

Full wwPDB X-ray Structure Validation Report (i)

Nov 22, 2023 – 12:18 PM JST

PDB ID : 7W6J

Title: The crystal structure of MLL1 (N3861I/Q3867L/C3882SS)-RBBP5-ASH2L

in complex with H3K4me2 peptide

Authors : Zhao, L.; Li, Y.; Chen, Y.

Deposited on : 2021-12-01

Resolution : 2.68 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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 : 2.36

buster-report : 1.1.7 (2018)

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

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

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

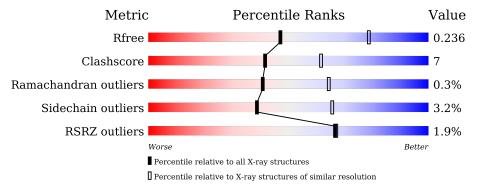
Validation Pipeline (wwPDB-VP) : 2.36

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 2.68 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	Whole archive $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}(\mathring{\rm A})) \end{array}$
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		Qua	ality of chain		
1	A	184	.%	78%			17% • •
2	С	159	2%	849	%		15% •
3	F	27		3%	22%	•	26%
4	В	9	33%		56%	·	11%



2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 2987 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 Set1/Ash2 histone methyltransferase complex subunit ASH2.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	A	177	Total 1405	C 907	N 236	O 256	S 6	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	285	SER	-	expression tag	UNP Q9UBL3
A	439	ILE	-	linker	UNP Q9UBL3
A	440	SER	-	linker	UNP Q9UBL3
A	441	GLY	-	linker	UNP Q9UBL3
A	442	ARG	-	linker	UNP Q9UBL3
A	443	GLY	-	linker	UNP Q9UBL3
A	444	SER	-	linker	UNP Q9UBL3

• Molecule 2 is a protein called Histone-lysine N-methyltransferase 2A.

Mo	l Chain	Residues		\mathbf{A}	toms			ZeroOcc	AltConf	Trace
2	С	158	Total 1273	C 803	N 230	O 228	S 12	0	0	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
С	3812	SER	-	expression tag	UNP Q03164
С	3861	ILE	ASN	engineered mutation	UNP Q03164
С	3867	LEU	GLN	engineered mutation	UNP Q03164
С	3882	SER	-	insertion	UNP Q03164
С	3883	SER	CYS	engineered mutation	UNP Q03164

• Molecule 3 is a protein called Retinoblastoma-binding protein 5.

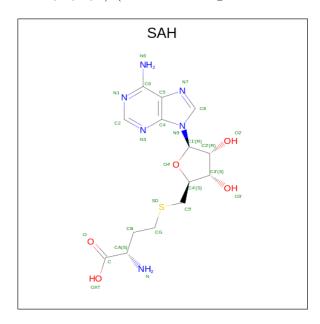


Mol	Chain	Residues		Aton	ns		ZeroOcc	AltConf	Trace
3	F	20	Total 178	C 110	N 25	O 43	0	0	0

• Molecule 4 is a protein called Histone H3.3C.

Mol	Chain	Residues	1	Ator	ns		ZeroOcc	AltConf	Trace
4	В	8	Total 66	C 39	N 16	O 11	0	0	0

• Molecule 5 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: $C_{14}H_{20}N_6O_5S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues		Ato	ms			ZeroOcc	AltConf
5	С	1	Total 26	C 14	N 6	O 5	S 1	0	0

• Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	С	1	Total Zn 1 1	0	0

• Molecule 7 is water.



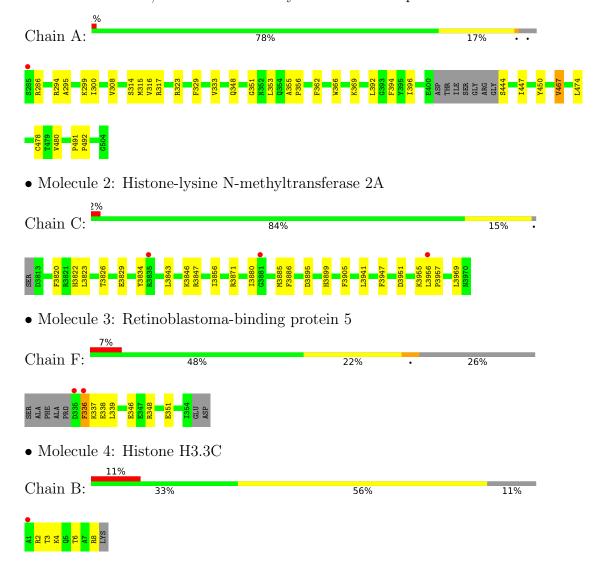
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	30	Total O 30 30	0	0
7	С	5	Total O 5 5	0	0
7	F	3	Total O 3 3	0	0



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: Set1/Ash2 histone methyltransferase complex subunit ASH2





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	75.49Å 44.30Å 119.38Å	Depositor
a, b, c, α , β , γ	90.00° 107.18° 90.00°	Depositor
Resolution (Å)	38.02 - 2.68	Depositor
Resolution (A)	38.02 - 2.68	EDS
% Data completeness	94.7 (38.02-2.68)	Depositor
(in resolution range)	94.7 (38.02-2.68)	EDS
R_{merge}	0.23	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.61 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
D D.	0.204 , 0.252	Depositor
R, R_{free}	0.203 , 0.236	DCC
R_{free} test set	514 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	40.7	Xtriage
Anisotropy	0.201	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.34, 32.7	EDS
L-test for twinning ²	$< L > = 0.48, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	0.027 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	2987	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.56% 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: MLY, ZN, SAH

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	Chain	$\mid \text{RMSZ} \mid \# Z > 5$		RMSZ	# Z > 5	
1	A	0.96	0/1446	0.76	0/1954	
2	С	0.38	0/1299	0.54	0/1740	
3	F	0.66	0/180	0.65	0/240	
4	В	0.58	0/54	1.25	0/71	
All	All	0.74	0/2979	0.68	0/4005	

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	A	1405	0	1371	19	0
2	С	1273	0	1271	18	0
3	F	178	0	148	6	0
4	В	66	0	76	3	0
5	С	26	0	19	1	0
6	С	1	0	0	0	0
7	A	30	0	0	0	0
7	С	5	0	0	0	0
7	F	3	0	0	0	0
All	All	2987	0	2885	41	0



The all-atom clash score is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clash score for this structure is 7.

All (41) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

C:C:3956:LEU:HD13 2:C:3969:LEU:HD12 1.71 0.73	Atom-1	Atom-2	Interatomic	Clash
2:C:3834:TYR:OH 2:C:3846:LYS:NZ 2.27 0.66 1:A:323:ARG:HG3 1:A:467:VAL:HG13 1.82 0.61 2:C:3885:MET:HB2 4:B:3:THR:HG22 1.81 0.61 2:C:3956:LEU:CD1 2:C:3969:LEU:HD12 2.31 0.60 1:A:315:MET:HB3 1:A:353:LEU:HD23 1.84 0.58 1:A:299:LYS:HB2 1:A:308:VAL:HB 1.85 0.58 2:C:3829:GLU:HB3 2:C:3847:ARG:HH22 1.68 0.57 2:C:3947:PHE:CE1 4:B:4:MLY:HG2 2.39 0.57 3:F:336:PHE:N 3:F:336:PHE:CD1 2.73 0.56 1:A:294:ARG:HD2 1:A:300:ILE:HD12 1.89 0.55 1:A:348:GLN:HB2 1:A:362:PHE:HB3 1.90 0.54 2:C:3820:PHE:O 2:C:3823:LEU:HB3 2.09 0.52 2:C:3829:GLU:HB3 2:C:3827:LEU:HB3 2.09 0.52 2:C:3829:GLU:HB3 2:C:3847:ARG:NH2 2.26 0.49 2:C:3951:ASP:O 2:C:3854:HB2 2.13 0.48 2:C:3955:HE:O 2:C:3852:HB2 2.14			distance (Å)	overlap (Å)
1:A:323:ARG:HG3 1:A:467:VAL:HG13 1.82 0.61 2:C:3885:MET:HB2 4:B:3:THR:HG22 1.81 0.61 2:C:3956:LEU:CD1 2:C:3969:LEU:HD12 2.31 0.60 1:A:315:MET:HB3 1:A:353:LEU:HD23 1.84 0.58 1:A:299:LYS:HB2 1:A:308:VAL:HB 1.85 0.58 2:C:3829:GLU:HB3 2:C:3847:ARG:HH22 1.68 0.57 2:C:3947:PHE:CE1 4:B:4:MLY:HG2 2.39 0.57 3:F:336:PHE:N 3:F:336:PHE:CD1 2.73 0.56 1:A:294:ARG:HD2 1:A:300:ILE:HD12 1.89 0.55 1:A:348:GLN:HB2 1:A:360:PHE:HB3 1.90 0.54 2:C:3820:PHE:O 2:C:3827:LEU:HB3 2.09 0.52 2:C:3829:GLU:HB3 2:C:3847:ARG:NH2 2.26 0.49 2:C:3951:ASP:O 2:C:3847:ARG:NH2 2.26 0.49 2:C:3951:HS:O 2:C:3826:THR:HG22 2.14 0.47 1:A:366:TRP:CZ3 1:A:399:LEU:HD12 2.50 0.48 2:C:3871:ARG:NH1 2:C:3895:ASP:OD2 2.47 0.44 1:A:325:MET:HB3 1:A:351:GLY:O 2.51				
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1:A:450:TYR:CE2 1:A:492:PRO:HB3 2.54 0.43 1:A:295:ALA:CB 1:A:314:SER:HB2 2.49 0.43 1:A:333:VAL:HA 1:A:480:VAL:HG12 2.01 0.43 2:C:3843:LEU:HG 2:C:3941:LEU:HD12 2.01 0.43 2:C:3899:HIS:HB3 3:F:339:LEU:HD22 2.01 0.43 1:A:355:ALA:HB1 1:A:356:PRO:HD2 2.01 0.43 1:A:394:PHE:CD1 1:A:394:PHE:N 2.86 0.43 3:F:336:PHE:N 3:F:336:PHE:HD1 2.17 0.42 1:A:329:PHE:CE1 1:A:394:PHE:HB2 2.54 0.42 2:C:3823:LEU:HD11 2:C:3856:ILE:HA 2.02 0.42 2:C:3885:MET:CB 4:B:3:THR:HG22 2.49 0.41	2:C:3956:LEU:HA	2:C:3957:PRO:HD3	1.68	0.43
1:A:295:ALA:CB 1:A:314:SER:HB2 2.49 0.43 1:A:333:VAL:HA 1:A:480:VAL:HG12 2.01 0.43 2:C:3843:LEU:HG 2:C:3941:LEU:HD12 2.01 0.43 2:C:3899:HIS:HB3 3:F:339:LEU:HD22 2.01 0.43 1:A:355:ALA:HB1 1:A:356:PRO:HD2 2.01 0.43 1:A:394:PHE:CD1 1:A:394:PHE:N 2.86 0.43 3:F:336:PHE:N 3:F:336:PHE:HD1 2.17 0.42 1:A:329:PHE:CE1 1:A:394:PHE:HB2 2.54 0.42 2:C:3823:LEU:HD11 2:C:3856:ILE:HA 2.02 0.42 2:C:3885:MET:CB 4:B:3:THR:HG22 2.49 0.41	1:A:396:ILE:HG13	1:A:447:ILE:HG13	2.00	0.43
1:A:333:VAL:HA 1:A:480:VAL:HG12 2.01 0.43 2:C:3843:LEU:HG 2:C:3941:LEU:HD12 2.01 0.43 2:C:3899:HIS:HB3 3:F:339:LEU:HD22 2.01 0.43 1:A:355:ALA:HB1 1:A:356:PRO:HD2 2.01 0.43 1:A:394:PHE:CD1 1:A:394:PHE:N 2.86 0.43 3:F:336:PHE:N 3:F:336:PHE:HD1 2.17 0.42 1:A:329:PHE:CE1 1:A:394:PHE:HB2 2.54 0.42 2:C:3823:LEU:HD11 2:C:3856:ILE:HA 2.02 0.42 2:C:3885:MET:CB 4:B:3:THR:HG22 2.49 0.41	1:A:450:TYR:CE2	1:A:492:PRO:HB3	2.54	0.43
2:C:3843:LEU:HG 2:C:3941:LEU:HD12 2.01 0.43 2:C:3899:HIS:HB3 3:F:339:LEU:HD22 2.01 0.43 1:A:355:ALA:HB1 1:A:356:PRO:HD2 2.01 0.43 1:A:394:PHE:CD1 1:A:394:PHE:N 2.86 0.43 3:F:336:PHE:N 3:F:336:PHE:HD1 2.17 0.42 1:A:329:PHE:CE1 1:A:394:PHE:HB2 2.54 0.42 2:C:3823:LEU:HD11 2:C:3856:ILE:HA 2.02 0.42 2:C:3885:MET:CB 4:B:3:THR:HG22 2.49 0.41	1:A:295:ALA:CB	1:A:314:SER:HB2	2.49	0.43
2:C:3899:HIS:HB3 3:F:339:LEU:HD22 2.01 0.43 1:A:355:ALA:HB1 1:A:356:PRO:HD2 2.01 0.43 1:A:394:PHE:CD1 1:A:394:PHE:N 2.86 0.43 3:F:336:PHE:N 3:F:336:PHE:HD1 2.17 0.42 1:A:329:PHE:CE1 1:A:394:PHE:HB2 2.54 0.42 2:C:3823:LEU:HD11 2:C:3856:ILE:HA 2.02 0.42 2:C:3885:MET:CB 4:B:3:THR:HG22 2.49 0.41	1:A:333:VAL:HA	1:A:480:VAL:HG12	2.01	0.43
1:A:355:ALA:HB1 1:A:356:PRO:HD2 2.01 0.43 1:A:394:PHE:CD1 1:A:394:PHE:N 2.86 0.43 3:F:336:PHE:N 3:F:336:PHE:HD1 2.17 0.42 1:A:329:PHE:CE1 1:A:394:PHE:HB2 2.54 0.42 2:C:3823:LEU:HD11 2:C:3856:ILE:HA 2.02 0.42 2:C:3885:MET:CB 4:B:3:THR:HG22 2.49 0.41	2:C:3843:LEU:HG	2:C:3941:LEU:HD12	2.01	0.43
1:A:394:PHE:CD1 1:A:394:PHE:N 2.86 0.43 3:F:336:PHE:N 3:F:336:PHE:HD1 2.17 0.42 1:A:329:PHE:CE1 1:A:394:PHE:HB2 2.54 0.42 2:C:3823:LEU:HD11 2:C:3856:ILE:HA 2.02 0.42 2:C:3885:MET:CB 4:B:3:THR:HG22 2.49 0.41	2:C:3899:HIS:HB3	3:F:339:LEU:HD22	2.01	0.43
3:F:336:PHE:N 3:F:336:PHE:HD1 2.17 0.42 1:A:329:PHE:CE1 1:A:394:PHE:HB2 2.54 0.42 2:C:3823:LEU:HD11 2:C:3856:ILE:HA 2.02 0.42 2:C:3885:MET:CB 4:B:3:THR:HG22 2.49 0.41	1:A:355:ALA:HB1	1:A:356:PRO:HD2	2.01	0.43
1:A:329:PHE:CE1 1:A:394:PHE:HB2 2.54 0.42 2:C:3823:LEU:HD11 2:C:3856:ILE:HA 2.02 0.42 2:C:3885:MET:CB 4:B:3:THR:HG22 2.49 0.41	1:A:394:PHE:CD1	1:A:394:PHE:N	2.86	0.43
2:C:3823:LEU:HD11 2:C:3856:ILE:HA 2.02 0.42 2:C:3885:MET:CB 4:B:3:THR:HG22 2.49 0.41	3:F:336:PHE:N	3:F:336:PHE:HD1	2.17	0.42
2:C:3823:LEU:HD11 2:C:3856:ILE:HA 2.02 0.42 2:C:3885:MET:CB 4:B:3:THR:HG22 2.49 0.41	1:A:329:PHE:CE1	1:A:394:PHE:HB2	2.54	0.42
	2:C:3823:LEU:HD11	2:C:3856:ILE:HA	2.02	0.42
	2:C:3885:MET:CB	4:B:3:THR:HG22	2.49	0.41
	3:F:348:ARG:NH1	3:F:351:GLU:OE2		
1:A:315:MET:HG2 1:A:316:VAL:N 2.36 0.41	1:A:315:MET:HG2	1:A:316:VAL:N	2.36	0.41

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Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	$egin{aligned} ext{Clash} \ ext{overlap } (ext{Å}) \end{aligned}$
1:A:474:LEU:HD22	1:A:478:CYS:SG	2.60	0.41
1:A:491:PRO:HA	1:A:492:PRO:HD3	1.98	0.41
3:F:336:PHE:HD1	3:F:336:PHE:H	1.64	0.41
2:C:3880:ILE:HD12	2:C:3880:ILE:H	1.87	0.40

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	Perce	ntiles
1	A	173/184 (94%)	167 (96%)	5 (3%)	1 (1%)	25	47
2	C	156/159 (98%)	147 (94%)	9 (6%)	0	100	100
3	F	18/27 (67%)	18 (100%)	0	0	100	100
4	В	5/9~(56%)	4 (80%)	1 (20%)	0	100	100
All	All	352/379 (93%)	336 (96%)	15 (4%)	1 (0%)	41	64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	286	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	150/155~(97%)	147 (98%)	3 (2%)	55 79
2	С	138/139 (99%)	137 (99%)	1 (1%)	84 93
3	F	20/25~(80%)	17 (85%)	3 (15%)	3 6
4	В	5/6 (83%)	2 (40%)	3 (60%)	0 0
All	All	313/325~(96%)	303 (97%)	10 (3%)	39 65

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	369	LYS
1	A	444	SER
1	A	467	VAL
2	С	3886	PHE
3	F	336	PHE
3	F	337	LYS
3	F	338	GLU
4	В	2	ARG
4	В	6	THR
4	В	8	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	376	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)

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).



Mol	Type	Chain	Res	Link	\mathbf{B}_{0}	ond leng	gths	В	ond ang	gles
WIOI	Туре	Chain	rtes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
4	MLY	В	4	4	9,10,11	0.59	0	6,11,13	0.65	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.

\mathbf{Mol}	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	MLY	В	4	4	-	3/8/9/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	В	4	MLY	C-CA-CB-CG
4	В	4	MLY	CD-CE-NZ-CH1
4	В	4	MLY	CA-CB-CG-CD

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	В	4	MLY	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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).

	Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
						Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
	5	SAH	С	4001	-	24,28,28	1.19	3 (12%)	25,40,40	1.84	5 (20%)

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
5	SAH	С	4001	-	-	4/11/31/31	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	$\mathbf{Ideal}(exttt{\AA})$
5	С	4001	SAH	C2-N3	3.90	1.38	1.32
5	С	4001	SAH	C2-N1	2.43	1.38	1.33
5	С	4001	SAH	OXT-C	-2.12	1.23	1.30

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
5	С	4001	SAH	N3-C2-N1	-5.56	119.99	128.68
5	С	4001	SAH	C5'-SD-CG	-4.21	89.64	102.27
5	С	4001	SAH	C3'-C2'-C1'	3.11	105.66	100.98
5	С	4001	SAH	OXT-C-O	-2.66	118.04	124.09
5	С	4001	SAH	OXT-C-CA	2.17	120.77	113.38

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	С	4001	SAH	O4'-C4'-C5'-SD
5	С	4001	SAH	C3'-C4'-C5'-SD
5	С	4001	SAH	CA-CB-CG-SD
5	С	4001	SAH	CB-CG-SD-C5'

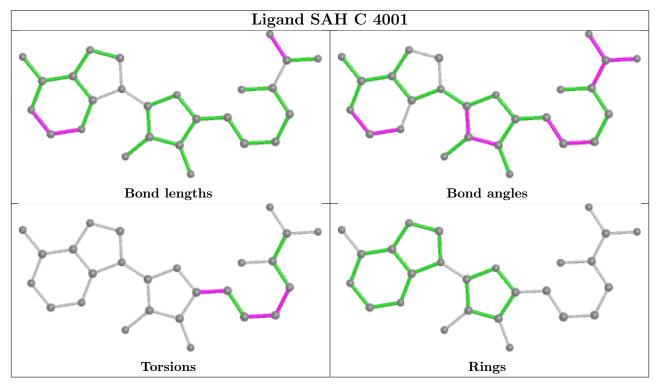
There are no ring outliers.

1 monomer is involved in 1 short contact:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	С	4001	SAH	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 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	<rsrz></rsrz>	$\# \mathrm{RSRZ}{>}2$	$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q < 0.9
1	A	177/184~(96%)	-0.31	1 (0%) 89 90	24, 32, 43, 55	0
2	С	158/159 (99%)	0.19	3 (1%) 66 67	35, 49, 77, 117	0
3	F	20/27 (74%)	0.49	2 (10%) 7 5	30, 45, 64, 70	0
4	В	7/9 (77%)	1.19	1 (14%) 2 1	57, 59, 76, 80	0
All	All	362/379~(95%)	-0.02	7 (1%) 66 67	24, 40, 70, 117	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	335	ASP	5.5
1	A	285	SER	4.5
2	С	3956	LEU	4.2
4	В	1	ALA	3.7
2	С	3835	ARG	2.8
2	С	3881	GLY	2.2
3	F	336	PHE	2.1

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.

ľ	Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
	4	MLY	В	4	11/12	0.93	0.23	47,50,53,55	0



6.3 Carbohydrates (i)

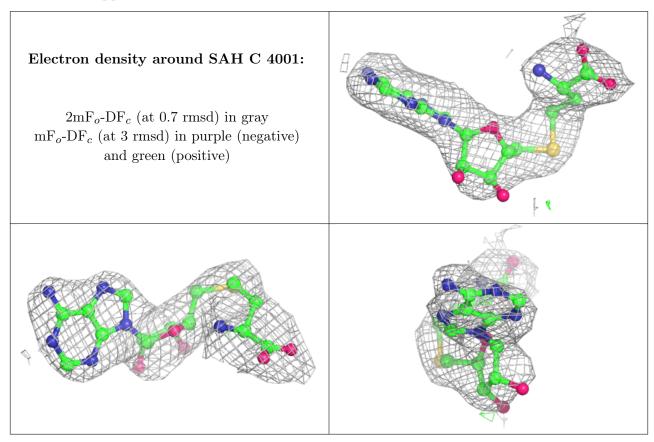
There are no monosaccharides in this entry.

6.4 Ligands (i)

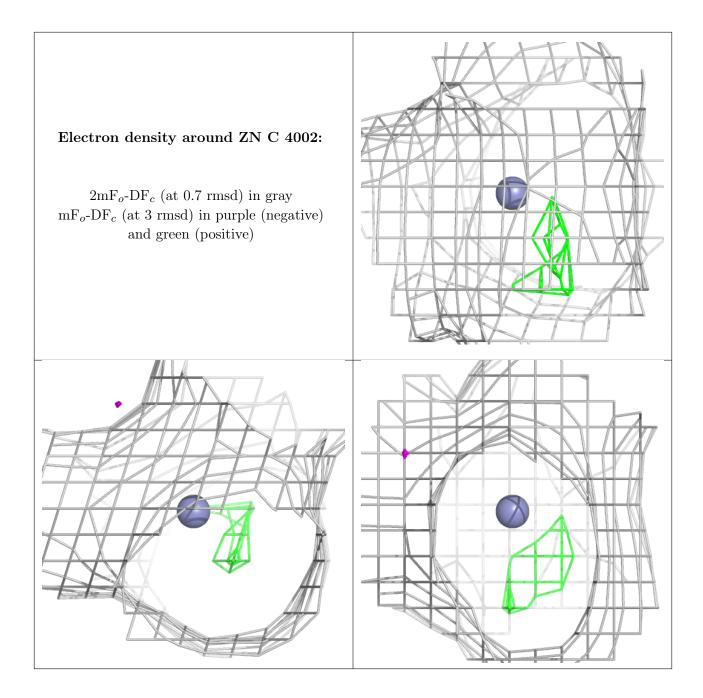
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	${f B-factors}({f \AA}^2)$	Q<0.9
5	SAH	С	4001	26/26	0.89	0.20	50,55,61,70	0
6	ZN	С	4002	1/1	0.93	0.12	60,60,60,60	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.

