



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 13, 2018 – 03:16 pm GMT

PDB ID : 3S8P  
Title : Crystal Structure of the SET Domain of Human Histone-Lysine N-Methyltransferase SUV420H1 In Complex With S-Adenosyl-L-Methionine  
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Deposited on : 2011-05-30  
Resolution : 1.85 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

<https://www.wwpdb.org/validation/2017/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 : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : trunk31020  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk31020

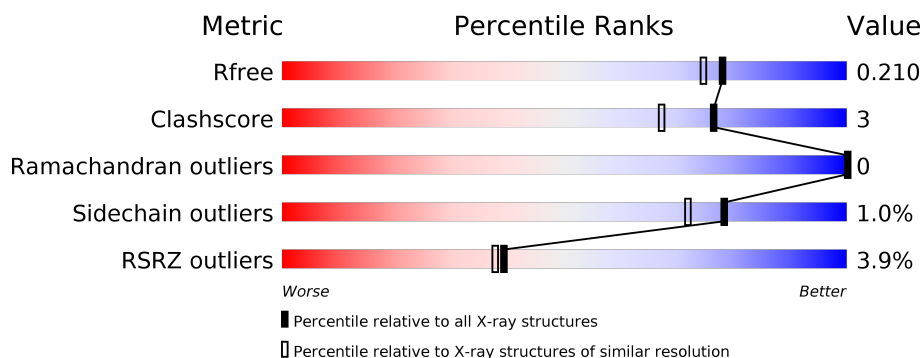
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.85 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))
$R_{free}$	111664	2111 (1.86-1.86)
Clashscore	122126	2258 (1.86-1.86)
Ramachandran outliers	120053	2234 (1.86-1.86)
Sidechain outliers	120020	2234 (1.86-1.86)
RSRZ outliers	108989	2075 (1.86-1.86)

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	273	<div> <div>2%</div> <div> <div></div> <div>79%</div> <div>6%</div> <div>15%</div> </div> </div>
1	B	273	<div> <div>4%</div> <div> <div></div> <div>79%</div> <div>8%</div> <div>13%</div> </div> </div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4042 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.

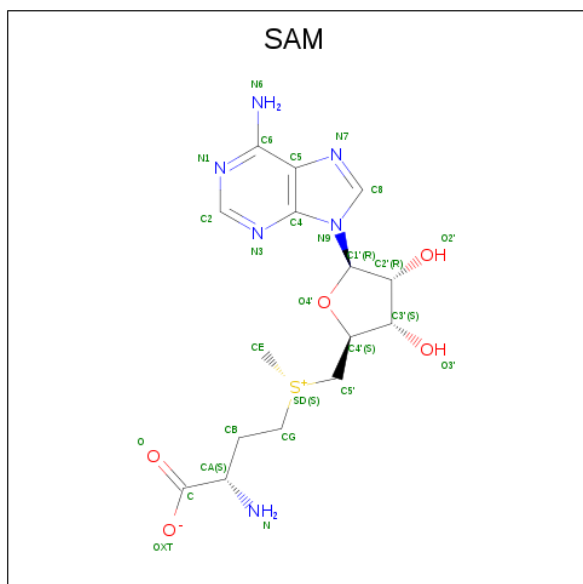
- Molecule 1 is a protein called Histone-lysine N-methyltransferase SUV420H1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	233	Total	C	N	O	S	Se	0	2	0
			1840	1157	312	353	12	6			
1	B	238	Total	C	N	O	S	Se	0	2	0
			1876	1178	321	358	12	7			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 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
3	A	1	Total 27	C 15	N 6	O 5	S 1	0	0
3	B	1	Total 27	C 15	N 6	O 5	S 1	0	0

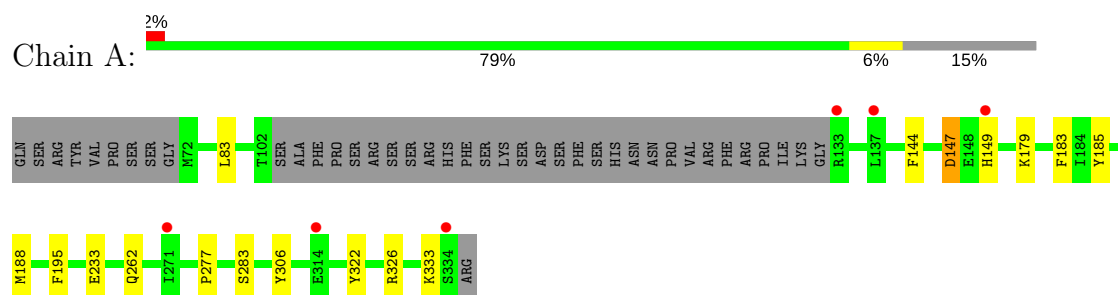
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	134	Total 134	O 134	0	0
4	B	136	Total 136	O 136	0	0

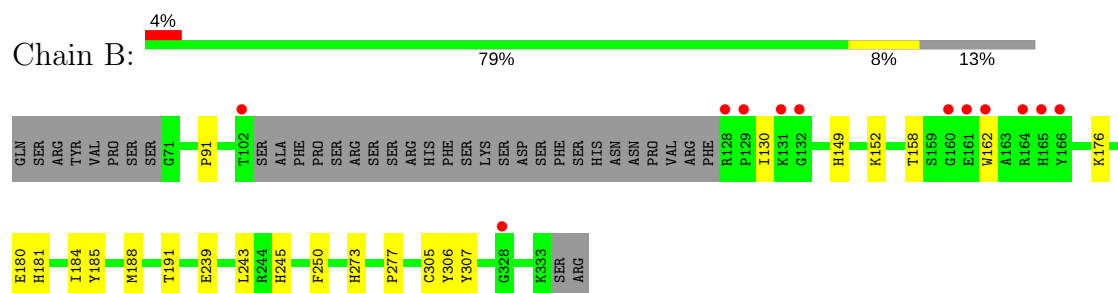
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: Histone-lysine N-methyltransferase SUV420H1



- Molecule 1: Histone-lysine N-methyltransferase SUV420H1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	46.42Å 50.13Å 74.84Å 100.99° 108.05° 89.76°	Depositor
Resolution (Å)	33.94 – 1.85 31.75 – 1.85	Depositor EDS
% Data completeness (in resolution range)	97.8 (33.94-1.85) 97.8 (31.75-1.85)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.01 (at 1.85Å)	Xtriage
Refinement program	REFMAC refmac _5.6.0081	Depositor
R, $R_{free}$	0.187 , 0.212 0.187 , 0.210	Depositor DCC
$R_{free}$ test set	2672 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.9	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 41.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.015 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4042	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.86% 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: ZN, SAM

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	0.50	0/1876	0.58	0/2514
1	B	0.52	0/1912	0.58	0/2561
All	All	0.51	0/3788	0.58	0/5075

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	1840	0	1737	11	0
1	B	1876	0	1772	15	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	27	0	22	0	0
3	B	27	0	22	1	0
4	A	134	0	0	0	0
4	B	136	0	0	0	0
All	All	4042	0	3553	24	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 3.

All (24) 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:273:HIS:HD2	1:B:307:TYR:H	1.12	0.92
1:B:273:HIS:CD2	1:B:307:TYR:H	2.00	0.79
1:A:185:TYR:O	1:A:188:MSE:HG2	1.83	0.78
1:A:233:GLU:HG2	1:A:262:GLN:HE21	1.57	0.68
1:A:283:SER:HB2	1:B:245:HIS:CD2	2.32	0.65
1:A:144:PHE:HA	1:A:147:ASP:HB2	1.85	0.57
1:B:181:HIS:O	1:B:184:ILE:HG12	2.07	0.54
1:B:185:TYR:O	1:B:188:MSE:HG2	2.08	0.53
1:B:149:HIS:HD2	1:B:152:LYS:H	1.55	0.53
1:A:283:SER:HB2	1:B:245:HIS:CG	2.49	0.48
1:B:176:LYS:HD3	1:B:180:GLU:OE2	2.15	0.47
1:A:179:LYS:HE2	1:A:183:PHE:CZ	2.50	0.46
1:A:147:ASP:HB3	1:A:149:HIS:H	1.80	0.46
1:A:233:GLU:HG2	1:A:262:GLN:NE2	2.29	0.46
1:B:239:GLU:HG2	1:B:243:LEU:HD12	1.98	0.46
1:A:322:TYR:O	1:A:326:ARG:HG3	2.17	0.44
1:B:273:HIS:HA	1:B:305:CYS:O	2.18	0.43
1:A:188:MSE:HE3	1:A:195:PHE:CE1	2.54	0.42
1:B:250:PHE:O	3:B:500:SAM:H5'1	2.20	0.42
1:A:277:PRO:HG3	1:A:306:TYR:HB2	2.01	0.41
1:B:158:THR:HG22	1:B:162:TRP:HZ2	1.85	0.41
1:B:158:THR:HA	1:B:162:TRP:HE1	1.84	0.41
1:B:91:PRO:HA	1:B:130:ILE:HG23	2.03	0.41
1:B:277:PRO:HG3	1:B:306:TYR:HB2	2.03	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	231/273 (85%)	227 (98%)	4 (2%)	0	100	100
1	B	236/273 (86%)	231 (98%)	5 (2%)	0	100	100
All	All	467/546 (86%)	458 (98%)	9 (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	195/236 (83%)	192 (98%)	3 (2%)	67	56
1	B	197/236 (84%)	196 (100%)	1 (0%)	90	87
All	All	392/472 (83%)	388 (99%)	4 (1%)	78	72

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	83	LEU
1	A	147	ASP
1	A	333	LYS
1	B	191	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	101	ASN
1	A	169	ASN
1	A	208	ASN
1	A	262	GLN
1	B	149	HIS
1	B	273	HIS

### 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 monoatomic - 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
3	SAM	A	500	-	21,29,29	1.67	3 (14%)	16,42,42	1.97	2 (12%)
3	SAM	B	500	-	21,29,29	1.69	2 (9%)	16,42,42	2.07	4 (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
3	SAM	A	500	-	-	0/8/33/33	0/3/3/3
3	SAM	B	500	-	-	0/8/33/33	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	500	SAM	CG-SD	-5.55	1.68	1.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	500	SAM	CG-SD	-5.54	1.68	1.80
3	A	500	SAM	C2-N3	2.00	1.35	1.32
3	B	500	SAM	C5-C4	3.11	1.47	1.40
3	A	500	SAM	C5-C4	3.14	1.47	1.40

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	500	SAM	N3-C2-N1	-7.06	122.82	128.86
3	A	500	SAM	N3-C2-N1	-6.58	123.23	128.86
3	B	500	SAM	C4'-O4'-C1'	2.10	112.02	109.83
3	B	500	SAM	N6-C6-N1	2.15	123.03	118.57
3	B	500	SAM	C2-N1-C6	2.44	122.90	118.75
3	A	500	SAM	C4'-O4'-C1'	2.50	112.44	109.83

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
3	B	500	SAM	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 [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	227/273 (83%)	-0.01	6 (2%) 56 54	19, 31, 57, 67	0
1	B	232/273 (84%)	0.08	12 (5%) 27 26	19, 31, 70, 119	0
All	All	459/546 (84%)	0.04	18 (3%) 39 38	19, 31, 58, 119	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	165	HIS	6.6
1	B	166	TYR	6.4
1	B	162	TRP	6.2
1	B	129	PRO	5.4
1	B	160	GLY	4.4
1	B	161	GLU	4.3
1	B	132	GLY	3.7
1	A	334	SER	3.4
1	B	164	ARG	3.3
1	A	137	LEU	3.3
1	B	128	ARG	2.6
1	B	131	LYS	2.6
1	A	314	GLU	2.3
1	B	102	THR	2.3
1	B	328	GLY	2.1
1	A	271	ILE	2.1
1	A	149	HIS	2.0
1	A	133	ARG	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. 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	B-factors( $\text{\AA}^2$ )	Q<0.9
3	SAM	A	500	27/27	0.96	0.10	19,22,27,29	0
3	SAM	B	500	27/27	0.96	0.11	19,23,25,27	0
2	ZN	B	400	1/1	0.98	0.06	28,28,28,28	0
2	ZN	A	400	1/1	0.99	0.07	26,26,26,26	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.