



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 26, 2018 – 11:14 AM EDT

PDB ID : 1F3L
Title : CRYSTAL STRUCTURE OF THE CONSERVED CORE OF PROTEIN
ARGININE METHYLTRANSFERASE PRMT3
Authors : Zhang, X.; Zhou, L.; Cheng, X.
Deposited on : 2000-06-05
Resolution : 2.03 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/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	:	1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20031021

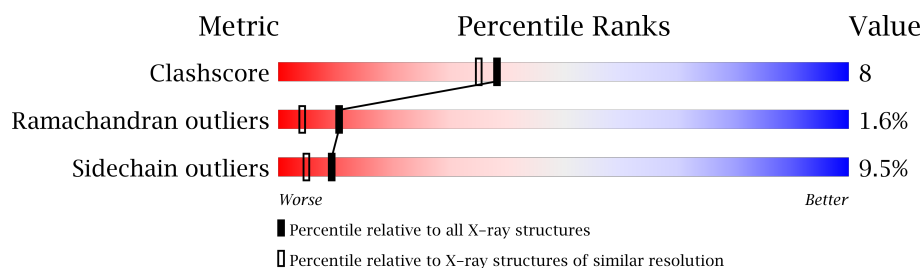
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.03 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))
Clashscore	122126	10355 (2.04-2.00)
Ramachandran outliers	120053	10237 (2.04-2.00)
Sidechain outliers	120020	10236 (2.04-2.00)

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 ≥ 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	321	

2 Entry composition [i](#)

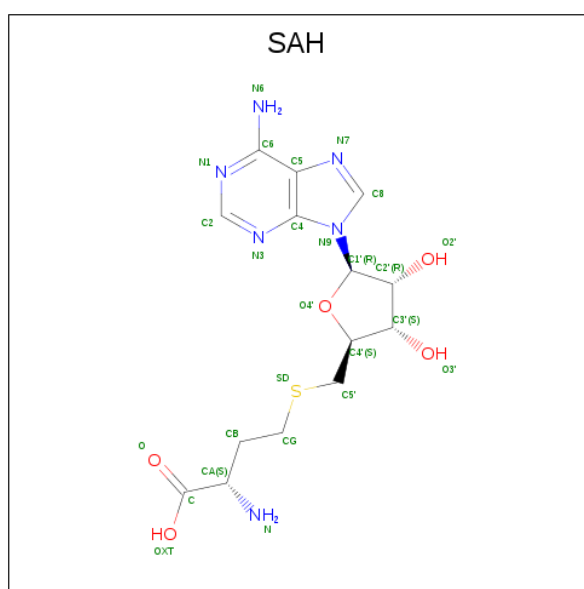
There are 3 unique types of molecules in this entry. The entry contains 2671 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PROTEIN ARGININE METHYLTRANSFERASE PRMT3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	321	Total	C	N	O	S	0	0	0
			2496	1607	405	469	15			

- 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		

- Molecule 3 is water.

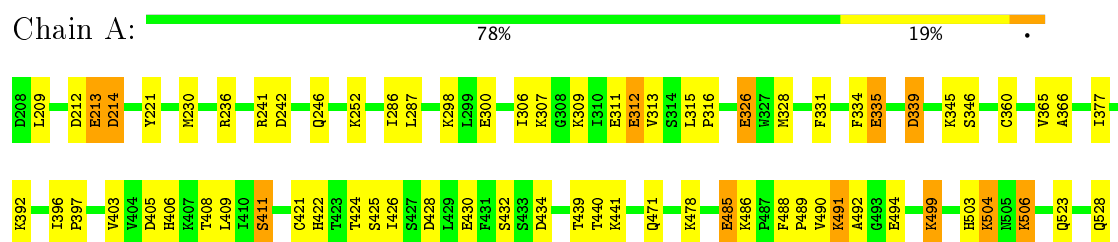
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	149	Total	O	0	0
			149	149		

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. 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. 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.

Note EDS was not executed.

- Molecule 1: PROTEIN ARGININE METHYLTRANSFERASE PRMT3



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	70.91Å 70.91Å 177.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.87 – 2.03	Depositor
% Data completeness (in resolution range)	86.6 (29.87-2.03)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.209 , 0.262	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2671	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.41	0/2549	0.63	0/3450

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	2496	0	2481	41	0
2	A	26	0	19	1	0
3	A	149	0	0	2	0
All	All	2671	0	2500	41	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 8.

All (41) 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:334:PHE:O	1:A:335:GLU:HB2	1.75	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:242:ASP:O	1:A:246:GLN:HG3	1.86	0.76
1:A:491:LYS:O	1:A:494:GLU:HB2	1.90	0.71
1:A:485:GLU:H	1:A:523:GLN:HE22	1.41	0.68
1:A:309:LYS:HB3	1:A:312:GLU:CG	2.25	0.66
1:A:230:MET:HE2	3:A:26:HOH:O	1.99	0.62
1:A:439:THR:HG22	1:A:492:ALA:HA	1.82	0.61
1:A:366:ALA:HB3	1:A:411:SER:HB3	1.82	0.61
1:A:242:ASP:O	1:A:246:GLN:CG	2.47	0.61
1:A:503:HIS:HE1	1:A:506:LYS:CD	2.15	0.59
1:A:236:ARG:HH11	1:A:326:GLU:HG3	1.69	0.56
1:A:440:THR:HG21	3:A:77:HOH:O	2.06	0.56
1:A:396:ILE:N	1:A:397:PRO:HD2	2.21	0.55
1:A:430:GLU:OE2	1:A:504:LYS:HG2	2.06	0.55
1:A:506:LYS:H	1:A:506:LYS:HD3	1.73	0.54
1:A:506:LYS:CD	1:A:506:LYS:H	2.23	0.52
1:A:309:LYS:HB3	1:A:312:GLU:HG3	1.93	0.50
1:A:236:ARG:NH1	1:A:326:GLU:HG3	2.28	0.49
1:A:503:HIS:HE1	1:A:506:LYS:HD3	1.78	0.49
1:A:405:ASP:HB3	1:A:408:THR:HG23	1.95	0.48
1:A:377:ILE:CD1	1:A:396:ILE:HG13	2.44	0.48
1:A:221:TYR:CD2	2:A:529:SAH:H3'	2.50	0.47
1:A:377:ILE:HD12	1:A:396:ILE:HG13	1.96	0.46
1:A:424:THR:HG22	1:A:425:SER:N	2.29	0.46
1:A:377:ILE:HG22	1:A:392:LYS:HE2	1.96	0.46
1:A:339:ASP:OD2	1:A:426:ILE:HD11	2.16	0.45
1:A:309:LYS:HB3	1:A:312:GLU:HG2	1.97	0.45
1:A:309:LYS:O	1:A:313:VAL:HG13	2.16	0.45
1:A:434:ASP:OD1	1:A:499:LYS:HG3	2.17	0.45
1:A:287:LEU:HG	1:A:287:LEU:O	2.16	0.45
1:A:298:LYS:HA	1:A:300:GLU:OE1	2.17	0.44
1:A:406:HIS:HB2	1:A:471:GLN:OE1	2.18	0.43
1:A:506:LYS:N	1:A:506:LYS:HD3	2.33	0.43
1:A:403:VAL:HG23	1:A:478:LYS:HD3	2.02	0.42
1:A:306:ILE:HD11	1:A:316:PRO:HD3	2.02	0.41
1:A:345:LYS:HE3	1:A:422:HIS:HA	2.02	0.41
1:A:213:GLU:O	1:A:214:ASP:CB	2.69	0.41
1:A:286:ILE:O	1:A:286:ILE:HG13	2.20	0.41
1:A:488:PHE:HA	1:A:489:PRO:HD3	1.95	0.40
1:A:424:THR:CG2	1:A:425:SER:N	2.85	0.40
1:A:440:THR:HG22	1:A:441:LYS:HG3	2.03	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	319/321 (99%)	304 (95%)	10 (3%)	5 (2%)	11 4

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	212	ASP
1	A	213	GLU
1	A	335	GLU
1	A	214	ASP
1	A	421	CYS

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	275/287 (96%)	249 (90%)	26 (10%)	9 5

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	209	LEU
1	A	241	ARG
1	A	252	LYS
1	A	307	LYS
1	A	311	GLU
1	A	312	GLU

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Mol	Chain	Res	Type
1	A	315	LEU
1	A	326	GLU
1	A	328	MET
1	A	331	PHE
1	A	339	ASP
1	A	346	SER
1	A	360	CYS
1	A	365	VAL
1	A	409	LEU
1	A	411	SER
1	A	428	ASP
1	A	432	SER
1	A	485	GLU
1	A	486	LYS
1	A	490	VAL
1	A	491	LYS
1	A	499	LYS
1	A	504	LYS
1	A	506	LYS
1	A	528	GLN

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	223	HIS
1	A	227	HIS
1	A	459	ASN
1	A	503	HIS
1	A	523	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

1 ligand is 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	529	-	20,28,28	0.58	0	19,40,40	1.08	2 (10%)

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	529	-	-	0/7/31/31	0/3/3/3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	529	SAH	CB-CG-SD	-2.45	107.82	113.31
2	A	529	SAH	C4'-C5'-SD	-2.25	105.65	113.71

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	A	529	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 ⓘ

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.