



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 16, 2024 – 11:04 PM EDT

PDB ID : 5GM1
Title : Crystal structure of methyltransferase TleD complexed with SAH
Authors : Yu, F.; Li, M.J.; Xu, C.Y.; Zhou, H.; Sun, B.; Wang, Z.J.; Xu, Q.; Xie, M.Y.;
Zuo, G.; Huang, P.; Wang, Q.S.; He, J.H.
Deposited on : 2016-07-12
Resolution : 2.50 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 ⓘ 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 ⓘ](#)) 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 : 2.37.1
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) : 2.37.1

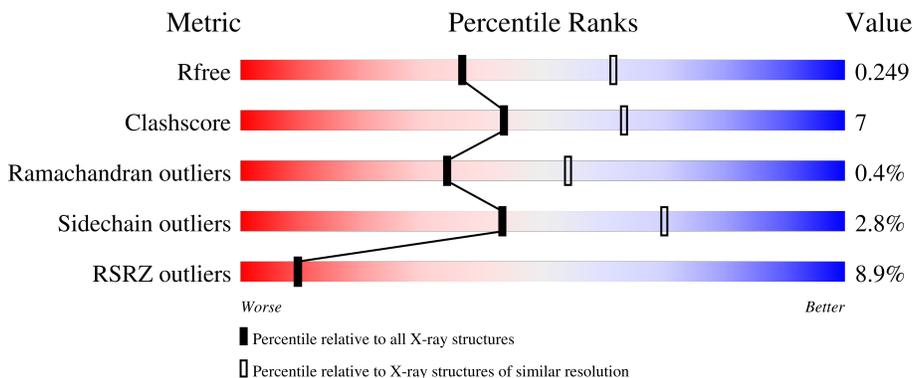
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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.



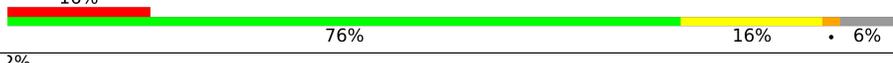
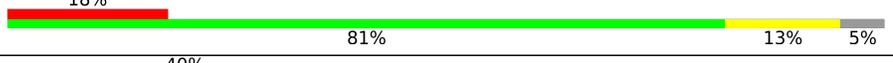
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 $\leq 5\%$. 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	297	79% 15% 5%
1	B	297	79% 14% 6%
1	C	297	76% 17% 6% 1%
1	D	297	81% 12% 6% 1%
1	E	297	80% 13% 6% 1%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	297	
1	G	297	
1	H	297	
1	I	297	
1	J	297	
1	K	297	
1	L	297	
1	M	297	
1	N	297	
1	O	297	
1	P	297	
1	Q	297	
1	R	297	

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
2	SAH	R	301	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 40182 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	281	2184	1384	371	417	12	0	2	0
1	B	280	2164	1372	367	414	11	0	1	0
1	C	280	2157	1370	365	411	11	0	0	0
1	D	280	2169	1375	370	413	11	0	1	0
1	E	279	2149	1364	364	410	11	0	0	0
1	F	280	2158	1369	366	412	11	0	0	0
1	G	280	2158	1369	366	412	11	0	0	0
1	H	279	2149	1364	364	410	11	0	0	0
1	I	280	2169	1375	370	413	11	3	1	0
1	J	281	2167	1374	368	414	11	0	0	0
1	K	281	2166	1375	367	413	11	0	0	0
1	L	280	2158	1369	366	412	11	0	0	0
1	M	281	2184	1384	371	417	12	0	2	0
1	N	281	2184	1384	371	417	12	0	2	0
1	O	280	2158	1369	366	412	11	0	0	0
1	P	280	2158	1369	366	412	11	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	Q	281	2184	1384	371	417	12	0	2	0
1	R	281	2176	1379	370	416	11	0	1	0

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	290	LEU	-	expression tag	UNP A0A077K7L1
A	291	GLU	-	expression tag	UNP A0A077K7L1
A	292	HIS	-	expression tag	UNP A0A077K7L1
A	293	HIS	-	expression tag	UNP A0A077K7L1
A	294	HIS	-	expression tag	UNP A0A077K7L1
A	295	HIS	-	expression tag	UNP A0A077K7L1
A	296	HIS	-	expression tag	UNP A0A077K7L1
A	297	HIS	-	expression tag	UNP A0A077K7L1
B	290	LEU	-	expression tag	UNP A0A077K7L1
B	291	GLU	-	expression tag	UNP A0A077K7L1
B	292	HIS	-	expression tag	UNP A0A077K7L1
B	293	HIS	-	expression tag	UNP A0A077K7L1
B	294	HIS	-	expression tag	UNP A0A077K7L1
B	295	HIS	-	expression tag	UNP A0A077K7L1
B	296	HIS	-	expression tag	UNP A0A077K7L1
B	297	HIS	-	expression tag	UNP A0A077K7L1
C	290	LEU	-	expression tag	UNP A0A077K7L1
C	291	GLU	-	expression tag	UNP A0A077K7L1
C	292	HIS	-	expression tag	UNP A0A077K7L1
C	293	HIS	-	expression tag	UNP A0A077K7L1
C	294	HIS	-	expression tag	UNP A0A077K7L1
C	295	HIS	-	expression tag	UNP A0A077K7L1
C	296	HIS	-	expression tag	UNP A0A077K7L1
C	297	HIS	-	expression tag	UNP A0A077K7L1
D	290	LEU	-	expression tag	UNP A0A077K7L1
D	291	GLU	-	expression tag	UNP A0A077K7L1
D	292	HIS	-	expression tag	UNP A0A077K7L1
D	293	HIS	-	expression tag	UNP A0A077K7L1
D	294	HIS	-	expression tag	UNP A0A077K7L1
D	295	HIS	-	expression tag	UNP A0A077K7L1
D	296	HIS	-	expression tag	UNP A0A077K7L1
D	297	HIS	-	expression tag	UNP A0A077K7L1
E	290	LEU	-	expression tag	UNP A0A077K7L1
E	291	GLU	-	expression tag	UNP A0A077K7L1

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	292	HIS	-	expression tag	UNP A0A077K7L1
E	293	HIS	-	expression tag	UNP A0A077K7L1
E	294	HIS	-	expression tag	UNP A0A077K7L1
E	295	HIS	-	expression tag	UNP A0A077K7L1
E	296	HIS	-	expression tag	UNP A0A077K7L1
E	297	HIS	-	expression tag	UNP A0A077K7L1
F	290	LEU	-	expression tag	UNP A0A077K7L1
F	291	GLU	-	expression tag	UNP A0A077K7L1
F	292	HIS	-	expression tag	UNP A0A077K7L1
F	293	HIS	-	expression tag	UNP A0A077K7L1
F	294	HIS	-	expression tag	UNP A0A077K7L1
F	295	HIS	-	expression tag	UNP A0A077K7L1
F	296	HIS	-	expression tag	UNP A0A077K7L1
F	297	HIS	-	expression tag	UNP A0A077K7L1
G	290	LEU	-	expression tag	UNP A0A077K7L1
G	291	GLU	-	expression tag	UNP A0A077K7L1
G	292	HIS	-	expression tag	UNP A0A077K7L1
G	293	HIS	-	expression tag	UNP A0A077K7L1
G	294	HIS	-	expression tag	UNP A0A077K7L1
G	295	HIS	-	expression tag	UNP A0A077K7L1
G	296	HIS	-	expression tag	UNP A0A077K7L1
G	297	HIS	-	expression tag	UNP A0A077K7L1
H	290	LEU	-	expression tag	UNP A0A077K7L1
H	291	GLU	-	expression tag	UNP A0A077K7L1
H	292	HIS	-	expression tag	UNP A0A077K7L1
H	293	HIS	-	expression tag	UNP A0A077K7L1
H	294	HIS	-	expression tag	UNP A0A077K7L1
H	295	HIS	-	expression tag	UNP A0A077K7L1
H	296	HIS	-	expression tag	UNP A0A077K7L1
H	297	HIS	-	expression tag	UNP A0A077K7L1
I	290	LEU	-	expression tag	UNP A0A077K7L1
I	291	GLU	-	expression tag	UNP A0A077K7L1
I	292	HIS	-	expression tag	UNP A0A077K7L1
I	293	HIS	-	expression tag	UNP A0A077K7L1
I	294	HIS	-	expression tag	UNP A0A077K7L1
I	295	HIS	-	expression tag	UNP A0A077K7L1
I	296	HIS	-	expression tag	UNP A0A077K7L1
I	297	HIS	-	expression tag	UNP A0A077K7L1
J	290	LEU	-	expression tag	UNP A0A077K7L1
J	291	GLU	-	expression tag	UNP A0A077K7L1
J	292	HIS	-	expression tag	UNP A0A077K7L1
J	293	HIS	-	expression tag	UNP A0A077K7L1

Continued on next page...

Continued from previous page...

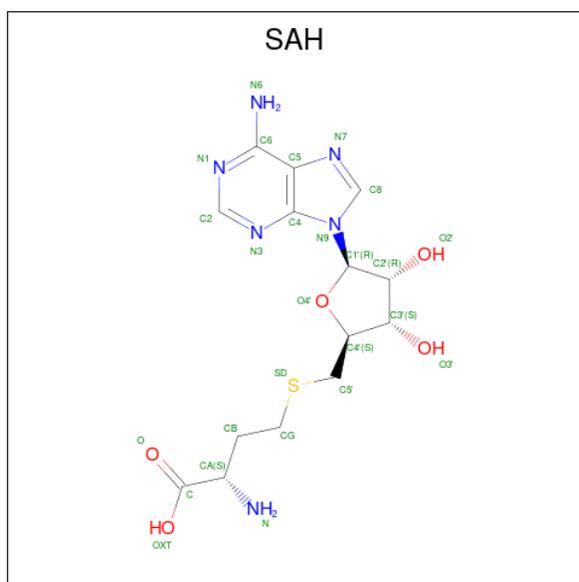
Chain	Residue	Modelled	Actual	Comment	Reference
J	294	HIS	-	expression tag	UNP A0A077K7L1
J	295	HIS	-	expression tag	UNP A0A077K7L1
J	296	HIS	-	expression tag	UNP A0A077K7L1
J	297	HIS	-	expression tag	UNP A0A077K7L1
K	290	LEU	-	expression tag	UNP A0A077K7L1
K	291	GLU	-	expression tag	UNP A0A077K7L1
K	292	HIS	-	expression tag	UNP A0A077K7L1
K	293	HIS	-	expression tag	UNP A0A077K7L1
K	294	HIS	-	expression tag	UNP A0A077K7L1
K	295	HIS	-	expression tag	UNP A0A077K7L1
K	296	HIS	-	expression tag	UNP A0A077K7L1
K	297	HIS	-	expression tag	UNP A0A077K7L1
L	290	LEU	-	expression tag	UNP A0A077K7L1
L	291	GLU	-	expression tag	UNP A0A077K7L1
L	292	HIS	-	expression tag	UNP A0A077K7L1
L	293	HIS	-	expression tag	UNP A0A077K7L1
L	294	HIS	-	expression tag	UNP A0A077K7L1
L	295	HIS	-	expression tag	UNP A0A077K7L1
L	296	HIS	-	expression tag	UNP A0A077K7L1
L	297	HIS	-	expression tag	UNP A0A077K7L1
M	290	LEU	-	expression tag	UNP A0A077K7L1
M	291	GLU	-	expression tag	UNP A0A077K7L1
M	292	HIS	-	expression tag	UNP A0A077K7L1
M	293	HIS	-	expression tag	UNP A0A077K7L1
M	294	HIS	-	expression tag	UNP A0A077K7L1
M	295	HIS	-	expression tag	UNP A0A077K7L1
M	296	HIS	-	expression tag	UNP A0A077K7L1
M	297	HIS	-	expression tag	UNP A0A077K7L1
N	290	LEU	-	expression tag	UNP A0A077K7L1
N	291	GLU	-	expression tag	UNP A0A077K7L1
N	292	HIS	-	expression tag	UNP A0A077K7L1
N	293	HIS	-	expression tag	UNP A0A077K7L1
N	294	HIS	-	expression tag	UNP A0A077K7L1
N	295	HIS	-	expression tag	UNP A0A077K7L1
N	296	HIS	-	expression tag	UNP A0A077K7L1
N	297	HIS	-	expression tag	UNP A0A077K7L1
O	290	LEU	-	expression tag	UNP A0A077K7L1
O	291	GLU	-	expression tag	UNP A0A077K7L1
O	292	HIS	-	expression tag	UNP A0A077K7L1
O	293	HIS	-	expression tag	UNP A0A077K7L1
O	294	HIS	-	expression tag	UNP A0A077K7L1
O	295	HIS	-	expression tag	UNP A0A077K7L1

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
O	296	HIS	-	expression tag	UNP A0A077K7L1
O	297	HIS	-	expression tag	UNP A0A077K7L1
P	290	LEU	-	expression tag	UNP A0A077K7L1
P	291	GLU	-	expression tag	UNP A0A077K7L1
P	292	HIS	-	expression tag	UNP A0A077K7L1
P	293	HIS	-	expression tag	UNP A0A077K7L1
P	294	HIS	-	expression tag	UNP A0A077K7L1
P	295	HIS	-	expression tag	UNP A0A077K7L1
P	296	HIS	-	expression tag	UNP A0A077K7L1
P	297	HIS	-	expression tag	UNP A0A077K7L1
Q	290	LEU	-	expression tag	UNP A0A077K7L1
Q	291	GLU	-	expression tag	UNP A0A077K7L1
Q	292	HIS	-	expression tag	UNP A0A077K7L1
Q	293	HIS	-	expression tag	UNP A0A077K7L1
Q	294	HIS	-	expression tag	UNP A0A077K7L1
Q	295	HIS	-	expression tag	UNP A0A077K7L1
Q	296	HIS	-	expression tag	UNP A0A077K7L1
Q	297	HIS	-	expression tag	UNP A0A077K7L1
R	290	LEU	-	expression tag	UNP A0A077K7L1
R	291	GLU	-	expression tag	UNP A0A077K7L1
R	292	HIS	-	expression tag	UNP A0A077K7L1
R	293	HIS	-	expression tag	UNP A0A077K7L1
R	294	HIS	-	expression tag	UNP A0A077K7L1
R	295	HIS	-	expression tag	UNP A0A077K7L1
R	296	HIS	-	expression tag	UNP A0A077K7L1
R	297	HIS	-	expression tag	UNP A0A077K7L1

- 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
			Total	C	N	O	S		
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	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		
2	G	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	H	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	I	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	J	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	K	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	L	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	M	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	N	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	O	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	P	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	Q	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	R	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	81	Total	O	0	0
			81	81		
3	B	90	Total	O	0	0
			90	90		
3	C	51	Total	O	0	0
			51	51		
3	D	35	Total	O	0	0
			35	35		
3	E	48	Total	O	0	0
			48	48		
3	F	72	Total	O	0	0
			72	72		
3	G	22	Total	O	0	0
			22	22		
3	H	19	Total	O	0	0
			19	19		
3	I	46	Total	O	0	0
			46	46		
3	J	21	Total	O	0	0
			21	21		
3	K	11	Total	O	0	0
			11	11		
3	L	21	Total	O	0	0
			21	21		
3	M	28	Total	O	0	0
			28	28		
3	N	19	Total	O	0	0
			19	19		

Continued on next page...

Continued from previous page...

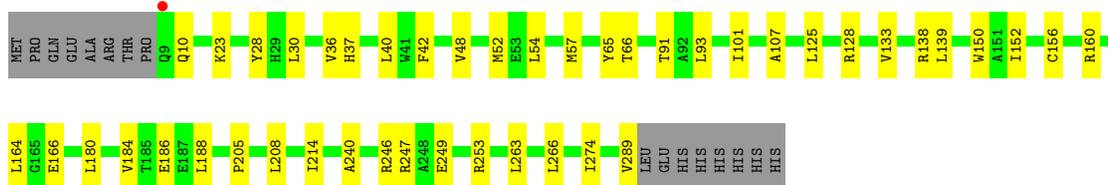
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	O	38	Total 38	O 38	0	0
3	P	25	Total 25	O 25	0	0
3	Q	24	Total 24	O 24	0	0
3	R	45	Total 45	O 45	0	0

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.

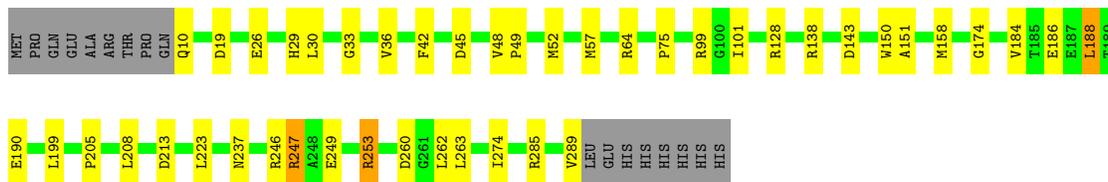
- Molecule 1: O-methyltransferase

Chain A: 



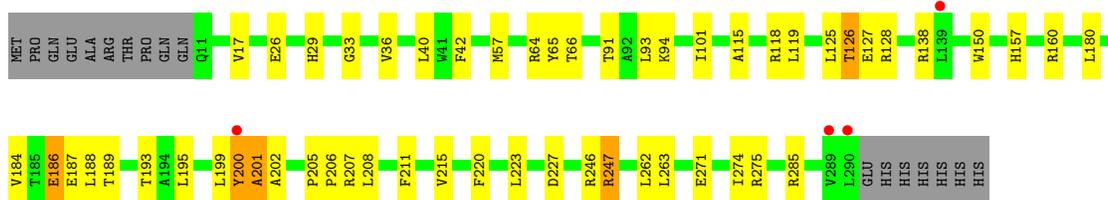
- Molecule 1: O-methyltransferase

Chain B: 



- Molecule 1: O-methyltransferase

Chain C: 



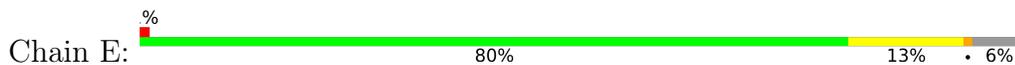
- Molecule 1: O-methyltransferase

Chain D: 

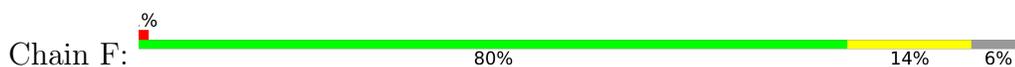




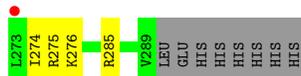
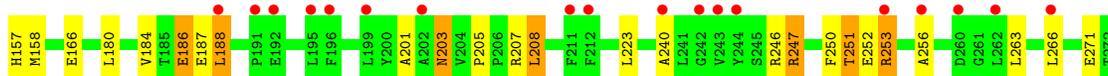
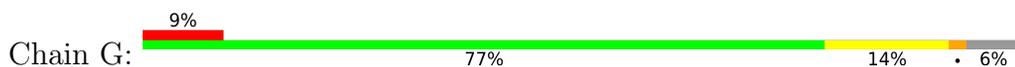
• Molecule 1: O-methyltransferase



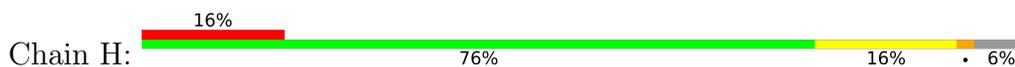
• Molecule 1: O-methyltransferase



• Molecule 1: O-methyltransferase

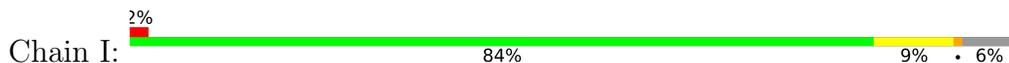


• Molecule 1: O-methyltransferase

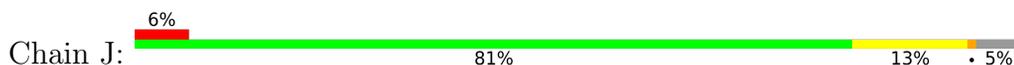




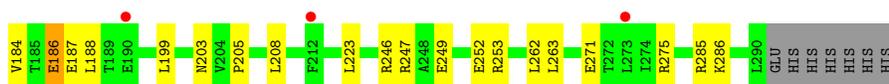
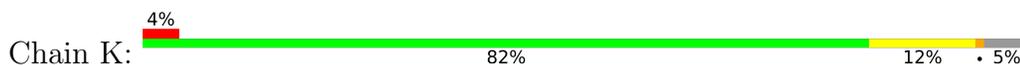
- Molecule 1: O-methyltransferase



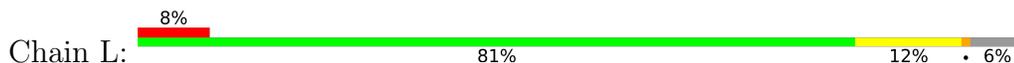
- Molecule 1: O-methyltransferase



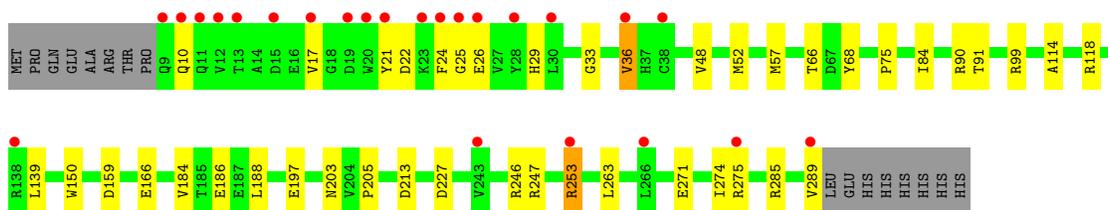
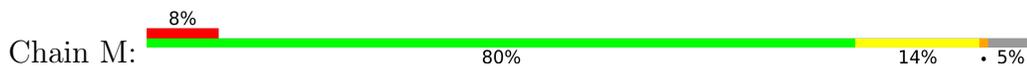
- Molecule 1: O-methyltransferase



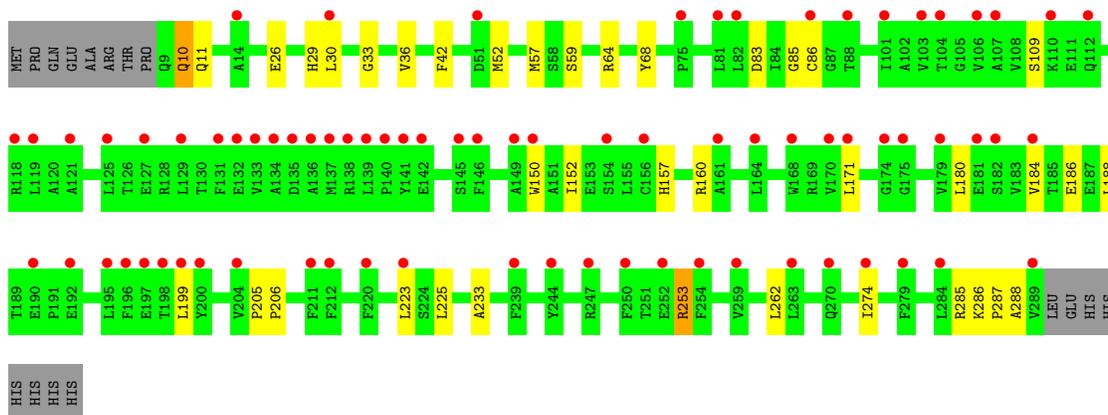
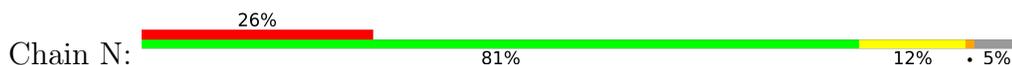
- Molecule 1: O-methyltransferase



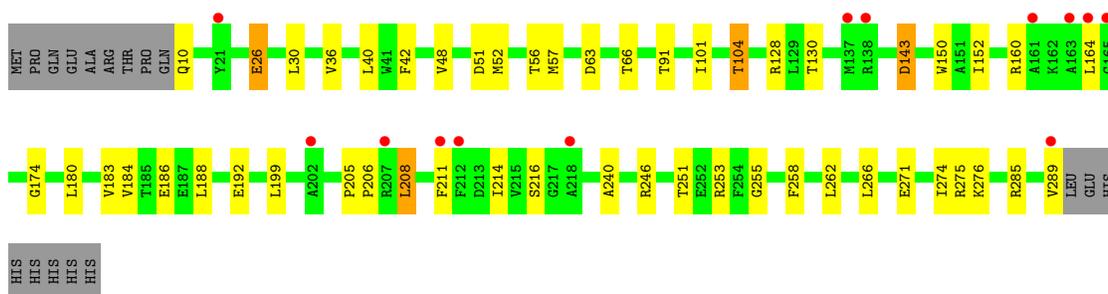
- Molecule 1: O-methyltransferase



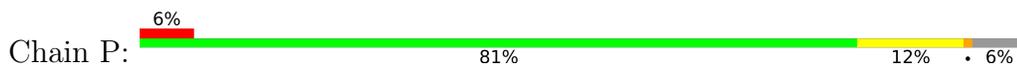
- Molecule 1: O-methyltransferase

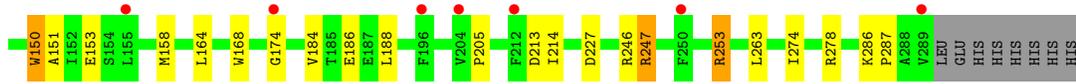


- Molecule 1: O-methyltransferase

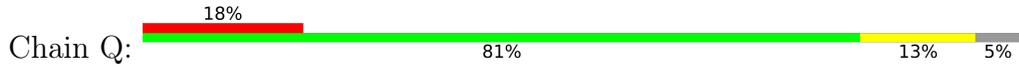


- Molecule 1: O-methyltransferase

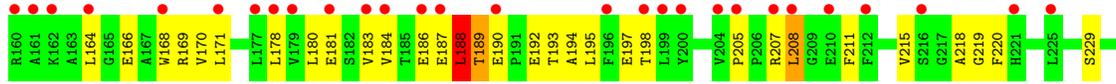
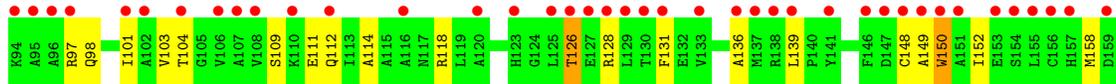




• Molecule 1: O-methyltransferase



• Molecule 1: O-methyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	259.62Å 152.90Å 154.79Å 90.00° 93.33° 90.00°	Depositor
Resolution (Å)	102.27 – 2.50 154.53 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.0 (102.27-2.50) 99.0 (154.53-2.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.54 (at 2.52Å)	Xtrriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.207 , 0.248 0.208 , 0.249	Depositor DCC
R_{free} test set	10316 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	46.4	Xtrriage
Anisotropy	0.291	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 58.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	40182	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.27% 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: 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	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.29	0/2229	0.48	0/3024
1	B	0.28	0/2209	0.46	0/2998
1	C	0.28	0/2202	0.46	0/2989
1	D	0.27	0/2214	0.45	0/3004
1	E	0.28	0/2194	0.47	0/2978
1	F	0.28	0/2203	0.47	0/2990
1	G	0.26	0/2203	0.45	0/2990
1	H	0.27	0/2194	0.44	0/2978
1	I	0.27	0/2214	0.47	0/3004
1	J	0.27	0/2212	0.44	0/3002
1	K	0.26	0/2211	0.44	0/3001
1	L	0.26	0/2203	0.44	0/2990
1	M	0.28	0/2229	0.46	0/3024
1	N	0.26	0/2229	0.44	0/3024
1	O	0.27	0/2203	0.46	0/2990
1	P	0.27	0/2203	0.45	0/2990
1	Q	0.28	0/2229	0.45	0/3024
1	R	0.26	0/2221	0.45	0/3014
All	All	0.27	0/39802	0.45	0/54014

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	2184	0	2139	29	0
1	B	2164	0	2120	31	0
1	C	2157	0	2119	33	0
1	D	2169	0	2128	25	0
1	E	2149	0	2108	26	0
1	F	2158	0	2116	30	0
1	G	2158	0	2116	33	0
1	H	2149	0	2108	41	0
1	I	2169	0	2128	23	0
1	J	2167	0	2124	30	0
1	K	2166	0	2127	25	0
1	L	2158	0	2116	26	0
1	M	2184	0	2139	36	0
1	N	2184	0	2139	34	0
1	O	2158	0	2116	33	0
1	P	2158	0	2116	32	0
1	Q	2184	0	2139	36	0
1	R	2176	0	2131	80	1
2	A	26	0	19	1	0
2	B	52	0	38	4	0
2	C	26	0	19	1	0
2	D	26	0	19	3	0
2	E	26	0	19	1	0
2	F	26	0	19	1	0
2	G	26	0	19	1	0
2	H	26	0	19	1	0
2	I	26	0	19	0	0
2	J	26	0	19	3	0
2	K	26	0	19	3	0
2	L	26	0	19	3	0
2	M	26	0	19	1	0
2	N	26	0	19	4	0
2	O	26	0	19	2	0
2	P	26	0	19	3	0
2	Q	26	0	19	0	0
2	R	26	0	19	1	0
3	A	81	0	0	2	0
3	B	90	0	0	8	0
3	C	51	0	0	7	0
3	D	35	0	0	3	0
3	E	48	0	0	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	72	0	0	6	0
3	G	22	0	0	6	0
3	H	19	0	0	10	0
3	I	46	0	0	8	0
3	J	21	0	0	3	0
3	K	11	0	0	4	0
3	L	21	0	0	7	0
3	M	28	0	0	10	0
3	N	19	0	0	7	0
3	O	38	0	0	4	0
3	P	25	0	0	13	0
3	Q	24	0	0	12	0
3	R	45	0	0	27	0
All	All	40182	0	38590	525	1

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

The worst 5 of 525 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:G:417:HOH:O	2:H:301:SAH:SD	1.97	1.23
1:F:22:ASP:O	3:F:401:HOH:O	1.67	1.09
1:R:57:MET:SD	3:R:442:HOH:O	2.14	1.03
1:N:86:CYS:SG	3:N:411:HOH:O	2.22	0.98
1:G:166:GLU:OE1	3:G:401:HOH:O	1.82	0.95

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:126:THR:OG1	1:R:126:THR:OG1[2_555]	2.14	0.06

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	281/297 (95%)	275 (98%)	4 (1%)	2 (1%)	22	39
1	B	279/297 (94%)	275 (99%)	4 (1%)	0	100	100
1	C	278/297 (94%)	269 (97%)	5 (2%)	4 (1%)	11	20
1	D	279/297 (94%)	275 (99%)	3 (1%)	1 (0%)	34	54
1	E	277/297 (93%)	275 (99%)	2 (1%)	0	100	100
1	F	278/297 (94%)	274 (99%)	4 (1%)	0	100	100
1	G	278/297 (94%)	267 (96%)	9 (3%)	2 (1%)	22	39
1	H	277/297 (93%)	269 (97%)	7 (2%)	1 (0%)	34	54
1	I	279/297 (94%)	275 (99%)	3 (1%)	1 (0%)	34	54
1	J	279/297 (94%)	273 (98%)	6 (2%)	0	100	100
1	K	279/297 (94%)	271 (97%)	7 (2%)	1 (0%)	34	54
1	L	278/297 (94%)	272 (98%)	5 (2%)	1 (0%)	34	54
1	M	281/297 (95%)	273 (97%)	7 (2%)	1 (0%)	34	54
1	N	281/297 (95%)	273 (97%)	6 (2%)	2 (1%)	22	39
1	O	278/297 (94%)	270 (97%)	7 (2%)	1 (0%)	34	54
1	P	278/297 (94%)	271 (98%)	5 (2%)	2 (1%)	22	39
1	Q	281/297 (95%)	274 (98%)	6 (2%)	1 (0%)	34	54
1	R	280/297 (94%)	269 (96%)	9 (3%)	2 (1%)	22	39
All	All	5021/5346 (94%)	4900 (98%)	99 (2%)	22 (0%)	34	54

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	126	THR
1	C	201	ALA
1	K	188	LEU
1	O	188	LEU
1	P	188	LEU

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	226/239 (95%)	222 (98%)	4 (2%)	59 81
1	B	224/239 (94%)	214 (96%)	10 (4%)	27 51
1	C	223/239 (93%)	216 (97%)	7 (3%)	40 67
1	D	224/239 (94%)	216 (96%)	8 (4%)	35 61
1	E	222/239 (93%)	217 (98%)	5 (2%)	50 76
1	F	223/239 (93%)	219 (98%)	4 (2%)	59 81
1	G	223/239 (93%)	215 (96%)	8 (4%)	35 61
1	H	222/239 (93%)	214 (96%)	8 (4%)	35 61
1	I	224/239 (94%)	217 (97%)	7 (3%)	40 67
1	J	224/239 (94%)	219 (98%)	5 (2%)	52 77
1	K	224/239 (94%)	217 (97%)	7 (3%)	40 67
1	L	223/239 (93%)	216 (97%)	7 (3%)	40 67
1	M	226/239 (95%)	221 (98%)	5 (2%)	52 77
1	N	226/239 (95%)	223 (99%)	3 (1%)	69 87
1	O	223/239 (93%)	214 (96%)	9 (4%)	31 56
1	P	223/239 (93%)	219 (98%)	4 (2%)	59 81
1	Q	226/239 (95%)	222 (98%)	4 (2%)	59 81
1	R	225/239 (94%)	217 (96%)	8 (4%)	35 61
All	All	4031/4302 (94%)	3918 (97%)	113 (3%)	43 70

5 of 113 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	208	LEU
1	R	195	LEU
1	K	252	GLU
1	R	190	GLU
1	P	186	GLU

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

Mol	Chain	Res	Type
1	N	231	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

19 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
2	SAH	F	301	-	24,28,28	1.24	3 (12%)	25,40,40	1.68	5 (20%)
2	SAH	B	302	-	24,28,28	1.20	3 (12%)	25,40,40	1.70	6 (24%)
2	SAH	L	301	-	24,28,28	1.20	3 (12%)	25,40,40	1.80	5 (20%)
2	SAH	J	301	-	24,28,28	1.20	3 (12%)	25,40,40	1.72	4 (16%)
2	SAH	A	301	-	24,28,28	1.19	3 (12%)	25,40,40	1.71	4 (16%)
2	SAH	E	301	-	24,28,28	1.21	3 (12%)	25,40,40	1.66	4 (16%)
2	SAH	B	301	-	24,28,28	1.18	3 (12%)	25,40,40	1.71	4 (16%)
2	SAH	P	301	-	24,28,28	1.21	3 (12%)	25,40,40	1.69	5 (20%)
2	SAH	O	301	-	24,28,28	1.20	3 (12%)	25,40,40	1.69	4 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SAH	C	301	-	24,28,28	1.18	3 (12%)	25,40,40	1.71	4 (16%)
2	SAH	Q	301	-	24,28,28	1.17	3 (12%)	25,40,40	1.68	4 (16%)
2	SAH	H	301	-	24,28,28	1.24	3 (12%)	25,40,40	1.78	6 (24%)
2	SAH	G	301	-	24,28,28	1.25	3 (12%)	25,40,40	1.64	4 (16%)
2	SAH	D	301	-	24,28,28	1.22	3 (12%)	25,40,40	1.73	4 (16%)
2	SAH	I	301	-	24,28,28	1.17	3 (12%)	25,40,40	1.62	4 (16%)
2	SAH	K	301	-	24,28,28	1.18	3 (12%)	25,40,40	1.75	4 (16%)
2	SAH	M	301	-	24,28,28	1.21	3 (12%)	25,40,40	1.71	4 (16%)
2	SAH	N	301	-	24,28,28	1.21	3 (12%)	25,40,40	1.69	5 (20%)
2	SAH	R	301	-	24,28,28	1.20	3 (12%)	25,40,40	1.71	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
2	SAH	F	301	-	-	2/11/31/31	0/3/3/3
2	SAH	B	302	-	-	6/11/31/31	0/3/3/3
2	SAH	L	301	-	-	3/11/31/31	0/3/3/3
2	SAH	J	301	-	-	2/11/31/31	0/3/3/3
2	SAH	A	301	-	-	2/11/31/31	0/3/3/3
2	SAH	E	301	-	-	2/11/31/31	0/3/3/3
2	SAH	B	301	-	-	2/11/31/31	0/3/3/3
2	SAH	P	301	-	-	3/11/31/31	0/3/3/3
2	SAH	O	301	-	-	4/11/31/31	0/3/3/3
2	SAH	C	301	-	-	1/11/31/31	0/3/3/3
2	SAH	Q	301	-	-	3/11/31/31	0/3/3/3
2	SAH	H	301	-	-	4/11/31/31	0/3/3/3
2	SAH	G	301	-	-	2/11/31/31	0/3/3/3
2	SAH	D	301	-	-	4/11/31/31	0/3/3/3
2	SAH	I	301	-	-	2/11/31/31	0/3/3/3
2	SAH	K	301	-	-	2/11/31/31	0/3/3/3
2	SAH	M	301	-	-	3/11/31/31	0/3/3/3
2	SAH	N	301	-	-	3/11/31/31	0/3/3/3
2	SAH	R	301	-	-	3/11/31/31	0/3/3/3

The worst 5 of 57 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	301	SAH	C2-N3	4.06	1.38	1.32
2	B	302	SAH	C2-N3	4.06	1.38	1.32
2	H	301	SAH	C2-N3	4.03	1.38	1.32
2	D	301	SAH	C2-N3	3.98	1.38	1.32
2	M	301	SAH	C2-N3	3.97	1.38	1.32

The worst 5 of 85 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	301	SAH	N3-C2-N1	-5.79	119.62	128.68
2	I	301	SAH	N3-C2-N1	-5.71	119.76	128.68
2	B	301	SAH	N3-C2-N1	-5.70	119.77	128.68
2	A	301	SAH	N3-C2-N1	-5.67	119.82	128.68
2	K	301	SAH	N3-C2-N1	-5.62	119.90	128.68

There are no chirality outliers.

5 of 53 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	302	SAH	N-CA-CB-CG
2	E	301	SAH	C-CA-CB-CG
2	I	301	SAH	C-CA-CB-CG
2	O	301	SAH	C-CA-CB-CG
2	P	301	SAH	N-CA-CB-CG

There are no ring outliers.

17 monomers are involved in 33 short contacts:

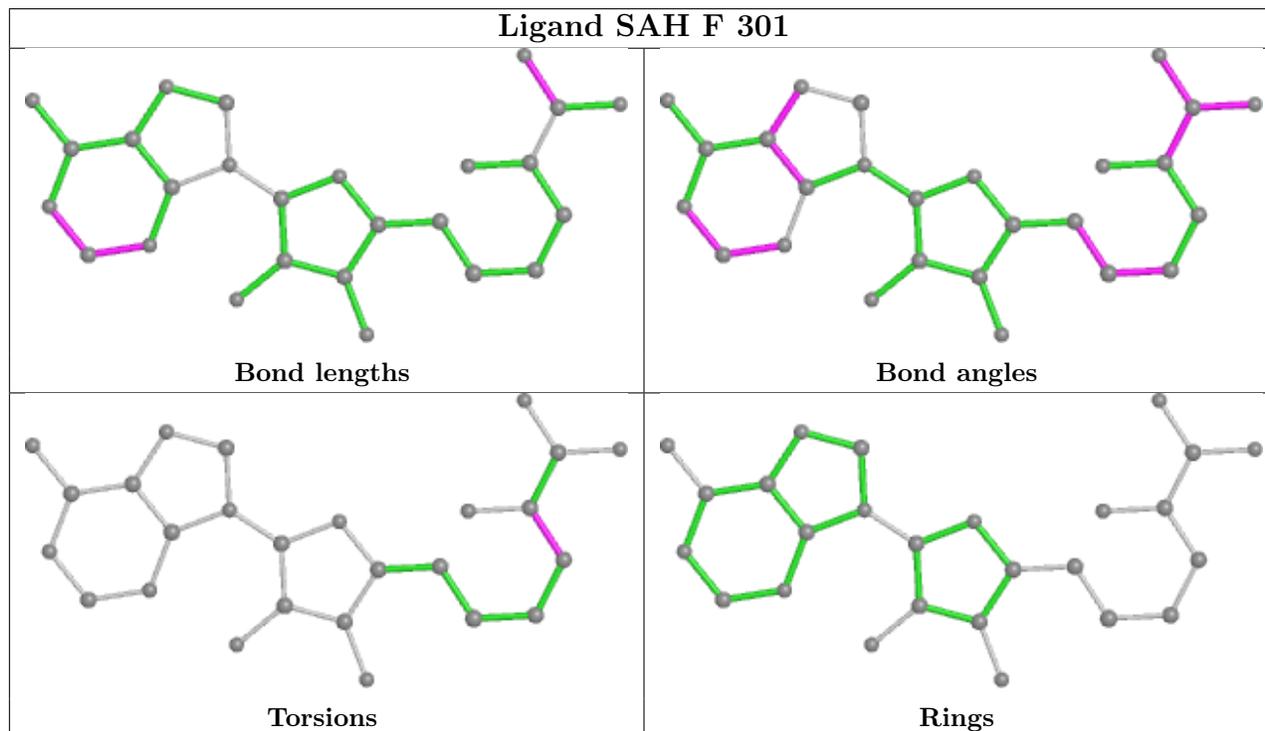
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	301	SAH	1	0
2	B	302	SAH	1	0
2	L	301	SAH	3	0
2	J	301	SAH	3	0
2	A	301	SAH	1	0
2	E	301	SAH	1	0
2	B	301	SAH	3	0
2	P	301	SAH	3	0
2	O	301	SAH	2	0
2	C	301	SAH	1	0
2	H	301	SAH	1	0

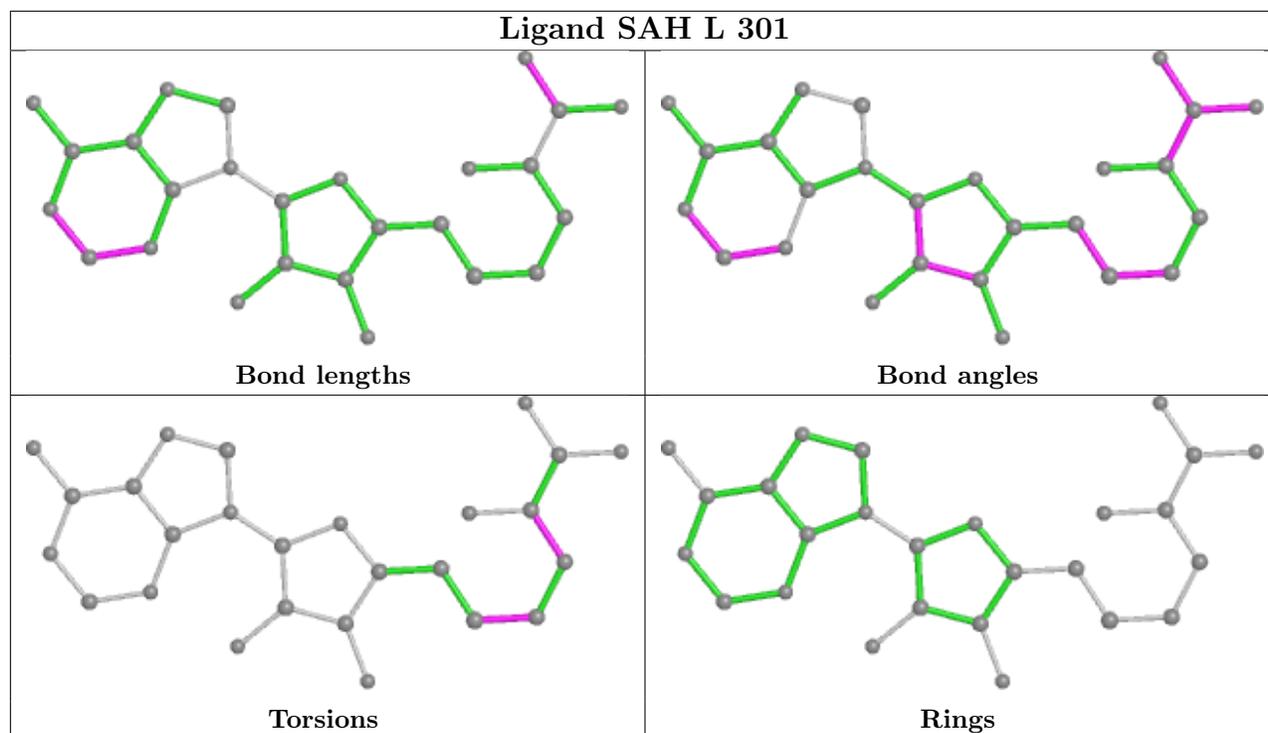
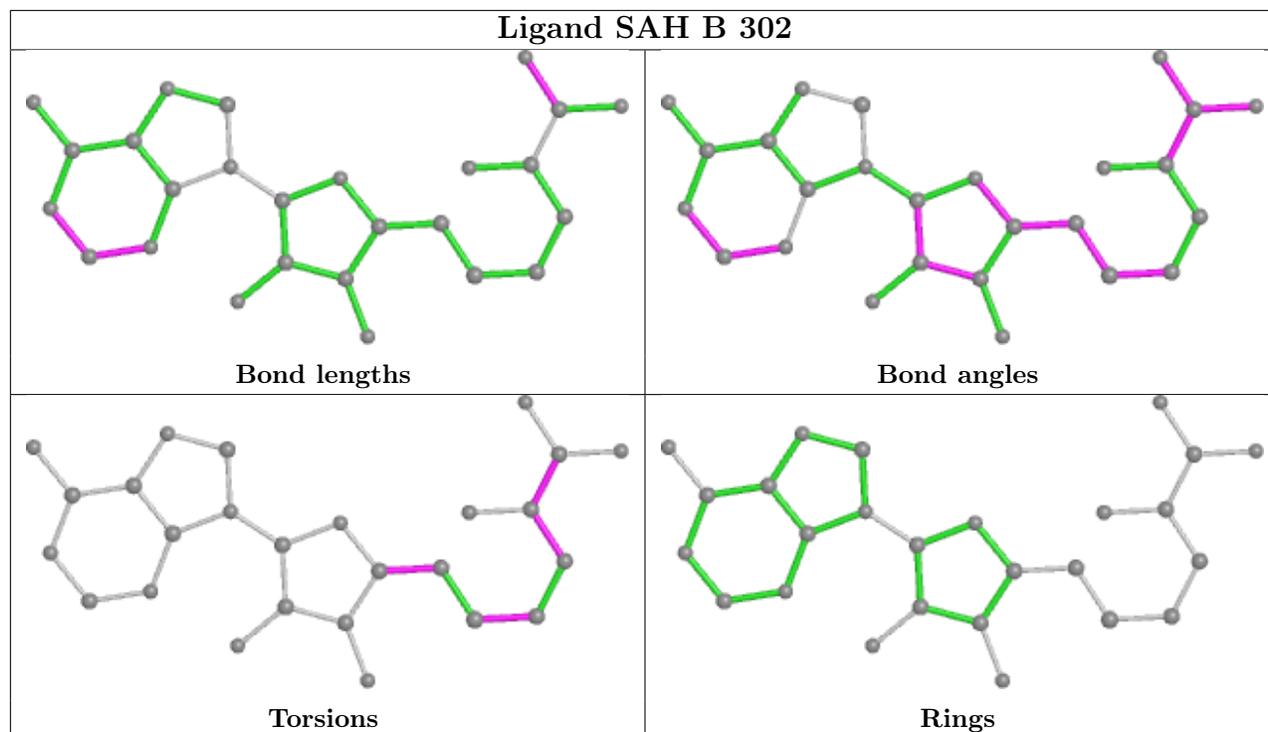
Continued on next page...

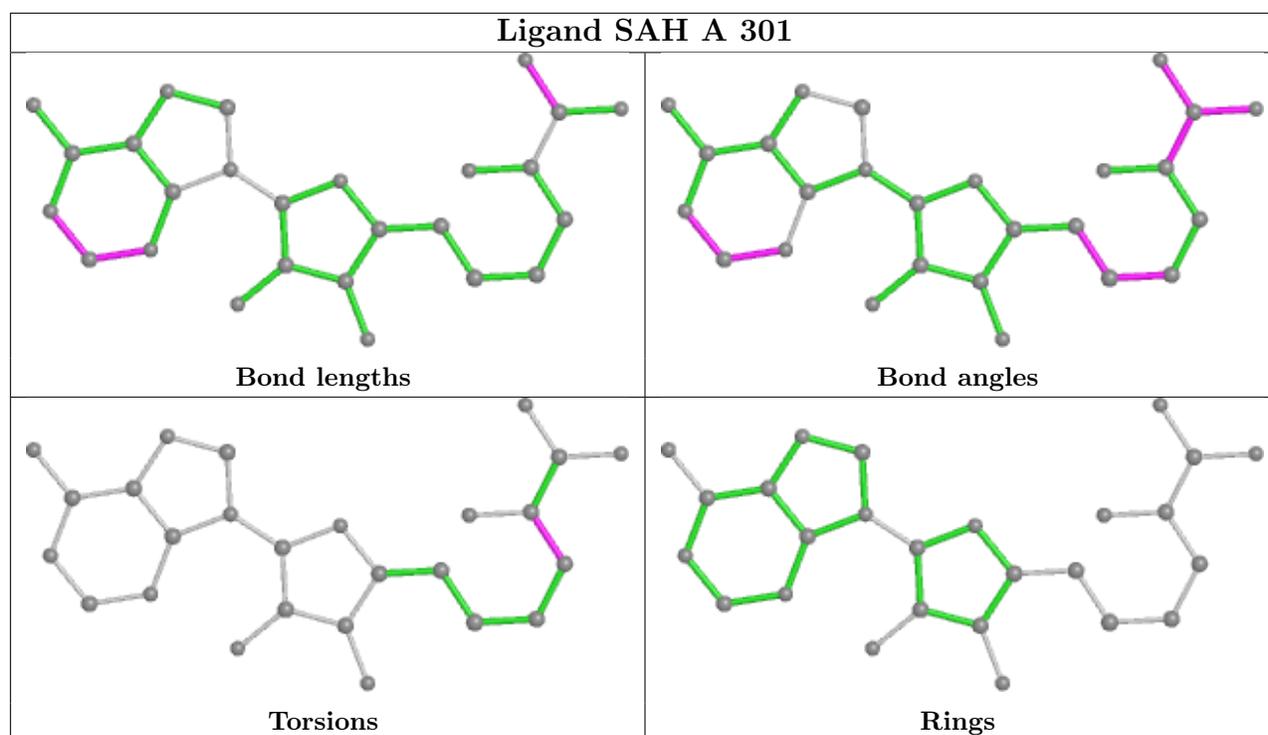
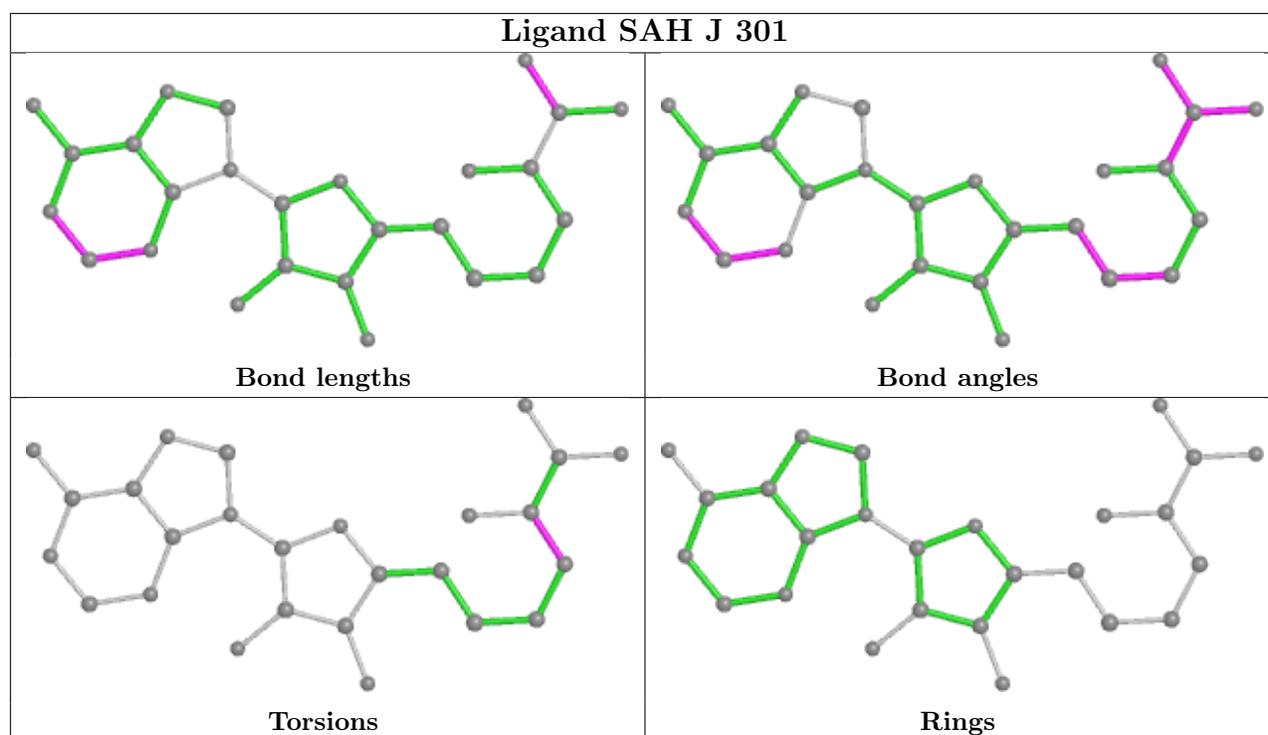
Continued from previous page...

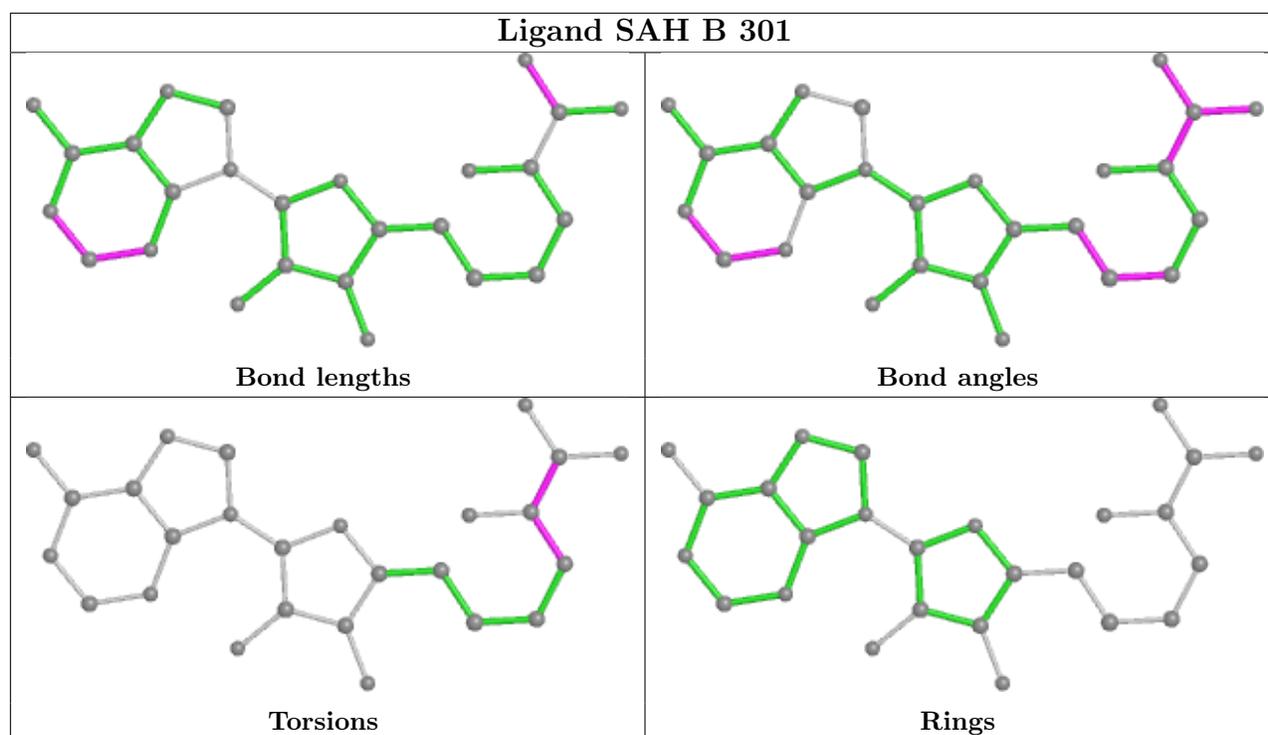
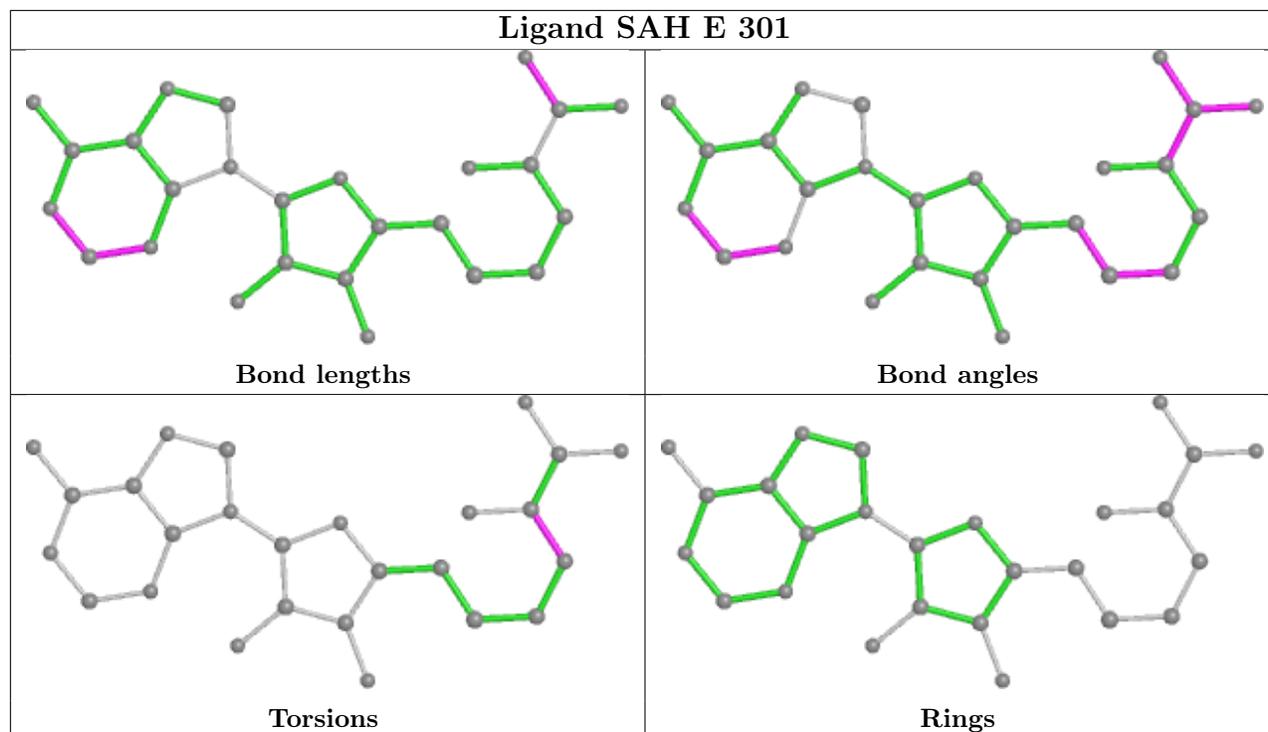
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	301	SAH	1	0
2	D	301	SAH	3	0
2	K	301	SAH	3	0
2	M	301	SAH	1	0
2	N	301	SAH	4	0
2	R	301	SAH	1	0

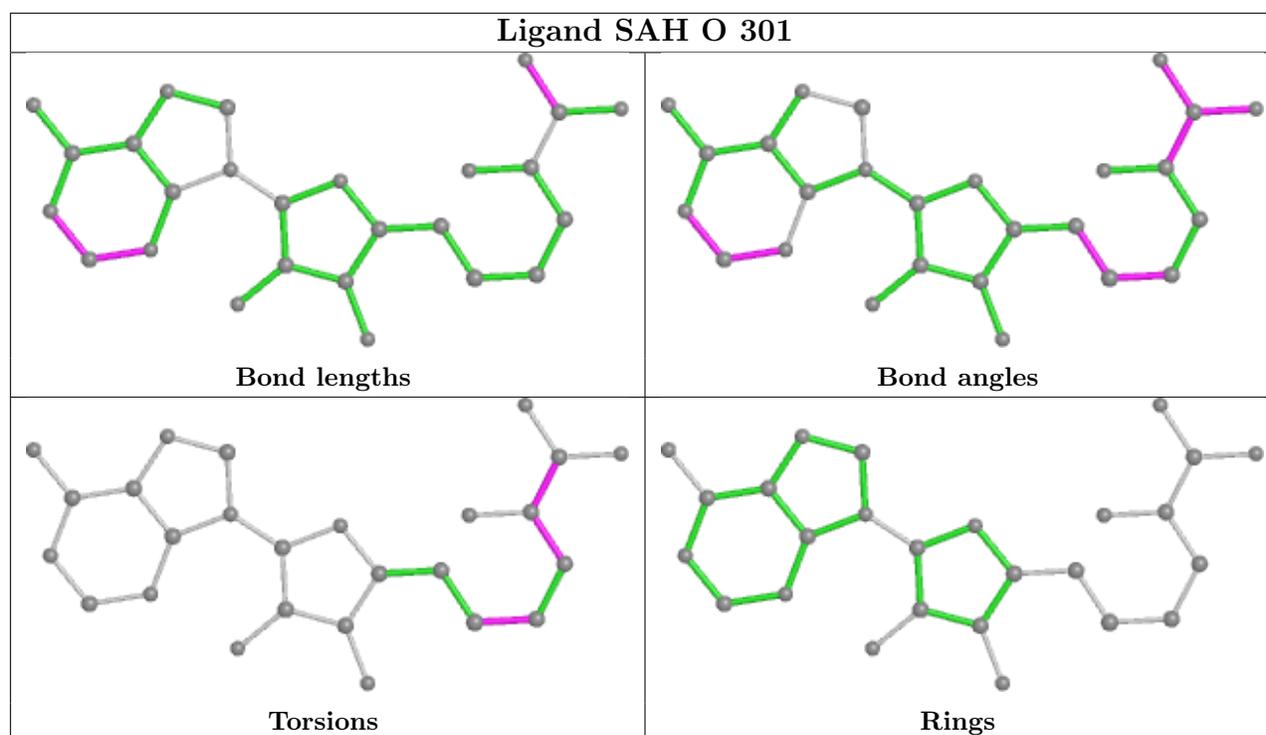
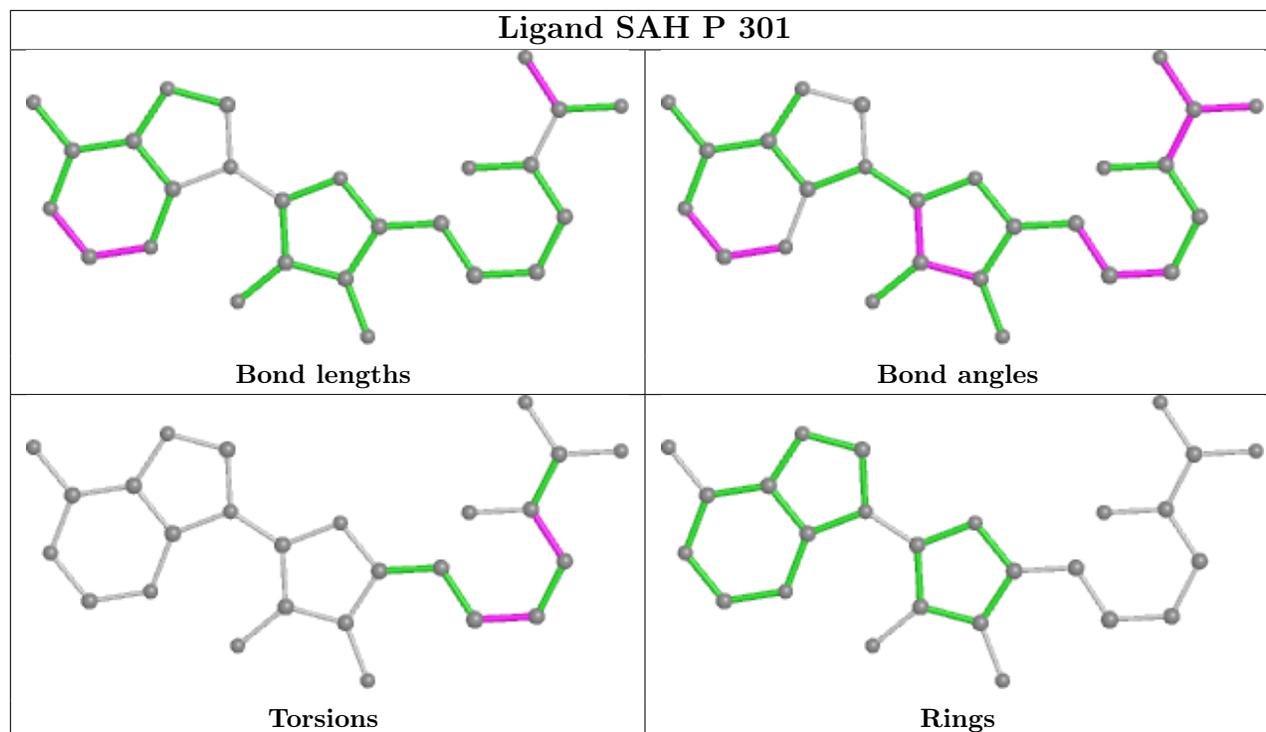
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.

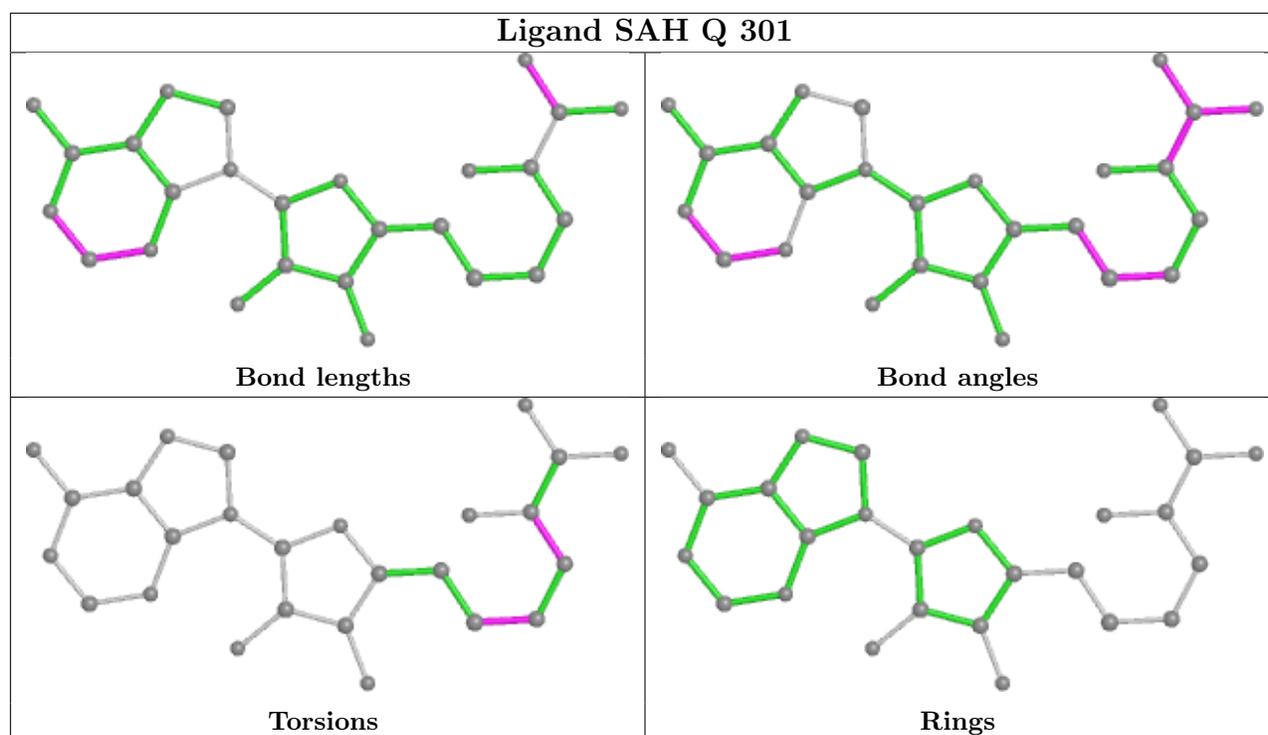
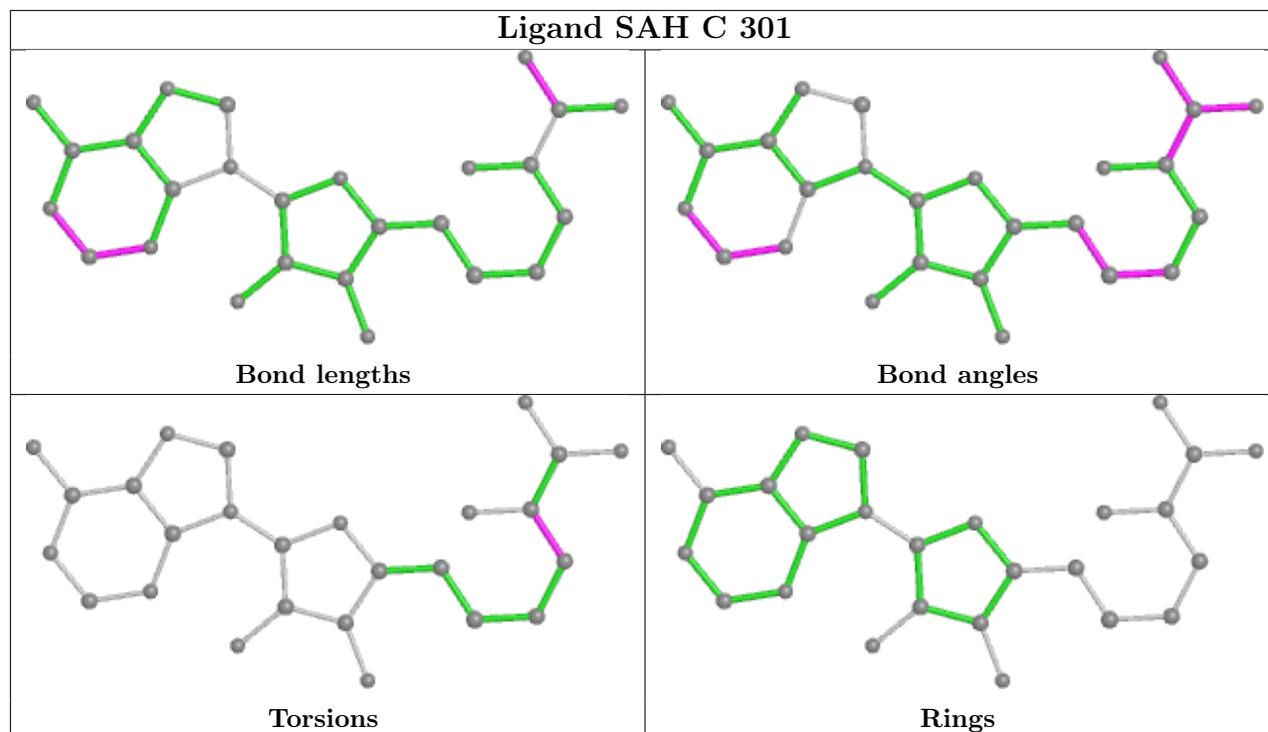


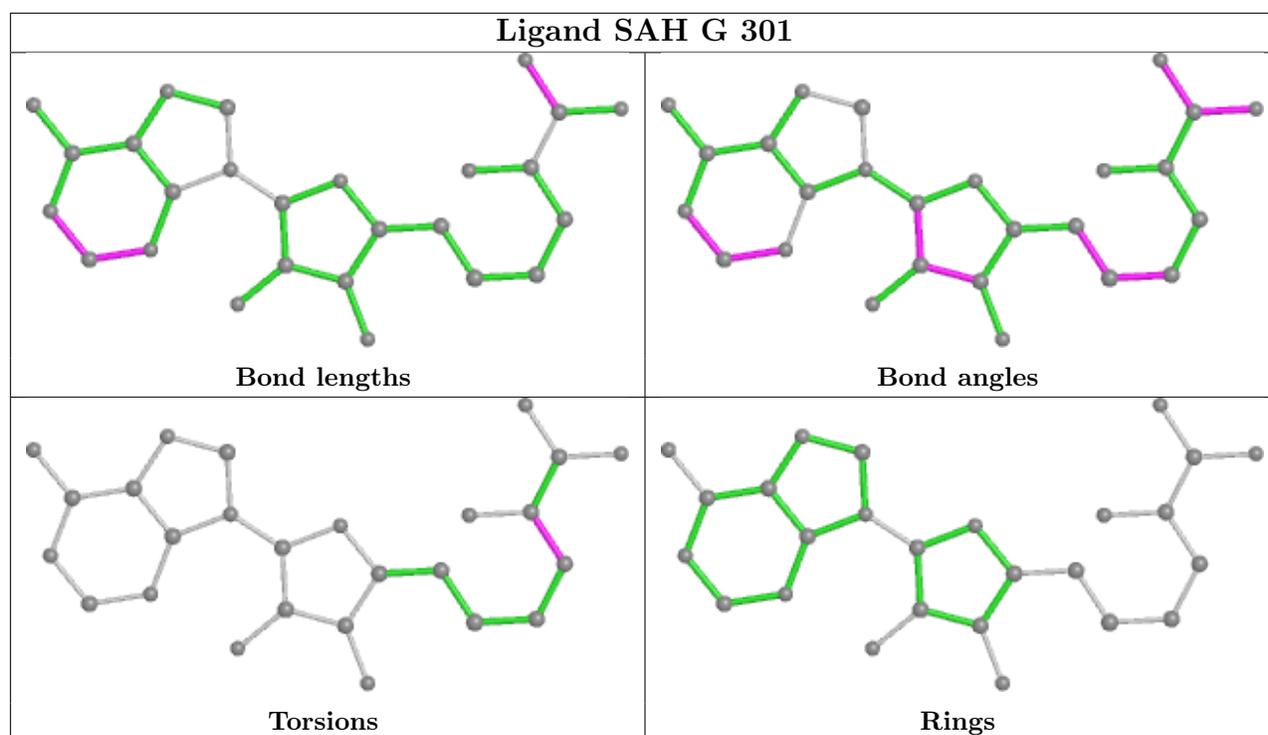
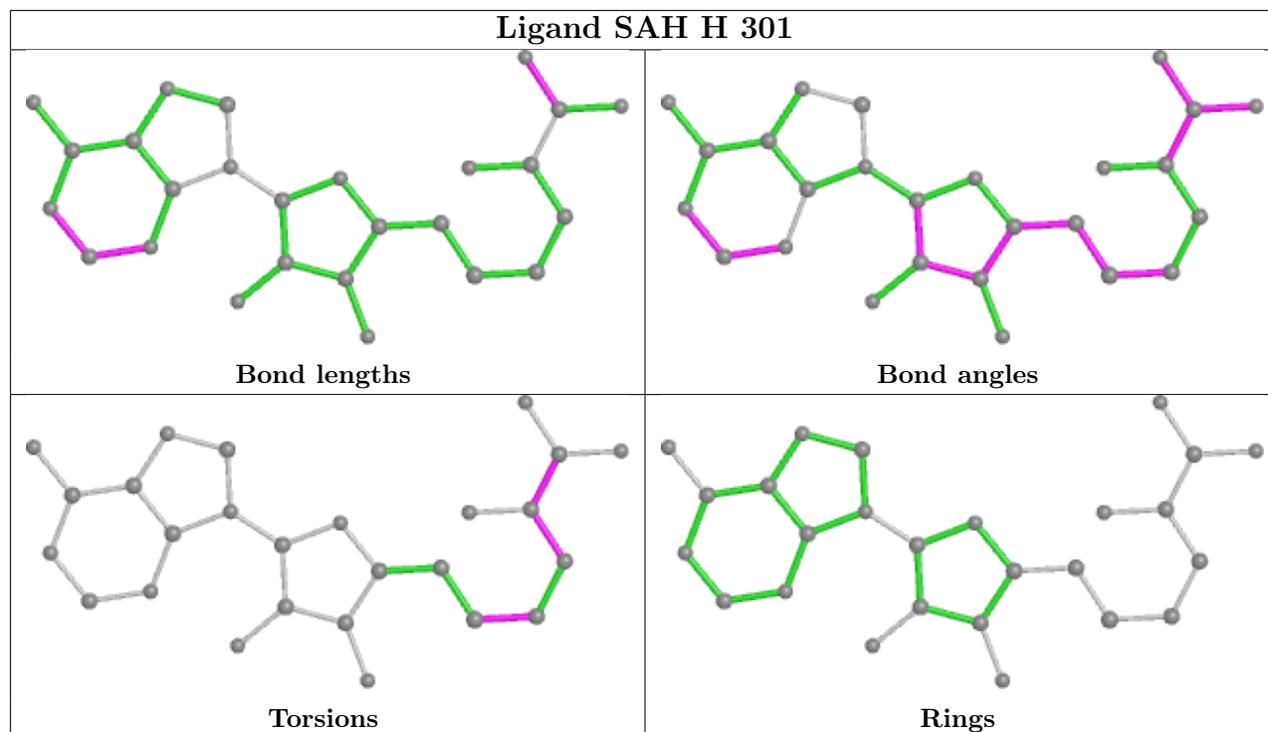


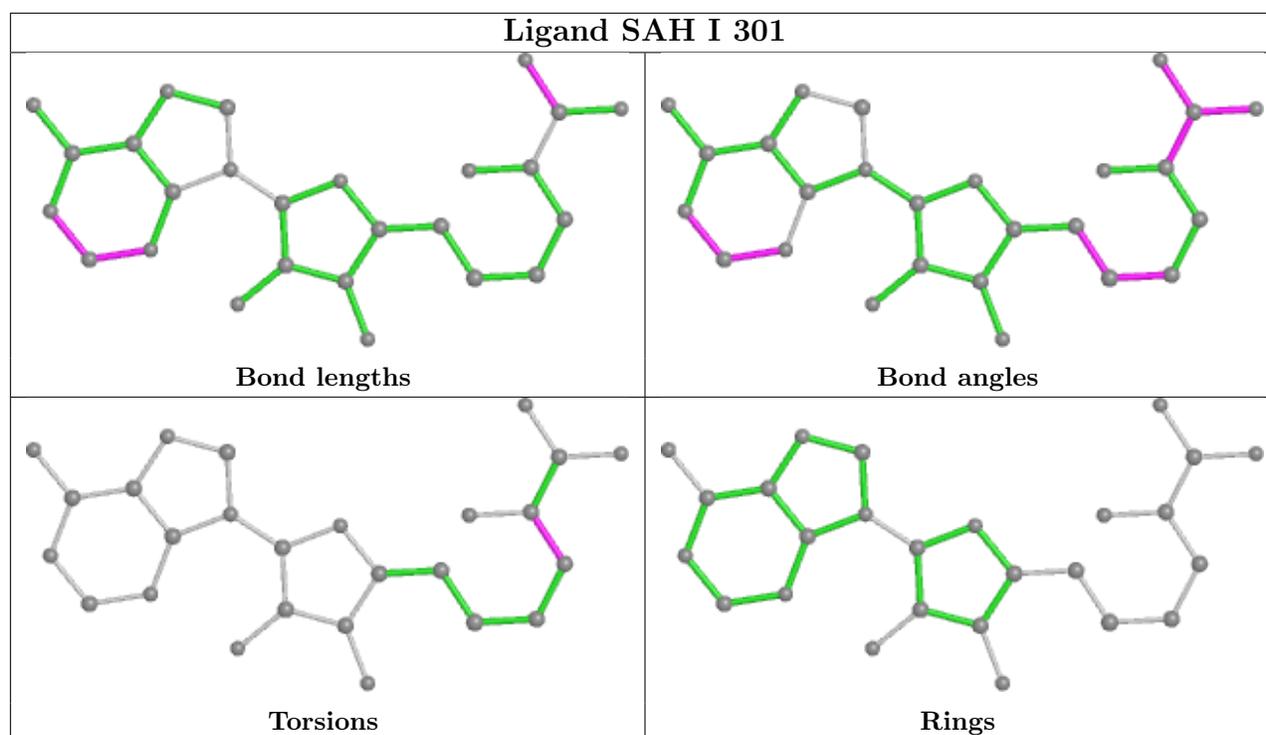
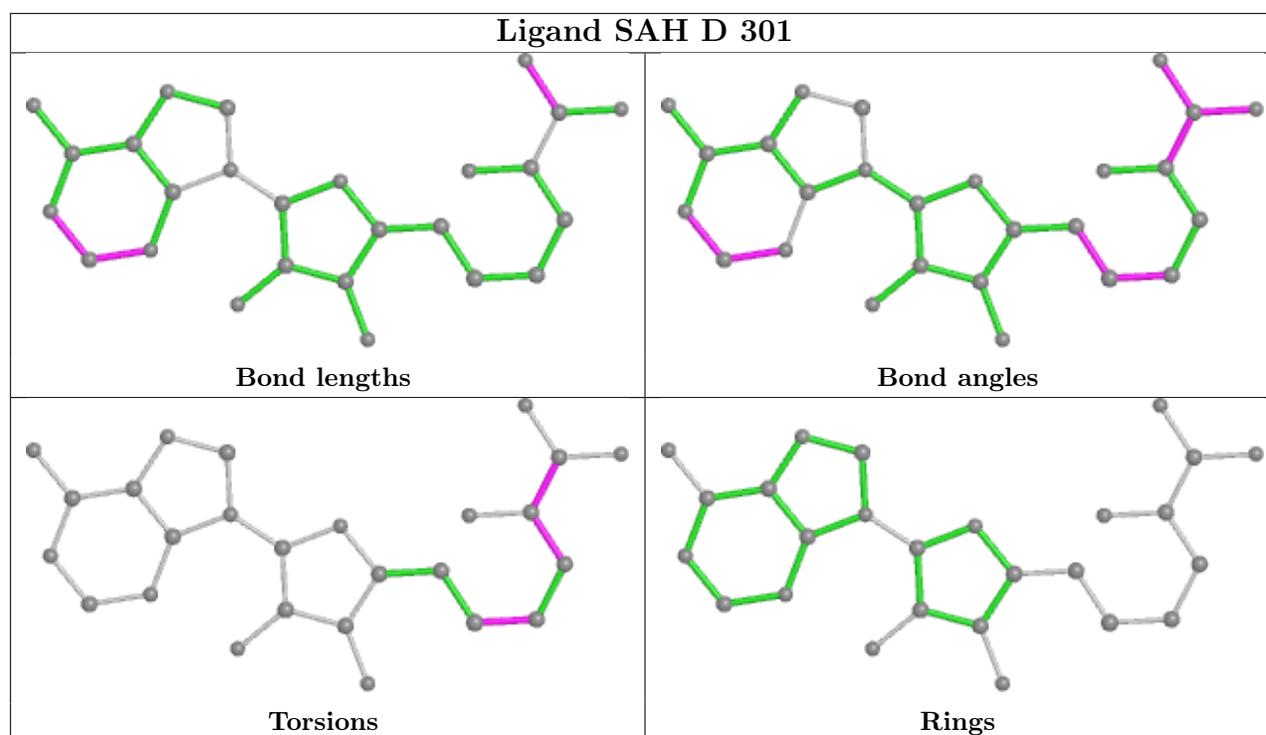


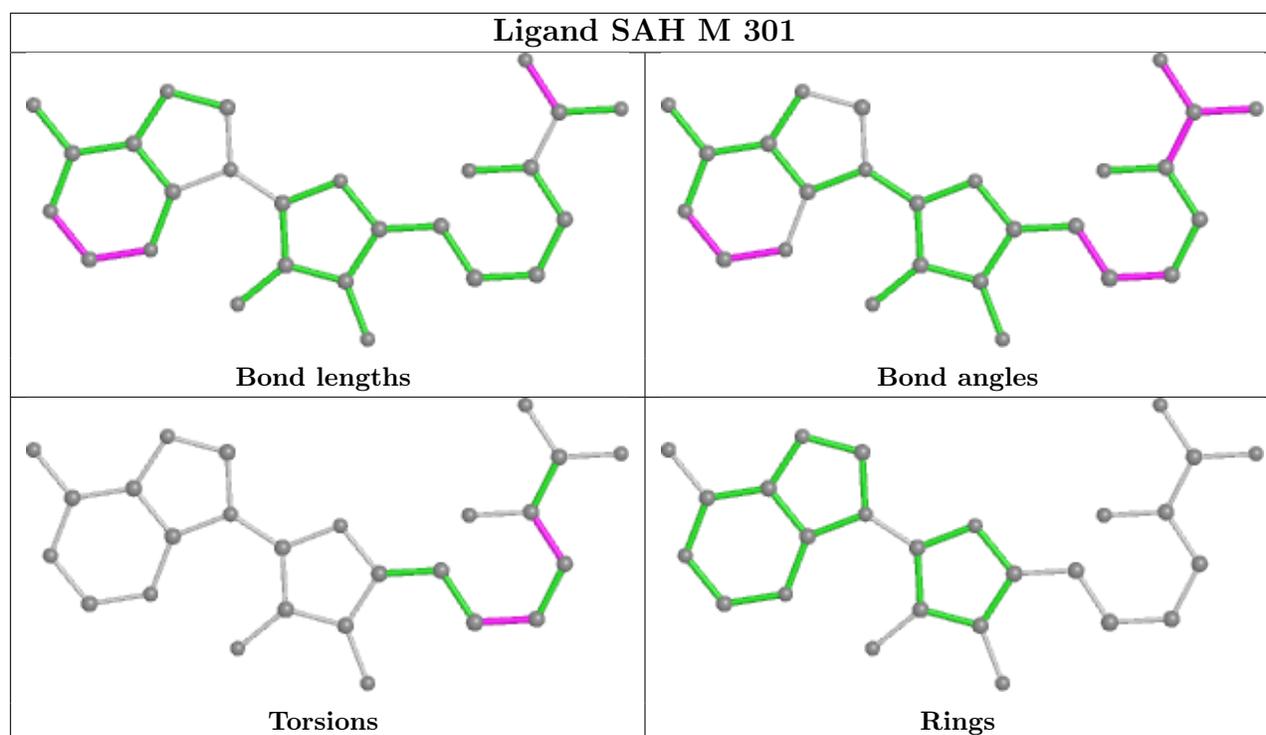
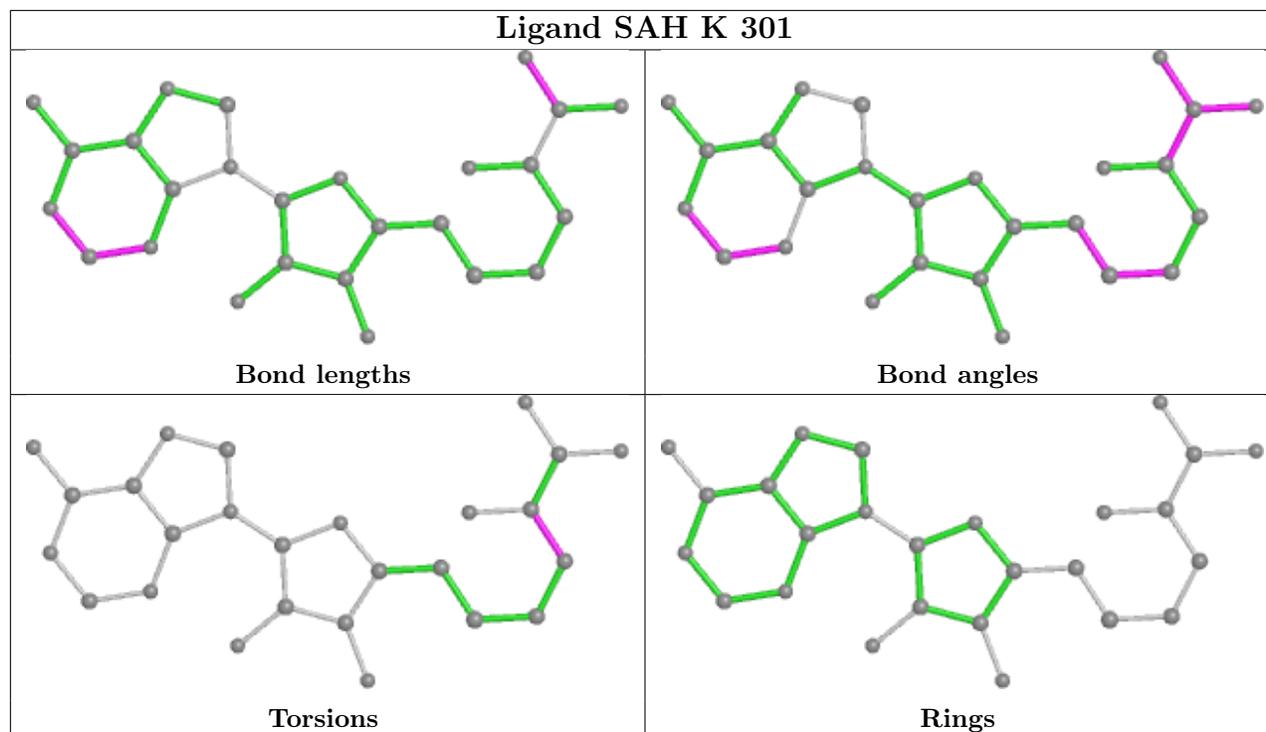


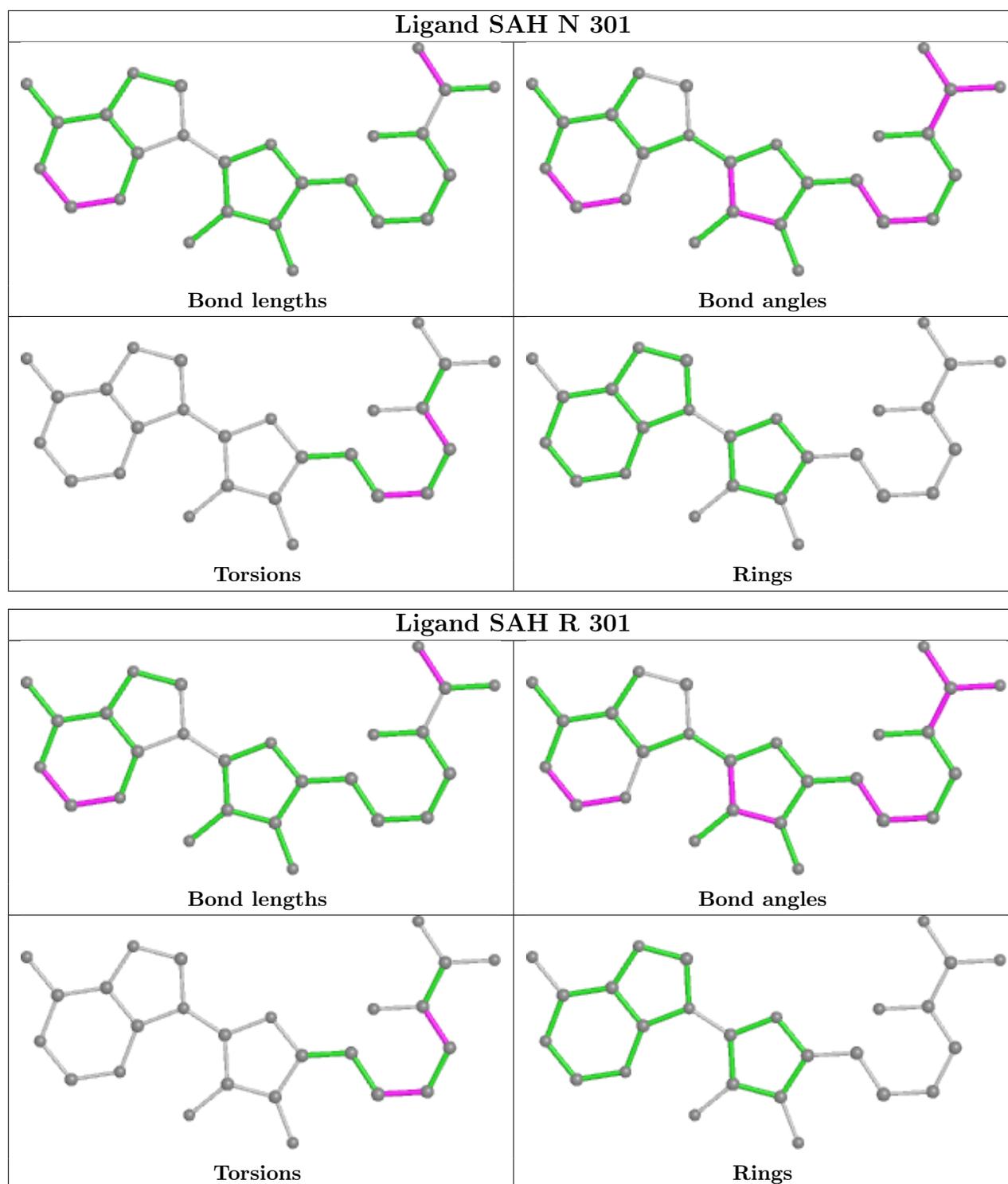












5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

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	281/297 (94%)	0.16	1 (0%) 92 93	29, 46, 71, 105	0
1	B	280/297 (94%)	0.15	0 100 100	32, 49, 77, 95	0
1	C	280/297 (94%)	0.32	4 (1%) 75 77	38, 61, 87, 101	0
1	D	280/297 (94%)	0.19	3 (1%) 80 82	40, 60, 86, 101	0
1	E	279/297 (93%)	0.19	3 (1%) 80 82	30, 56, 77, 94	0
1	F	280/297 (94%)	0.19	2 (0%) 87 89	28, 49, 75, 102	0
1	G	280/297 (94%)	0.77	26 (9%) 8 8	53, 85, 122, 138	0
1	H	279/297 (93%)	1.05	47 (16%) 1 1	64, 99, 123, 137	0
1	I	280/297 (94%)	0.18	5 (1%) 68 71	25, 47, 96, 132	1 (0%)
1	J	281/297 (94%)	0.54	17 (6%) 21 22	35, 85, 113, 133	0
1	K	281/297 (94%)	0.54	13 (4%) 32 34	46, 76, 117, 127	0
1	L	280/297 (94%)	0.70	24 (8%) 10 10	51, 88, 120, 147	0
1	M	281/297 (94%)	0.58	24 (8%) 10 10	40, 63, 141, 169	0
1	N	281/297 (94%)	1.42	76 (27%) 0 0	50, 107, 137, 152	0
1	O	280/297 (94%)	0.46	13 (4%) 32 34	36, 70, 100, 124	0
1	P	280/297 (94%)	0.48	17 (6%) 21 22	42, 78, 105, 116	0
1	Q	281/297 (94%)	1.11	53 (18%) 1 1	36, 77, 159, 191	0
1	R	281/297 (94%)	2.11	119 (42%) 0 0	73, 115, 149, 173	0
All	All	5045/5346 (94%)	0.62	447 (8%) 9 9	25, 70, 124, 191	1 (0%)

The worst 5 of 447 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Q	11	GLN	19.2
1	M	9	GLN	11.9
1	R	250	PHE	8.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	M	17	VAL	8.5
1	R	243	VAL	8.3

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.

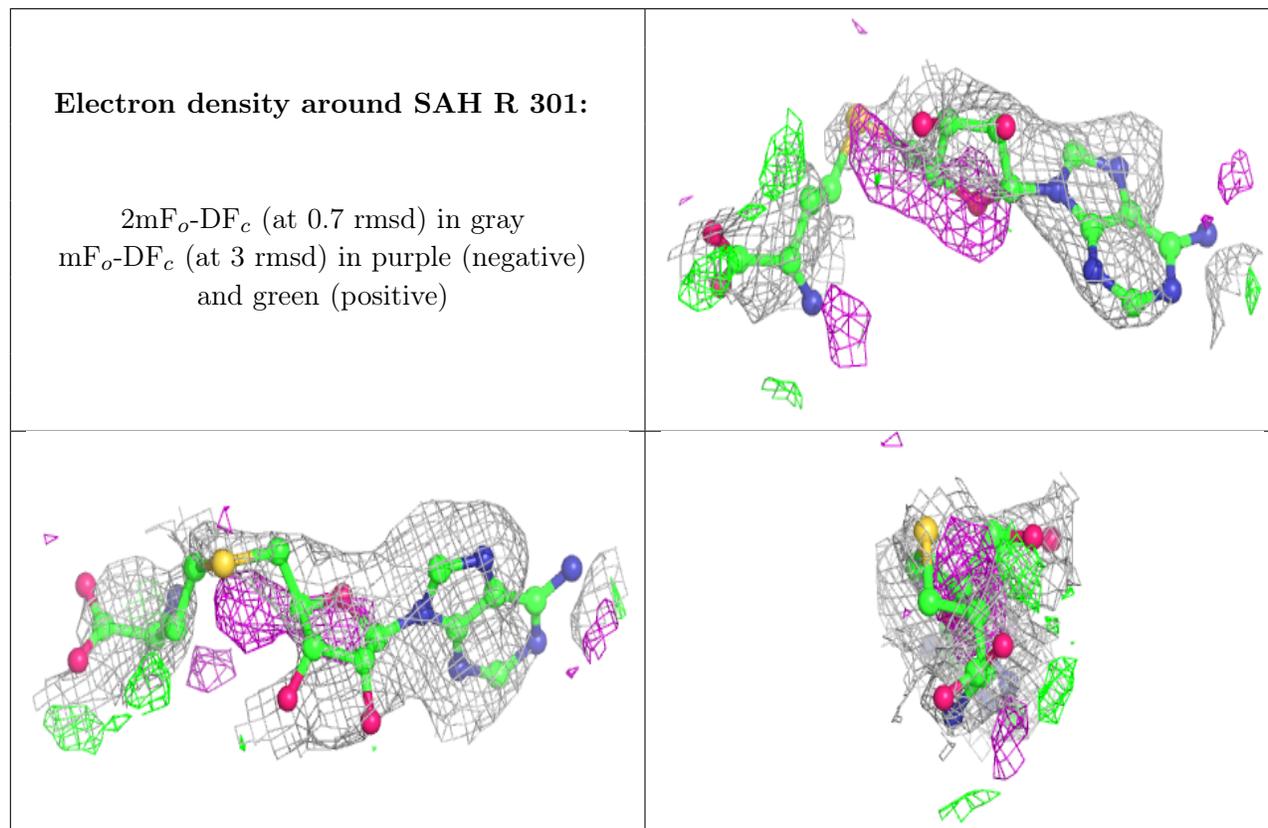
6.4 Ligands [i](#)

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
2	SAH	R	301	26/26	0.54	0.42	118,121,122,123	0
2	SAH	N	301	26/26	0.69	0.29	105,107,108,108	0
2	SAH	B	302	26/26	0.71	0.25	105,107,108,108	0
2	SAH	H	301	26/26	0.78	0.29	98,102,105,106	0
2	SAH	J	301	26/26	0.86	0.22	88,89,91,91	0
2	SAH	P	301	26/26	0.88	0.22	72,74,75,75	0
2	SAH	K	301	26/26	0.88	0.20	75,79,80,81	0
2	SAH	L	301	26/26	0.91	0.26	85,87,89,89	0
2	SAH	O	301	26/26	0.91	0.21	80,82,83,83	0
2	SAH	G	301	26/26	0.93	0.19	74,75,77,77	0
2	SAH	C	301	26/26	0.94	0.19	61,63,64,64	0
2	SAH	Q	301	26/26	0.94	0.18	61,62,64,65	0
2	SAH	B	301	26/26	0.94	0.20	49,51,52,53	0
2	SAH	D	301	26/26	0.95	0.15	57,58,59,59	0
2	SAH	M	301	26/26	0.96	0.18	57,61,62,62	0
2	SAH	E	301	26/26	0.97	0.18	48,49,50,50	0
2	SAH	A	301	26/26	0.98	0.15	36,38,39,39	0
2	SAH	F	301	26/26	0.98	0.17	34,35,36,37	0
2	SAH	I	301	26/26	0.98	0.15	34,36,37,38	0

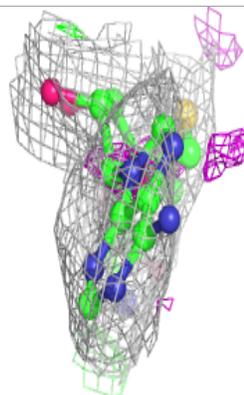
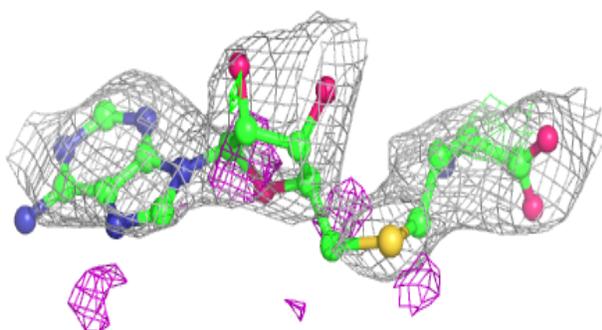
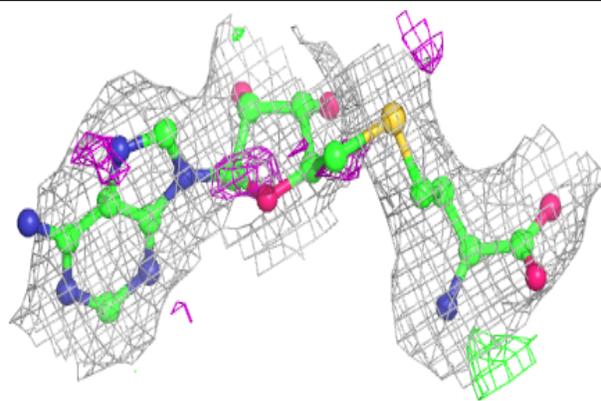
The following is a graphical depiction of the model fit to experimental electron density of all

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.

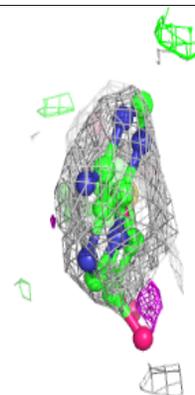
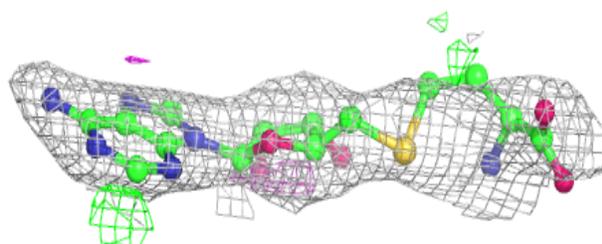
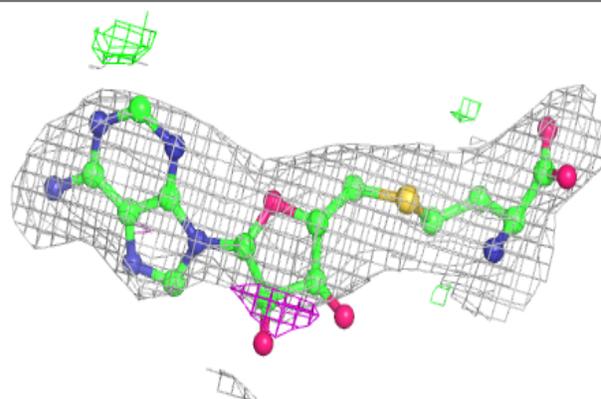


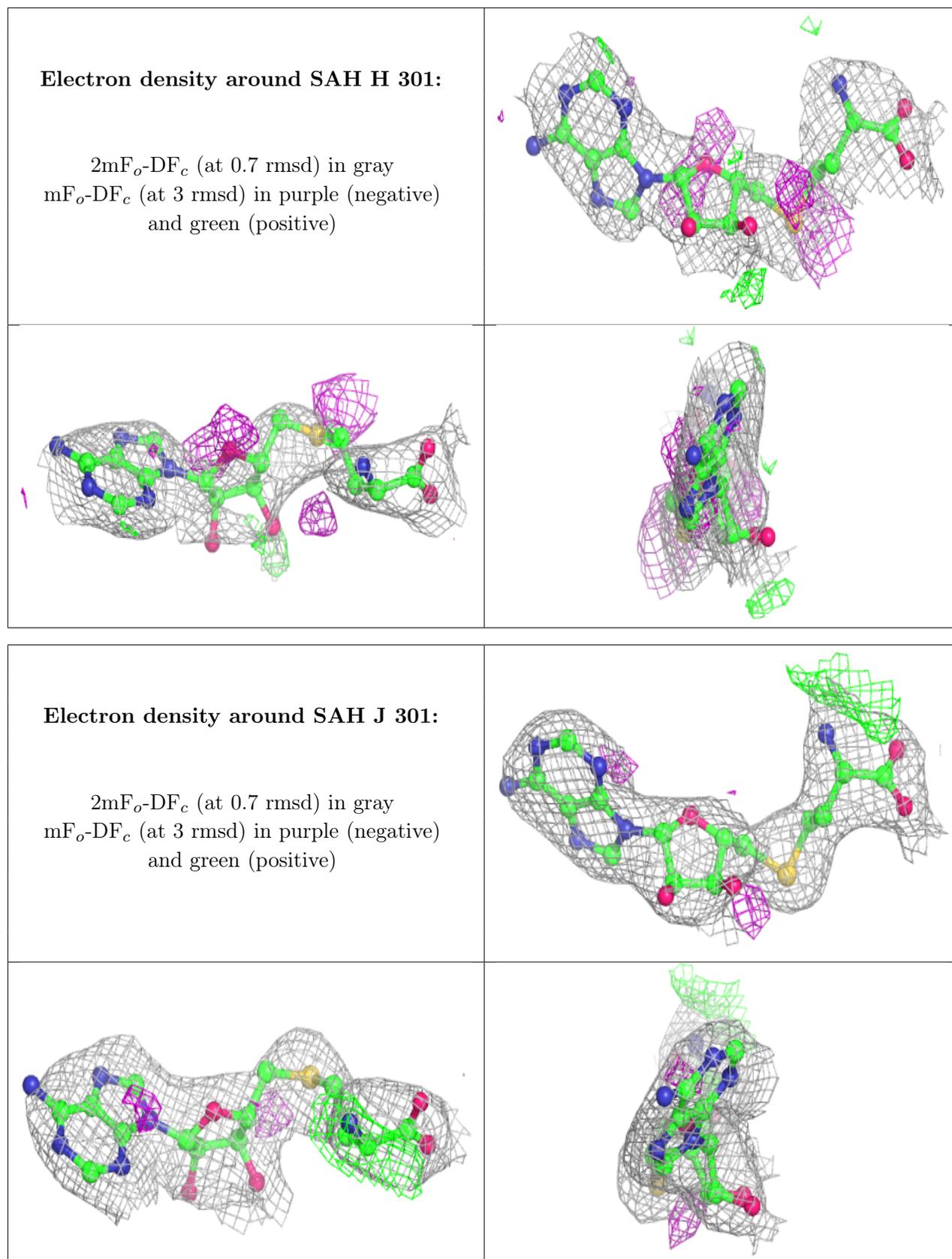
Electron density around SAH N 301:

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

**Electron density around SAH B 302:**

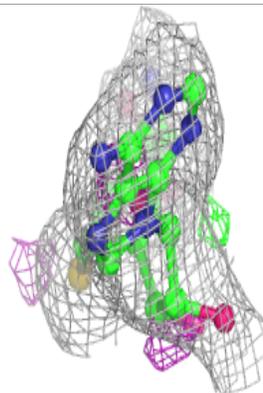
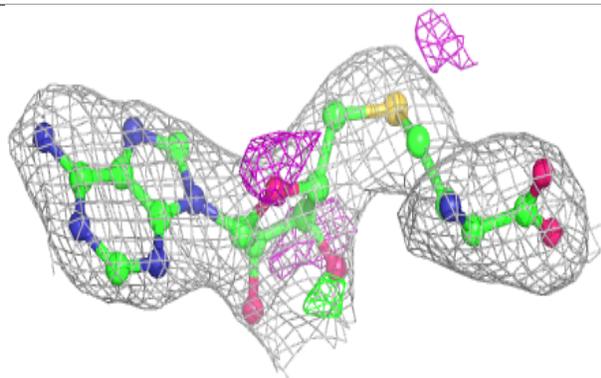
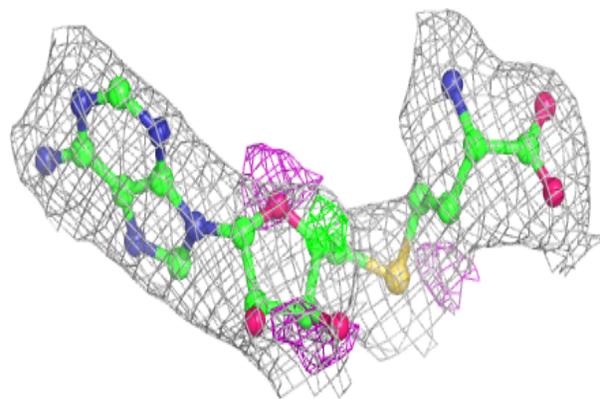
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



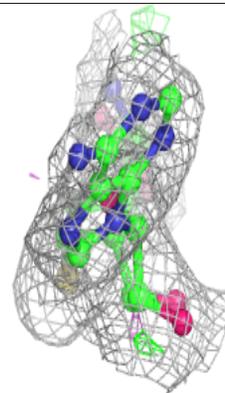
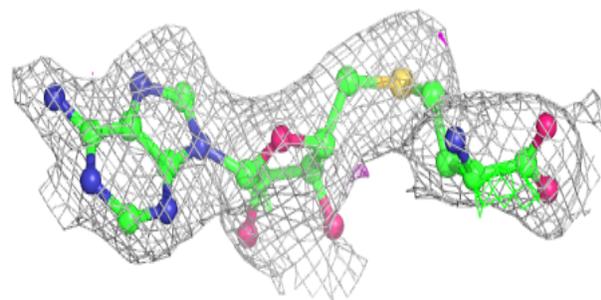
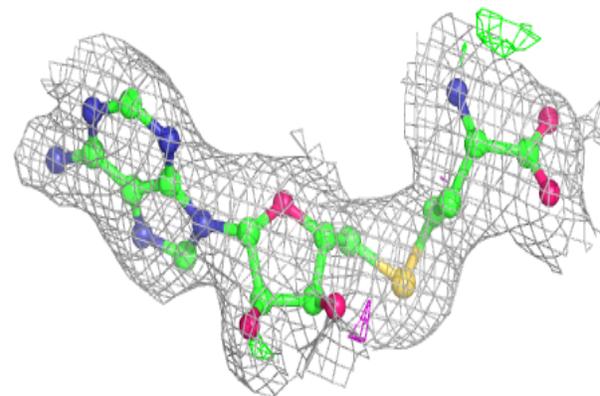


Electron density around SAH P 301:

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

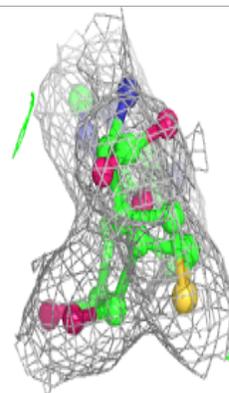
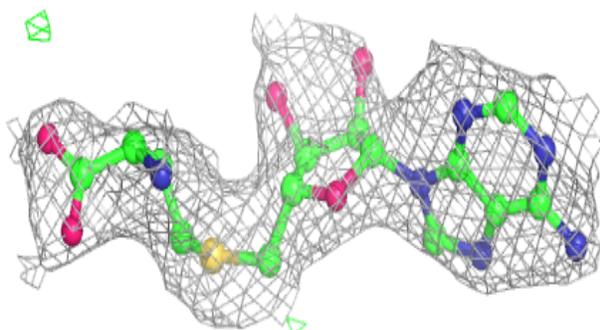
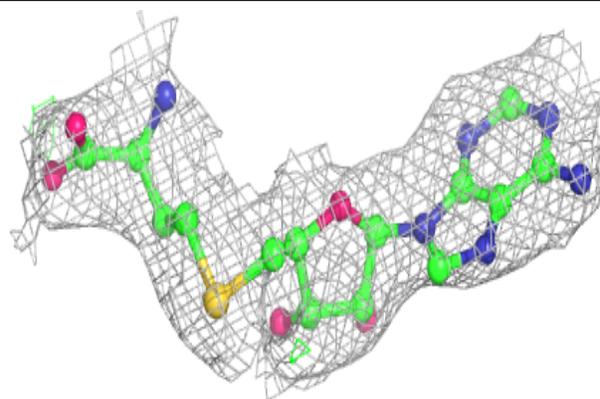
**Electron density around SAH K 301:**

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

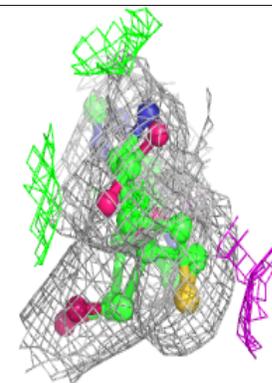
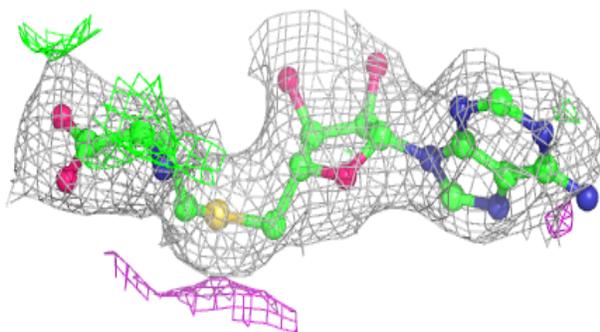
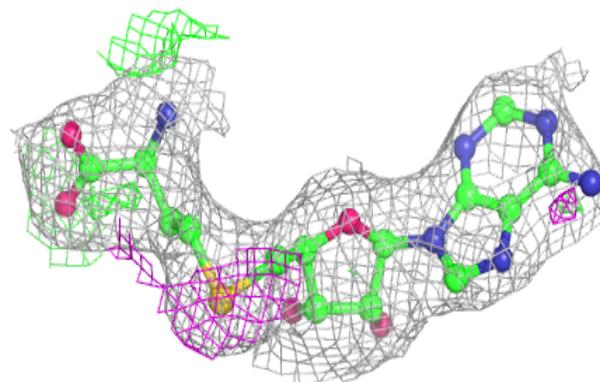


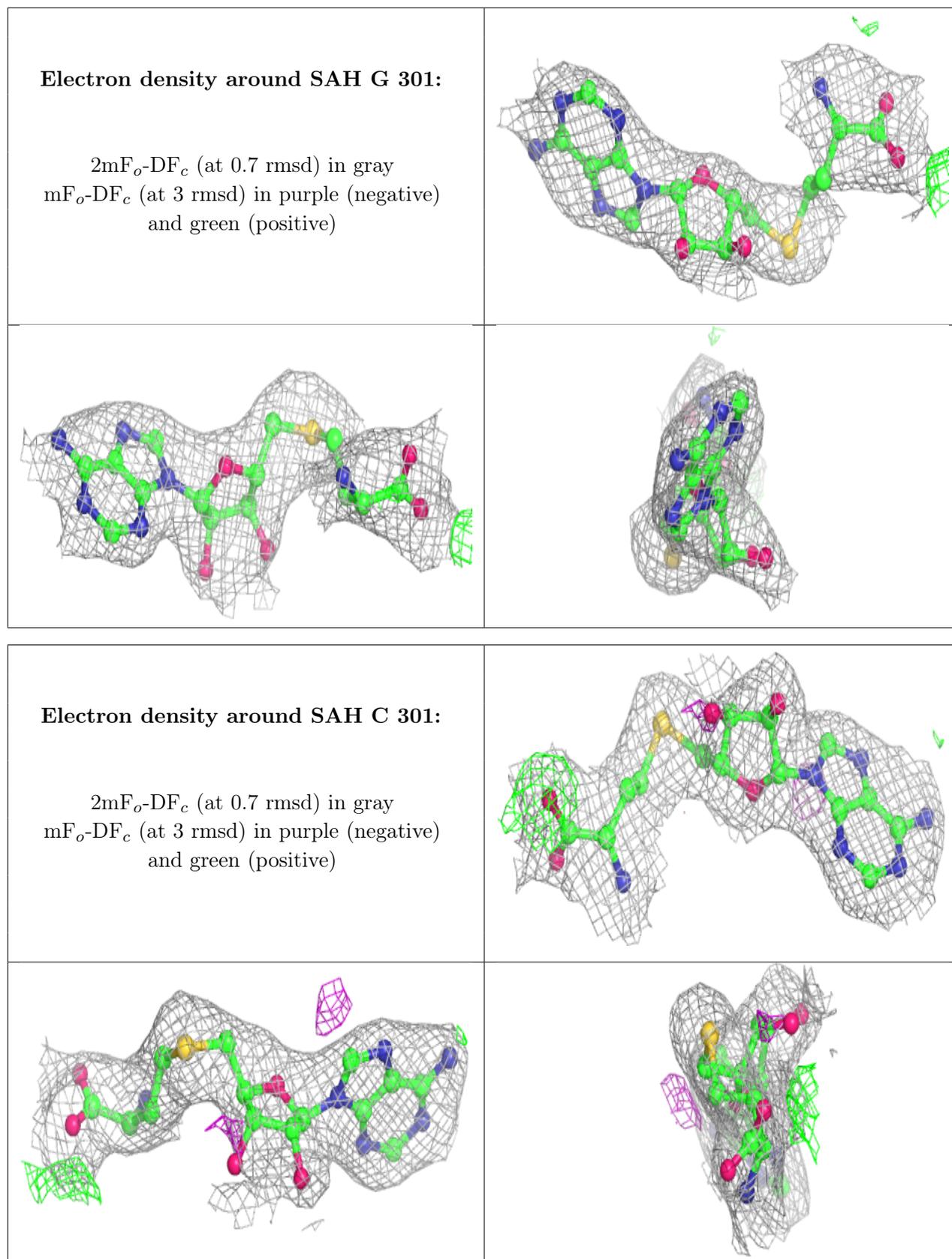
Electron density around SAH L 301:

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

**Electron density around SAH O 301:**

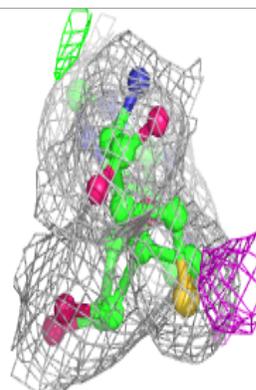
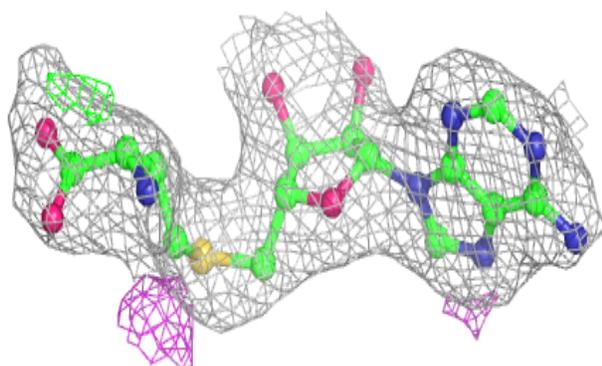
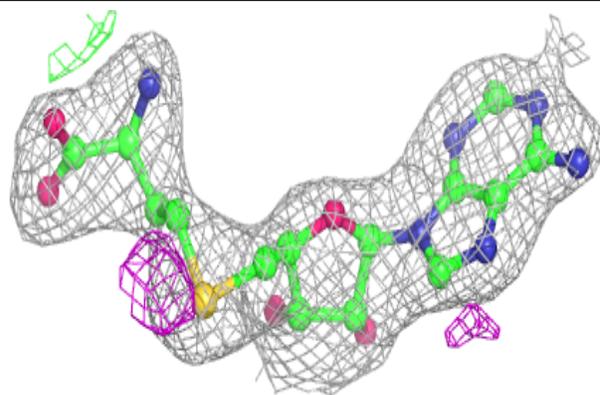
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



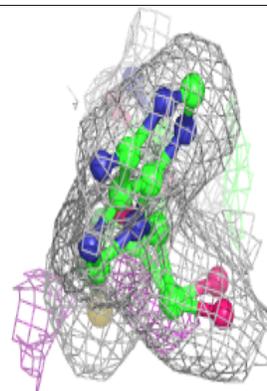
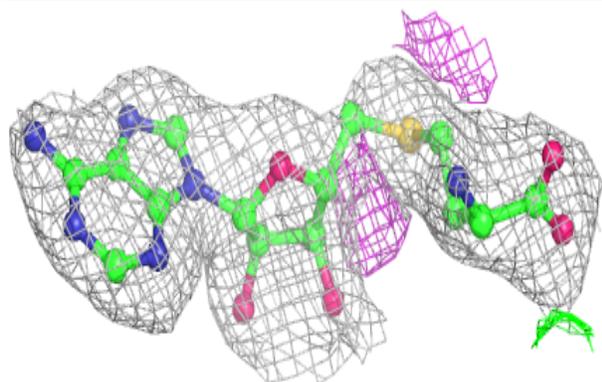
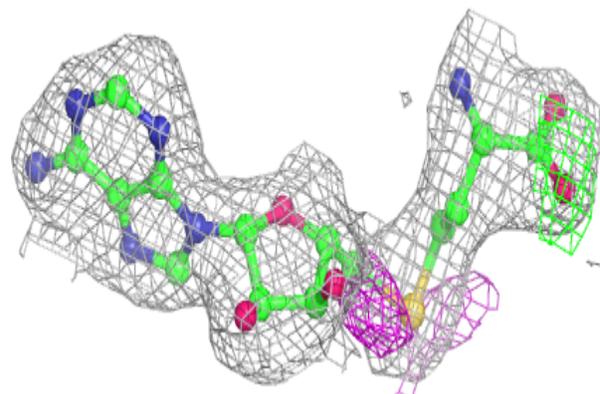


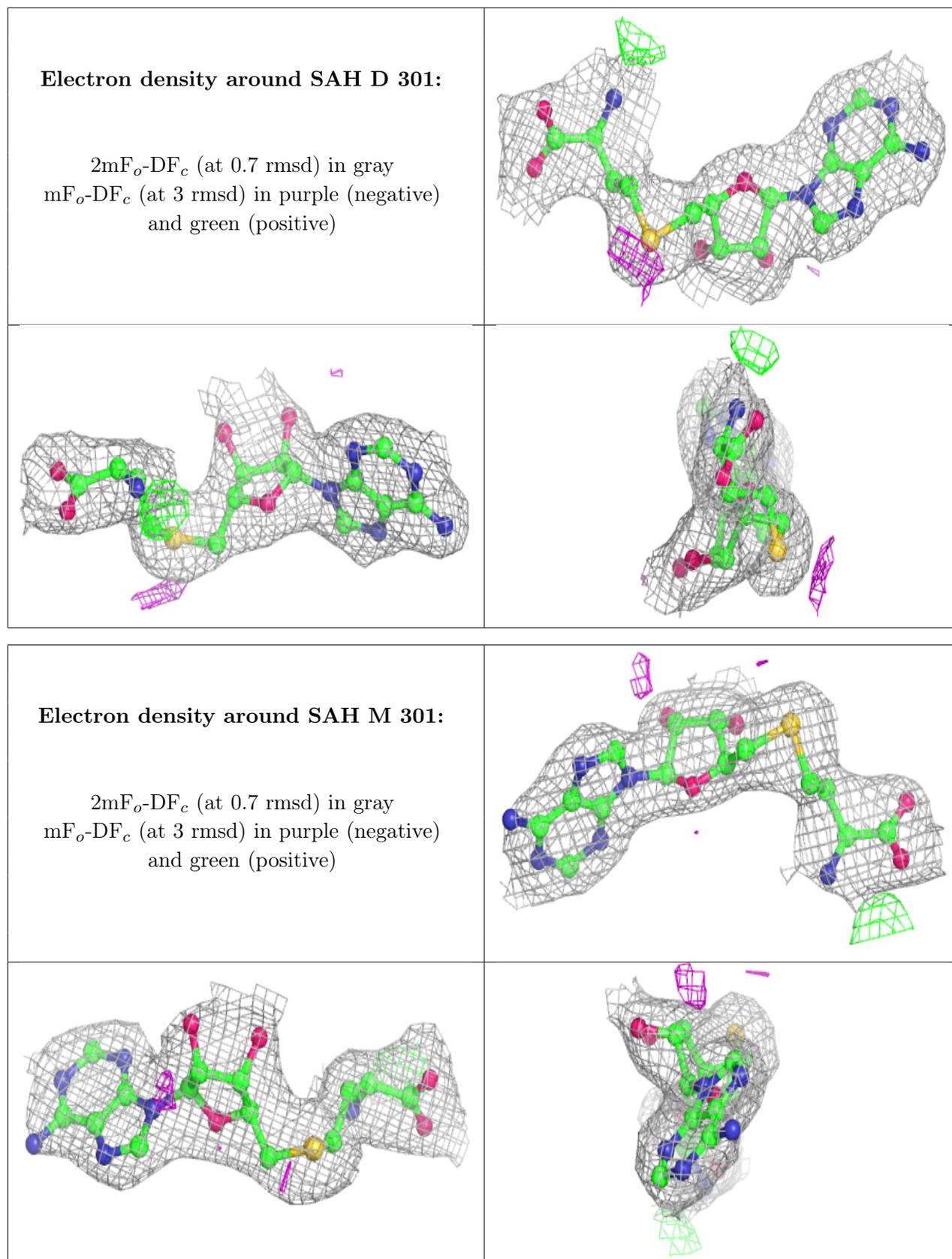
Electron density around SAH Q 301:

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

**Electron density around SAH B 301:**

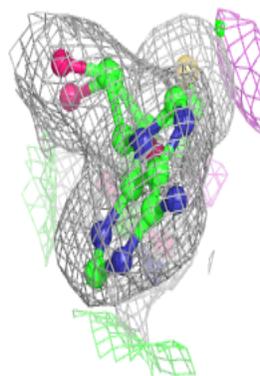
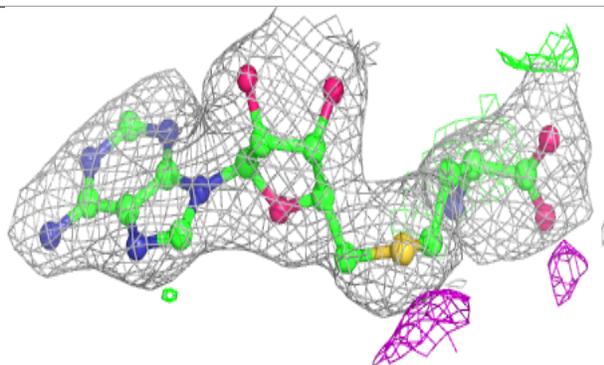
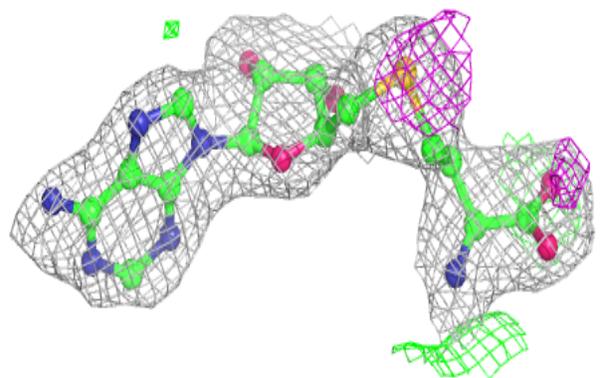
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



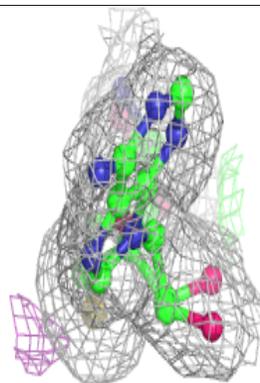
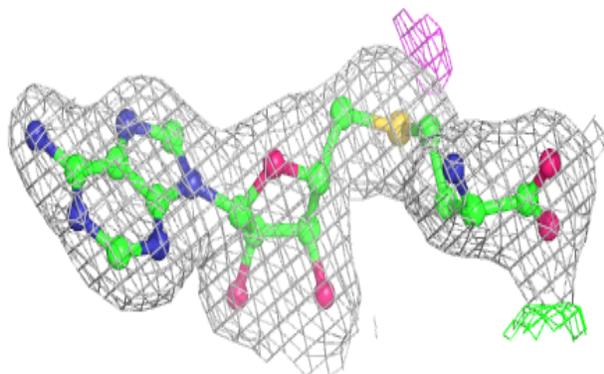
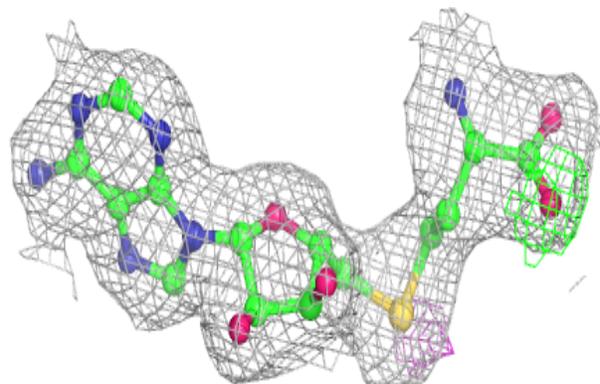


Electron density around SAH E 301:

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

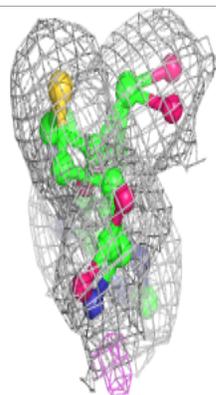
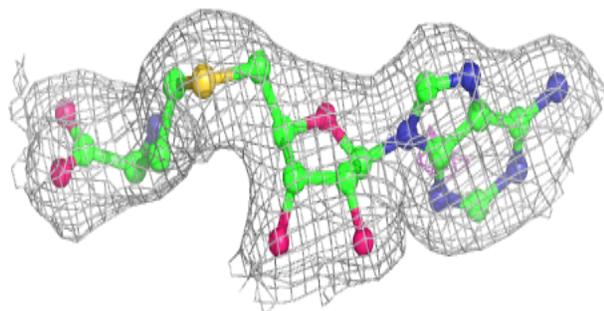
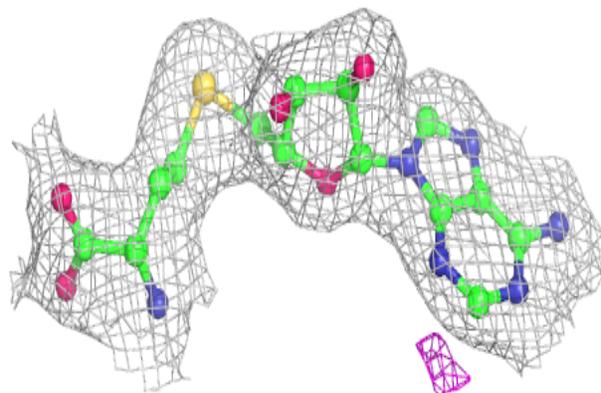
**Electron density around SAH A 301:**

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

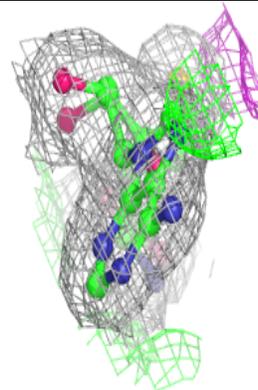
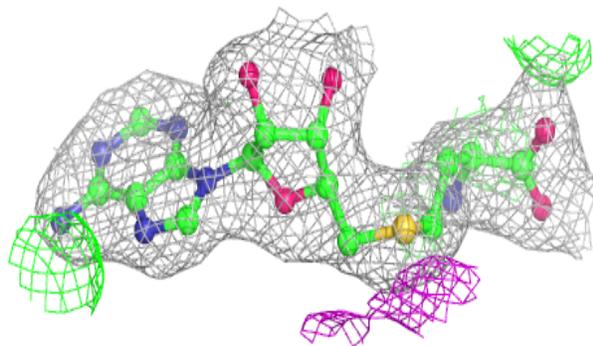
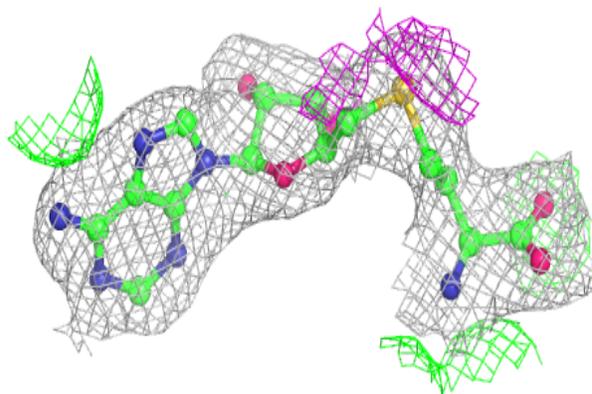


Electron density around SAH F 301:

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

**Electron density around SAH I 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

There are no such residues in this entry.