

# Full wwPDB X-ray Structure Validation Report (i)

#### May 14, 2020 - 07:36 am BST

PDB ID	:	5IL0
Title	:	Crystal structural of the METTL3-METTL14 complex for N6-adenosine
		methylation
Authors	:	Wang, X.; Guan, Z.; Zou, T.; Yin, P.
Deposited on	:	2016-03-04
Resolution	:	1.88 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 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 as 541 be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
$\operatorname{Refmac}$	:	5.8.0158
$\operatorname{CCP4}$	:	7.0.044  (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.88 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 <sub>free</sub>	130704	9470(1.90-1.86)
Clashscore	141614	10282(1.90-1.86)
Ramachandran outliers	138981	10152(1.90-1.86)
Sidechain outliers	138945	10152(1.90-1.86)
RSRZ outliers	127900	9303 (1.90-1.86)

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 >=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	212	9%	14% •				
2	В	300	<u>6%</u> 83%	9% • 6%				

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:



Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	EDO	В	501	-	_	Х	-



# 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4347 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 METTL3.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	211	Total 1706	C 1090	N 304	O 302	S 10	0	0	0

• Molecule 2 is a protein called METTL14.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
2	В	282	Total 2301	C 1463	N 398	0 427	Р 1	S 12	0	0	0

• Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



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



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• Molecule 4 is BROMIDE ION (three-letter code: BR) (formula: Br).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	1	Total Br 1 1	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	102	Total O 102 102	0	0
5	В	229	Total         O           229         229	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: METTL3



# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants	101.69Å 101.69Å 116.48Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
$\mathbf{B}_{\text{assolution}}(\hat{\lambda})$	36.27 - 1.88	Depositor
Resolution (A)	36.27 - 1.88	EDS
% Data completeness	99.9 (36.27-1.88)	Depositor
(in resolution range)	95.0(36.27-1.88)	EDS
$R_{merge}$	(Not available)	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.99 (at 1.88 \text{\AA})$	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
B B.	0.175 , $0.205$	Depositor
$\Pi, \Pi_{free}$	0.175 , $0.205$	DCC
$R_{free}$ test set	2511 reflections $(5.01%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	27.3	Xtriage
Anisotropy	0.011	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.33 , $45.2$	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4347	wwPDB-VP
Average B, all atoms $(Å^2)$	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.29% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities 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, BR, SEP

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	А	0.34	0/1752	0.55	0/2381	
2	В	0.39	0/2348	0.58	0/3180	
All	All	0.37	0/4100	0.56	0/5561	

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	1706	0	1685	20	0
2	В	2301	0	2246	22	0
3	А	4	0	6	2	0
3	В	4	0	6	6	0
4	В	1	0	0	0	0
5	А	102	0	0	0	0
5	В	229	0	0	1	0
All	All	4347	0	3943	39	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 5.



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		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
2:B:276:ASP:HB2	2:B:277:PRO:HD3	1.57	0.86
2:B:311:ILE:HG22	3:B:501:EDO:H11	1.58	0.84
1:A:537:PRO:HB3	3:A:601:EDO:H22	1.77	0.65
2:B:168:MET:HE3	2:B:369:TYR:HA	1.80	0.64
1:A:373:TRP:HB2	1:A:551:LEU:HD13	1.81	0.62
1:A:383:VAL:HG22	1:A:422:LEU:HD21	1.83	0.60
2:B:200:ARG:NH1	5:B:604:HOH:O	2.34	0.60
1:A:456:ILE:HD11	2:B:262:ILE:HD11	1.84	0.59
2:B:276:ASP:HB2	2:B:277:PRO:CD	2.31	0.59
1:A:411:ASP:CG	1:A:435:ARG:HH22	2.05	0.58
2:B:191:LEU:HD22	2:B:193:PRO:HD3	1.85	0.58
1:A:411:ASP:OD1	1:A:435:ARG:NH2	2.39	0.56
2:B:311:ILE:H	3:B:501:EDO:C1	2.20	0.55
1:A:533:LEU:HD12	1:A:547:LEU:HD12	1.88	0.55
2:B:297:LYS:HB2	2:B:300:THR:HG22	1.90	0.54
2:B:325:GLU:CD	2:B:349:ARG:HH11	2.12	0.53
2:B:311:ILE:H	3:B:501:EDO:H12	1.72	0.53
1:A:377:ASP:OD2	1:A:379:ARG:HD3	2.08	0.53
1:A:480:LYS:HD2	2:B:313:LEU:HD21	1.91	0.52
2:B:200:ARG:NH2	2:B:276:ASP:HB3	2.24	0.52
1:A:434:GLY:O	1:A:437:MET:HG2	2.11	0.50
2:B:310:ASP:HA	3:B:501:EDO:H12	1.93	0.49
1:A:468:ARG:HD3	3:B:501:EDO:O1	2.13	0.48
2:B:310:ASP:OD1	3:B:501:EDO:H21	2.13	0.48
2:B:196:GLU:HG2	2:B:210:CYS:HB3	1.93	0.48
1:A:396:PRO:HG2	1:A:398:TRP:CE2	2.52	0.45
1:A:381:LEU:HD23	1:A:574:ILE:HG21	2.00	0.44
1:A:456:ILE:HD11	2:B:262:ILE:CD1	2.47	0.44
2:B:277:PRO:HB2	2:B:278:LYS:H	1.50	0.44
1:A:459:LYS:HE2	1:A:481:GLU:HG2	1.99	0.44
2:B:142:ARG:NH2	2:B:329:GLU:OE2	2.39	0.42
1:A:436:ALA:HA	1:A:439:LEU:HB3	2.02	0.42
1:A:552:ASP:N	3:A:601:EDO:O2	2.40	0.42
1:A:378:ILE:HG13	1:A:534:PHE:CE1	2.55	0.41
2:B:390:GLU:OE1	2:B:394:ARG:HD3	2.19	0.41
1:A:383:VAL:CG2	1:A:422:LEU:HD21	2.50	0.41
2:B:261:TRP:CE2	2:B:327:PRO:HG3	2.56	0.40
2:B:269:PRO:HA	2:B:270:GLY:HA2	1.67	0.40
1:A:388:LYS:O	1:A:529:ARG:HD3	2.20	0.40

All (39) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



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	А	209/212 (99%)	203~(97%)	5(2%)	1 (0%)	29 17
2	В	275/300 (92%)	267 (97%)	5 (2%)	3 (1%)	14 5
All	All	484/512~(94%)	470 (97%)	10 (2%)	4 (1%)	19 9

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	В	276	ASP
2	В	277	PRO
1	А	578	LYS
2	В	270	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 sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric Outliers		Percentiles		
1	А	186/188~(99%)	180~(97%)	6 (3%)	39 27		
2	В	250/268~(93%)	242 (97%)	8 (3%)	39 27		
All	All	436/456~(96%)	422 (97%)	14 (3%)	39 27		

All (14) residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	А	369	PHE
1	А	474	HIS
1	А	480	LYS
1	А	529	ARG
1	А	533	LEU
1	А	556	LEU
2	В	191	LEU
2	В	207	ASN
2	В	243	LEU
2	В	271	LYS
2	В	274	THR
2	В	278	LYS
2	В	298	ARG
2	В	320	GLU

Some 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)

1 non-standard protein/DNA/RNA residue 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).

Mal	Tune	Chain	Dog	Link	B	ond leng	$\mathbf{gths}$	E	Bond ang	gles
	туре	Chain	nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SEP	В	399	2	8,9,10	1.58	1 (12%)	8,12,14	2.15	2 (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
2	SEP	В	399	2	-	3/5/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	Ideal(Å)
2	В	399	SEP	P-O1P	3.31	1.61	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
2	В	399	SEP	P-OG-CB	-4.26	106.56	118.30
2	В	399	SEP	OG-CB-CA	3.91	111.95	108.14

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	$\mathbf{Res}$	Type	Atoms
2	В	399	SEP	CB-OG-P-O2P
2	В	399	SEP	CB-OG-P-O3P
2	В	399	SEP	CB-OG-P-O1P

There are no ring outliers.

No monomer is involved in short contacts.

### 5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 1 is 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).



Mal	Turne	Type Chain		Timle	Bond lengths			Bond angles		
	туре	Chain	nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	EDO	В	501	-	3,3,3	0.44	0	$^{2,2,2}$	0.15	0
3	EDO	А	601	-	3,3,3	0.43	0	$2,\!2,\!2$	0.45	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
3	EDO	В	501	-	-	0/1/1/1	-
3	EDO	А	601	-	-	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.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	В	501	EDO	6	0
3	А	601	EDO	2	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,  $95^{th}$  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	<RSRZ $>$	#RSRZ>2	$OWAB(Å^2)$	Q < 0.9
1	А	211/212 (99%)	0.34	19 (9%) 9 10	20, 43, 80, 102	0
2	В	281/300~(93%)	0.10	18 (6%) 19 20	19, 31, 70, 109	0
All	All	492/512~(96%)	0.20	37 (7%) 14 15	19, 37, 77, 109	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	В	272	THR	6.4
2	В	206	ALA	5.6
2	В	321	ILE	5.2
1	А	402	MET	4.6
2	В	270	GLY	4.3
1	А	369	PHE	4.0
2	В	274	THR	3.8
2	В	199	TYR	3.7
1	А	579	ASN	3.5
2	В	207	ASN	3.4
2	В	205	THR	3.4
2	В	401	PRO	3.3
1	А	403	GLU	3.3
1	А	492	GLN	3.1
1	А	573	ILE	3.1
1	А	571	ASP	3.0
2	В	322	GLY	3.0
1	А	578	LYS	2.9
2	В	116	HIS	2.8
1	A	566	LYS	2.8
2	В	208	GLU	2.7
1	A	490	ASN	2.7
1	A	400(A)	HIS	2.6
2	B	269	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
1	А	577	PRO	2.6
2	В	271	LYS	2.6
1	А	572	GLY	2.5
1	А	575	SER	2.5
2	В	268	ASN	2.5
2	В	200	ARG	2.3
1	А	370	PRO	2.3
1	А	565	PHE	2.3
1	А	554	ILE	2.3
2	В	260	CYS	2.2
2	В	277	PRO	2.2
1	А	561	VAL	2.2
1	A	559	PRO	2.0

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### 6.2 Non-standard residues in protein, DNA, RNA chains (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	$\mathbf{B} ext{-factors}(\mathbf{\AA}^2)$	Q<0.9
2	SEP	В	399	10/11	0.81	0.15	$32,\!55,\!86,\!87$	0

### 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,  $95^{th}$  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	B-factors(Å <sup>2</sup> )	Q<0.9
3	EDO	В	501	4/4	0.87	0.28	$41,\!45,\!45,\!52$	0
3	EDO	А	601	4/4	0.92	0.14	54,63,64,65	0
4	BR	В	502	1/1	1.00	0.04	38,38,38,38	0



# 6.5 Other polymers (i)

There are no such residues in this entry.

