



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 26, 2024 – 04:08 AM EDT

PDB ID : 6ZXO  
Title : Crystal structure of His-tagged human thymidylate synthase (HT-hTS) in complex with FdUMP and Raltitrexed (Tomudex)  
Authors : Pozzi, C.; Mangani, S.  
Deposited on : 2020-07-30  
Resolution : 2.60 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>.

---

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

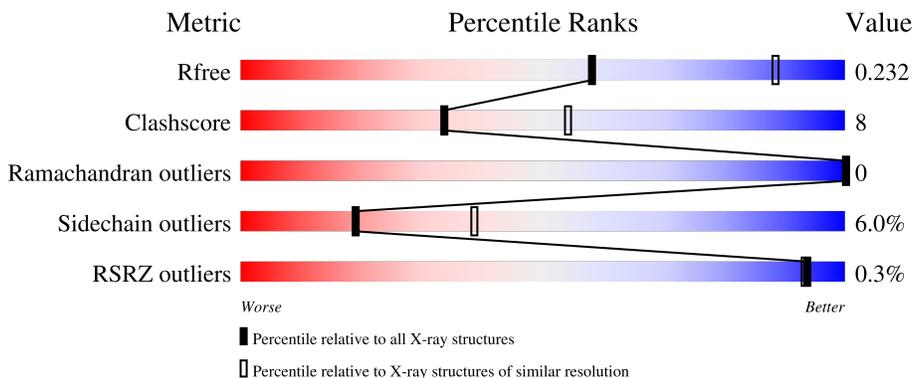
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

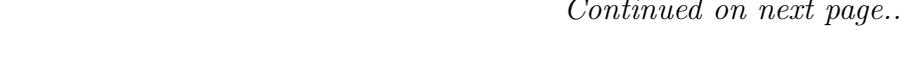
The reported resolution of this entry is 2.60 Å.

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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	325	 74% 14% • 11%
1	B	325	 75% 13% • 11%
1	C	325	 71% 16% • 11%
1	D	325	 73% 15% • 11%
1	E	325	 66% 21% • 11%

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
2	F	325	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a green segment on the left labeled '64%', a yellow segment in the middle labeled '23%', and a red segment on the right labeled '12%'. A small red square is positioned at the beginning of the bar, and a small black dot is at the end of the red segment.</p>

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	D16	C	401	-	-	X	-

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 14315 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 Thymidylate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	288	2286	1467	396	410	13	0	0	0
1	B	288	2286	1471	396	406	13	0	0	0
1	C	288	2240	1449	382	396	13	0	0	0
1	D	288	2281	1465	394	409	13	0	0	0
1	E	288	2271	1462	389	407	13	0	0	0

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	initiating methionine	UNP P04818
A	-10	ARG	-	expression tag	UNP P04818
A	-9	GLY	-	expression tag	UNP P04818
A	-8	SER	-	expression tag	UNP P04818
A	-7	HIS	-	expression tag	UNP P04818
A	-6	HIS	-	expression tag	UNP P04818
A	-5	HIS	-	expression tag	UNP P04818
A	-4	HIS	-	expression tag	UNP P04818
A	-3	HIS	-	expression tag	UNP P04818
A	-2	HIS	-	expression tag	UNP P04818
A	-1	GLY	-	expression tag	UNP P04818
A	0	SER	-	expression tag	UNP P04818
B	-11	MET	-	initiating methionine	UNP P04818
B	-10	ARG	-	expression tag	UNP P04818
B	-9	GLY	-	expression tag	UNP P04818
B	-8	SER	-	expression tag	UNP P04818
B	-7	HIS	-	expression tag	UNP P04818
B	-6	HIS	-	expression tag	UNP P04818
B	-5	HIS	-	expression tag	UNP P04818

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	HIS	-	expression tag	UNP P04818
B	-3	HIS	-	expression tag	UNP P04818
B	-2	HIS	-	expression tag	UNP P04818
B	-1	GLY	-	expression tag	UNP P04818
B	0	SER	-	expression tag	UNP P04818
C	-11	MET	-	initiating methionine	UNP P04818
C	-10	ARG	-	expression tag	UNP P04818
C	-9	GLY	-	expression tag	UNP P04818
C	-8	SER	-	expression tag	UNP P04818
C	-7	HIS	-	expression tag	UNP P04818
C	-6	HIS	-	expression tag	UNP P04818
C	-5	HIS	-	expression tag	UNP P04818
C	-4	HIS	-	expression tag	UNP P04818
C	-3	HIS	-	expression tag	UNP P04818
C	-2	HIS	-	expression tag	UNP P04818
C	-1	GLY	-	expression tag	UNP P04818
C	0	SER	-	expression tag	UNP P04818
D	-11	MET	-	initiating methionine	UNP P04818
D	-10	ARG	-	expression tag	UNP P04818
D	-9	GLY	-	expression tag	UNP P04818
D	-8	SER	-	expression tag	UNP P04818
D	-7	HIS	-	expression tag	UNP P04818
D	-6	HIS	-	expression tag	UNP P04818
D	-5	HIS	-	expression tag	UNP P04818
D	-4	HIS	-	expression tag	UNP P04818
D	-3	HIS	-	expression tag	UNP P04818
D	-2	HIS	-	expression tag	UNP P04818
D	-1	GLY	-	expression tag	UNP P04818
D	0	SER	-	expression tag	UNP P04818
E	-11	MET	-	initiating methionine	UNP P04818
E	-10	ARG	-	expression tag	UNP P04818
E	-9	GLY	-	expression tag	UNP P04818
E	-8	SER	-	expression tag	UNP P04818
E	-7	HIS	-	expression tag	UNP P04818
E	-6	HIS	-	expression tag	UNP P04818
E	-5	HIS	-	expression tag	UNP P04818
E	-4	HIS	-	expression tag	UNP P04818
E	-3	HIS	-	expression tag	UNP P04818
E	-2	HIS	-	expression tag	UNP P04818
E	-1	GLY	-	expression tag	UNP P04818
E	0	SER	-	expression tag	UNP P04818

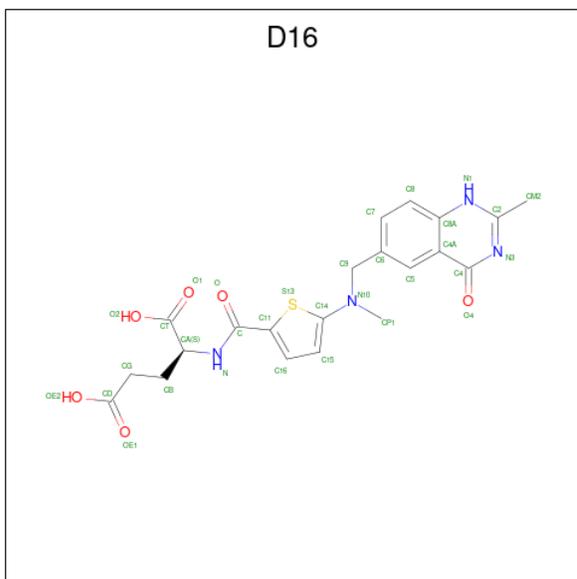
- Molecule 2 is a protein called Thymidylate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	F	287	2245	1440	384	407	14	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-11	MET	-	initiating methionine	UNP P04818
F	-10	ARG	-	expression tag	UNP P04818
F	-9	GLY	-	expression tag	UNP P04818
F	-8	SER	-	expression tag	UNP P04818
F	-7	HIS	-	expression tag	UNP P04818
F	-6	HIS	-	expression tag	UNP P04818
F	-5	HIS	-	expression tag	UNP P04818
F	-4	HIS	-	expression tag	UNP P04818
F	-3	HIS	-	expression tag	UNP P04818
F	-2	HIS	-	expression tag	UNP P04818
F	-1	GLY	-	expression tag	UNP P04818
F	0	SER	-	expression tag	UNP P04818

- Molecule 3 is TOMUDEX (three-letter code: D16) (formula: C<sub>21</sub>H<sub>22</sub>N<sub>4</sub>O<sub>6</sub>S) (labeled as "Ligand of Interest" by depositor).



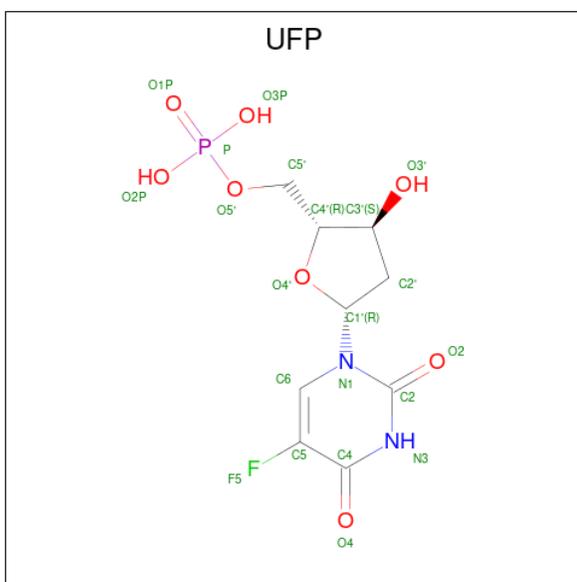
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	A	1	32	21	4	6	1	0	0
3	B	1	32	21	4	6	1	0	0

*Continued on next page...*

Continued from previous page...

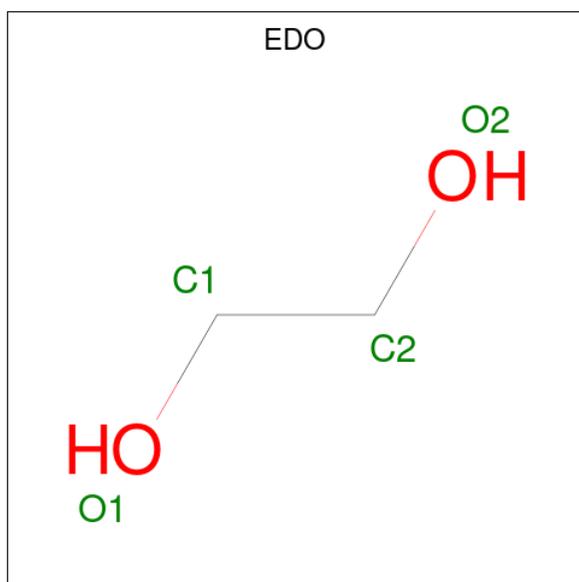
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	C	1	Total	C	N	O	S	0	0
			32	21	4	6	1		
3	D	1	Total	C	N	O	S	0	0
			32	21	4	6	1		
3	E	1	Total	C	N	O	S	0	0
			32	21	4	6	1		
3	F	1	Total	C	N	O	S	0	0
			32	21	4	6	1		

- Molecule 4 is 5-FLUORO-2'-DEOXYURIDINE-5'-MONOPHOSPHATE (three-letter code: UFP) (formula: C<sub>9</sub>H<sub>12</sub>FN<sub>2</sub>O<sub>8</sub>P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
4	A	1	Total	C	F	N	O	P	0	0
			21	9	1	2	8	1		
4	B	1	Total	C	F	N	O	P	0	0
			21	9	1	2	8	1		
4	C	1	Total	C	F	N	O	P	0	0
			21	9	1	2	8	1		
4	D	1	Total	C	F	N	O	P	0	0
			21	9	1	2	8	1		
4	E	1	Total	C	F	N	O	P	0	0
			21	9	1	2	8	1		
4	F	1	Total	C	F	N	O	P	0	0
			21	9	1	2	8	1		

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

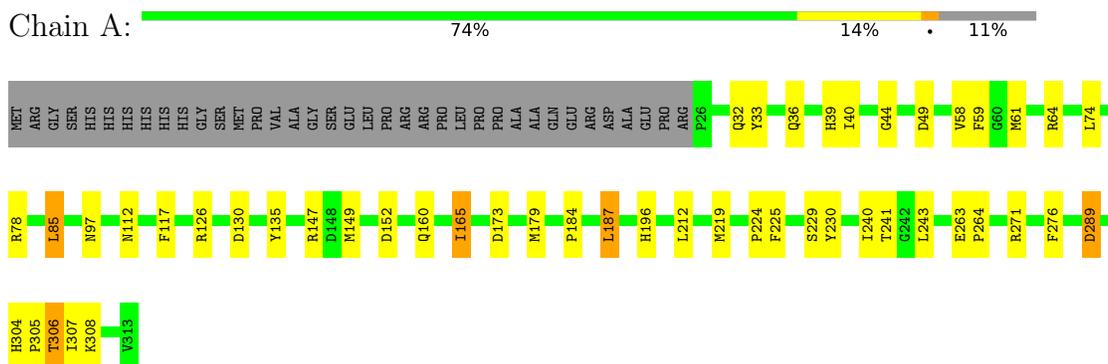
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	66	Total O 66 66	0	0
6	B	80	Total O 80 80	0	0
6	C	66	Total O 66 66	0	0
6	D	65	Total O 65 65	0	0
6	E	50	Total O 50 50	0	0
6	F	49	Total O 49 49	0	0

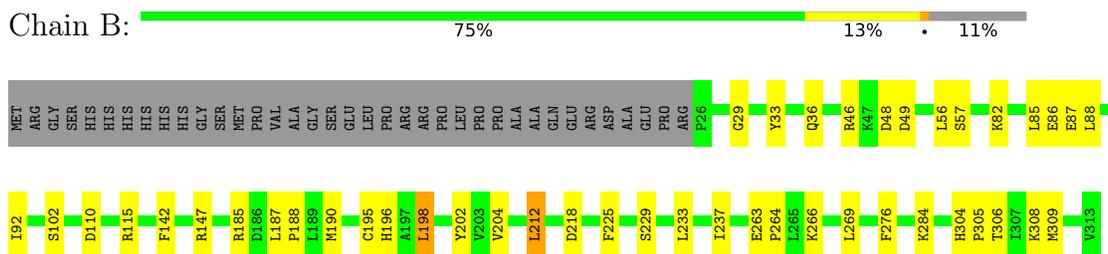
### 3 Residue-property plots [i](#)

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.

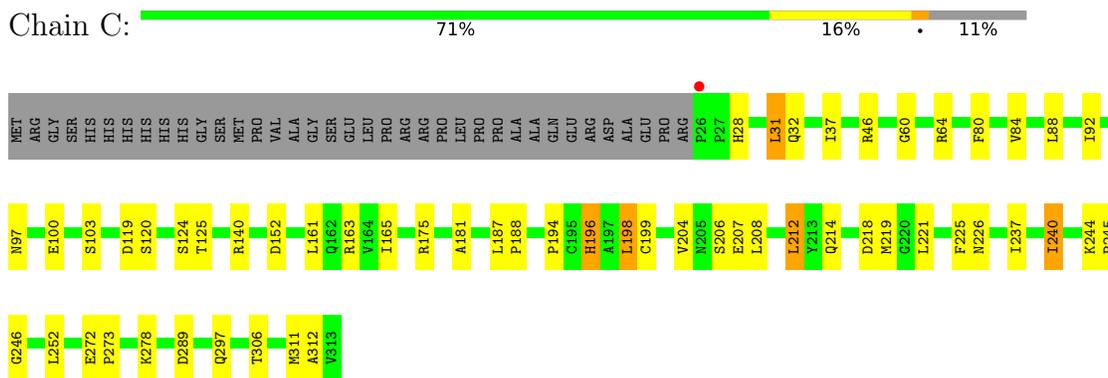
- Molecule 1: Thymidylate synthase



- Molecule 1: Thymidylate synthase



- Molecule 1: Thymidylate synthase



- Molecule 1: Thymidylate synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	61.72Å 95.87Å 103.84Å 112.39° 91.47° 109.17°	Depositor
Resolution (Å)	47.33 – 2.60 47.29 – 2.60	Depositor EDS
% Data completeness (in resolution range)	96.0 (47.33-2.60) 96.0 (47.29-2.60)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.10 (at 2.61Å)	Xtrriage
Refinement program	REFMAC 5.8.0258	Depositor
R, $R_{free}$	0.172 , 0.232 0.173 , 0.232	Depositor DCC
$R_{free}$ test set	3084 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	53.1	Xtrriage
Anisotropy	0.020	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 42.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.043 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	14315	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.06% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: D16, EDO, CME, UFP

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	0.34	0/2346	0.75	0/3178
1	B	0.35	0/2346	0.79	0/3177
1	C	0.33	0/2300	0.76	0/3121
1	D	0.34	0/2341	0.76	0/3172
1	E	0.34	0/2331	0.74	0/3160
2	F	0.34	0/2294	0.73	0/3115
All	All	0.34	0/13958	0.75	0/18923

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	2286	0	2218	35	0
1	B	2286	0	2229	24	0
1	C	2240	0	2152	36	0
1	D	2281	0	2220	32	0
1	E	2271	0	2190	53	0
2	F	2245	0	2129	52	0
3	A	32	0	20	2	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	32	0	20	2	0
3	C	32	0	20	9	0
3	D	32	0	20	4	0
3	E	32	0	20	6	0
3	F	32	0	20	1	0
4	A	21	0	10	0	0
4	B	21	0	10	1	0
4	C	21	0	10	3	0
4	D	21	0	10	0	0
4	E	21	0	10	2	0
4	F	21	0	10	0	0
5	A	4	0	6	2	0
5	B	4	0	6	0	0
5	C	4	0	6	0	0
6	A	66	0	0	1	0
6	B	80	0	0	1	0
6	C	66	0	0	2	0
6	D	65	0	0	1	0
6	E	50	0	0	2	0
6	F	49	0	0	1	0
All	All	14315	0	13336	231	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 8.

The worst 5 of 231 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)
2:F:123:PHE:HB3	2:F:126:ARG:HD2	1.45	0.99
1:C:225:PHE:CD2	3:C:401:D16:H16	2.04	0.93
1:E:221:LEU:HD11	3:E:401:D16:HB2	1.52	0.92
1:A:271:ARG:HH11	1:A:304:HIS:HB3	1.34	0.91
2:F:123:PHE:HB3	2:F:126:ARG:CD	2.05	0.86

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	286/325 (88%)	266 (93%)	20 (7%)	0	100	100
1	B	286/325 (88%)	272 (95%)	14 (5%)	0	100	100
1	C	286/325 (88%)	267 (93%)	19 (7%)	0	100	100
1	D	286/325 (88%)	263 (92%)	23 (8%)	0	100	100
1	E	286/325 (88%)	258 (90%)	28 (10%)	0	100	100
2	F	284/325 (87%)	261 (92%)	23 (8%)	0	100	100
All	All	1714/1950 (88%)	1587 (93%)	127 (7%)	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	237/281 (84%)	228 (96%)	9 (4%)	33	59
1	B	236/281 (84%)	223 (94%)	13 (6%)	21	43
1	C	224/281 (80%)	207 (92%)	17 (8%)	13	26
1	D	238/281 (85%)	224 (94%)	14 (6%)	19	39
1	E	231/281 (82%)	219 (95%)	12 (5%)	23	46
2	F	226/280 (81%)	208 (92%)	18 (8%)	12	24
All	All	1392/1685 (83%)	1309 (94%)	83 (6%)	19	39

5 of 83 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	125	THR
2	F	115	ARG
1	E	196	HIS
2	F	45	VAL
2	F	190	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	HIS
1	A	156	GLN
1	A	211	GLN
2	F	112	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](#)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	CME	F	199	2	8,9,10	0.65	0	5,9,11	0.86	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
2	CME	F	199	2	-	2/5/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	199	CME	CE-SD-SG-CB
2	F	199	CME	SD-CE-CZ-OH

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	199	CME	3	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

15 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
3	D16	D	401	-	30,34,34	1.59	4 (13%)	37,48,48	2.20	10 (27%)
4	UFP	D	402	-	22,22,22	1.46	2 (9%)	33,33,33	2.50	10 (30%)
4	UFP	E	402	-	22,22,22	1.64	4 (18%)	33,33,33	2.35	9 (27%)
4	UFP	F	402	-	22,22,22	1.65	5 (22%)	33,33,33	2.95	12 (36%)
3	D16	C	401	-	30,34,34	1.30	3 (10%)	37,48,48	1.19	2 (5%)
4	UFP	A	402	-	22,22,22	1.54	4 (18%)	33,33,33	2.51	12 (36%)
5	EDO	B	403	-	3,3,3	0.15	0	2,2,2	0.27	0
3	D16	B	401	-	30,34,34	1.42	3 (10%)	37,48,48	1.44	5 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	D16	E	401	-	30,34,34	1.33	4 (13%)	37,48,48	1.27	2 (5%)
4	UFP	B	402	-	22,22,22	1.64	6 (27%)	33,33,33	2.20	10 (30%)
4	UFP	C	402	-	22,22,22	1.46	4 (18%)	33,33,33	2.64	10 (30%)
5	EDO	C	403	-	3,3,3	0.19	0	2,2,2	0.35	0
3	D16	A	401	-	30,34,34	1.50	2 (6%)	37,48,48	1.63	6 (16%)
3	D16	F	401	-	30,34,34	1.36	4 (13%)	37,48,48	1.29	2 (5%)
5	EDO	A	403	-	3,3,3	0.10	0	2,2,2	0.13	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	D16	D	401	-	-	2/19/25/25	0/3/3/3
4	UFP	D	402	-	-	2/10/22/22	0/2/2/2
4	UFP	E	402	-	-	2/10/22/22	0/2/2/2
4	UFP	F	402	-	-	2/10/22/22	0/2/2/2
3	D16	C	401	-	-	5/19/25/25	0/3/3/3
4	UFP	A	402	-	-	2/10/22/22	0/2/2/2
5	EDO	B	403	-	-	1/1/1/1	-
3	D16	B	401	-	-	7/19/25/25	0/3/3/3
3	D16	E	401	-	-	4/19/25/25	0/3/3/3
4	UFP	B	402	-	-	1/10/22/22	0/2/2/2
4	UFP	C	402	-	-	1/10/22/22	0/2/2/2
5	EDO	C	403	-	-	1/1/1/1	-
3	D16	A	401	-	-	5/19/25/25	0/3/3/3
3	D16	F	401	-	-	4/19/25/25	0/3/3/3
5	EDO	A	403	-	-	1/1/1/1	-

The worst 5 of 45 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	401	D16	C4A-C8A	5.71	1.50	1.41
3	B	401	D16	C4A-C8A	5.60	1.49	1.41
3	A	401	D16	C4A-C8A	5.26	1.49	1.41
4	A	402	UFP	C6-C5	4.65	1.40	1.33
3	C	401	D16	C4A-C8A	4.53	1.48	1.41

The worst 5 of 90 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	402	UFP	O4-C4-C5	-8.48	118.07	125.72
4	F	402	UFP	C5-C4-N3	7.95	120.39	112.56
4	F	402	UFP	O4-C4-C5	-7.77	118.71	125.72
3	D	401	D16	C11-C-N	6.88	127.96	115.21
4	D	402	UFP	O4-C4-C5	-6.86	119.53	125.72

There are no chirality outliers.

5 of 40 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	401	D16	CB-CA-N-C
3	E	401	D16	CB-CA-N-C
3	A	401	D16	N-CA-CB-CG
3	C	401	D16	N-CA-CB-CG
3	D	401	D16	N-CA-CB-CG

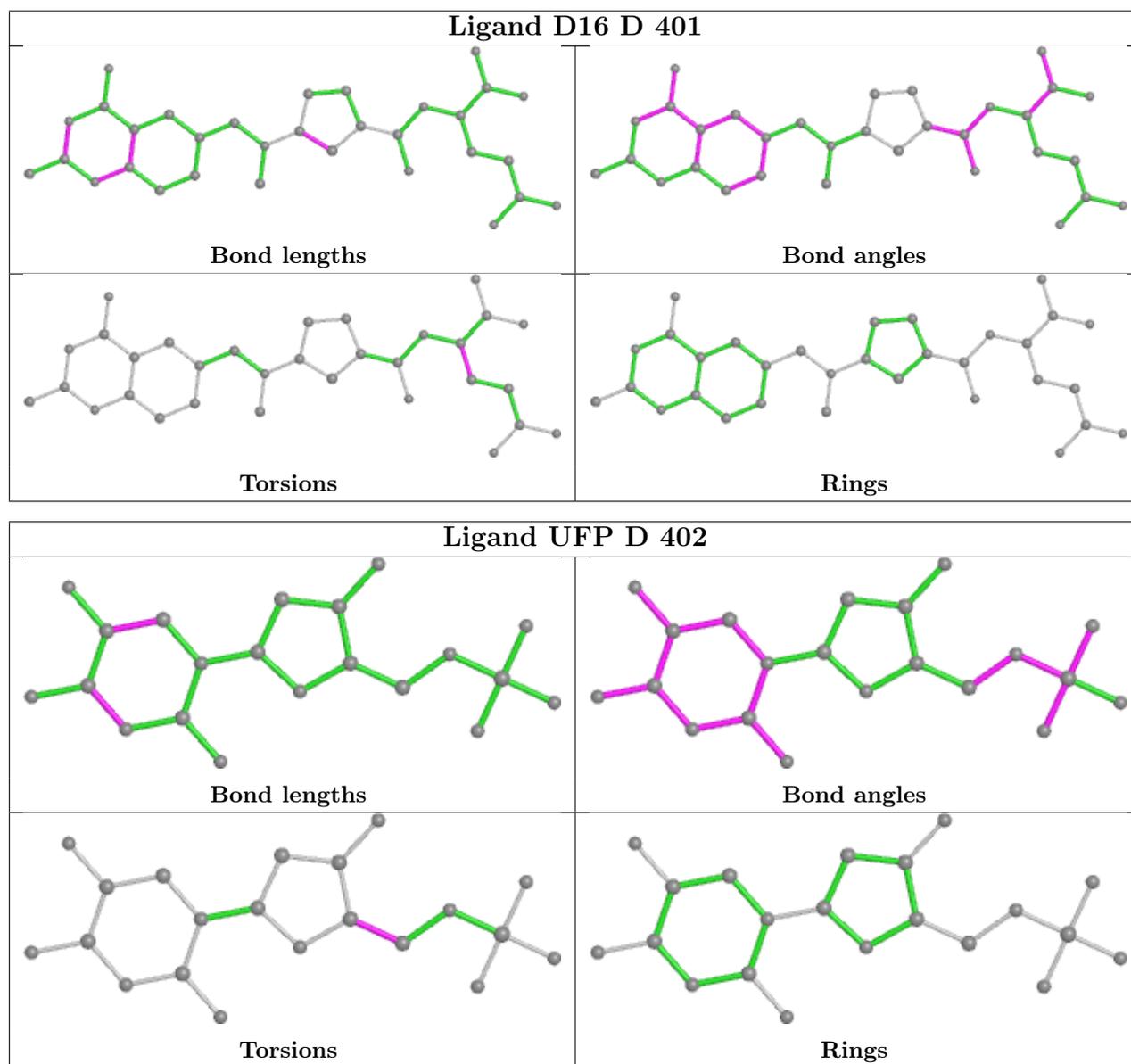
There are no ring outliers.

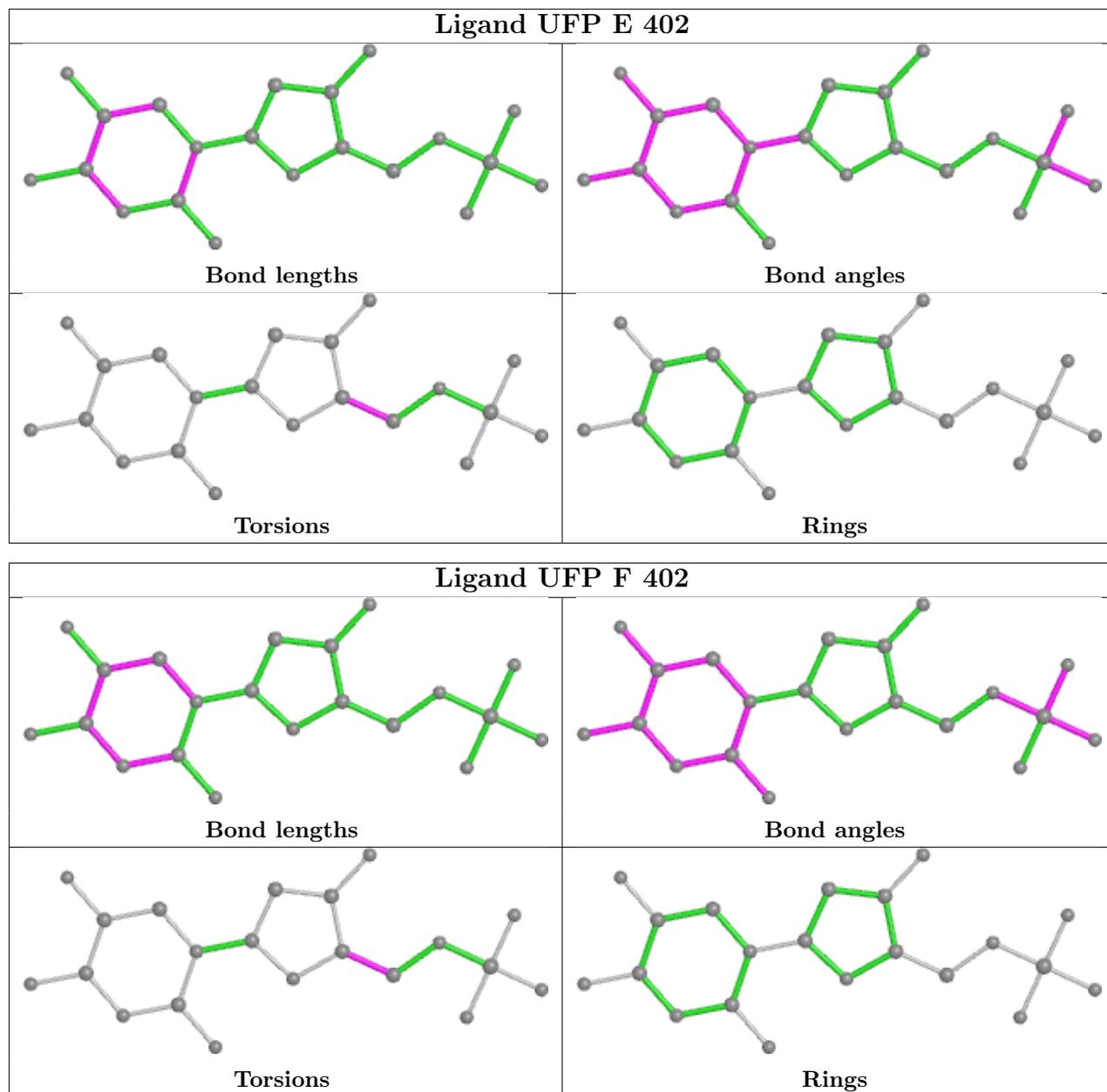
10 monomers are involved in 29 short contacts:

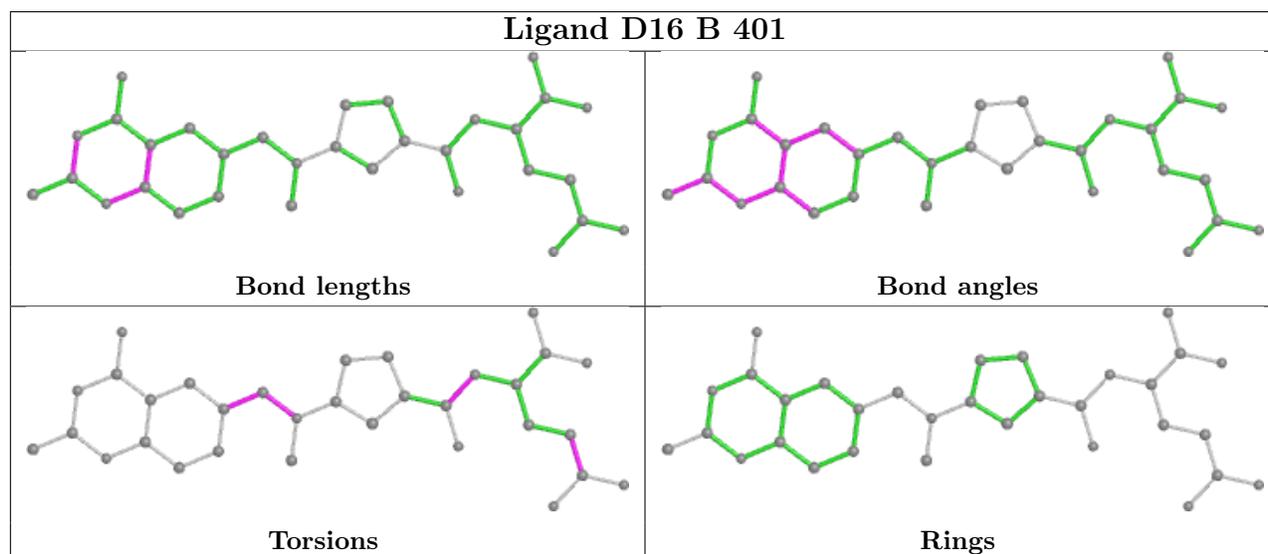
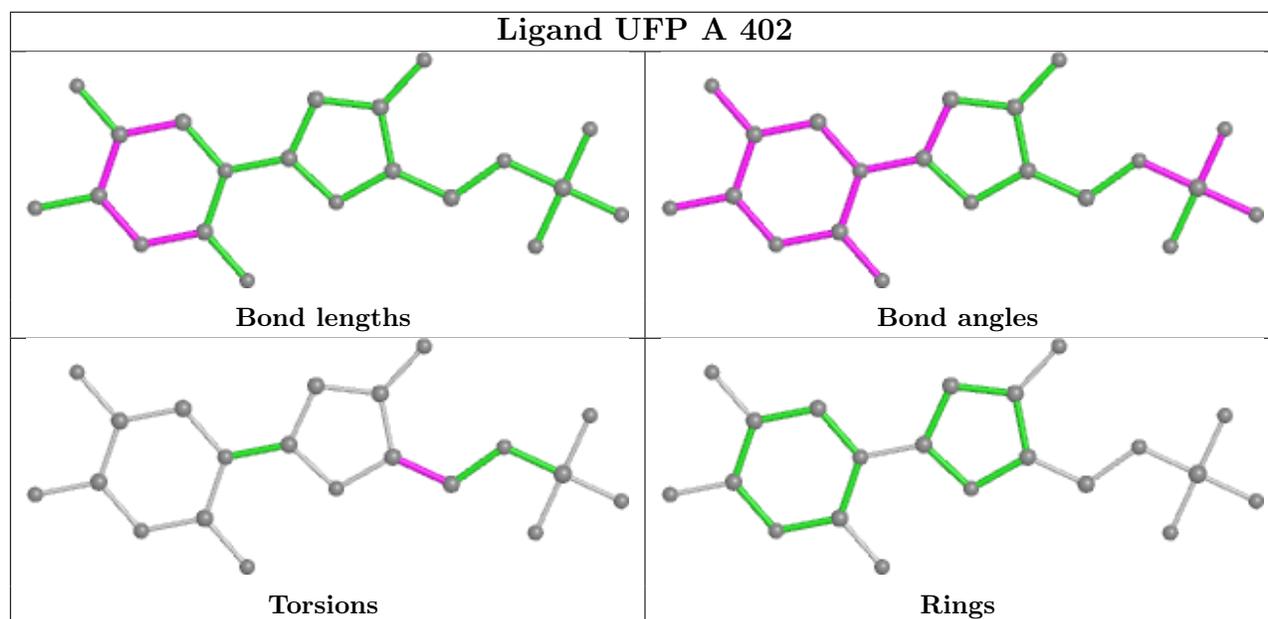
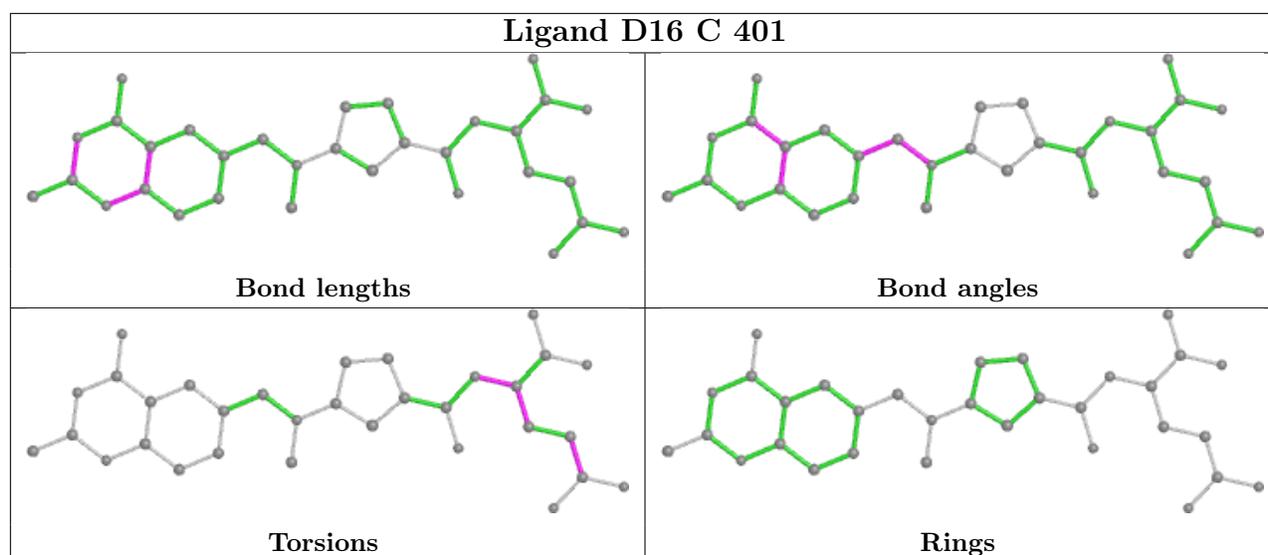
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	401	D16	4	0
4	E	402	UFP	2	0
3	C	401	D16	9	0
3	B	401	D16	2	0
3	E	401	D16	6	0
4	B	402	UFP	1	0
4	C	402	UFP	3	0
3	A	401	D16	2	0
3	F	401	D16	1	0
5	A	403	EDO	2	0

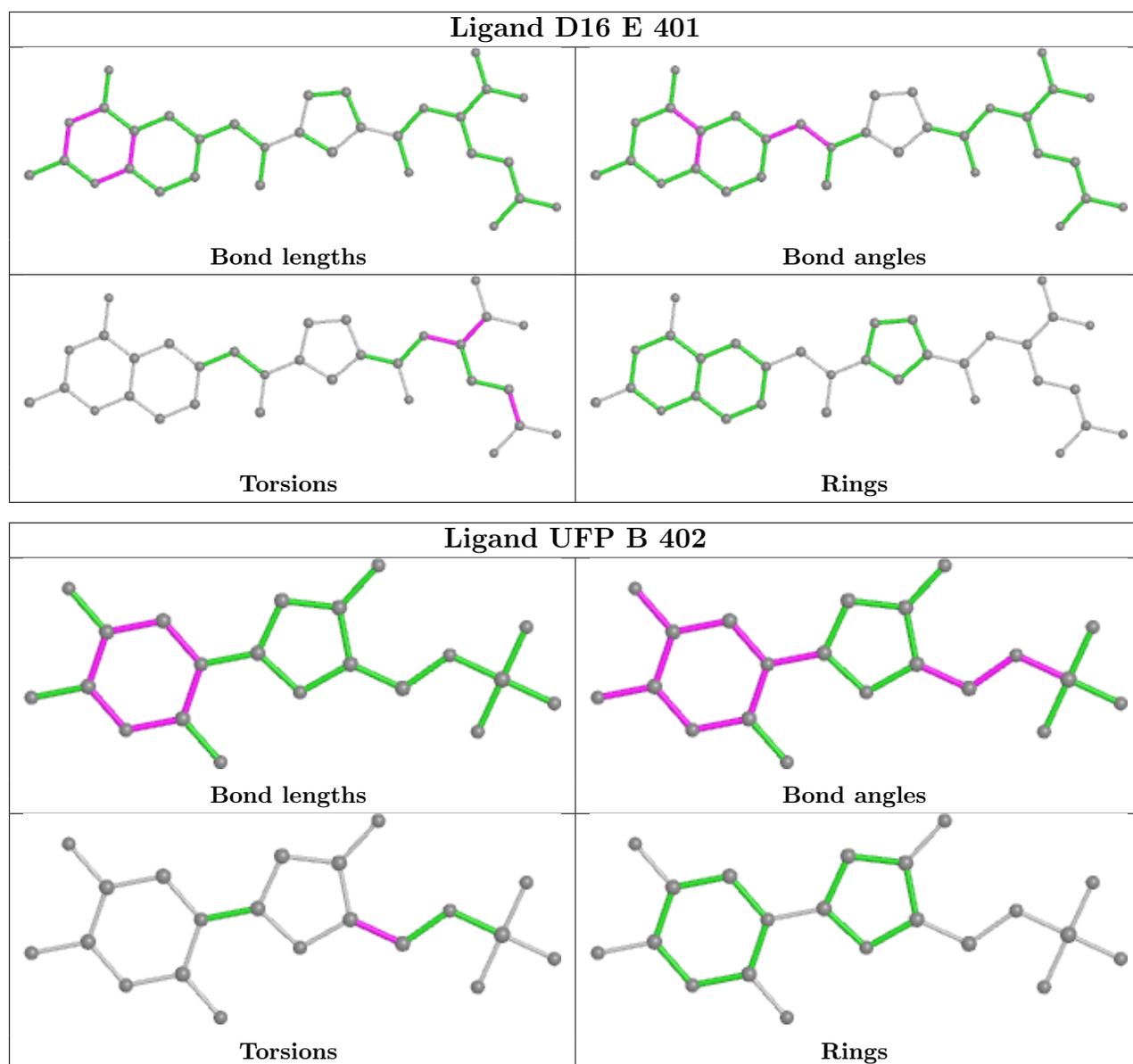
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

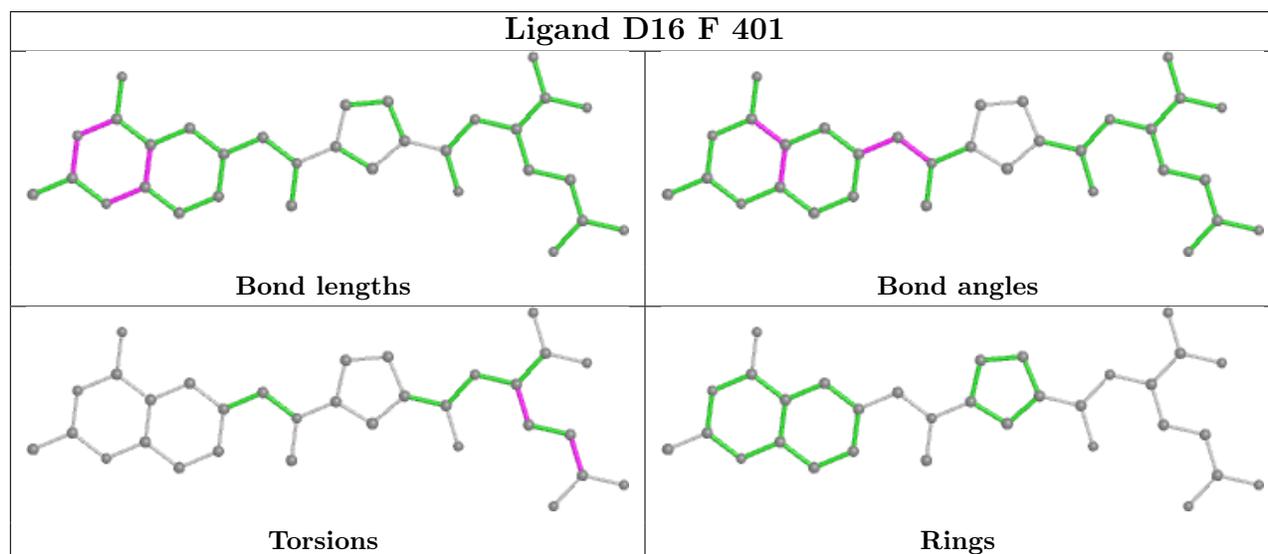
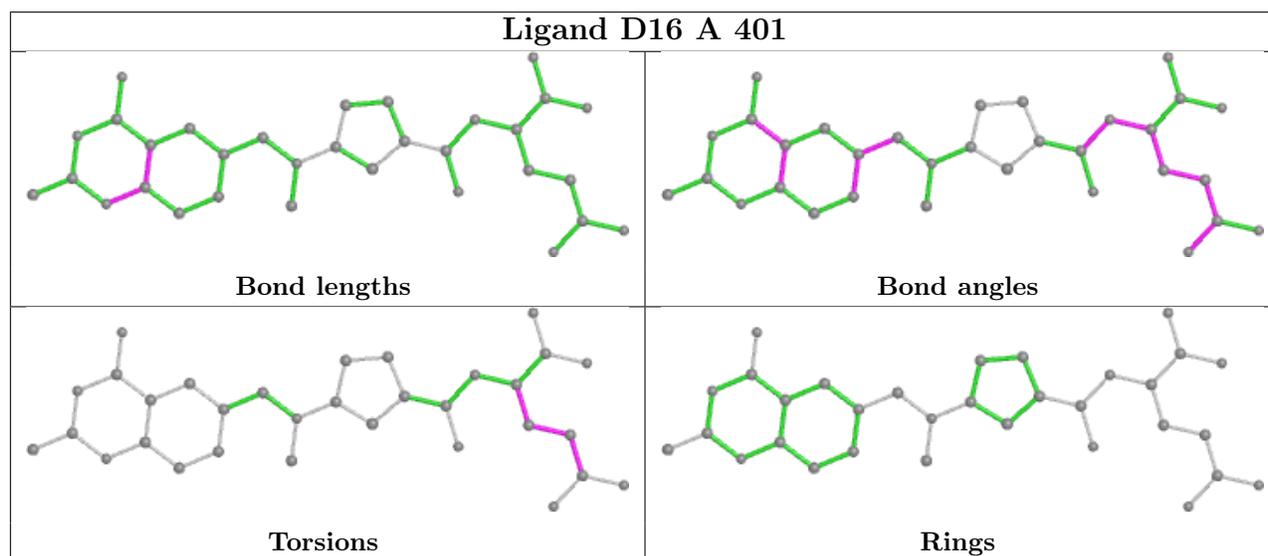
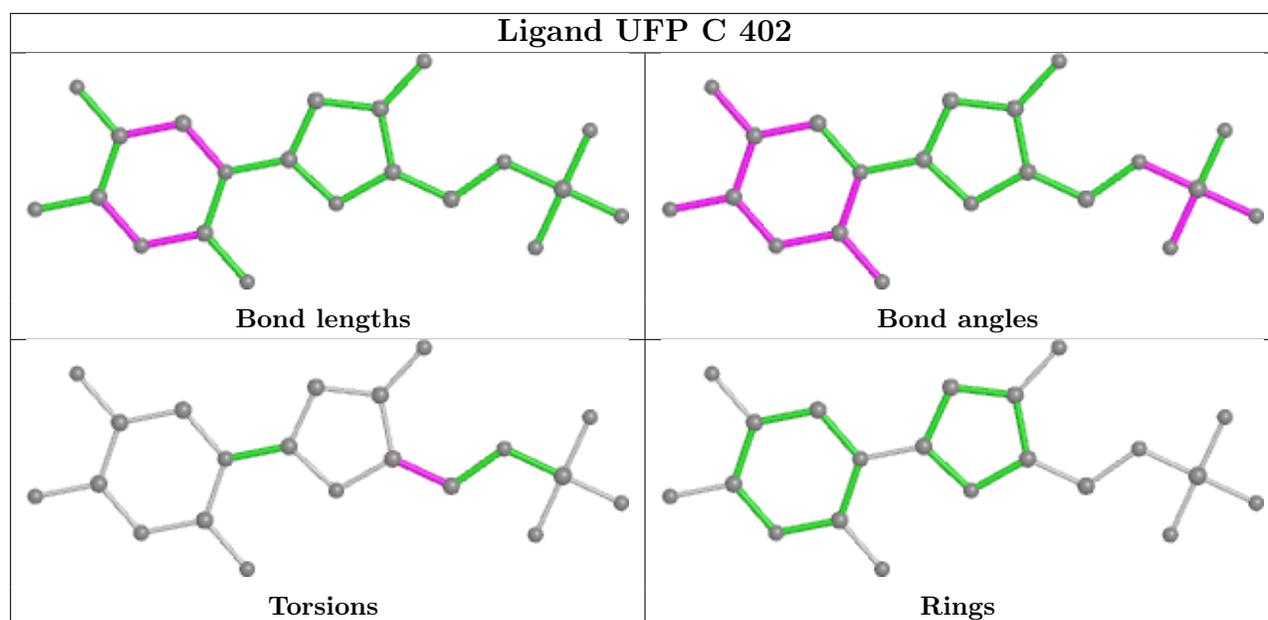
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.











## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<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	288/325 (88%)	-0.68	0 100 100	26, 49, 75, 94	0
1	B	288/325 (88%)	-0.85	0 100 100	25, 44, 66, 85	0
1	C	288/325 (88%)	-0.66	1 (0%) 94 93	28, 49, 81, 98	0
1	D	288/325 (88%)	-0.65	1 (0%) 94 93	27, 49, 73, 99	0
1	E	288/325 (88%)	-0.61	1 (0%) 94 93	30, 56, 81, 99	0
2	F	286/325 (88%)	-0.53	3 (1%) 82 80	27, 60, 91, 97	0
All	All	1726/1950 (88%)	-0.67	6 (0%) 94 93	25, 51, 81, 99	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	313	VAL	2.5
2	F	281	ILE	2.4
1	D	26	PRO	2.3
2	F	282	LEU	2.3
2	F	26	PRO	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	CME	F	199	10/11	0.93	0.21	37,52,84,98	0

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

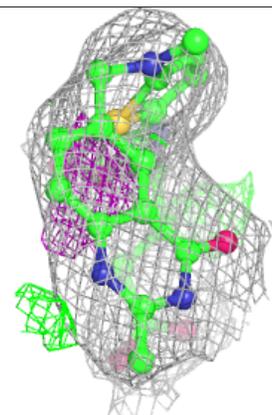
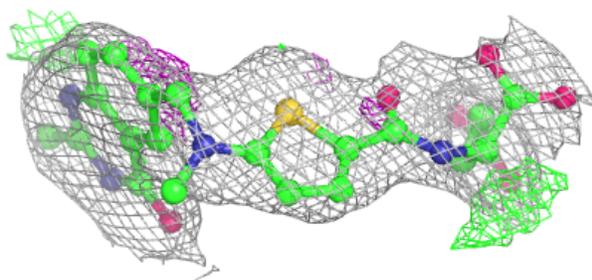
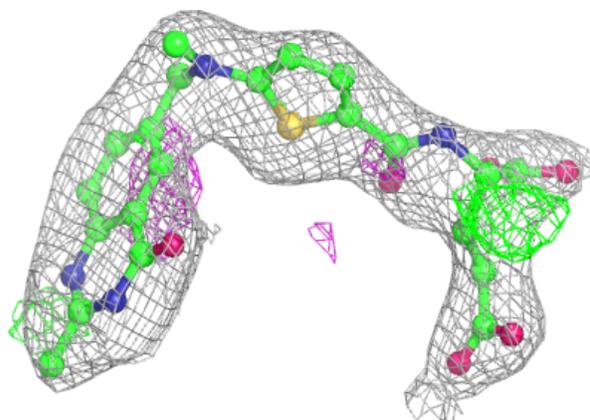
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	EDO	C	403	4/4	0.87	0.18	58,62,64,67	0
5	EDO	B	403	4/4	0.89	0.31	62,64,66,69	0
3	D16	C	401	32/32	0.93	0.16	30,46,80,83	0
3	D16	E	401	32/32	0.93	0.13	38,56,77,82	0
3	D16	B	401	32/32	0.95	0.12	40,55,91,99	0
5	EDO	A	403	4/4	0.95	0.14	64,65,66,73	0
3	D16	D	401	32/32	0.96	0.14	37,49,75,80	0
3	D16	A	401	32/32	0.96	0.15	36,55,96,99	0
3	D16	F	401	32/32	0.96	0.15	44,62,99,99	0
4	UFP	D	402	21/21	0.98	0.15	36,40,46,54	0
4	UFP	E	402	21/21	0.98	0.12	31,40,49,64	0
4	UFP	F	402	21/21	0.98	0.15	38,42,49,68	0
4	UFP	A	402	21/21	0.99	0.17	32,37,49,61	0
4	UFP	B	402	21/21	0.99	0.13	30,39,51,77	0
4	UFP	C	402	21/21	0.99	0.15	34,38,42,58	0

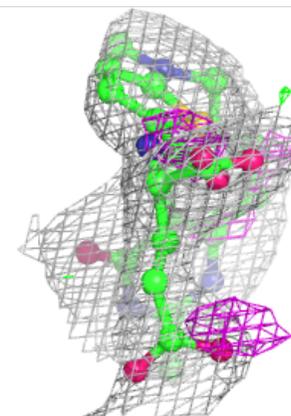
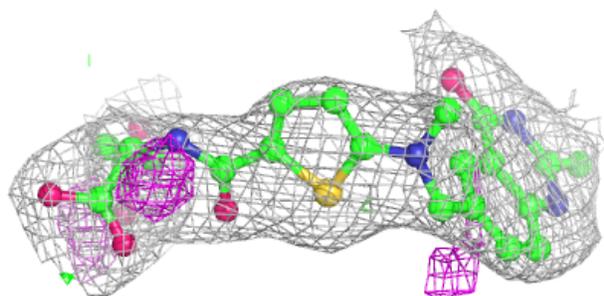
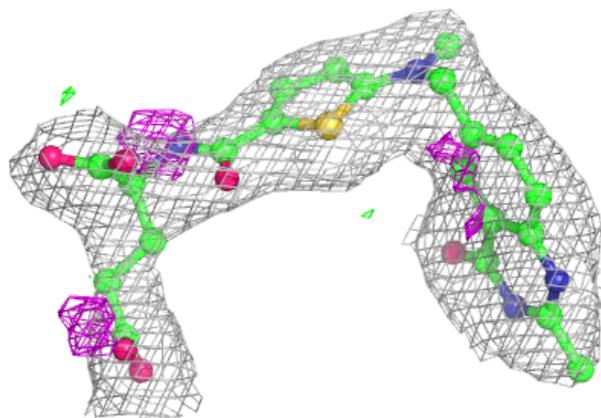
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around D16 C 401:**

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

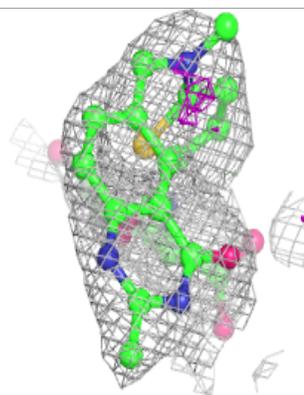
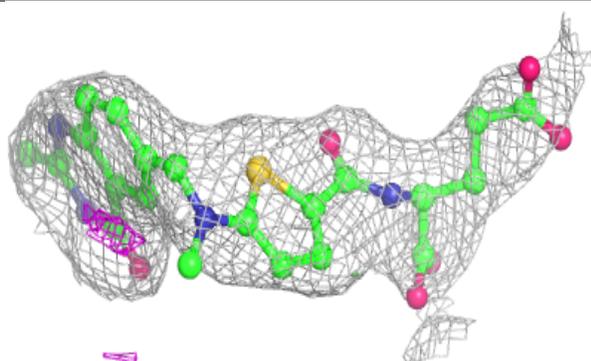
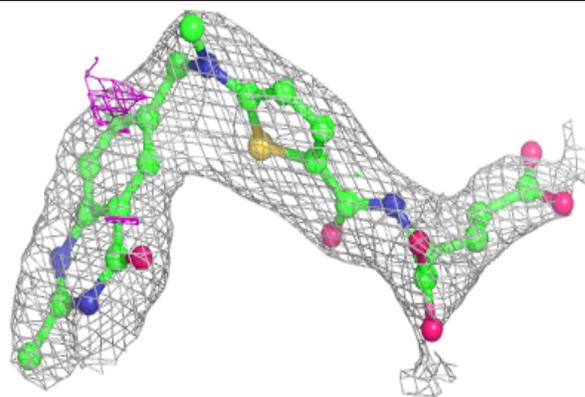
**Electron density around D16 E 401:**

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

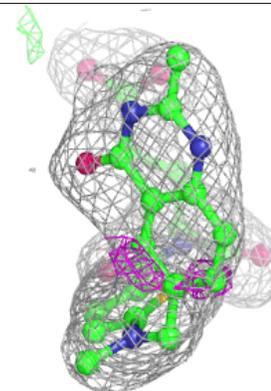
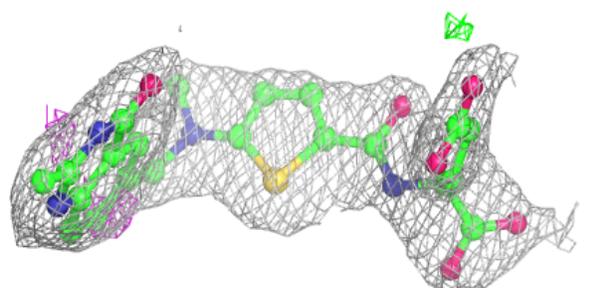
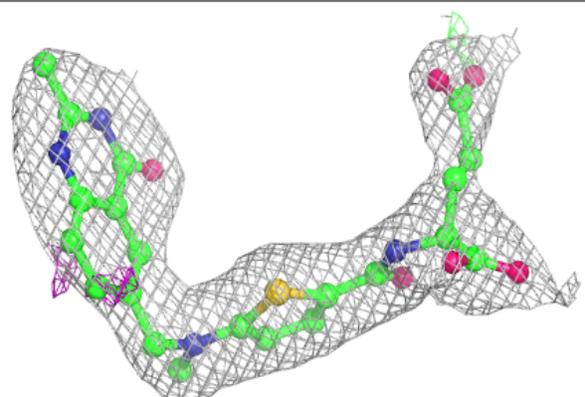


**Electron density around D16 B 401:**

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

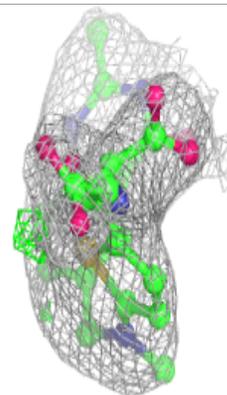
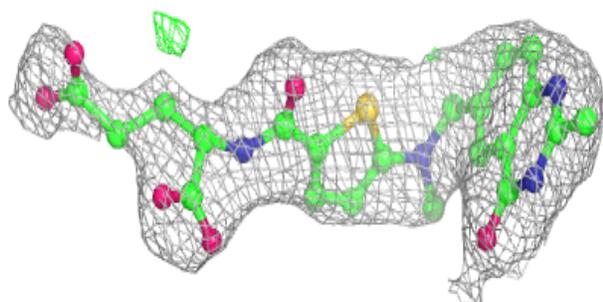
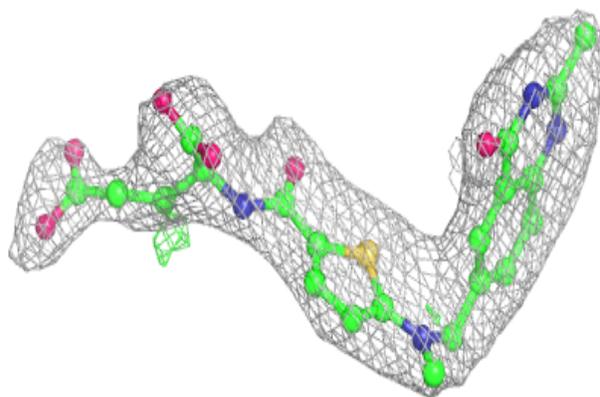
**Electron density around D16 D 401:**

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

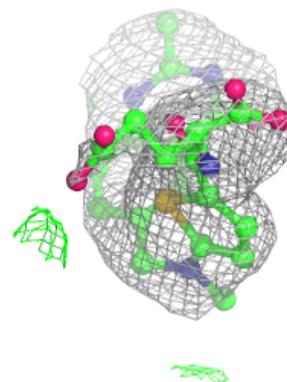
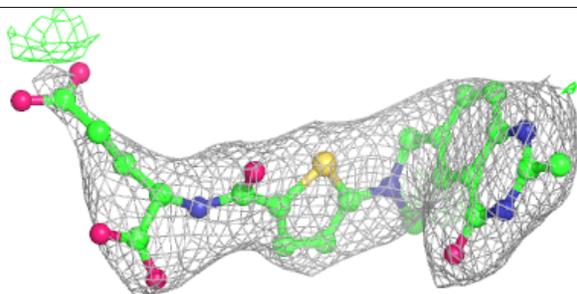
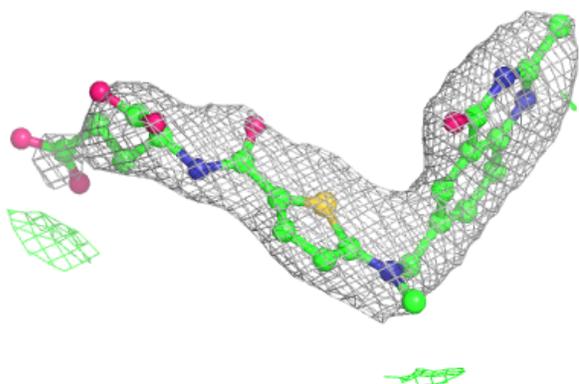


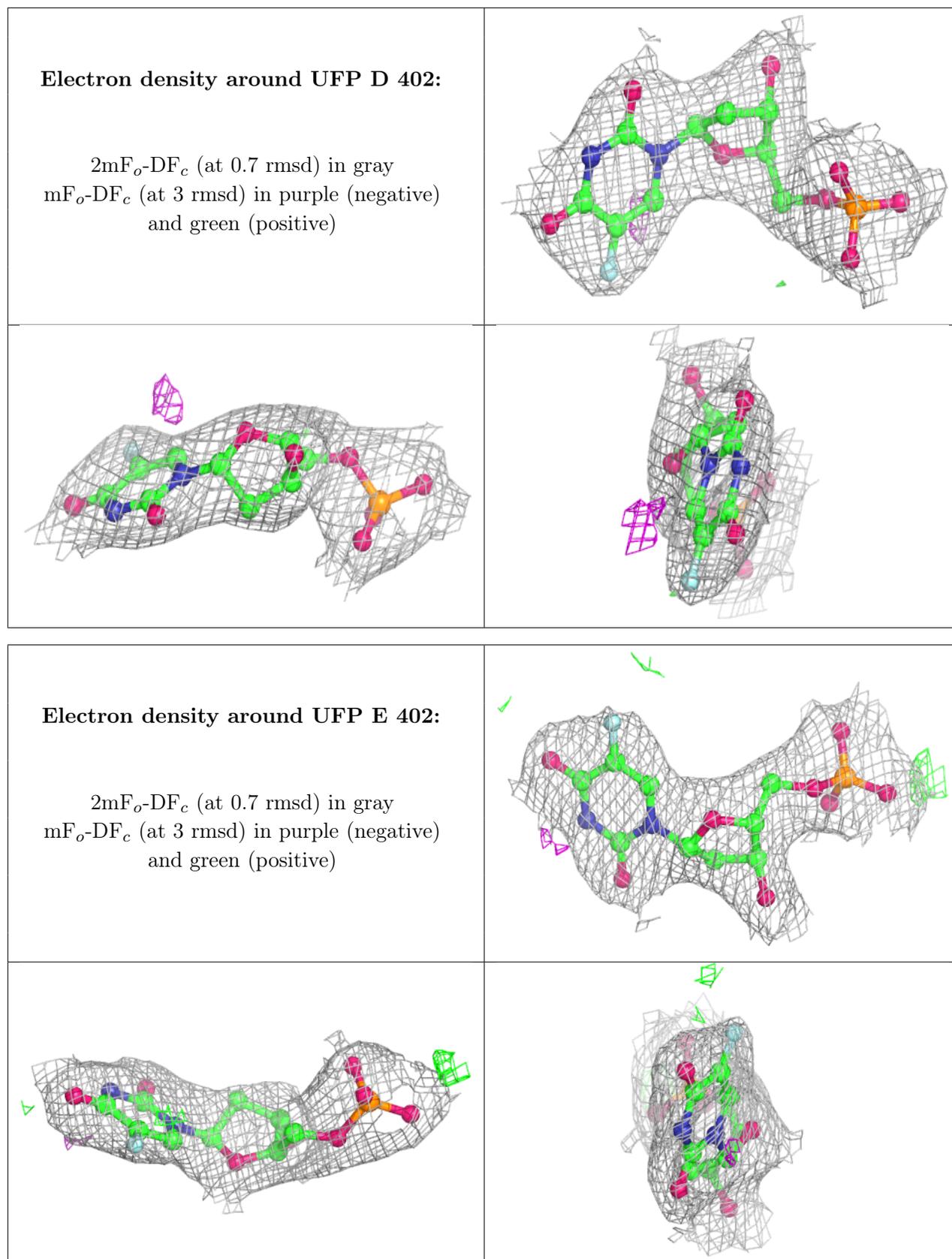
**Electron density around D16 A 401:**

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

**Electron density around D16 F 401:**

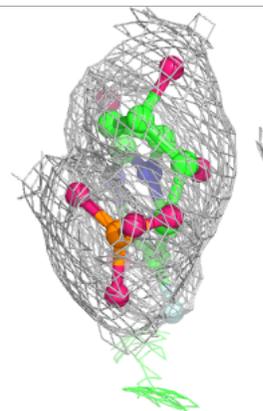
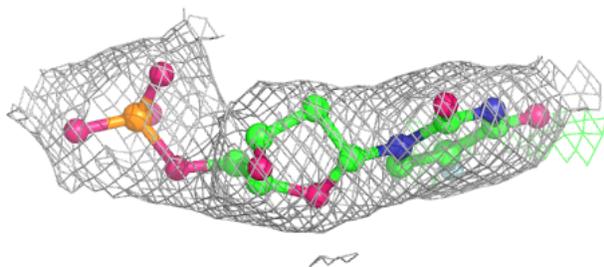
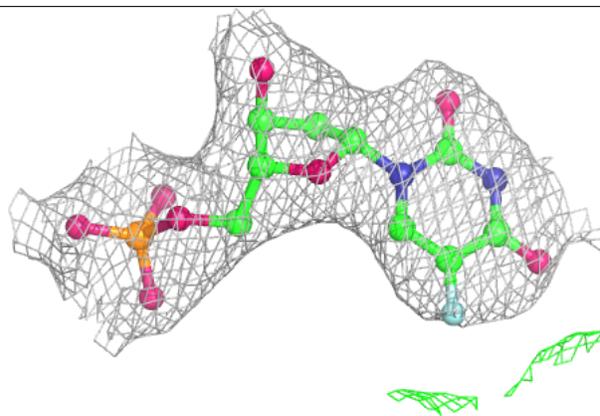
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



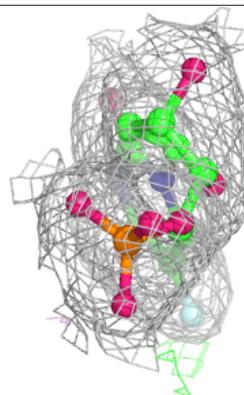
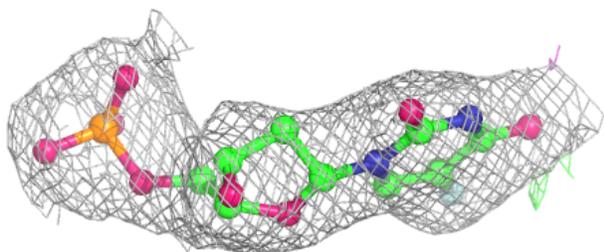
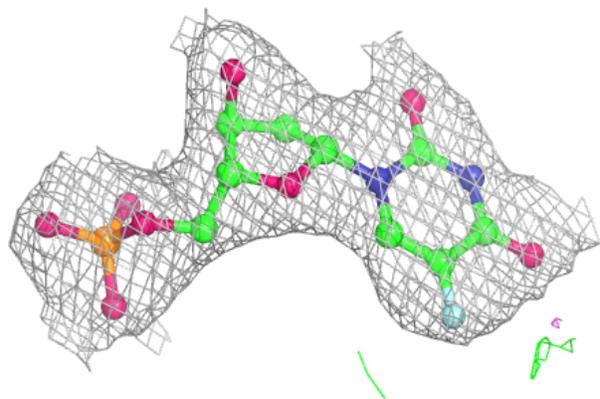


**Electron density around UFP F 402:**

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

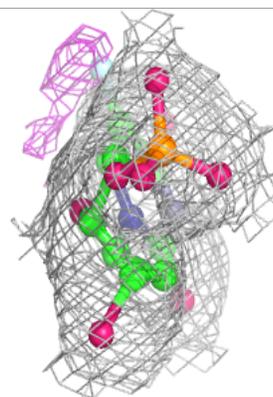
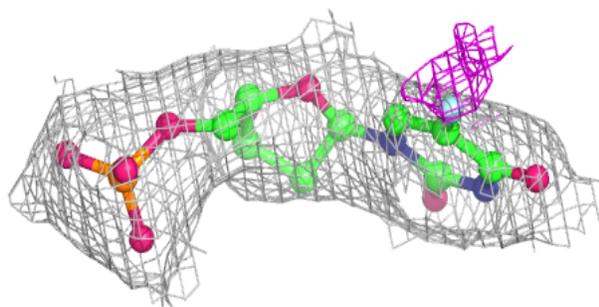
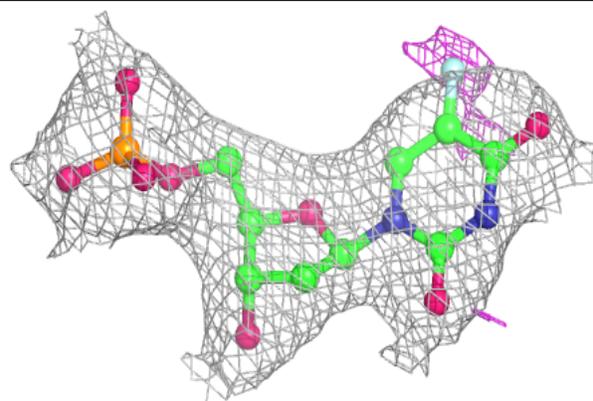
**Electron density around UFP A 402:**

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

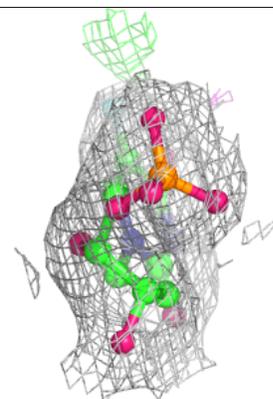
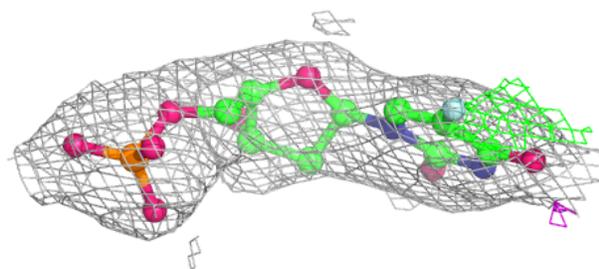
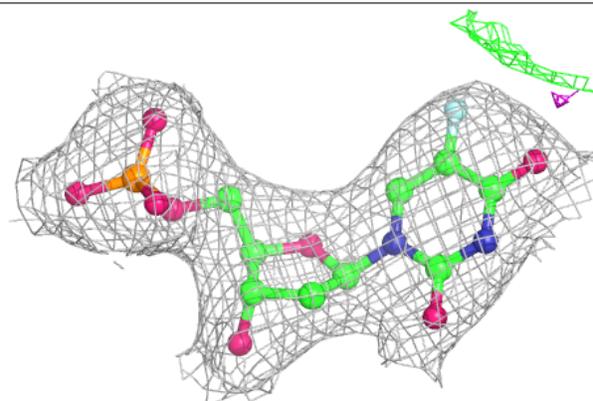


**Electron density around UFP B 402:**

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

**Electron density around UFP C 402:**

$2mF_o-DF_c$  (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.