at 2.3 Å resolution  
Authors : Bosch, J.; Arakaki, T.L.; Le Trong, I.; Merritt, E.A.; Hol, W.G.J.; Structural Genomics of Pathogenic Protozoa Consortium (SGPP)  
Deposited on : 2008-01-09  
Resolution : 2.30 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

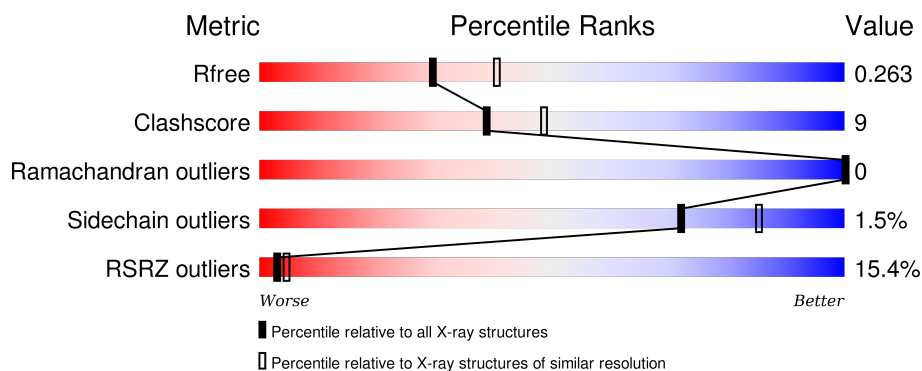
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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	304	
1	B	304	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4921 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 Spermidine synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	282	Total	C	N	O	S	Se	5	8	0
			2267	1441	386	422	10	8			
1	B	271	Total	C	N	O	S	Se	2	7	0
			2174	1383	369	402	10	10			

There are 16 discrepancies between the modelled and reference sequences:

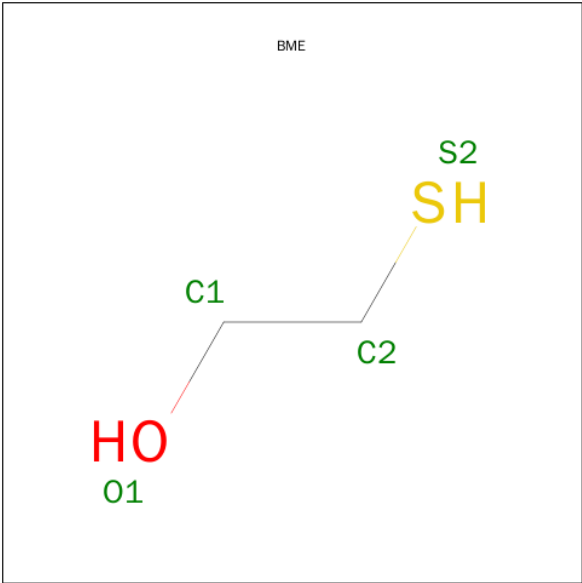
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	EXPRESSION TAG	UNP Q4DA73
A	2	ALA	-	EXPRESSION TAG	UNP Q4DA73
A	3	HIS	-	EXPRESSION TAG	UNP Q4DA73
A	4	HIS	-	EXPRESSION TAG	UNP Q4DA73
A	5	HIS	-	EXPRESSION TAG	UNP Q4DA73
A	6	HIS	-	EXPRESSION TAG	UNP Q4DA73
A	7	HIS	-	EXPRESSION TAG	UNP Q4DA73
A	8	HIS	-	EXPRESSION TAG	UNP Q4DA73
B	1	MSE	-	EXPRESSION TAG	UNP Q4DA73
B	2	ALA	-	EXPRESSION TAG	UNP Q4DA73
B	3	HIS	-	EXPRESSION TAG	UNP Q4DA73
B	4	HIS	-	EXPRESSION TAG	UNP Q4DA73
B	5	HIS	-	EXPRESSION TAG	UNP Q4DA73
B	6	HIS	-	EXPRESSION TAG	UNP Q4DA73
B	7	HIS	-	EXPRESSION TAG	UNP Q4DA73
B	8	HIS	-	EXPRESSION TAG	UNP Q4DA73

- Molecule 2 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula: C<sub>15</sub>H<sub>22</sub>N<sub>6</sub>O<sub>5</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			27	15	6	5	1		
2	B	1	Total	C	N	O	S	0	0
			27	15	6	5	1		

- Molecule 3 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C<sub>2</sub>H<sub>6</sub>OS).



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

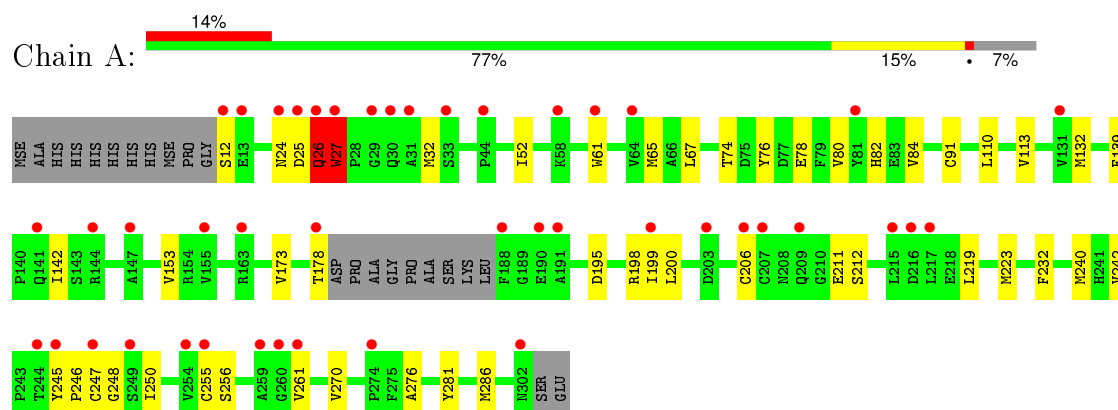
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	203	Total 203	O 203	0	0
4	B	221	Total 221	O 221	0	0

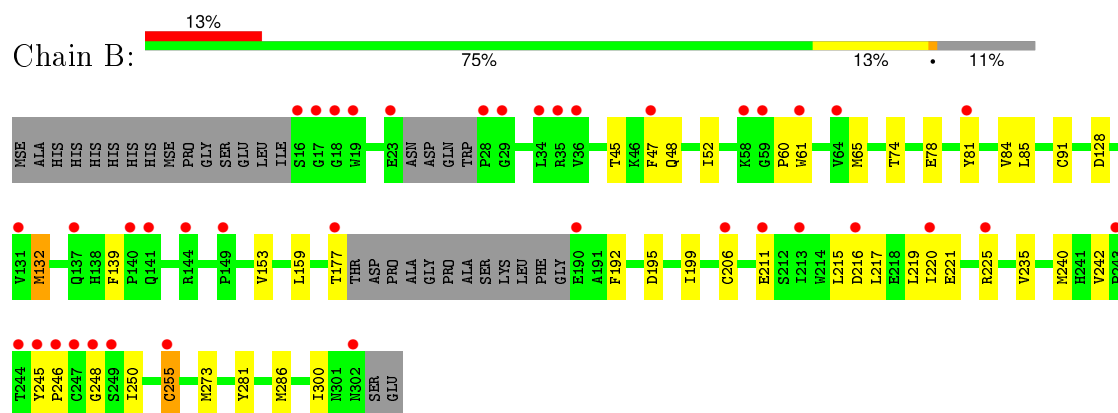
### 3 Residue-property plots [i](#)

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 ( $RSRZ > 2$ ). 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: Spermidine synthase



#### • Molecule 1: Spermidine synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	44.08 Å 99.94 Å 69.99 Å 90.00° 106.26° 90.00°	Depositor
Resolution (Å)	20.00 – 2.30 19.69 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-2.30) 98.6 (19.69-2.30)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.80 (at 2.30 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.203 , 0.259 0.207 , 0.263	Depositor DCC
$R_{free}$ test set	1274 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	26.9	Xtriage
Anisotropy	0.113	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 50.7	EDS
Estimated twinning fraction	0.037 for h,-k,-h-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 25509 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	4921	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.70% 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: SAM, BME

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	2.64	9/2338 (0.4%)	3.28	13/3154 (0.4%)
1	B	0.58	1/2241 (0.0%)	0.57	2/3020 (0.1%)
All	All	1.93	10/4579 (0.2%)	2.38	15/6174 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	27	TRP	CG-CD1	-81.32	0.23	1.36
1	A	27	TRP	CB-CG	79.67	2.93	1.50
1	A	26	GLN	CG-CD	46.42	2.57	1.51
1	B	177	THR	CB-OG1	23.68	1.90	1.43
1	A	26	GLN	CB-CG	18.42	2.02	1.52
1	A	27	TRP	CE3-CZ3	15.28	1.64	1.38
1	A	178	THR	CB-OG1	-13.34	1.16	1.43
1	A	12	SER	CB-OG	9.11	1.54	1.42
1	A	27	TRP	CZ3-CH2	8.73	1.54	1.40
1	A	178	THR	CB-CG2	7.18	1.76	1.52

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	27	TRP	CG-CD2-CE3	-143.39	4.85	133.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	27	TRP	CD1-CG-CD2	54.88	150.21	106.30
1	A	27	TRP	NE1-CE2-CZ2	-52.55	72.59	130.40
1	A	27	TRP	CB-CG-CD1	-43.18	70.87	127.00
1	A	26	GLN	CG-CD-OE1	-42.75	36.10	121.60
1	A	27	TRP	NE1-CE2-CD2	-37.11	70.19	107.30
1	A	27	TRP	CG-CD1-NE1	-30.78	79.32	110.10
1	A	27	TRP	CA-CB-CG	-16.38	82.58	113.70
1	A	27	TRP	CD2-CE2-CZ2	15.45	140.84	122.30
1	B	177	THR	CA-CB-CG2	10.80	127.52	112.40
1	A	178	THR	CA-CB-CG2	-10.29	97.99	112.40
1	B	177	THR	OG1-CB-CG2	-9.60	87.93	110.00
1	A	27	TRP	CD1-NE1-CE2	9.22	117.30	109.00
1	A	26	GLN	CB-CG-CD	-8.35	89.89	111.60
1	A	27	TRP	CH2-CZ2-CE2	-6.99	110.42	117.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	26	GLN	Sidechain

## 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	2267	0	2231	49	0
1	B	2174	0	2151	42	0
2	A	27	0	22	2	0
2	B	27	0	22	0	0
3	A	1	0	0	1	0
3	B	1	0	0	2	0
4	A	203	0	0	2	0
4	B	221	0	0	0	0
All	All	4921	0	4426	80	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 9.

All (80) 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:27:TRP:CZ2	1:B:61:TRP:CE2	2.67	0.83
1:A:27:TRP:HE3	1:A:27:TRP:CB	1.92	0.81
1:A:91:CYS:SG	3:A:401:BME:S2	2.82	0.77
1:B:91:CYS:SG	3:B:401:BME:S2	2.82	0.77
1:B:45:THR:HG21	1:B:128:ASP:OD2	1.84	0.76
1:B:273[C]:MSE:SE	3:B:401:BME:S2	2.94	0.76
1:A:27:TRP:CZ2	1:B:61:TRP:NE1	2.58	0.72
1:B:159:LEU:HD23	1:B:192:PHE:CD1	2.31	0.65
1:B:45:THR:HG22	1:B:48:GLN:O	1.97	0.65
1:B:84:VAL:HG11	1:B:240:MSE:HE2	1.82	0.62
1:A:52:ILE:HD11	1:A:65:MSE:HE2	1.81	0.61
1:A:27:TRP:HZ2	1:B:61:TRP:CE2	2.17	0.61
1:B:45:THR:HG23	1:B:47:PHE:H	1.65	0.61
1:A:110:LEU:O	1:A:113:VAL:HG22	2.02	0.59
1:B:221[A]:GLU:CD	1:B:225[A]:ARG:HH21	2.06	0.59
2:A:501:SAM:SD	4:A:695:HOH:O	2.57	0.58
1:B:221[A]:GLU:HG2	1:B:225[A]:ARG:HE	1.68	0.57
1:A:270:VAL:O	1:A:276:ALA:HB2	2.04	0.57
1:A:27:TRP:CZ2	1:B:60:PRO:HD2	2.41	0.56
1:A:27:TRP:HD1	1:A:27:TRP:CB	2.18	0.56
1:A:84:VAL:HG11	1:A:240:MSE:HE2	1.88	0.55
1:A:25:ASP:C	1:A:27:TRP:H	2.10	0.55
1:B:220:ILE:HG21	1:B:300:ILE:HD13	1.88	0.54
1:A:27:TRP:CD1	1:A:27:TRP:CB	2.87	0.54
1:B:52:ILE:HD11	1:B:65:MSE:HE2	1.90	0.53
1:B:273[B]:MSE:HE2	1:B:273[B]:MSE:HA	1.89	0.53
1:B:281:TYR:CZ	1:B:286:MSE:HE2	2.44	0.53
1:A:27:TRP:HZ2	1:B:61:TRP:CD1	2.27	0.53
1:A:211:GLU:HG3	1:A:219:LEU:HD22	1.91	0.53
1:A:25:ASP:O	1:A:26:GLN:HB3	2.08	0.52
1:A:173:VAL:HG23	1:A:200:LEU:HD21	1.90	0.52
1:A:248:GLY:HA3	1:B:248:GLY:HA3	1.91	0.52
1:A:212:SER:OG	1:A:247:CYS:SG	2.68	0.52
1:A:219:LEU:CD2	1:A:223[A]:MSE:HE3	2.41	0.51
1:A:74:THR:O	1:A:78:GLU:HB2	2.11	0.51
1:A:61:TRP:HA	1:A:76:TYR:HB2	1.92	0.51
1:A:27:TRP:CZ2	1:B:61:TRP:CD1	2.98	0.51
1:A:27:TRP:CH2	1:B:60:PRO:CG	2.94	0.50
1:A:206[A]:CYS:SG	1:A:232:PHE:CE1	3.05	0.49
1:B:217:LEU:HD12	1:B:300:ILE:HD11	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:GLU:HG3	1:B:219:LEU:HD23	1.94	0.48
1:A:27:TRP:CH2	1:B:60:PRO:HG2	2.48	0.48
1:A:132:MSE:HE3	1:A:153:VAL:CG1	2.44	0.48
1:A:245:TYR:CE1	1:A:250:ILE:HD12	2.49	0.48
1:A:27:TRP:HZ2	1:B:61:TRP:CD2	2.32	0.47
1:A:256:SER:OG	1:A:261:VAL:HG21	2.14	0.47
1:B:132:MSE:HE2	1:B:153:VAL:CG1	2.43	0.47
1:B:245:TYR:CE1	1:B:250:ILE:HD12	2.50	0.46
1:A:52:ILE:CD1	1:A:65:MSE:HE2	2.44	0.46
1:A:132:MSE:HE3	1:A:153:VAL:HG11	1.98	0.46
1:A:195:ASP:O	1:A:199:ILE:HG23	2.16	0.46
1:B:217:LEU:CD1	1:B:300:ILE:HD11	2.46	0.45
1:A:281:TYR:CZ	1:A:286:MSE:HE2	2.51	0.45
1:B:215:LEU:HD12	1:B:216:ASP:CG	2.38	0.44
1:A:67:LEU:HD12	2:A:501:SAM:HE2	2.00	0.44
1:B:81:TYR:CZ	1:B:85:LEU:HD11	2.53	0.44
1:B:215:LEU:HD12	1:B:216:ASP:OD1	2.18	0.43
1:A:78:GLU:HG2	1:A:82:HIS:CE1	2.54	0.43
1:A:110:LEU:HA	1:A:113:VAL:HG22	2.00	0.43
1:A:27:TRP:CA	1:A:27:TRP:HE3	2.31	0.42
1:B:45:THR:HG22	1:B:48:GLN:H	1.83	0.42
1:B:240:MSE:HG3	1:B:242:VAL:HG23	2.01	0.42
1:A:65:MSE:HE3	1:A:139:PHE:CE2	2.54	0.42
1:A:139:PHE:HB3	1:A:142:ILE:HD12	2.00	0.42
1:B:74:THR:O	1:B:78:GLU:HB2	2.19	0.42
1:A:80:VAL:O	1:A:84:VAL:HG23	2.20	0.42
1:A:195:ASP:HA	1:A:198:ARG:HG2	2.01	0.42
1:B:235:VAL:HG22	1:B:255[B]:CYS:HB3	2.01	0.42
1:A:32:MSE:HE2	4:A:686:HOH:O	2.19	0.42
1:A:245:TYR:CG	1:A:246:PRO:HD2	2.55	0.41
1:A:219:LEU:O	1:A:219:LEU:HD23	2.19	0.41
1:A:240:MSE:HG3	1:A:242:VAL:HG23	2.02	0.41
1:B:245:TYR:CG	1:B:246:PRO:HD2	2.55	0.41
1:A:27:TRP:HZ2	1:B:61:TRP:CG	2.39	0.41
1:B:221[A]:GLU:HG2	1:B:225[A]:ARG:NE	2.35	0.41
1:A:173:VAL:HG23	1:A:200:LEU:CD2	2.51	0.41
1:A:27:TRP:CE2	1:B:61:TRP:NE1	2.89	0.40
1:B:65:MSE:HE3	1:B:139:PHE:CE2	2.56	0.40
1:B:235:VAL:HG22	1:B:255[A]:CYS:HB2	2.03	0.40
1:B:195:ASP:O	1:B:199:ILE:HG23	2.21	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	286/304 (94%)	273 (96%)	13 (4%)	0	100	100
1	B	273/304 (90%)	262 (96%)	11 (4%)	0	100	100
All	All	559/608 (92%)	535 (96%)	24 (4%)	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	253/253 (100%)	248 (98%)	5 (2%)	63	79
1	B	243/253 (96%)	238 (98%)	5 (2%)	61	78
All	All	496/506 (98%)	486 (98%)	10 (2%)	72	79

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	ASN
1	A	26	GLN
1	A	27	TRP
1	A	255[A]	CYS
1	A	255[B]	CYS
1	B	132	MSE
1	B	206[A]	CYS
1	B	206[B]	CYS

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Mol	Chain	Res	Type
1	B	255[A]	CYS
1	B	255[B]	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	ASN
1	A	30	GLN
1	A	208	ASN
1	B	30	GLN
1	B	164	GLN

### 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 4 ligands modelled in this entry, 2 are modelled with single atom - leaving 2 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	SAM	A	501	-	21,29,29	1.10	2 (9%)	17,42,42	3.07	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SAM	B	501	-	21,29,29	1.12	2 (9%)	17,42,42	3.21	3 (17%)

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	SAM	A	501	-	-	0/8/33/33	0/3/3/3
2	SAM	B	501	-	-	0/8/33/33	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	SAM	C2-N1	2.46	1.38	1.33
2	B	501	SAM	C2-N1	2.59	1.38	1.33
2	B	501	SAM	C2-N3	3.60	1.38	1.32
2	A	501	SAM	C2-N3	3.61	1.38	1.32

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	SAM	N3-C2-N1	-12.42	119.39	128.89
2	A	501	SAM	N3-C2-N1	-11.93	119.76	128.89
2	B	501	SAM	C1'-N9-C4	-2.13	123.73	126.94
2	A	501	SAM	C4-C5-N7	-2.04	107.60	109.48
2	B	501	SAM	O4'-C1'-N9	2.44	113.20	108.10

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	SAM	2	0

## 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	275/304 (90%)	1.01	44 (16%) 3 4	22, 34, 56, 79	3 (1%)
1	B	264/304 (86%)	0.87	39 (14%) 3 5	19, 32, 56, 62	1 (0%)
All	All	539/608 (88%)	0.94	83 (15%) 3 4	19, 33, 56, 79	4 (0%)

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	27	TRP	11.8
1	A	12	SER	9.5
1	A	26	GLN	7.0
1	B	17	GLY	6.8
1	B	141	GLN	6.5
1	B	245	TYR	6.2
1	B	244	THR	5.6
1	B	247	CYS	5.3
1	B	16	SER	5.2
1	B	18	GLY	5.1
1	B	302	ASN	5.0
1	B	47	PHE	4.9
1	A	24	ASN	4.8
1	B	246	PRO	4.5
1	B	23	GLU	4.3
1	A	191	ALA	4.2
1	A	302	ASN	4.2
1	B	149	PRO	4.2
1	A	206[A]	CYS	4.0
1	A	178	THR	3.9
1	B	34	LEU	3.8
1	B	36	VAL	3.7
1	A	29	GLY	3.7
1	B	144	ARG	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	61	TRP	3.6
1	B	190	GLU	3.4
1	A	215	LEU	3.3
1	A	25	ASP	3.3
1	A	58	LYS	3.3
1	B	19	TRP	3.3
1	B	140	PRO	3.2
1	A	255[A]	CYS	3.2
1	B	81	TYR	3.2
1	B	248	GLY	3.1
1	A	216	ASP	3.1
1	A	13	GLU	3.1
1	B	28	PRO	3.0
1	A	245	TYR	3.0
1	A	260	GLY	2.9
1	A	261	VAL	2.9
1	B	213	ILE	2.9
1	B	243	PRO	2.9
1	A	30	GLN	2.9
1	A	188	PHE	2.8
1	B	35	ARG	2.7
1	A	64	VAL	2.7
1	B	59	GLY	2.7
1	B	225[A]	ARG	2.6
1	A	254	VAL	2.6
1	A	190	GLU	2.6
1	B	255[A]	CYS	2.5
1	A	131	VAL	2.5
1	A	33[A]	SER	2.5
1	A	249	SER	2.5
1	A	44	PRO	2.5
1	B	137	GLN	2.4
1	B	29	GLY	2.4
1	A	163	ARG	2.4
1	B	216	ASP	2.4
1	A	81	TYR	2.4
1	A	203	ASP	2.4
1	A	31	ALA	2.4
1	B	64	VAL	2.3
1	A	244	THR	2.3
1	A	259	ALA	2.3
1	B	177	THR	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	155	VAL	2.3
1	A	141	GLN	2.2
1	A	274	PRO	2.2
1	A	147	ALA	2.2
1	A	61	TRP	2.2
1	A	207	CYS	2.2
1	A	247	CYS	2.2
1	A	144[A]	ARG	2.2
1	B	220	ILE	2.2
1	A	199	ILE	2.2
1	A	217	LEU	2.1
1	B	206[A]	CYS	2.1
1	B	58	LYS	2.1
1	B	249	SER	2.1
1	A	209	GLN	2.0
1	B	211	GLU	2.0
1	B	131	VAL	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
2	SAM	A	501	27/27	0.85	0.24	1.40	44,48,68,68	0
2	SAM	B	501	27/27	0.86	0.24	1.30	42,46,68,69	0
3	BME	B	401	1/4	0.98	0.13	-0.90	28,28,28,28	0
3	BME	A	401	1/4	0.95	0.10	-	35,35,35,35	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.