

wwPDB X-ray Structure Validation Summary Report (i)

Oct 14, 2023 – 04:53 PM EDT

PDB ID	:	7TWK
Title	:	Structure of a borosin methyltransferase from Mycena rosella with native pep-
		tide (MroMA1) in complex with SAH
Authors	:	Zheng, Y.; Ongpipattanakul, C.; Nair, S.K.
Deposited on	:	2022-02-07
Resolution	:	1.79 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

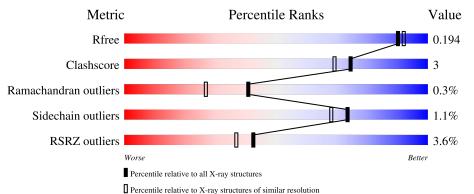
MolProbity Mogul Xtriage (Phenix) EDS	:	4.02b-467 1.8.5 (274361), CSD as541be (2020) 1.13 2.36
buster-report Percentile statistics Refmac	: : :	1.1.7 (2018) 20191225.v01 (using entries in the PDB archive December 25th 2019) 5.8.0158 7.0.044 (Gargrove)
Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)		Parkinson et al. (1996) 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.79 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	5950(1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	А	400	3% 87%	6% 6%
1	С	400	4% 87%	• 9%
2	В	400	3% 	8% •
2	D	400	3% 90%	6% ••



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 13661 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.

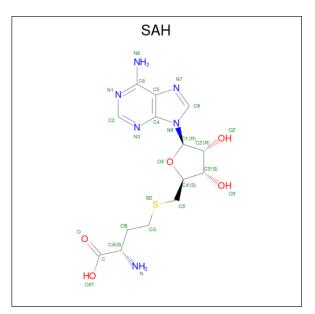
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	1 A	A 374	Total	С	Ν	Ο	\mathbf{S}	0	2	0
1			2901	1852	493	543	13	0		
1	С	365	Total	\mathbf{C}	Ν	Ο	\mathbf{S}	0	3	0
1		305	2844	1814	483	535	12			

• Molecule 1 is a protein called MroMA1.

• Molecule 2 is a protein called MroMA1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
0	Р	392	Total	С	Ν	0	S	0	2	0
		392	3050	1952	514	572	12	0		
0	Л	201	Total	С	Ν	0	S	0	15	0
	2 D	391	3126	2002	524	587	13	0		

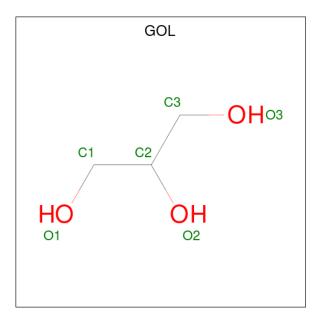
• Molecule 3 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: $C_{14}H_{20}N_6O_5S$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	0	0
3	В	1	Total C N O S 26 14 6 5 1	0	0
3	С	1	Total C N O S 26 14 6 5 1	0	0
3	D	1	Total C N O S 26 14 6 5 1	0	0

• Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
4	С	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0

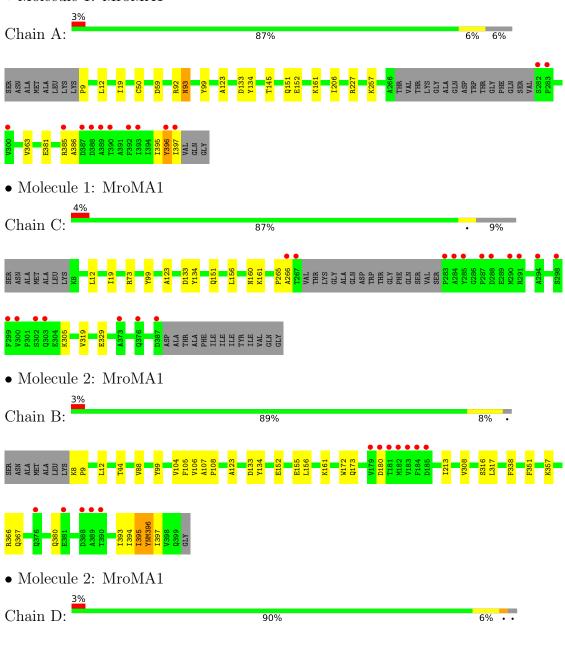
• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	407	Total O 407 407	0	0
5	В	417	Total O 417 417	0	0
5	С	343	Total O 343 343	0	0
5	D	457	Total O 457 457	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: MroMA1









4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65	Depositor
Cell constants	191.83Å 191.83Å 93.71Å	Deperitor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	25.00 - 1.79	Depositor
Resolution (A)	95.92 - 1.79	EDS
% Data completeness	99.9 (25.00-1.79)	Depositor
(in resolution range)	$100.0 \ (95.92 - 1.79)$	EDS
R _{merge}	0.10	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.33 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
D D.	0.167 , 0.192	Depositor
R, R_{free}	0.169 , 0.194	DCC
R_{free} test set	9018 reflections (4.92%)	wwPDB-VP
Wilson B-factor $(Å^2)$	22.5	Xtriage
Anisotropy	0.325	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.37, 57.1	EDS
L-test for twinning ²	$< L > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.019 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	13661	wwPDB-VP
Average B, all atoms $(Å^2)$	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.02% of the height of the origin peak. No significant pseudotranslation is detected.

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.



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: SAH, GOL, IML, YNM

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	Unain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.28	0/2970	0.56	1/4028~(0.0%)	
1	С	0.28	0/2915	0.57	0/3952	
2	В	0.28	0/3091	0.56	0/4194	
2	D	0.28	0/3192	0.56	1/4333~(0.0%)	
All	All	0.28	0/12168	0.56	2/16507~(0.0%)	

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
2	D	9	PRO	N-CA-CB	6.07	110.58	103.30
1	А	93	ASN	CB-CA-C	5.35	121.09	110.40

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	2901	0	2901	19	0
1	С	2844	0	2848	7	0
2	В	3050	0	3058	32	0
2	D	3126	0	3139	26	0
3	А	26	0	19	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	В	26	0	19	0	0
3	С	26	0	19	0	0
3	D	26	0	19	0	0
4	В	6	0	8	2	0
4	С	6	0	8	2	0
5	А	407	0	0	5	0
5	В	417	0	0	5	0
5	С	343	0	0	2	0
5	D	457	0	0	5	0
All	All	13661	0	12038	76	0

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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.

The worst 5 of 76 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)
5:A:628:HOH:O	4:C:502:GOL:H2	1.54	1.05
1:A:93:ASN:HB3	5:A:916:HOH:O	1.64	0.94
2:B:8:LYS:N	2:B:9:PRO:HD3	1.89	0.88
2:D:397:ILE:HG13	5:D:720:HOH:O	1.72	0.88
2:D:317[B]:LEU:HD11	2:D:338:PHE:HE2	1.40	0.85

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	А	372/400~(93%)	364 (98%)	7 (2%)	1 (0%)	41	27
1	С	364/400~(91%)	353~(97%)	9 (2%)	2~(0%)	29	15

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Mol	Chain	Analysed	vsed Favoured Allowed		Outliers	Percentiles	
2	В	389/400~(97%)	379~(97%)	9~(2%)	1 (0%)	41	27
2	D	401/400 (100%)	393~(98%)	8 (2%)	0	100	100
All	All	1526/1600~(95%)	1489 (98%)	33 (2%)	4 (0%)	41	27

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All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	396	TYR
1	С	265	PRO
1	С	266	ALA
2	В	180	ASP

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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
1	А	309/329~(94%)	306~(99%)	3~(1%)	76	71
1	С	305/329~(93%)	299~(98%)	6(2%)	55	44
2	В	323/326~(99%)	322 (100%)	1 (0%)	92	91
2	D	334/326~(102%)	328~(98%)	6 (2%)	59	48
All	All	1271/1310~(97%)	1255~(99%)	16 (1%)	73	62

5 of 16 residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
2	D	177	VAL
2	D	162	LYS
1	С	329[A]	GLU
2	D	134	TYR
1	С	160[B]	ASN

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such side chains are listed below:



Mol	Chain	Res	Type
1	А	173	GLN
2	В	315	GLN
1	С	173	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)

6 non-standard protein/DNA/RNA residues 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).

Mal	Mol Type		pe Chain Res		Bo	Bond lengths			Bond angles		
	туре	Chain	ries	Link	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2	
2	IML	В	394	2	7,8,9	0.52	0	7,9,11	0.92	0	
2	IML	D	395	2	7,8,9	0.76	0	7,9,11	1.25	2 (28%)	
2	IML	D	394	2	7,8,9	0.57	0	7,9,11	1.01	1 (14%)	
2	IML	В	395	2	7,8,9	0.67	0	7,9,11	1.24	1 (14%)	
2	YNM	D	396	2	12,13,14	0.63	0	15,16,18	1.35	1 (6%)	
2	YNM	В	396	2	12,13,14	0.61	0	15,16,18	1.57	2 (13%)	

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	IML	В	394	2	-	3/8/10/12	-
2	IML	D	395	2	-	4/8/10/12	-
2	IML	D	394	2	-	3/8/10/12	-
2	IML	В	395	2	-	4/8/10/12	-
2	YNM	D	396	2	-	1/5/8/10	0/1/1/1
2	YNM	В	396	2	-	1/5/8/10	0/1/1/1



There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	В	396	YNM	CG-CB-CA	-3.39	108.78	113.63
2	В	396	YNM	CB-CA-C	-3.38	105.25	111.65
2	D	396	YNM	CB-CA-C	-3.06	105.84	111.65
2	В	395	IML	O-C-CA	-2.69	117.32	124.83
2	D	395	IML	O-C-CA	-2.26	118.53	124.83

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	394	IML	CB-CA-N-CN
2	В	394	IML	C-CA-CB-CG1
2	D	394	IML	CB-CA-N-CN
2	В	396	YNM	O-C-CA-CB
2	D	396	YNM	O-C-CA-CB

There are no ring outliers.

6 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	394	IML	1	0
2	D	395	IML	2	0
2	D	394	IML	1	0
2	В	395	IML	1	0
2	D	396	YNM	4	0
2	В	396	YNM	4	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

6 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 length (or angles).

Mol	Type	Chain	Res	es Link	Bo	ond leng	ths	Bond angles		
MIOI	туре		nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
3	SAH	А	500	-	24,28,28	0.62	0	$25,\!40,\!40$	0.99	3 (12%)
3	SAH	С	501	-	24,28,28	0.64	0	$25,\!40,\!40$	1.05	3 (12%)
3	SAH	В	501	-	$24,\!28,\!28$	0.70	1 (4%)	$25,\!40,\!40$	1.07	2 (8%)
3	SAH	D	500	-	24,28,28	0.62	0	$25,\!40,\!40$	0.96	2 (8%)
4	GOL	С	502	-	$5,\!5,\!5$	0.16	0	$5,\!5,\!5$	0.45	0
4	GOL	В	502	-	$5,\!5,\!5$	0.09	0	$5,\!5,\!5$	0.29	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	SAH	А	500	-	-	2/11/31/31	0/3/3/3
3	SAH	С	501	-	-	4/11/31/31	0/3/3/3
3	SAH	В	501	-	-	4/11/31/31	0/3/3/3
3	SAH	D	500	-	-	5/11/31/31	0/3/3/3
4	GOL	С	502	-	-	0/4/4/4	-
4	GOL	В	502	-	-	4/4/4/4	-

All (1) bond length outliers are listed below:

ľ	Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	$\operatorname{Ideal}(\operatorname{\AA})$
	3	В	501	SAH	OXT-C	-2.19	1.23	1.30

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$\mathbf{Ideal}(^{o})$
3	В	501	SAH	OXT-C-O	-3.58	115.97	124.09
3	С	501	SAH	OXT-C-O	-2.76	117.81	124.09
3	D	500	SAH	OXT-C-O	-2.76	117.81	124.09
3	В	501	SAH	C5-C6-N6	2.44	124.05	120.35
3	D	500	SAH	C5-C6-N6	2.38	123.97	120.35

There are no chirality outliers.



Mol	Chain	Res	Type	Atoms
3	А	500	SAH	N-CA-CB-CG
3	А	500	SAH	C-CA-CB-CG
3	С	501	SAH	N-CA-CB-CG
4	В	502	GOL	O1-C1-C2-C3
4	В	502	GOL	O2-C2-C3-O3

5 of 19 torsion outliers are listed below:

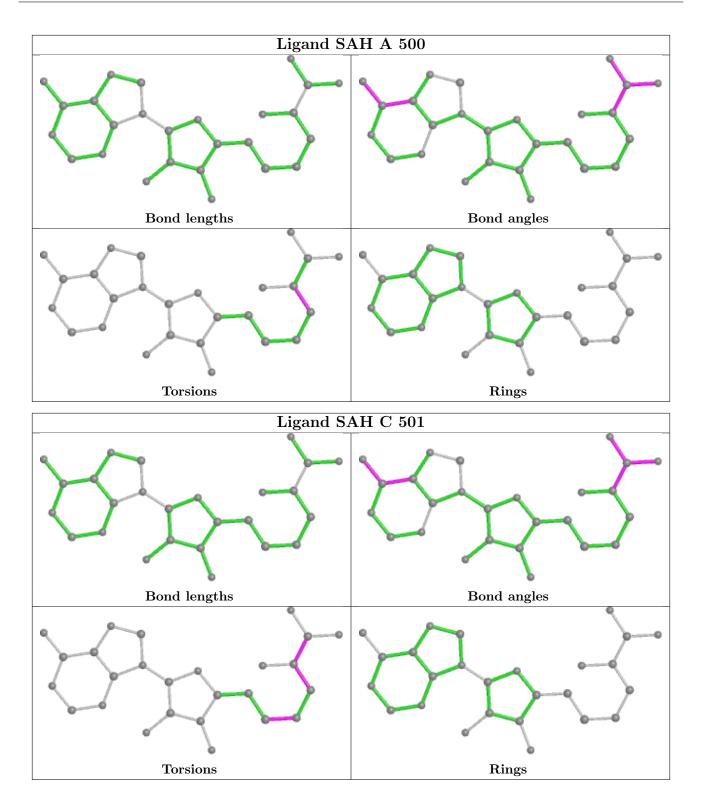
There are no ring outliers.

2 monomers are involved in 4 short contacts:

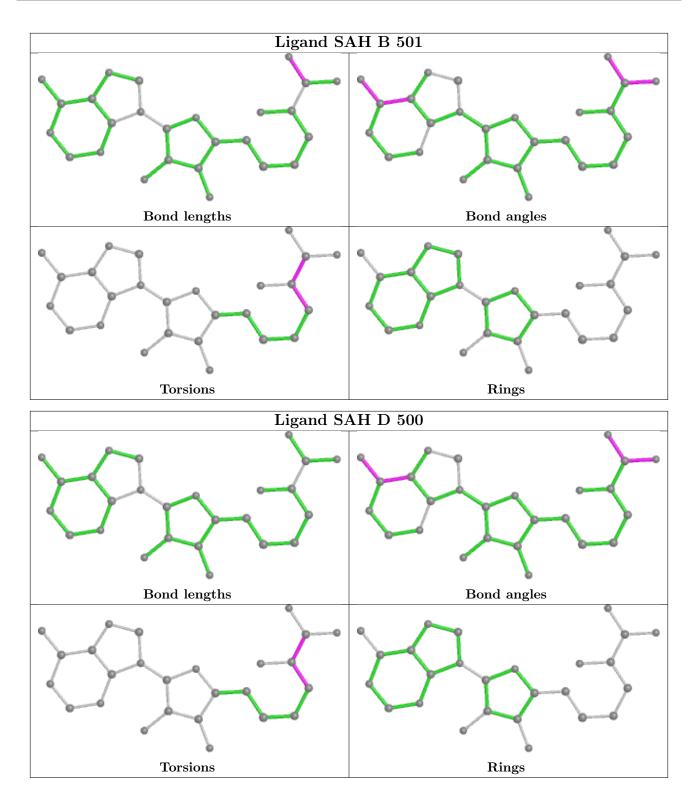
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	С	502	GOL	2	0
4	В	502	GOL	2	0

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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	374/400~(93%)	-0.09	12 (3%) 47 41	15, 25, 56, 94	0
1	С	365/400~(91%)	0.09	18 (4%) 29 24	16, 26, 65, 107	0
2	В	389/400~(97%)	0.04	12 (3%) 49 43	15, 27, 55, 150	0
2	D	388/400~(97%)	-0.12	12 (3%) 49 43	16, 24, 45, 91	0
All	All	1516/1600~(94%)	-0.02	54 (3%) 42 37	15, 25, 56, 150	0

The worst 5 of 54 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	С	267	THR	12.5
2	В	181	THR	11.3
2	В	182	MET	10.4
2	В	183	VAL	9.1
2	В	184	PHE	7.9

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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
2	IML	D	394	9/10	0.89	0.17	$27,\!28,\!28,\!29$	0
2	IML	В	394	9/10	0.90	0.11	23,25,26,26	0
2	YNM	В	396	13/14	0.93	0.13	20,25,29,30	0
2	YNM	D	396	13/14	0.93	0.16	20,26,33,35	0
2	IML	D	395	9/10	0.95	0.13	22,27,32,34	0
2	IML	В	395	9/10	0.96	0.11	22,24,27,30	0



7TWK

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

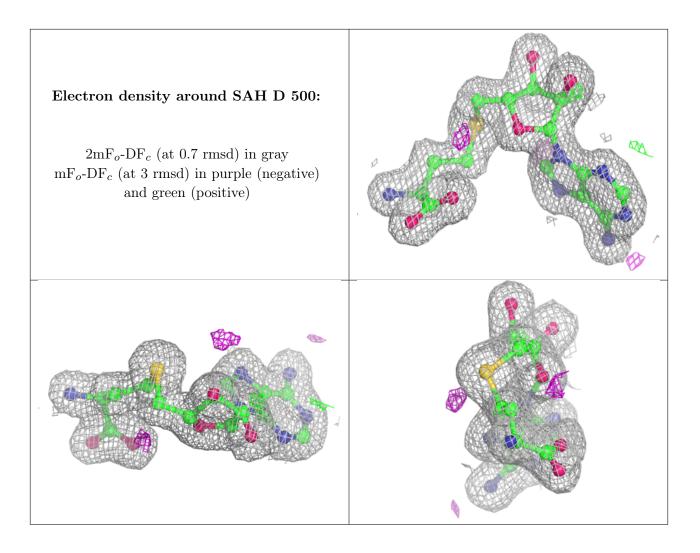
6.4 Ligands (i)

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.

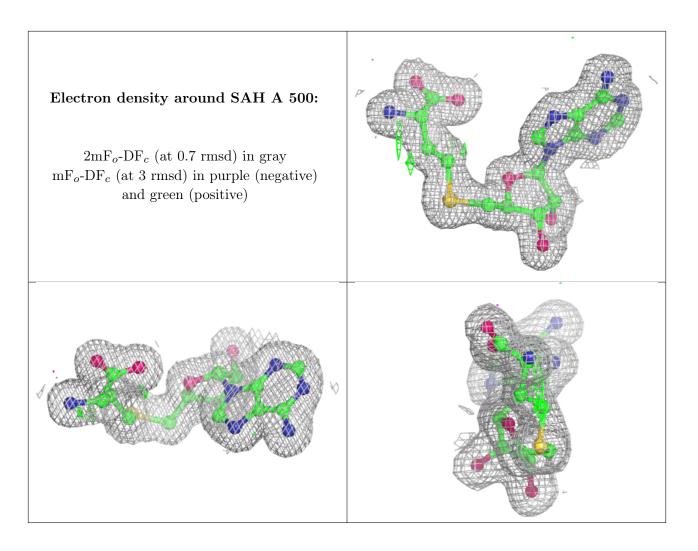
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GOL	В	502	6/6	0.74	0.18	$37,\!46,\!48,\!48$	0
4	GOL	С	502	6/6	0.82	0.15	31,39,39,43	0
3	SAH	D	500	26/26	0.98	0.07	17,17,19,19	0
3	SAH	А	500	26/26	0.98	0.09	16,17,20,21	0
3	SAH	С	501	26/26	0.98	0.08	17,19,22,24	0
3	SAH	В	501	26/26	0.99	0.08	16,18,19,19	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.

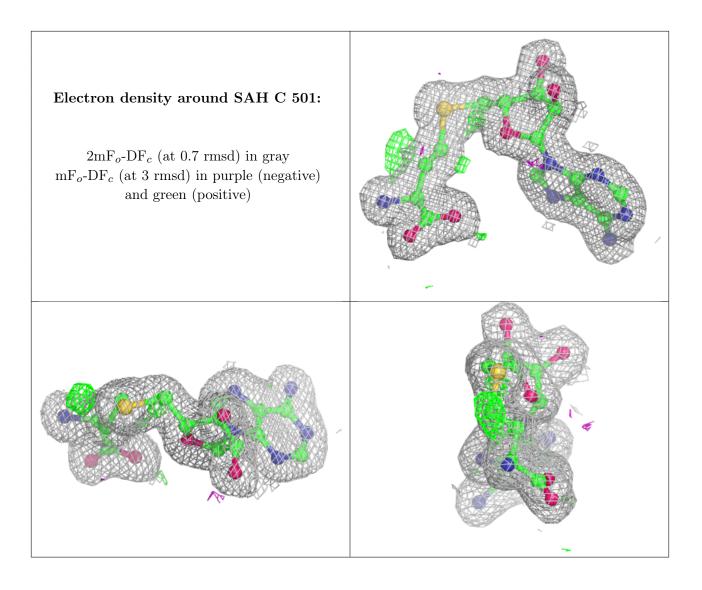




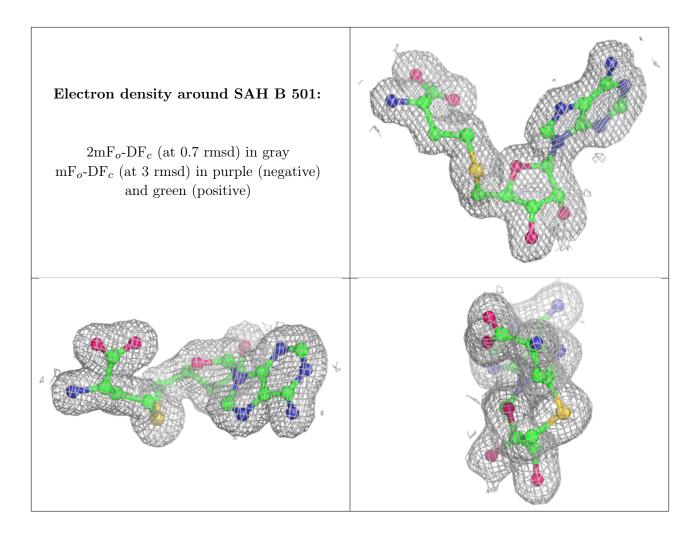












6.5 Other polymers (i)

There are no such residues in this entry.

