



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 14, 2020 – 09:45 AM BST

PDB ID : 6TU1
Title : Crystal structure of the human METTL3-METTL14 complex bound to Compound 8 (ASI_M3M_091)
Authors : Bedi, R.K.; Huang, D.; Sledz, P.; Caffisch, A.
Deposited on : 2019-12-31
Resolution : 2.31 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 ⓘ symbol.

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) : 1.13
EDS : 2.14.4.dev1
buster-report : 1.1.7 (2018)
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) : 2.14.4.dev1

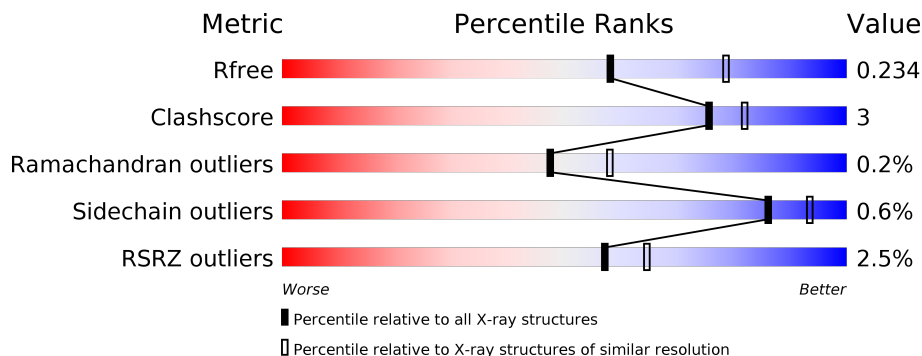
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.31 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5974 (2.34-2.30)
Clashscore	141614	6604 (2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)
RSRZ outliers	127900	5855 (2.34-2.30)

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 $\leq 5\%$. 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	580	 31% 66%
2	B	456	 48% 48%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3620 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.

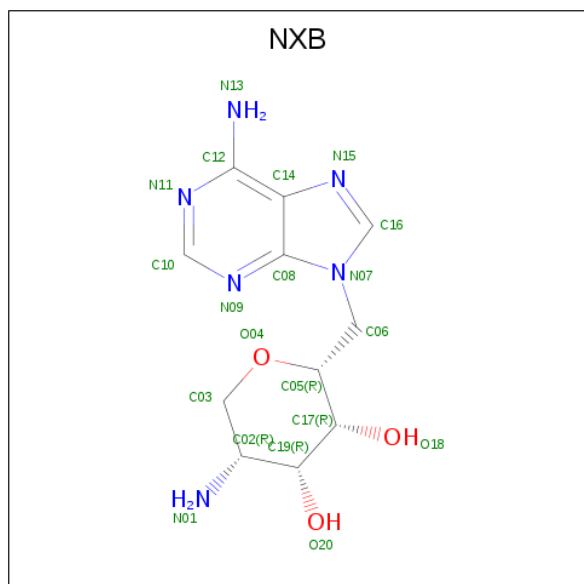
- Molecule 1 is a protein called N6-adenosine-methyltransferase catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	197	1565	1003	274	279	9	0	0	0

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

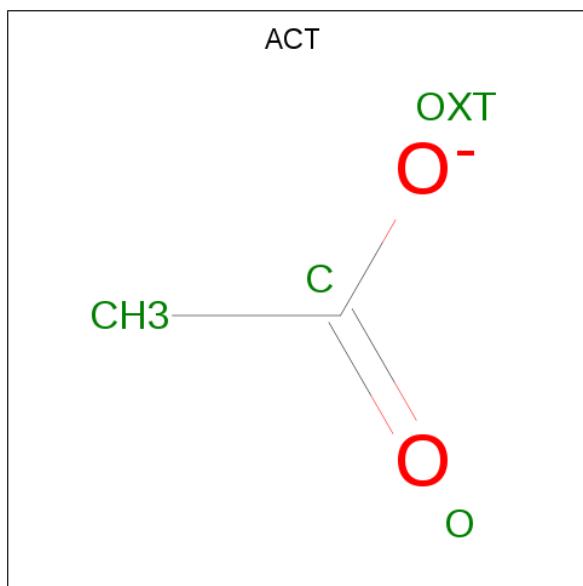
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	236	1854	1189	311	341	13	0	1	0

- Molecule 3 is (2 {R},3 {R},4 {R},5 {R})-2-[(6-aminopurin-9-yl)methyl]-5-azanyl-oxane-3,4-diol (three-letter code: NXB) (formula: C₁₁H₁₆N₆O₃) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	20	11	6	3	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	70	Total	O	0	0
			70	70		
5	B	107	Total	O	0	0
			107	107		

ASP	PHE	ILE	HIS	ALA	ASN	Y809	L313	I321	F337	C338	L339	L364	Y369	E391	ILE	GLU	ARG	LEU	ARG	PRO	LYS	SER	PRO	PRO	PRO	LYS	SER	SER	ASP	ARG	GLY	GLY	GLY	ALA	PRO	ARG	GLY	GLY	GLY	ARG	GLY	THR	SER	ALA	GLY	ARG	GLY	ARG	GLU	ARG	ASN
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ARG	SER	ASN	PHE	ARG	GLY	GLU	ARG	GLY	PHE	ARG	GLY	GLY	ARG	GLY	GLY	ALA	HIS	ARG	GLY	GLY	PHE	PRO	PRO	ARG
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4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	64.21Å 64.21Å 226.57Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.78 - 2.31 44.78 - 2.31	Depositor EDS
% Data completeness (in resolution range)	99.4 (44.78-2.31) 99.4 (44.78-2.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 2.32Å)	Xtrriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.195 , 0.234 0.195 , 0.234	Depositor DCC
R_{free} test set	1238 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	43.4	Xtrriage
Anisotropy	0.185	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 39.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.031 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3620	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.25% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NXB, 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	0.42	0/1604	0.58	0/2182
2	B	0.41	0/1901	0.61	0/2586
All	All	0.41	0/3505	0.59	0/4768

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

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	1565	0	1510	11	0
2	B	1854	0	1728	12	0
3	A	20	0	0	1	0
4	B	4	0	3	0	0
5	A	70	0	0	0	0
5	B	107	0	0	1	0
All	All	3620	0	3241	21	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 3.

All (21) 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:321:ILE:O	2:B:321:ILE:HD12	1.80	0.81
2:B:168:MET:HE3	2:B:369:TYR:HA	1.69	0.74
1:A:391:VAL:HB	1:A:530:LYS:HG2	1.78	0.66
2:B:151:GLU:N	5:B:604:HOH:O	2.31	0.63
1:A:428:LEU:HD12	1:A:444:LEU:HD11	1.82	0.61
2:B:151:GLU:HG2	2:B:151:GLU:O	2.04	0.57
1:A:501:ASP:OD2	2:B:285:LYS:HE3	2.08	0.54
1:A:373:TRP:HB2	1:A:551:LEU:HD13	1.90	0.54
2:B:156:LYS:O	2:B:160:ILE:HG13	2.10	0.51
2:B:260[B]:CYS:SG	2:B:287:HIS:CE1	3.04	0.50
1:A:559:PRO:HA	1:A:562:VAL:HG22	1.97	0.47
1:A:428:LEU:HD12	1:A:444:LEU:CD1	2.46	0.46
1:A:476:LEU:HG	2:B:337:PHE:HZ	1.81	0.46
1:A:392:VAL:HB	1:A:428:LEU:HD23	1.98	0.46
2:B:262:ILE:HD12	2:B:313:LEU:HD22	2.01	0.43
1:A:397:PRO:HB2	1:A:408:THR:HA	2.01	0.42
1:A:415:ARG:NH2	1:A:442:GLU:OE2	2.48	0.42
2:B:169:TYR:HB2	2:B:364:LEU:HD23	2.02	0.42
2:B:230:PHE:CE1	2:B:339:LEU:HD22	2.54	0.42
2:B:321:ILE:C	2:B:321:ILE:HD12	2.37	0.41
1:A:534:PHE:HB3	3:A:601:NXB:O04	2.21	0.41

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	191/580 (33%)	185 (97%)	5 (3%)	1 (0%)	29	35
2	B	227/456 (50%)	221 (97%)	6 (3%)	0	100	100
All	All	418/1036 (40%)	406 (97%)	11 (3%)	1 (0%)	47	58

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	573	ILE

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	165/502 (33%)	164 (99%)	1 (1%)	86	93
2	B	192/392 (49%)	191 (100%)	1 (0%)	88	95
All	All	357/894 (40%)	355 (99%)	2 (1%)	86	93

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

Mol	Chain	Res	Type
1	A	369	PHE
2	B	285	LYS

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](#)

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

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
4	ACT	B	501	-	1,3,3	7.44	1 (100%)	0,3,3	0.00	-
3	NXB	A	601	-	20,22,22	1.71	6 (30%)	15,32,32	2.47	4 (26%)

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	NXB	A	601	-	-	2/2/21/21	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	501	ACT	CH3-C	7.44	1.58	1.48
3	A	601	NXB	C14-N15	3.42	1.52	1.39
3	A	601	NXB	C12-N13	3.15	1.45	1.34
3	A	601	NXB	C06-N07	-2.47	1.45	1.48
3	A	601	NXB	C08-N09	-2.37	1.32	1.35
3	A	601	NXB	O04-C03	-2.23	1.40	1.43
3	A	601	NXB	O04-C05	-2.11	1.39	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	NXB	C03-O04-C05	-5.64	104.55	112.19
3	A	601	NXB	N09-C10-N11	-4.70	121.33	128.68
3	A	601	NXB	C08-C14-N15	-4.15	105.08	109.40
3	A	601	NXB	C17-C19-C02	2.85	116.18	111.37

There are no chirality outliers.

All (2) torsion outliers are listed below:

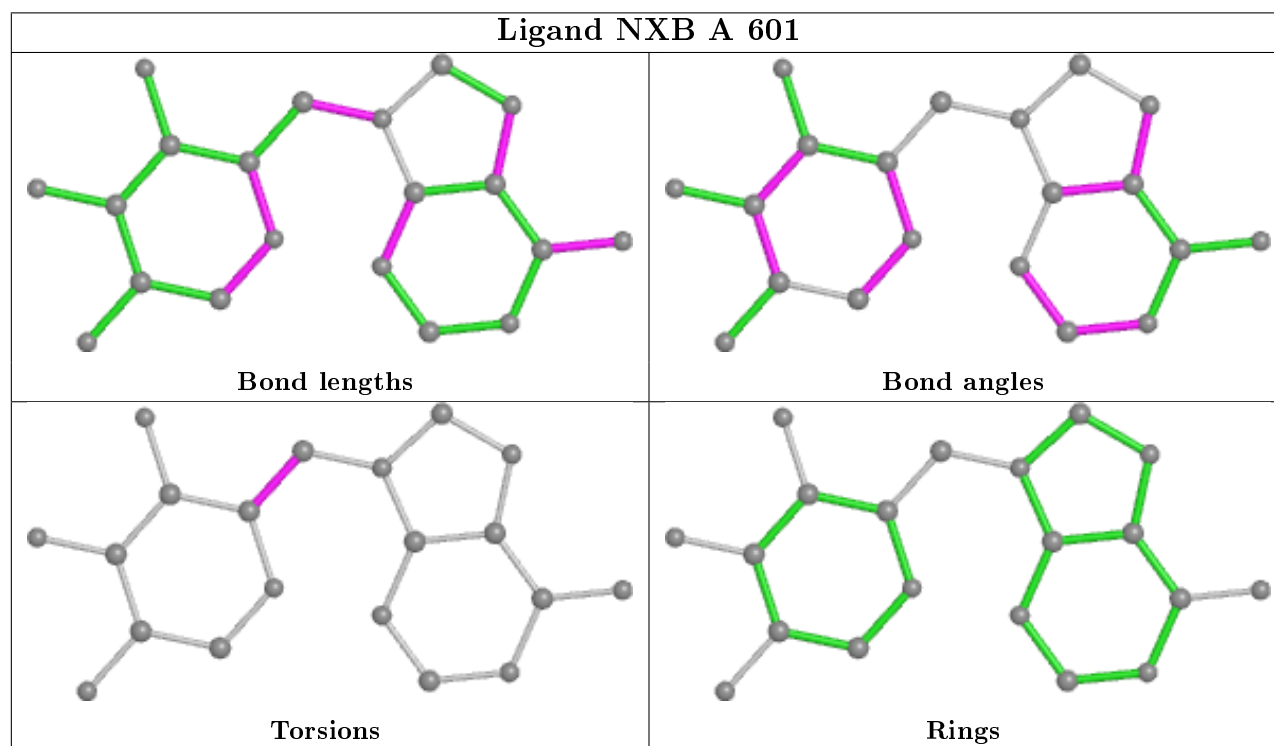
Mol	Chain	Res	Type	Atoms
3	A	601	NXB	O04-C05-C06-N07
3	A	601	NXB	C17-C05-C06-N07

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	601	NXB	1	0

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 than 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, 95th 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	A	197/580 (33%)	-0.12	7 (3%) 42 49	32, 44, 68, 86	0
2	B	236/456 (51%)	-0.17	4 (1%) 70 76	30, 43, 75, 86	0
All	All	433/1036 (41%)	-0.15	11 (2%) 57 64	30, 43, 72, 86	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	574	ILE	5.5
2	B	136	ASP	5.2
1	A	575	SER	3.6
2	B	137	VAL	3.6
1	A	573	ILE	3.6
1	A	570	PRO	3.1
2	B	155	LEU	2.6
1	A	467	ILE	2.4
2	B	151	GLU	2.3
1	A	567	GLN	2.2
1	A	571	ASP	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](#)

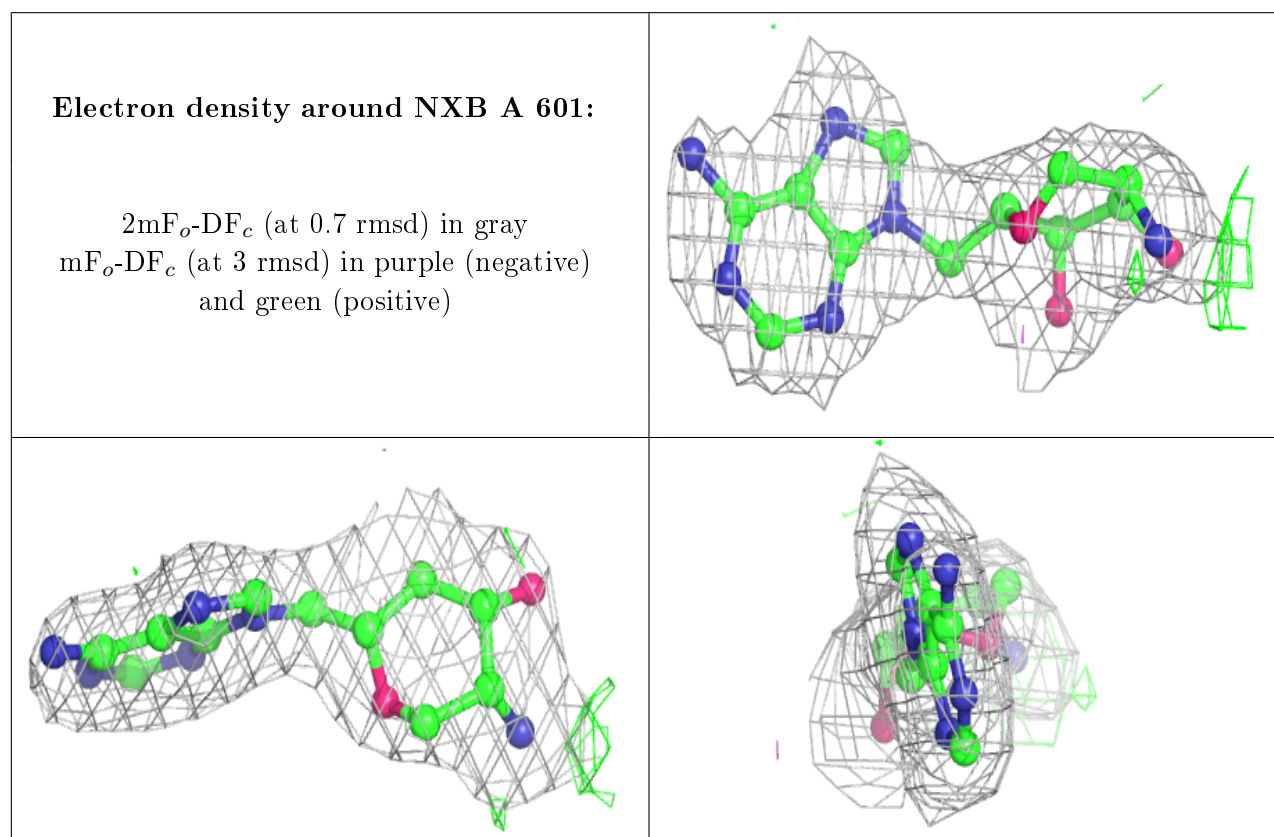
There are no monosaccharides in this entry.

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, 95th 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 ²)	Q<0.9
3	NXB	A	601	20/20	0.93	0.12	41,46,55,61	0
4	ACT	B	501	4/4	0.97	0.13	37,40,41,50	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.