



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 14, 2023 – 12:48 PM EDT

PDB ID : 1QZF  
Title : Crystal structure of DHFR-TS from *Cryptosporidium hominis*  
Authors : O'Neil, R.H.; Lilien, R.H.; Donald, B.R.; Stroud, R.M.; Anderson, A.C.  
Deposited on : 2003-09-16  
Resolution : 2.80 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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35  
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) : 2.35

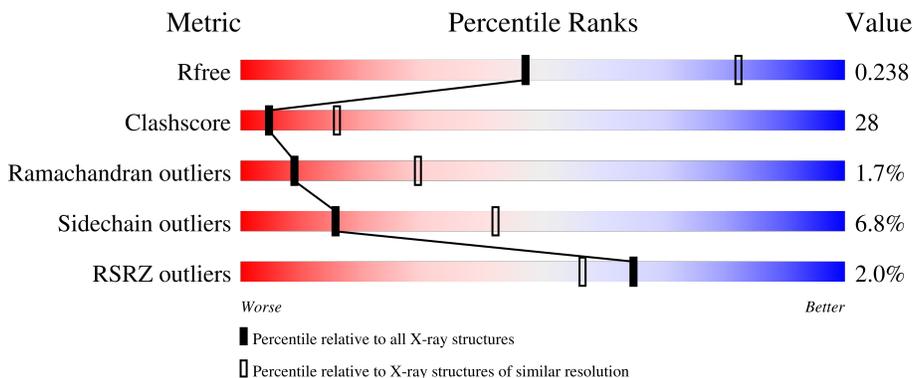
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	521	
1	B	521	
1	C	521	
1	D	521	
1	E	521	

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:

<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
2	UMP	A	603	-	-	X	-
2	UMP	B	607	-	-	X	-
2	UMP	C	611	-	-	X	-
3	CB3	A	604	X	-	-	-
3	CB3	B	608	X	-	-	-
3	CB3	C	612	X	-	-	-
3	CB3	D	616	X	-	-	-
3	CB3	E	620	X	-	-	-
4	FOL	A	605	-	-	X	-
4	FOL	D	617	-	-	X	-
4	FOL	E	621	-	-	X	-

## 2 Entry composition [i](#)

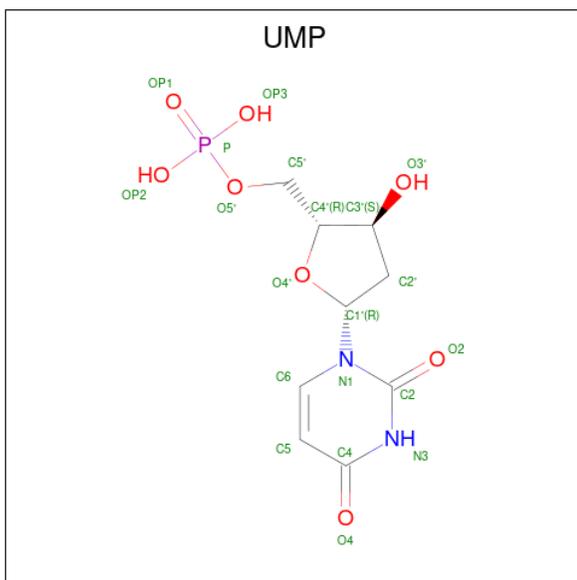
There are 6 unique types of molecules in this entry. The entry contains 22196 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 bifunctional dihydrofolate reductase-thymidylate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	519	Total 4223	C 2694	N 713	O 793	S 23	0	0	0
1	B	519	Total 4223	C 2694	N 713	O 793	S 23	0	0	0
1	C	519	Total 4223	C 2694	N 713	O 793	S 23	0	0	0
1	D	519	Total 4223	C 2694	N 713	O 793	S 23	0	0	0
1	E	519	Total 4223	C 2694	N 713	O 793	S 23	0	0	0

- Molecule 2 is 2'-DEOXYURIDINE 5'-MONOPHOSPHATE (three-letter code: UMP) (formula: C<sub>9</sub>H<sub>13</sub>N<sub>2</sub>O<sub>8</sub>P).



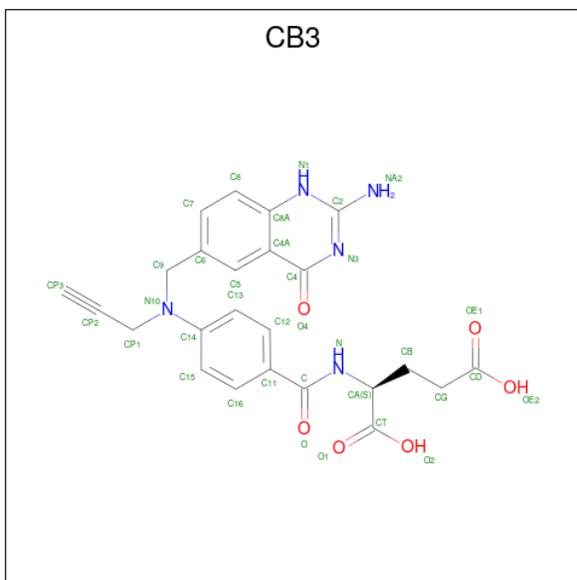
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total 20	C 9	N 2	O 8	P 1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
2	C	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
2	D	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
2	E	1	Total	C	N	O	P	0	0
			20	9	2	8	1		

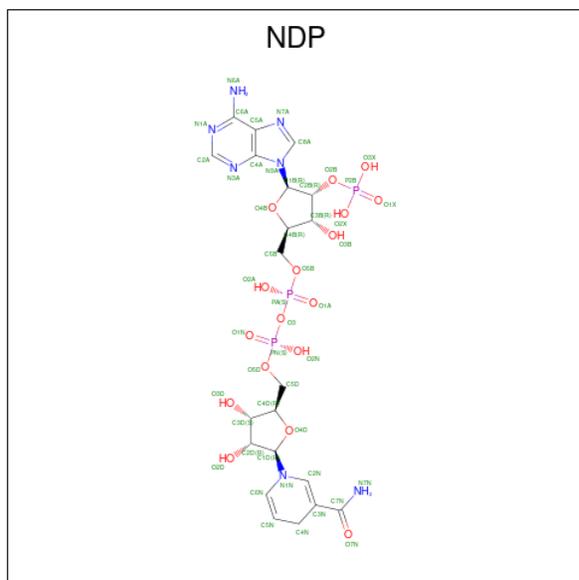
- Molecule 3 is 10-PROPARGYL-5,8-DIDEAZAFOLIC ACID (three-letter code: CB3) (formula: C<sub>24</sub>H<sub>23</sub>N<sub>5</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			35	24	5	6		
3	B	1	Total	C	N	O	0	0
			35	24	5	6		
3	C	1	Total	C	N	O	0	0
			35	24	5	6		
3	D	1	Total	C	N	O	0	0
			35	24	5	6		
3	E	1	Total	C	N	O	0	0
			35	24	5	6		

- Molecule 4 is FOLIC ACID (three-letter code: FOL) (formula: C<sub>19</sub>H<sub>19</sub>N<sub>7</sub>O<sub>6</sub>).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
5	A	1	Total 48	C 21	N 7	O 17	P 3	0	0
5	B	1	Total 48	C 21	N 7	O 17	P 3	0	0
5	C	1	Total 48	C 21	N 7	O 17	P 3	0	0
5	D	1	Total 48	C 21	N 7	O 17	P 3	0	0
5	E	1	Total 48	C 21	N 7	O 17	P 3	0	0

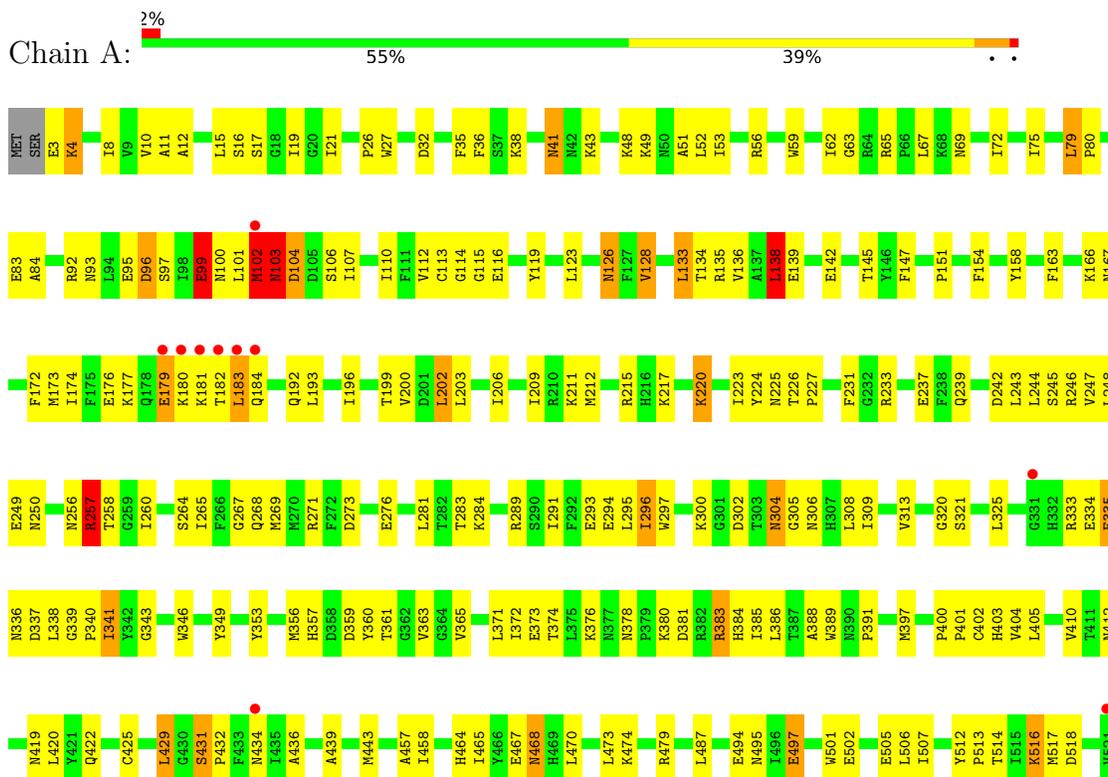
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	101	Total 101	O 101	0	0
6	B	116	Total 116	O 116	0	0
6	C	83	Total 83	O 83	0	0
6	D	71	Total 71	O 71	0	0
6	E	35	Total 35	O 35	0	0

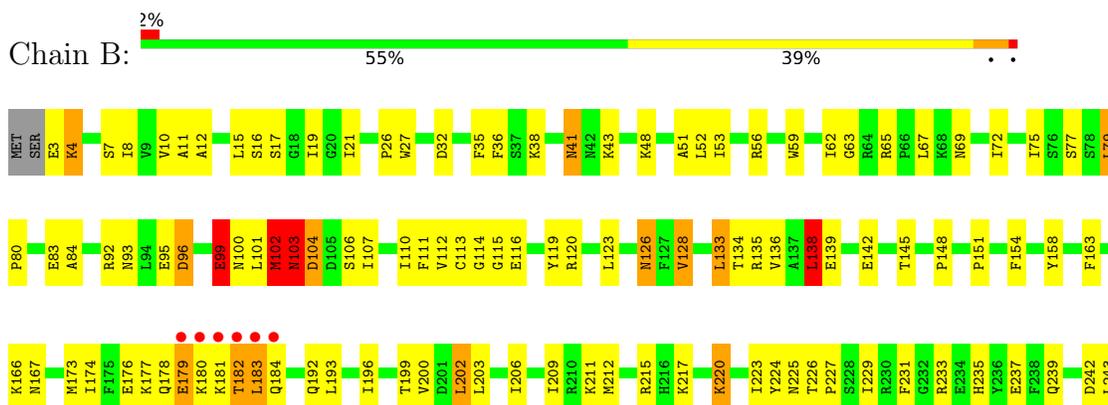
### 3 Residue-property plots

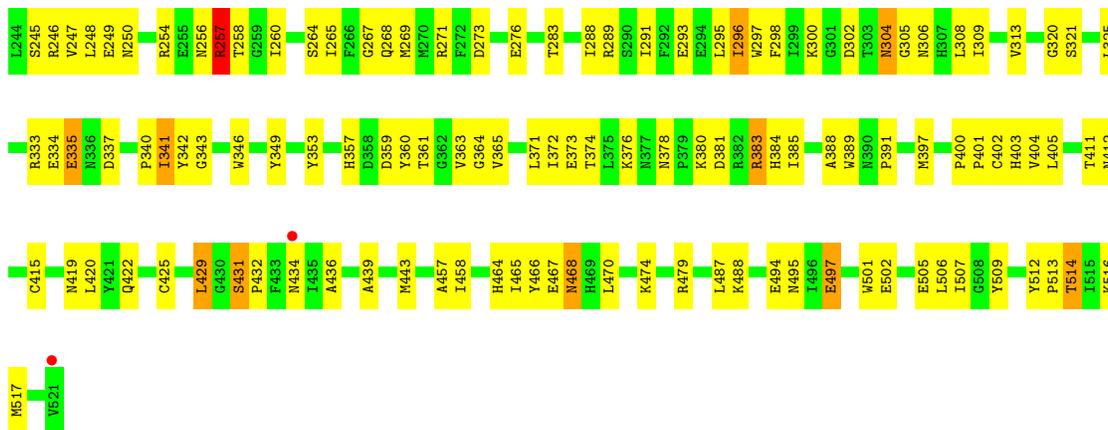
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: bifunctional dihydrofolate reductase-thymidylate synthase

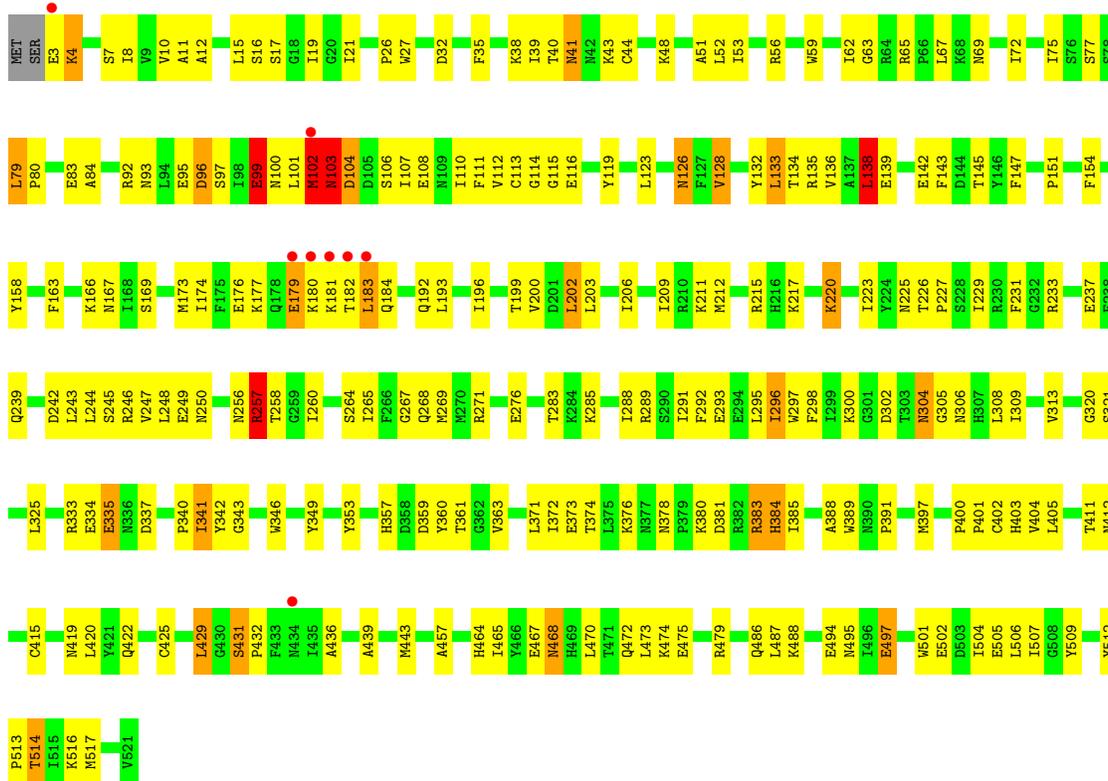


- Molecule 1: bifunctional dihydrofolate reductase-thymidylate synthase



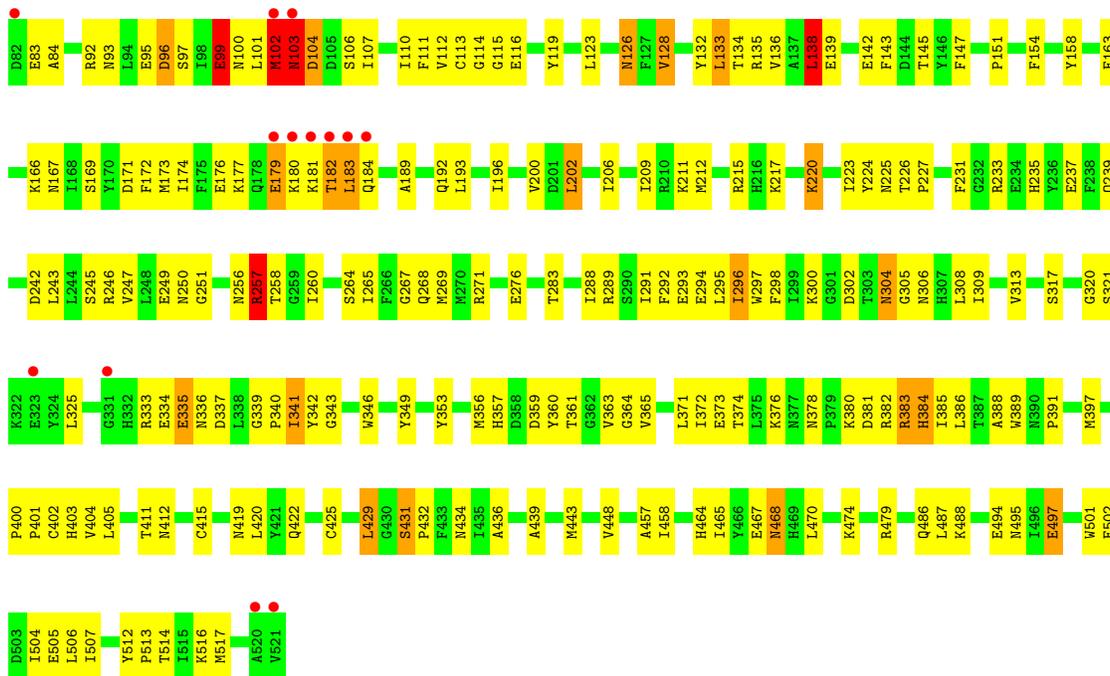


• Molecule 1: bifunctional dihydrofolate reductase-thymidylate synthase

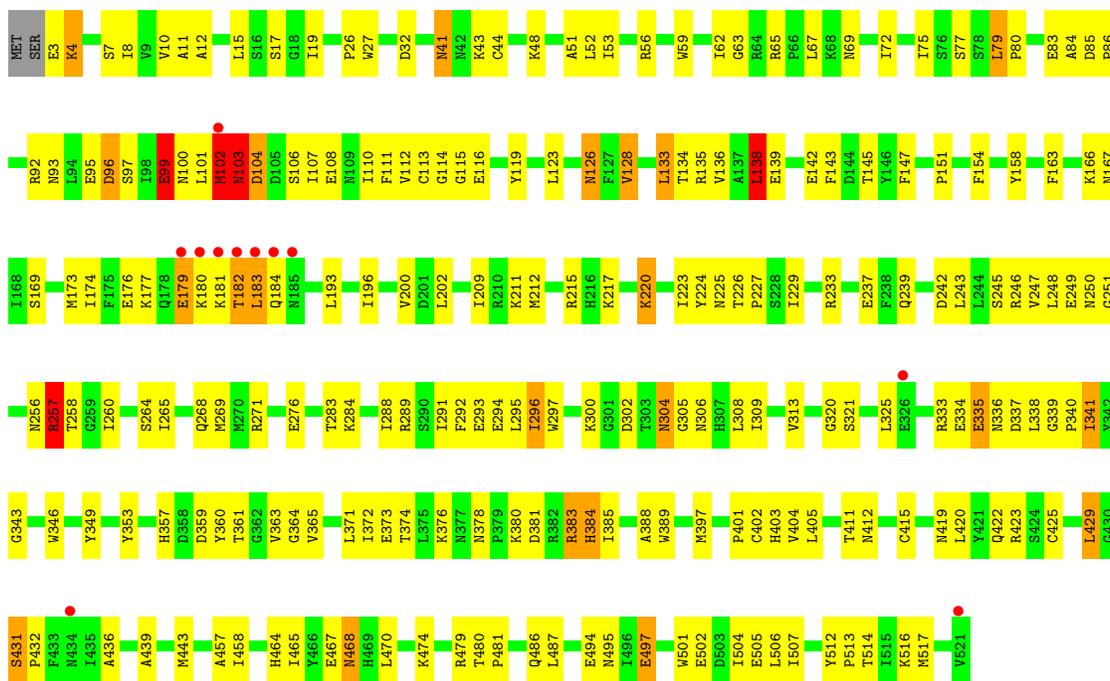


• Molecule 1: bifunctional dihydrofolate reductase-thymidylate synthase





• Molecule 1: bifunctional dihydrofolate reductase-thymidylate synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	214.90Å 116.30Å 219.70Å 90.00° 95.23° 90.00°	Depositor
Resolution (Å)	29.80 – 2.80 29.80 – 2.78	Depositor EDS
% Data completeness (in resolution range)	83.6 (29.80-2.80) 82.5 (29.80-2.78)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.39 (at 2.76Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.225 , 0.245 0.221 , 0.238	Depositor DCC
$R_{free}$ test set	5618 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.5	Xtrriage
Anisotropy	0.527	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 46.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	22196	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.69% 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: FOL, CB3, UMP, NDP

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	0.44	0/4320	0.70	3/5838 (0.1%)
1	B	0.44	0/4320	0.73	4/5838 (0.1%)
1	C	0.44	0/4320	0.70	3/5838 (0.1%)
1	D	0.45	0/4320	0.71	3/5838 (0.1%)
1	E	0.47	0/4320	0.74	4/5838 (0.1%)
All	All	0.45	0/21600	0.72	17/29190 (0.1%)

There are no bond length outliers.

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	E	257	ARG	NE-CZ-NH2	-14.81	112.90	120.30
1	B	257	ARG	NE-CZ-NH2	-14.37	113.11	120.30
1	E	257	ARG	NE-CZ-NH1	14.27	127.44	120.30
1	B	257	ARG	NE-CZ-NH1	13.94	127.27	120.30
1	D	257	ARG	NE-CZ-NH1	-10.18	115.21	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	4223	0	4159	253	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	4223	0	4159	239	0
1	C	4223	0	4159	244	0
1	D	4223	0	4159	248	0
1	E	4223	0	4159	226	0
2	A	20	0	11	7	0
2	B	20	0	11	8	0
2	C	20	0	11	7	0
2	D	20	0	11	3	0
2	E	20	0	11	6	0
3	A	35	0	21	3	0
3	B	35	0	21	3	0
3	C	35	0	21	3	0
3	D	35	0	21	3	0
3	E	35	0	21	4	0
4	A	32	0	17	9	0
4	B	32	0	17	8	0
4	C	32	0	17	8	0
4	D	32	0	17	9	0
4	E	32	0	17	10	0
5	A	48	0	26	10	0
5	B	48	0	26	7	0
5	C	48	0	26	9	0
5	D	48	0	26	10	0
5	E	48	0	26	10	0
6	A	101	0	0	8	0
6	B	116	0	0	3	0
6	C	83	0	0	1	0
6	D	71	0	0	6	0
6	E	35	0	0	2	0
All	All	22196	0	21170	1204	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 28.

The worst 5 of 1204 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:A:341:ILE:HA	1:A:397:MET:HE3	1.43	1.01
1:E:341:ILE:HA	1:E:397:MET:HE3	1.43	1.01
1:C:341:ILE:HA	1:C:397:MET:HE3	1.43	1.00
1:D:341:ILE:HA	1:D:397:MET:HE3	1.43	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:341:ILE:HA	1:B:397:MET:HE3	1.42	0.99

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	517/521 (99%)	468 (90%)	40 (8%)	9 (2%)	9	29
1	B	517/521 (99%)	466 (90%)	43 (8%)	8 (2%)	10	33
1	C	517/521 (99%)	466 (90%)	42 (8%)	9 (2%)	9	29
1	D	517/521 (99%)	466 (90%)	42 (8%)	9 (2%)	9	29
1	E	517/521 (99%)	468 (90%)	40 (8%)	9 (2%)	9	29
All	All	2585/2605 (99%)	2334 (90%)	207 (8%)	44 (2%)	9	29

5 of 44 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	84	ALA
1	A	102	MET
1	A	103	ASN
1	B	84	ALA
1	B	102	MET

### 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	468/470 (100%)	436 (93%)	32 (7%)	16	42
1	B	468/470 (100%)	436 (93%)	32 (7%)	16	42
1	C	468/470 (100%)	436 (93%)	32 (7%)	16	42
1	D	468/470 (100%)	436 (93%)	32 (7%)	16	42
1	E	468/470 (100%)	436 (93%)	32 (7%)	16	42
All	All	2340/2350 (100%)	2180 (93%)	160 (7%)	16	42

5 of 160 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	296	ILE
1	E	202	LEU
1	D	383	ARG
1	E	96	ASP
1	E	373	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 109 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	256	ASN
1	D	41	ASN
1	E	268	GLN
1	C	304	ASN
1	C	422	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

20 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
4	FOL	C	613	-	34,34,34	2.32	9 (26%)	44,47,47	2.37	17 (38%)
5	NDP	E	622	-	45,52,52	1.76	9 (20%)	53,80,80	1.58	13 (24%)
5	NDP	B	610	-	45,52,52	1.76	8 (17%)	53,80,80	1.54	11 (20%)
4	FOL	E	621	-	34,34,34	2.33	8 (23%)	44,47,47	2.38	16 (36%)
3	CB3	D	616	-	36,37,37	2.05	10 (27%)	46,51,51	2.00	5 (10%)
2	UMP	D	615	-	21,21,21	3.07	7 (33%)	31,31,31	2.18	9 (29%)
3	CB3	E	620	-	36,37,37	2.05	11 (30%)	46,51,51	2.00	5 (10%)
5	NDP	A	606	-	45,52,52	1.79	9 (20%)	53,80,80	1.54	12 (22%)
3	CB3	C	612	-	36,37,37	1.97	9 (25%)	46,51,51	1.96	6 (13%)
3	CB3	B	608	-	36,37,37	2.01	8 (22%)	46,51,51	1.98	6 (13%)
5	NDP	C	614	-	45,52,52	1.74	8 (17%)	53,80,80	1.49	10 (18%)
5	NDP	D	618	-	45,52,52	1.73	9 (20%)	53,80,80	1.51	11 (20%)
2	UMP	A	603	-	21,21,21	3.01	7 (33%)	31,31,31	2.18	9 (29%)
3	CB3	A	604	-	36,37,37	2.11	11 (30%)	46,51,51	2.00	5 (10%)
4	FOL	B	609	-	34,34,34	2.32	9 (26%)	44,47,47	2.38	16 (36%)
2	UMP	C	611	-	21,21,21	2.96	5 (23%)	31,31,31	2.19	9 (29%)
2	UMP	B	607	-	21,21,21	2.95	5 (23%)	31,31,31	2.22	9 (29%)
2	UMP	E	619	-	21,21,21	3.00	6 (28%)	31,31,31	2.21	9 (29%)
4	FOL	D	617	-	34,34,34	2.32	9 (26%)	44,47,47	2.41	15 (34%)
4	FOL	A	605	-	34,34,34	2.32	9 (26%)	44,47,47	2.38	16 (36%)

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	FOL	C	613	-	-	6/22/22/22	0/3/3/3
5	NDP	E	622	-	-	5/30/77/77	0/5/5/5
5	NDP	B	610	-	-	6/30/77/77	0/5/5/5
4	FOL	E	621	-	-	6/22/22/22	0/3/3/3
3	CB3	D	616	-	1/1/5/6	7/27/28/28	0/3/3/3
2	UMP	D	615	-	-	2/10/22/22	0/2/2/2
3	CB3	E	620	-	1/1/5/6	7/27/28/28	0/3/3/3
5	NDP	A	606	-	-	6/30/77/77	0/5/5/5
3	CB3	C	612	-	1/1/5/6	7/27/28/28	0/3/3/3
3	CB3	B	608	-	1/1/5/6	7/27/28/28	0/3/3/3
5	NDP	C	614	-	-	6/30/77/77	0/5/5/5
5	NDP	D	618	-	-	6/30/77/77	0/5/5/5
2	UMP	A	603	-	-	3/10/22/22	0/2/2/2
3	CB3	A	604	-	1/1/5/6	7/27/28/28	0/3/3/3
4	FOL	B	609	-	-	6/22/22/22	0/3/3/3
2	UMP	C	611	-	-	3/10/22/22	0/2/2/2
2	UMP	B	607	-	-	3/10/22/22	0/2/2/2
2	UMP	E	619	-	-	3/10/22/22	0/2/2/2
4	FOL	D	617	-	-	6/22/22/22	0/3/3/3
4	FOL	A	605	-	-	6/22/22/22	0/3/3/3

The worst 5 of 166 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	615	UMP	C6-C5	8.62	1.55	1.35
2	E	619	UMP	C6-C5	8.46	1.54	1.35
2	A	603	UMP	C6-C5	8.43	1.54	1.35
2	C	611	UMP	C6-C5	8.43	1.54	1.35
2	B	607	UMP	C6-C5	8.41	1.54	1.35

The worst 5 of 209 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	616	CB3	C4A-C8A-N1	-7.53	119.51	123.60
3	A	604	CB3	C4A-C8A-N1	-7.49	119.54	123.60
4	D	617	FOL	C6-C9-N10	7.43	129.50	113.07
4	B	609	FOL	C6-C9-N10	7.30	129.22	113.07
4	C	613	FOL	C6-C9-N10	7.30	129.21	113.07

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	604	CB3	CA
3	B	608	CB3	CA
3	C	612	CB3	CA
3	D	616	CB3	CA
3	E	620	CB3	CA

5 of 108 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	605	FOL	C6-C9-N10-C14
4	B	609	FOL	C6-C9-N10-C14
4	C	613	FOL	C6-C9-N10-C14
4	D	617	FOL	C6-C9-N10-C14
4	E	621	FOL	C6-C9-N10-C14

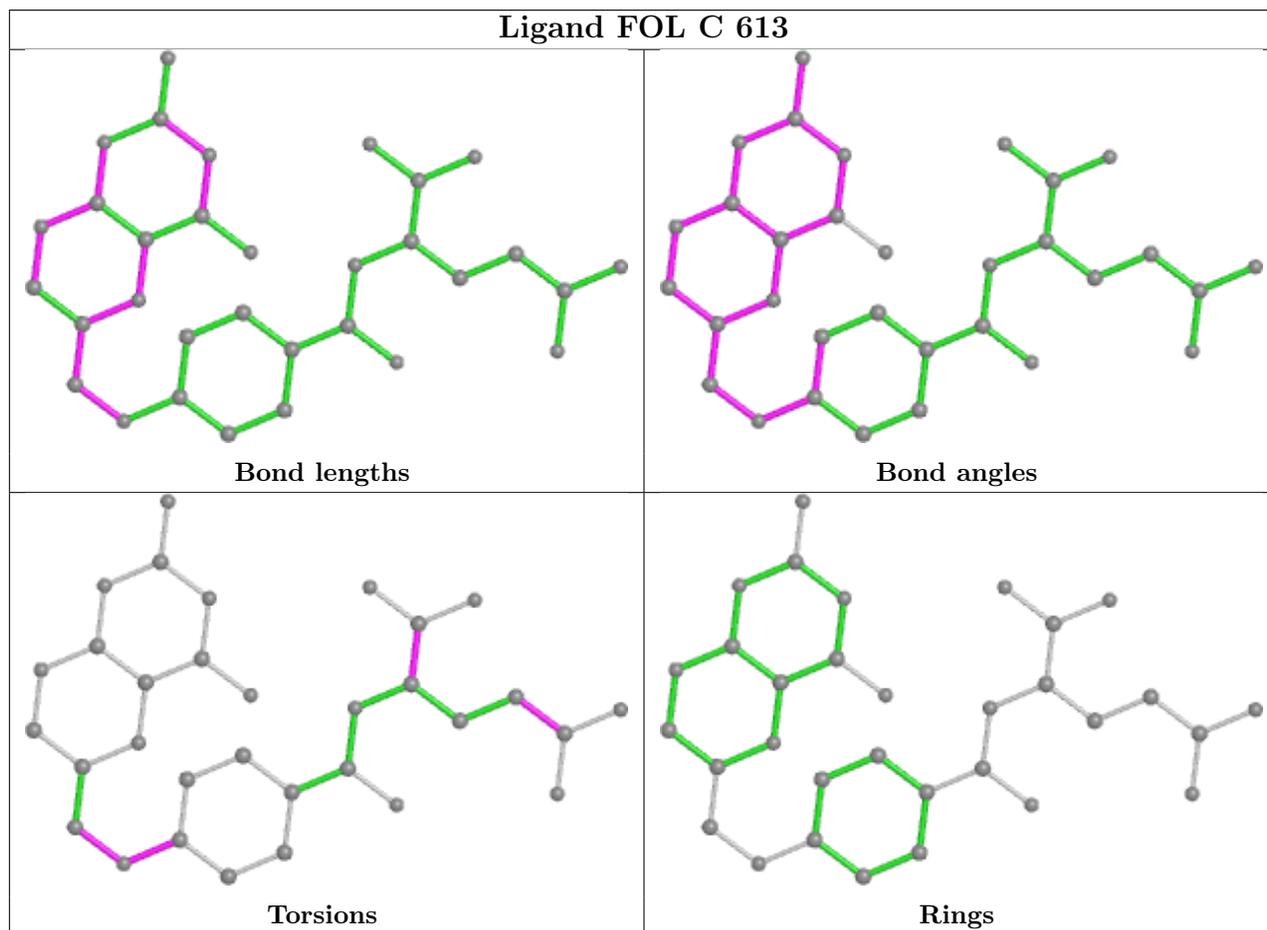
There are no ring outliers.

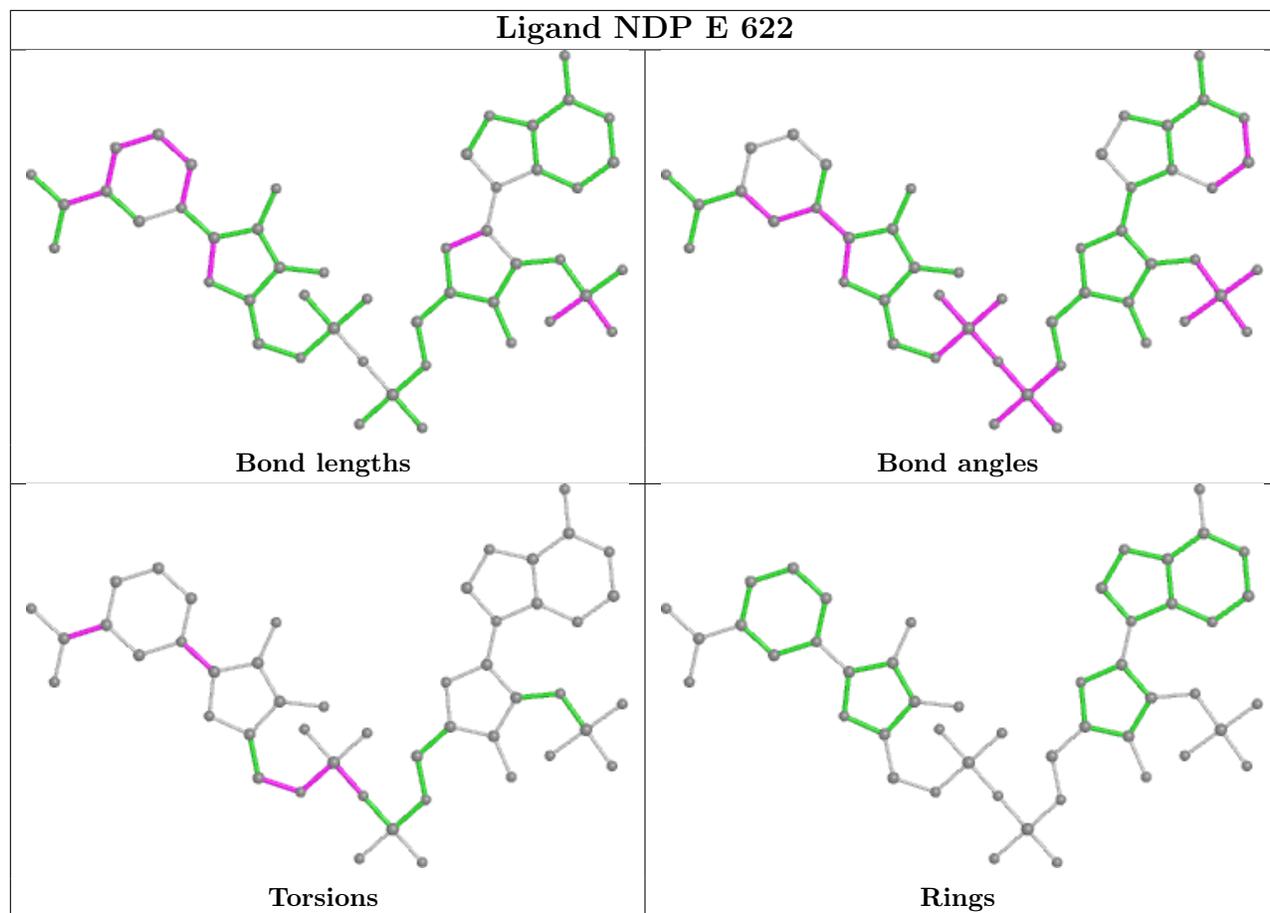
20 monomers are involved in 119 short contacts:

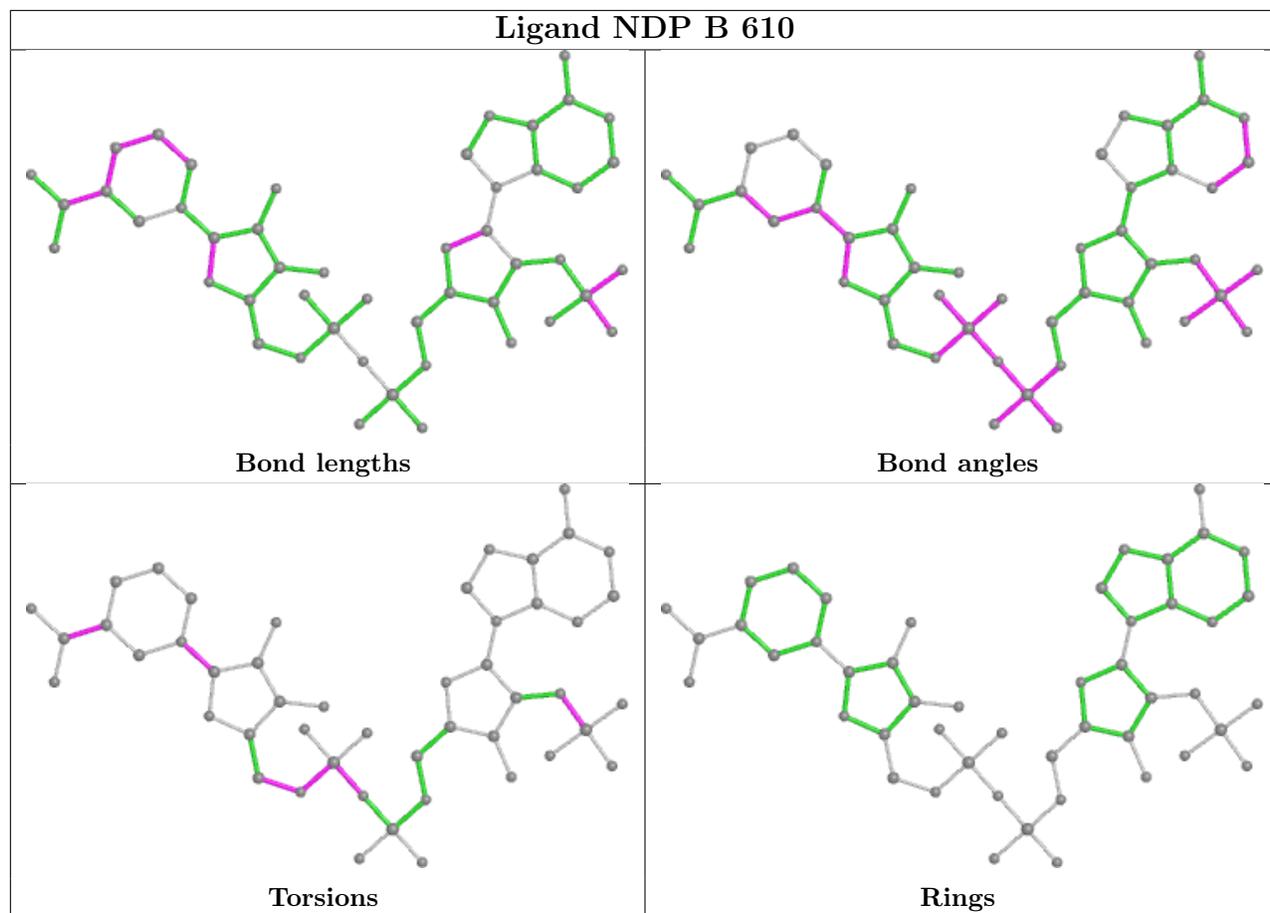
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	613	FOL	8	0
5	E	622	NDP	10	0
5	B	610	NDP	7	0
4	E	621	FOL	10	0
3	D	616	CB3	3	0
2	D	615	UMP	3	0
3	E	620	CB3	4	0
5	A	606	NDP	10	0
3	C	612	CB3	3	0
3	B	608	CB3	3	0
5	C	614	NDP	9	0
5	D	618	NDP	10	0
2	A	603	UMP	7	0
3	A	604	CB3	3	0
4	B	609	FOL	8	0
2	C	611	UMP	7	0
2	B	607	UMP	8	0
2	E	619	UMP	6	0
4	D	617	FOL	9	0
4	A	605	FOL	9	0

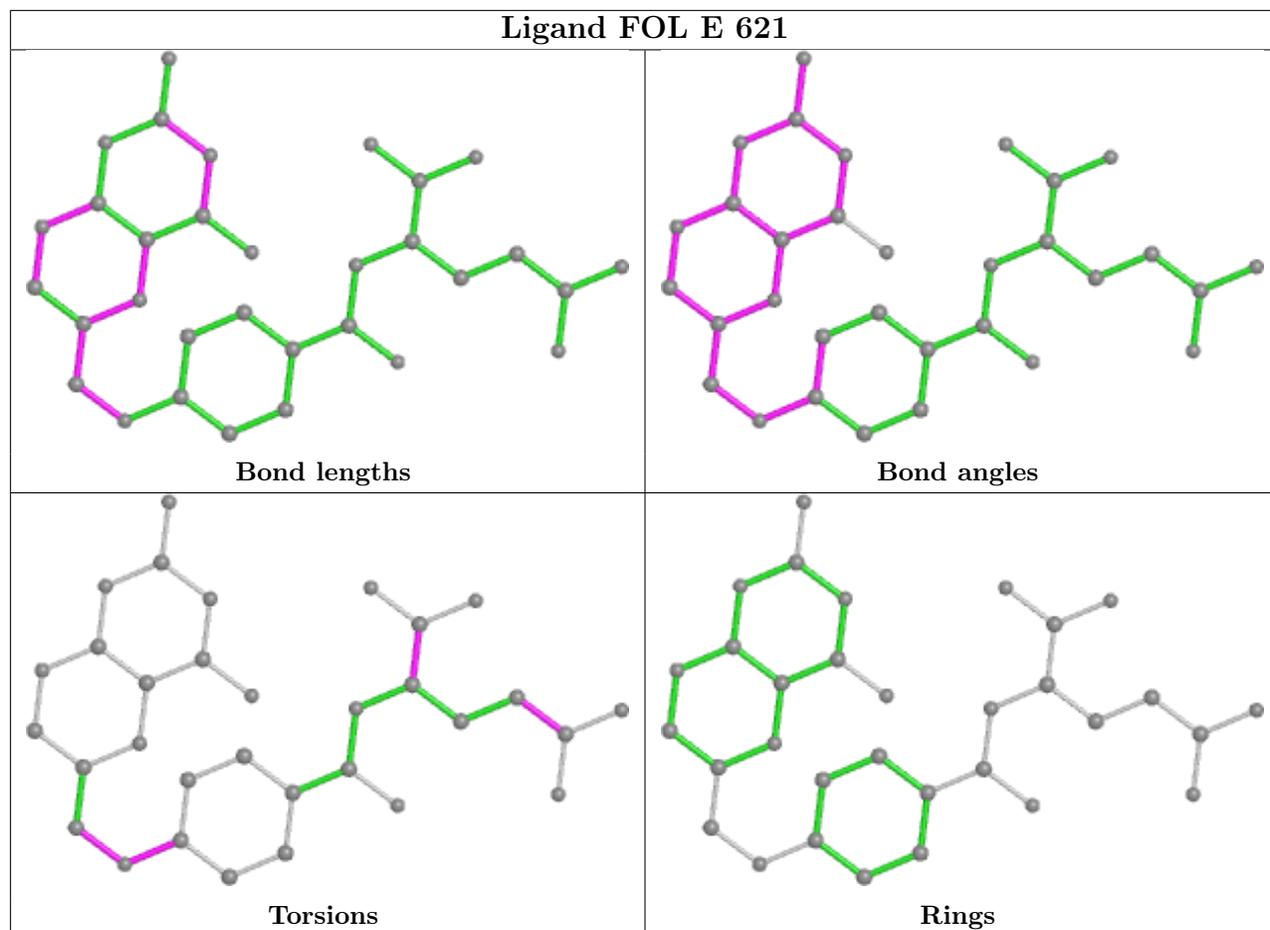
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

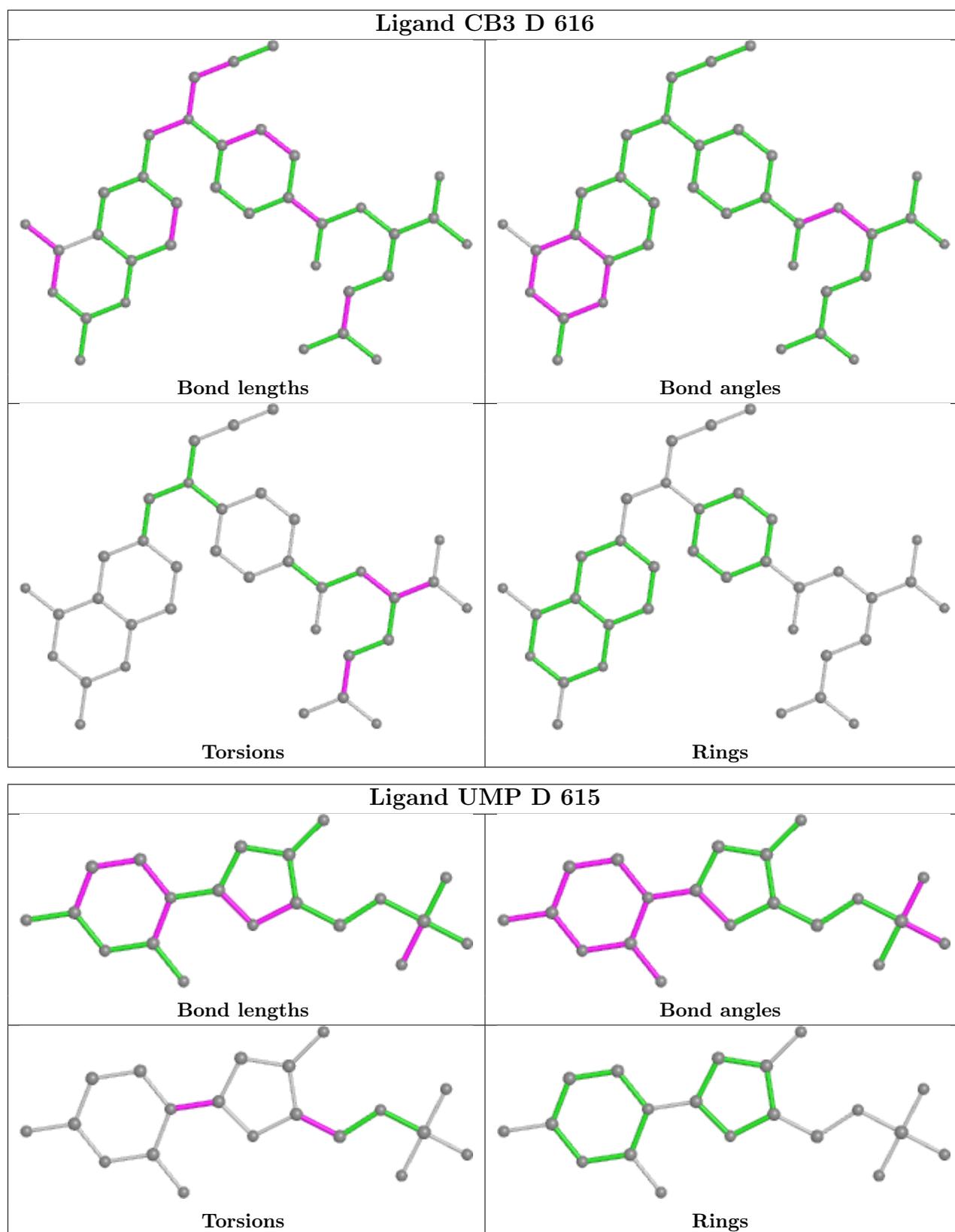
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 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.

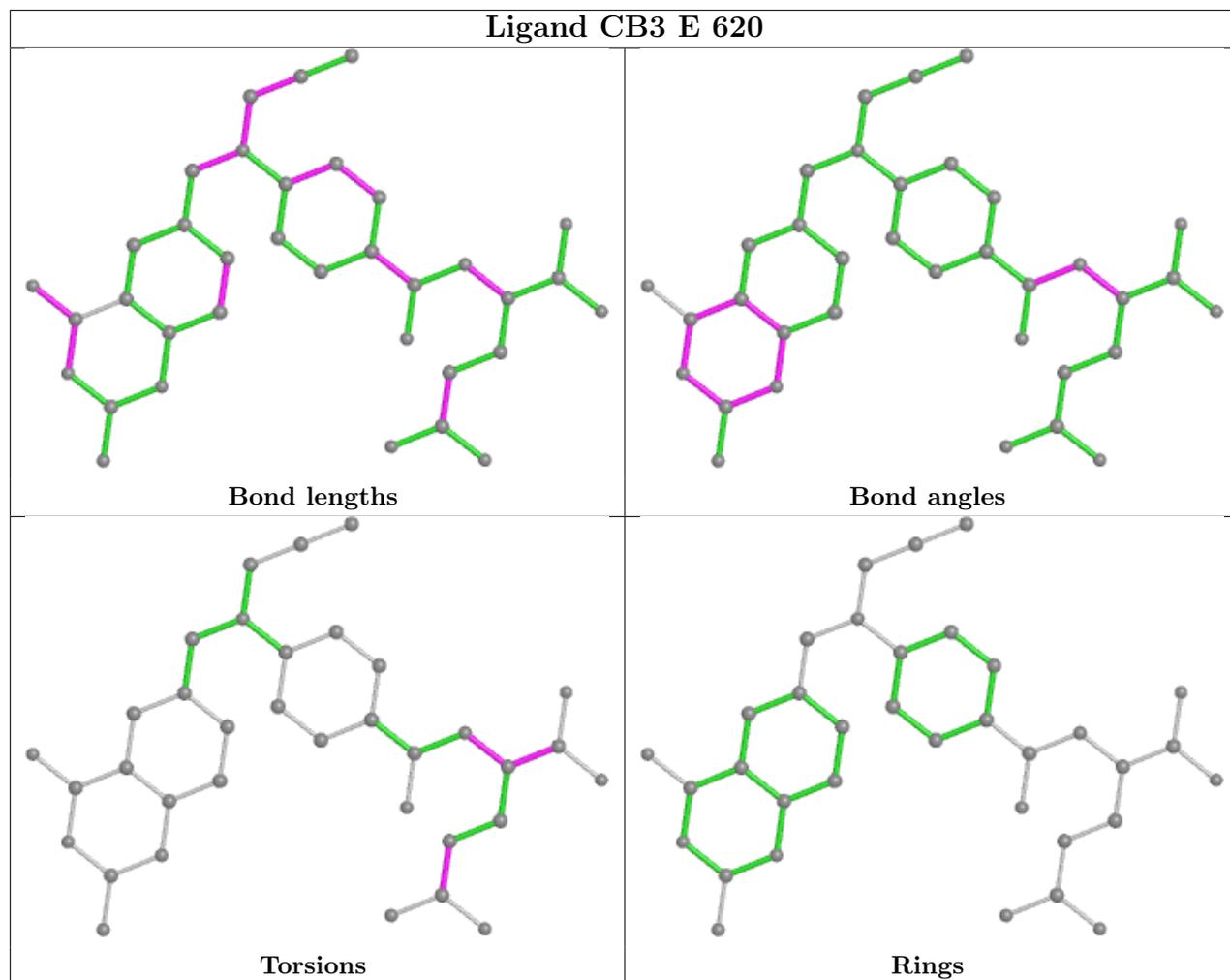


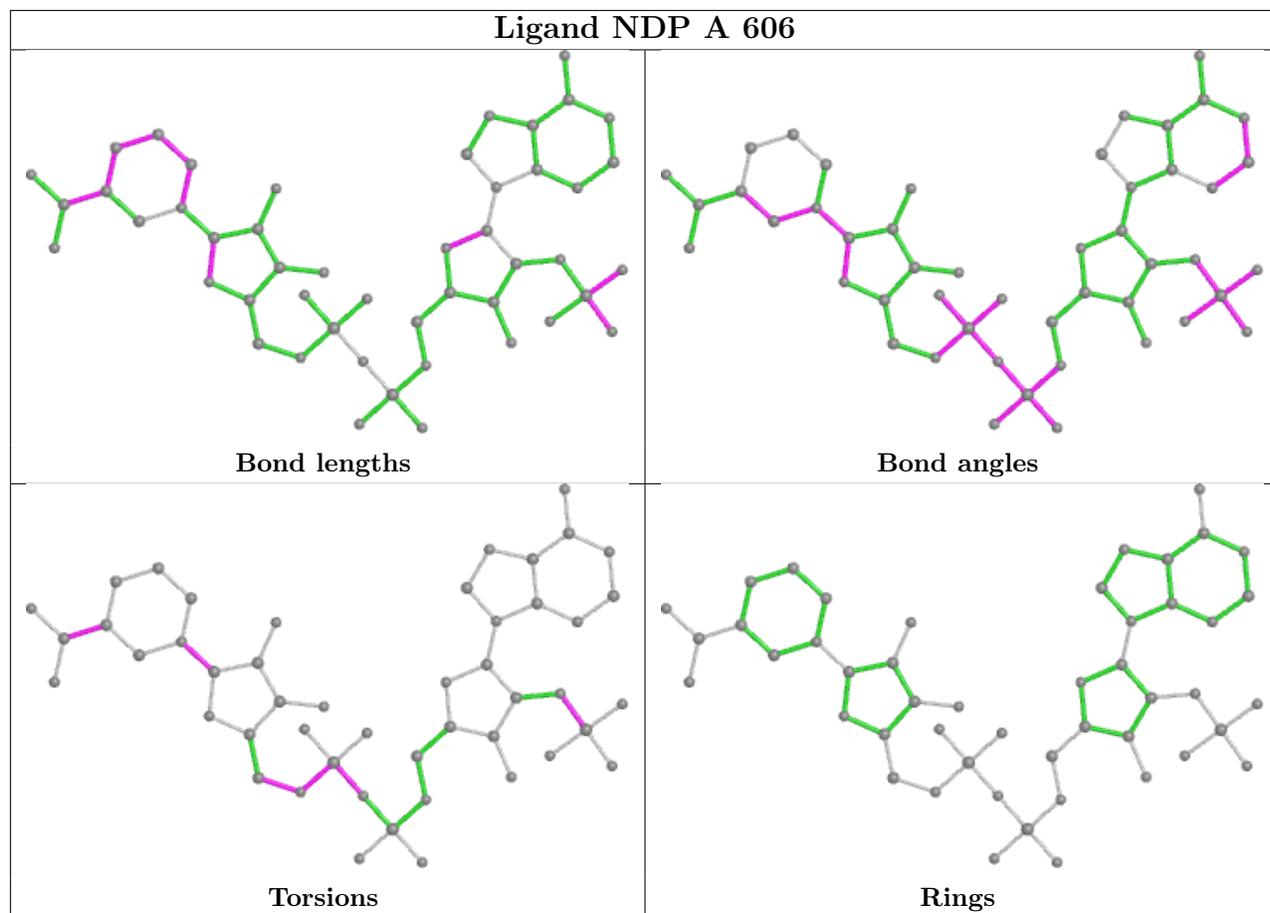


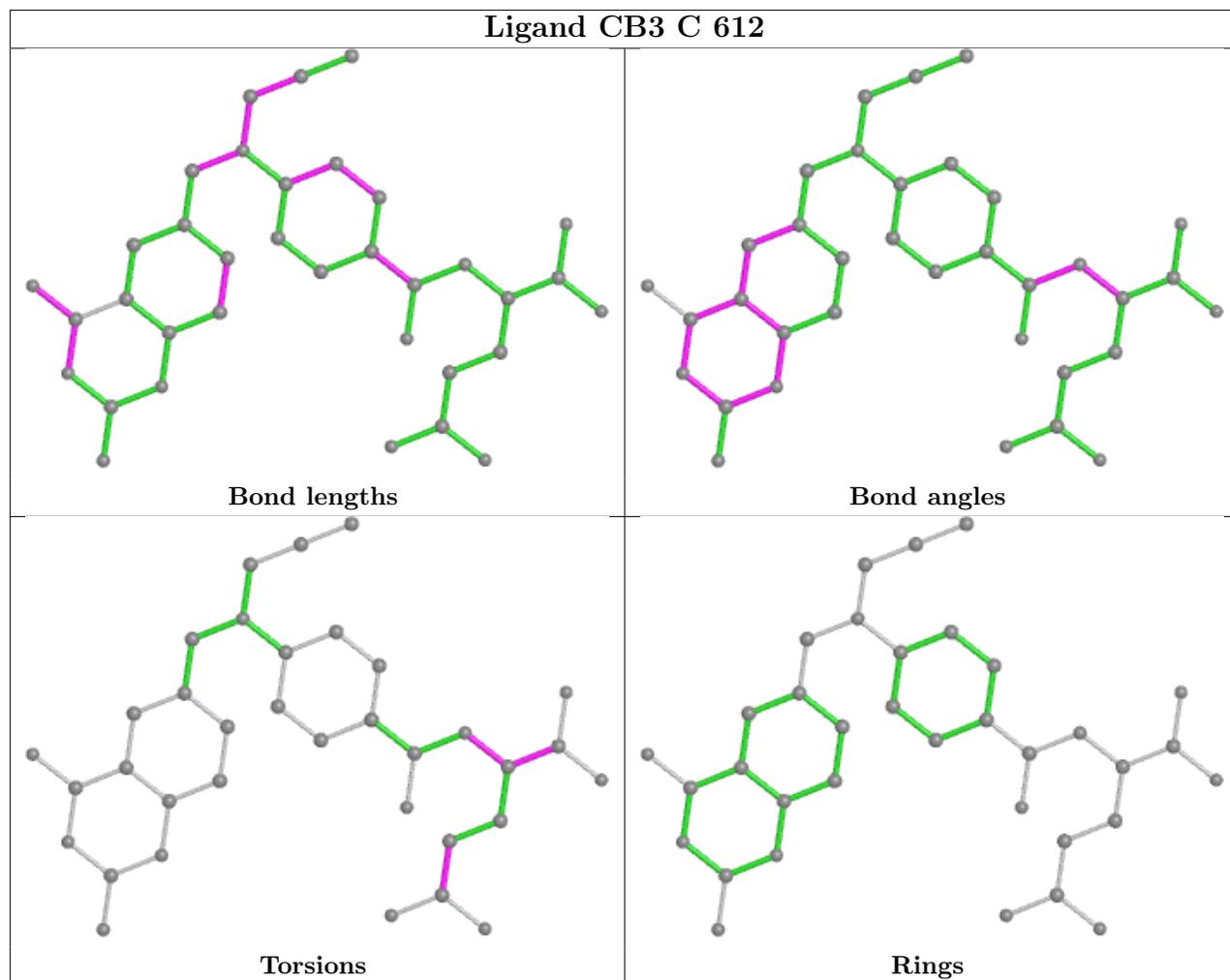


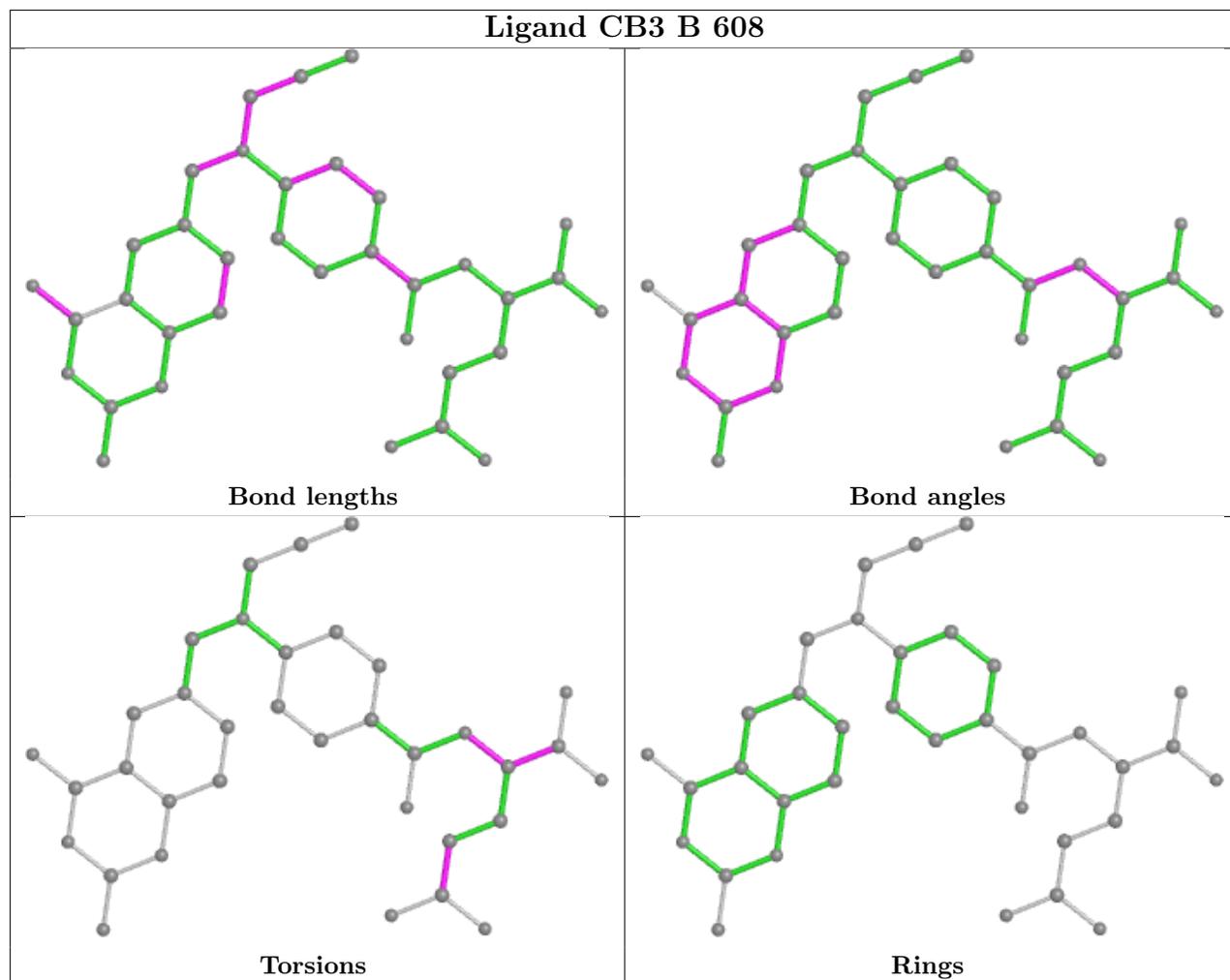


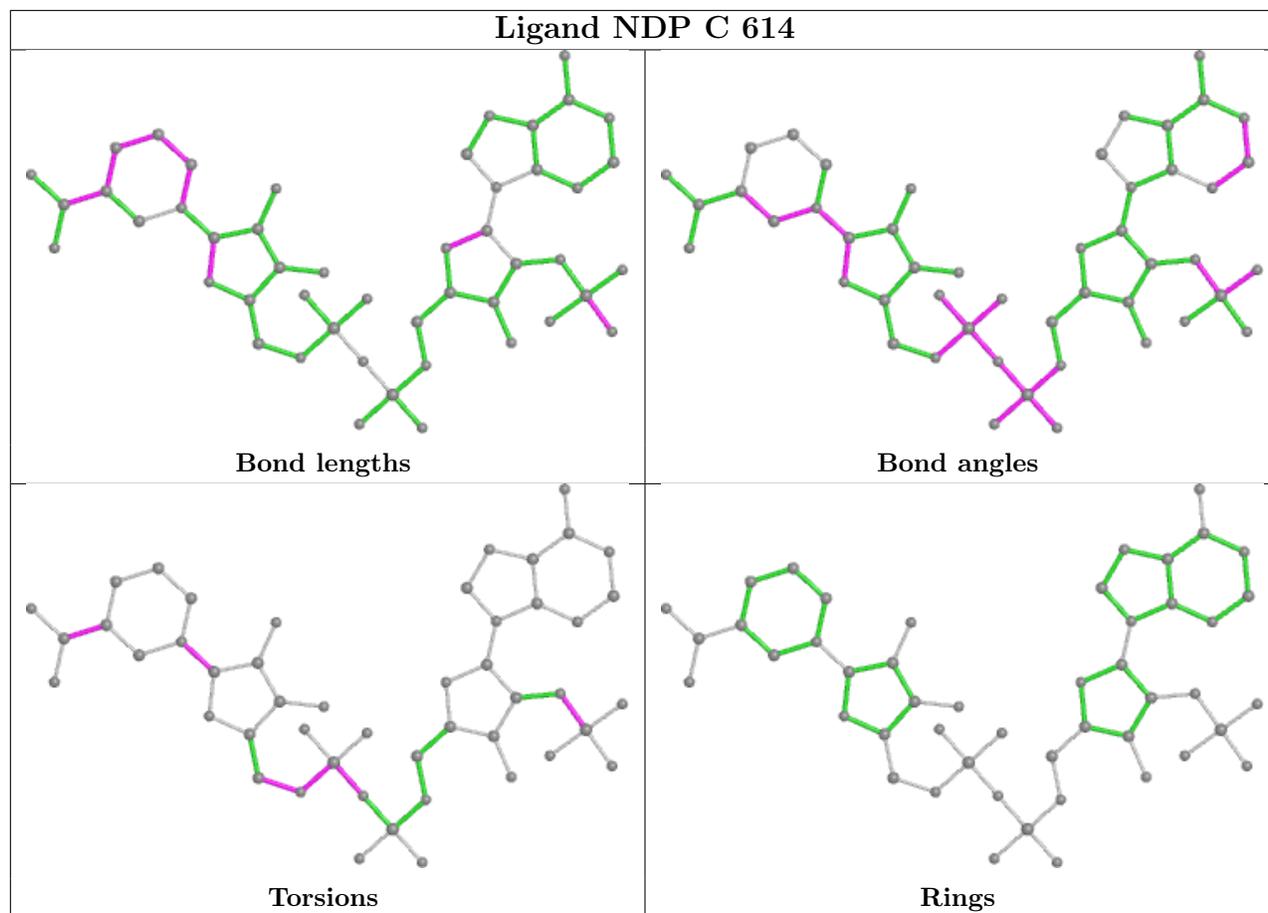


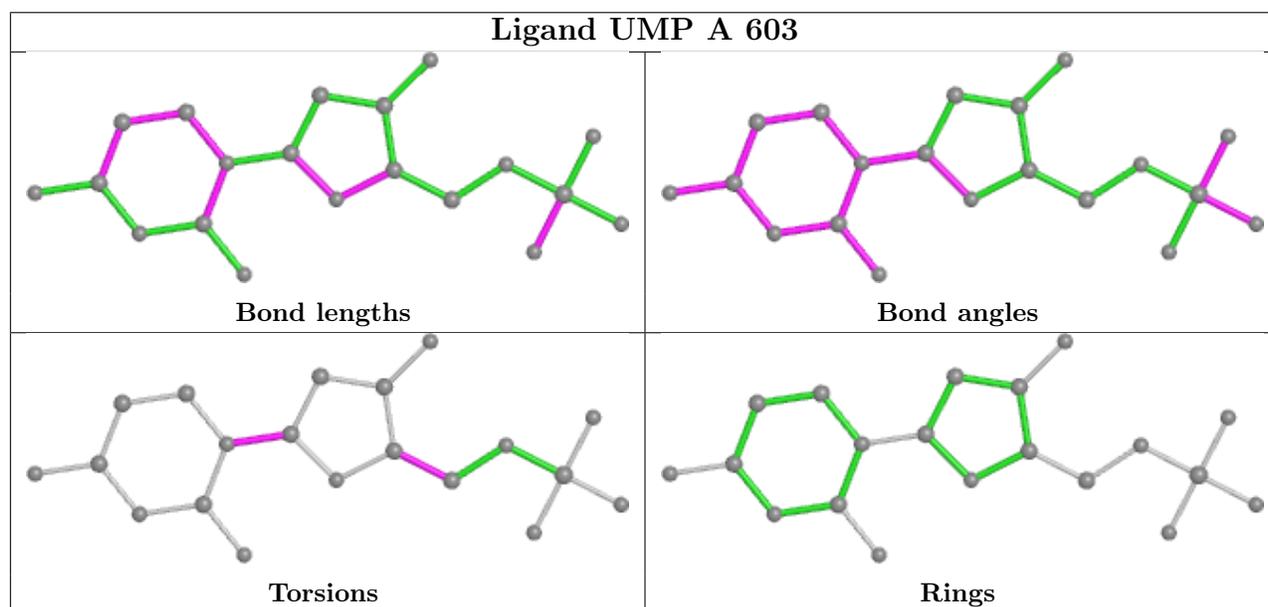
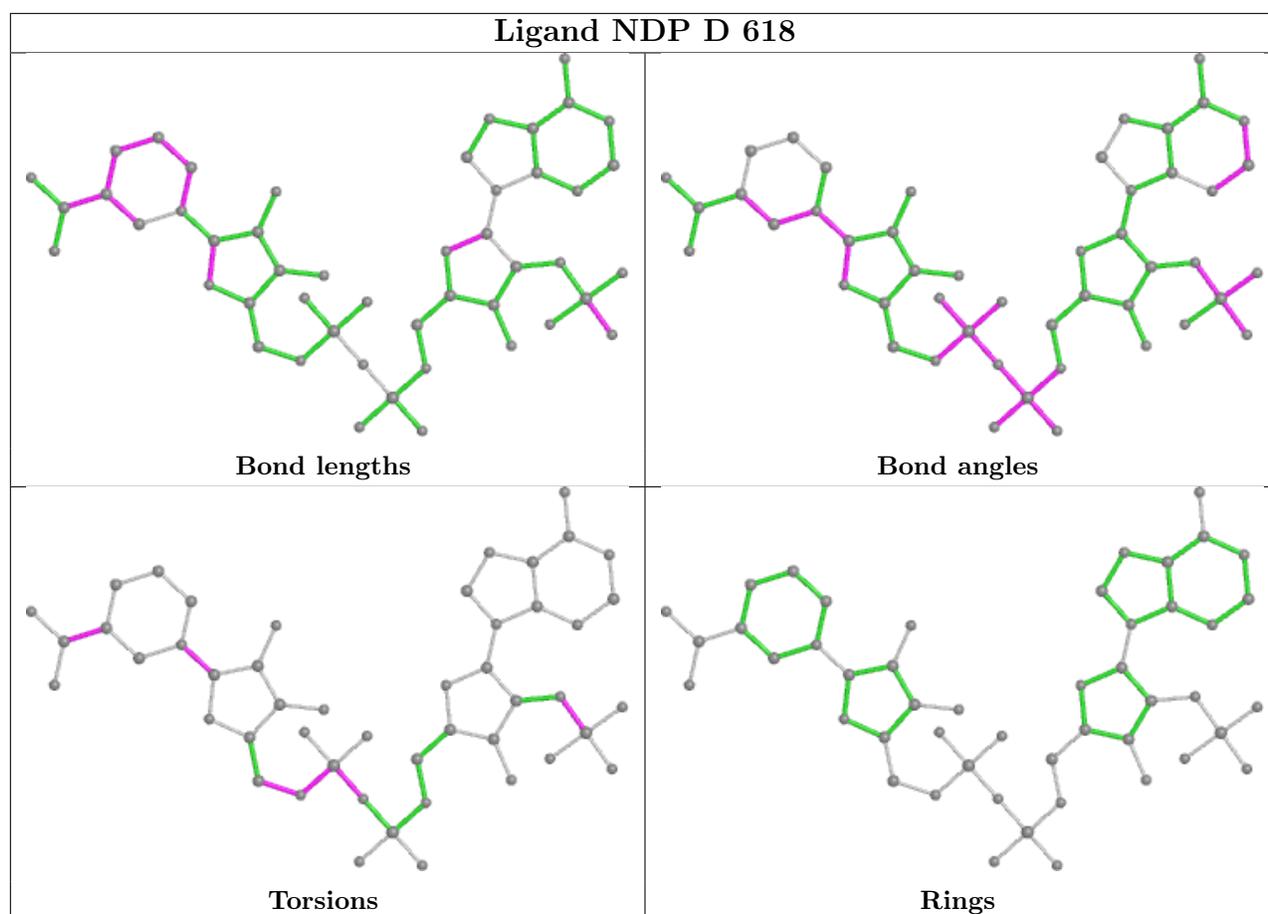


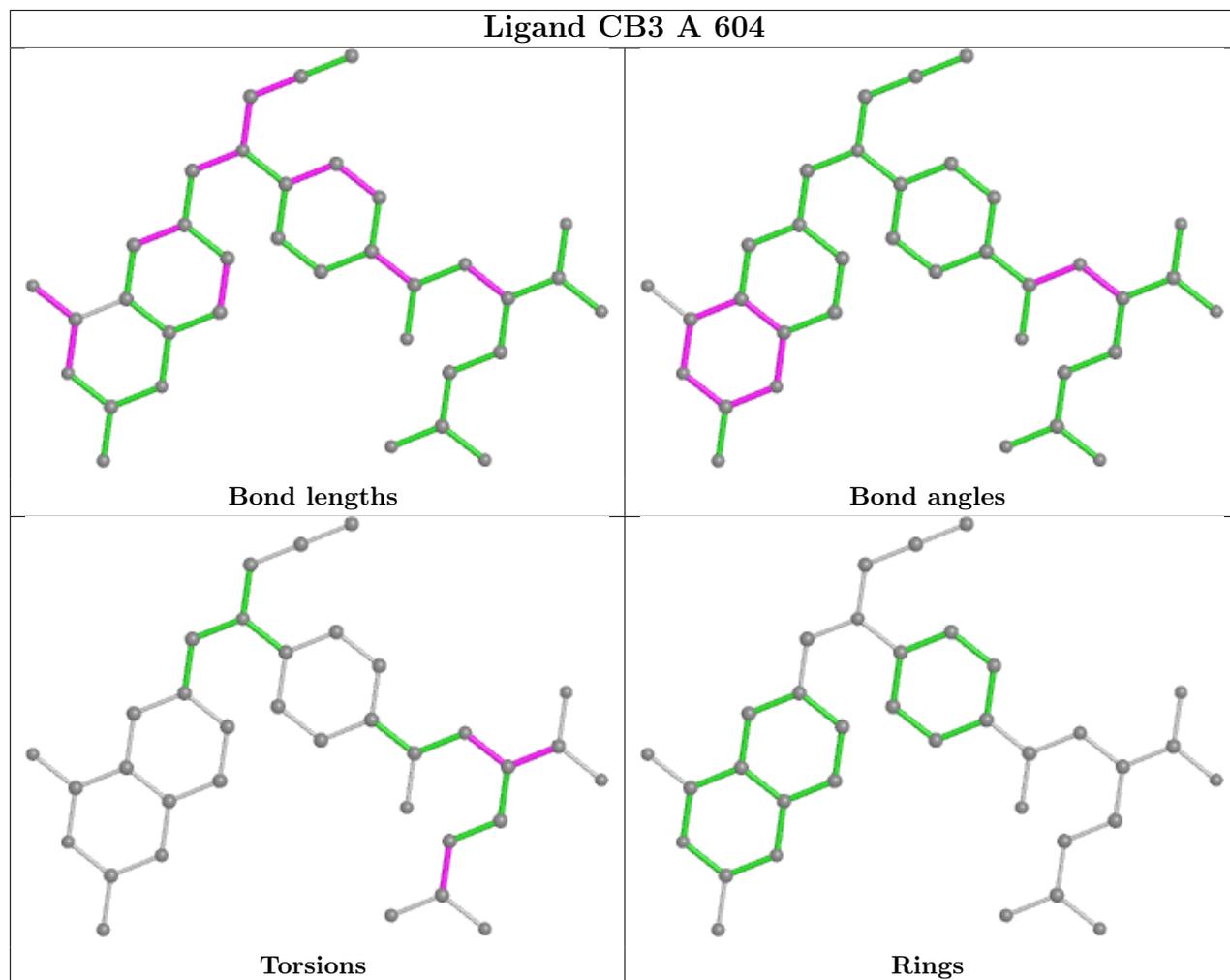


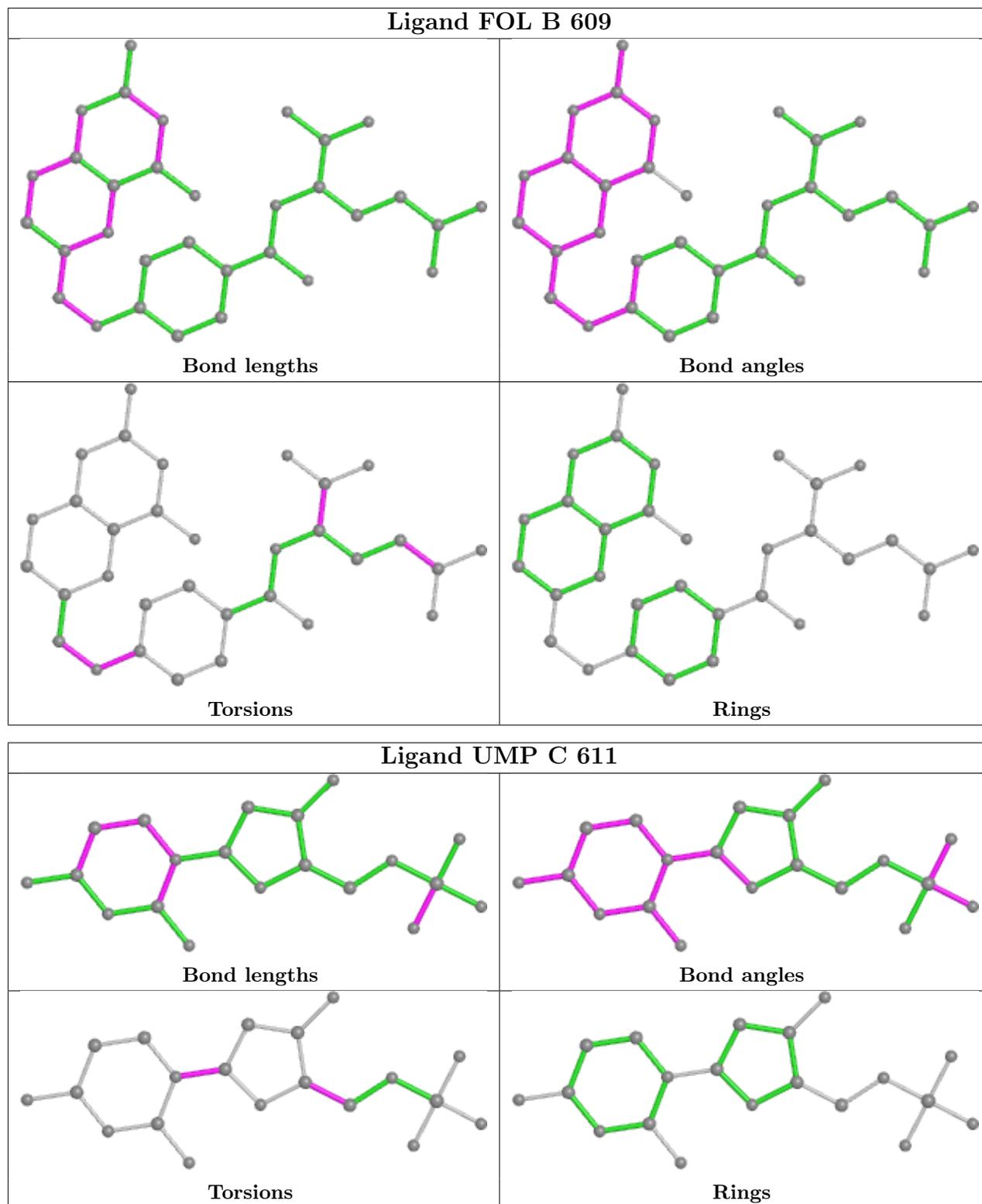


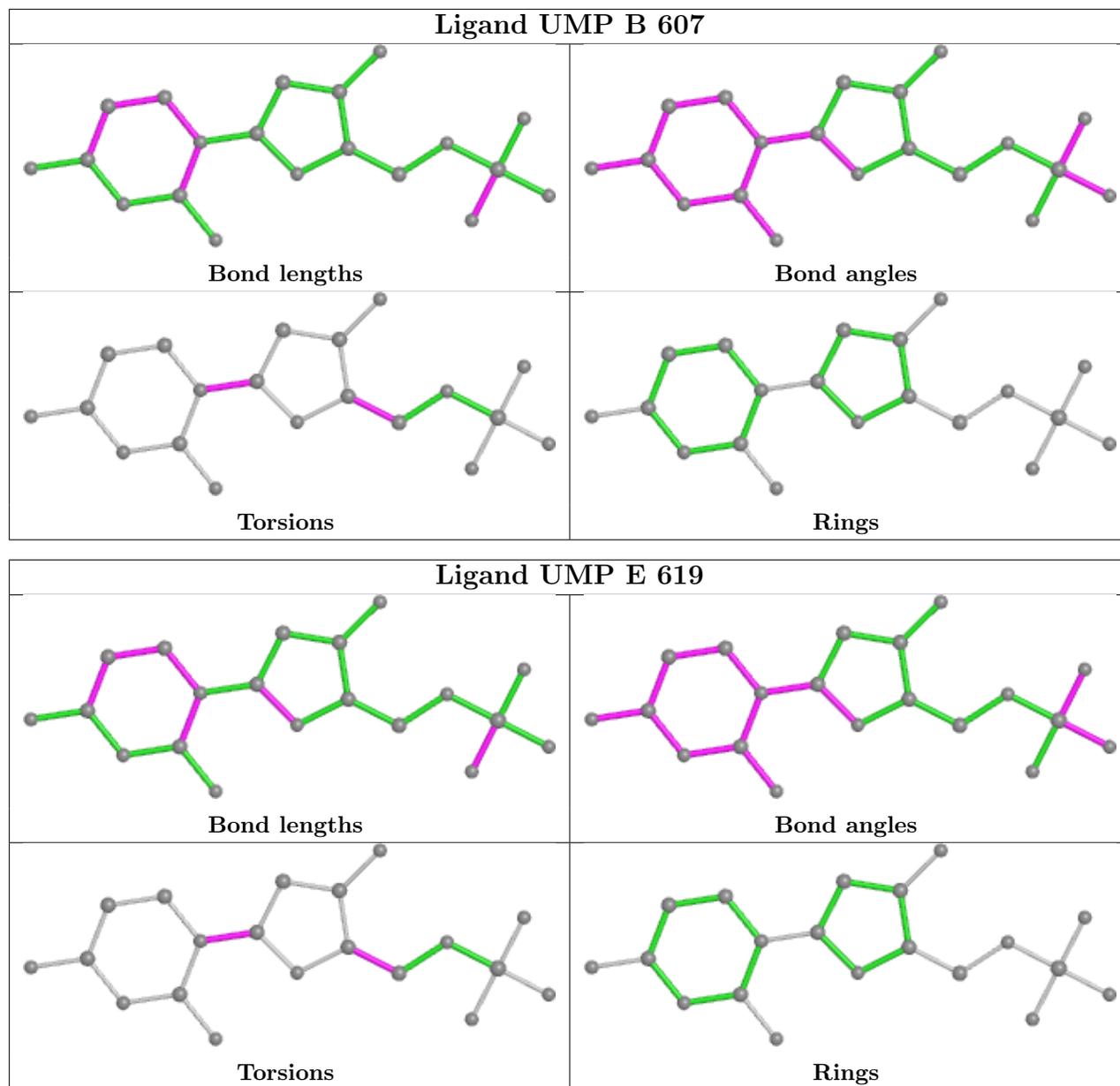


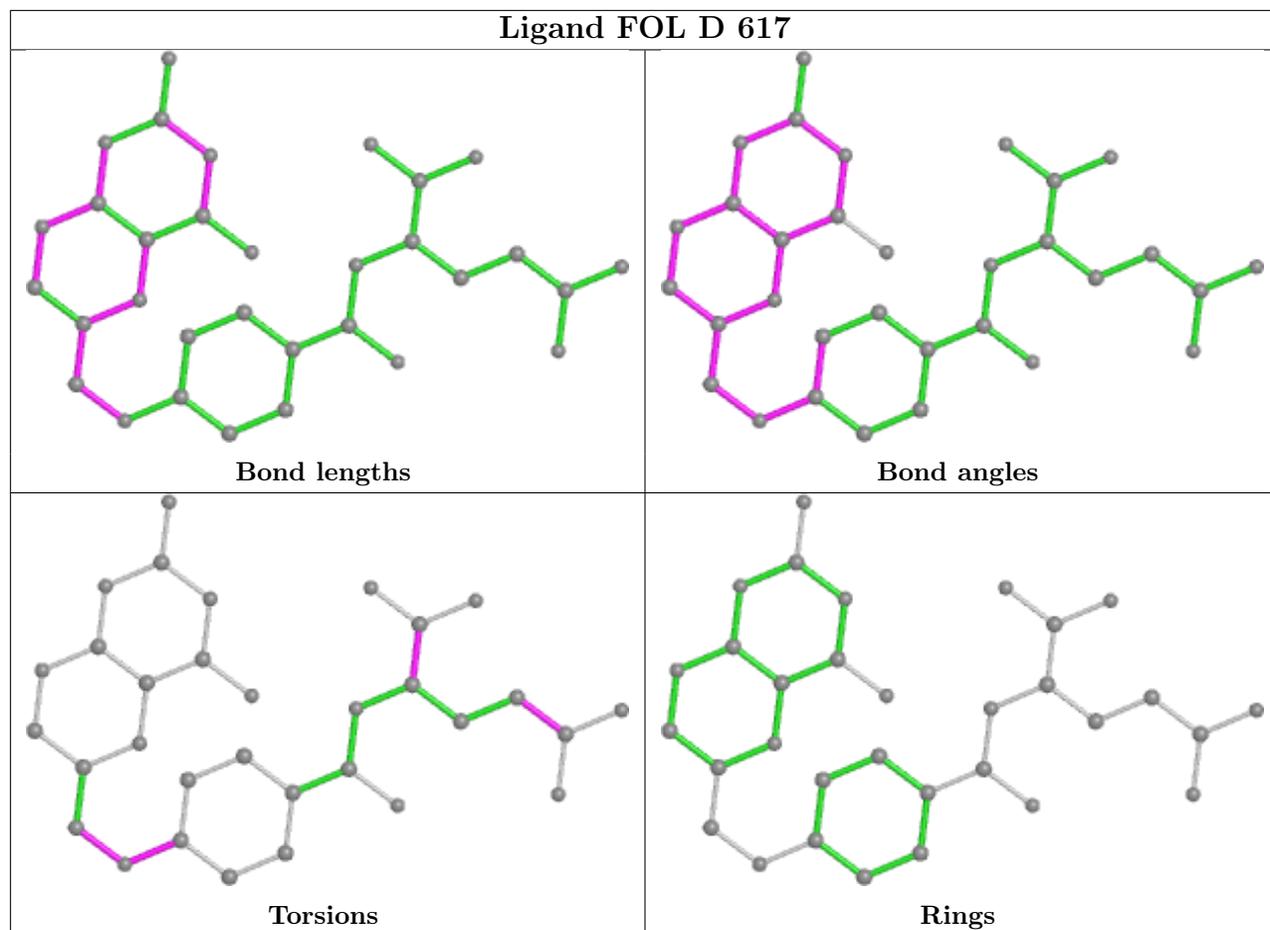


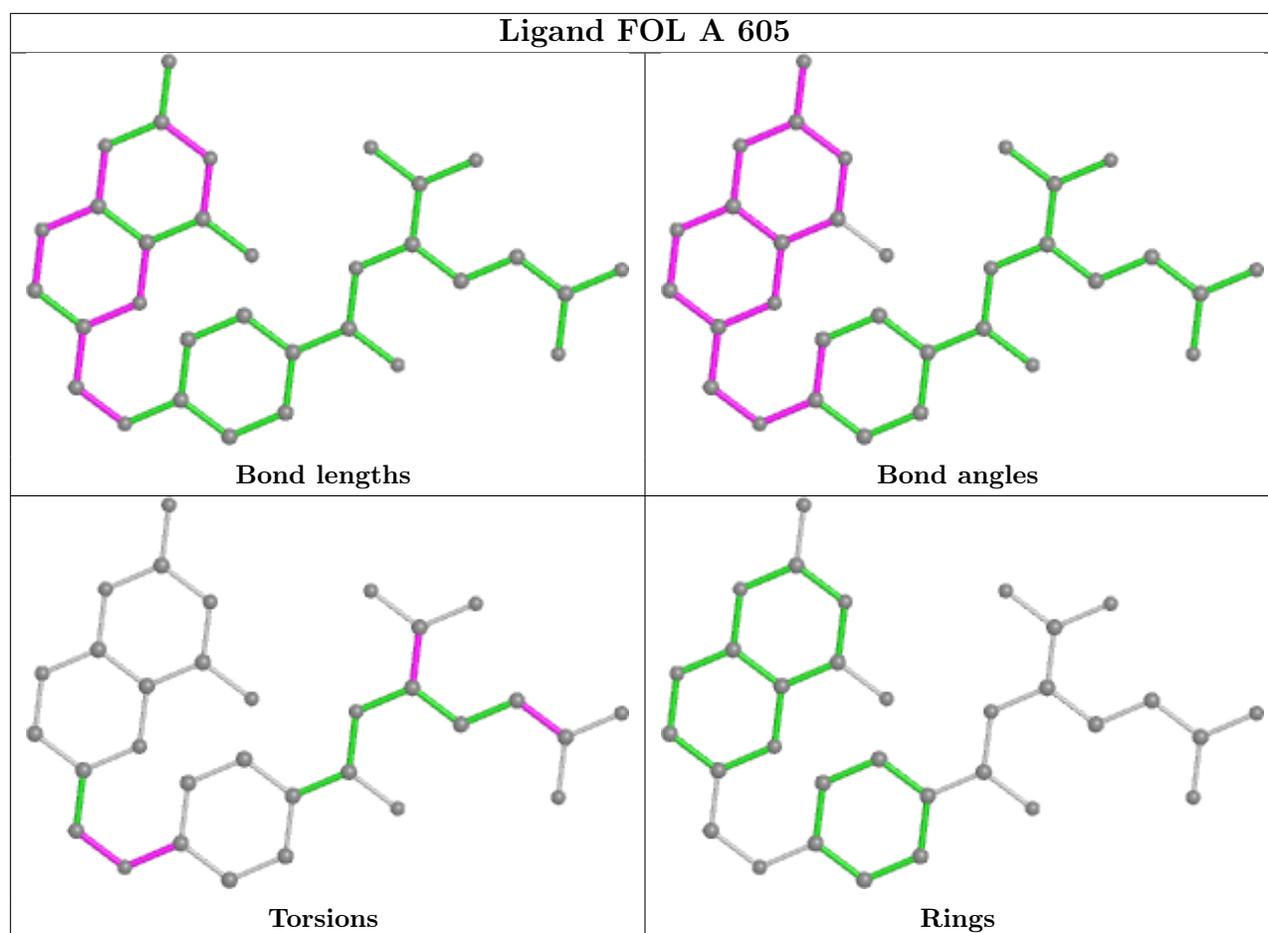












## 5.7 Other polymers [i](#)

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	519/521 (99%)	-0.29	10 (1%) 66 59	21, 35, 59, 82	0
1	B	519/521 (99%)	-0.28	8 (1%) 73 68	21, 34, 56, 81	0
1	C	519/521 (99%)	-0.36	8 (1%) 73 68	22, 36, 57, 82	0
1	D	519/521 (99%)	-0.29	14 (2%) 54 44	24, 36, 60, 82	0
1	E	519/521 (99%)	-0.27	11 (2%) 63 54	25, 38, 60, 82	0
All	All	2595/2605 (99%)	-0.30	51 (1%) 65 56	21, 36, 59, 82	0

The worst 5 of 51 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	182	THR	6.3
1	C	182	THR	5.9
1	A	182	THR	5.3
1	E	182	THR	5.0
1	B	182	THR	4.9

### 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,

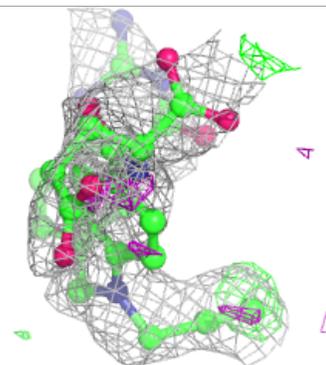
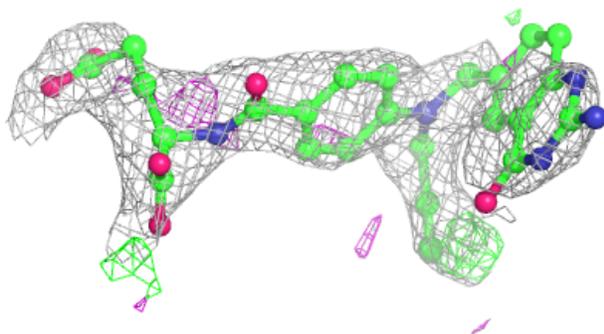
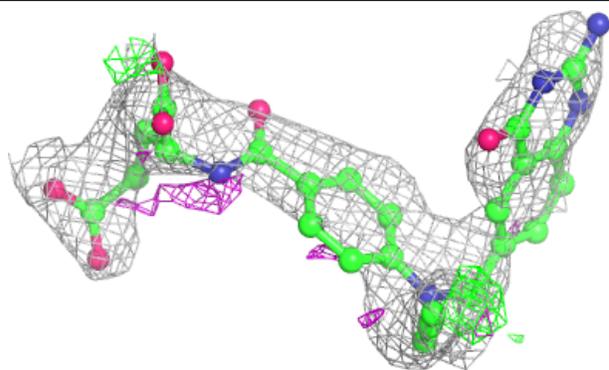
median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	CB3	D	616	35/35	0.73	0.36	66,71,77,78	0
3	CB3	A	604	35/35	0.80	0.32	66,71,77,78	0
3	CB3	C	612	35/35	0.82	0.29	65,69,76,76	0
3	CB3	B	608	35/35	0.83	0.28	63,69,76,76	0
3	CB3	E	620	35/35	0.83	0.28	67,71,76,77	0
2	UMP	C	611	20/20	0.85	0.26	55,66,73,73	0
2	UMP	A	603	20/20	0.85	0.29	55,68,73,73	0
2	UMP	D	615	20/20	0.86	0.28	57,69,74,74	0
2	UMP	B	607	20/20	0.87	0.30	52,66,72,72	0
4	FOL	E	621	32/32	0.88	0.21	40,45,47,47	0
4	FOL	D	617	32/32	0.90	0.21	37,43,47,48	0
4	FOL	B	609	32/32	0.91	0.22	36,43,44,45	0
4	FOL	C	613	32/32	0.92	0.20	37,44,47,47	0
4	FOL	A	605	32/32	0.92	0.21	34,43,44,44	0
2	UMP	E	619	20/20	0.92	0.22	60,70,74,74	0
5	NDP	C	614	48/48	0.93	0.18	39,48,57,58	0
5	NDP	E	622	48/48	0.93	0.17	40,48,57,58	0
5	NDP	D	618	48/48	0.94	0.17	40,48,56,57	0
5	NDP	B	610	48/48	0.96	0.18	37,43,53,55	0
5	NDP	A	606	48/48	0.96	0.17	36,43,52,54	0

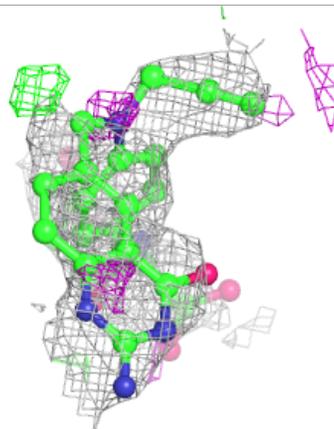
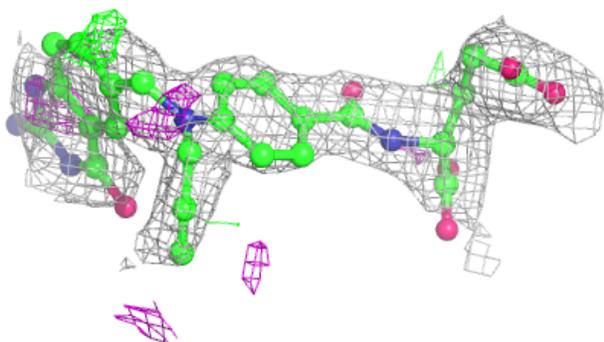
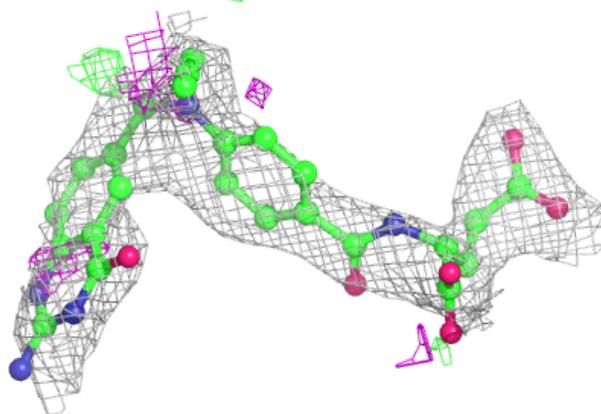
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around CB3 D 616:**

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

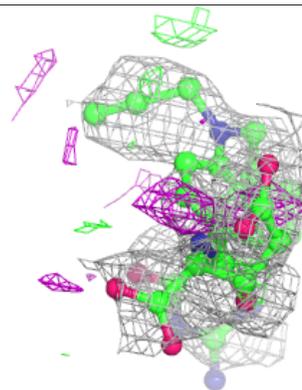
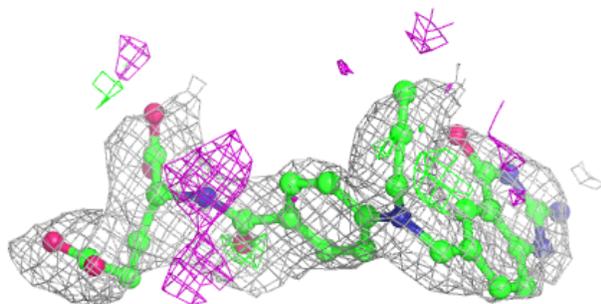
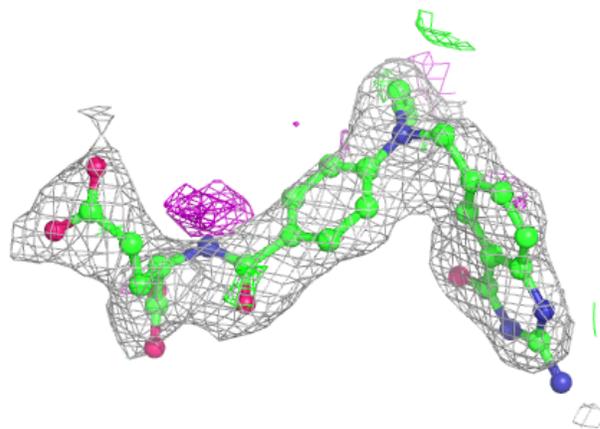
**Electron density around CB3 A 604:**

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

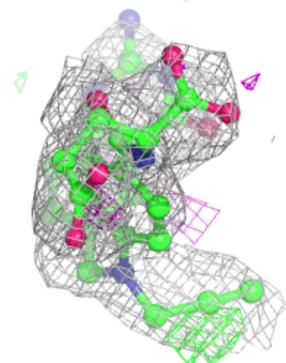
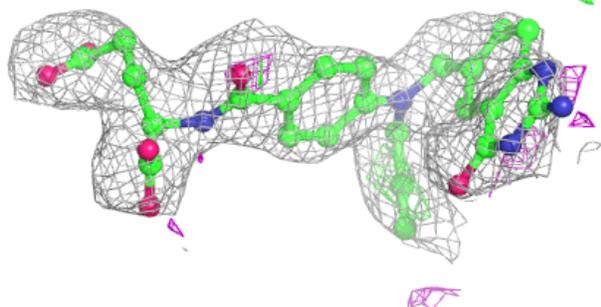
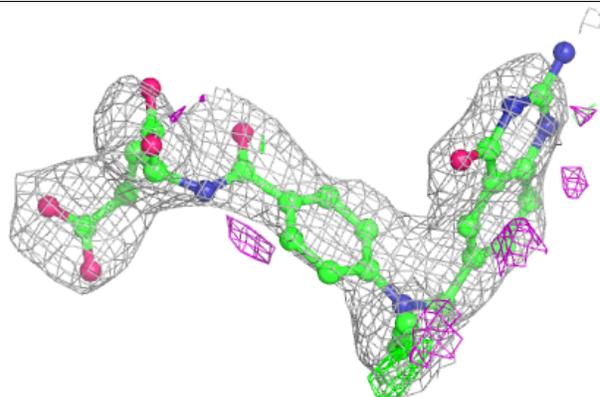


**Electron density around CB3 C 612:**

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

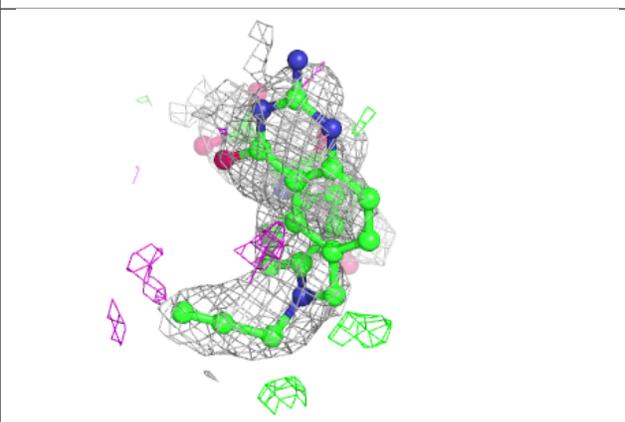
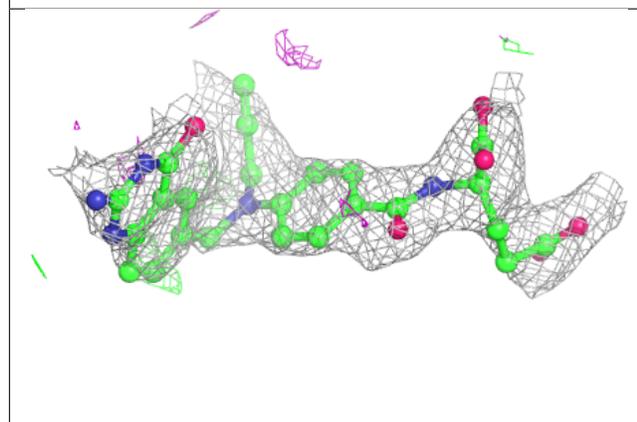
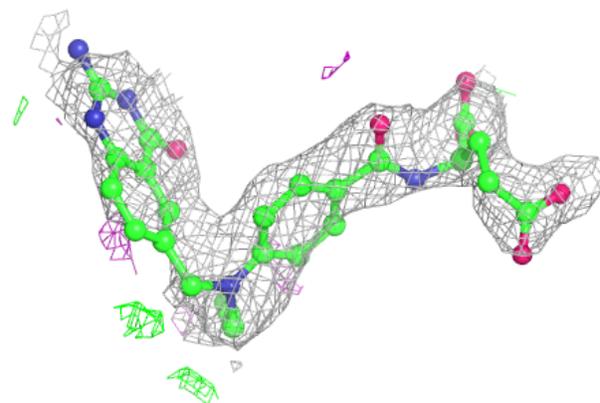
**Electron density around CB3 B 608:**

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

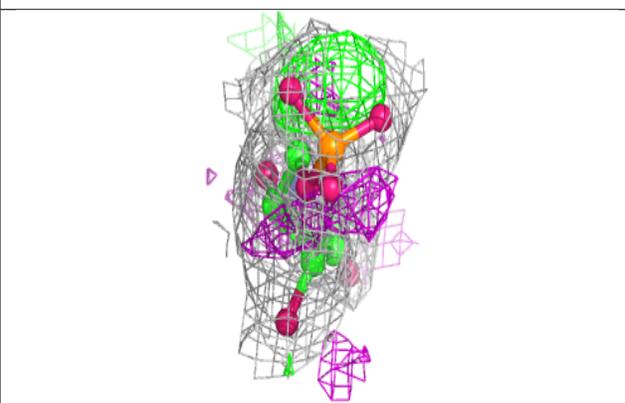
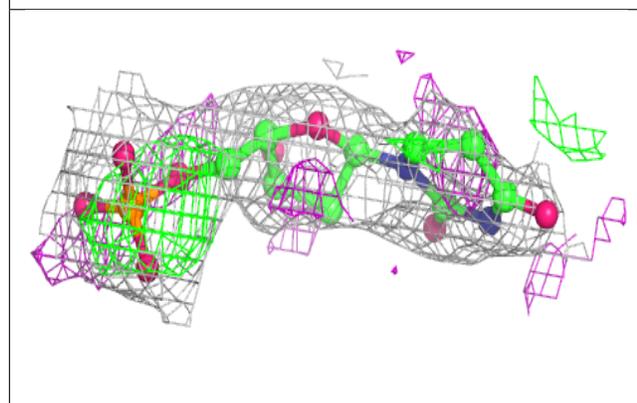
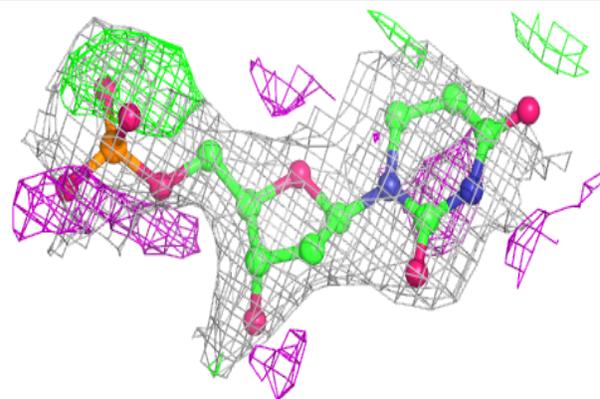


**Electron density around CB3 E 620:**

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

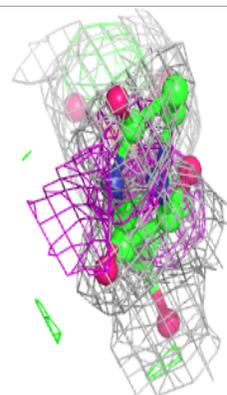
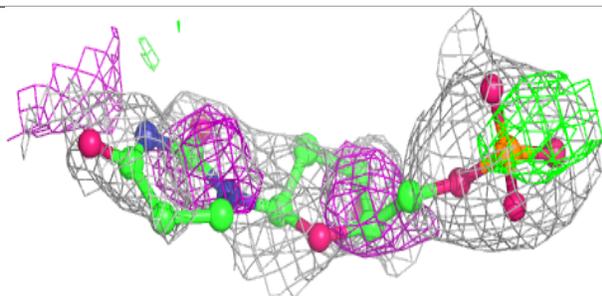
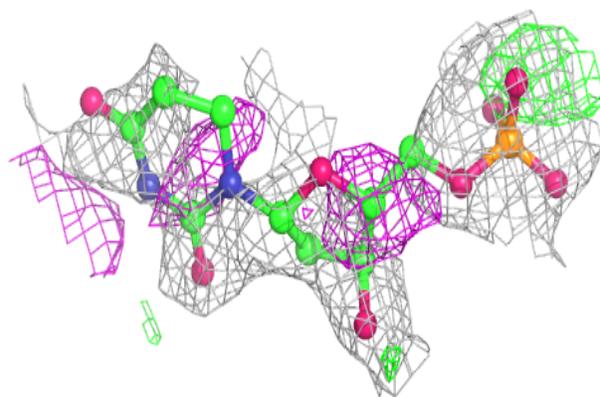
**Electron density around UMP C 611:**

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

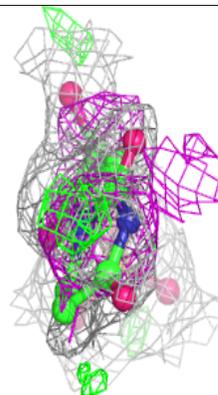
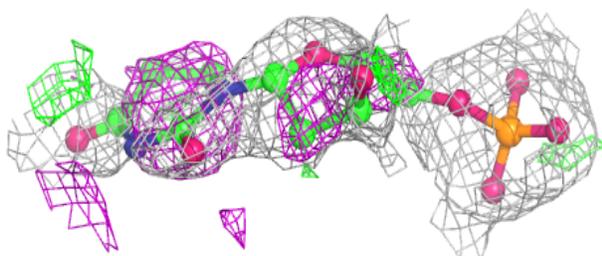
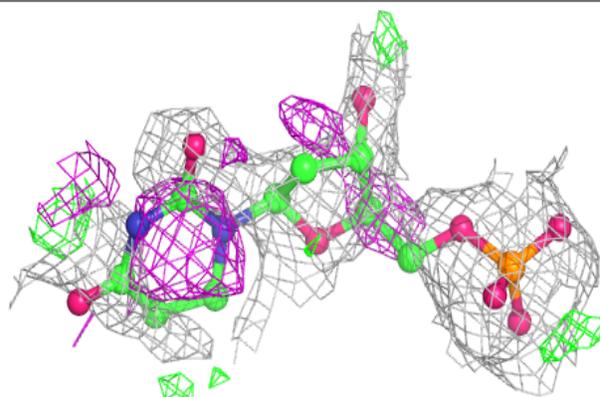


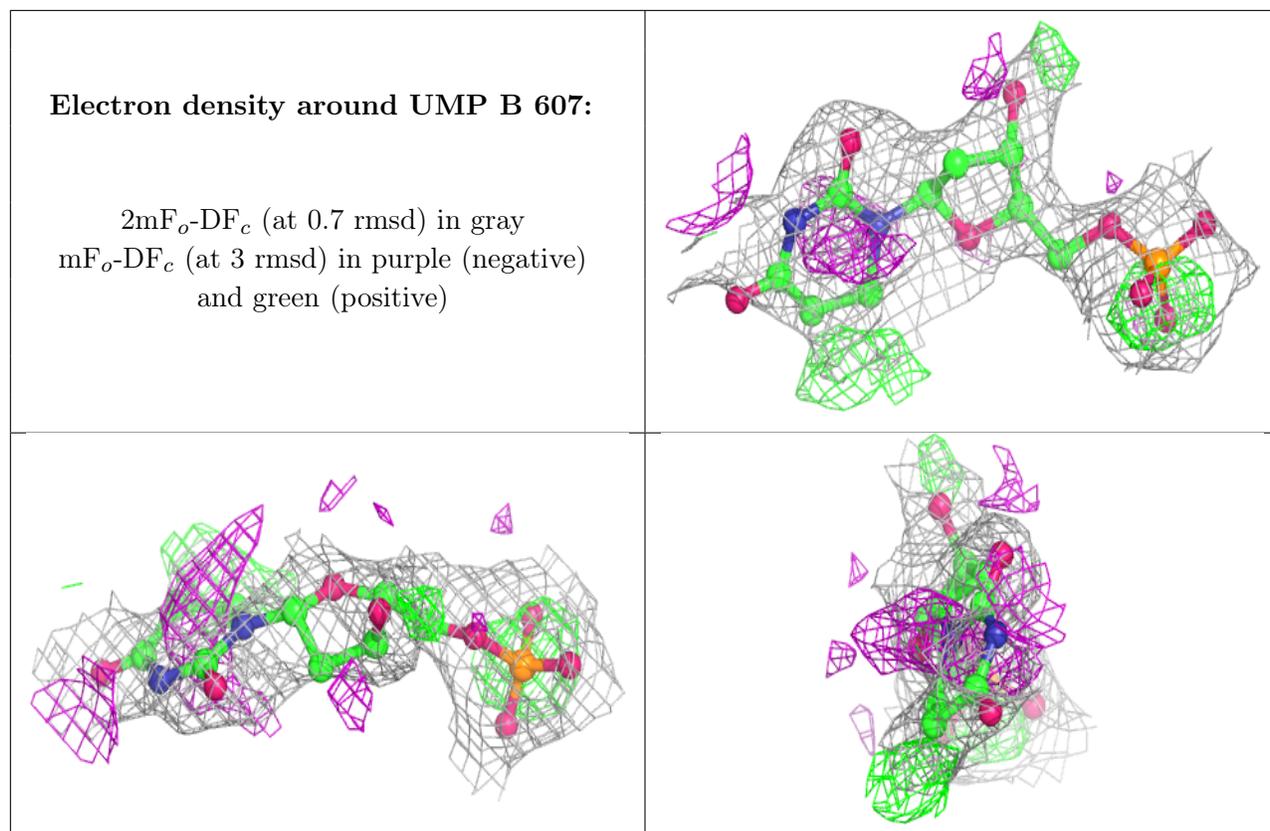
**Electron density around UMP A 603:**

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

**Electron density around UMP D 615:**

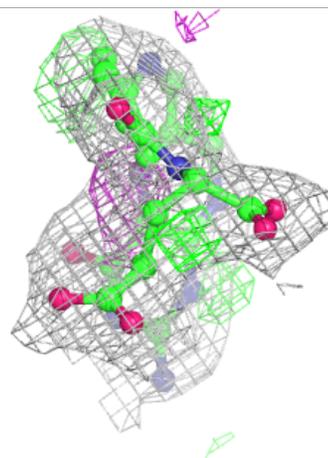
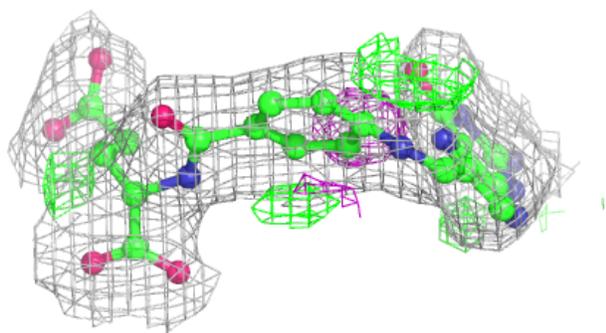
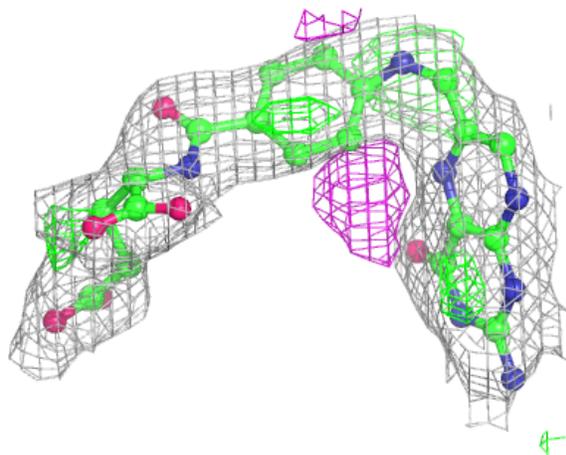
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





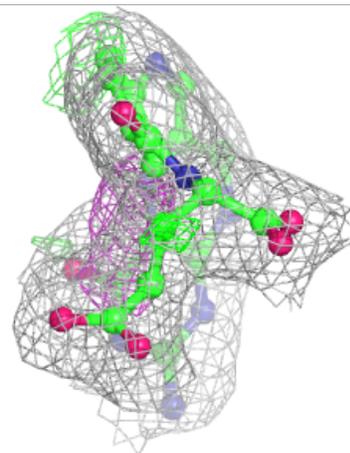
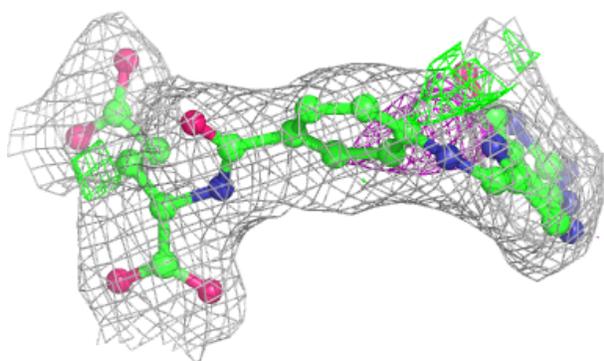
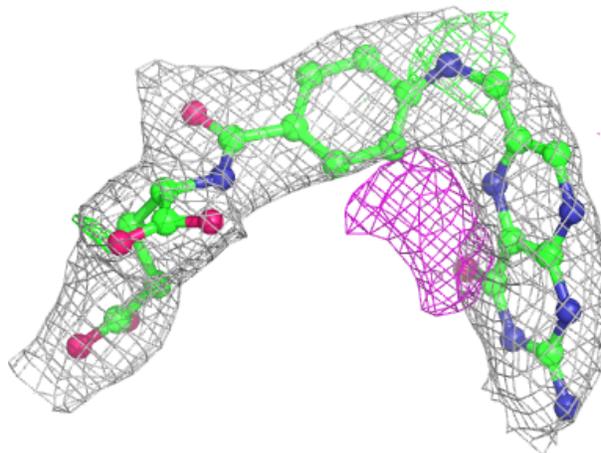
**Electron density around FOL E 621:**

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



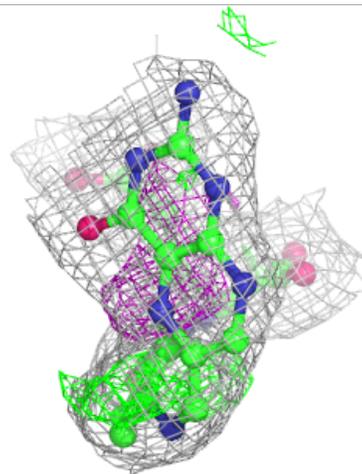
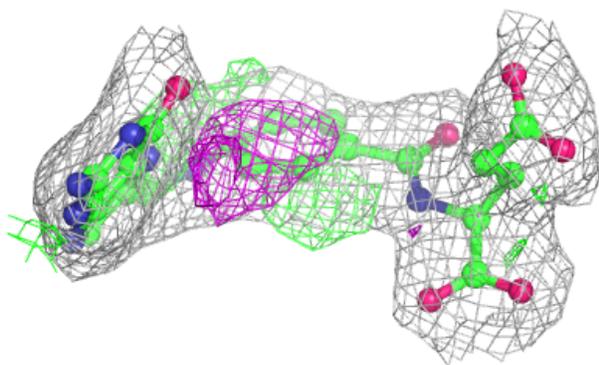
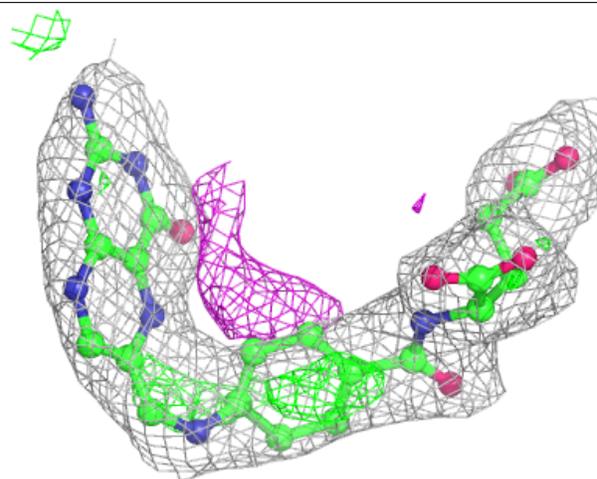
**Electron density around FOL D 617:**

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



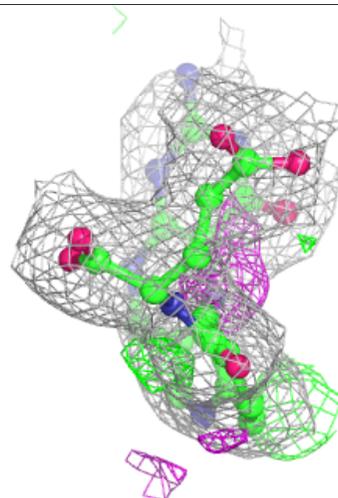
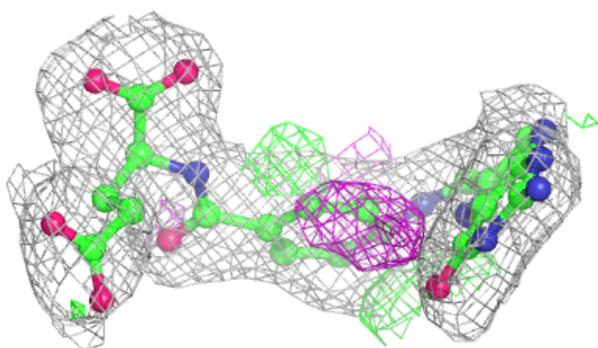
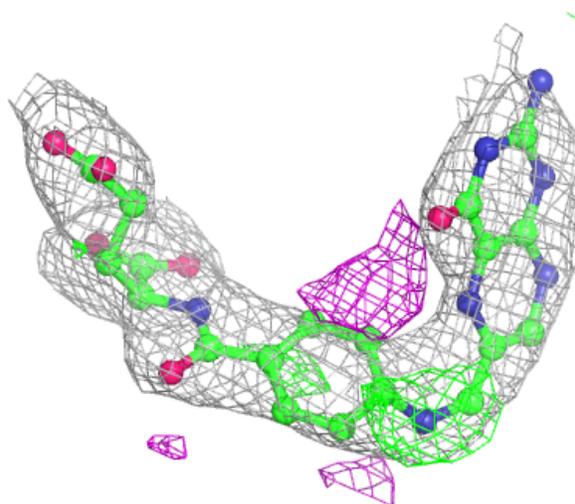
**Electron density around FOL B 609:**

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



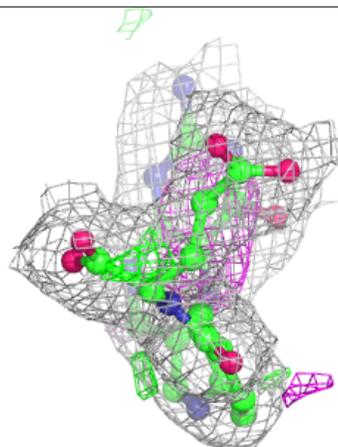
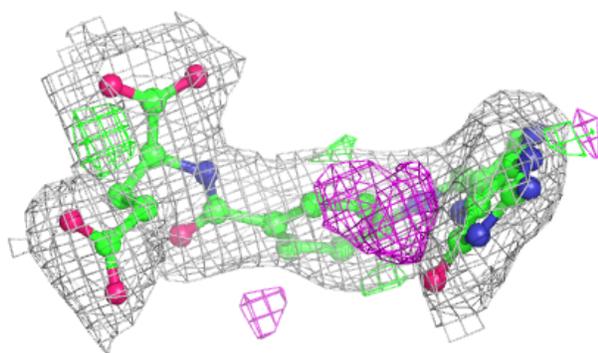
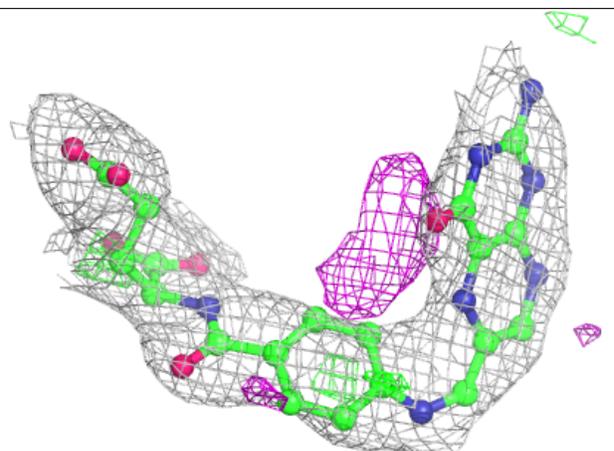
**Electron density around FOL C 613:**

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

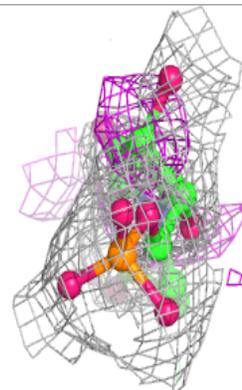
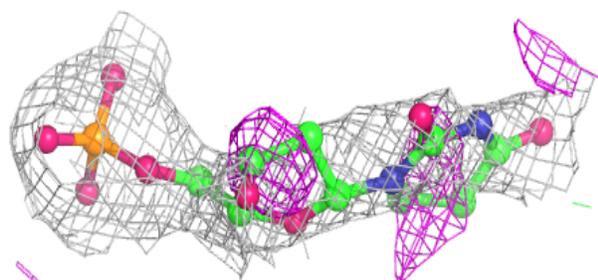
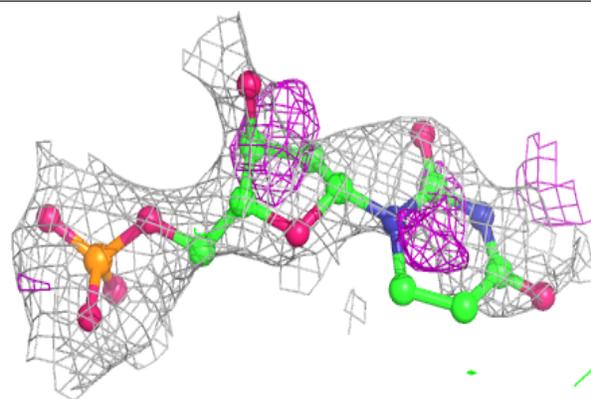


**Electron density around FOL A 605:**

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

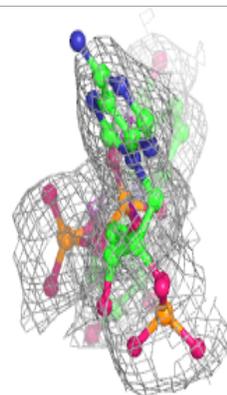
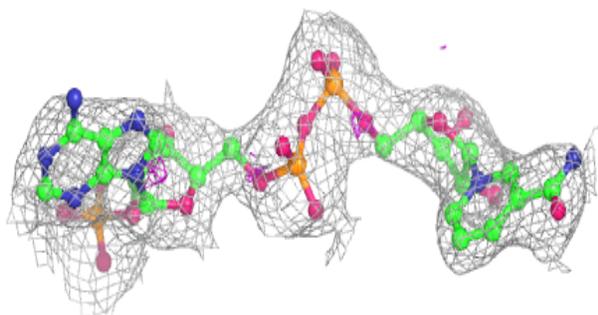
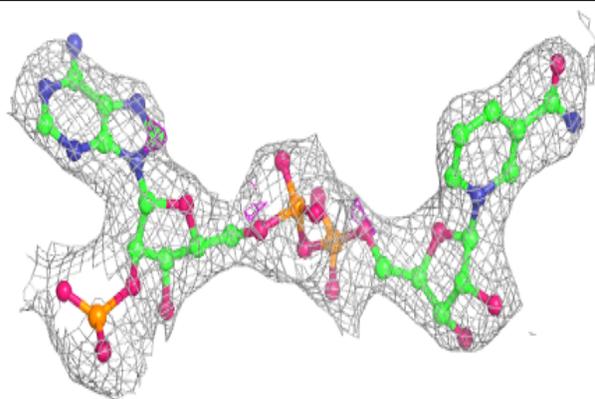
**Electron density around UMP E 619:**

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

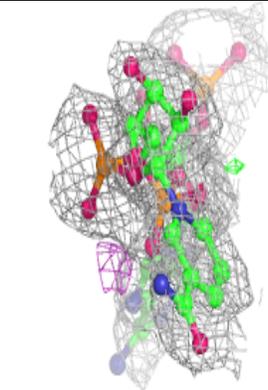
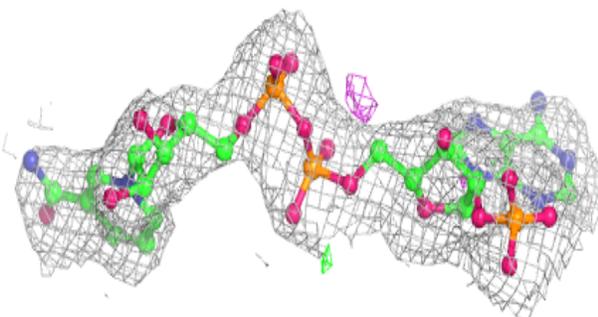
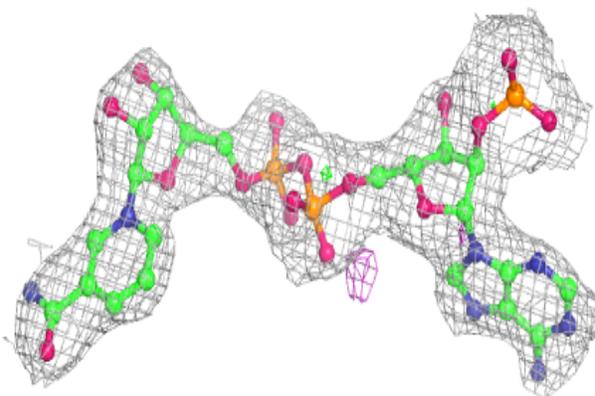


**Electron density around NDP C 614:**

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

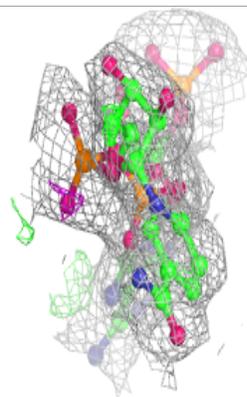
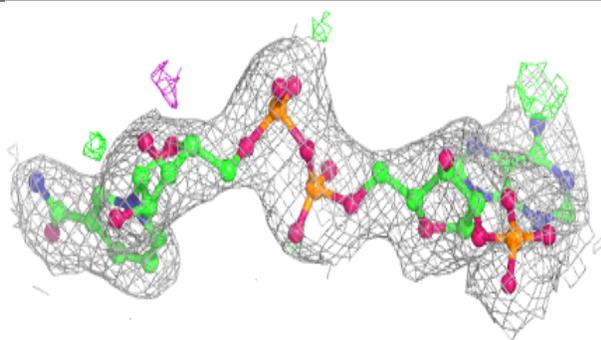
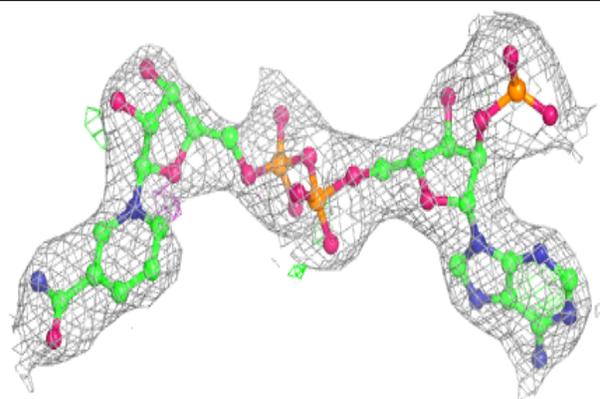
**Electron density around NDP E 622:**

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

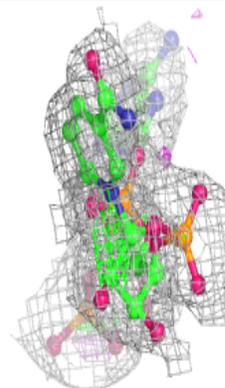
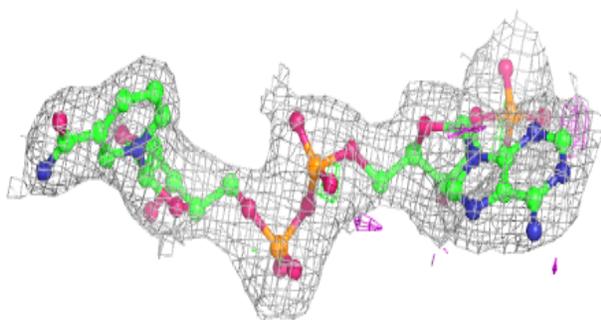
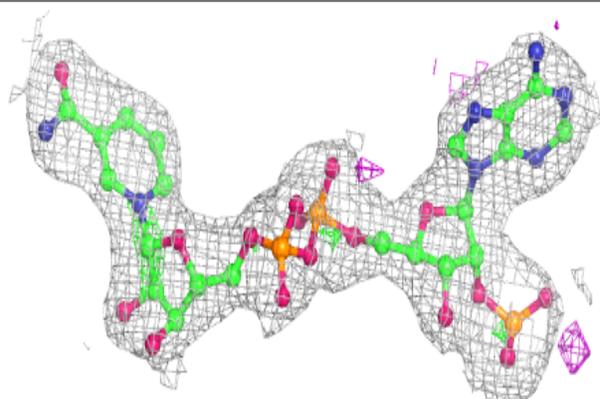


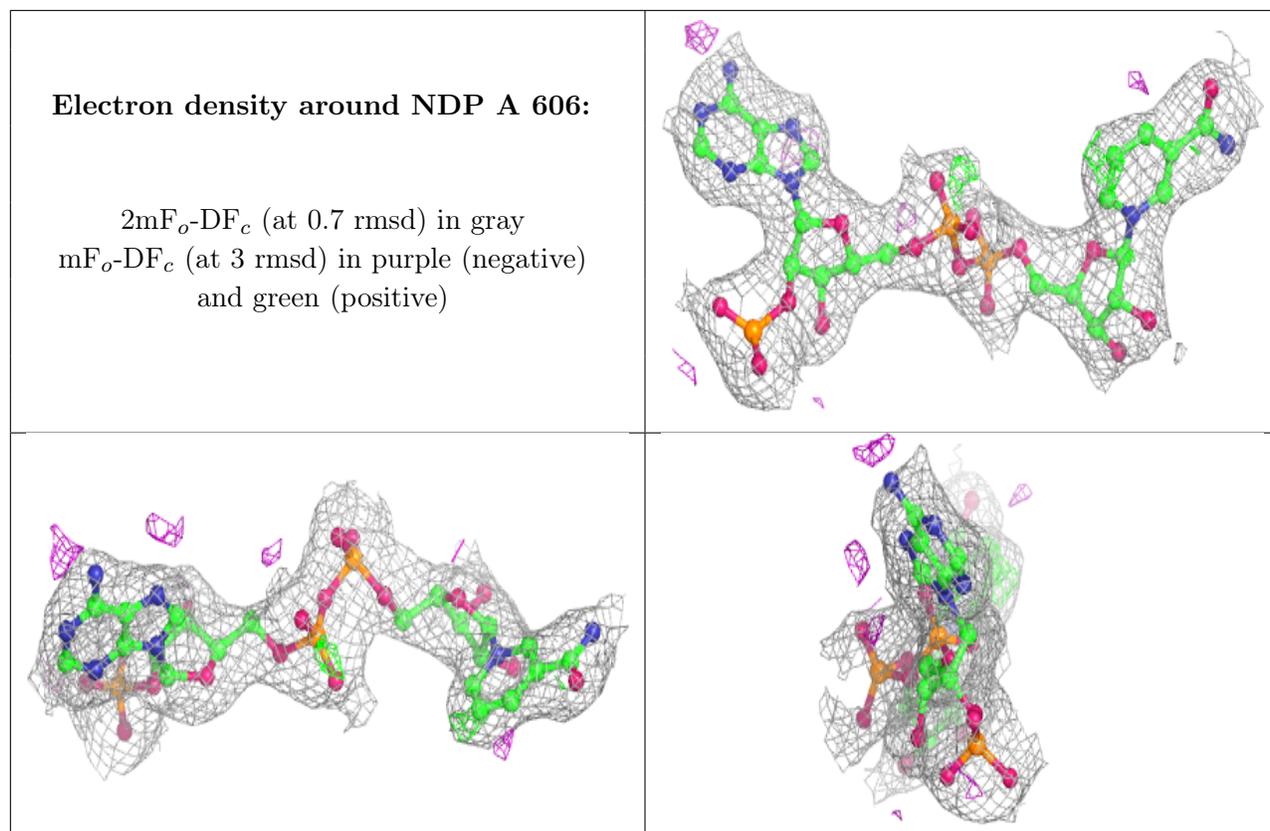
**Electron density around NDP D 618:**

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

**Electron density around NDP B 610:**

$2mF_o-DF_c$  (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.