

Full wwPDB X-ray Structure Validation Report (i)

Feb 6, 2024 – 11:21 AM EST

PDB ID	:	2DPM
Title	:	DPNM DNA ADENINE METHYLTRANSFERASE FROM STREPTOCCO-
		CUS PNEUMONIAE COMPLEXED WITH S-ADENOSYLMETHIONINE
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Deposited on		
Resolution	:	1.80 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 (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

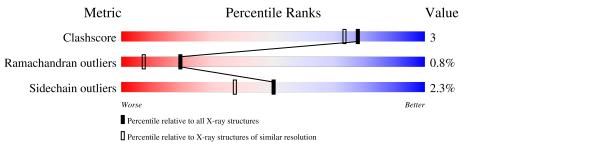
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.80 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	Similar resolution
Metric	$(\# {\rm Entries})$	$(\# { m Entries}, { m resolution} { m range}({ m \AA}))$
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain		
1	А	284	81%	9%	9%



2DPM

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2295 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.

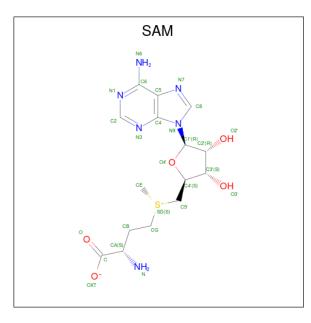
• Molecule 1 is a protein called PROTEIN (ADENINE-SPECIFIC METHYLTRANSFERASE DPNII 1).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	258	Total 2089	C 1348	N 350	O 386	${S \atop 5}$	0	0	0

• Molecule 2 is MERCURY (II) ION (three-letter code: HG) (formula: Hg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	Total Hg 1 1	0	0

• Molecule 3 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula: $C_{15}H_{22}N_6O_5S$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	Δ	1	Total	С	Ν	0	S	0	0
5	A	1	27	15	6	5	1	0	0

• Molecule 4 is water.



Mol	Chain	Residues	Ato	ms	ZeroOcc	AltConf
4	А	178	Total 178	O 178	0	0

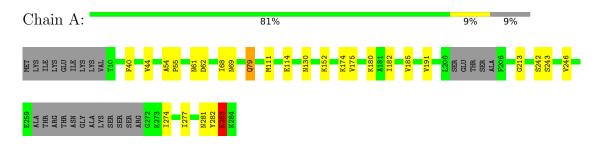


3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 (ADENINE-SPECIFIC METHYLTRANSFERASE DPNII 1)





4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	56.60Å 68.10Å 85.20Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 - 1.80	Depositor
% Data completeness	99.9 (20.00-1.80)	Depositor
(in resolution range)	55.5 (20.00-1.00)	Depositor
R_{merge}	(Not available)	Depositor
R _{sym}	0.05	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.238 , 0.284	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2295	wwPDB-VP
Average B, all atoms $(Å^2)$	37.0	wwPDB-VP



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: SAM, HG

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).

Mal	Chain	Bond	lengths	Bond angles	
Mol	Unain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.43	0/2136	0.61	1/2893~(0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	283	GLU	N-CA-C	-5.06	97.34	111.00

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	А	2089	0	2023	12	1
2	А	1	0	0	0	0
3	А	27	0	22	0	0
4	А	178	0	0	0	0
All	All	2295	0	2045	12	1

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 (12) close contacts within the same asymmetric unit are listed below, sorted by their clash



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:ILE:HG21	1:A:175:VAL:HG22	1.69	0.75
1:A:69:ASN:HD21	1:A:114:GLU:HB3	1.60	0.67
1:A:79:GLN:H	1:A:79:GLN:NE2	2.03	0.56
1:A:182:ILE:O	1:A:185:VAL:HG23	2.10	0.51
1:A:54:ALA:N	1:A:55:PRO:HD3	2.27	0.50
1:A:281:ASN:OD1	1:A:282:TYR:HD2	1.95	0.49
1:A:40:PHE:HB2	1:A:191:VAL:HG22	1.95	0.49
1:A:243:SER:HB3	1:A:246:VAL:HG23	1.94	0.49
1:A:61:ASN:HD22	1:A:174:LYS:HB2	1.81	0.46
1:A:242:SER:HA	1:A:277:ILE:CD1	2.48	0.43
1:A:44:VAL:HG12	1:A:62:ASP:HB2	2.01	0.41
1:A:68:ILE:HG21	1:A:175:VAL:CG2	2.46	0.40

magnitude.

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:ASN:ND2	1:A:283:GLU:OE1[3_646]	2.19	0.01

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	А	252/284~(89%)	243~(96%)	7 (3%)	2(1%)	19 7	

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	274	ILE
1	А	213	GLY



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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	А	222/255~(87%)	217~(98%)	5(2%)	50	37

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

Mol	Chain	\mathbf{Res}	Type
1	А	79	GLN
1	А	111	MET
1	А	152	LYS
1	А	180	LYS
1	А	283	GLU

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

Mol	Chain	Res	Type
1	А	61	ASN
1	А	69	ASN
1	А	73	GLN
1	А	77	ASN
1	А	79	GLN
1	А	211	HIS

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 monosaccharides in this entry.



5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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				B	ond ang	les		
wioi Type	Chain	nes	S LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2	
3	SAM	А	300	-	24,29,29	1.63	5 (20%)	23,42,42	2.02	5 (21%)

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.

Μ	ol	Type	Chain	Res	Link	Chirals	Torsions	Rings
	}	SAM	А	300	-	-	0/12/33/33	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\operatorname{Observed}(\operatorname{\AA})$	$\mathrm{Ideal}(\mathrm{\AA})$
3	А	300	SAM	C4-N3	3.75	1.40	1.35
3	А	300	SAM	O4'-C1'	2.86	1.45	1.41
3	А	300	SAM	O-C	2.76	1.30	1.22
3	А	300	SAM	C2-N3	2.61	1.36	1.32
3	А	300	SAM	C5'-C4'	-2.08	1.47	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	А	300	SAM	O4'-C1'-C2'	-6.27	97.76	106.93
3	А	300	SAM	OXT-C-O	-5.14	112.42	124.09
3	А	300	SAM	CE-SD-C5'	-2.61	79.99	100.54
3	А	300	SAM	C5-C6-N6	2.14	123.60	120.35
3	А	300	SAM	C5-C6-N1	-2.09	115.61	120.35

There are no chirality outliers.

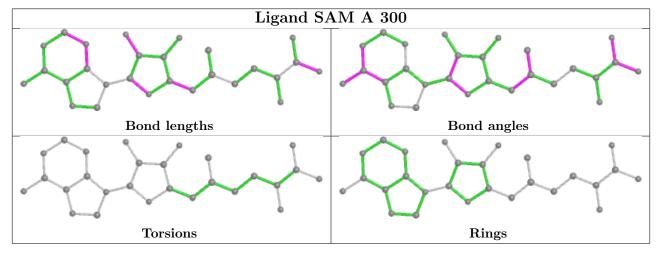
There are no torsion outliers.



There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and sufficient must be highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

