



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 20, 2020 – 03:00 PM BST

PDB ID : 4OA5  
Title : X-ray crystal structure of an O-methyltransferase from Anaplasma phagocytophilum bound to SAH solved by iodide SAD phasing  
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)  
Deposited on : 2014-01-03  
Resolution : 2.30 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](mailto: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.

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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	:	2.13.1
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)	:	2.13.1

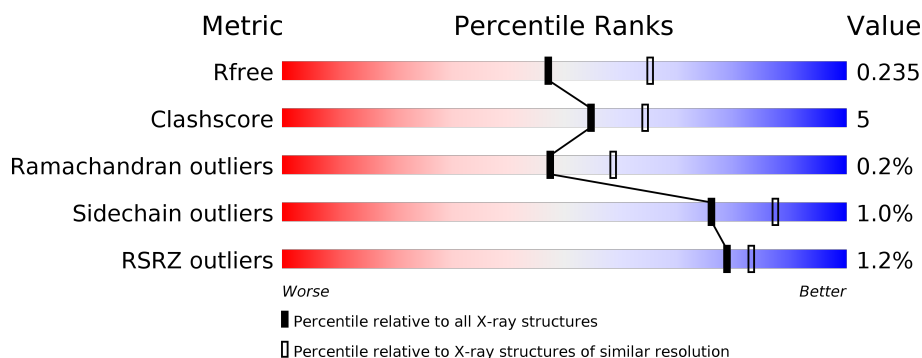
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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  $\geq 3$ , 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	227	<div> <div>%</div> <div> <div></div> <div>84%</div> <div>8%</div> <div>7%</div> </div> </div>
1	B	227	<div> <div></div> <div>90%</div> <div>7%</div> </div>
1	C	227	<div> <div>4%</div> <div> <div></div> <div>85%</div> <div>8%</div> <div>7%</div> </div> </div>
1	D	227	<div> <div></div> <div>89%</div> <div>5%</div> <div>6%</div> </div>
1	E	227	<div> <div>%</div> <div> <div></div> <div>84%</div> <div>10%</div> <div>6%</div> </div> </div>
1	F	227	<div> <div></div> <div>84%</div> <div>9%</div> <div>6%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	IOD	A	304	-	-	X	-
3	IOD	A	318	-	-	X	X
3	IOD	C	303	-	-	X	-
3	IOD	C	307	-	-	X	-
3	IOD	C	312	-	-	X	-
3	IOD	C	314	-	-	X	-
3	IOD	D	304	-	-	X	-
3	IOD	D	318	-	-	X	-
3	IOD	E	309	-	-	X	-
3	IOD	E	311	-	-	X	-
3	IOD	E	317	-	-	-	X
3	IOD	F	310	-	-	X	-
4	EDO	F	326	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10988 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 O-methyltransferase family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	212	Total	C	N	O	S	0	8	0
			1652	1053	274	313	12			
1	B	212	Total	C	N	O	S	0	2	0
			1608	1022	265	310	11			
1	C	212	Total	C	N	O	S	0	4	0
			1628	1037	267	311	13			
1	D	213	Total	C	N	O	S	0	4	0
			1632	1037	269	313	13			
1	E	214	Total	C	N	O	S	0	4	0
			1655	1054	275	314	12			
1	F	213	Total	C	N	O	S	0	2	0
			1630	1036	269	312	13			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MET	-	EXPRESSION TAG	UNP Q2GKC7
A	-7	ALA	-	EXPRESSION TAG	UNP Q2GKC7
A	-6	HIS	-	EXPRESSION TAG	UNP Q2GKC7
A	-5	HIS	-	EXPRESSION TAG	UNP Q2GKC7
A	-4	HIS	-	EXPRESSION TAG	UNP Q2GKC7
A	-3	HIS	-	EXPRESSION TAG	UNP Q2GKC7
A	-2	HIS	-	EXPRESSION TAG	UNP Q2GKC7
A	-1	HIS	-	EXPRESSION TAG	UNP Q2GKC7
A	0	MET	-	EXPRESSION TAG	UNP Q2GKC7
A	1	VAL	-	EXPRESSION TAG	UNP Q2GKC7
B	-8	MET	-	EXPRESSION TAG	UNP Q2GKC7
B	-7	ALA	-	EXPRESSION TAG	UNP Q2GKC7
B	-6	HIS	-	EXPRESSION TAG	UNP Q2GKC7
B	-5	HIS	-	EXPRESSION TAG	UNP Q2GKC7
B	-4	HIS	-	EXPRESSION TAG	UNP Q2GKC7
B	-3	HIS	-	EXPRESSION TAG	UNP Q2GKC7
B	-2	HIS	-	EXPRESSION TAG	UNP Q2GKC7

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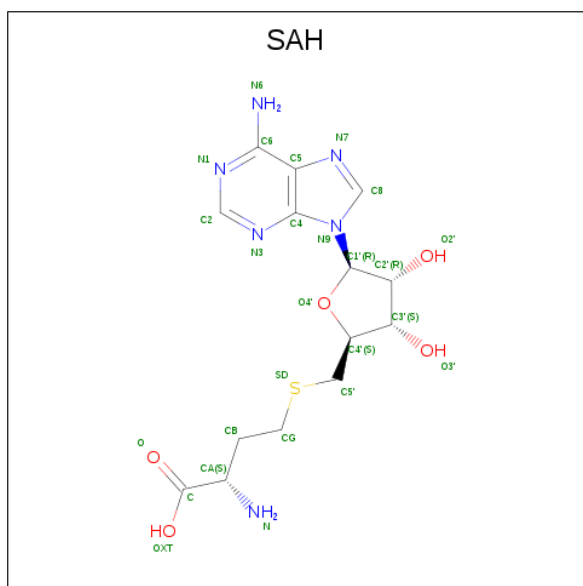
Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	HIS	-	EXPRESSION TAG	UNP Q2GKC7
B	0	MET	-	EXPRESSION TAG	UNP Q2GKC7
B	1	VAL	-	EXPRESSION TAG	UNP Q2GKC7
C	-8	MET	-	EXPRESSION TAG	UNP Q2GKC7
C	-7	ALA	-	EXPRESSION TAG	UNP Q2GKC7
C	-6	HIS	-	EXPRESSION TAG	UNP Q2GKC7
C	-5	HIS	-	EXPRESSION TAG	UNP Q2GKC7
C	-4	HIS	-	EXPRESSION TAG	UNP Q2GKC7
C	-3	HIS	-	EXPRESSION TAG	UNP Q2GKC7
C	-2	HIS	-	EXPRESSION TAG	UNP Q2GKC7
C	-1	HIS	-	EXPRESSION TAG	UNP Q2GKC7
C	0	MET	-	EXPRESSION TAG	UNP Q2GKC7
C	1	VAL	-	EXPRESSION TAG	UNP Q2GKC7
D	-8	MET	-	EXPRESSION TAG	UNP Q2GKC7
D	-7	ALA	-	EXPRESSION TAG	UNP Q2GKC7
D	-6	HIS	-	EXPRESSION TAG	UNP Q2GKC7
D	-5	HIS	-	EXPRESSION TAG	UNP Q2GKC7
D	-4	HIS	-	EXPRESSION TAG	UNP Q2GKC7
D	-3	HIS	-	EXPRESSION TAG	UNP Q2GKC7
D	-2	HIS	-	EXPRESSION TAG	UNP Q2GKC7
D	-1	HIS	-	EXPRESSION TAG	UNP Q2GKC7
D	0	MET	-	EXPRESSION TAG	UNP Q2GKC7
D	1	VAL	-	EXPRESSION TAG	UNP Q2GKC7
E	-8	MET	-	EXPRESSION TAG	UNP Q2GKC7
E	-7	ALA	-	EXPRESSION TAG	UNP Q2GKC7
E	-6	HIS	-	EXPRESSION TAG	UNP Q2GKC7
E	-5	HIS	-	EXPRESSION TAG	UNP Q2GKC7
E	-4	HIS	-	EXPRESSION TAG	UNP Q2GKC7
E	-3	HIS	-	EXPRESSION TAG	UNP Q2GKC7
E	-2	HIS	-	EXPRESSION TAG	UNP Q2GKC7
E	-1	HIS	-	EXPRESSION TAG	UNP Q2GKC7
E	0	MET	-	EXPRESSION TAG	UNP Q2GKC7
E	1	VAL	-	EXPRESSION TAG	UNP Q2GKC7
F	-8	MET	-	EXPRESSION TAG	UNP Q2GKC7
F	-7	ALA	-	EXPRESSION TAG	UNP Q2GKC7
F	-6	HIS	-	EXPRESSION TAG	UNP Q2GKC7
F	-5	HIS	-	EXPRESSION TAG	UNP Q2GKC7
F	-4	HIS	-	EXPRESSION TAG	UNP Q2GKC7
F	-3	HIS	-	EXPRESSION TAG	UNP Q2GKC7
F	-2	HIS	-	EXPRESSION TAG	UNP Q2GKC7
F	-1	HIS	-	EXPRESSION TAG	UNP Q2GKC7
F	0	MET	-	EXPRESSION TAG	UNP Q2GKC7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	1	VAL	-	EXPRESSION TAG	UNP Q2GKC7

- Molecule 2 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula:  $C_{14}H_{20}N_6O_5S$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	B	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	C	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	D	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	E	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	F	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

- Molecule 3 is IODIDE ION (three-letter code: IOD) (formula: I).

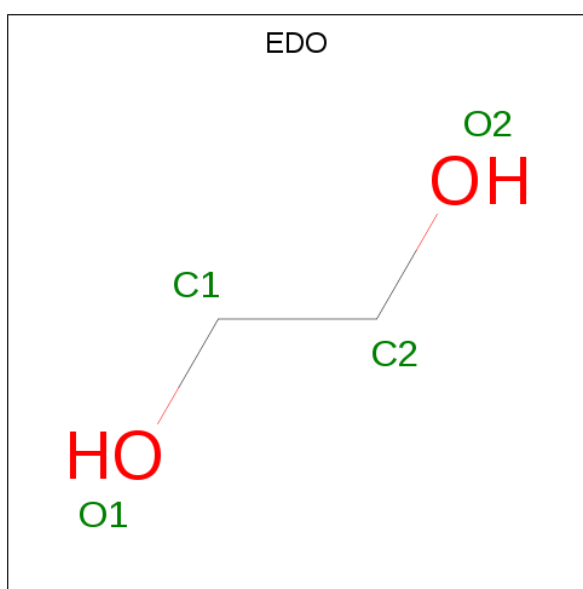
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	21	Total	I	0	0
			21	21		
3	E	16	Total	I	0	0
			16	16		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	16	Total	I	0	0
			16	16		
3	C	20	Total	I	0	0
			20	20		
3	A	19	Total	I	0	0
			19	19		
3	F	22	Total	I	0	0
			22	22		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



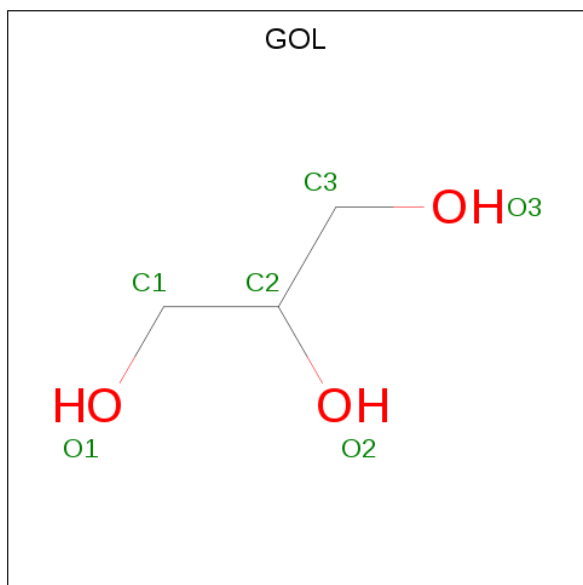
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	E	1	Total	C	O	0	0
			4	2	2		
4	E	1	Total	C	O	0	0
			4	2	2		
4	F	1	Total	C	O	0	0
			4	2	2		
4	F	1	Total	C	O	0	0
			4	2	2		

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

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	C	O	0	0
			6	3	3		
5	D	1	Total	C	O	0	0
			6	3	3		
5	E	1	Total	C	O	0	0
			6	3	3		
5	F	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	151	Total	O	0	0
			151	151		
6	B	127	Total	O	0	0
			127	127		

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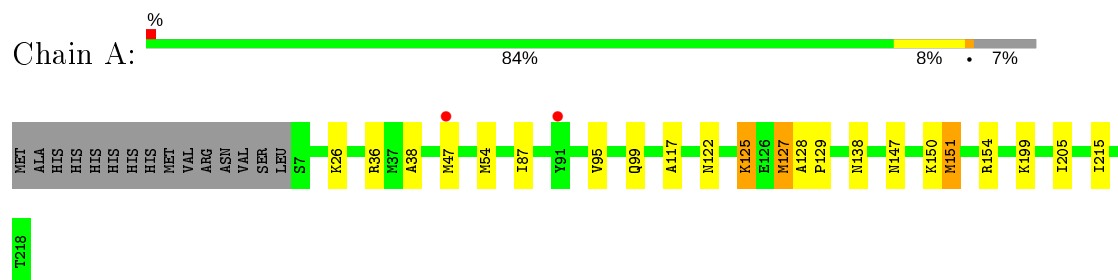
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	135	Total 135	O 135	0	0
6	D	158	Total 158	O 158	0	0
6	E	139	Total 139	O 139	0	0
6	F	139	Total 139	O 139	0	0

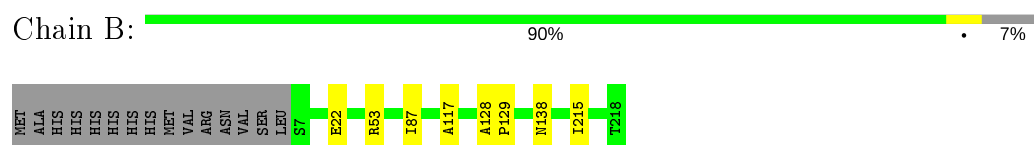
### 3 Residue-property plots

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 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.

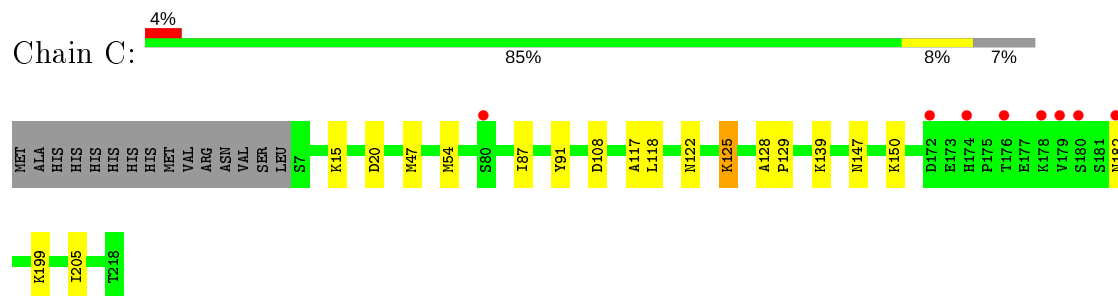
- Molecule 1: O-methyltransferase family protein



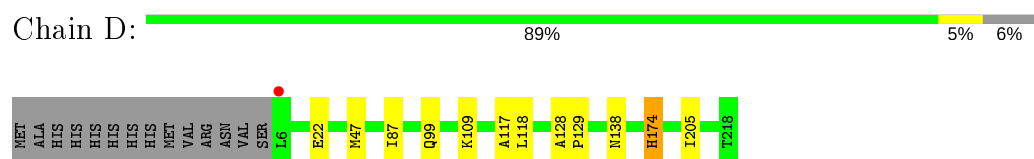
- Molecule 1: O-methyltransferase family protein



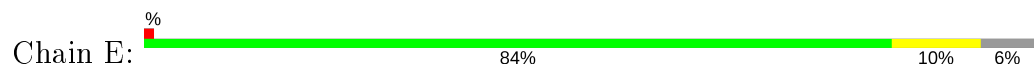
- Molecule 1: O-methyltransferase family protein

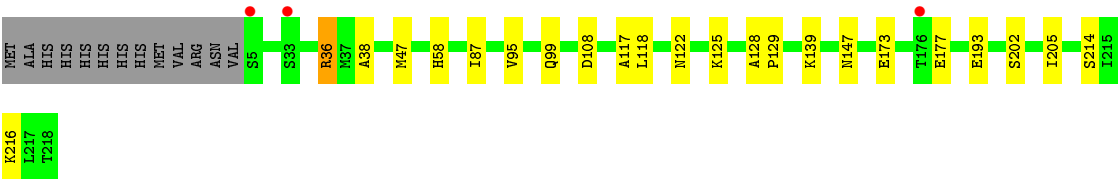


- Molecule 1: O-methyltransferase family protein

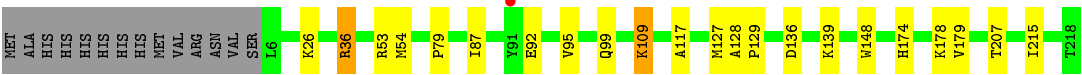
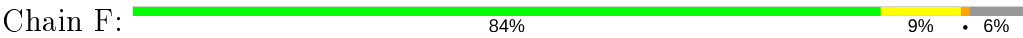


- Molecule 1: O-methyltransferase family protein





● Molecule 1: O-methyltransferase family protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	192.36Å 72.27Å 130.84Å 90.00° 124.94° 90.00°	Depositor
Resolution (Å)	47.83 – 2.30 47.83 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.6 (47.83-2.30) 99.7 (47.83-2.30)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.23 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, $R_{free}$	0.195 , 0.231 0.200 , 0.235	Depositor DCC
$R_{free}$ test set	3320 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.4	Xtriage
Anisotropy	0.134	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 41.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	10988	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.96% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, SAH, EDO, IOD

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	0.57	0/1700	0.73	2/2301 (0.1%)
1	B	0.48	0/1642	0.68	0/2228
1	C	0.53	0/1669	0.67	2/2263 (0.1%)
1	D	0.59	0/1669	0.72	1/2260 (0.0%)
1	E	0.59	1/1696 (0.1%)	0.69	1/2295 (0.0%)
1	F	0.55	0/1664	0.72	4/2254 (0.2%)
All	All	0.55	1/10040 (0.0%)	0.70	10/13601 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	193	GLU	CD-OE2	5.18	1.31	1.25

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	53	ARG	NE-CZ-NH2	-5.98	117.31	120.30
1	A	199	LYS	CD-CE-NZ	5.75	124.92	111.70
1	F	127	MET	CA-CB-CG	5.66	122.91	113.30
1	C	125	LYS	CB-CA-C	-5.30	99.80	110.40
1	E	125	LYS	CG-CD-CE	-5.27	96.09	111.90

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	1652	0	1660	21	1
1	B	1608	0	1572	5	0
1	C	1628	0	1608	17	1
1	D	1632	0	1611	14	0
1	E	1655	0	1659	20	1
1	F	1630	0	1610	15	0
2	A	26	0	19	1	0
2	B	26	0	19	1	0
2	C	26	0	19	0	0
2	D	26	0	19	1	0
2	E	26	0	19	0	0
2	F	26	0	19	2	0
3	A	19	0	0	7	0
3	B	16	0	0	5	0
3	C	20	0	0	14	0
3	D	21	0	0	7	0
3	E	16	0	0	10	0
3	F	22	0	0	10	0
4	A	8	0	12	0	0
4	B	4	0	6	0	0
4	E	8	0	12	0	0
4	F	20	0	30	3	0
5	D	12	0	16	3	0
5	E	6	0	8	0	0
5	F	6	0	8	0	0
6	A	151	0	0	5	1
6	B	127	0	0	1	0
6	C	135	0	0	4	0
6	D	158	0	0	3	0
6	E	139	0	0	4	0
6	F	139	0	0	6	0
All	All	10988	0	9926	104	2

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 5.

The worst 5 of 104 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)
3:C:312:IOD:I	1:E:118:LEU:HD11	2.00	1.32
3:E:311:IOD:I	3:E:312:IOD:I	2.97	1.22
3:C:313:IOD:I	3:C:314:IOD:I	2.99	1.20
1:C:47:MET:SD	3:C:303:IOD:I	2.71	1.18
1:A:47:MET:SD	3:A:304:IOD:I	2.74	1.15

All (2) 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	Interatomic distance (Å)	Clash overlap (Å)
1:A:154[B]:ARG:NH2	6:A:488:HOH:O[2_656]	2.02	0.18
1:C:91:TYR:OH	1:E:177:GLU:O[2_555]	2.10	0.10

## 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	218/227 (96%)	212 (97%)	4 (2%)	2 (1%)	17	20
1	B	212/227 (93%)	205 (97%)	5 (2%)	2 (1%)	17	20
1	C	214/227 (94%)	209 (98%)	5 (2%)	0	100	100
1	D	215/227 (95%)	207 (96%)	6 (3%)	2 (1%)	17	20
1	E	216/227 (95%)	211 (98%)	5 (2%)	0	100	100
1	F	213/227 (94%)	207 (97%)	6 (3%)	0	100	100
All	All	1288/1362 (95%)	1251 (97%)	31 (2%)	6 (0%)	47	35

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	138[A]	ASN
1	B	138[B]	ASN
1	D	138[A]	ASN

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Mol	Chain	Res	Type
1	D	138[B]	ASN
1	A	138[A]	ASN

### 5.3.2 Protein sidechains ⓘ

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	178/193 (92%)	175 (98%)	3 (2%)	60	76
1	B	170/193 (88%)	169 (99%)	1 (1%)	86	94
1	C	175/193 (91%)	175 (100%)	0	100	100
1	D	174/193 (90%)	174 (100%)	0	100	100
1	E	180/193 (93%)	178 (99%)	2 (1%)	73	86
1	F	174/193 (90%)	170 (98%)	4 (2%)	50	67
All	All	1051/1158 (91%)	1041 (99%)	10 (1%)	76	87

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	36	ARG
1	E	173	GLU
1	F	92	GLU
1	B	22	GLU
1	F	36	ARG

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

Mol	Chain	Res	Type
1	D	174	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.



## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 134 ligands modelled in this entry, 114 are monoatomic - leaving 20 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	$\# Z  > 2$
2	SAH	D	301	-	21,28,28	1.05	1 (4%)	20,40,40	1.31	3 (15%)
4	EDO	F	324	-	3,3,3	0.69	0	2,2,2	0.64	0
2	SAH	A	301	-	21,28,28	1.07	2 (9%)	20,40,40	1.74	5 (25%)
4	EDO	E	319	-	3,3,3	0.68	0	2,2,2	0.22	0
4	EDO	B	318	-	3,3,3	0.66	0	2,2,2	0.28	0
2	SAH	F	301	-	21,28,28	1.05	1 (4%)	20,40,40	1.43	3 (15%)
4	EDO	E	318	-	3,3,3	0.49	0	2,2,2	0.30	0
4	EDO	F	327	-	3,3,3	0.31	0	2,2,2	0.07	0
2	SAH	B	301	-	21,28,28	1.16	2 (9%)	20,40,40	1.52	3 (15%)
4	EDO	F	326	-	3,3,3	0.63	0	2,2,2	0.10	0
2	SAH	C	301	-	21,28,28	0.97	1 (4%)	20,40,40	1.52	4 (20%)
4	EDO	A	321	-	3,3,3	0.43	0	2,2,2	0.14	0
5	GOL	D	323	-	5,5,5	0.58	0	5,5,5	0.85	0
4	EDO	F	325	-	3,3,3	0.59	0	2,2,2	0.19	0
5	GOL	F	329	-	5,5,5	0.46	0	5,5,5	0.35	0
2	SAH	E	301	-	21,28,28	0.97	1 (4%)	20,40,40	1.35	3 (15%)
5	GOL	E	320	-	5,5,5	0.41	0	5,5,5	0.44	0
4	EDO	F	328	-	3,3,3	0.53	0	2,2,2	0.42	0
4	EDO	A	322	-	3,3,3	0.73	0	2,2,2	0.23	0
5	GOL	D	324	-	5,5,5	0.57	0	5,5,5	1.26	1 (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
2	SAH	D	301	-	-	1/7/31/31	0/3/3/3
4	EDO	F	324	-	-	0/1/1/1	-
2	SAH	A	301	-	-	2/7/31/31	0/3/3/3
4	EDO	E	319	-	-	0/1/1/1	-
4	EDO	B	318	-	-	1/1/1/1	-
2	SAH	F	301	-	-	2/7/31/31	0/3/3/3
4	EDO	E	318	-	-	1/1/1/1	-
4	EDO	F	327	-	-	0/1/1/1	-
2	SAH	B	301	-	-	0/7/31/31	0/3/3/3
4	EDO	F	326	-	-	1/1/1/1	-
2	SAH	C	301	-	-	1/7/31/31	0/3/3/3
4	EDO	A	321	-	-	1/1/1/1	-
5	GOL	D	323	-	-	4/4/4/4	-
4	EDO	F	325	-	-	0/1/1/1	-
5	GOL	F	329	-	-	2/4/4/4	-
2	SAH	E	301	-	-	1/7/31/31	0/3/3/3
5	GOL	E	320	-	-	3/4/4/4	-
4	EDO	F	328	-	-	0/1/1/1	-
4	EDO	A	322	-	-	1/1/1/1	-
5	GOL	D	324	-	-	2/4/4/4	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	SAH	C5-C4	2.57	1.47	1.40
2	A	301	SAH	O4'-C1'	2.41	1.44	1.41
2	F	301	SAH	O4'-C1'	2.39	1.44	1.41
2	D	301	SAH	C2-N3	2.34	1.35	1.32
2	E	301	SAH	C5-C4	2.32	1.47	1.40

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	SAH	N3-C2-N1	-4.33	121.91	128.68
2	B	301	SAH	N3-C2-N1	-4.07	122.31	128.68
2	C	301	SAH	N3-C2-N1	-4.02	122.39	128.68
2	A	301	SAH	N6-C6-N1	3.65	126.15	118.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	301	SAH	N3-C2-N1	-3.53	123.16	128.68

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	E	320	GOL	C1-C2-C3-O3
5	D	323	GOL	C1-C2-C3-O3
5	D	324	GOL	C1-C2-C3-O3
5	D	324	GOL	O2-C2-C3-O3
5	D	323	GOL	O2-C2-C3-O3

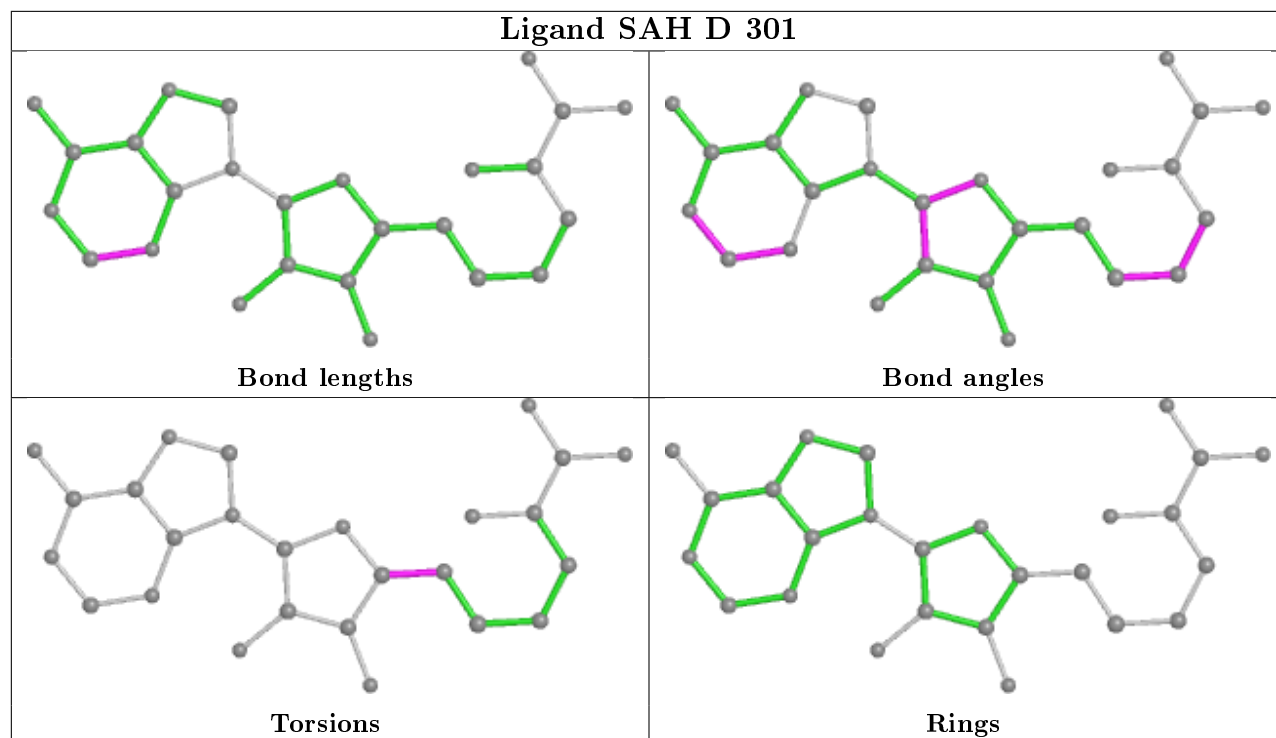
There are no ring outliers.

8 monomers are involved in 11 short contacts:

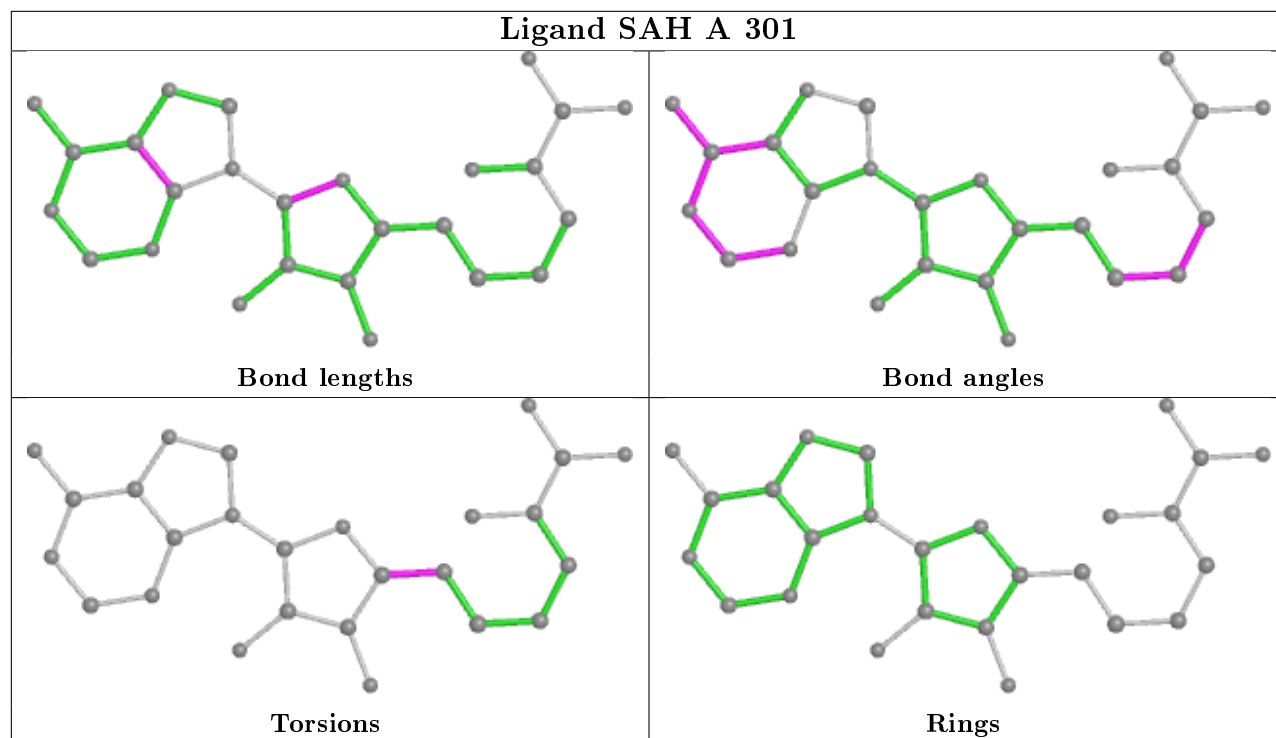
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	301	SAH	1	0
2	A	301	SAH	1	0
2	F	301	SAH	2	0
4	F	327	EDO	1	0
2	B	301	SAH	1	0
4	F	326	EDO	1	0
4	F	328	EDO	1	0
5	D	324	GOL	3	0

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.

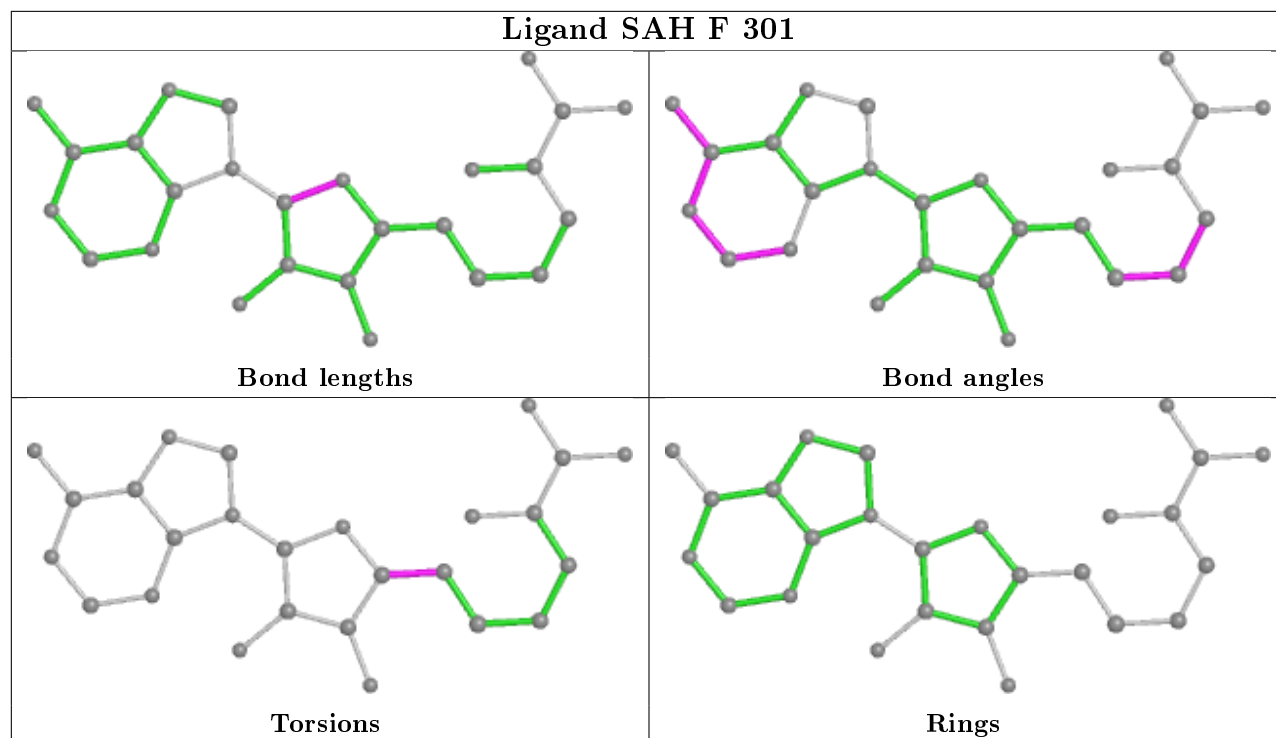
## Ligand SAH D 301



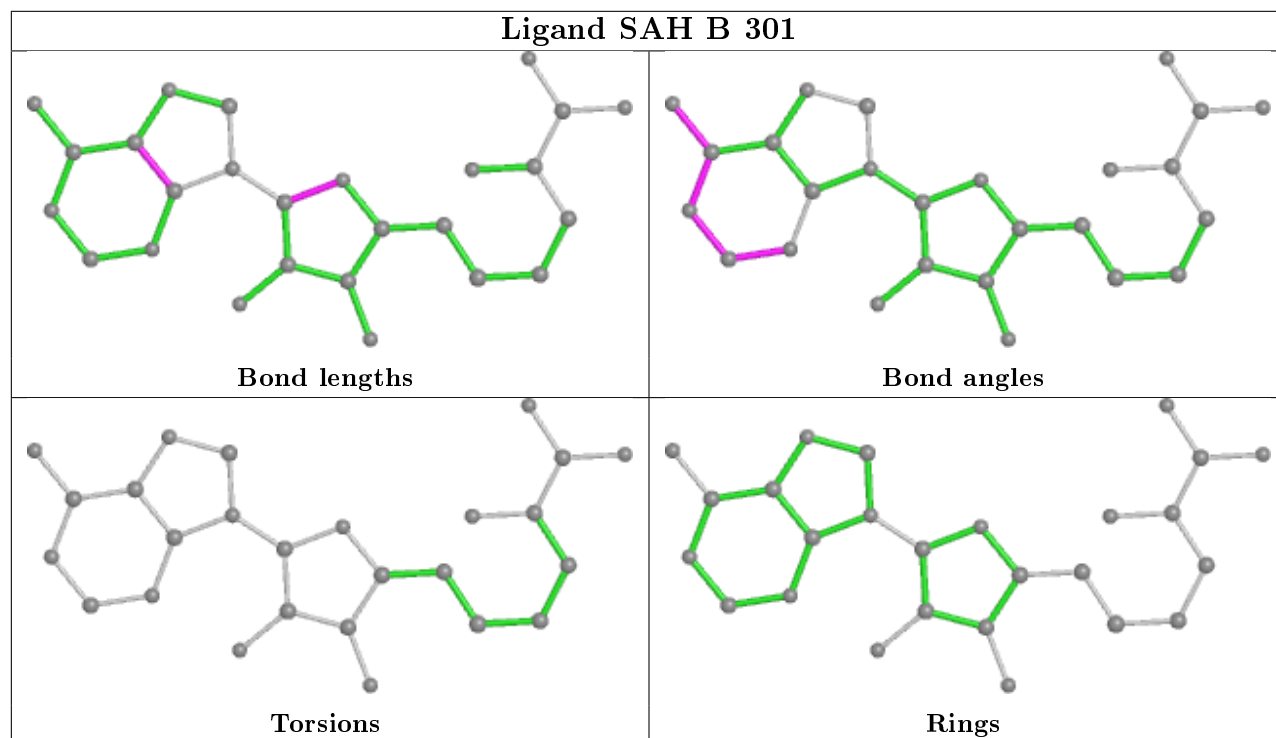
## Ligand SAH A 301

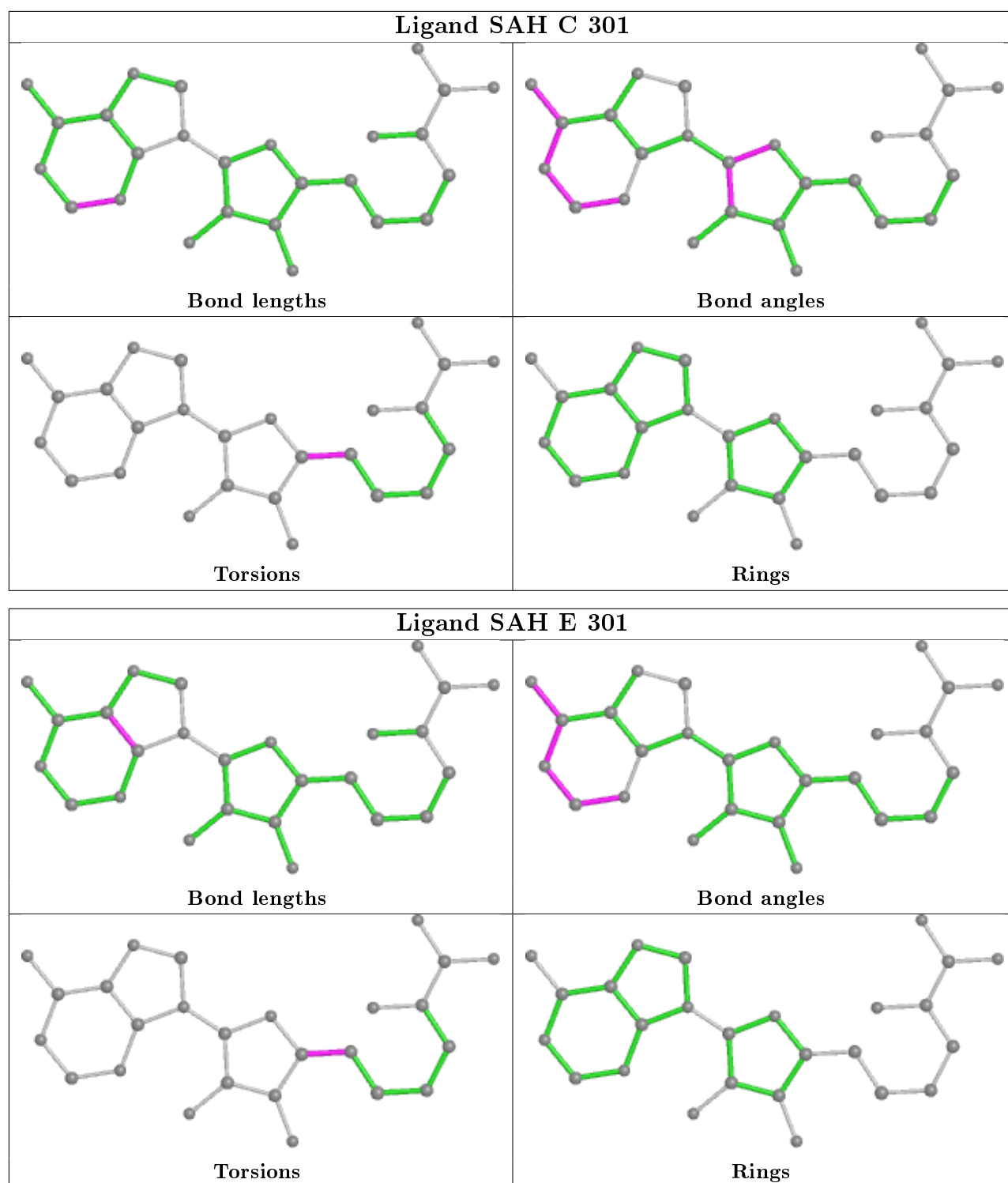


## Ligand SAH F 301



## Ligand SAH B 301





## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	212/227 (93%)	-0.10	2 (0%) 84 88	8, 17, 32, 44	1 (0%)
1	B	212/227 (93%)	-0.17	0 100 100	13, 23, 43, 65	0
1	C	212/227 (93%)	-0.11	8 (3%) 40 47	11, 20, 43, 85	0
1	D	213/227 (93%)	-0.32	1 (0%) 91 94	6, 13, 28, 49	0
1	E	214/227 (94%)	-0.14	3 (1%) 75 80	7, 16, 32, 52	0
1	F	213/227 (93%)	-0.09	1 (0%) 91 94	11, 19, 36, 46	0
All	All	1276/1362 (93%)	-0.16	15 (1%) 79 83	6, 18, 39, 85	1 (0%)

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	47	MET	4.9
1	C	182[A]	ASN	4.2
1	C	179	VAL	3.8
1	C	176	THR	3.7
1	C	178	LYS	3.3

### 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 ⓘ

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	IOD	A	318	1/1	0.63	0.68	58,58,58,58	1
3	IOD	C	320	1/1	0.64	0.17	58,58,58,58	1
3	IOD	F	319	1/1	0.65	0.40	73,73,73,73	1
3	IOD	C	302	1/1	0.69	0.13	55,55,55,55	1
3	IOD	A	310	1/1	0.69	0.14	55,55,55,55	1
3	IOD	D	322	1/1	0.69	0.09	70,70,70,70	1
3	IOD	E	317	1/1	0.70	0.52	32,32,32,32	1
3	IOD	F	321	1/1	0.70	0.34	50,50,50,50	1
3	IOD	D	302	1/1	0.71	0.18	50,50,50,50	1
5	GOL	F	329	6/6	0.71	0.26	57,61,62,63	0
3	IOD	C	318	1/1	0.72	0.11	61,61,61,61	1
3	IOD	E	314	1/1	0.74	0.11	53,53,53,53	1
5	GOL	E	320	6/6	0.74	0.25	41,45,46,47	0
3	IOD	F	317	1/1	0.75	0.14	35,35,35,35	1
3	IOD	F	310	1/1	0.75	0.13	42,42,42,42	1
4	EDO	E	319	4/4	0.75	0.23	35,37,38,40	0
4	EDO	F	326	4/4	0.76	0.56	41,42,43,44	0
3	IOD	A	315	1/1	0.77	0.10	78,78,78,78	1
4	EDO	A	322	4/4	0.79	0.39	33,34,37,39	0
3	IOD	D	321	1/1	0.80	0.35	44,44,44,44	1
3	IOD	D	319	1/1	0.80	0.33	82,82,82,82	1
4	EDO	F	328	4/4	0.80	0.28	51,53,55,56	0
4	EDO	F	324	4/4	0.81	0.19	24,25,26,27	0
4	EDO	F	325	4/4	0.81	0.15	45,50,50,53	0
5	GOL	D	324	6/6	0.81	0.26	28,34,35,37	0
5	GOL	D	323	6/6	0.82	0.25	27,33,34,38	0
3	IOD	A	311	1/1	0.82	0.17	49,49,49,49	1
4	EDO	B	318	4/4	0.82	0.25	35,36,38,40	0
3	IOD	B	311	1/1	0.84	0.09	54,54,54,54	1
4	EDO	F	327	4/4	0.84	0.24	46,46,47,51	0
3	IOD	C	316	1/1	0.85	0.13	56,56,56,56	1
3	IOD	E	307	1/1	0.86	0.14	60,60,60,60	1
3	IOD	F	313	1/1	0.87	0.11	51,51,51,51	1
3	IOD	D	316	1/1	0.87	0.24	38,38,38,38	1
3	IOD	A	316	1/1	0.87	0.12	61,61,61,61	1
3	IOD	F	320	1/1	0.88	0.12	57,57,57,57	1
3	IOD	D	307	1/1	0.88	0.11	64,64,64,64	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	IOD	B	317	1/1	0.88	0.14	63,63,63,63	1
3	IOD	E	311	1/1	0.88	0.15	38,38,38,38	1
3	IOD	F	315	1/1	0.88	0.22	52,52,52,52	1
4	EDO	A	321	4/4	0.88	0.20	28,29,29,29	0
3	IOD	B	314	1/1	0.89	0.09	55,55,55,55	1
3	IOD	B	306	1/1	0.89	0.13	43,43,43,43	1
3	IOD	F	305	1/1	0.89	0.07	59,59,59,59	1
3	IOD	E	315	1/1	0.89	0.09	44,44,44,44	1
4	EDO	E	318	4/4	0.89	0.18	36,37,38,40	0
3	IOD	F	322	1/1	0.89	0.26	39,39,39,39	1
3	IOD	E	305	1/1	0.89	0.18	58,58,58,58	1
3	IOD	D	304	1/1	0.90	0.20	35,35,35,35	1
3	IOD	F	314	1/1	0.90	0.08	38,38,38,38	1
3	IOD	C	313	1/1	0.90	0.12	34,34,34,34	1
3	IOD	D	320	1/1	0.90	0.09	41,41,41,41	1
3	IOD	A	317	1/1	0.91	0.19	51,51,51,51	1
3	IOD	A	312	1/1	0.91	0.16	45,45,45,45	1
3	IOD	D	318	1/1	0.91	0.13	50,50,50,50	1
3	IOD	C	308	1/1	0.91	0.09	69,69,69,69	1
3	IOD	E	303	1/1	0.92	0.12	30,30,30,30	1
3	IOD	D	315	1/1	0.92	0.16	36,36,36,36	1
3	IOD	F	309	1/1	0.92	0.13	66,66,66,66	1
3	IOD	D	317	1/1	0.93	0.10	49,49,49,49	1
3	IOD	C	307	1/1	0.93	0.07	53,53,53,53	1
3	IOD	F	318	1/1	0.93	0.23	30,30,30,30	1
3	IOD	F	316	1/1	0.93	0.10	38,38,38,38	1
3	IOD	F	302	1/1	0.93	0.13	49,49,49,49	1
3	IOD	C	321	1/1	0.93	0.11	48,48,48,48	1
3	IOD	A	320	1/1	0.93	0.22	46,46,46,46	1
3	IOD	C	309	1/1	0.93	0.09	39,39,39,39	1
3	IOD	C	312	1/1	0.94	0.09	56,56,56,56	1
3	IOD	F	323	1/1	0.94	0.15	45,45,45,45	1
3	IOD	D	310	1/1	0.94	0.11	44,44,44,44	1
3	IOD	C	317	1/1	0.94	0.12	51,51,51,51	1
3	IOD	A	309	1/1	0.94	0.07	28,28,28,28	1
3	IOD	F	306	1/1	0.94	0.07	38,38,38,38	1
3	IOD	C	319	1/1	0.95	0.12	43,43,43,43	1
3	IOD	E	316	1/1	0.95	0.07	45,45,45,45	1
3	IOD	E	313	1/1	0.95	0.14	50,50,50,50	1
3	IOD	C	305	1/1	0.95	0.06	32,32,32,32	1
3	IOD	A	319	1/1	0.95	0.14	49,49,49,49	1
3	IOD	B	312	1/1	0.95	0.06	57,57,57,57	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	SAH	F	301	26/26	0.95	0.11	16,17,19,20	0
3	IOD	E	312	1/1	0.95	0.13	36,36,36,36	1
2	SAH	B	301	26/26	0.95	0.11	20,24,25,27	0
3	IOD	C	315	1/1	0.96	0.10	32,32,32,32	1
2	SAH	D	301	26/26	0.96	0.10	9,11,12,12	0
3	IOD	C	306	1/1	0.96	0.04	34,34,34,34	1
3	IOD	C	303	1/1	0.96	0.08	23,23,23,23	1
3	IOD	B	315	1/1	0.96	0.04	46,46,46,46	1
3	IOD	B	313	1/1	0.96	0.15	48,48,48,48	1
3	IOD	A	307	1/1	0.96	0.06	51,51,51,51	1
2	SAH	A	301	26/26	0.96	0.12	13,15,16,17	0
3	IOD	B	305	1/1	0.96	0.08	36,36,36,36	1
3	IOD	E	308	1/1	0.96	0.10	32,32,32,32	1
3	IOD	A	308	1/1	0.96	0.07	44,44,44,44	1
3	IOD	B	304	1/1	0.96	0.05	48,48,48,48	1
3	IOD	A	314	1/1	0.96	0.10	41,41,41,41	1
2	SAH	E	301	26/26	0.97	0.10	14,15,17,17	0
3	IOD	D	306	1/1	0.97	0.07	38,38,38,38	0
3	IOD	F	312	1/1	0.97	0.10	33,33,33,33	1
3	IOD	B	302	1/1	0.97	0.18	26,26,26,26	1
3	IOD	B	308	1/1	0.97	0.07	58,58,58,58	1
2	SAH	C	301	26/26	0.97	0.10	12,14,15,15	0
3	IOD	B	303	1/1	0.97	0.07	39,39,39,39	1
3	IOD	E	310	1/1	0.97	0.13	33,33,33,33	1
3	IOD	B	309	1/1	0.98	0.04	42,42,42,42	0
3	IOD	A	306	1/1	0.98	0.04	38,38,38,38	1
3	IOD	A	305	1/1	0.98	0.14	30,30,30,30	1
3	IOD	F	311	1/1	0.98	0.16	46,46,46,46	1
3	IOD	D	303	1/1	0.98	0.04	35,35,35,35	0
3	IOD	A	302	1/1	0.98	0.04	30,30,30,30	0
3	IOD	D	312	1/1	0.98	0.10	26,26,26,26	1
3	IOD	E	302	1/1	0.98	0.05	39,39,39,39	1
3	IOD	F	308	1/1	0.98	0.04	30,30,30,30	0
3	IOD	C	311	1/1	0.98	0.04	51,51,51,51	1
3	IOD	A	303	1/1	0.98	0.05	39,39,39,39	0
3	IOD	C	314	1/1	0.98	0.08	31,31,31,31	1
3	IOD	F	303	1/1	0.98	0.15	34,34,34,34	1
3	IOD	F	307	1/1	0.98	0.05	37,37,37,37	0
3	IOD	A	304	1/1	0.98	0.11	34,34,34,34	1
3	IOD	D	313	1/1	0.98	0.06	37,37,37,37	1
3	IOD	A	313	1/1	0.98	0.23	44,44,44,44	1
3	IOD	B	310	1/1	0.99	0.04	34,34,34,34	0

*Continued on next page...*

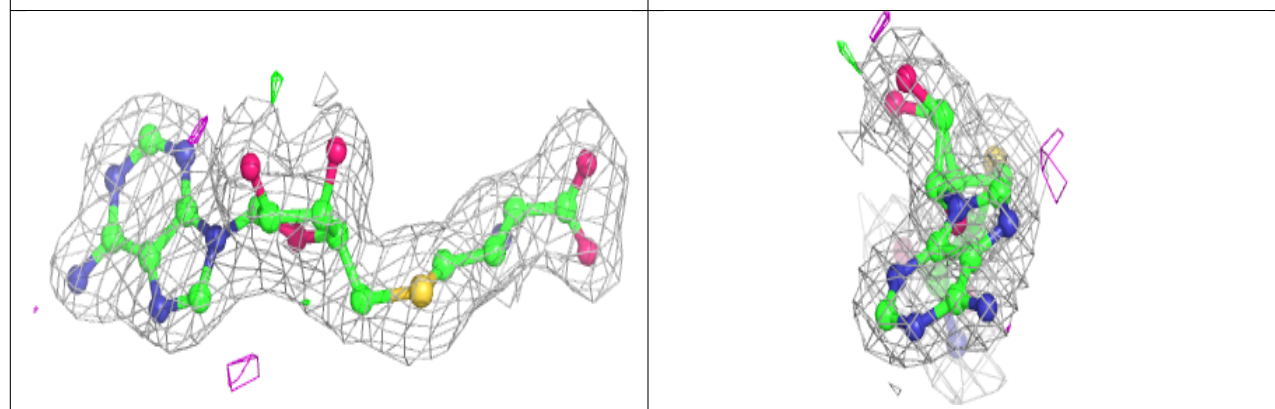
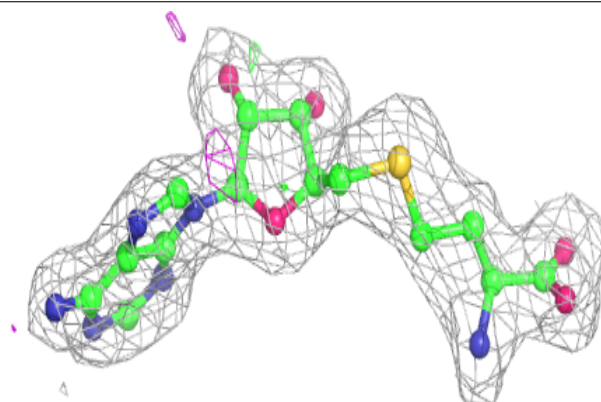
*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	IOD	D	309	1/1	0.99	0.04	32,32,32,32	1
3	IOD	D	308	1/1	0.99	0.11	23,23,23,23	1
3	IOD	D	314	1/1	0.99	0.11	40,40,40,40	1
3	IOD	F	304	1/1	0.99	0.06	44,44,44,44	1
3	IOD	C	304	1/1	0.99	0.05	44,44,44,44	1
3	IOD	E	306	1/1	0.99	0.04	47,47,47,47	1
3	IOD	D	305	1/1	0.99	0.06	27,27,27,27	1
3	IOD	D	311	1/1	0.99	0.06	30,30,30,30	1
3	IOD	E	309	1/1	0.99	0.09	22,22,22,22	1
3	IOD	B	316	1/1	0.99	0.09	44,44,44,44	1
3	IOD	B	307	1/1	0.99	0.03	48,48,48,48	1
3	IOD	C	310	1/1	0.99	0.06	36,36,36,36	1
3	IOD	E	304	1/1	0.99	0.04	27,27,27,27	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.

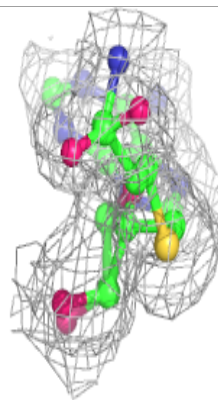
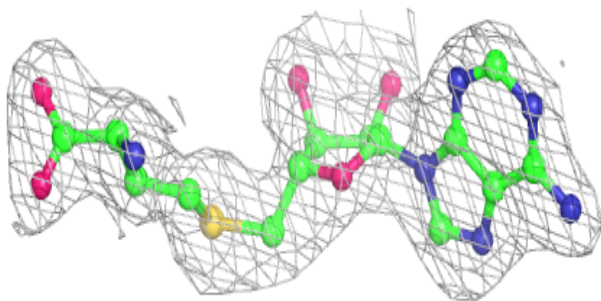
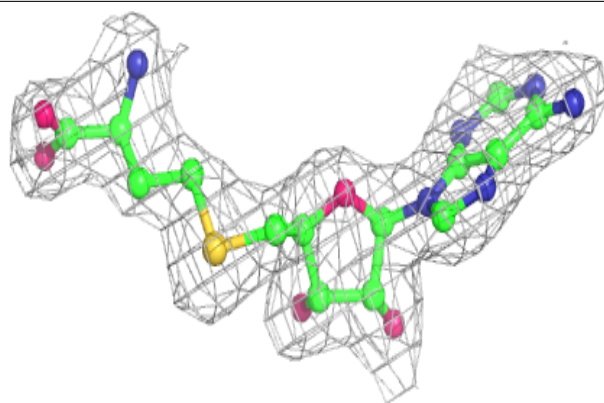
**Electron density around SAH F 301:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)

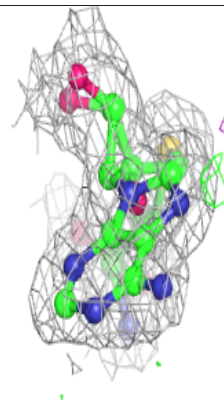
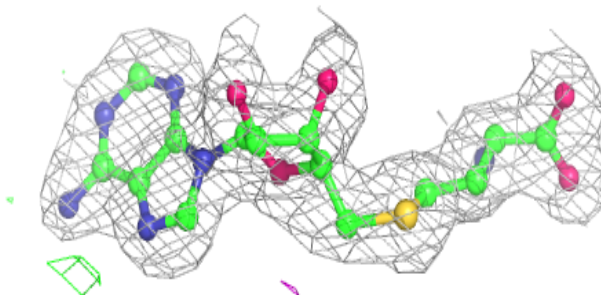
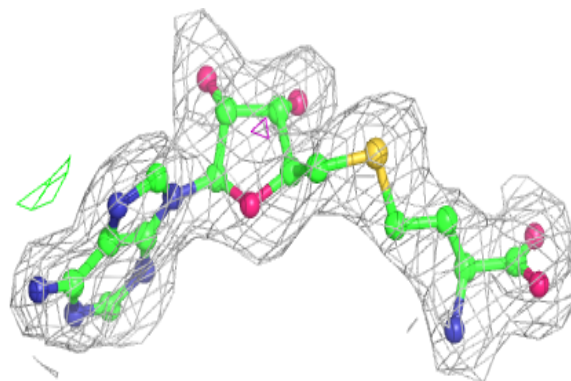


**Electron density around SAH B 301:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

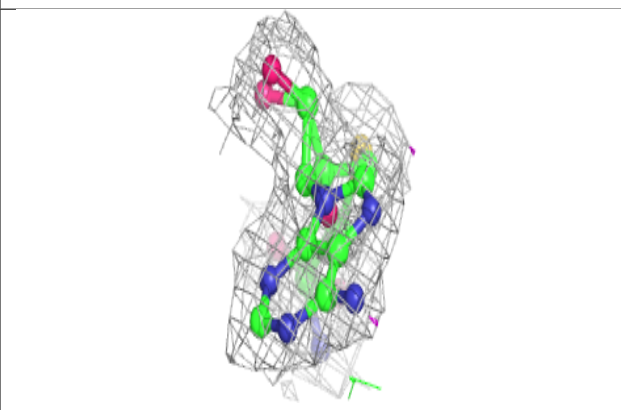
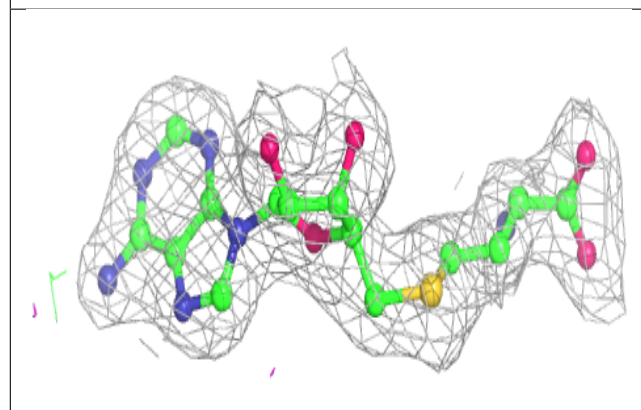
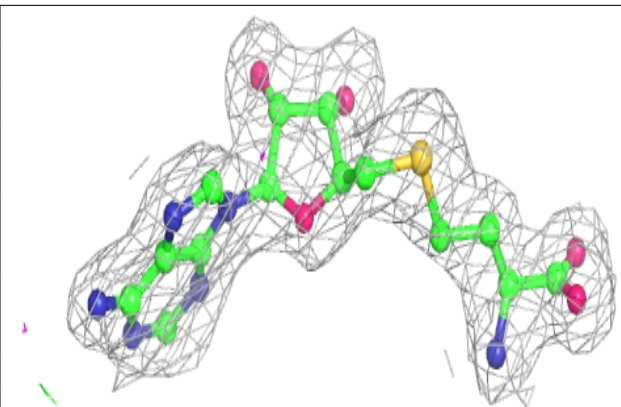
**Electron density around SAH D 301:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

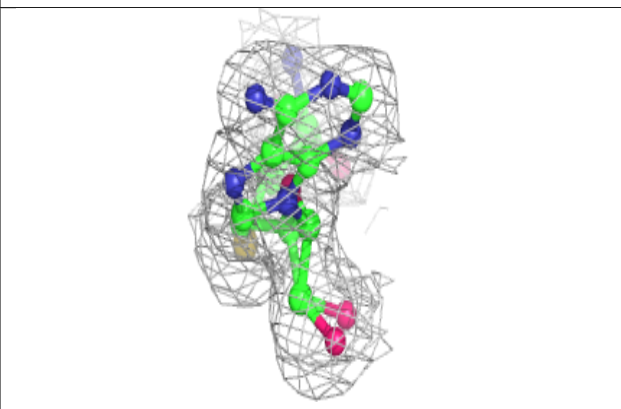
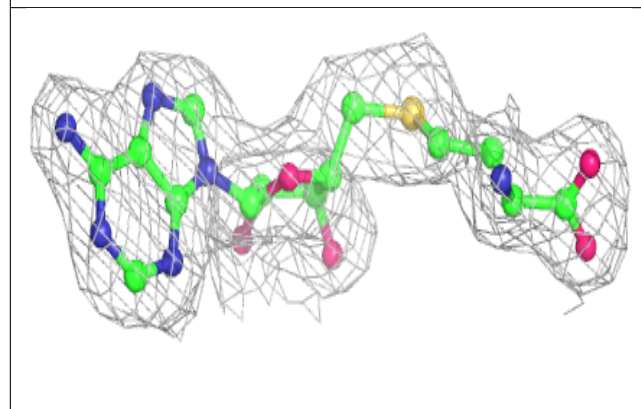
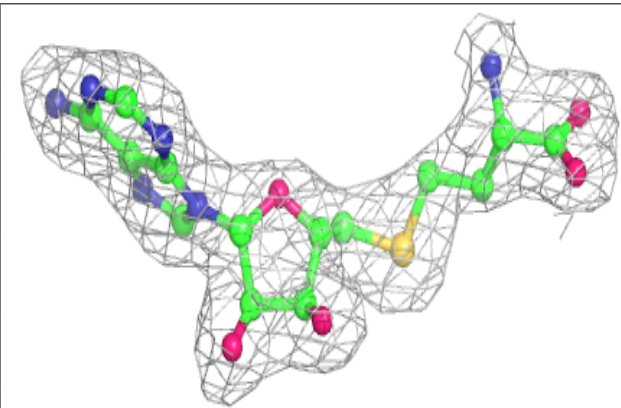


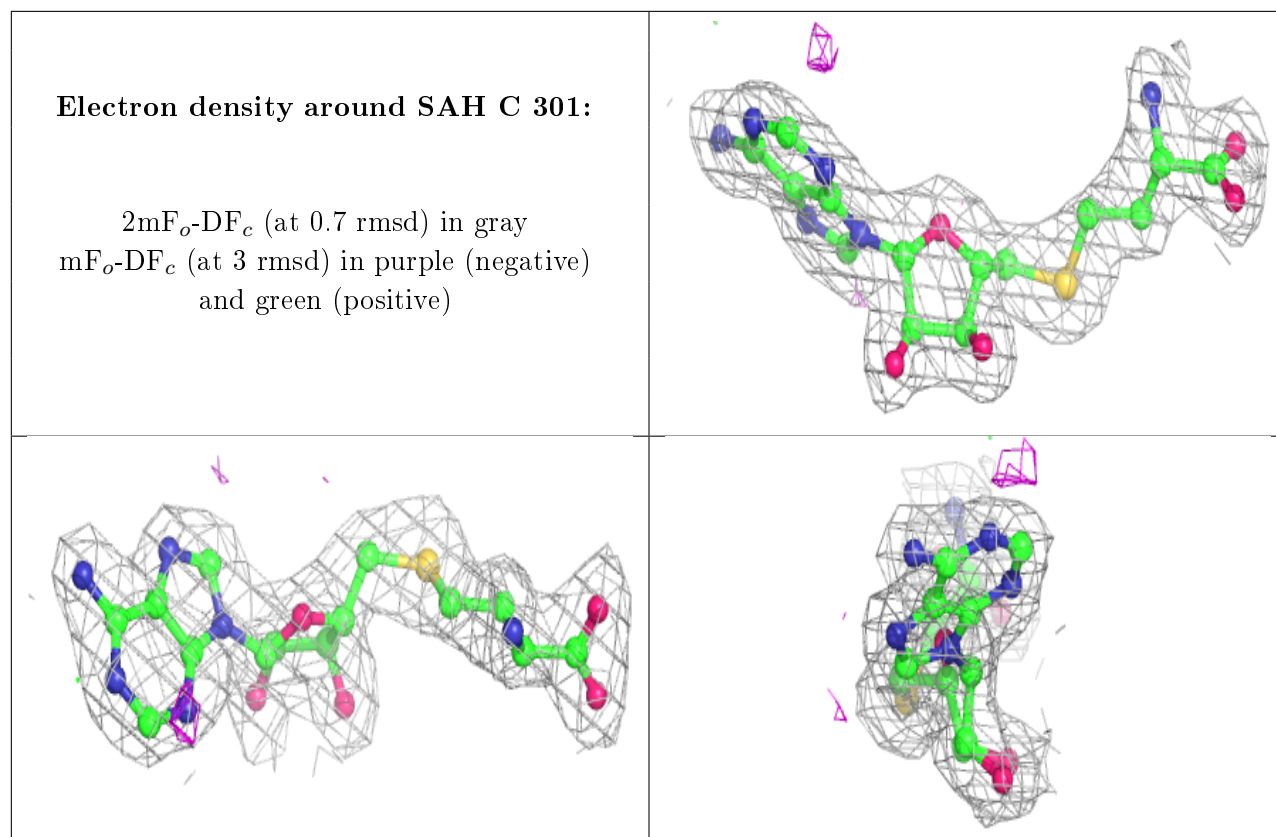
**Electron density around SAH A 301:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around SAH E 301:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.