

Full wwPDB X-ray Structure Validation Report (i)

Oct 12, 2021 – 05:34 pm BST

PDB ID : 70ED

Title : Crystal structure of the human METTL3-METTL14 complex with compound

UOZ019a

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Deposited on : 2021-05-03

Resolution : 2.00 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 as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.23.2

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac: 5.8.0267

CCP4 : 7.1.010 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

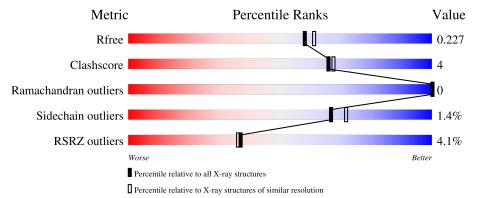
Validation Pipeline (wwPDB-VP) : 2.23.2

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 2.00 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	$(\# ext{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 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	A	246	75%	6%	18%				
2	В	290	72%	8% •	19%				



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3759 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 1591	C 1022	N 275	O 285	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.

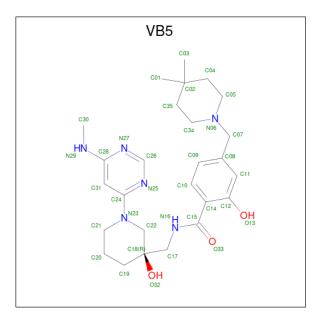
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	В	236	Total 1863	C 1197	N 314	O 339	S 13	0	2	0



There is a discrepancy between the modelled and reference sequences:

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

• Molecule 3 is 4-[(4,4-dimethylpiperidin-1-yl)methyl]- {N}-[[(3 {R})-1-[6-(methylamino)p yrimidin-4-yl]-3-oxidanyl-piperidin-3-yl]methyl]-2-oxidanyl-benzamide (three-letter code: VB5) (formula: $C_{26}H_{38}N_6O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 35	C 26	N 6	O 3	0	0

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





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

• Molecule 5 is water.

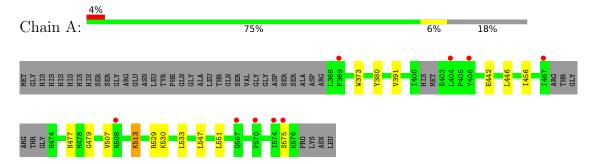
\mathbf{Mol}	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
5	A	111	Total O 111 111	0	0
5	В	155	Total O 155 155	0	0



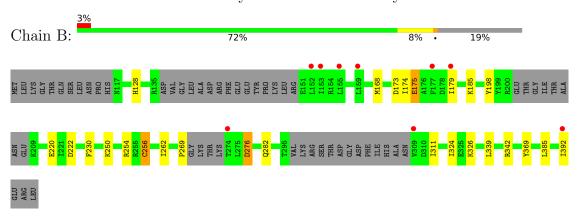
3 Residue-property plots (i)

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: N6-adenosine-methyltransferase catalytic subunit



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





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants	64.03Å 64.03Å 225.88Å	Denogitor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.78 - 2.00	Depositor
rtesolution (A)	49.78 - 2.00	EDS
% Data completeness	99.9 (49.78-2.00)	Depositor
(in resolution range)	99.9 (49.78-2.00)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.72 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
D D.	0.186 , 0.228	Depositor
R, R_{free}	0.184 , 0.227	DCC
R_{free} test set	1862 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	34.2	Xtriage
Anisotropy	0.155	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning ²	$< L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	0.027 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3759	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.59% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ 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: ACT, VB5

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		
IVIOI		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.39	0/1632	0.61	0/2222	
2	В	0.42	0/1913	0.64	1/2600 (0.0%)	
All	All	0.41	0/3545	0.63	1/4822 (0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}(^{o})$
2	В	276	ASP	CB-CG-OD1	7.08	124.67	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	1591	0	1529	10	0
2	В	1863	0	1750	20	0
3	A	35	0	0	0	0
4	В	4	0	3	0	0
5	A	111	0	0	3	1
5	В	155	0	0	8	1
All	All	3759	0	3282	27	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 4.

All (27) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${ m distance}({ m \AA})$	overlap (Å)
2:B:276:ASP:OD2	5:B:501:HOH:O	2.08	0.71
1:A:391:VAL:HB	1:A:530:LYS:HG2	1.80	0.64
2:B:174:ILE:O	5:B:502:HOH:O	2.16	0.62
2:B:254:ARG:NH1	5:B:508:HOH:O	2.32	0.60
2:B:168:MET:HE3	2:B:369:TYR:HA	1.85	0.59
1:A:529:ARG:HG3	5:A:731:HOH:O	2.06	0.55
2:B:250:LYS:NZ	5:B:512:HOH:O	2.45	0.50
1:A:442:GLU:O	1:A:446:LEU:HG	2.13	0.49
1:A:380:TYR:OH	5:A:701:HOH:O	2.18	0.47
2:B:198:TYR:HB3	2:B:324:ILE:HG22	1.97	0.47
2:B:230:PHE:CE1	2:B:339:LEU:HD22	2.50	0.46
2:B:173:ASP:HB3	2:B:175:GLU:OE1	2.16	0.46
2:B:282:GLN:NE2	5:B:506:HOH:O	2.29	0.46
1:A:456:ILE:HD11	2:B:262:ILE:HD11	1.98	0.46
2:B:128:HIS:CE1	2:B:269:PRO:HG3	2.52	0.45
2:B:185:LYS:O	2:B:342[B]:ARG:NH1	2.50	0.44
2:B:222:ASP:OD2	5:B:503:HOH:O	2.21	0.44
5:A:808:HOH:O	2:B:256:CYS:HB3	2.18	0.44
1:A:477:ASN:O	2:B:311:ILE:HD12	2.19	0.43
2:B:326:LYS:NZ	5:B:513:HOH:O	2.46	0.42
2:B:179:ILE:HD11	2:B:220:GLU:HB2	2.00	0.42
2:B:385:LEU:HD21	2:B:392:ILE:HD11	2.02	0.42
2:B:311:ILE:HG22	5:B:554:HOH:O	2.19	0.42
1:A:513:LYS:HB3	1:A:513:LYS:HE3	1.91	0.41
1:A:533:LEU:HD22	1:A:547:LEU:HD12	2.02	0.41
1:A:479:GLY:N	2:B:311:ILE:HD11	2.36	0.41
1:A:373:TRP:HB2	1:A:551:LEU:HD13	2.02	0.40

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	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
5:A:794:HOH:O	5:B:642:HOH:O[6 664]	1.90	0.30



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	Perce	entiles
1	A	195/246~(79%)	190 (97%)	5 (3%)	0	100	100
2	В	228/290~(79%)	221 (97%)	7 (3%)	0	100	100
All	All	423/536 (79%)	411 (97%)	12 (3%)	0	100	100

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	Analysed	Rotameric	Outliers	Percentiles
1	A	168/215 (78%)	165 (98%)	3 (2%)	59 63
2	В	193/259 (74%)	191 (99%)	2 (1%)	76 81
All	All	361/474 (76%)	356 (99%)	5 (1%)	67 72

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

Mol	Chain	Res	Type
1	A	507	VAL
1	A	513	LYS
1	A	575	SER
2	В	175	GLU
2	В	256	CYS

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



Mol	Chain	Res	Type
2	В	122	HIS
2	В	282	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	Trus	Chain	Dag	Timle	Bond lengths			В	ond ang	gles
MIOI	Type	Chain	Res	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	VB5	A	601	-	36,38,38	2.70	12 (33%)	48,55,55	2.04	10 (20%)
4	ACT	В	401	-	1,3,3	7.62	1 (100%)	0,3,3	-	-

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	VB5	A	601	-	-	2/20/44/44	0/4/4/4

All (13) bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
4	В	401	ACT	СН3-С	7.62	1.58	1.48
3	A	601	VB5	C15-N16	6.18	1.47	1.33
3	A	601	VB5	C24-N23	6.12	1.50	1.37
3	A	601	VB5	C07-N06	-5.87	1.36	1.47
3	A	601	VB5	C28-N29	5.32	1.47	1.36
3	A	601	VB5	C05-N06	-5.09	1.32	1.46
3	A	601	VB5	C34-N06	-5.02	1.33	1.46
3	A	601	VB5	C07-C08	3.71	1.58	1.51
3	A	601	VB5	C22-N23	3.50	1.49	1.46
3	A	601	VB5	O32-C18	-2.72	1.39	1.44
3	A	601	VB5	C14-C15	2.67	1.55	1.50
3	A	601	VB5	C35-C34	2.39	1.58	1.52
3	A	601	VB5	O33-C15	-2.08	1.19	1.23

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$Ideal(^{o})$
3	A	601	VB5	C26-N25-C24	5.62	119.85	114.94
3	A	601	VB5	N27-C26-N25	-5.32	120.27	128.60
3	A	601	VB5	C30-N29-C28	-4.56	119.05	122.97
3	A	601	VB5	C21-N23-C22	4.44	121.90	114.00
3	A	601	VB5	C04-C05-N06	4.42	115.59	111.23
3	A	601	VB5	C17-N16-C15	-3.64	116.88	122.89
3	A	601	VB5	C35-C34-N06	3.00	114.20	111.23
3	A	601	VB5	C08-C07-N06	-2.31	108.64	113.12
3	A	601	VB5	C14-C15-N16	2.24	121.77	117.36
3	A	601	VB5	C34-N06-C05	2.11	113.58	108.83

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	VB5	N27-C28-N29-C30
3	A	601	VB5	N16-C17-C18-O32

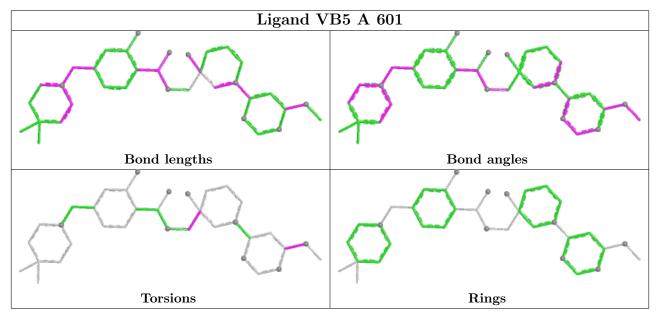
There are no ring outliers.

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.



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	$\langle { m RSRZ} \rangle$	$\# \mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	201/246 (81%)	-0.12	9 (4%) 33 32	23, 36, 64, 73	0
2	В	236/290 (81%)	-0.11	9 (3%) 40 39	22, 34, 67, 90	0
All	All	437/536 (81%)	-0.11	18 (4%) 37 36	22, 35, 66, 90	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	В	274	THR	4.0
1	A	574	ILE	3.8
2	В	392	ILE	3.8
2	В	309	VAL	3.5
1	A	575	SER	3.5
2	В	155	LEU	3.4
1	A	406	TYR	2.7
2	В	152	LEU	2.6
2	В	179	ILE	2.5
2	В	177	PHE	2.5
1	A	570	PRO	2.4
1	A	467	ILE	2.4
1	A	567	GLN	2.3
1	A	369	PHE	2.2
1	A	508	ARG	2.2
2	В	153	ILE	2.1
2	В	159	LEU	2.1
1	A	404	LEU	2.1

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)

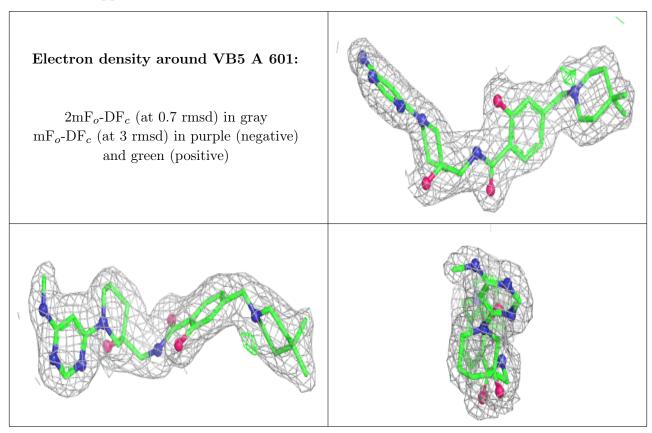
There are no monosaccharides in this entry.

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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
3	VB5	A	601	35/35	0.94	0.10	29,35,41,46	0
4	ACT	В	401	4/4	0.97	0.10	26,28,29,30	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





6.5 Other polymers (i)

There are no such residues in this entry.

