

wwPDB X-ray Structure Validation Summary Report (i)

May 12, 2021 – 12:11 PM EDT

PDB ID	:	7LNI
Title	:	SeMet CamA Adenine Methyltransferase Complexed to Cognate Substrate
		DNA
Authors	:	Horton, J.R.; Cheng, X.; Zhou, J.
Deposited on	:	2021-02-07
Resolution	:	2.68 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 following versions of software and data (see references (1)) were used in the production of this report:

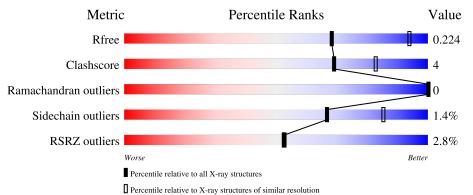
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.18
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.18

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 2.68 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	3863 (2.70-2.66)
Clashscore	141614	4210 (2.70-2.66)
Ramachandran outliers	138981	4141 (2.70-2.66)
Sidechain outliers	138945	4141 (2.70-2.66)
RSRZ outliers	127900	3780 (2.70-2.66)

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% 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	А	578	86%	9%	5%
1	В	578	^{2%} 84%	12%	5%
1	С	578	83%	11%	7%
2	Е	14	64%	36%	
2	G	14	50% 50%	6	

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Mol	Chain	Length	Quality of chain	
2	Ι	14	7% 64% 30	6%
3	D	14	7%86%	14%
3	F	14	86%	14%
3	Н	14	7%100%	



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 15353 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.

Mol	Chain	Residues		Atoms					ZeroOcc	AltConf	Trace
1	Λ	547	Total	С	Ν	0	\mathbf{S}	Se	0	1	0
	A	047	4521	2944	721	839	12	5			
1	В	551	Total	С	Ν	0	S	Se	0	0	0
	D	551	4544	2961	726	840	12	5	0		
1	C	540	Total	С	Ν	0	S	Se	0	0	0
		040	4306	2801	687	801	12	5	U	U	U

• Molecule 1 is a protein called Site-specific DNA-methyltransferase (adenine-specific).

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	HIS	-	expression tag	UNP Q183J3
В	0	HIS	-	expression tag	UNP Q183J3
С	0	HIS	_	expression tag	UNP Q183J3

• Molecule 2 is a DNA chain called DNA Strand 2.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	E	14	Total	С	Ν	Ο	Р	0	0	0
	Ľ	14	287	139	50	85	13	0		
2	С	14	Total	С	Ν	Ο	Р	0	0	0
	G	14	287	139	50	85	13	0	0	0
2	Т	14	Total	С	Ν	0	Р	0	0	0
2	1	14	287	139	50	85	13	0	0	0

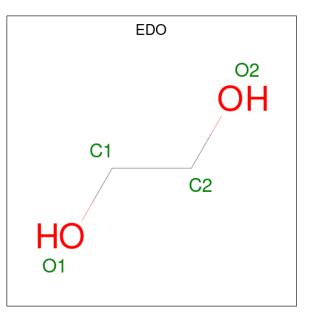
• Molecule 3 is a DNA chain called DNA Strand 1.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
3	D	14	Total 281		N 53		Р 13	0	0	0
3	F	14	Total 281			O 79	Р 13	0	0	0
3	Н	14	Total 281	C 136	N 53	O 79	Р 13	0	0	0





• Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
4	F	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
4	Ι	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	68	Total O 68 68	0	0
5	В	78	Total O 78 78	0	0
5	С	42	$\begin{array}{cc} \text{Total} & \text{O} \\ 42 & 42 \end{array}$	0	0
5	Е	10	Total O 10 10	0	0
5	D	18	Total O 18 18	0	0
5	F	22	Total O 22 22	0	0
5	G	8	Total O 8 8	0	0
5	Н	13	Total O 13 13	0	0

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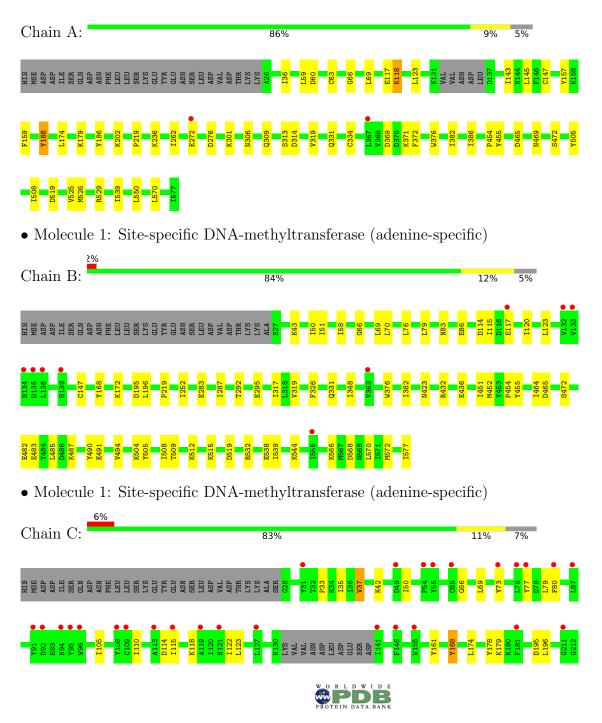
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	Ι	7	Total O 7 7	0	0



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 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: Site-specific DNA-methyltransferase (adenine-specific)



1213 2219 1244 1262 1262	1280 1280 1285 1285 1287 1287 1287 1287 1287 1287 1287 1285 1333 1333 1333 1333 1339 1337 8339 8339 8339 8339 8339 8339 8339 8	1382 1386 1386 1386 1401 1402 1403 1402 1419 1419 1437 1419 1464 1437 1464 1437 1464
V494 Y505 I508 K511 K511 M513	15 19 15 26 15 30 15 47 15 47 15 77	
• Molecule 2:	DNA Strand 2	
Chain E:	64%	36%
A1 12 63 11 11 11 11		
• Molecule 2:	DNA Strand 2	
Chain G:	50%	50%
A1 72 64 65 65 71 11 711	A14	
	DNA Strand 2	
Chain I:	64%	36%
A1 12 63 19 110 111 111 114		
	DNA Strand 1	
Chain D:	86%	14%
11 C13 A14		
• Molecule 3:	DNA Strand 1	
Chain F:	86%	14%
T1 C13 A14		
	DNA Strand 1	
Chain H:	100%	
11 A14		



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	82.07Å 160.99Å 231.32Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.76 - 2.68	Depositor
Resolution (A)	48.68 - 2.68	EDS
% Data completeness	99.2 (40.76-2.68)	Depositor
(in resolution range)	90.8 (48.68-2.68)	EDS
R _{merge}	0.31	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$0.92 (at 2.69 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.19_4092	Depositor
D D.	0.203 , 0.223	Depositor
R, R_{free}	0.202 , 0.224	DCC
R_{free} test set	1999 reflections (2.33%)	wwPDB-VP
Wilson B-factor $(Å^2)$	43.4	Xtriage
Anisotropy	0.363	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.32 , 40.2	EDS
L-test for twinning ²	$ \langle L \rangle = 0.49, \langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	15353	wwPDB-VP
Average B, all atoms $(Å^2)$	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.67% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: EDO

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		
INIOI	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.24	0/4612	0.43	0/6201	
1	В	0.24	0/4633	0.43	0/6230	
1	С	0.24	0/4388	0.42	0/5918	
2	Е	0.51	0/321	0.99	0/495	
2	G	0.53	0/321	1.00	0/495	
2	Ι	0.51	0/321	0.99	0/495	
3	D	0.47	0/315	0.84	0/483	
3	F	0.45	0/315	0.84	0/483	
3	Н	0.45	0/315	0.82	0/483	
All	All	0.28	0/15541	0.52	0/21283	

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	А	4521	0	4484	26	0
1	В	4544	0	4522	39	0
1	С	4306	0	4138	32	0
2	Е	287	0	162	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G	287	0	162	5	0
2	Ι	287	0	162	3	0
3	D	281	0	159	1	0
3	F	281	0	159	1	0
3	Н	281	0	159	0	0
4	В	4	0	6	0	0
4	F	4	0	6	0	0
4	Ι	4	0	6	0	0
5	А	68	0	0	0	0
5	В	78	0	0	1	0
5	С	42	0	0	0	0
5	D	18	0	0	0	0
5	Е	10	0	0	0	0
5	F	22	0	0	0	0
5	G	8	0	0	0	0
5	Н	13	0	0	0	0
5	Ι	7	0	0	0	0
All	All	15353	0	14125	107	0

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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 4.

The worst 5 of 107 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1			Clash overlap (Å)
1:A:69:LEU:HD12	1:A:123:LEU:HD21	1.75	0.69
1:C:66:GLY:HA3	1:C:123:LEU:HD13	1.75	0.69
1:B:538:GLU:OE2	1:B:566:LYS:NZ	2.25	0.69
2:G:1:DA:H2"	2:G:2:DT:H5"	1.77	0.66
1:C:252:ILE:HD12	1:C:287:ILE:HD12	1.77	0.66

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.



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	А	544/578~(94%)	533~(98%)	11 (2%)	0	100 10	00
1	В	549/578~(95%)	537~(98%)	12 (2%)	0	100 10	00
1	С	536/578~(93%)	525~(98%)	11 (2%)	0	100 10	00
All	All	1629/1734~(94%)	1595 (98%)	34 (2%)	0	100 10	00

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

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	nain Analysed Rotameric Outliers		Percentiles		
1	А	494/542~(91%)	488 (99%)	6 (1%)	71 87	
1	В	497/542~(92%)	493~(99%)	4 (1%)	81 92	
1	С	449/542~(83%)	439 (98%)	10 (2%)	52 77	
All	All	1440/1626~(89%)	1420 (99%)	20 (1%)	67 85	

5 of 20 residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	С	168	TYR
1	С	420	LYS
1	С	519	ASP
1	С	455	TYR
1	В	70	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

3 ligands are 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	B	ond leng	gths	B	ond ang	gles
	туре	Unam	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
4	EDO	В	601	-	3,3,3	0.46	0	2,2,2	0.32	0
4	EDO	F	101	-	3,3,3	0.46	0	2,2,2	0.32	0
4	EDO	Ι	101	-	3,3,3	0.47	0	2,2,2	0.31	0

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
4	EDO	В	601	-	-	0/1/1/1	-
4	EDO	F	101	-	-	0/1/1/1	-
4	EDO	Ι	101	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

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 (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^{th} 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	$\langle RSRZ \rangle$	#RSRZ>2	$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q < 0.9
1	А	542/578~(93%)	-0.21	2 (0%) 92 93	27, 47, 83, 137	0
1	В	546/578~(94%)	-0.09	9 (1%) 72 73	27, 46, 83, 193	0
1	С	535/578~(92%)	0.26	32 (5%) 21 20	34, 60, 121, 172	0
2	Ε	14/14~(100%)	-0.17	1 (7%) 16 13	35, 41, 155, 176	0
2	G	14/14~(100%)	-0.58	0 100 100	32, 38, 64, 69	0
2	Ι	14/14~(100%)	0.11	1 (7%) 16 13	42, 52, 134, 178	0
3	D	14/14~(100%)	-0.12	1 (7%) 16 13	30, 40, 117, 147	0
3	F	14/14~(100%)	-0.35	0 100 100	29, 36, 74, 75	0
3	Н	14/14~(100%)	0.13	1 (7%) 16 13	38, 52, 125, 164	0
All	All	1707/1818 (93%)	-0.02	47 (2%) 53 52	27, 51, 109, 193	0

The worst 5 of 47 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	С	119	ALA	5.9
1	В	134	ASN	5.4
1	В	135	ASP	5.4
1	В	139	SER	5.3
1	С	95	TYR	4.5

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 monosaccharides 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^{th} 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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
4	EDO	Ι	101	4/4	0.80	0.29	$51,\!56,\!61,\!68$	0
4	EDO	В	601	4/4	0.83	0.26	59,72,78,78	0
4	EDO	F	101	4/4	0.89	0.21	33,48,53,59	0

6.5 Other polymers (i)

There are no such residues in this entry.

