W O R L D W I D E
wwPDB
PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 16, 2021 – 02:02 pm BST

PDB ID	:	7O2E
Title	:	Crystal structure of the human METTL3-METTL14 complex bound to Compound 21 (ADO_AD_089)
Authors	:	Bedi, R.K.; Dolbois, A.; Caflisch, A.
Deposited on	:	2021-03-30
Resolution	:	2.50 Å(reported)

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

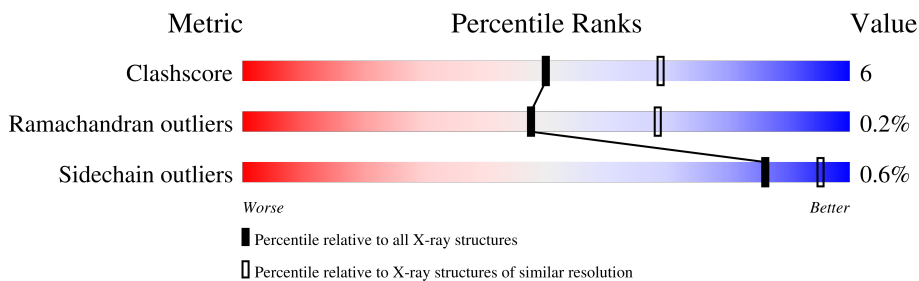|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.1

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 2.50 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	Percentile Ranks	Value
Clashscore		6
Ramachandran outliers		0.2%
Sidechain outliers		0.6%

Worse ← → *Better*

▮ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)

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	A	246	66%　　15%　　18%
2	B	290	72%　　11%　　17%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3460 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 N6-adenosine-methyltransferase catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	201	Total 1563	C 1003	N 272	O 279	S 9	0	0	0

There are 19 discrepancies between the modelled and reference sequences:

| Chain	Residue	Modelled	Actual	Comment	Reference
A	335	MET	-	initiating methionine	UNP Q86U44
A	336	GLY	-	expression tag	UNP Q86U44
A	337	HIS	-	expression tag	UNP Q86U44
A	338	HIS	-	expression tag	UNP Q86U44
A	339	HIS	-	expression tag	UNP Q86U44
A	340	HIS	-	expression tag	UNP Q86U44
A	341	HIS	-	expression tag	UNP Q86U44
A	342	HIS	-	expression tag	UNP Q86U44
A	343	SER	-	expression tag	UNP Q86U44
A	344	SER	-	expression tag	UNP Q86U44
A	345	GLY	-	expression tag	UNP Q86U44
A	346	ARG	-	expression tag	UNP Q86U44
A	347	GLU	-	expression tag	UNP Q86U44
A	348	ASN	-	expression tag	UNP Q86U44
A	349	LEU	-	expression tag	UNP Q86U44
A	350	TYR	-	expression tag	UNP Q86U44
A	351	PHE	-	expression tag	UNP Q86U44
A	352	GLN	-	expression tag	UNP Q86U44
A	353	GLY	-	expression tag	UNP Q86U44

- Molecule 2 is a protein called N6-adenosine-methyltransferase non-catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	241	Total 1833	C 1176	N 311	O 334	S 12	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	106	MET	-	initiating methionine	UNP Q9HCE5

- Molecule 3 is 4-[4-[(4,4-dimethylpiperidin-1-yl)methyl]-3-fluoranyl-phenyl]-9-[6-(methylamino)pyrimidin-4-yl]-1,4,9-triazaspiro[5.5]undecan-2-one (three-letter code: UZH) (formula: $C_{27}H_{38}FN_7O$) (labeled as "Ligand of Interest" by depositor).
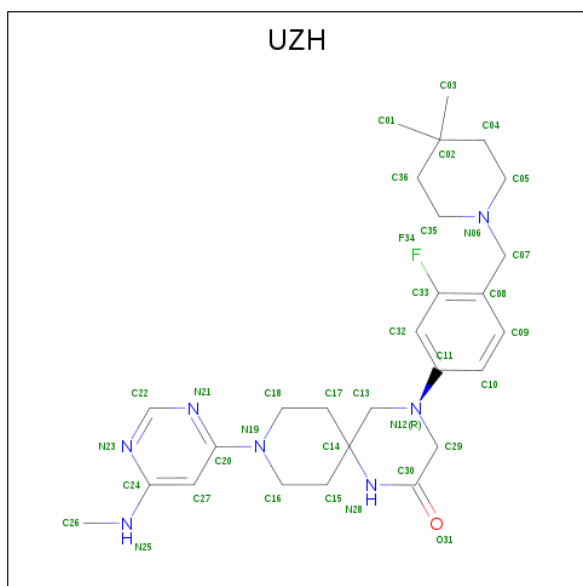
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	F	N	O		
3	A	1	36	27	1	7	1	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).

ACT

OXT

O⁻

C

CH3

O

O

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total 4	C 2	O 2	0	0

- Molecule 5 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	8	Total 8	O 8	0	0
5	B	16	Total 16	O 16	0	0

3 Residue-property plots ⓘ

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: N6-adenosine-methyltransferase catalytic subunit

Chain A:
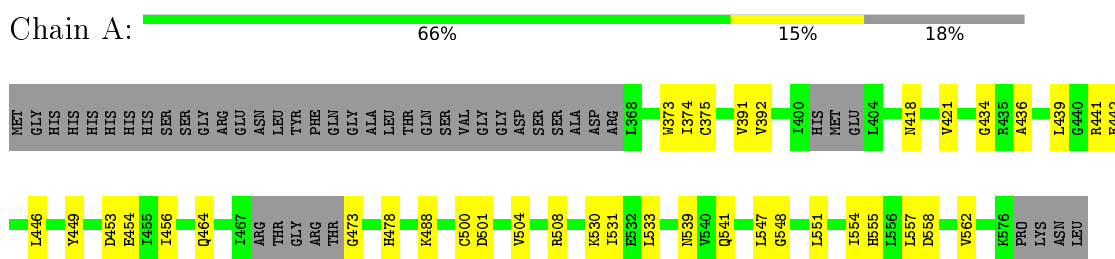
• Molecule 2: N6-adenosine-methyltransferase non-catalytic subunit

Chain B:
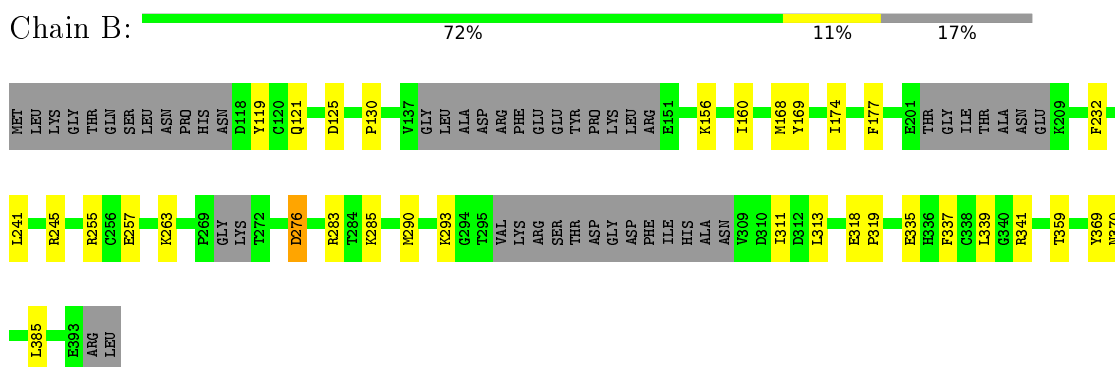
4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	63.93Å 63.93Å 224.60Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.52 – 2.50	Depositor
% Data completeness (in resolution range)	99.9 (44.52-2.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.206 , 0.273	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3460	wwPDB-VP
Average B, all atoms (Å²)	62.0	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: UZH, ACT

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	0.45	0/1604	0.64	0/2187
2	B	0.48	0/1879	0.66	1/2560 (0.0%)
All	All	0.46	0/3483	0.65	1/4747 (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})
2	B	276	ASP	CB-CG-OD1	7.66	125.19	118.30

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	A	1563	0	1470	21	0
2	B	1833	0	1673	23	0
3	A	36	0	0	0	0
4	B	4	0	3	0	0
5	A	8	0	0	0	0
5	B	16	0	0	0	0
All	All	3460	0	3146	38	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 6.

The worst 5 of 38 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)
2:B:168:MET:HE3	2:B:369:TYR:HA	1.58	0.85
1:A:464:GLN:OE1	2:B:119:TYR:OH	2.04	0.76
1:A:373:TRP:HB2	1:A:551:LEU:HD23	1.78	0.65
2:B:311:ILE:HG23	2:B:313:LEU:H	1.65	0.62
1:A:374:ILE:HG23	1:A:554:ILE:HD12	1.85	0.57

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	195/246 (79%)	184 (94%)	10 (5%)	1 (0%)	29	48
2	B	231/290 (80%)	222 (96%)	9 (4%)	0	100	100
All	All	426/536 (80%)	406 (95%)	19 (4%)	1 (0%)	47	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	508	ARG

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	159/215 (74%)	158 (99%)	1 (1%)		86	95
2	B	181/259 (70%)	180 (99%)	1 (1%)		86	95
All	All	340/474 (72%)	338 (99%)	2 (1%)		86	95

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	453	ASP
2	B	276	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	478	HIS
2	B	121	GLN

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)

2 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	Bond lengths			Bond angles		
					Counts	RMSZ	#$|Z| > 2$	Counts	RMSZ	#$|Z| > 2$
3	UZH	A	601	-	39,40,40	2.83	12 (30%)	48,59,59	3.03	20 (41%)
4	ACT	B	401	-	1,3,3	8.79	1 (100%)	0,3,3	0.00	-

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	UZH	A	601	-	-	2/14/52/52	0/5/5/5

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	401	ACT	CH3-C	8.79	1.59	1.48
3	A	601	UZH	C30-N28	8.40	1.45	1.34
3	A	601	UZH	C07-N06	-7.12	1.33	1.47
3	A	601	UZH	C05-N06	-5.32	1.32	1.46
3	A	601	UZH	C24-N25	5.27	1.47	1.36

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	UZH	C17-C14-C13	11.79	132.87	110.62
3	A	601	UZH	C15-C14-C13	-7.82	95.87	110.62
3	A	601	UZH	C22-N21-C20	4.89	119.22	114.94
3	A	601	UZH	N23-C22-N21	-4.83	121.04	128.60
3	A	601	UZH	C18-N19-C16	4.82	122.16	111.52

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	UZH	C27-C24-N25-C26
3	A	601	UZH	N23-C24-N25-C26

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 any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand UZH A 601

Bond lengths — Bond angles — Torsions — Rings
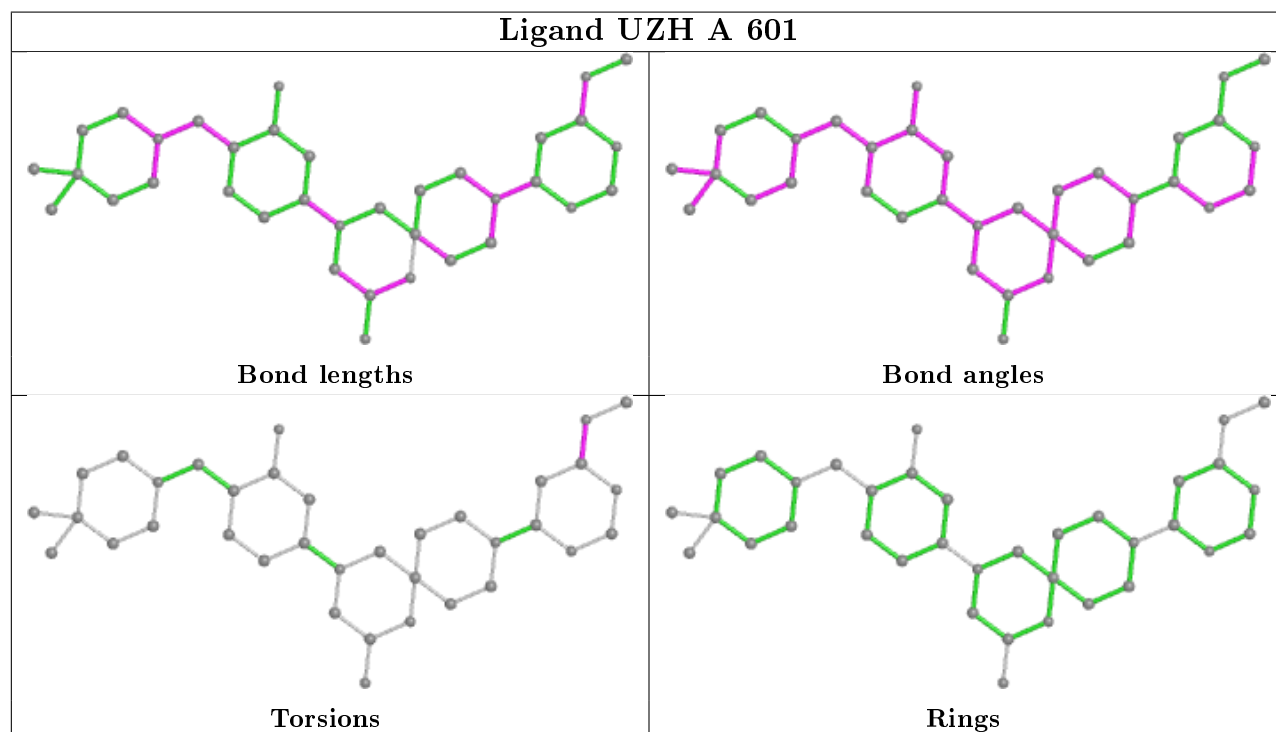
5.7 Other polymers (i)

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.