



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 24, 2024 – 12:38 PM EDT

PDB ID : 6XVG  
Title : Human Sirt6 3-318 in complex with ADP-ribose and the activator MDL-801  
Authors : You, W.; Steegborn, C.  
Deposited on : 2020-01-22  
Resolution : 2.10 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 1.20.1  
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

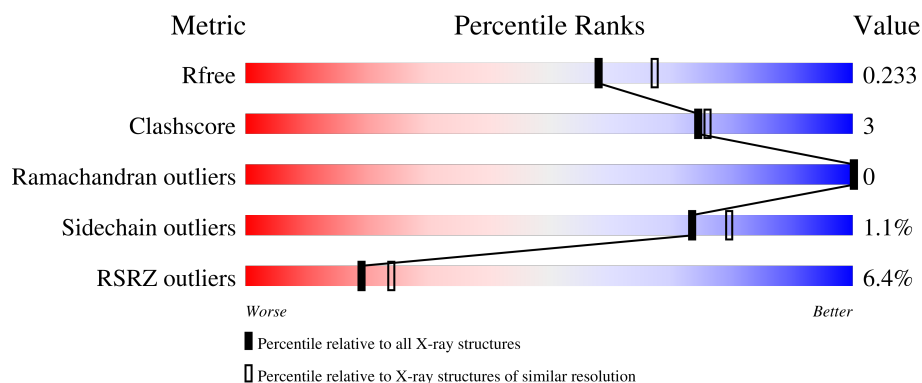
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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  $\geq 3$ , 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	316	<div> <div>5%</div> <div> <div></div> <div>81%</div> <div>6%</div> <div>12%</div> </div> </div>
1	B	316	<div> <div>5%</div> <div> <div></div> <div>81%</div> <div>9%</div> <div>10%</div> </div> </div>
1	C	316	<div> <div>6%</div> <div> <div></div> <div>80%</div> <div>8%</div> <div>12%</div> </div> </div>
1	D	316	<div> <div>3%</div> <div> <div></div> <div>82%</div> <div>5%</div> <div>12%</div> </div> </div>
1	E	316	<div> <div>5%</div> <div> <div></div> <div>82%</div> <div>6%</div> <div>12%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	316	

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
6	SO4	B	409	-	-	X	-

## 2 Entry composition [i](#)

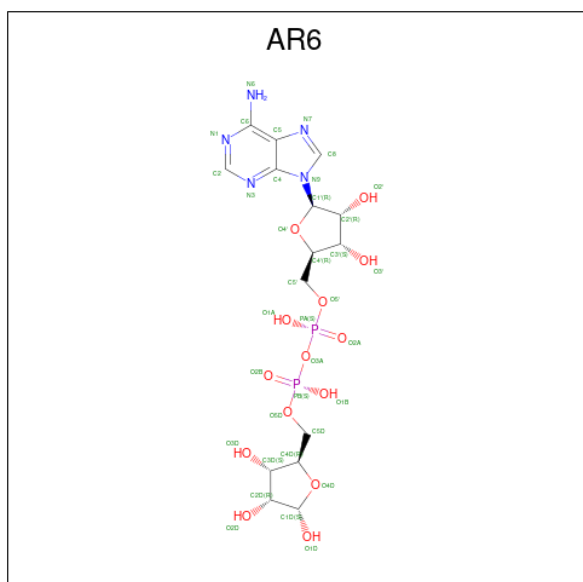
There are 7 unique types of molecules in this entry. The entry contains 13647 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 NAD-dependent protein deacetylase sirtuin-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	278	Total	C	N	O	S	0	0	0
			2152	1354	393	394	11			
1	B	284	Total	C	N	O	S	0	0	0
			2199	1383	403	402	11			
1	C	279	Total	C	N	O	S	0	0	0
			2151	1353	390	397	11			
1	D	277	Total	C	N	O	S	0	0	0
			2140	1346	390	393	11			
1	E	279	Total	C	N	O	S	0	0	0
			2149	1353	388	397	11			
1	F	278	Total	C	N	O	S	0	0	0
			2148	1349	390	398	11			

- Molecule 2 is [(2R,3S,4R,5R)-5-(6-AMINOPURIN-9-YL)-3,4-DIHYDROXY-OXOLAN-2-YL]METHYL [HYDROXY-[(2R,3S,4R,5S)-3,4,5-TRIHYDROXYOXOLAN-2-YL]METHOXY]PHOSPHORYL] HYDROGEN PHOSPHATE (three-letter code: AR6) (formula:  $C_{15}H_{23}N_5O_{14}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	B	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	C	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	D	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	E	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	F	1	Total	C	N	O	P	0	0
			36	15	5	14	2		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

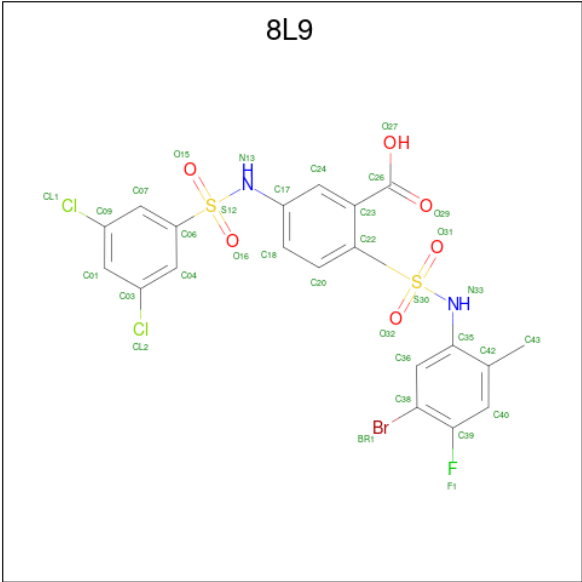
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		
3	B	1	Total	Zn	0	0
			1	1		
3	C	1	Total	Zn	0	0
			1	1		
3	D	1	Total	Zn	0	0
			1	1		
3	E	1	Total	Zn	0	0
			1	1		
3	F	1	Total	Zn	0	0
			1	1		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



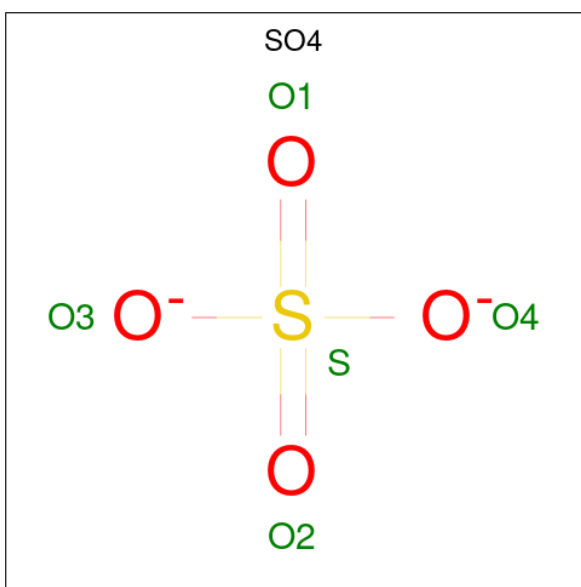
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is 5-[[3,5-bis(chloranyl)phenyl]sulfonylamino]-2-[(5-bromanyl-4-fluoranyl-2-methyl-phenyl)sulfamoyl]benzoic acid (three-letter code: 8L9) (formula: C<sub>20</sub>H<sub>14</sub>BrCl<sub>2</sub>FN<sub>2</sub>O<sub>6</sub>S<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms								ZeroOcc	AltConf
5	A	1	Total	Br	C	Cl	F	N	O	S	0	0
			34	1	20	2	1	2	6	2		
5	B	1	Total	Br	C	Cl	F	N	O	S	0	0
			34	1	20	2	1	2	6	2		
5	C	1	Total	Br	C	Cl	F	N	O	S	0	0
			34	1	20	2	1	2	6	2		
5	D	1	Total	Br	C	Cl	F	N	O	S	0	0
			34	1	20	2	1	2	6	2		
5	E	1	Total	Br	C	Cl	F	N	O	S	0	0
			34	1	20	2	1	2	6	2		
5	F	1	Total	Br	C	Cl	F	N	O	S	0	0
			34	1	20	2	1	2	6	2		

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	C	1	Total	O	S	0	0
			5	4	1		
6	D	1	Total	O	S	0	0
			5	4	1		
6	D	1	Total	O	S	0	0
			5	4	1		
6	D	1	Total	O	S	0	0
			5	4	1		
6	E	1	Total	O	S	0	0
			5	4	1		
6	E	1	Total	O	S	0	0
			5	4	1		
6	E	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is water.

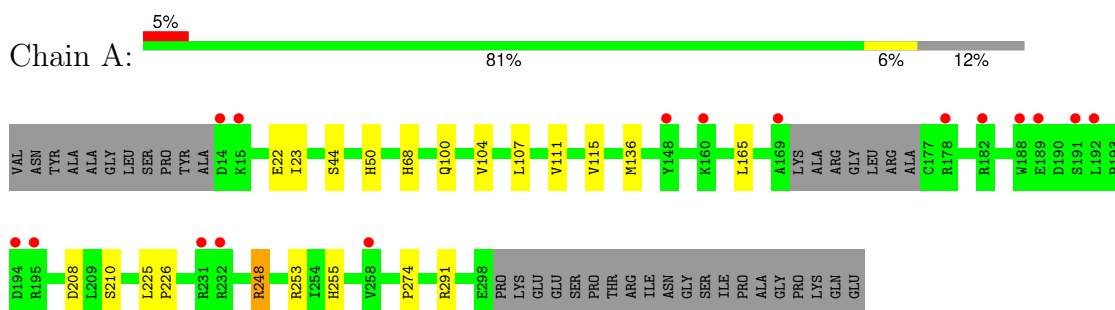


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	29	Total 29	O 29	0	0
7	B	32	Total 32	O 32	0	0
7	C	40	Total 40	O 40	0	0
7	D	29	Total 29	O 29	0	0
7	E	25	Total 25	O 25	0	0
7	F	14	Total 14	O 14	0	0

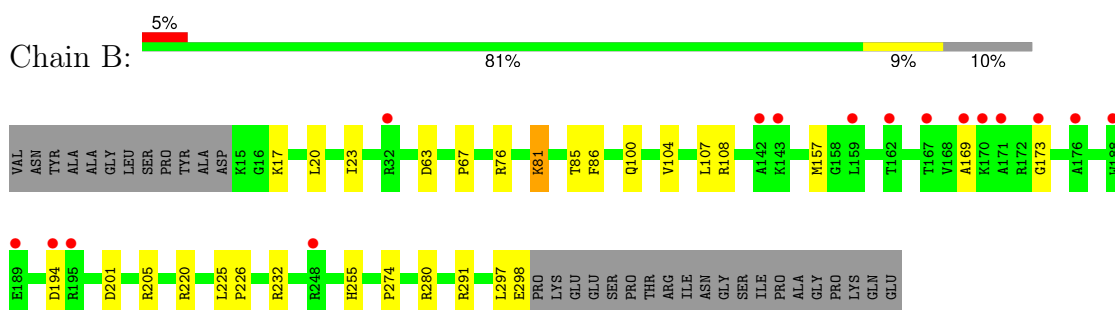
### 3 Residue-property plots [i](#)

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.

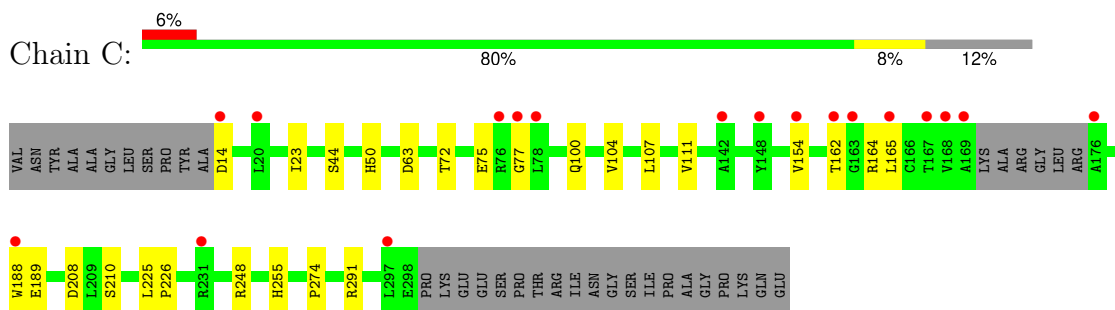
- Molecule 1: NAD-dependent protein deacetylase sirtuin-6



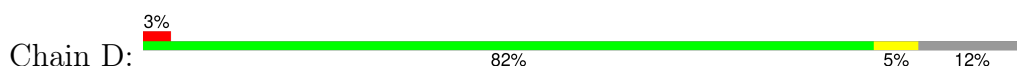
- Molecule 1: NAD-dependent protein deacetylase sirtuin-6

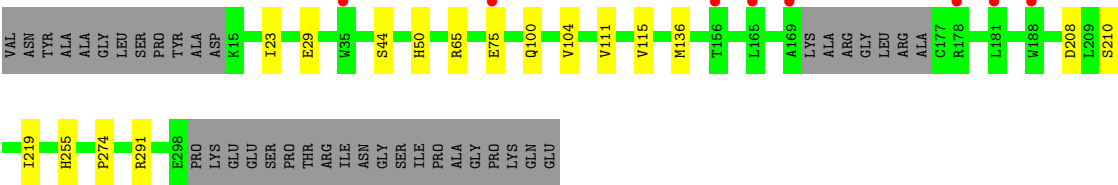


- Molecule 1: NAD-dependent protein deacetylase sirtuin-6

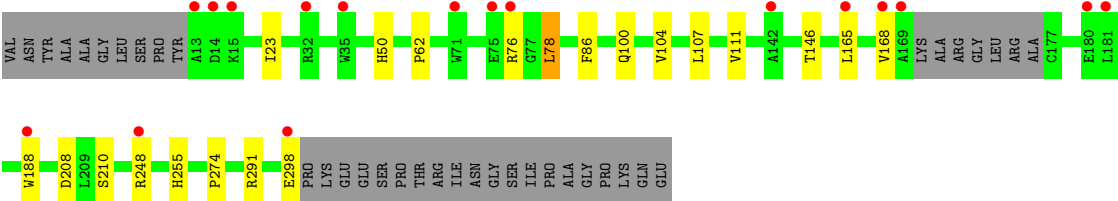
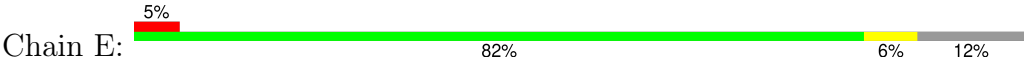


- Molecule 1: NAD-dependent protein deacetylase sirtuin-6

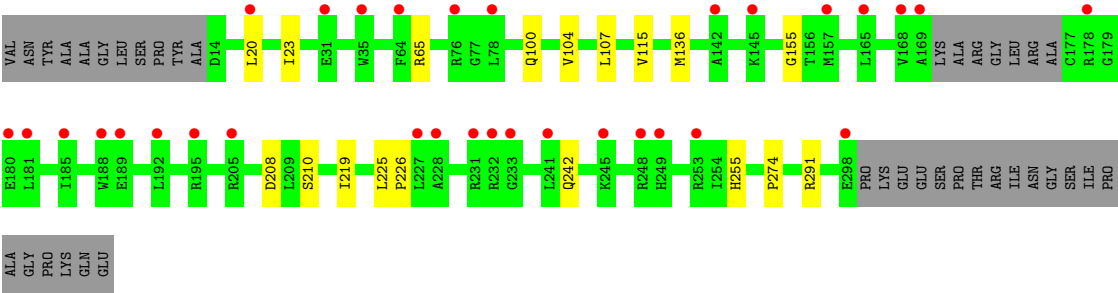
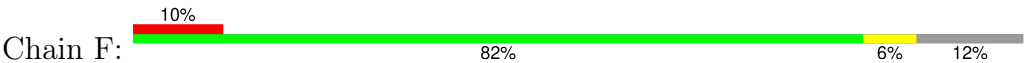




• Molecule 1: NAD-dependent protein deacetylase sirtuin-6



• Molecule 1: NAD-dependent protein deacetylase sirtuin-6



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.51Å 136.53Å 89.87Å 90.00° 117.71° 90.00°	Depositor
Resolution (Å)	46.39 – 2.10 46.39 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.6 (46.39-2.10) 99.6 (46.39-2.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.11 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, $R_{free}$	0.204 , 0.230 0.212 , 0.233	Depositor DCC
$R_{free}$ test set	2101 reflections (1.89%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	45.7	Xtriage
Anisotropy	0.272	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 44.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for -h-l,k,h 0.000 for l,k,-h-l 0.007 for h,-k,-h-l 0.012 for -h-l,-k,l 0.006 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	13647	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.33% 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: 8L9, AR6, ZN, GOL, SO4

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	0.67	0/2199	0.81	1/2986 (0.0%)
1	B	0.67	0/2247	0.81	0/3050
1	C	0.66	0/2198	0.81	0/2987
1	D	0.66	0/2187	0.78	0/2972
1	E	0.67	0/2196	0.80	1/2984 (0.0%)
1	F	0.70	2/2195 (0.1%)	0.81	1/2984 (0.0%)
All	All	0.67	2/13222 (0.0%)	0.80	3/17963 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	20	LEU	C-N	8.16	1.49	1.34
1	F	242	GLN	C-N	7.90	1.49	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	208	ASP	CB-CA-C	-6.26	97.89	110.40
1	F	208	ASP	CB-CA-C	-5.68	99.03	110.40
1	A	253	ARG	NE-CZ-NH1	-5.30	117.65	120.30

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	2152	0	2149	11	0
1	B	2199	0	2206	20	0
1	C	2151	0	2136	17	0
1	D	2140	0	2127	11	0
1	E	2149	0	2136	13	0
1	F	2148	0	2124	9	0
2	A	36	0	21	0	0
2	B	36	0	21	1	0
2	C	36	0	21	1	0
2	D	36	0	21	1	0
2	E	36	0	21	0	0
2	F	36	0	21	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	6	0	8	0	0
4	B	6	0	8	2	0
4	C	18	0	24	1	0
4	D	6	0	8	3	0
4	E	12	0	16	2	0
5	A	34	0	0	1	0
5	B	34	0	0	1	0
5	C	34	0	0	1	0
5	D	34	0	0	3	0
5	E	34	0	0	1	0
5	F	34	0	0	1	0
6	A	5	0	0	0	0
6	B	25	0	0	3	0
6	C	5	0	0	0	0
6	D	15	0	0	0	0
6	E	15	0	0	0	0
7	A	29	0	0	0	0
7	B	32	0	0	1	0
7	C	40	0	0	0	0
7	D	29	0	0	0	0
7	E	25	0	0	0	0
7	F	14	0	0	0	0
All	All	13647	0	13068	85	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 85 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)
1:C:14:ASP:O	1:C:188:TRP:CH2	2.42	0.72
1:B:220:ARG:NH2	6:B:409:SO4:O1	2.23	0.72
1:E:86:PHE:H	4:E:704:GOL:H31	1.55	0.71
1:C:77:GLY:HA3	1:F:155:GLY:O	1.91	0.70
1:D:219:ILE:HD12	1:D:219:ILE:N	2.10	0.67

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	274/316 (87%)	272 (99%)	2 (1%)	0	100	100
1	B	282/316 (89%)	278 (99%)	4 (1%)	0	100	100
1	C	275/316 (87%)	274 (100%)	1 (0%)	0	100	100
1	D	273/316 (86%)	270 (99%)	3 (1%)	0	100	100
1	E	275/316 (87%)	272 (99%)	3 (1%)	0	100	100
1	F	274/316 (87%)	272 (99%)	2 (1%)	0	100	100
All	All	1653/1896 (87%)	1638 (99%)	15 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 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	232/265 (88%)	229 (99%)	3 (1%)	69	75
1	B	236/265 (89%)	233 (99%)	3 (1%)	69	75
1	C	231/265 (87%)	228 (99%)	3 (1%)	69	75
1	D	230/265 (87%)	228 (99%)	2 (1%)	78	84
1	E	231/265 (87%)	228 (99%)	3 (1%)	69	75
1	F	231/265 (87%)	230 (100%)	1 (0%)	91	94
All	All	1391/1590 (88%)	1376 (99%)	15 (1%)	73	79

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	210	SER
1	E	248	ARG
1	C	248	ARG
1	F	210	SER
1	E	78	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	68	HIS
1	F	249	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 39 ligands modelled in this entry, 6 are monoatomic - leaving 33 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$
6	SO4	D	407	-	4,4,4	0.33	0	6,6,6	0.13	0
4	GOL	C	1005	-	5,5,5	0.17	0	5,5,5	0.44	0
6	SO4	B	407	-	4,4,4	0.35	0	6,6,6	0.15	0
2	AR6	C	1002	-	35,39,39	0.66	0	42,60,60	0.96	3 (7%)
6	SO4	B	405	-	4,4,4	0.36	0	6,6,6	0.13	0
4	GOL	C	1004	-	5,5,5	0.12	0	5,5,5	0.35	0
6	SO4	E	706	-	4,4,4	0.29	0	6,6,6	0.22	0
6	SO4	D	405	-	4,4,4	0.24	0	6,6,6	0.19	0
2	AR6	B	401	-	35,39,39	0.84	2 (5%)	42,60,60	1.07	4 (9%)
2	AR6	D	401	-	35,39,39	0.75	0	42,60,60	1.15	3 (7%)
4	GOL	C	1001	-	5,5,5	0.09	0	5,5,5	0.26	0
4	GOL	A	403	-	5,5,5	0.22	0	5,5,5	0.44	0
2	AR6	F	401	-	35,39,39	1.04	4 (11%)	42,60,60	0.81	1 (2%)
4	GOL	B	403	-	5,5,5	0.19	0	5,5,5	0.45	0
5	8L9	D	404	-	36,36,36	1.87	9 (25%)	54,55,55	3.56	19 (35%)
6	SO4	B	408	-	4,4,4	0.31	0	6,6,6	0.12	0
5	8L9	E	705	-	36,36,36	1.68	7 (19%)	54,55,55	3.53	11 (20%)
5	8L9	C	1006	-	36,36,36	1.97	10 (27%)	54,55,55	4.22	24 (44%)
6	SO4	B	409	-	4,4,4	0.32	0	6,6,6	0.08	0
2	AR6	E	702	-	35,39,39	0.68	0	42,60,60	1.10	3 (7%)
4	GOL	E	704	-	5,5,5	0.22	0	5,5,5	0.56	0
2	AR6	A	401	-	35,39,39	0.64	0	42,60,60	1.04	3 (7%)
5	8L9	B	404	-	36,36,36	1.99	9 (25%)	54,55,55	3.73	17 (31%)
4	GOL	E	701	-	5,5,5	0.12	0	5,5,5	0.24	0
6	SO4	C	1007	-	4,4,4	0.31	0	6,6,6	0.14	0
6	SO4	E	707	-	4,4,4	0.30	0	6,6,6	0.12	0
5	8L9	F	403	-	36,36,36	2.07	10 (27%)	54,55,55	3.66	18 (33%)
6	SO4	A	405	-	4,4,4	0.32	0	6,6,6	0.10	0
5	8L9	A	404	-	36,36,36	2.06	10 (27%)	54,55,55	3.66	21 (38%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	SO4	E	708	-	4,4,4	0.29	0	6,6,6	0.13	0
6	SO4	B	406	-	4,4,4	0.24	0	6,6,6	0.19	0
6	SO4	D	406	-	4,4,4	0.31	0	6,6,6	0.08	0
4	GOL	D	403	-	5,5,5	0.15	0	5,5,5	0.41	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	C	1005	-	-	4/4/4/4	-
2	AR6	C	1002	-	-	1/18/54/54	0/4/4/4
4	GOL	C	1004	-	-	4/4/4/4	-
2	AR6	B	401	-	-	0/18/54/54	0/4/4/4
2	AR6	D	401	-	-	1/18/54/54	0/4/4/4
4	GOL	C	1001	-	-	2/4/4/4	-
4	GOL	A	403	-	-	2/4/4/4	-
2	AR6	F	401	-	-	2/18/54/54	0/4/4/4
4	GOL	B	403	-	-	0/4/4/4	-
5	8L9	D	404	-	-	10/26/26/26	0/3/3/3
5	8L9	E	705	-	-	11/26/26/26	0/3/3/3
5	8L9	C	1006	-	-	13/26/26/26	0/3/3/3
2	AR6	E	702	-	-	1/18/54/54	0/4/4/4
4	GOL	E	704	-	-	2/4/4/4	-
2	AR6	A	401	-	-	1/18/54/54	0/4/4/4
5	8L9	B	404	-	-	9/26/26/26	0/3/3/3
4	GOL	E	701	-	-	0/4/4/4	-
5	8L9	F	403	-	-	14/26/26/26	0/3/3/3
5	8L9	A	404	-	-	8/26/26/26	0/3/3/3
4	GOL	D	403	-	-	2/4/4/4	-

The worst 5 of 61 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	404	8L9	C06-S12	6.08	1.85	1.76
5	F	403	8L9	S12-N13	6.01	1.73	1.63
5	C	1006	8L9	S12-N13	5.49	1.72	1.63
5	D	404	8L9	S12-N13	5.30	1.71	1.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	404	8L9	S12-N13	4.87	1.71	1.63

The worst 5 of 127 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	1006	8L9	O16-S12-O15	-17.90	97.78	119.52
5	A	404	8L9	O16-S12-O15	-17.76	97.95	119.52
5	E	705	8L9	O32-S30-O31	-17.68	98.04	119.52
5	F	403	8L9	O32-S30-O31	-16.02	100.07	119.52
5	B	404	8L9	O16-S12-O15	-15.66	100.50	119.52

There are no chirality outliers.

5 of 87 torsion outliers are listed below:

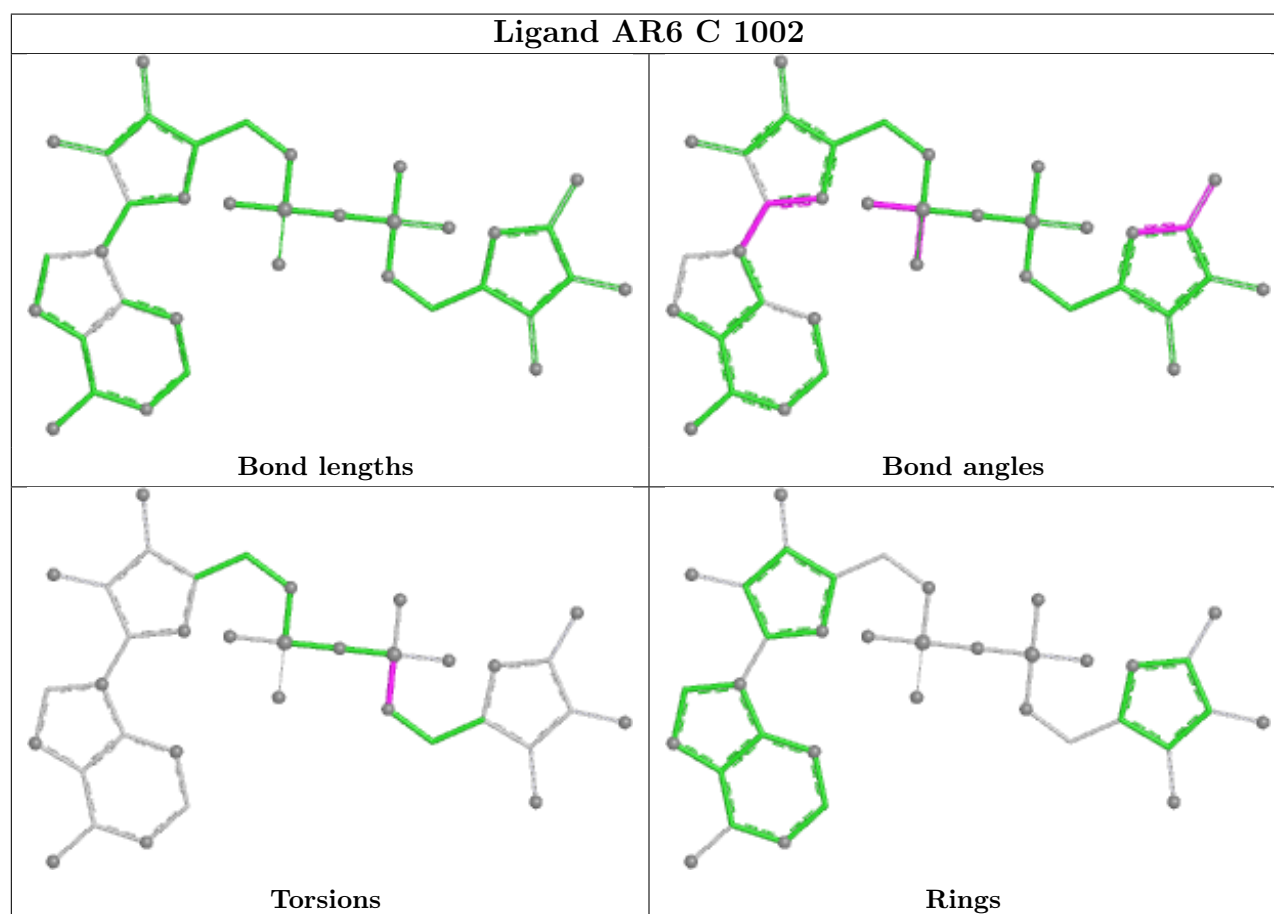
Mol	Chain	Res	Type	Atoms
2	D	401	AR6	C5D-O5D-PB-O2B
2	E	702	AR6	C5D-O5D-PB-O2B
4	A	403	GOL	C1-C2-C3-O3
4	C	1004	GOL	O1-C1-C2-O2
4	C	1004	GOL	O1-C1-C2-C3

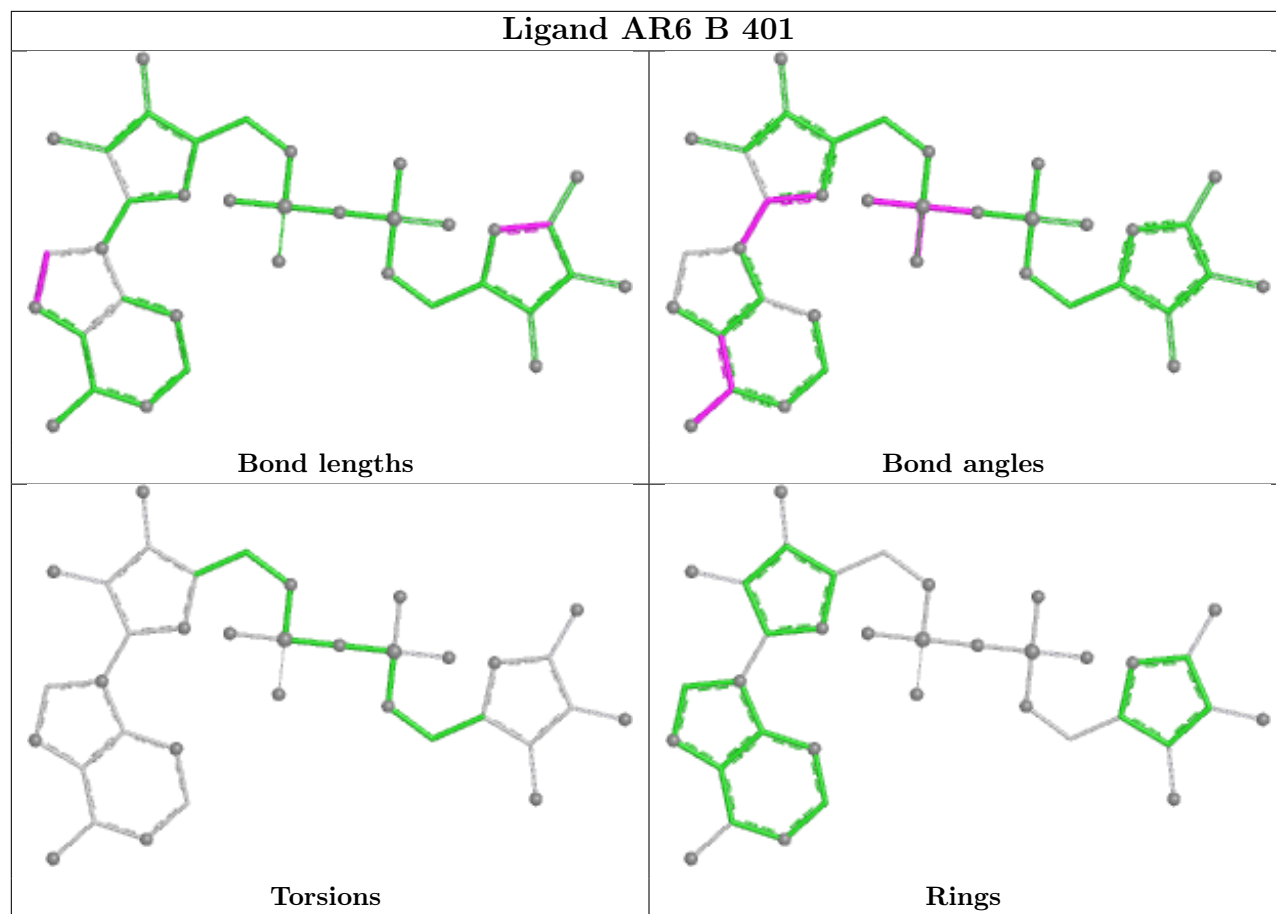
There are no ring outliers.

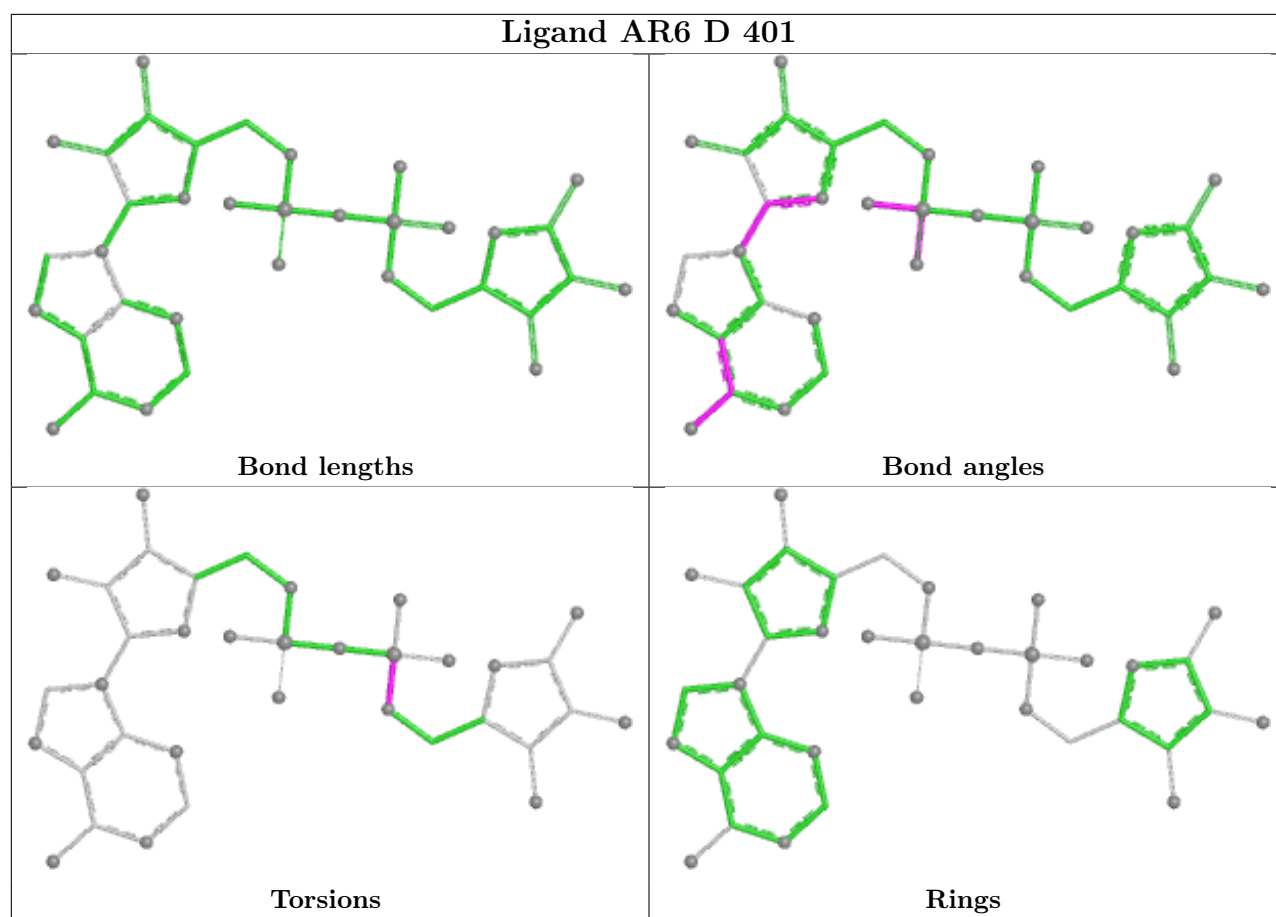
16 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1002	AR6	1	0
4	C	1004	GOL	1	0
2	B	401	AR6	1	0
2	D	401	AR6	1	0
4	B	403	GOL	2	0
5	D	404	8L9	3	0
6	B	408	SO4	1	0
5	E	705	8L9	1	0
5	C	1006	8L9	1	0
6	B	409	SO4	2	0
4	E	704	GOL	1	0
5	B	404	8L9	1	0
4	E	701	GOL	1	0
5	F	403	8L9	1	0
5	A	404	8L9	1	0
4	D	403	GOL	3	0

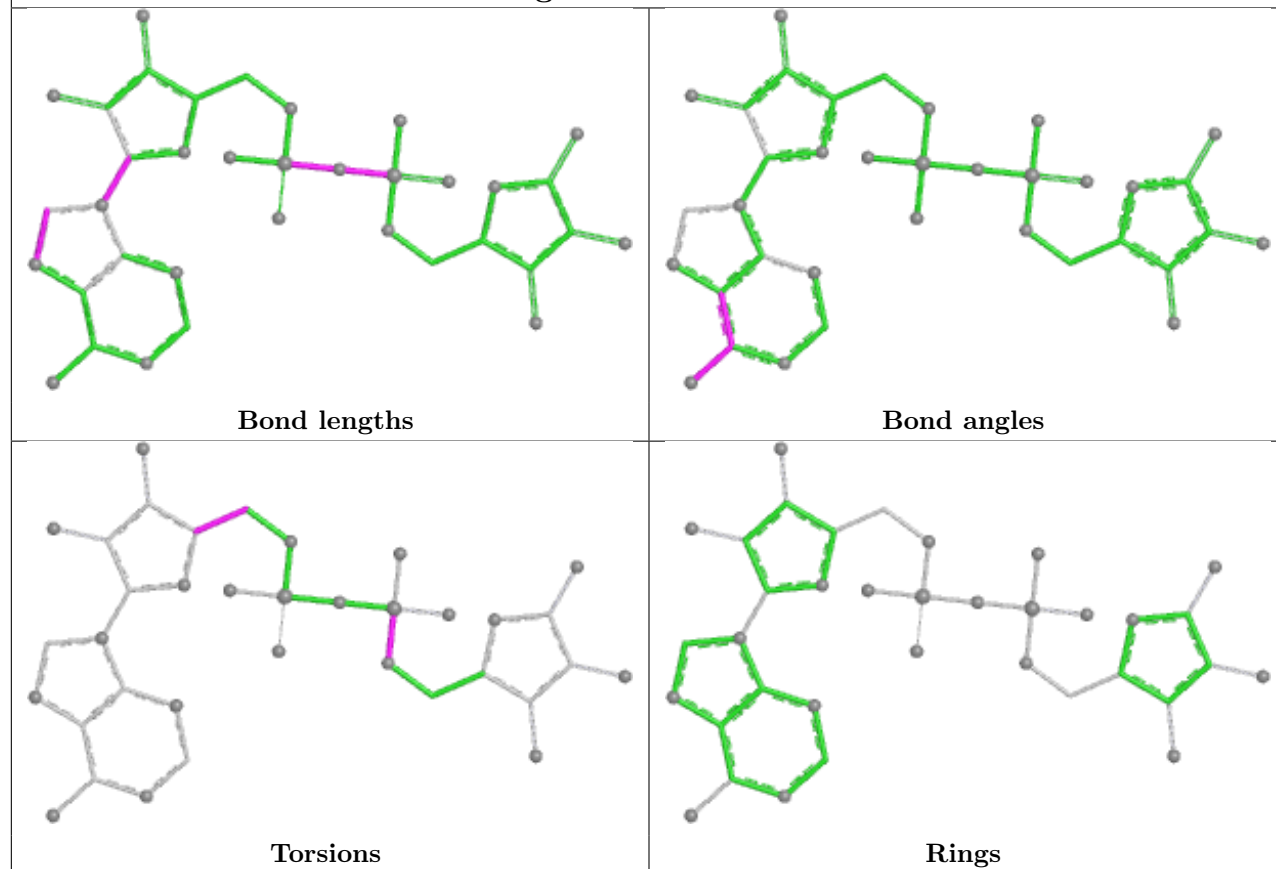
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



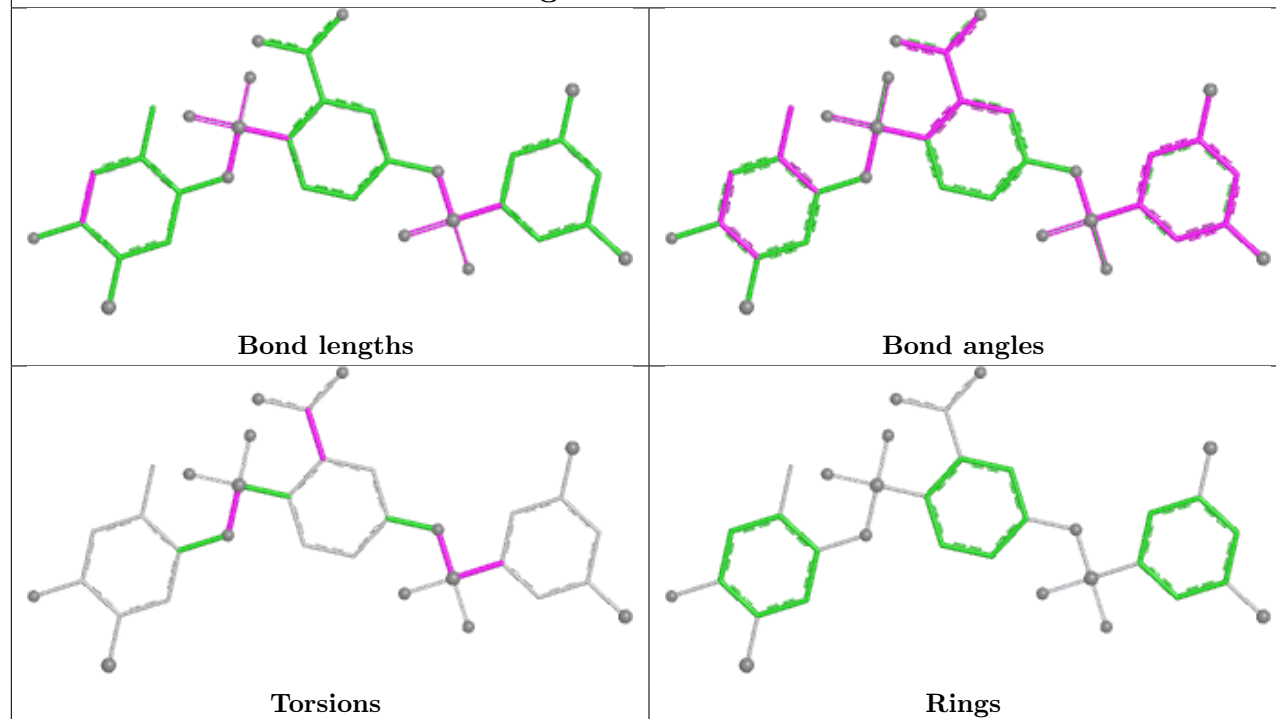




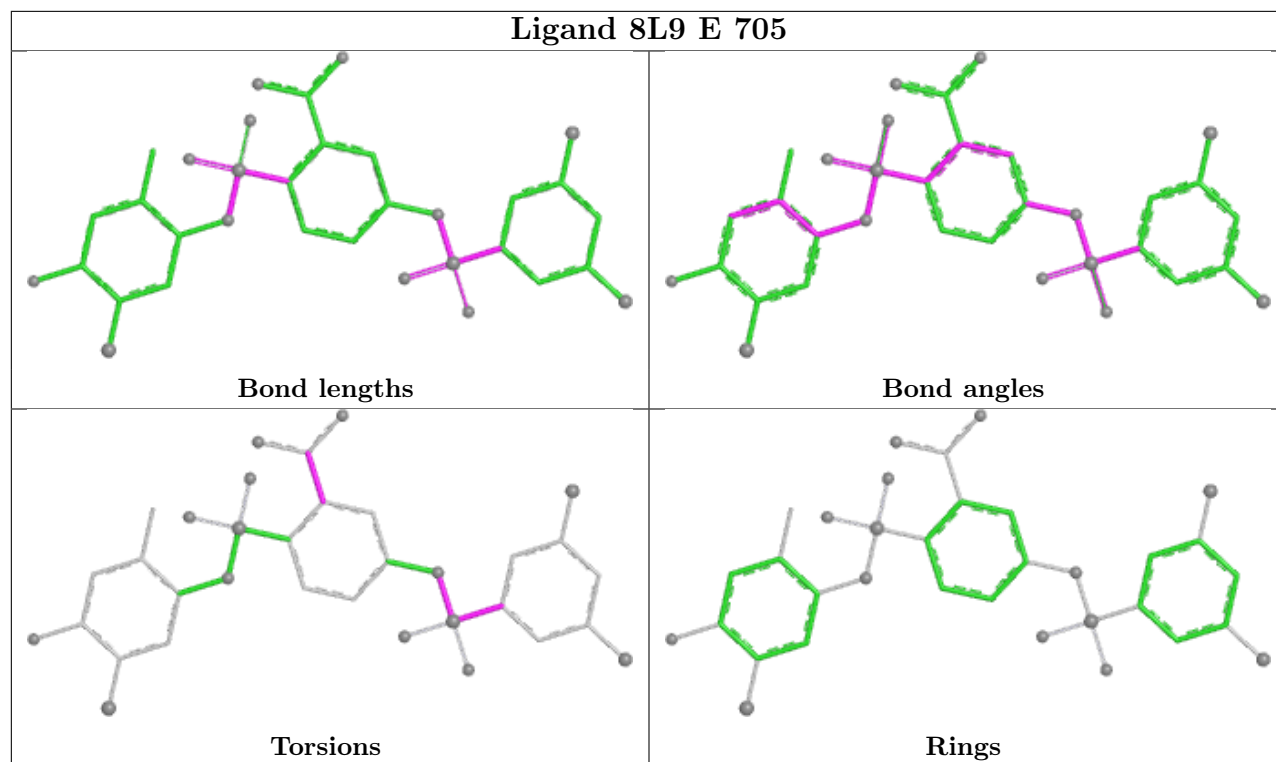
## Ligand AR6 F 401



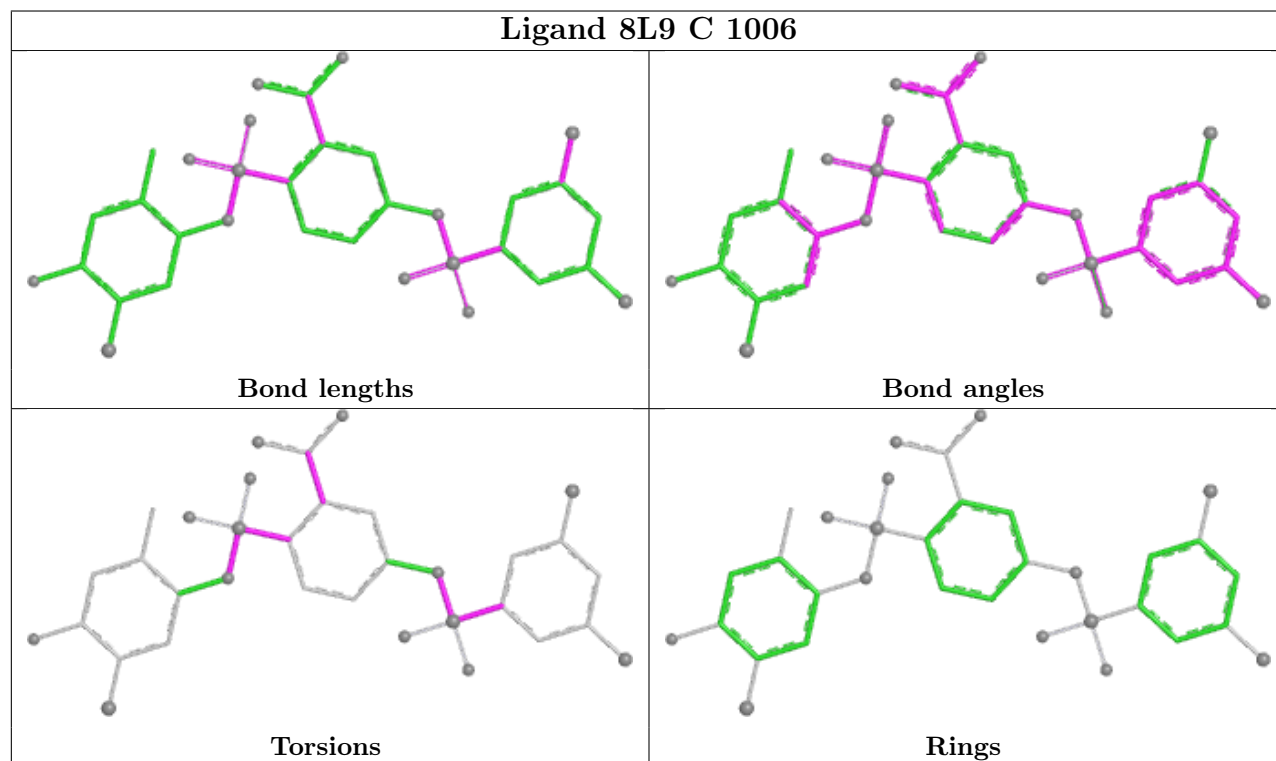
## Ligand 8L9 D 404



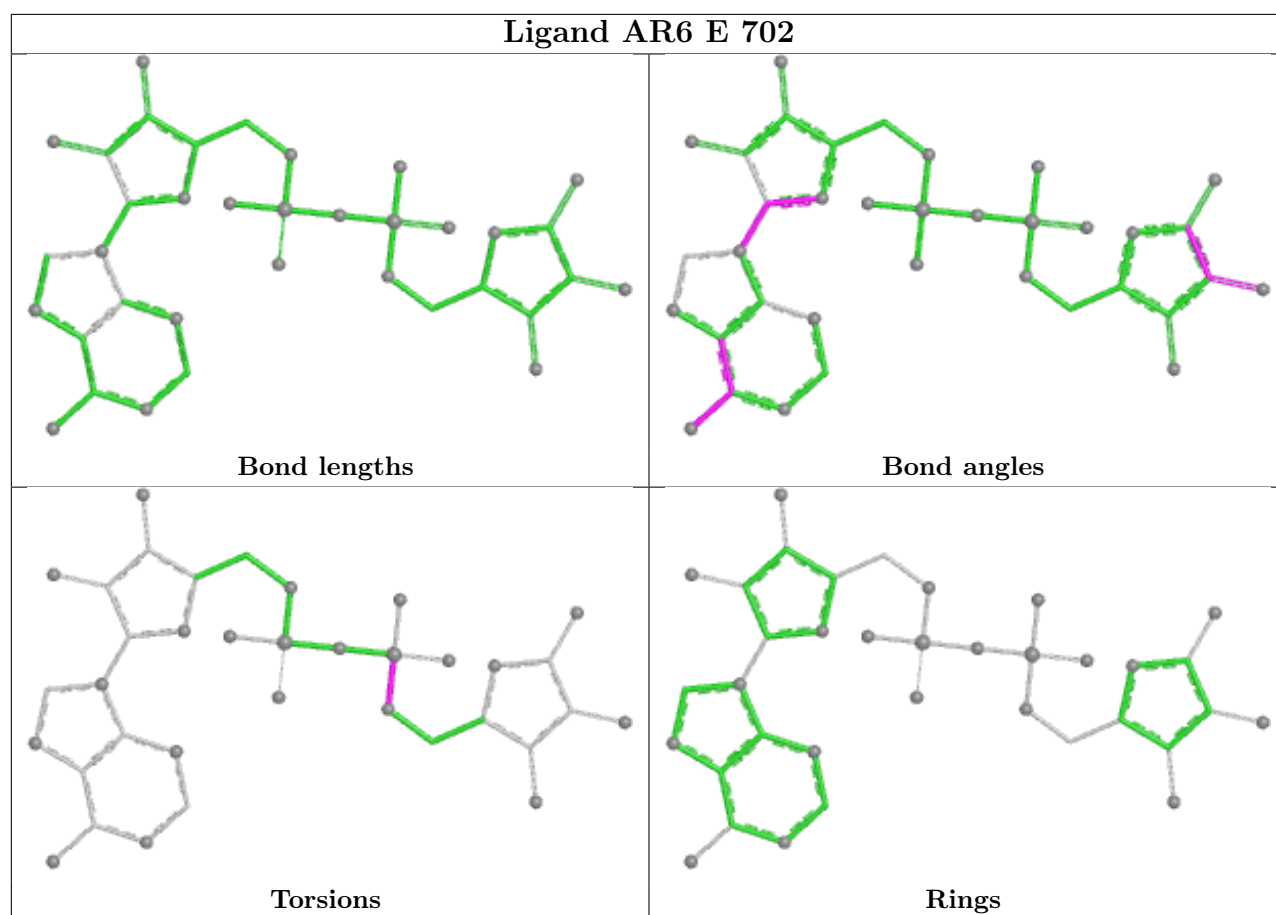
## Ligand 8L9 E 705



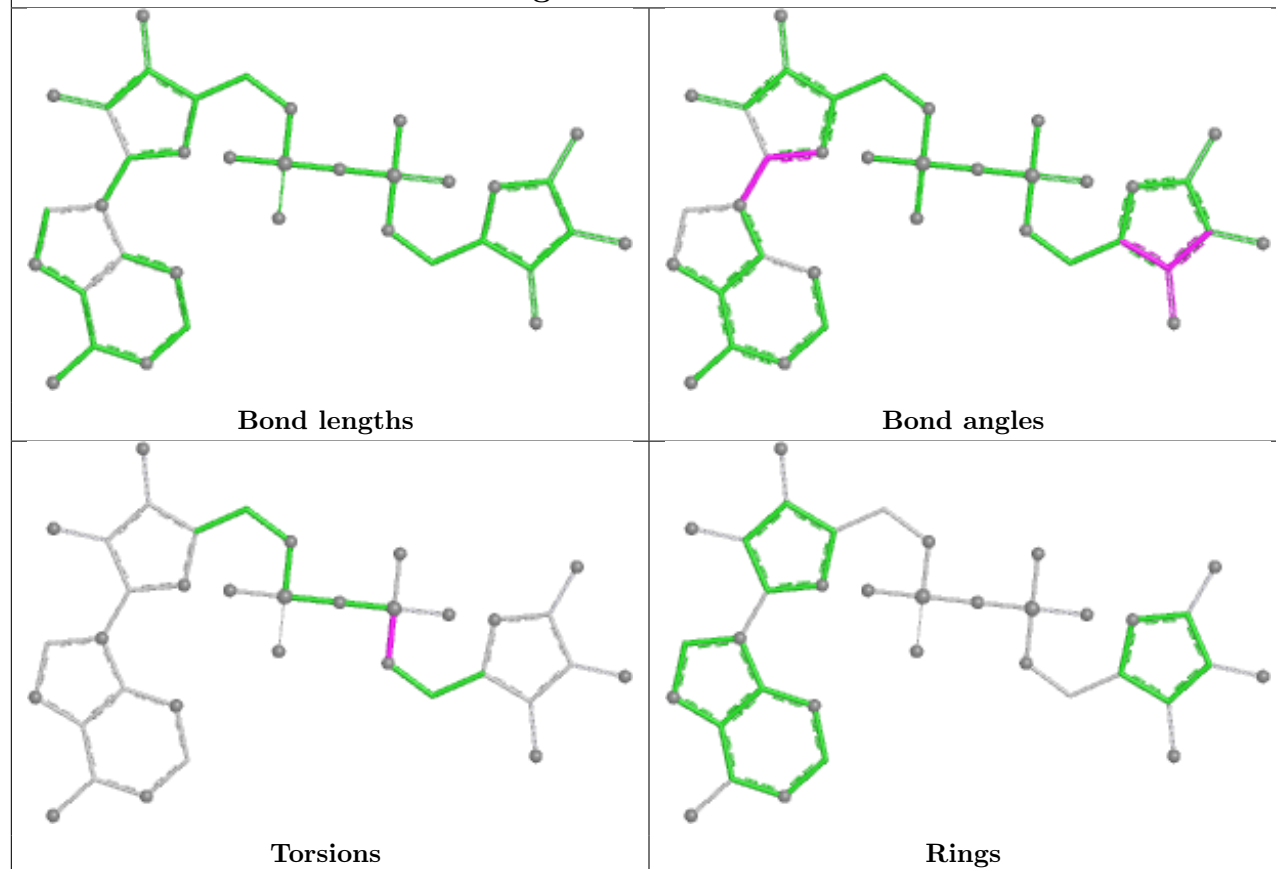
## Ligand 8L9 C 1006



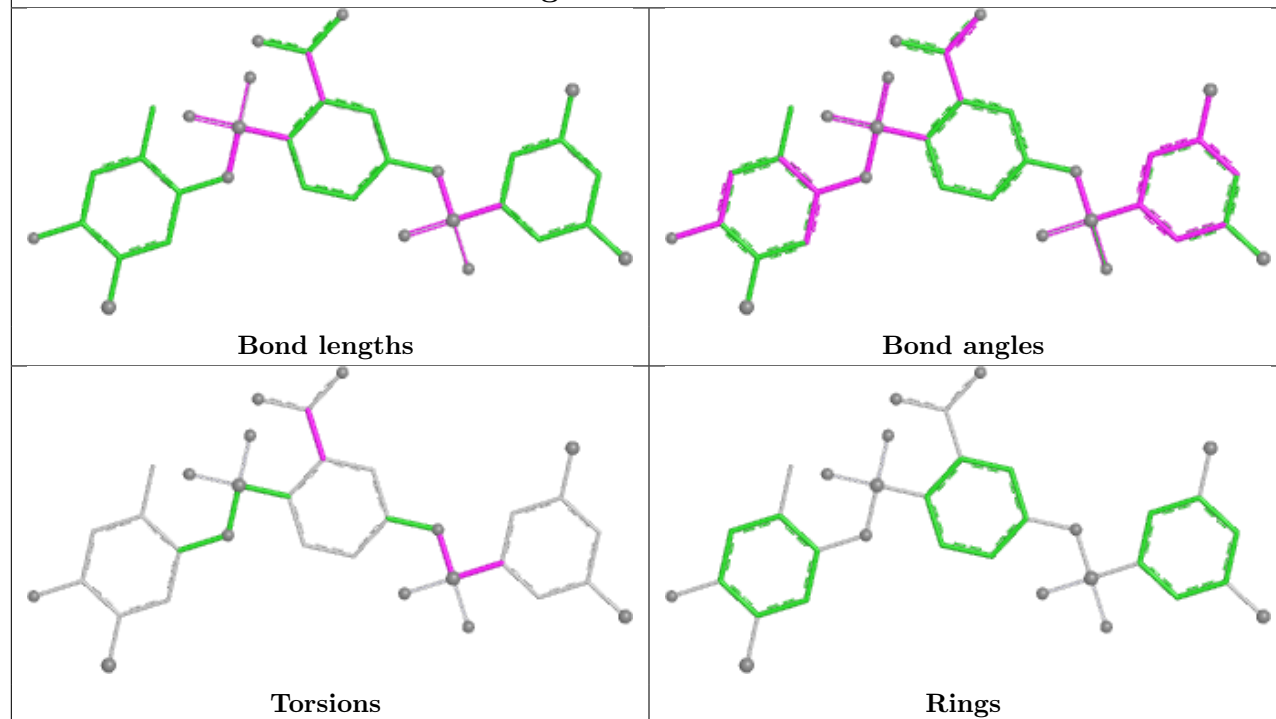


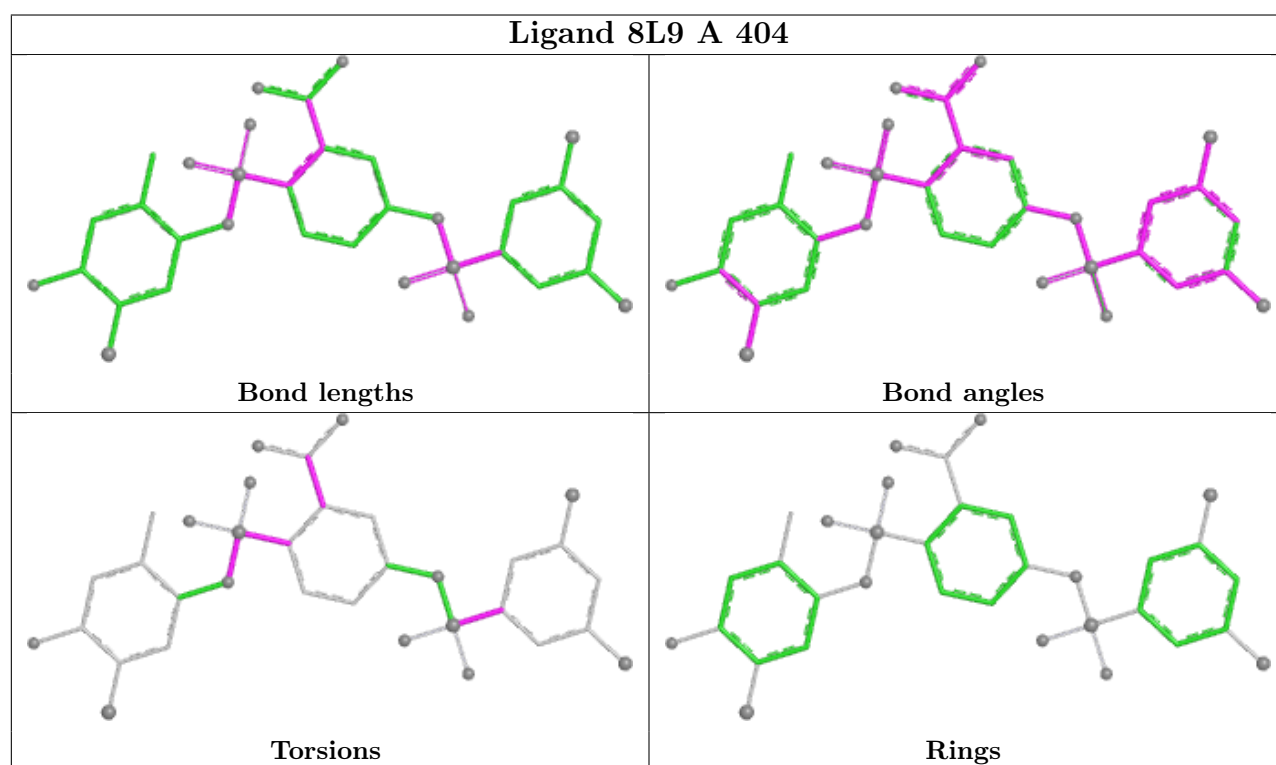
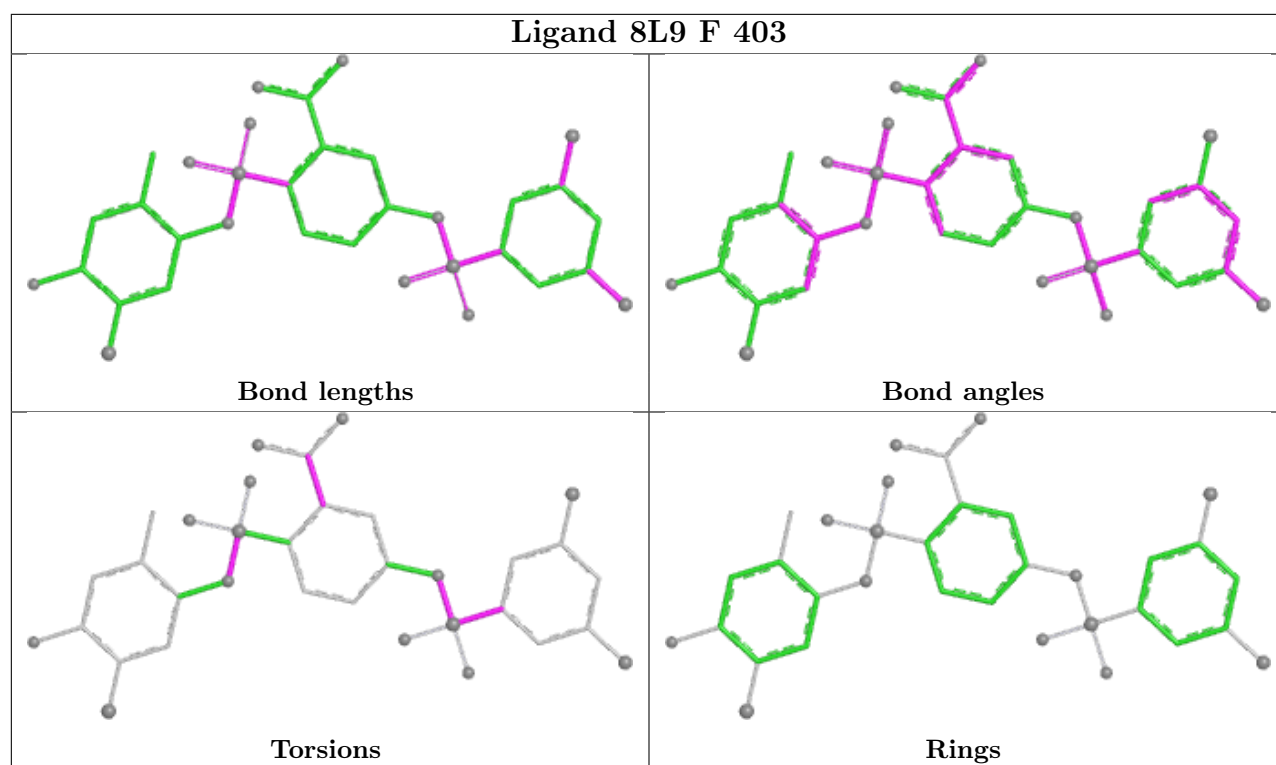


## Ligand AR6 A 401



## Ligand 8L9 B 404





## 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	278/316 (87%)	0.48	16 (5%) 23 28	34, 48, 84, 133	0
1	B	284/316 (89%)	0.35	16 (5%) 24 29	36, 50, 78, 123	0
1	C	279/316 (88%)	0.47	18 (6%) 18 23	34, 48, 91, 140	0
1	D	277/316 (87%)	0.28	8 (2%) 51 57	36, 52, 79, 117	0
1	E	279/316 (88%)	0.53	17 (6%) 21 26	37, 57, 90, 123	0
1	F	278/316 (87%)	0.60	32 (11%) 4 6	43, 62, 92, 121	0
All	All	1675/1896 (88%)	0.45	107 (6%) 19 24	34, 53, 87, 140	0

The worst 5 of 107 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	14	ASP	10.8
1	A	188	TRP	8.2
1	E	169	ALA	7.8
1	C	176	ALA	6.5
1	F	178	ARG	6.2

### 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.

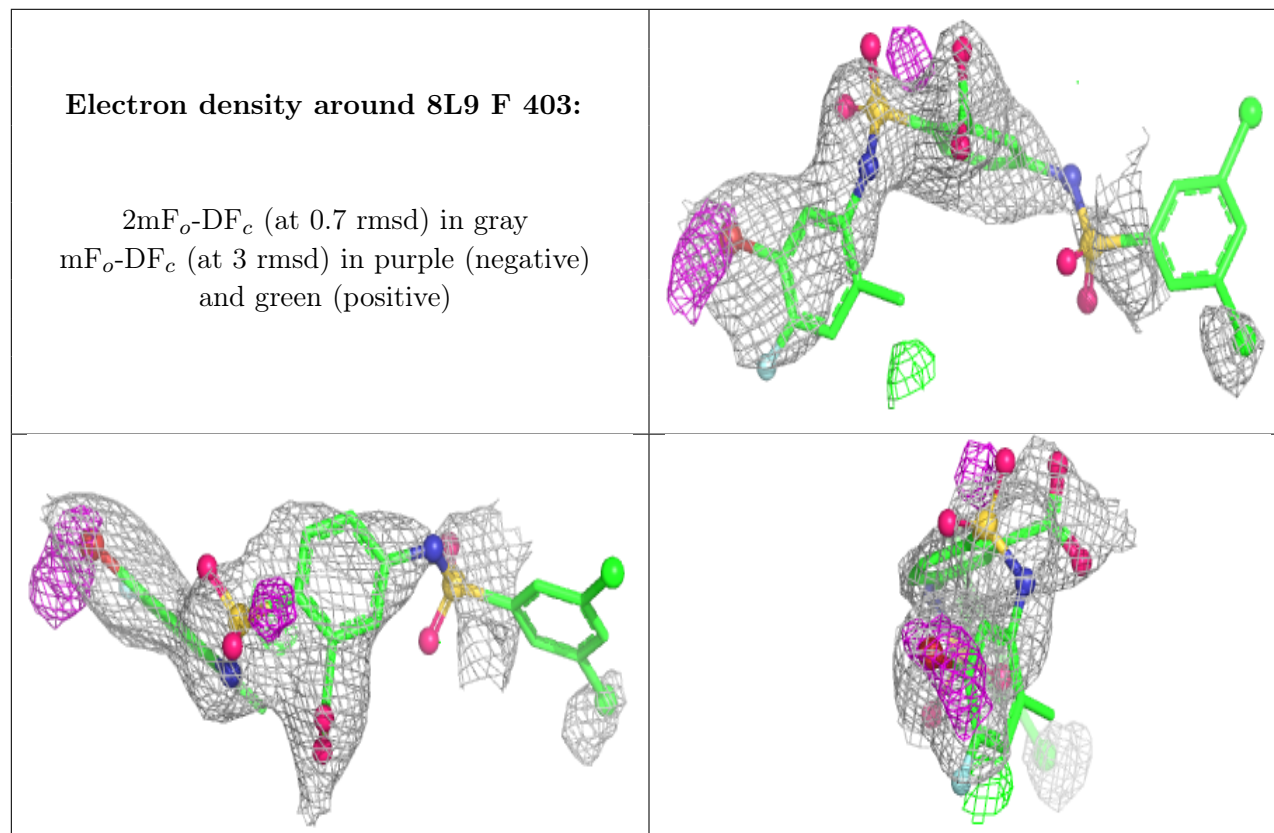
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	GOL	A	403	6/6	0.55	0.18	75,80,87,89	0
4	GOL	E	704	6/6	0.64	0.24	70,73,77,89	0
4	GOL	B	403	6/6	0.70	0.25	61,78,81,81	0
4	GOL	E	701	6/6	0.72	0.17	78,93,102,110	0
4	GOL	C	1004	6/6	0.80	0.12	75,85,91,91	0
5	8L9	F	403	34/34	0.80	0.26	92,130,180,193	0
6	SO4	C	1007	5/5	0.80	0.30	107,109,115,126	0
5	8L9	B	404	34/34	0.81	0.24	96,118,149,156	0
4	GOL	C	1005	6/6	0.81	0.38	61,68,73,76	0
4	GOL	D	403	6/6	0.81	0.21	72,77,79,83	0
4	GOL	C	1001	6/6	0.84	0.16	72,79,86,88	0
5	8L9	E	705	34/34	0.85	0.23	81,117,156,156	0
6	SO4	E	707	5/5	0.85	0.34	88,89,106,122	0
6	SO4	A	405	5/5	0.87	0.20	91,105,114,121	0
5	8L9	A	404	34/34	0.89	0.18	74,86,130,156	0
5	8L9	D	404	34/34	0.90	0.20	81,97,135,167	0
6	SO4	B	409	5/5	0.90	0.24	98,105,109,110	0
6	SO4	D	406	5/5	0.91	0.24	95,108,117,117	0
5	8L9	C	1006	34/34	0.91	0.24	78,108,156,157	0
6	SO4	E	708	5/5	0.91	0.21	92,106,118,120	0
6	SO4	B	408	5/5	0.92	0.18	82,94,96,101	0
6	SO4	D	407	5/5	0.92	0.17	100,106,112,115	0
6	SO4	B	407	5/5	0.93	0.15	81,90,94,101	0
6	SO4	B	405	5/5	0.94	0.23	77,80,84,95	0
3	ZN	E	703	1/1	0.95	0.07	77,77,77,77	0
6	SO4	B	406	5/5	0.95	0.16	71,79,96,100	0
2	AR6	F	401	36/36	0.97	0.10	47,55,71,72	0
3	ZN	A	402	1/1	0.97	0.07	66,66,66,66	0
6	SO4	E	706	5/5	0.97	0.12	63,65,79,92	0
2	AR6	E	702	36/36	0.97	0.11	44,51,63,65	0
6	SO4	D	405	5/5	0.97	0.16	71,78,87,93	0
3	ZN	C	1003	1/1	0.98	0.09	63,63,63,63	0
2	AR6	A	401	36/36	0.98	0.11	32,38,47,55	0
3	ZN	F	402	1/1	0.98	0.07	79,79,79,79	0
2	AR6	B	401	36/36	0.98	0.12	35,42,50,60	0
2	AR6	D	401	36/36	0.98	0.10	42,45,52,53	0
3	ZN	D	402	1/1	0.99	0.06	68,68,68,68	0

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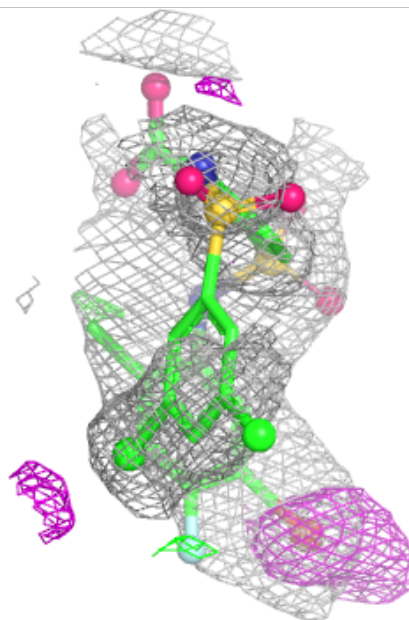
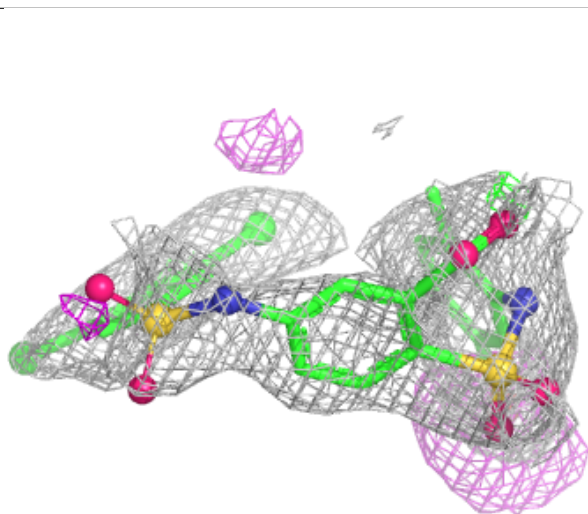
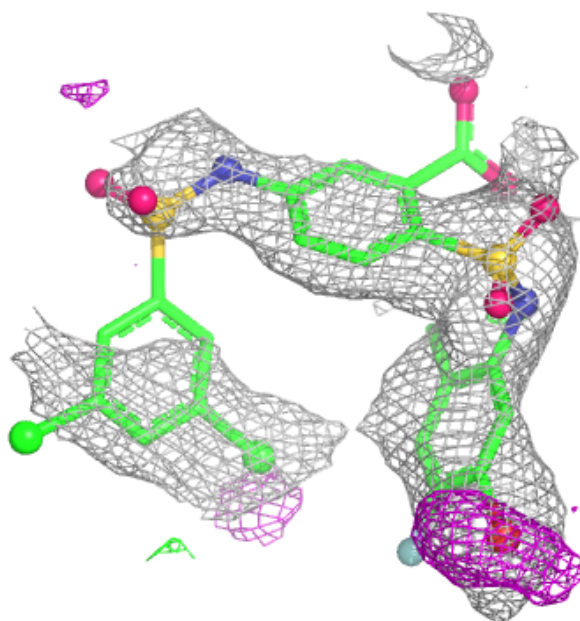
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	ZN	B	402	1/1	0.99	0.07	60,60,60,60	0
2	AR6	C	1002	36/36	0.99	0.11	33,40,50,57	0

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 8L9 B 404:**

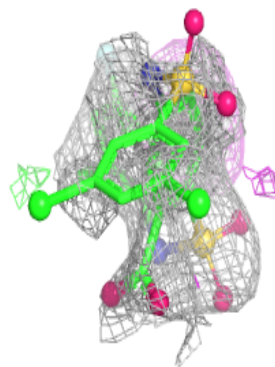
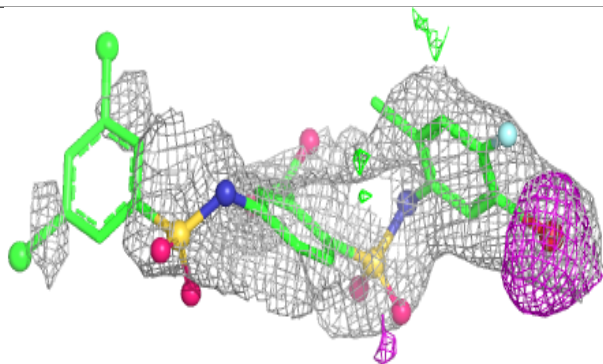
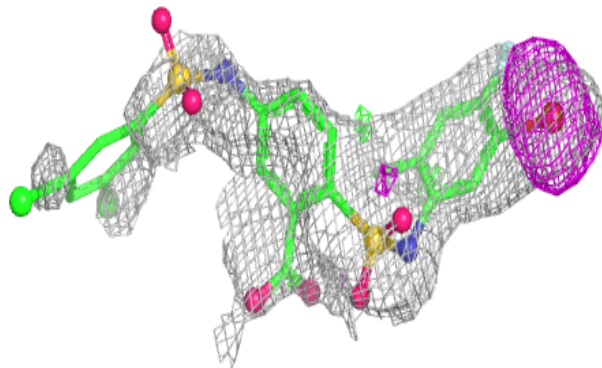
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





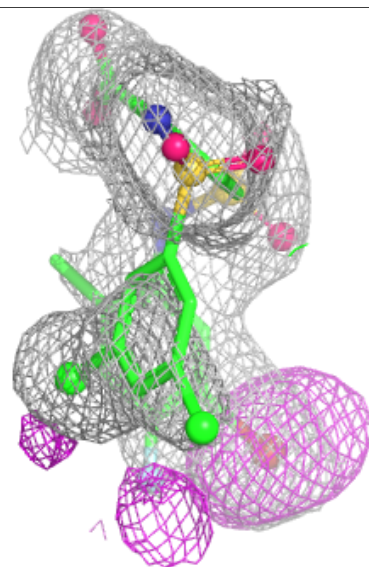
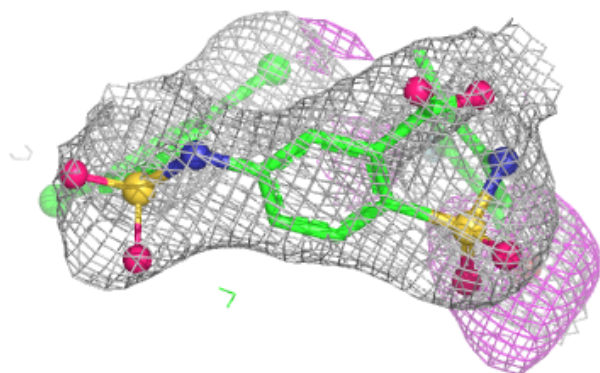
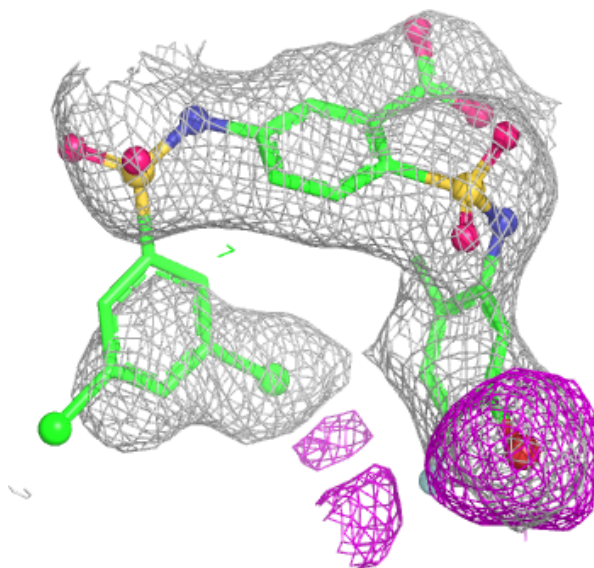
**Electron density around 8L9 E 705:**

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



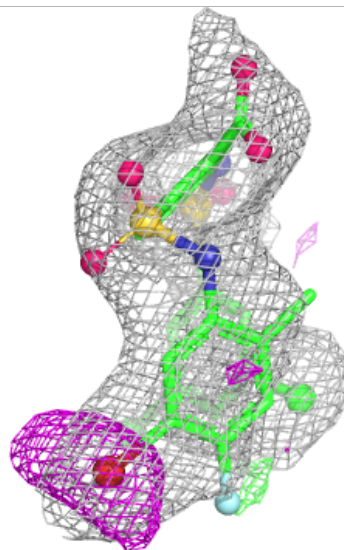
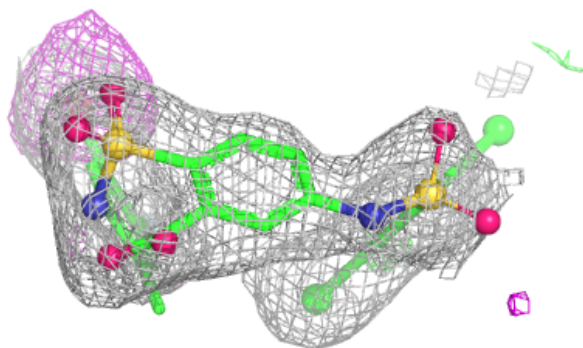
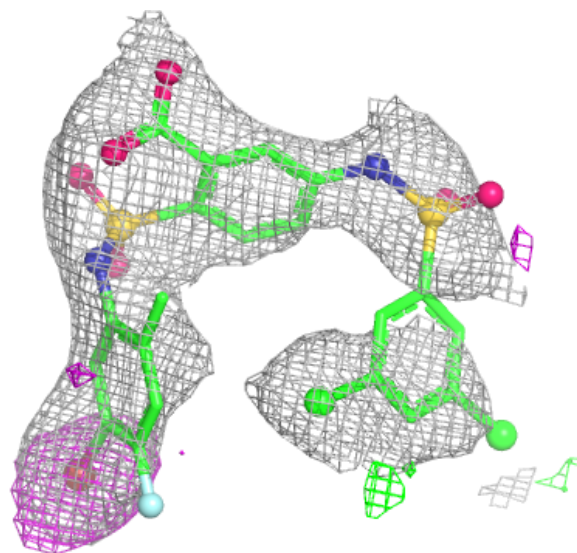
**Electron density around 8L9 A 404:**

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



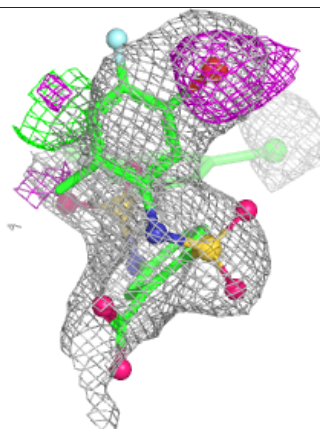
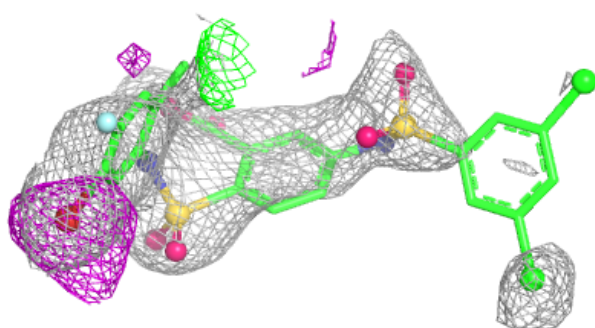
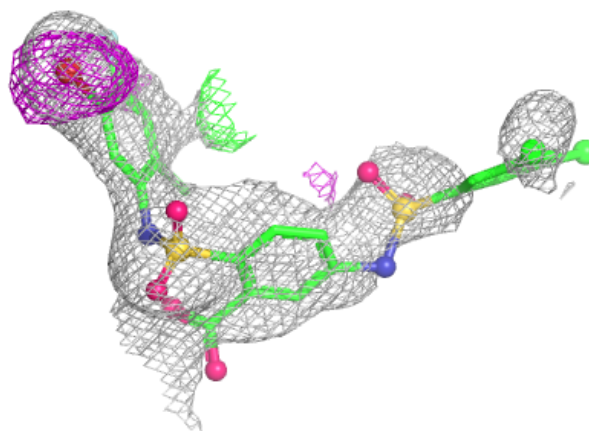
**Electron density around 8L9 D 404:**

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

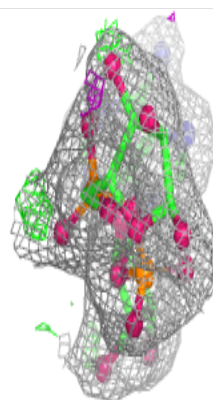
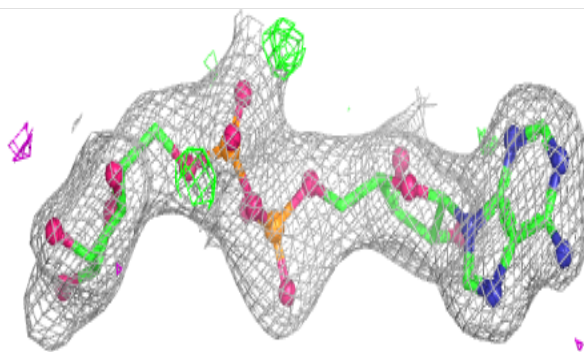
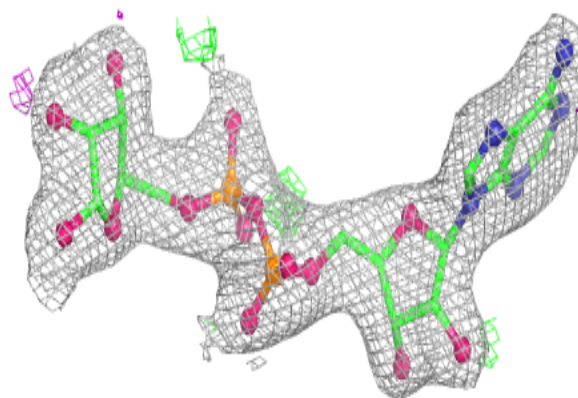


**Electron density around 8L9 C 1006:**

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

**Electron density around AR6 F 401:**

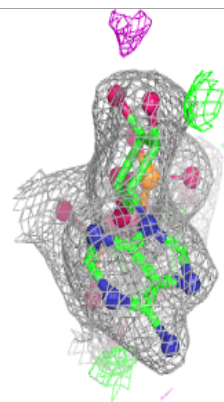
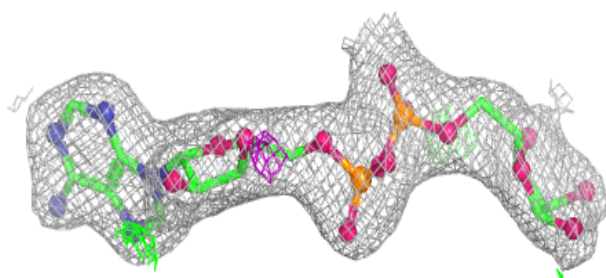
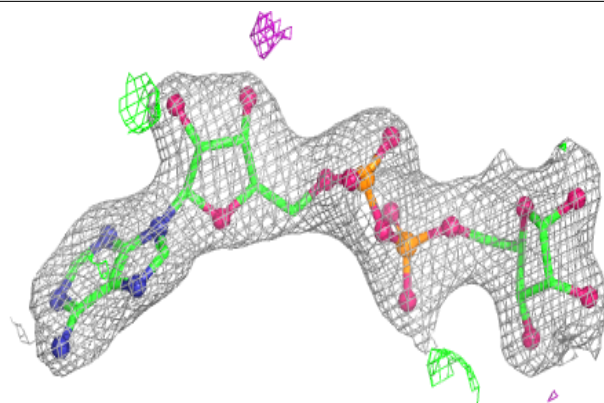
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



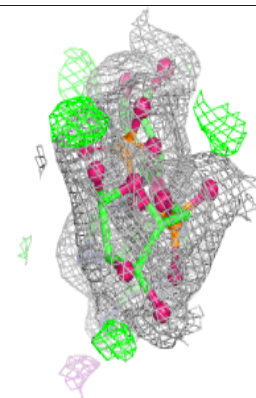
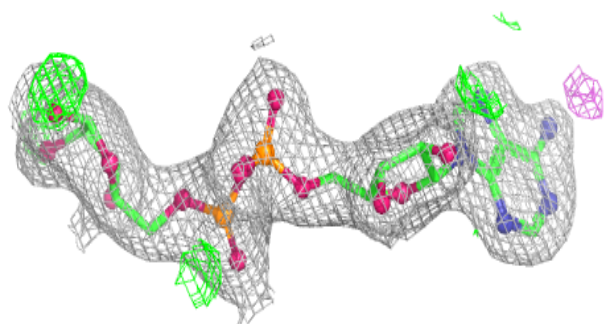
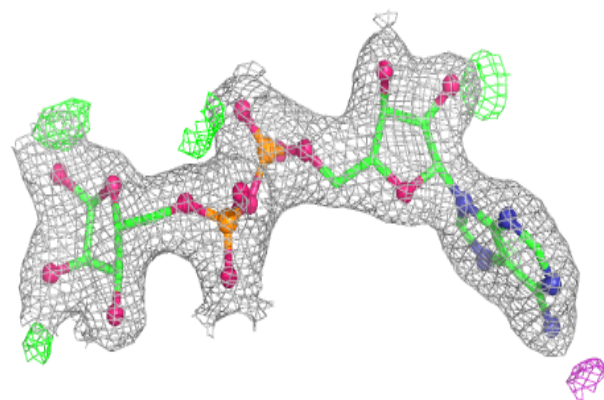


**Electron density around AR6 E 702:**

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

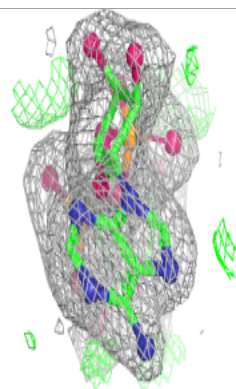
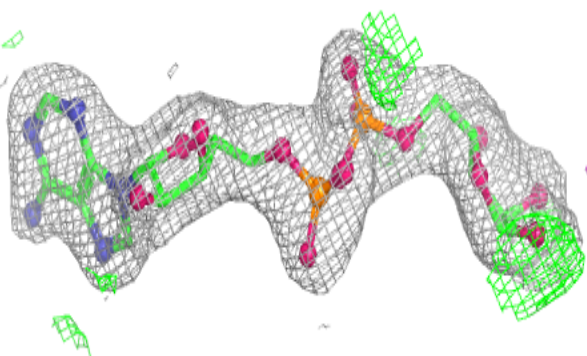
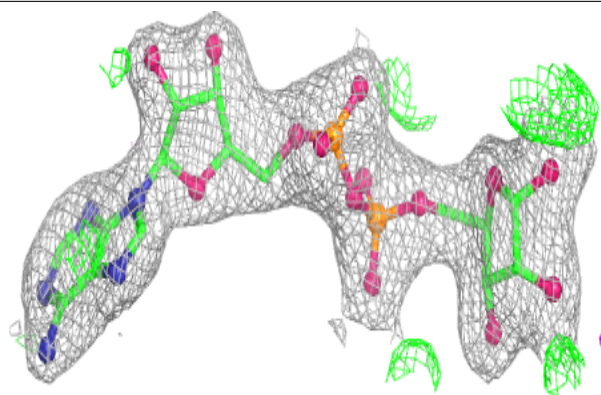
**Electron density around AR6 A 401:**

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

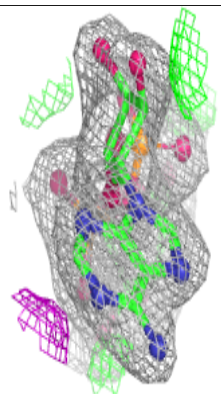
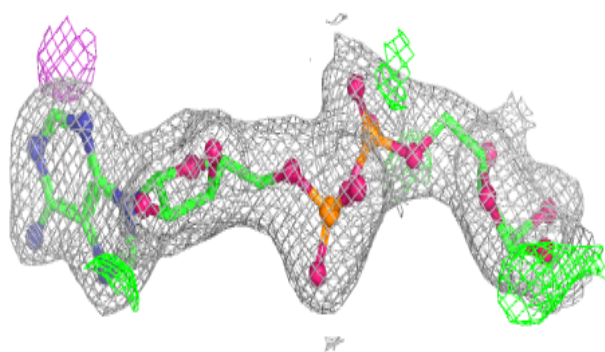
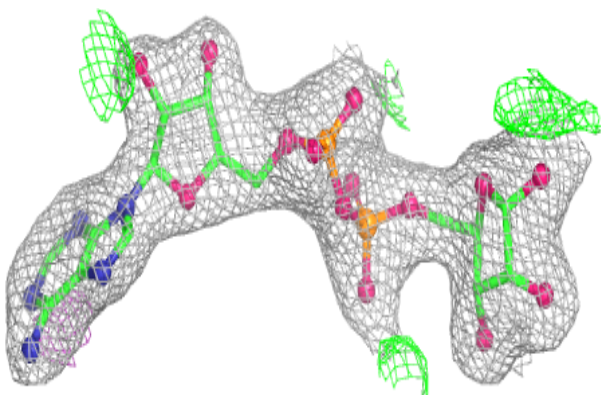


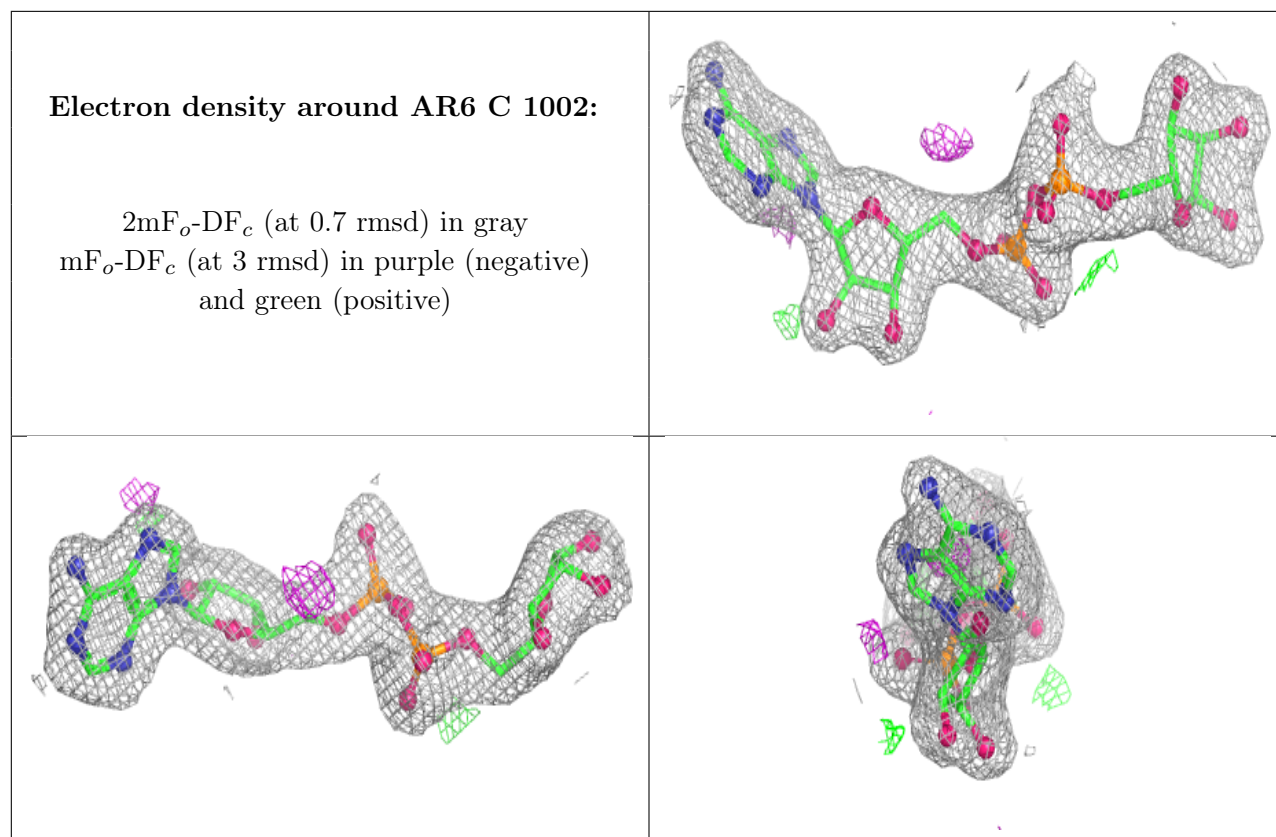
**Electron density around AR6 B 401:**

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

**Electron density around AR6 D 401:**

$2mF_o-DF_c$  (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.