



# Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 07:08 am BST

PDB ID : 6PFA  
Title : Crystal structure of TS-DHFR from *Cryptosporidium hominis* in complex with NADPH, FdUMP and 2-((4-((2-amino-4-oxo-4,7-dihydro-3H-pyrrolo[2,3-d]pyrimidin-5-yl)methyl)benzamido)methyl)benzoic acid.  
Authors : Czyzyk, D.J.; Valhondo, M.; Jorgensen, W.L.; Anderson, K.S.  
Deposited on : 2019-06-21  
Resolution : 2.79 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
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) : 2.11

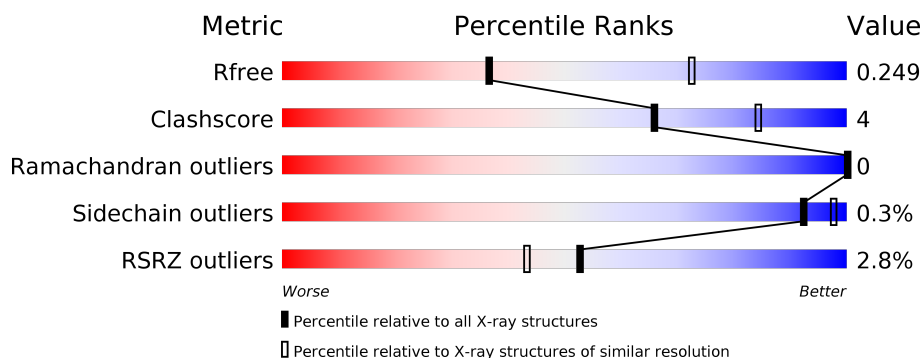
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.79 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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	521	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 1%, orange 1%, orange 87%, yellow 87%, yellow 97%, grey 97%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>87%</span> <span>10%</span> </div> </div>
1	B	521	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, orange 86%, yellow 86%, yellow 97%, grey 97%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>86%</span> <span>11%</span> </div> </div>
1	C	521	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 2%, orange 2%, orange 87%, yellow 87%, yellow 96%, grey 96%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>87%</span> <span>9%</span> </div> </div>
1	D	521	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 3%, orange 3%, orange 86%, yellow 86%, yellow 97%, grey 97%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>86%</span> <span>11%</span> </div> </div>
1	E	521	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 7%, orange 7%, orange 90%, yellow 90%, yellow 97%, grey 97%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>90%</span> <span>7%</span> </div> </div>

2 Entry composition ⓘ

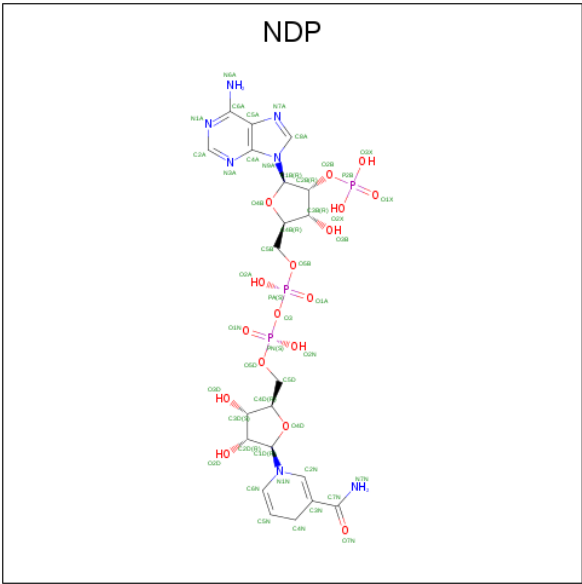
There are 7 unique types of molecules in this entry. The entry contains 21045 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
1	A	506	Total	C	N	O	S	0	0	0
			4076	2605	686	764	21			
1	B	506	Total	C	N	O	S	0	0	0
			4080	2608	687	764	21			
1	C	505	Total	C	N	O	S	0	0	0
			4037	2582	678	756	21			
1	D	506	Total	C	N	O	S	0	0	0
			4058	2595	681	761	21			
1	E	506	Total	C	N	O	S	0	0	0
			4003	2561	664	757	21			

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: C<sub>21</sub>H<sub>30</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).



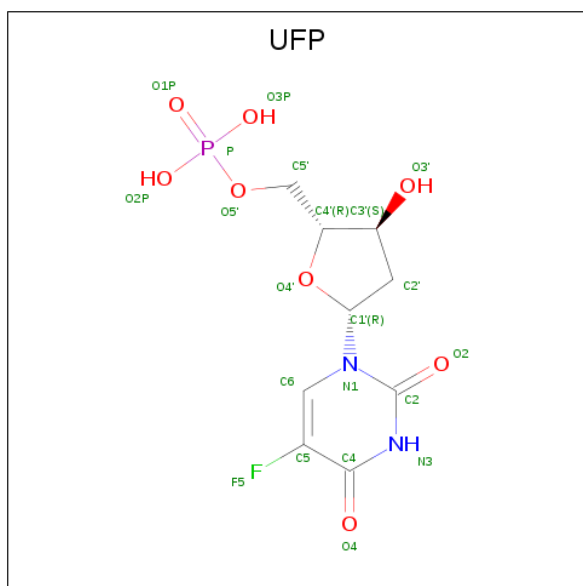
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

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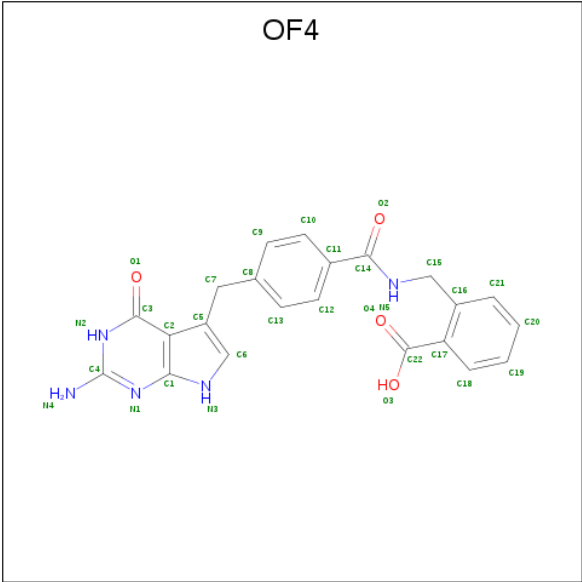
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	E	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 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).



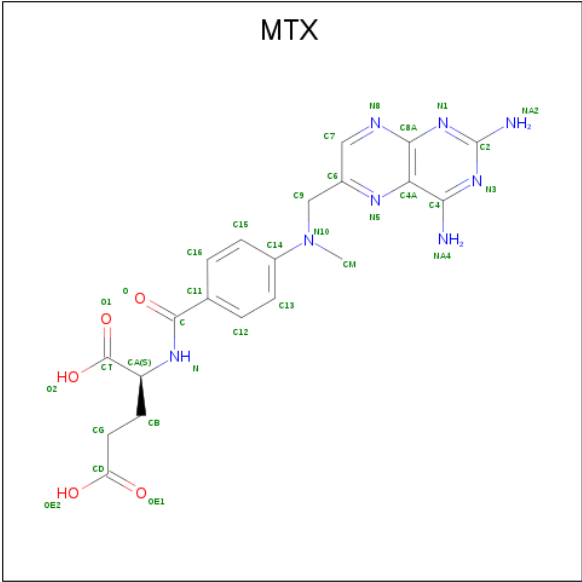
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total 21	C 9	F 1	N 2	O 8	P 1	0	0
3	B	1	Total 21	C 9	F 1	N 2	O 8	P 1	0	0
3	C	1	Total 21	C 9	F 1	N 2	O 8	P 1	0	0
3	D	1	Total 21	C 9	F 1	N 2	O 8	P 1	0	0
3	E	1	Total 21	C 9	F 1	N 2	O 8	P 1	0	0

- Molecule 4 is 2-[(4-[(2-amino-4-oxo-4,7-dihydro-3H-pyrrolo[2,3-d]pyrimidin-5-yl)methyl]benzene-1-carbonyl]amino)methyl]benzoic acid (three-letter code: OF4) (formula: C<sub>22</sub>H<sub>19</sub>N<sub>5</sub>O<sub>4</sub>) (labeled as "Ligand of Interest" by author).



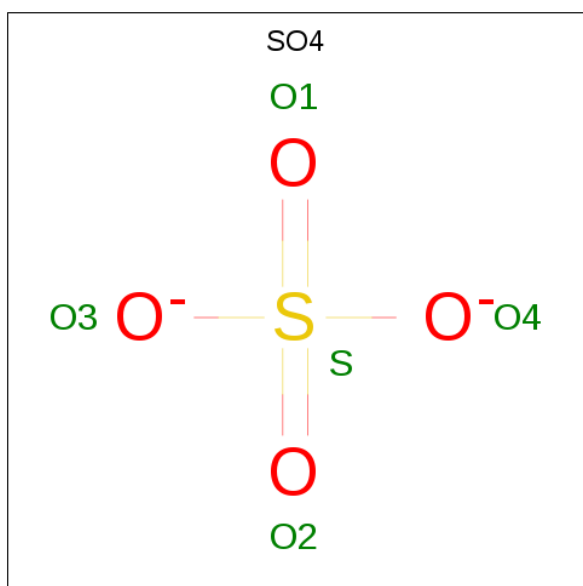
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			31	22	5	4		
4	B	1	Total	C	N	O	0	0
			31	22	5	4		
4	C	1	Total	C	N	O	0	0
			31	22	5	4		
4	D	1	Total	C	N	O	0	0
			31	22	5	4		
4	E	1	Total	C	N	O	0	0
			31	22	5	4		

- Molecule 5 is METHOTREXATE (three-letter code: MTX) (formula: C<sub>20</sub>H<sub>22</sub>N<sub>8</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			33	20	8	5		
5	B	1	Total	C	N	O	0	0
			33	20	8	5		
5	C	1	Total	C	N	O	0	0
			33	20	8	5		
5	D	1	Total	C	N	O	0	0
			33	20	8	5		
5	E	1	Total	C	N	O	0	0
			33	20	8	5		

- Molecule 6 is SULFATE ION (three-letter code: SO<sub>4</sub>) (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	C	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		

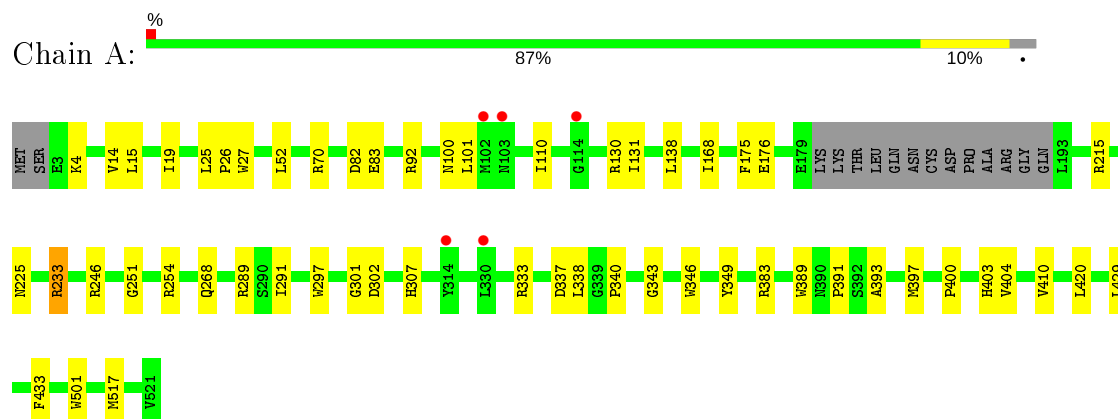
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	24	Total 24	O 24	0	0
7	B	37	Total 37	O 37	0	0
7	C	15	Total 15	O 15	0	0
7	D	18	Total 18	O 18	0	0
7	E	7	Total 7	O 7	0	0

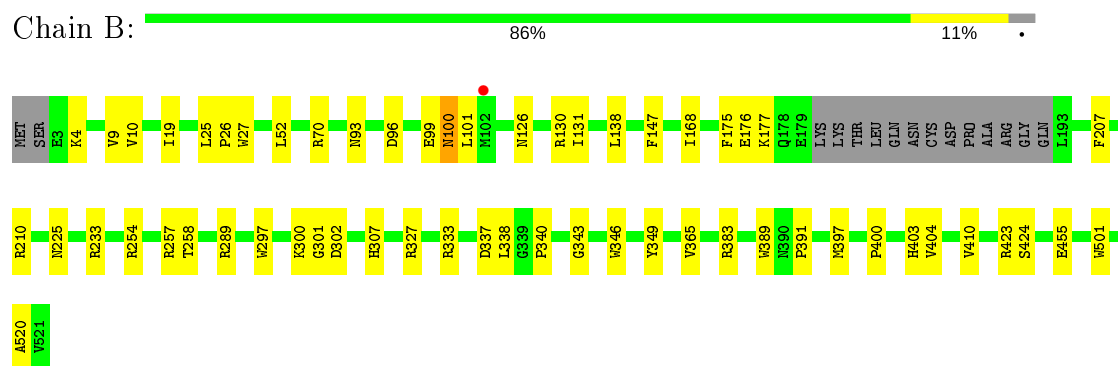
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

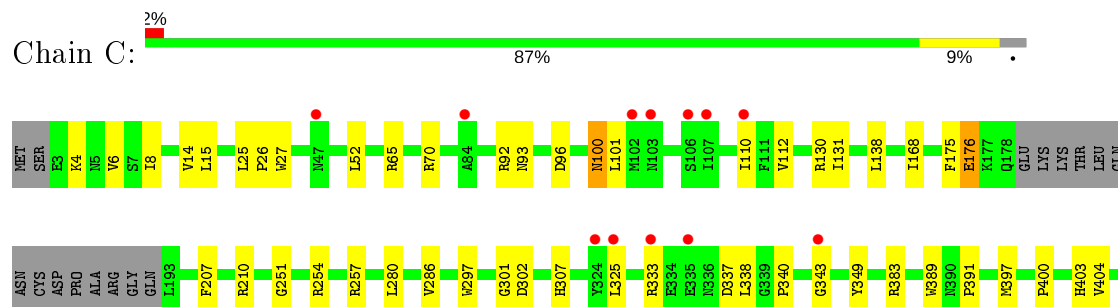
- Molecule 1: Bifunctional dihydrofolate reductase-thymidylate synthase



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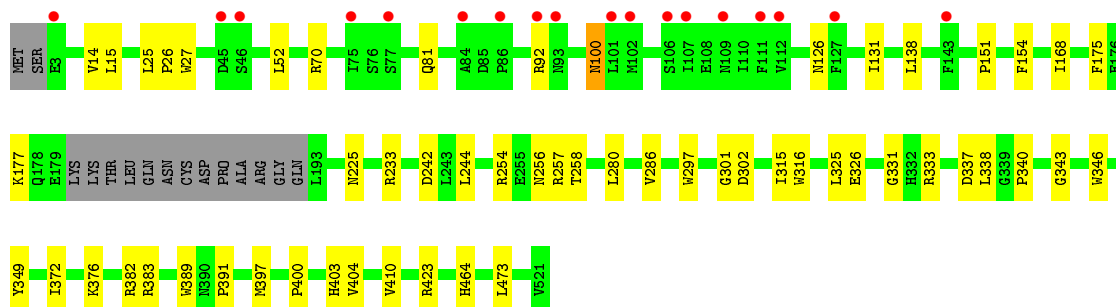






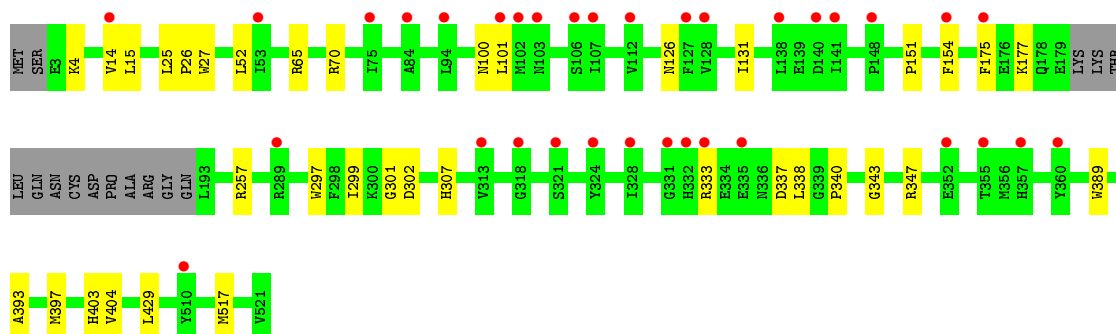
- Molecule 1: Bifunctional dihydrofolate reductase-thymidylate synthase

Chain D: 3% 86% 11%



- Molecule 1: Bifunctional dihydrofolate reductase-thymidylate synthase

Chain E: 7% 90% 7%



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	213.21Å 117.29Å 222.82Å 90.00° 95.72° 90.00°	Depositor
Resolution (Å)	48.93 – 2.79 48.93 – 2.79	Depositor EDS
% Data completeness (in resolution range)	99.0 (48.93-2.79) 99.2 (48.93-2.79)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.97 (at 2.77Å)	Xtriage
Refinement program	PHENIX (1.15.2 _3472: 000)	Depositor
R, $R_{free}$	0.221 , 0.249 0.222 , 0.249	Depositor DCC
$R_{free}$ test set	6780 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	66.7	Xtriage
Anisotropy	0.316	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 41.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	21045	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.27% 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: UFP, NDP, MTX, SO4, OF4

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	0.25	0/4171	0.42	0/5648
1	B	0.25	0/4175	0.42	0/5652
1	C	0.24	0/4132	0.41	0/5602
1	D	0.24	0/4153	0.41	0/5627
1	E	0.24	0/4097	0.40	0/5564
All	All	0.24	0/20728	0.41	0/28093

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 [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	4076	0	3962	39	0
1	B	4080	0	3973	41	0
1	C	4037	0	3898	35	0
1	D	4058	0	3926	40	0
1	E	4003	0	3814	21	0
2	A	48	0	26	1	0
2	B	48	0	26	1	0
2	C	48	0	26	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	48	0	26	0	0
2	E	48	0	26	0	0
3	A	21	0	10	0	0
3	B	21	0	10	3	0
3	C	21	0	10	2	0
3	D	21	0	10	3	0
3	E	21	0	10	1	0
4	A	31	0	0	0	0
4	B	31	0	0	1	0
4	C	31	0	0	0	0
4	D	31	0	0	0	0
4	E	31	0	0	0	0
5	A	33	0	20	1	0
5	B	33	0	20	2	0
5	C	33	0	20	2	0
5	D	33	0	20	1	0
5	E	33	0	20	1	0
6	A	5	0	0	0	0
6	B	5	0	0	0	0
6	C	5	0	0	0	0
6	D	5	0	0	0	0
6	E	5	0	0	0	0
7	A	24	0	0	0	0
7	B	37	0	0	2	0
7	C	15	0	0	0	0
7	D	18	0	0	0	0
7	E	7	0	0	0	0
All	All	21045	0	19853	161	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 4.

All (161) 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:B:258:THR:HG21	1:B:520:ALA:HB1	1.68	0.75
1:D:52:LEU:HD11	1:D:70:ARG:HD2	1.75	0.66
1:B:389:TRP:HB2	1:B:404:VAL:HG13	1.78	0.64
1:E:126:ASN:OD1	1:E:177:LYS:NZ	2.30	0.64
1:B:52:LEU:HD11	1:B:70:ARG:HD2	1.81	0.63
1:B:126:ASN:OD1	1:B:177:LYS:NZ	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:126:ASN:OD1	1:D:177:LYS:NZ	2.31	0.62
1:B:131:ILE:HB	1:B:175:PHE:HB2	1.81	0.62
1:A:225:ASN:O	1:A:233:ARG:NH2	2.31	0.62
1:B:257:ARG:HH21	3:B:602:UFP:H5'2	1.66	0.61
1:C:131:ILE:HB	1:C:175:PHE:HB2	1.84	0.60
1:E:131:ILE:HB	1:E:175:PHE:HB2	1.82	0.60
1:A:389:TRP:HB2	1:A:404:VAL:HG13	1.83	0.59
1:D:333:ARG:HG3	1:D:337:ASP:HB3	1.84	0.59
1:D:131:ILE:HB	1:D:175:PHE:HB2	1.83	0.59
1:A:131:ILE:HB	1:A:175:PHE:HB2	1.84	0.59
1:D:389:TRP:HB2	1:D:404:VAL:HG13	1.83	0.58
1:C:349:TYR:HH	1:D:349:TYR:HH	1.51	0.58
1:B:225:ASN:O	1:B:233:ARG:NH2	2.28	0.58
1:E:389:TRP:HB2	1:E:404:VAL:HG13	1.85	0.58
1:B:301:GLY:HA2	1:B:343:GLY:O	2.04	0.57
1:A:52:LEU:HD11	1:A:70:ARG:HD2	1.86	0.57
1:C:389:TRP:HB2	1:C:404:VAL:HG13	1.85	0.57
1:D:225:ASN:O	1:D:233:ARG:NH2	2.37	0.57
1:B:327:ARG:NH2	7:B:703:HOH:O	2.38	0.56
1:E:302:ASP:OD2	1:E:307:HIS:ND1	2.33	0.56
1:A:301:GLY:HA2	1:A:343:GLY:O	2.05	0.56
1:B:300:LYS:NZ	7:B:704:HOH:O	2.39	0.56
1:B:4:LYS:HG2	1:B:101:LEU:HD23	1.86	0.56
1:C:254:ARG:NH2	1:D:410:VAL:O	2.38	0.56
1:A:333:ARG:HG3	1:A:337:ASP:HB3	1.89	0.55
1:C:130:ARG:NH1	1:C:176:GLU:OE2	2.40	0.55
1:E:52:LEU:HD11	1:E:70:ARG:HD2	1.88	0.55
1:C:52:LEU:HD11	1:C:70:ARG:HD2	1.88	0.55
1:B:333:ARG:HG3	1:B:337:ASP:HB3	1.88	0.54
1:A:4:LYS:HG2	1:A:101:LEU:HD23	1.87	0.54
1:C:301:GLY:HA2	1:C:343:GLY:O	2.06	0.54
1:D:297:TRP:HH2	1:D:338:LEU:HD12	1.73	0.54
1:B:130:ARG:NH1	1:B:176:GLU:OE2	2.41	0.53
1:C:410:VAL:O	1:D:254:ARG:NH2	2.41	0.53
1:D:301:GLY:HA2	1:D:343:GLY:O	2.08	0.53
1:A:349:TYR:HH	1:B:349:TYR:HH	1.51	0.52
1:A:391:PRO:HD2	1:B:349:TYR:CE2	2.45	0.52
1:D:26:PRO:HG2	1:D:27:TRP:CE3	2.45	0.52
1:C:391:PRO:HD2	1:D:349:TYR:CE2	2.46	0.51
1:A:26:PRO:HG2	1:A:27:TRP:CE3	2.45	0.51
1:A:254:ARG:NH2	1:B:410:VAL:O	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:349:TYR:CE2	1:D:391:PRO:HD2	2.46	0.51
1:E:14:VAL:HG13	1:E:15:LEU:HG	1.92	0.51
1:C:302:ASP:OD2	1:C:307:HIS:ND1	2.33	0.51
1:E:403:HIS:H	1:E:403:HIS:CD2	2.28	0.51
1:B:26:PRO:HG2	1:B:27:TRP:CE3	2.46	0.50
1:C:26:PRO:HG2	1:C:27:TRP:CE3	2.47	0.50
1:A:410:VAL:O	1:B:254:ARG:NH2	2.44	0.50
1:A:302:ASP:OD2	1:A:307:HIS:ND1	2.37	0.50
1:C:25:LEU:HD11	5:C:604:MTX:H7	1.95	0.49
1:B:138:LEU:HD11	1:B:168:ILE:HD13	1.93	0.49
1:B:349:TYR:HB3	1:B:365:VAL:HB	1.94	0.49
1:B:93:ASN:ND2	1:B:96:ASP:OD2	2.31	0.49
1:E:25:LEU:HD11	5:E:604:MTX:H7	1.95	0.49
1:A:383:ARG:NE	1:B:400:PRO:HG2	2.28	0.49
1:A:349:TYR:CE2	1:B:391:PRO:HD2	2.48	0.49
1:D:256:ASN:OD1	1:D:258:THR:OG1	2.25	0.49
1:A:429:LEU:HD21	1:A:517:MET:HB2	1.94	0.49
1:A:26:PRO:HG2	1:A:27:TRP:CZ3	2.48	0.48
1:B:343:GLY:HA2	1:B:346:TRP:HB2	1.95	0.48
1:E:26:PRO:HG2	1:E:27:TRP:CE3	2.48	0.48
1:D:372:ILE:HG22	1:D:376:LYS:HE2	1.96	0.48
1:E:297:TRP:HH2	1:E:338:LEU:HD12	1.78	0.48
1:D:326:GLU:HG2	1:D:331:GLY:HA2	1.95	0.48
1:C:4:LYS:HG2	1:C:101:LEU:HD23	1.95	0.48
1:B:26:PRO:HG2	1:B:27:TRP:CZ3	2.49	0.48
1:C:333:ARG:HG3	1:C:337:ASP:HB3	1.95	0.48
1:E:4:LYS:H	1:E:101:LEU:HD22	1.78	0.48
1:E:299:ILE:O	1:E:347:ARG:NH1	2.45	0.48
1:E:301:GLY:HA2	1:E:343:GLY:O	2.13	0.48
1:A:215:ARG:NH1	1:B:455:GLU:OE2	2.46	0.48
1:C:297:TRP:HH2	1:C:338:LEU:HD12	1.79	0.48
1:A:297:TRP:CD1	1:A:302:ASP:HB3	2.49	0.48
1:C:403:HIS:H	1:C:403:HIS:CD2	2.31	0.48
1:D:14:VAL:HG13	1:D:15:LEU:HG	1.96	0.48
1:B:403:HIS:CD2	1:B:403:HIS:H	2.32	0.47
1:B:297:TRP:HH2	1:B:338:LEU:HD12	1.78	0.47
1:C:8:ILE:HG12	1:C:112:VAL:HB	1.97	0.47
1:A:138:LEU:HD11	1:A:168:ILE:HD13	1.96	0.47
3:C:602:UFP:O1P	1:D:382:ARG:NE	2.47	0.47
1:D:343:GLY:HA2	1:D:346:TRP:HB2	1.97	0.47
1:A:130:ARG:HG3	1:A:176:GLU:HG2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:297:TRP:CD1	1:C:302:ASP:HB3	2.49	0.47
1:B:302:ASP:OD2	1:B:307:HIS:ND1	2.33	0.46
1:C:14:VAL:HG13	1:C:15:LEU:HG	1.97	0.46
1:E:333:ARG:HG3	1:E:337:ASP:HB3	1.96	0.46
1:C:251:GLY:O	1:E:65:ARG:NH1	2.46	0.46
1:D:244:LEU:HD22	1:D:473:LEU:HD13	1.98	0.46
1:C:100:ASN:OD1	1:C:100:ASN:N	2.49	0.45
1:C:340:PRO:O	1:C:397:MET:HG2	2.16	0.45
1:D:100:ASN:N	1:D:100:ASN:OD1	2.48	0.45
1:A:25:LEU:HD11	5:A:604:MTX:H7	1.98	0.45
1:A:400:PRO:HG2	1:B:383:ARG:NE	2.31	0.45
1:B:423:ARG:NH2	3:B:602:UFP:O3P	2.49	0.45
1:E:340:PRO:O	1:E:397:MET:HG2	2.16	0.45
1:A:100:ASN:HB2	1:A:110:ILE:HD11	1.99	0.45
1:D:257:ARG:HH21	3:D:602:UFP:H5'2	1.81	0.45
1:C:325:LEU:HD23	1:C:333:ARG:HB3	1.99	0.45
1:C:383:ARG:NE	1:D:400:PRO:HG2	2.32	0.44
1:A:403:HIS:H	1:A:403:HIS:CD2	2.34	0.44
1:D:81:GLN:HG3	1:D:92:ARG:NH2	2.32	0.44
1:A:340:PRO:O	1:A:397:MET:HG2	2.18	0.44
1:D:26:PRO:HG2	1:D:27:TRP:CZ3	2.53	0.44
1:B:25:LEU:HD11	5:B:604:MTX:H7	1.98	0.44
1:A:251:GLY:O	1:C:65:ARG:NH1	2.49	0.44
1:D:151:PRO:HG2	1:D:154:PHE:HD1	1.83	0.44
1:D:403:HIS:CD2	1:D:403:HIS:H	2.34	0.44
1:A:291:ILE:HG12	1:A:433:PHE:CD2	2.53	0.43
1:A:289:ARG:HG3	1:A:501:TRP:CE2	2.53	0.43
1:A:297:TRP:HH2	1:A:338:LEU:HD12	1.82	0.43
1:E:151:PRO:HG2	1:E:154:PHE:HD1	1.84	0.43
1:C:138:LEU:HD11	1:C:168:ILE:HD13	1.99	0.43
1:A:4:LYS:HG2	1:A:101:LEU:CD2	2.49	0.43
1:B:207:PHE:HB3	1:B:210:ARG:HB2	2.01	0.43
1:B:289:ARG:HG3	1:B:501:TRP:CE2	2.54	0.43
1:C:6:VAL:HG22	1:C:110:ILE:HB	2.00	0.43
1:A:92:ARG:HD3	1:A:92:ARG:HA	1.89	0.42
1:C:207:PHE:HB3	1:C:210:ARG:HB2	2.01	0.42
1:B:100:ASN:N	1:B:100:ASN:OD1	2.51	0.42
1:E:393:ALA:O	1:E:397:MET:HG3	2.19	0.42
1:C:257:ARG:NE	3:C:602:UFP:O2P	2.49	0.42
1:A:246:ARG:NH2	1:A:268:GLN:OE1	2.30	0.42
1:B:19:ILE:O	2:B:601:NDP:H2N	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:400:PRO:HG2	1:D:383:ARG:NE	2.35	0.42
1:A:19:ILE:O	2:A:601:NDP:H2N	2.20	0.42
3:B:602:UFP:H4'	4:B:603:OF4:N4	2.35	0.42
1:B:9:VAL:O	5:B:604:MTX:NA4	2.50	0.42
1:C:26:PRO:HG2	1:C:27:TRP:CZ3	2.54	0.42
1:D:138:LEU:HD11	1:D:168:ILE:HD13	2.02	0.41
1:A:403:HIS:HB2	1:A:420:LEU:HD11	2.01	0.41
2:C:601:NDP:H42N	5:C:604:MTX:N5	2.34	0.41
1:A:393:ALA:O	1:A:397:MET:HG3	2.20	0.41
1:E:26:PRO:HG2	1:E:27:TRP:CZ3	2.54	0.41
1:C:280:LEU:HD11	1:C:286:VAL:HB	2.01	0.41
1:A:14:VAL:HG13	1:A:15:LEU:HG	2.03	0.41
1:A:343:GLY:HA2	1:A:346:TRP:HB2	2.03	0.41
1:D:233:ARG:NH1	1:D:242:ASP:OD1	2.53	0.41
1:D:340:PRO:O	1:D:397:MET:HG2	2.20	0.41
1:B:10:VAL:HG21	1:B:147:PHE:CD1	2.56	0.41
1:E:429:LEU:HD21	1:E:517:MET:HB2	2.03	0.41
1:B:340:PRO:O	1:B:397:MET:HG2	2.21	0.41
1:D:325:LEU:HD23	1:D:333:ARG:HB3	2.02	0.41
1:B:423:ARG:HG3	1:B:424:SER:N	2.36	0.41
1:C:93:ASN:ND2	1:C:96:ASP:OD2	2.39	0.41
1:D:280:LEU:HD11	1:D:286:VAL:HB	2.02	0.41
1:D:315:ILE:HG13	1:D:316:TRP:CD1	2.56	0.41
1:D:297:TRP:CD1	1:D:302:ASP:HB3	2.56	0.41
1:B:297:TRP:CD1	1:B:302:ASP:HB3	2.56	0.40
1:C:92:ARG:HA	1:C:92:ARG:HD3	1.89	0.40
1:D:464:HIS:NE2	3:D:602:UFP:O3'	2.45	0.40
1:E:257:ARG:HH21	3:E:602:UFP:H5'1	1.86	0.40
1:D:423:ARG:NH2	3:D:602:UFP:O3P	2.49	0.40
1:A:82:ASP:OD1	1:A:83:GLU:N	2.55	0.40
1:D:151:PRO:HG2	1:D:154:PHE:CD1	2.56	0.40
1:D:25:LEU:HD11	5:D:604:MTX:H7	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	502/521 (96%)	473 (94%)	29 (6%)	0	100	100
1	B	502/521 (96%)	473 (94%)	29 (6%)	0	100	100
1	C	501/521 (96%)	472 (94%)	29 (6%)	0	100	100
1	D	502/521 (96%)	474 (94%)	28 (6%)	0	100	100
1	E	502/521 (96%)	474 (94%)	28 (6%)	0	100	100
All	All	2509/2605 (96%)	2366 (94%)	143 (6%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	445/470 (95%)	444 (100%)	1 (0%)	93	98
1	B	446/470 (95%)	444 (100%)	2 (0%)	91	97
1	C	437/470 (93%)	435 (100%)	2 (0%)	88	96
1	D	440/470 (94%)	439 (100%)	1 (0%)	93	98
1	E	428/470 (91%)	427 (100%)	1 (0%)	93	98
All	All	2196/2350 (93%)	2189 (100%)	7 (0%)	92	98

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	233	ARG
1	B	99	GLU
1	B	100	ASN
1	C	100	ASN
1	C	176	GLU
1	D	100	ASN

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Mol	Chain	Res	Type
1	E	100	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

25 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	UFP	D	602	-	19,22,22	1.19	1 (5%)	24,33,33	2.12	4 (16%)
3	UFP	B	602	-	19,22,22	1.22	1 (5%)	24,33,33	2.17	6 (25%)
5	MTX	E	604	-	29,35,35	1.77	6 (20%)	38,49,49	1.90	9 (23%)
4	OF4	E	603	-	31,34,34	1.55	5 (16%)	32,48,48	2.40	8 (25%)
3	UFP	C	602	-	19,22,22	1.18	1 (5%)	24,33,33	2.11	4 (16%)
2	NDP	E	601	-	45,52,52	1.93	11 (24%)	53,80,80	1.11	6 (11%)
2	NDP	A	601	-	45,52,52	1.95	11 (24%)	53,80,80	1.10	7 (13%)
2	NDP	C	601	-	45,52,52	1.94	11 (24%)	53,80,80	1.12	6 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	MTX	A	604	-	29,35,35	1.79	6 (20%)	38,49,49	1.94	10 (26%)
5	MTX	B	604	-	29,35,35	1.79	6 (20%)	38,49,49	1.94	11 (28%)
6	SO4	D	605	-	4,4,4	0.15	0	6,6,6	0.04	0
6	SO4	B	605	-	4,4,4	0.15	0	6,6,6	0.07	0
2	NDP	D	601	-	45,52,52	1.95	11 (24%)	53,80,80	1.12	5 (9%)
6	SO4	E	605	-	4,4,4	0.14	0	6,6,6	0.05	0
2	NDP	B	601	-	45,52,52	1.93	11 (24%)	53,80,80	1.09	5 (9%)
6	SO4	C	605	-	4,4,4	0.15	0	6,6,6	0.06	0
4	OF4	D	603	-	31,34,34	1.51	4 (12%)	32,48,48	2.38	7 (21%)
3	UFP	A	602	-	19,22,22	1.18	1 (5%)	24,33,33	2.11	6 (25%)
6	SO4	A	605	-	4,4,4	0.13	0	6,6,6	0.06	0
5	MTX	C	604	-	29,35,35	1.78	6 (20%)	38,49,49	1.95	10 (26%)
5	MTX	D	604	-	29,35,35	1.79	6 (20%)	38,49,49	1.94	11 (28%)
4	OF4	A	603	-	31,34,34	1.52	4 (12%)	32,48,48	2.34	7 (21%)
4	OF4	C	603	-	31,34,34	1.54	5 (16%)	32,48,48	2.41	7 (21%)
3	UFP	E	602	-	19,22,22	1.38	2 (10%)	24,33,33	2.05	4 (16%)
4	OF4	B	603	-	31,34,34	1.52	4 (12%)	32,48,48	2.41	7 (21%)

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	OF4	D	603	-	-	1/13/17/17	0/4/4/4
3	UFP	D	602	-	-	3/7/22/22	0/2/2/2
2	NDP	A	601	-	-	3/30/77/77	0/5/5/5
3	UFP	B	602	-	-	3/7/22/22	0/2/2/2
2	NDP	C	601	-	-	3/30/77/77	0/5/5/5
5	MTX	A	604	-	-	5/19/25/25	0/3/3/3
3	UFP	A	602	-	-	1/7/22/22	0/2/2/2
5	MTX	B	604	-	-	5/19/25/25	0/3/3/3
5	MTX	E	604	-	-	4/19/25/25	0/3/3/3
2	NDP	B	601	-	-	2/30/77/77	0/5/5/5
5	MTX	C	604	-	-	5/19/25/25	0/3/3/3
5	MTX	D	604	-	-	5/19/25/25	0/3/3/3
4	OF4	A	603	-	-	1/13/17/17	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NDP	D	601	-	-	6/30/77/77	0/5/5/5
3	UFP	E	602	-	-	2/7/22/22	0/2/2/2
4	OF4	E	603	-	-	1/13/17/17	0/4/4/4
3	UFP	C	602	-	-	3/7/22/22	0/2/2/2
2	NDP	E	601	-	-	7/30/77/77	0/5/5/5
4	OF4	B	603	-	-	1/13/17/17	0/4/4/4
4	OF4	C	603	-	-	1/13/17/17	0/4/4/4

All (113) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	604	MTX	C2-NA2	5.32	1.44	1.33
5	B	604	MTX	C2-NA2	5.31	1.44	1.33
5	E	604	MTX	C2-NA2	5.25	1.44	1.33
5	C	604	MTX	C2-NA2	5.24	1.44	1.33
5	A	604	MTX	C2-NA2	5.20	1.44	1.33
5	B	604	MTX	C-N	5.06	1.45	1.34
5	E	604	MTX	C-N	5.05	1.45	1.34
5	D	604	MTX	C-N	5.03	1.45	1.34
5	A	604	MTX	C-N	4.99	1.45	1.34
5	C	604	MTX	C-N	4.94	1.44	1.34
4	C	603	OF4	C17-C22	4.59	1.51	1.47
4	E	603	OF4	C17-C22	4.52	1.51	1.47
2	C	601	NDP	C4N-C3N	-4.47	1.41	1.49
2	B	601	NDP	C4N-C3N	-4.45	1.41	1.49
2	A	601	NDP	C4N-C3N	-4.45	1.41	1.49
2	D	601	NDP	C4N-C3N	-4.42	1.41	1.49
2	E	601	NDP	C4N-C3N	-4.41	1.41	1.49
4	B	603	OF4	C17-C22	4.40	1.51	1.47
4	A	603	OF4	C17-C22	4.32	1.51	1.47
4	D	603	OF4	C17-C22	4.30	1.51	1.47
2	C	601	NDP	C6A-N6A	4.11	1.49	1.34
2	E	601	NDP	C6A-N6A	4.10	1.49	1.34
2	A	601	NDP	C6A-N6A	4.10	1.49	1.34
2	B	601	NDP	C6A-N6A	4.09	1.49	1.34
2	D	601	NDP	C6A-N6A	4.07	1.48	1.34
2	D	601	NDP	C7N-N7N	4.04	1.44	1.33
2	B	601	NDP	C7N-N7N	4.02	1.44	1.33
2	E	601	NDP	C7N-N7N	4.00	1.44	1.33
2	C	601	NDP	C7N-N7N	4.00	1.44	1.33
2	A	601	NDP	C7N-N7N	3.99	1.44	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	NDP	C2D-C3D	-3.94	1.42	1.53
2	D	601	NDP	C2D-C3D	-3.89	1.42	1.53
2	B	601	NDP	C2D-C3D	-3.89	1.42	1.53
2	E	601	NDP	C2D-C3D	-3.84	1.42	1.53
2	C	601	NDP	C2D-C3D	-3.82	1.42	1.53
2	D	601	NDP	C3B-C2B	-3.80	1.44	1.52
2	B	601	NDP	C3B-C2B	-3.73	1.44	1.52
2	E	601	NDP	C3B-C2B	-3.71	1.44	1.52
2	C	601	NDP	C3B-C2B	-3.71	1.44	1.52
2	A	601	NDP	C3B-C2B	-3.71	1.44	1.52
2	A	601	NDP	C6N-C5N	3.66	1.39	1.33
2	D	601	NDP	C6N-C5N	3.66	1.39	1.33
2	E	601	NDP	C6N-C5N	3.63	1.39	1.33
2	B	601	NDP	C6N-C5N	3.62	1.39	1.33
2	C	601	NDP	C6N-C5N	3.62	1.39	1.33
5	A	604	MTX	CB-CA	-3.40	1.49	1.53
3	E	602	UFP	P-O1P	3.28	1.61	1.50
5	C	604	MTX	CB-CA	-3.26	1.49	1.53
2	A	601	NDP	C4N-C5N	-3.21	1.40	1.48
2	D	601	NDP	C4N-C5N	-3.21	1.40	1.48
2	C	601	NDP	C4N-C5N	-3.19	1.40	1.48
2	E	601	NDP	C4N-C5N	-3.18	1.40	1.48
2	B	601	NDP	C4N-C5N	-3.17	1.40	1.48
5	B	604	MTX	CB-CA	-3.17	1.49	1.53
4	E	603	OF4	C4-N2	3.10	1.40	1.35
4	A	603	OF4	C4-N2	3.10	1.40	1.35
4	C	603	OF4	C4-N2	3.07	1.40	1.35
5	D	604	MTX	CB-CA	-3.07	1.49	1.53
4	D	603	OF4	C4-N2	3.06	1.40	1.35
4	B	603	OF4	C4-N2	3.03	1.40	1.35
5	E	604	MTX	CB-CA	-3.02	1.49	1.53
3	B	602	UFP	C4-C5	2.90	1.42	1.38
3	D	602	UFP	C4-C5	2.83	1.42	1.38
3	C	602	UFP	C4-C5	2.80	1.42	1.38
3	A	602	UFP	C4-C5	2.76	1.41	1.38
3	E	602	UFP	C4-C5	2.70	1.41	1.38
5	D	604	MTX	C4-NA4	2.59	1.43	1.34
5	C	604	MTX	C4-NA4	2.57	1.43	1.34
5	E	604	MTX	C4-NA4	2.57	1.43	1.34
5	D	604	MTX	C14-N10	2.56	1.46	1.39
5	B	604	MTX	C4-NA4	2.56	1.43	1.34
5	A	604	MTX	C4-NA4	2.55	1.43	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	604	MTX	C14-N10	2.53	1.46	1.39
5	B	604	MTX	C14-N10	2.51	1.46	1.39
5	C	604	MTX	C14-N10	2.50	1.46	1.39
5	A	604	MTX	C14-N10	2.48	1.46	1.39
2	D	601	NDP	C3B-C4B	-2.41	1.46	1.53
5	A	604	MTX	C7-N8	2.40	1.35	1.31
2	C	601	NDP	C3B-C4B	-2.39	1.46	1.53
2	A	601	NDP	C3B-C4B	-2.38	1.46	1.53
2	D	601	NDP	C4A-N3A	2.38	1.38	1.35
5	C	604	MTX	C7-N8	2.36	1.35	1.31
2	E	601	NDP	C3B-C4B	-2.35	1.47	1.53
2	B	601	NDP	C3B-C4B	-2.34	1.47	1.53
5	B	604	MTX	C7-N8	2.34	1.35	1.31
5	D	604	MTX	C7-N8	2.34	1.35	1.31
2	A	601	NDP	C3D-C4D	-2.34	1.47	1.53
2	E	601	NDP	C4A-N3A	2.33	1.38	1.35
2	A	601	NDP	C4A-N3A	2.33	1.38	1.35
2	B	601	NDP	C3D-C4D	-2.29	1.47	1.53
2	C	601	NDP	C3D-C4D	-2.29	1.47	1.53
5	E	604	MTX	C7-N8	2.28	1.35	1.31
2	C	601	NDP	C4A-N3A	2.28	1.38	1.35
2	D	601	NDP	C3D-C4D	-2.27	1.47	1.53
2	E	601	NDP	C3D-C4D	-2.27	1.47	1.53
4	E	603	OF4	C4-N4	2.24	1.38	1.33
4	E	603	OF4	C17-C16	2.22	1.43	1.40
4	D	603	OF4	C4-N4	2.22	1.38	1.33
2	B	601	NDP	C4A-N3A	2.20	1.38	1.35
4	A	603	OF4	C4-N4	2.18	1.38	1.33
4	C	603	OF4	C4-N4	2.17	1.38	1.33
4	D	603	OF4	C2-C1	-2.15	1.37	1.43
4	C	603	OF4	C17-C16	2.14	1.43	1.40
4	B	603	OF4	C4-N4	2.12	1.38	1.33
2	C	601	NDP	C2N-C3N	2.11	1.40	1.34
4	B	603	OF4	C2-C1	-2.10	1.37	1.43
2	D	601	NDP	C2N-C3N	2.08	1.40	1.34
4	A	603	OF4	C2-C1	-2.08	1.37	1.43
4	C	603	OF4	C2-C1	-2.08	1.37	1.43
4	E	603	OF4	C2-C1	-2.07	1.37	1.43
2	A	601	NDP	C2N-C3N	2.07	1.40	1.34
2	E	601	NDP	C2N-C3N	2.06	1.40	1.34
2	B	601	NDP	C2N-C3N	2.04	1.40	1.34

All (140) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	603	OF4	C2-C3-N2	-9.96	115.26	124.09
4	B	603	OF4	C2-C3-N2	-9.93	115.28	124.09
4	E	603	OF4	C2-C3-N2	-9.88	115.33	124.09
4	A	603	OF4	C2-C3-N2	-9.82	115.37	124.09
4	D	603	OF4	C2-C3-N2	-9.76	115.43	124.09
3	A	602	UFP	C4-N3-C2	7.69	121.63	115.14
3	B	602	UFP	C4-N3-C2	7.58	121.54	115.14
3	C	602	UFP	C4-N3-C2	7.50	121.48	115.14
3	E	602	UFP	C4-N3-C2	7.45	121.44	115.14
3	D	602	UFP	C4-N3-C2	7.36	121.36	115.14
5	C	604	MTX	C6-C7-N8	-4.80	118.42	123.13
5	B	604	MTX	C6-C7-N8	-4.76	118.46	123.13
5	D	604	MTX	C6-C7-N8	-4.72	118.50	123.13
5	A	604	MTX	C6-C7-N8	-4.67	118.55	123.13
5	E	604	MTX	C6-C7-N8	-4.56	118.66	123.13
4	C	603	OF4	C3-N2-C4	4.19	122.59	115.93
4	A	603	OF4	C3-N2-C4	4.19	122.58	115.93
4	E	603	OF4	C3-N2-C4	4.18	122.56	115.93
4	B	603	OF4	C3-N2-C4	4.12	122.48	115.93
4	D	603	OF4	C3-N2-C4	4.09	122.43	115.93
4	C	603	OF4	N4-C4-N1	4.02	124.34	117.79
4	A	603	OF4	N4-C4-N1	3.96	124.24	117.79
4	D	603	OF4	N4-C4-N1	3.95	124.23	117.79
4	B	603	OF4	N4-C4-N1	3.91	124.16	117.79
3	D	602	UFP	P-O5'-C5'	-3.90	107.55	118.30
5	A	604	MTX	N8-C8A-N1	3.90	120.27	115.82
4	E	603	OF4	N4-C4-N1	3.87	124.10	117.79
5	C	604	MTX	CG-CB-CA	3.86	120.84	113.04
4	C	603	OF4	N4-C4-N2	-3.85	111.26	117.25
5	D	604	MTX	C7-N8-C8A	3.85	120.56	116.69
5	D	604	MTX	N8-C8A-N1	3.85	120.21	115.82
5	C	604	MTX	C7-N8-C8A	3.83	120.54	116.69
2	E	601	NDP	N3A-C2A-N1A	-3.81	122.73	128.68
4	B	603	OF4	N4-C4-N2	-3.80	111.34	117.25
2	C	601	NDP	N3A-C2A-N1A	-3.78	122.77	128.68
5	E	604	MTX	C7-N8-C8A	3.77	120.48	116.69
5	B	604	MTX	N8-C8A-N1	3.77	120.12	115.82
4	D	603	OF4	N4-C4-N2	-3.77	111.39	117.25
5	E	604	MTX	N1-C2-N3	-3.76	122.21	127.22
5	A	604	MTX	CG-CB-CA	3.74	120.60	113.04
5	D	604	MTX	N1-C2-N3	-3.72	122.26	127.22
2	B	601	NDP	N3A-C2A-N1A	-3.72	122.87	128.68
5	C	604	MTX	N1-C2-N3	-3.70	122.28	127.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	604	MTX	N1-C2-N3	-3.70	122.29	127.22
3	C	602	UFP	P-O5'-C5'	-3.69	108.12	118.30
2	D	601	NDP	N3A-C2A-N1A	-3.69	122.91	128.68
5	C	604	MTX	N8-C8A-N1	3.69	120.03	115.82
4	E	603	OF4	N4-C4-N2	-3.68	111.52	117.25
4	A	603	OF4	N4-C4-N2	-3.68	111.53	117.25
4	C	603	OF4	C3-C2-C1	3.66	117.08	115.01
4	B	603	OF4	C3-C2-C1	3.66	117.08	115.01
5	D	604	MTX	CG-CB-CA	3.66	120.43	113.04
2	A	601	NDP	N3A-C2A-N1A	-3.64	122.98	128.68
5	A	604	MTX	N1-C2-N3	-3.62	122.39	127.22
5	A	604	MTX	C7-N8-C8A	3.61	120.32	116.69
3	B	602	UFP	C5-C4-N3	-3.61	118.58	122.39
3	E	602	UFP	P-O5'-C5'	-3.60	108.38	118.30
4	D	603	OF4	C3-C2-C1	3.59	117.04	115.01
5	A	604	MTX	C2-N1-C8A	3.55	119.41	115.36
5	B	604	MTX	C7-N8-C8A	3.53	120.24	116.69
5	E	604	MTX	CG-CB-CA	3.53	120.17	113.04
4	B	603	OF4	C5-C7-C8	-3.53	105.75	114.21
5	E	604	MTX	N8-C8A-N1	3.52	119.84	115.82
5	B	604	MTX	C2-N1-C8A	3.49	119.34	115.36
5	C	604	MTX	C2-N1-C8A	3.46	119.31	115.36
5	B	604	MTX	CG-CB-CA	3.46	120.02	113.04
5	E	604	MTX	C2-N1-C8A	3.45	119.29	115.36
5	D	604	MTX	C2-N1-C8A	3.44	119.28	115.36
3	C	602	UFP	C5-C4-N3	-3.41	118.79	122.39
2	C	601	NDP	PN-O3-PA	-3.39	121.19	132.83
3	D	602	UFP	C5-C4-N3	-3.39	118.81	122.39
3	A	602	UFP	C5-C4-N3	-3.39	118.81	122.39
4	A	603	OF4	C3-C2-C1	3.37	116.91	115.01
4	E	603	OF4	C3-C2-C1	3.36	116.91	115.01
3	B	602	UFP	P-O5'-C5'	-3.33	109.11	118.30
3	A	602	UFP	P-O5'-C5'	-3.31	109.18	118.30
3	E	602	UFP	C5-C4-N3	-3.31	118.90	122.39
4	D	603	OF4	C5-C7-C8	-3.22	106.48	114.21
2	B	601	NDP	PN-O3-PA	-3.10	122.19	132.83
5	D	604	MTX	C11-C-N	2.99	122.79	117.06
5	B	604	MTX	C11-C-N	2.97	122.75	117.06
3	B	602	UFP	O4'-C1'-C2'	-2.96	100.65	106.25
2	A	601	NDP	PN-O3-PA	-2.96	122.68	132.83
2	D	601	NDP	PN-O3-PA	-2.87	122.97	132.83
2	E	601	NDP	PN-O3-PA	-2.79	123.27	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	604	MTX	C11-C-N	2.75	122.34	117.06
3	C	602	UFP	O4'-C1'-C2'	-2.74	101.08	106.25
3	D	602	UFP	O4'-C1'-C2'	-2.73	101.09	106.25
4	C	603	OF4	C5-C7-C8	-2.70	107.73	114.21
5	E	604	MTX	C11-C-N	2.69	122.22	117.06
5	E	604	MTX	C4A-C4-N3	-2.67	119.26	121.01
5	A	604	MTX	C11-C-N	2.65	122.15	117.06
2	D	601	NDP	O5B-C5B-C4B	2.65	118.12	108.99
5	B	604	MTX	C4A-C4-N3	-2.62	119.29	121.01
5	D	604	MTX	C4A-C4-N3	-2.61	119.30	121.01
5	C	604	MTX	C4A-C4-N3	-2.58	119.32	121.01
4	E	603	OF4	C5-C7-C8	-2.55	108.10	114.21
5	A	604	MTX	C13-C14-N10	-2.53	117.98	121.62
2	D	601	NDP	O5D-C5D-C4D	2.43	117.37	108.99
2	E	601	NDP	O5B-C5B-C4B	2.42	117.31	108.99
5	A	604	MTX	C4A-C4-N3	-2.41	119.43	121.01
3	E	602	UFP	O4'-C1'-C2'	-2.40	101.72	106.25
2	C	601	NDP	C4A-C5A-N7A	-2.37	106.93	109.40
2	E	601	NDP	O5D-C5D-C4D	2.34	117.06	108.99
2	D	601	NDP	C4A-C5A-N7A	-2.32	106.98	109.40
3	A	602	UFP	C6-N1-C1'	-2.32	114.03	119.24
3	A	602	UFP	O4'-C1'-C2'	-2.31	101.89	106.25
5	B	604	MTX	C13-C14-N10	-2.30	118.31	121.62
5	C	604	MTX	CA-N-C	-2.30	119.37	122.34
2	B	601	NDP	C4A-C5A-N7A	-2.30	107.01	109.40
4	A	603	OF4	C5-C7-C8	-2.27	108.76	114.21
2	C	601	NDP	O5B-C5B-C4B	2.25	116.72	108.99
2	A	601	NDP	O5B-C5B-C4B	2.24	116.72	108.99
4	A	603	OF4	N1-C4-N2	-2.24	124.23	127.22
2	A	601	NDP	C4A-C5A-N7A	-2.24	107.06	109.40
2	E	601	NDP	C4A-C5A-N7A	-2.24	107.07	109.40
5	D	604	MTX	CA-N-C	-2.23	119.46	122.34
2	C	601	NDP	O5D-C5D-C4D	2.22	116.62	108.99
2	B	601	NDP	C3N-C7N-N7N	2.18	121.54	117.67
3	B	602	UFP	C6-N1-C1'	-2.17	114.36	119.24
5	B	604	MTX	CA-N-C	-2.16	119.56	122.34
3	A	602	UFP	C5-C6-N1	2.14	121.75	119.77
4	D	603	OF4	N1-C4-N2	-2.13	124.38	127.22
4	E	603	OF4	N1-C4-N2	-2.13	124.38	127.22
2	E	601	NDP	C3N-C7N-N7N	2.13	121.44	117.67
5	D	604	MTX	C13-C14-N10	-2.13	118.56	121.62
4	C	603	OF4	N1-C4-N2	-2.12	124.40	127.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	NDP	O5D-C5D-C4D	2.11	116.26	108.99
5	A	604	MTX	CB-CA-N	-2.11	107.13	110.19
3	B	602	UFP	C5-C6-N1	2.09	121.71	119.77
2	A	601	NDP	O4D-C1D-N1N	2.09	112.14	108.06
5	D	604	MTX	O-C-N	-2.09	118.61	122.45
5	C	604	MTX	C13-C14-N10	-2.07	118.64	121.62
2	C	601	NDP	C3N-C7N-N7N	2.05	121.31	117.67
4	B	603	OF4	N1-C4-N2	-2.04	124.50	127.22
2	B	601	NDP	O5B-C5B-C4B	2.04	116.01	108.99
5	B	604	MTX	O-C-N	-2.03	118.72	122.45
5	E	604	MTX	C13-C14-N10	-2.03	118.70	121.62
4	E	603	OF4	C15-C16-C21	-2.02	116.40	121.00
2	A	601	NDP	C3N-C7N-N7N	2.01	121.24	117.67

There are no chirality outliers.

All (62) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	602	UFP	C5'-O5'-P-O2P
3	D	602	UFP	C5'-O5'-P-O3P
3	B	602	UFP	C5'-O5'-P-O2P
3	B	602	UFP	C5'-O5'-P-O3P
3	C	602	UFP	C5'-O5'-P-O2P
3	C	602	UFP	C5'-O5'-P-O3P
5	A	604	MTX	CT-CA-CB-CG
5	B	604	MTX	CT-CA-CB-CG
5	C	604	MTX	N-CA-CB-CG
5	C	604	MTX	CT-CA-CB-CG
5	A	604	MTX	N-CA-CB-CG
5	B	604	MTX	N-CA-CB-CG
2	D	601	NDP	C3D-C4D-C5D-O5D
2	D	601	NDP	O4D-C4D-C5D-O5D
3	E	602	UFP	C3'-C4'-C5'-O5'
5	D	604	MTX	N-CA-CB-CG
2	E	601	NDP	C3D-C4D-C5D-O5D
3	E	602	UFP	O4'-C4'-C5'-O5'
3	D	602	UFP	C5'-O5'-P-O1P
3	B	602	UFP	C5'-O5'-P-O1P
3	C	602	UFP	C5'-O5'-P-O1P
5	E	604	MTX	N-CA-CB-CG
2	E	601	NDP	O4D-C4D-C5D-O5D
2	D	601	NDP	C5D-O5D-PN-O3

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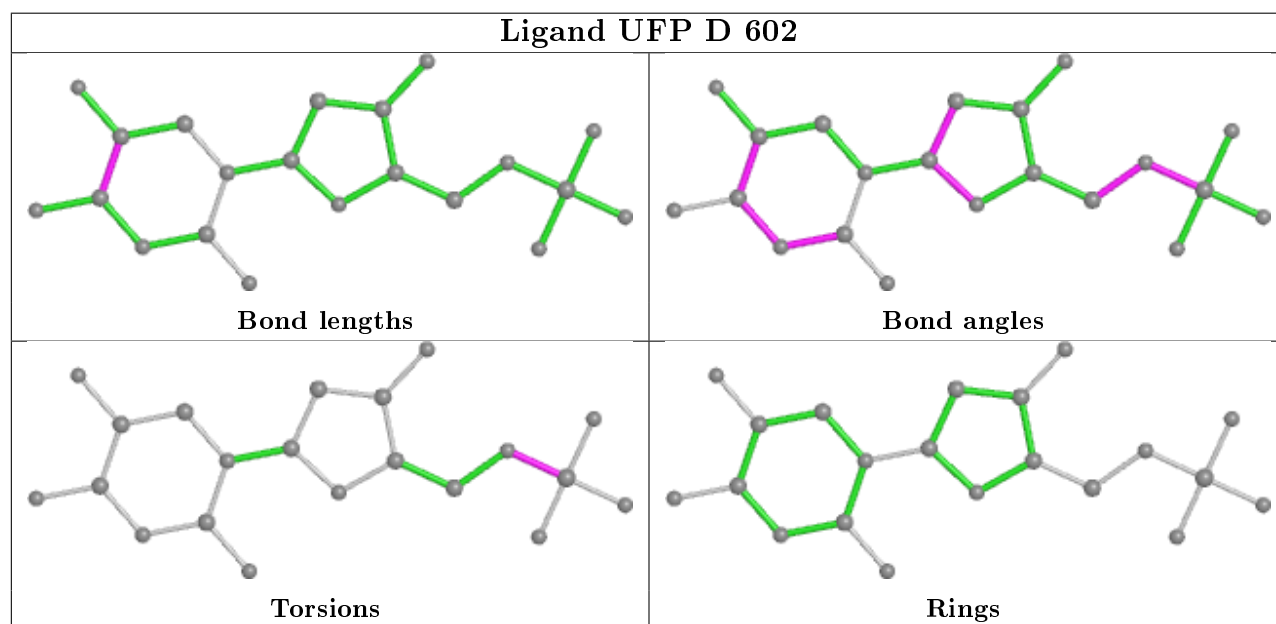
Mol	Chain	Res	Type	Atoms
2	D	601	NDP	C5D-O5D-PN-O2N
5	E	604	MTX	C6-C9-N10-CM
5	A	604	MTX	C6-C9-N10-CM
5	B	604	MTX	C6-C9-N10-CM
5	C	604	MTX	C6-C9-N10-CM
5	D	604	MTX	C6-C9-N10-CM
5	E	604	MTX	C13-C14-N10-CM
5	D	604	MTX	CT-CA-CB-CG
5	E	604	MTX	C15-C14-N10-CM
4	E	603	OF4	N5-C15-C16-C21
4	D	603	OF4	N5-C15-C16-C21
4	C	603	OF4	N5-C15-C16-C21
4	B	603	OF4	N5-C15-C16-C21
2	C	601	NDP	O4D-C1D-N1N-C2N
4	A	603	OF4	N5-C15-C16-C21
2	E	601	NDP	O4D-C1D-N1N-C2N
2	A	601	NDP	O4D-C1D-N1N-C2N
2	D	601	NDP	O4D-C1D-N1N-C2N
2	B	601	NDP	O4D-C1D-N1N-C2N
5	A	604	MTX	C15-C14-N10-CM
5	D	604	MTX	C15-C14-N10-CM
2	C	601	NDP	C2D-C1D-N1N-C2N
3	A	602	UFP	O4'-C4'-C5'-O5'
2	A	601	NDP	C2D-C1D-N1N-C2N
5	A	604	MTX	C13-C14-N10-CM
5	B	604	MTX	C13-C14-N10-CM
5	B	604	MTX	C15-C14-N10-CM
5	C	604	MTX	C13-C14-N10-CM
5	C	604	MTX	C15-C14-N10-CM
5	D	604	MTX	C13-C14-N10-CM
2	E	601	NDP	C2D-C1D-N1N-C2N
2	D	601	NDP	C4D-C5D-O5D-PN
2	E	601	NDP	C4D-C5D-O5D-PN
2	C	601	NDP	C4D-C5D-O5D-PN
2	E	601	NDP	C5D-O5D-PN-O2N
2	E	601	NDP	C2N-C3N-C7N-N7N
2	A	601	NDP	C4D-C5D-O5D-PN
2	B	601	NDP	C4D-C5D-O5D-PN

There are no ring outliers.

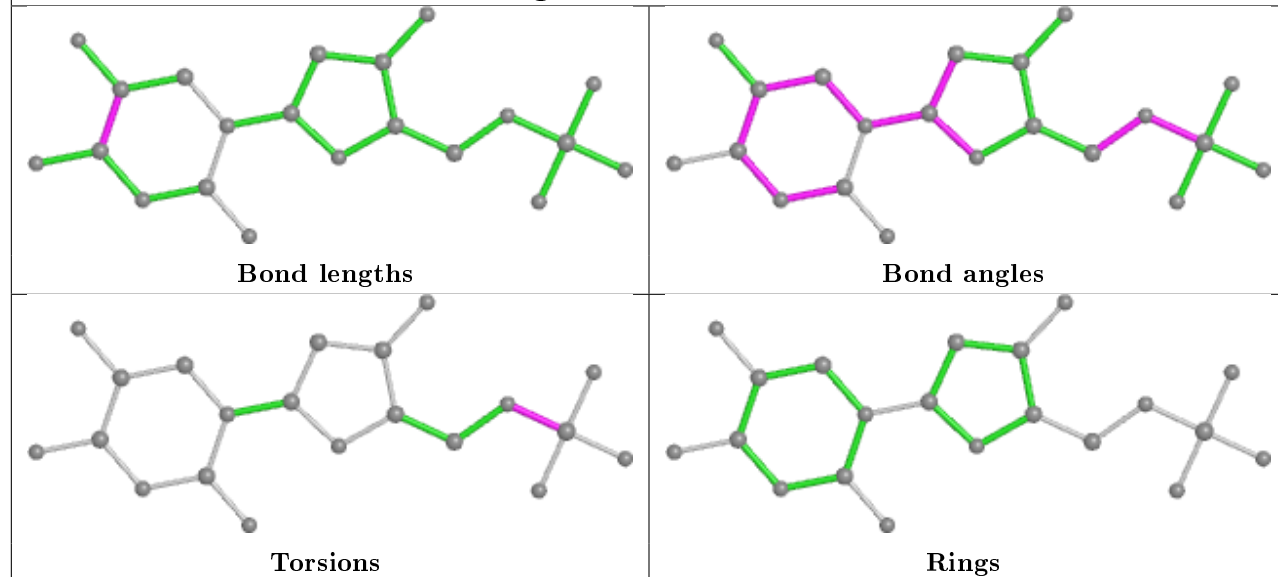
13 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	602	UFP	3	0
3	B	602	UFP	3	0
5	E	604	MTX	1	0
3	C	602	UFP	2	0
2	A	601	NDP	1	0
2	C	601	NDP	1	0
5	A	604	MTX	1	0
5	B	604	MTX	2	0
2	B	601	NDP	1	0
5	C	604	MTX	2	0
5	D	604	MTX	1	0
3	E	602	UFP	1	0
4	B	603	OF4	1	0

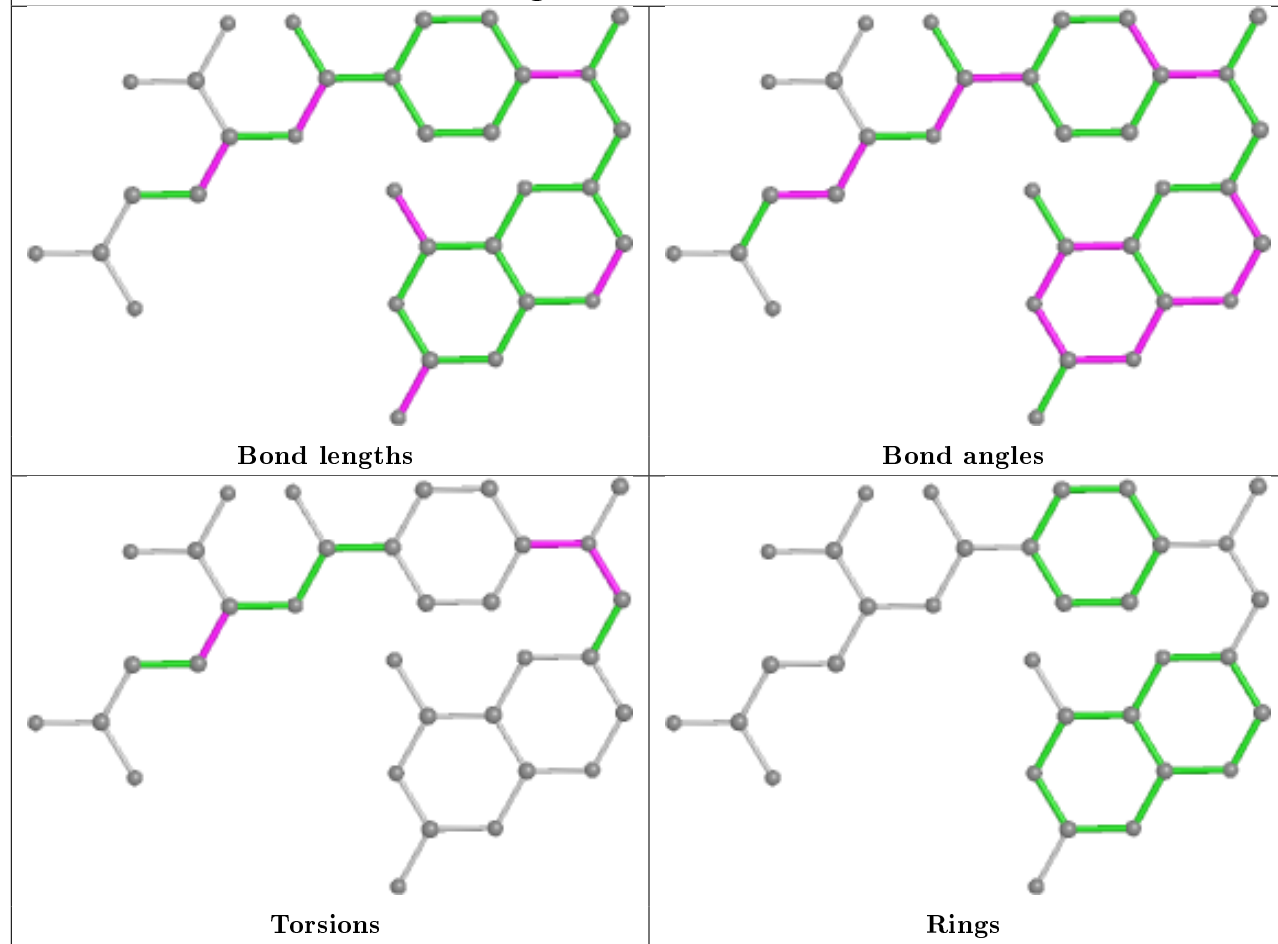
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



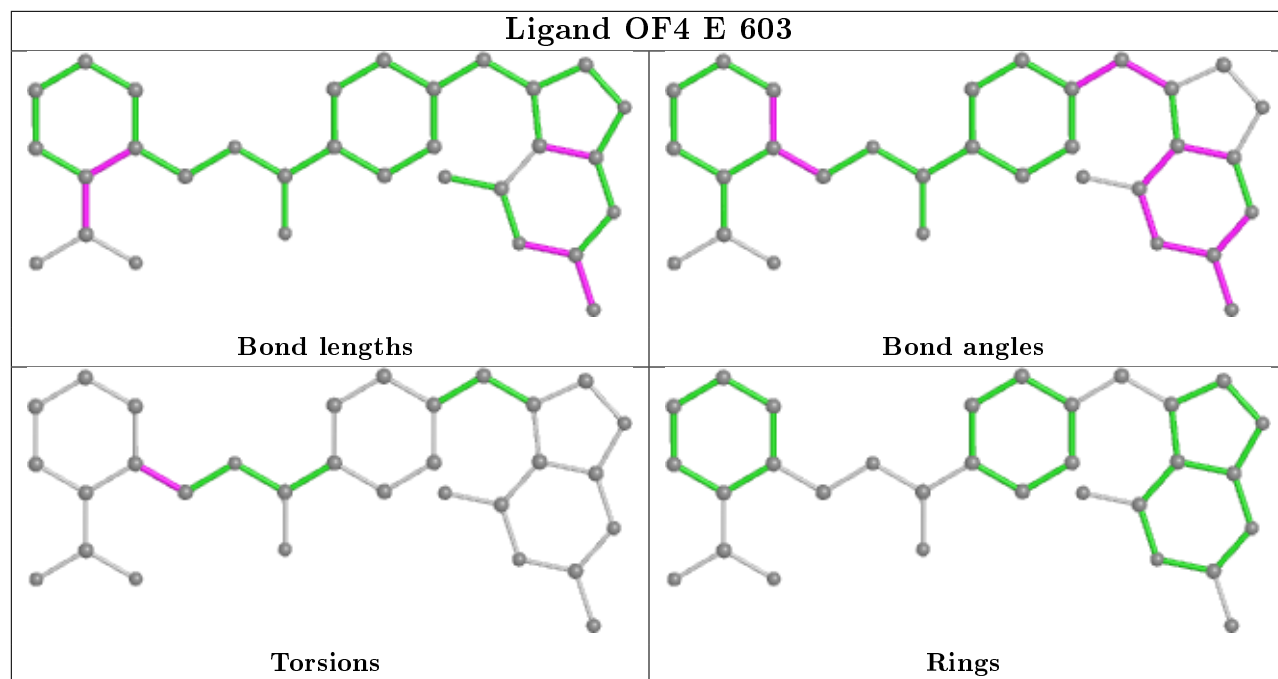
## Ligand UFP B 602



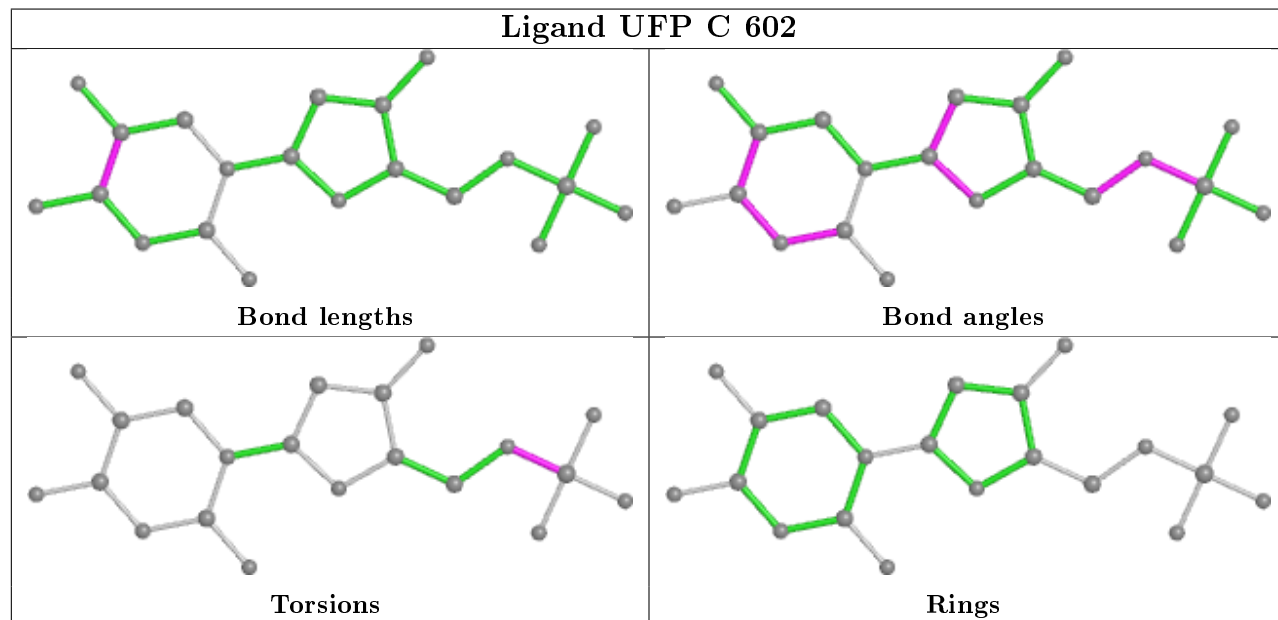
## Ligand MTX E 604

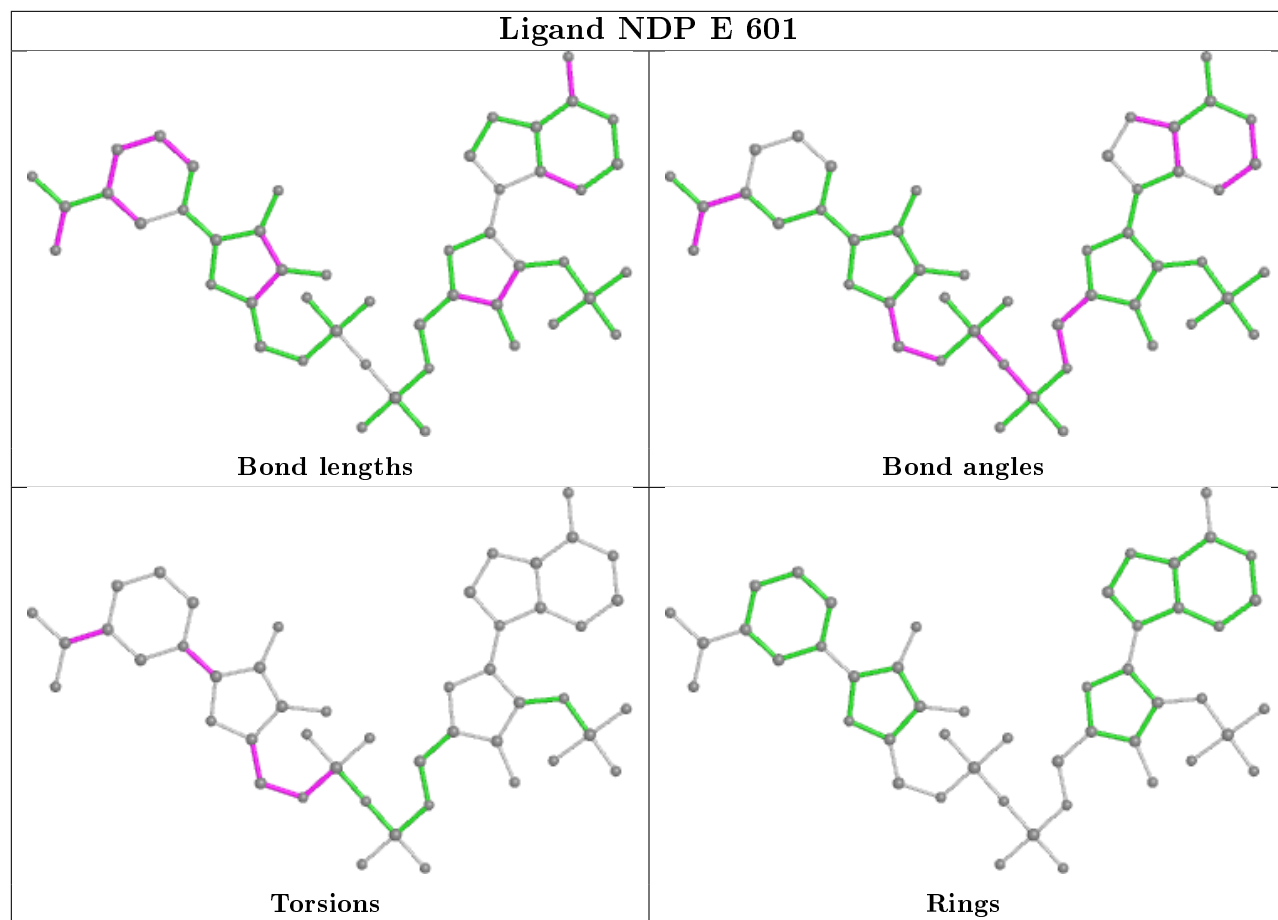


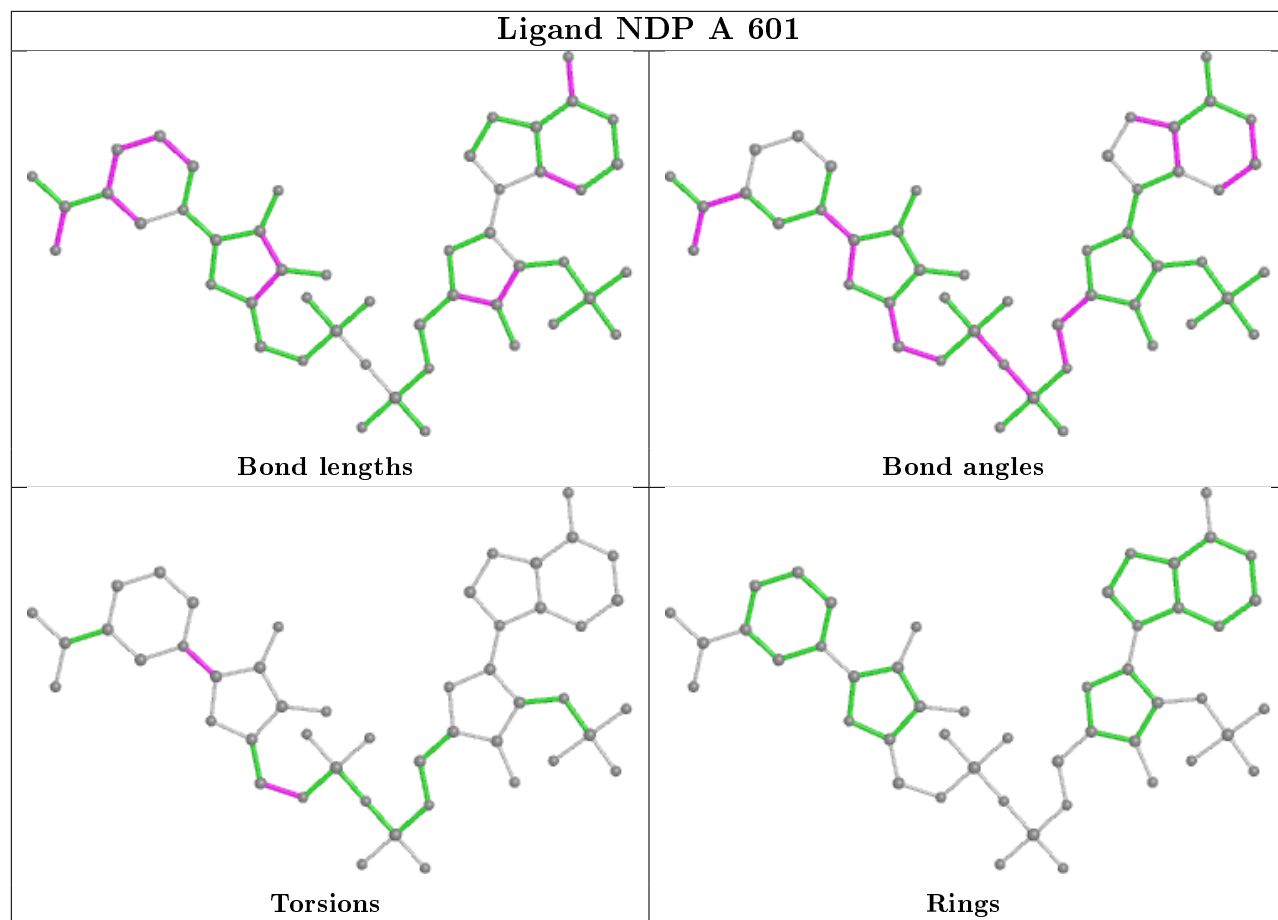
## Ligand OF4 E 603



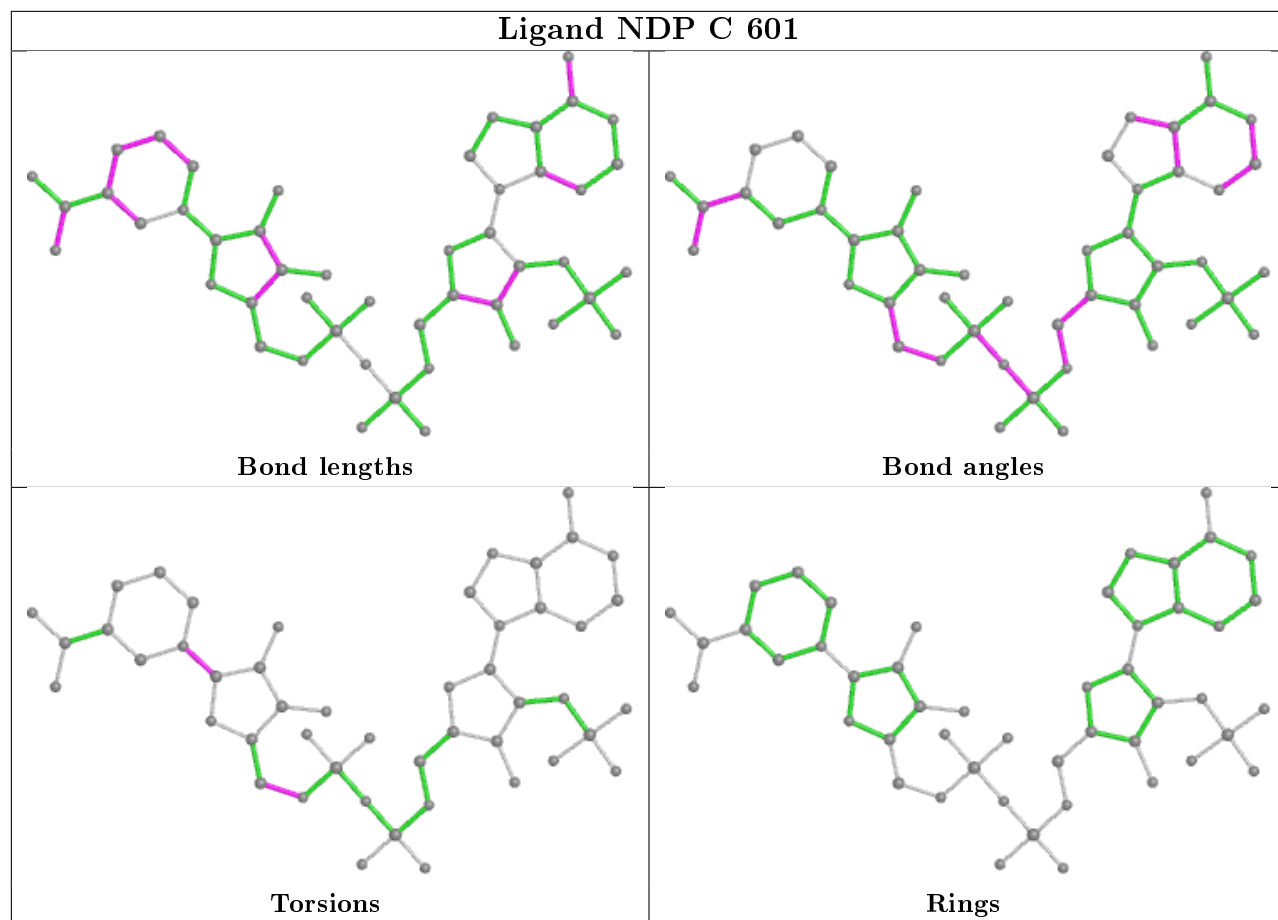
## Ligand UFP C 602

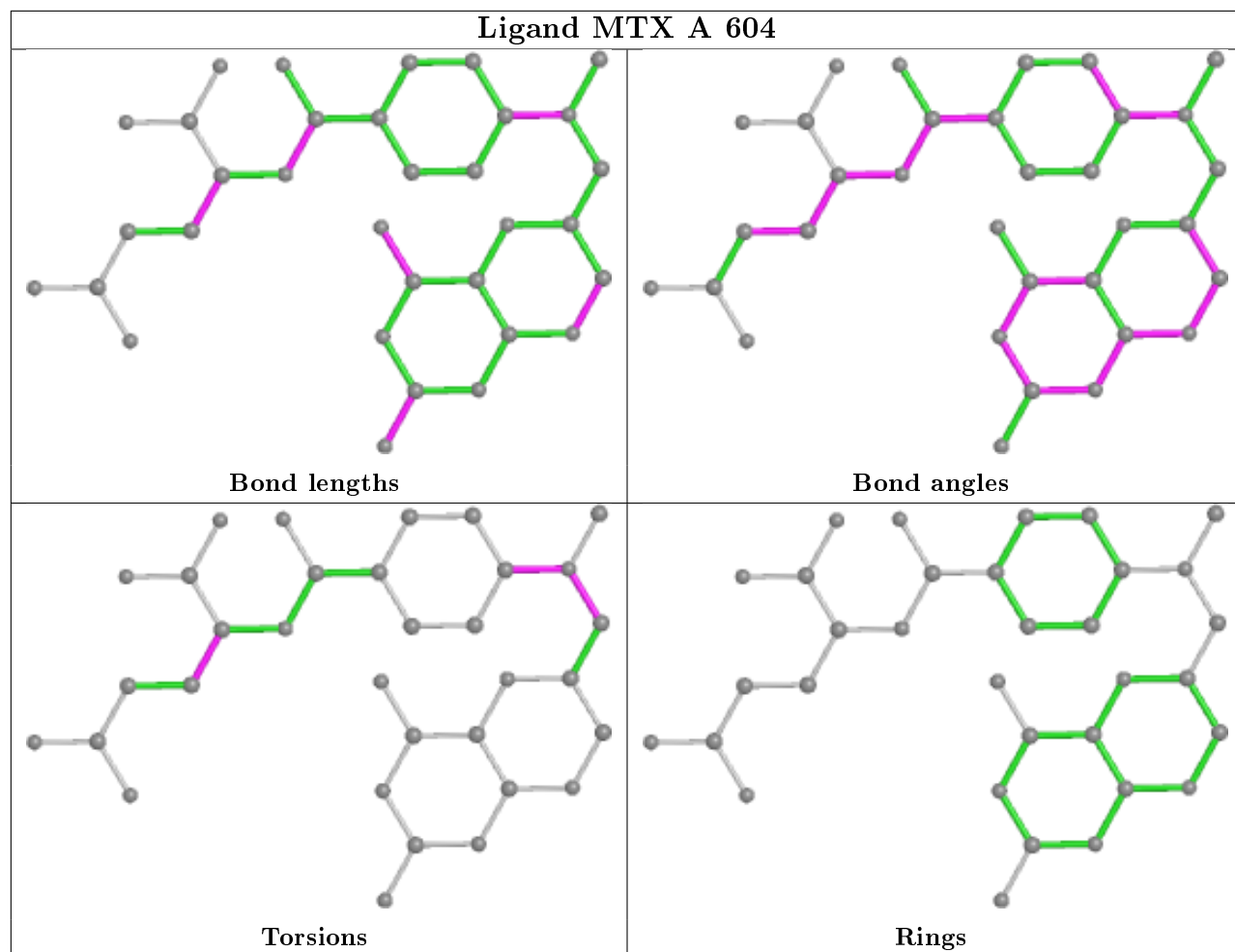


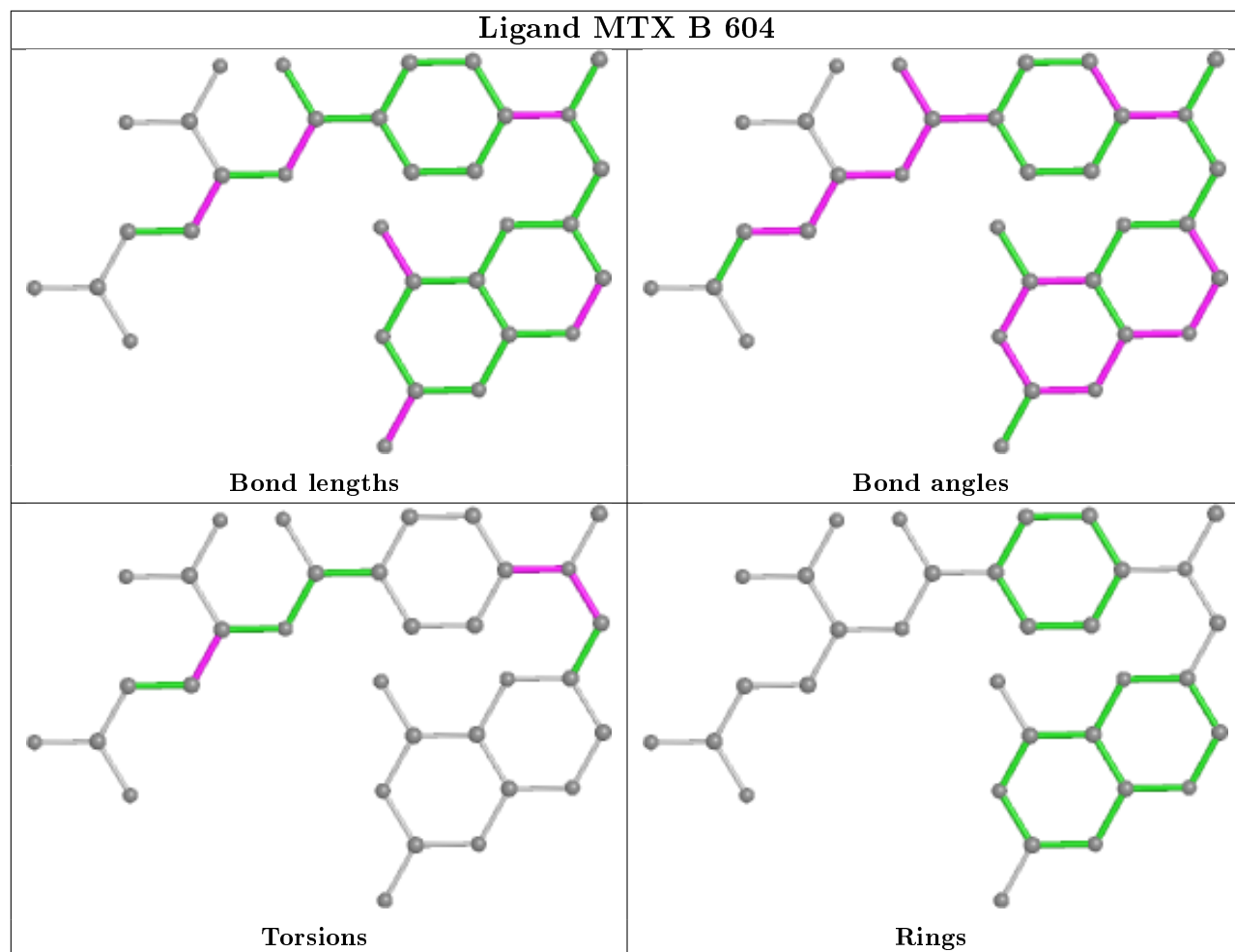


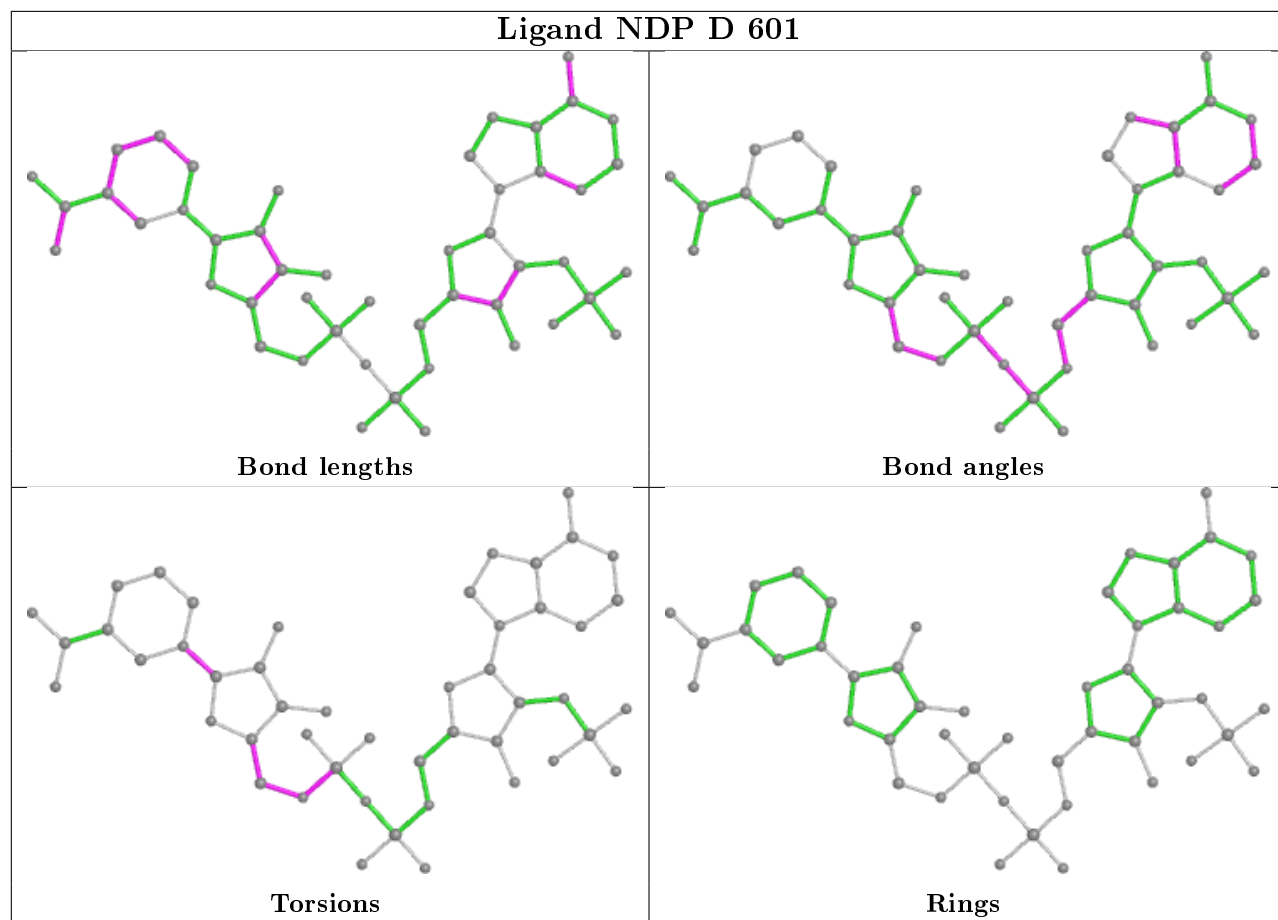


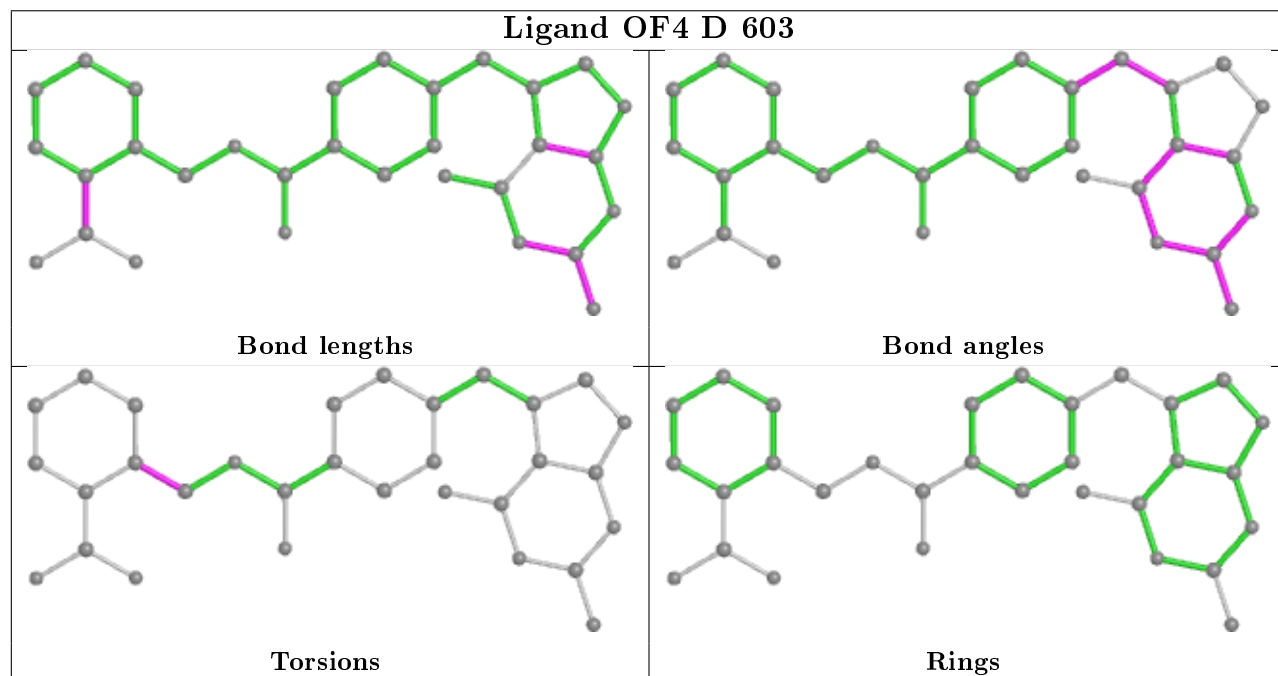
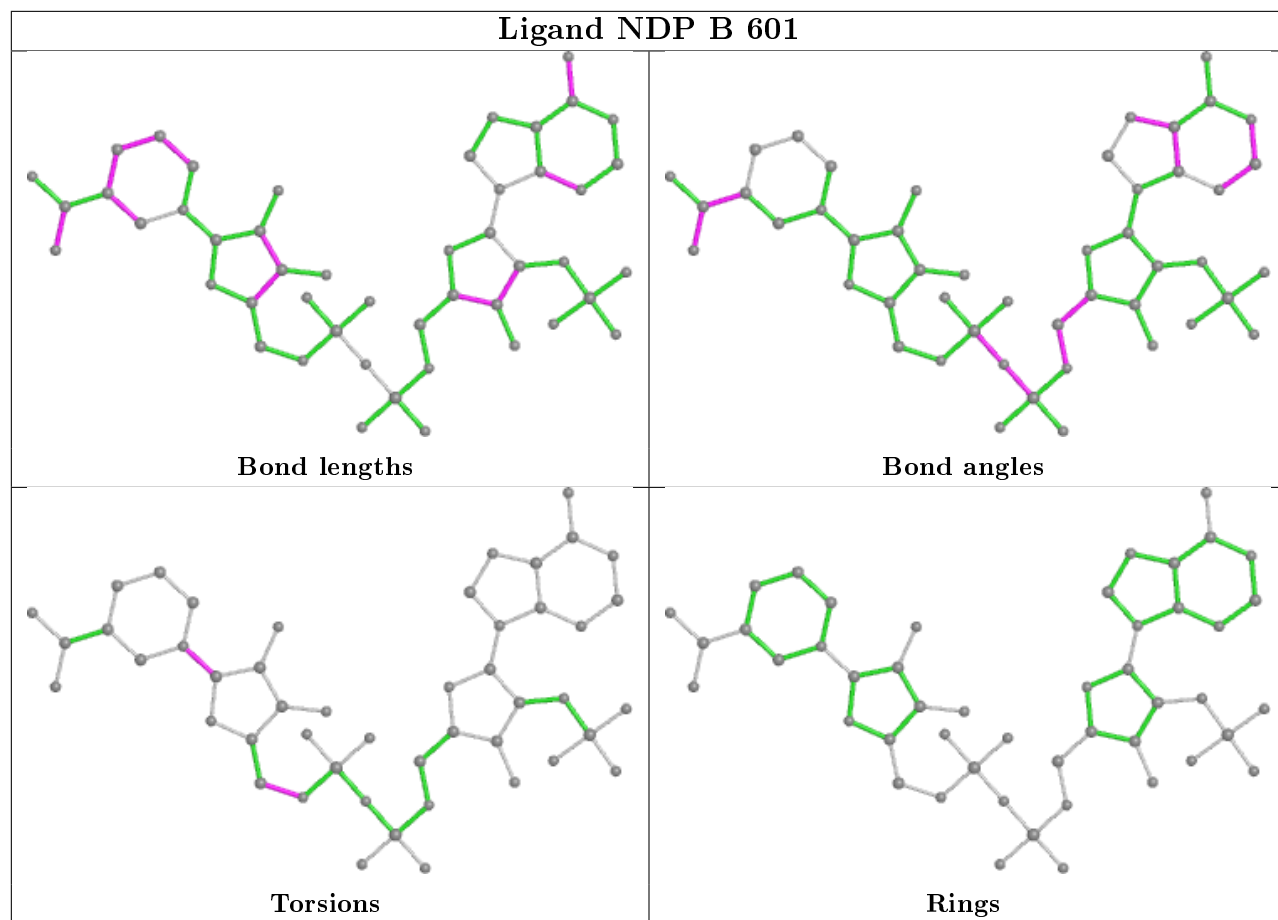




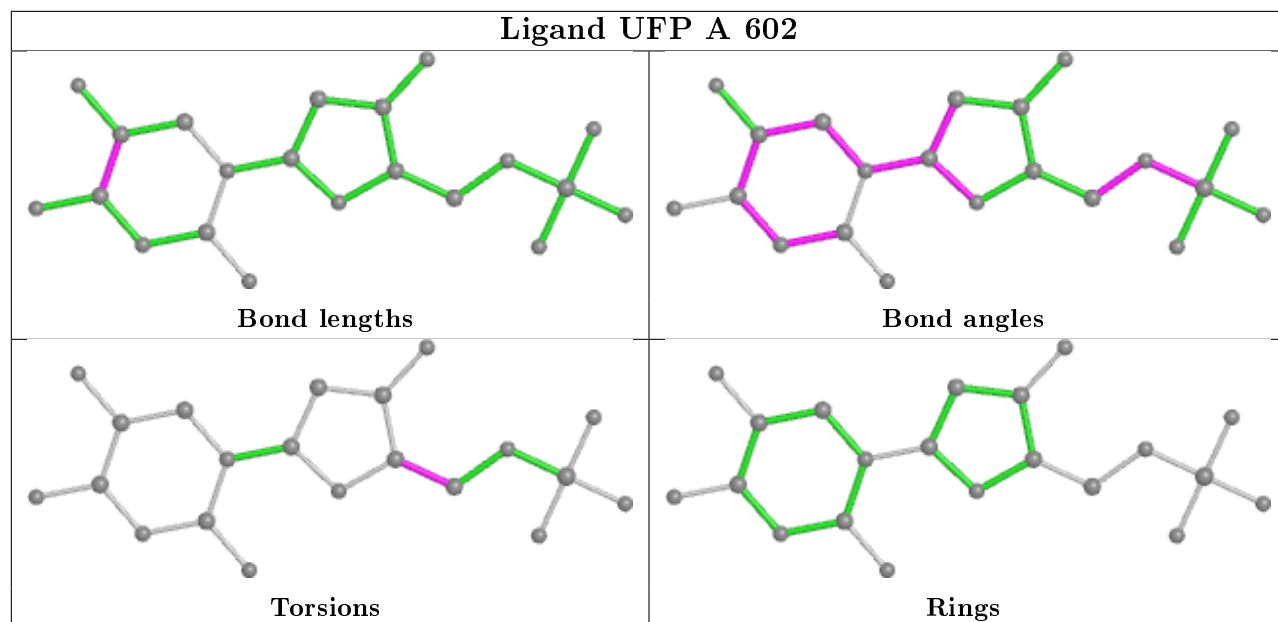




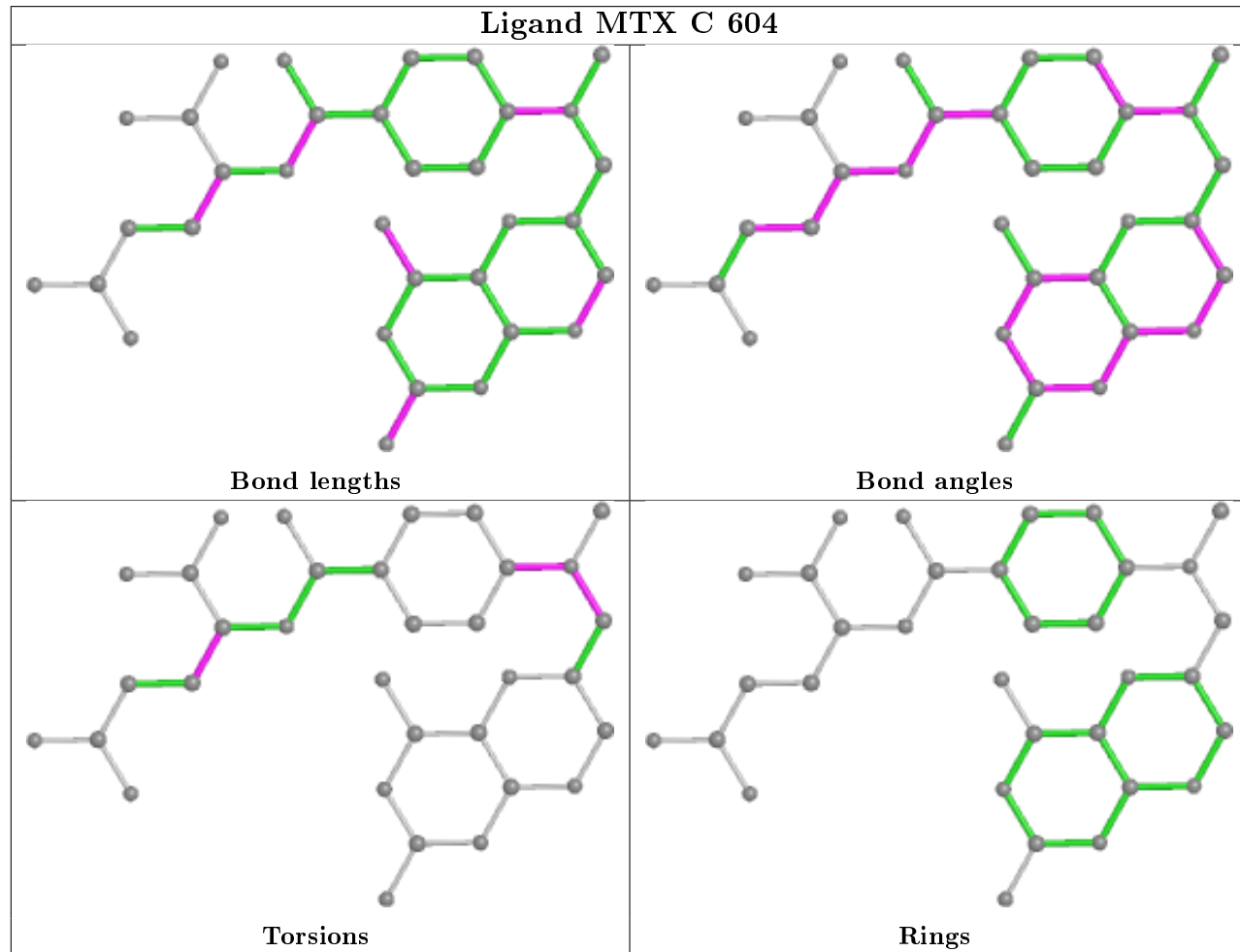


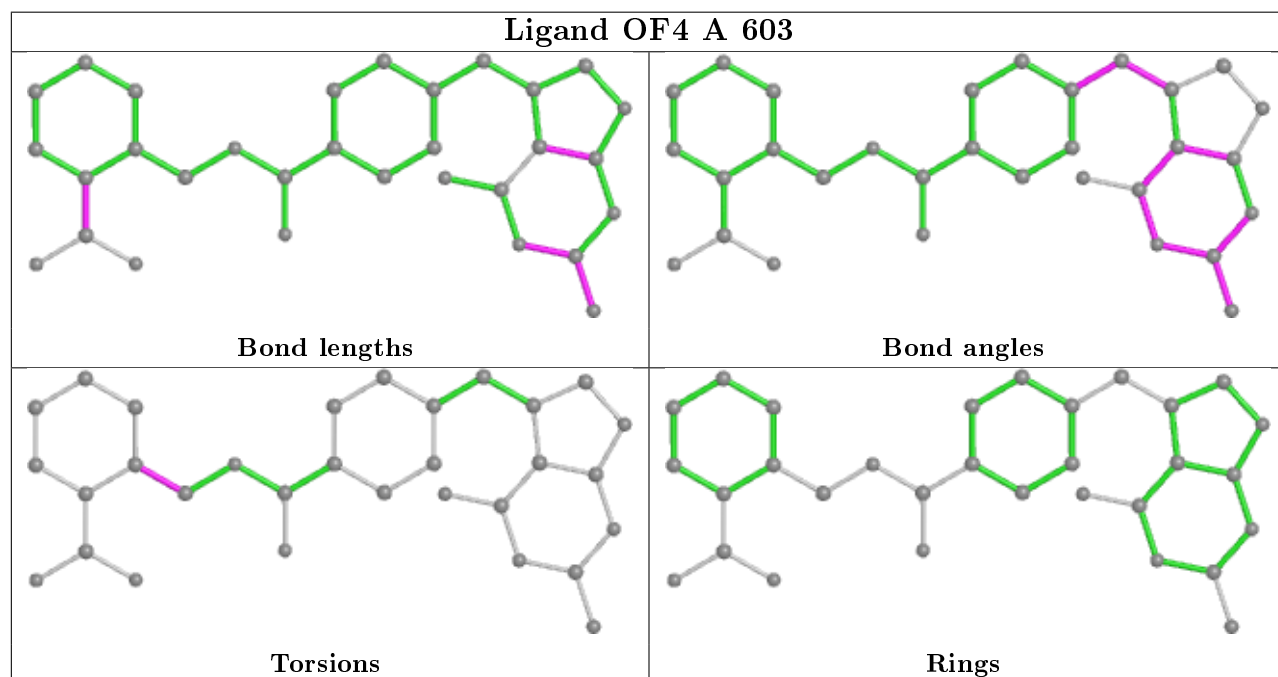
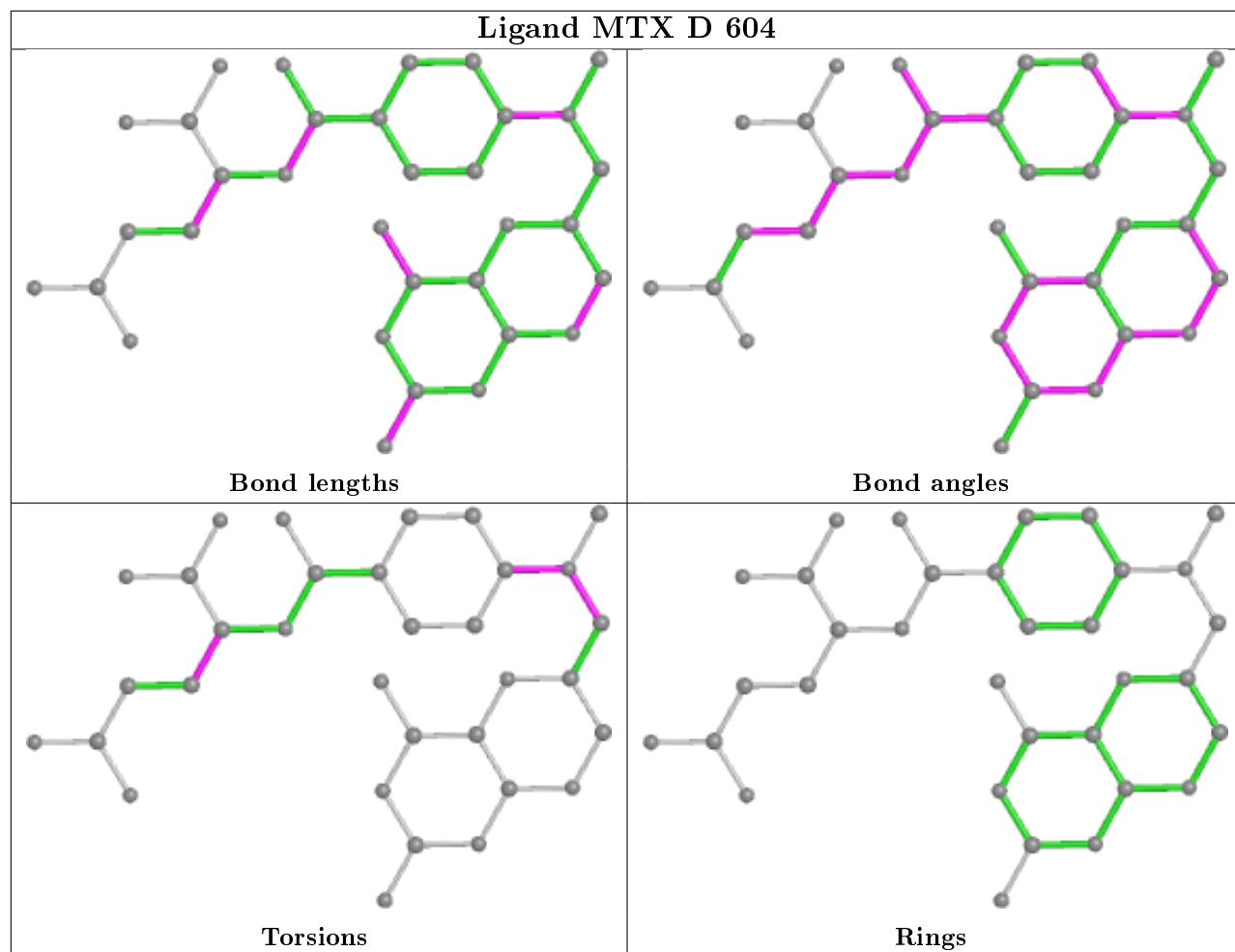


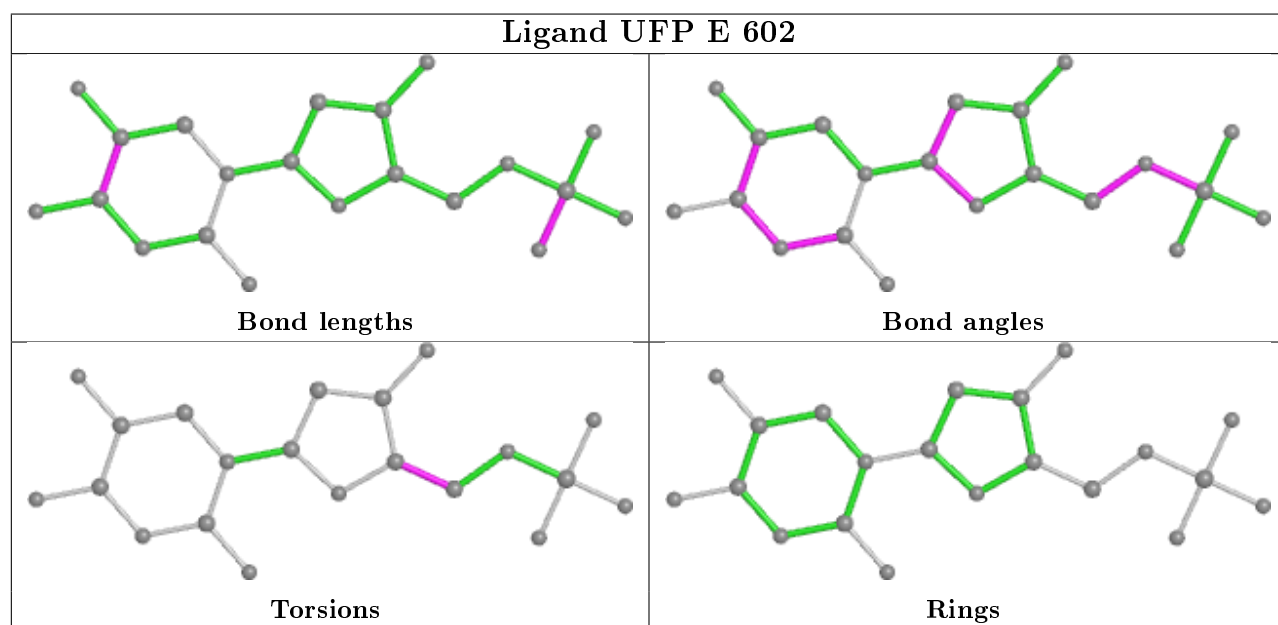
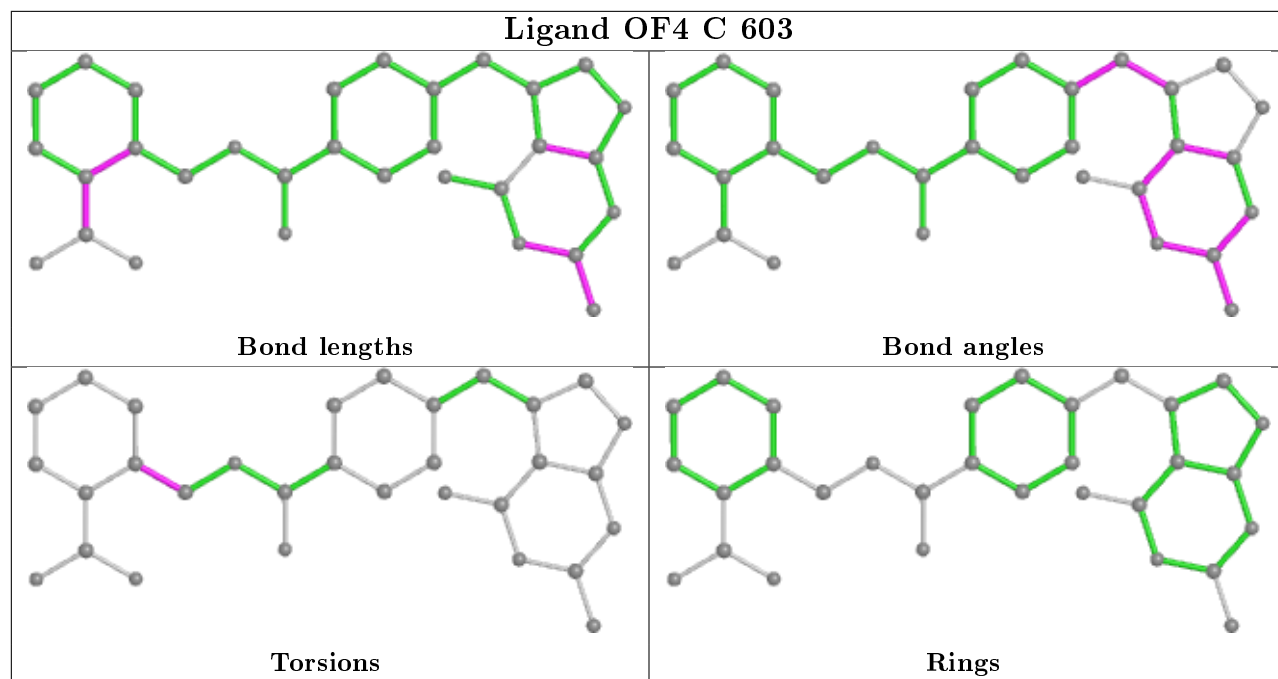
## Ligand UFP A 602



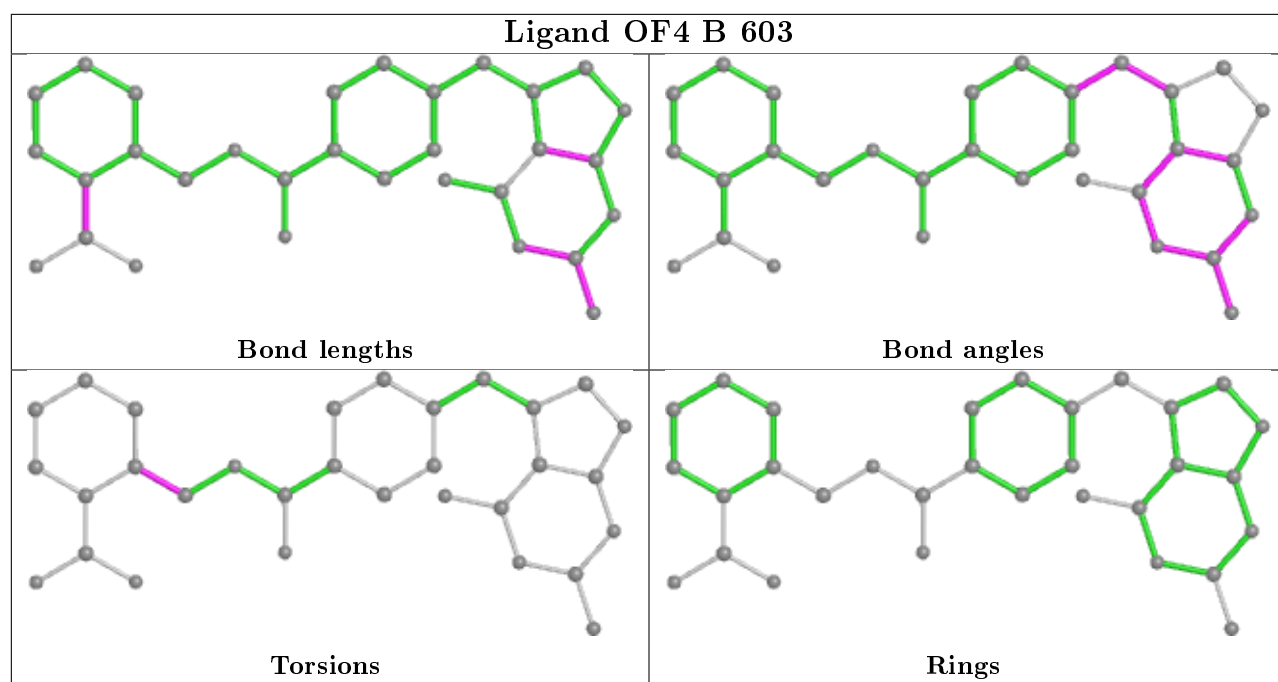
## Ligand MTX C 604











## 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

### 6.1 Protein, DNA and RNA chains

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	506/521 (97%)	0.13	5 (0%) 82 77	42, 60, 91, 120	0
1	B	506/521 (97%)	0.03	1 (0%) 95 94	40, 56, 82, 124	0
1	C	505/521 (96%)	0.14	12 (2%) 59 49	52, 73, 102, 140	0
1	D	506/521 (97%)	0.16	18 (3%) 42 32	48, 70, 108, 150	0
1	E	506/521 (97%)	0.52	34 (6%) 17 10	69, 90, 125, 143	0
All	All	2529/2605 (97%)	0.20	70 (2%) 53 43	40, 70, 113, 150	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	102	MET	5.4
1	E	318	GLY	4.2
1	D	101	LEU	4.1
1	A	102	MET	4.1
1	C	102	MET	4.1
1	E	102	MET	4.0
1	E	14	VAL	3.8
1	E	328	ILE	3.8
1	B	102	MET	3.7
1	E	324	TYR	3.4
1	D	107	ILE	3.3
1	E	510	TYR	3.1
1	C	106	SER	3.0
1	D	106	SER	2.8
1	E	128	VAL	2.8
1	E	333	ARG	2.8
1	E	107	ILE	2.8
1	E	101	LEU	2.8
1	E	127	PHE	2.7
1	E	84	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	107	ILE	2.7
1	E	106	SER	2.6
1	D	112	VAL	2.6
1	E	313	VAL	2.6
1	E	94	LEU	2.6
1	D	3	GLU	2.6
1	E	103	ASN	2.6
1	C	84	ALA	2.5
1	E	138	LEU	2.5
1	C	103	ASN	2.5
1	D	84	ALA	2.4
1	D	75	ILE	2.4
1	D	92	ARG	2.4
1	E	140	ASP	2.4
1	E	75	ILE	2.3
1	A	114	GLY	2.3
1	C	325	LEU	2.3
1	D	127	PHE	2.3
1	E	53	ILE	2.3
1	E	175	PHE	2.3
1	D	45	ASP	2.3
1	D	77	SER	2.2
1	C	343	GLY	2.2
1	E	112	VAL	2.2
1	D	111	PHE	2.2
1	D	109	ASN	2.2
1	A	314	TYR	2.2
1	E	331	GLY	2.2
1	C	333	ARG	2.2
1	E	352	GLU	2.1
1	E	357	HIS	2.1
1	D	143	PHE	2.1
1	C	110	ILE	2.1
1	E	148	PRO	2.1
1	C	335	GLU	2.1
1	D	93	ASN	2.1
1	E	321	SER	2.1
1	E	154	PHE	2.1
1	E	335	GLU	2.1
1	E	360	TYR	2.1
1	C	47	ASN	2.1
1	E	289	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	330	LEU	2.0
1	C	324	TYR	2.0
1	E	355	THR	2.0
1	E	332	HIS	2.0
1	E	141	ILE	2.0
1	A	103	ASN	2.0
1	D	46	SER	2.0
1	D	86	PRO	2.0

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

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	OF4	E	603	31/31	0.72	0.38	102,118,136,145	0
4	OF4	A	603	31/31	0.78	0.33	70,84,118,132	0
4	OF4	C	603	31/31	0.79	0.31	80,98,129,134	0
4	OF4	B	603	31/31	0.84	0.26	48,66,103,115	0
4	OF4	D	603	31/31	0.86	0.25	58,75,107,120	0
5	MTX	E	604	33/33	0.86	0.22	75,88,93,97	0
3	UFP	E	602	21/21	0.91	0.18	87,113,123,127	0
5	MTX	C	604	33/33	0.92	0.20	58,72,86,86	0
5	MTX	D	604	33/33	0.92	0.17	69,81,87,92	0
6	SO4	E	605	5/5	0.93	0.29	78,95,111,117	0
5	MTX	B	604	33/33	0.94	0.19	47,60,78,86	0
2	NDP	D	601	48/48	0.94	0.20	67,97,118,120	0
3	UFP	C	602	21/21	0.94	0.16	70,85,98,98	0
5	MTX	A	604	33/33	0.94	0.17	43,58,76,83	0
3	UFP	A	602	21/21	0.94	0.19	55,69,85,92	0

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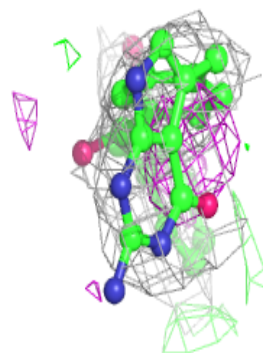
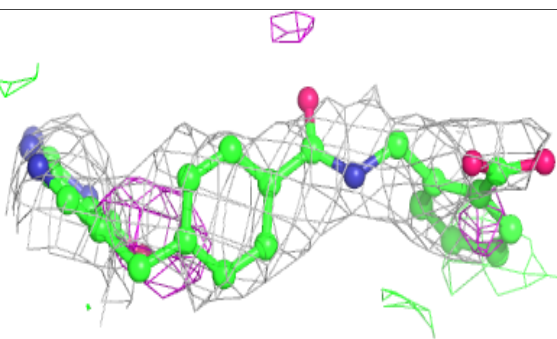
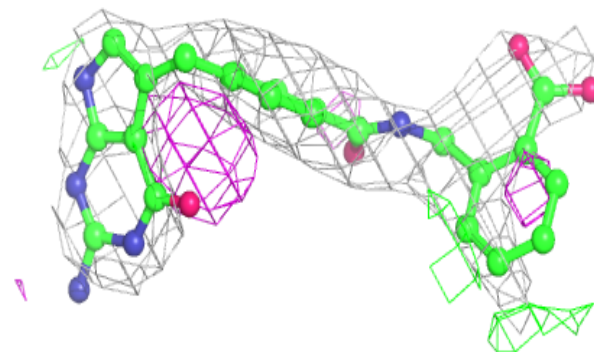
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
6	SO4	A	605	5/5	0.94	0.25	54,61,79,84	0
6	SO4	B	605	5/5	0.95	0.22	74,75,81,86	0
2	NDP	E	601	48/48	0.95	0.17	78,93,115,117	0
2	NDP	C	601	48/48	0.95	0.18	56,81,102,115	0
3	UFP	D	602	21/21	0.96	0.16	45,67,75,77	0
3	UFP	B	602	21/21	0.96	0.17	34,60,69,75	0
2	NDP	A	601	48/48	0.96	0.15	46,61,76,96	0
6	SO4	C	605	5/5	0.97	0.21	68,83,89,90	0
2	NDP	B	601	48/48	0.97	0.14	47,60,71,87	0
6	SO4	D	605	5/5	0.98	0.17	74,81,98,102	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.

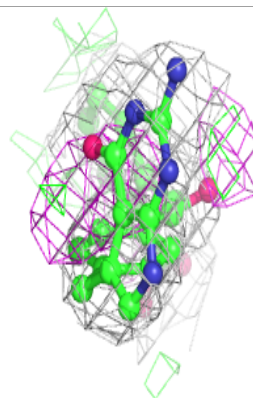
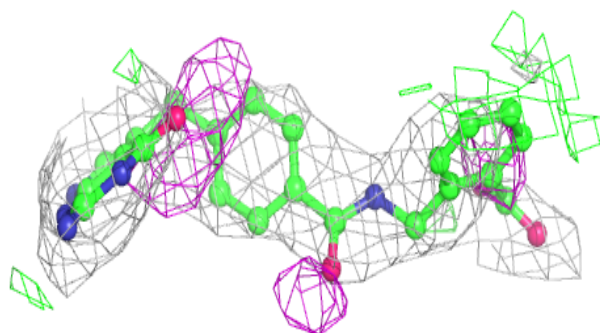
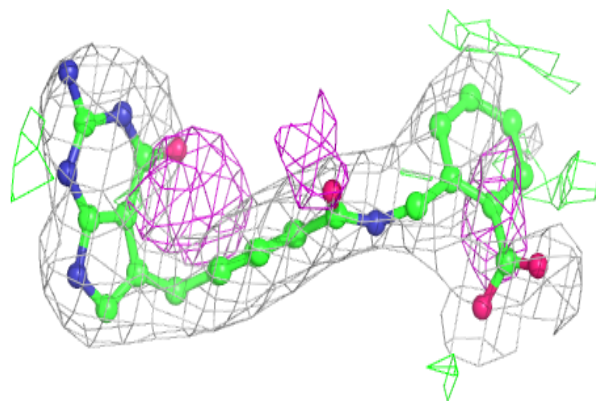
**Electron density around OF4 E 603:**

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

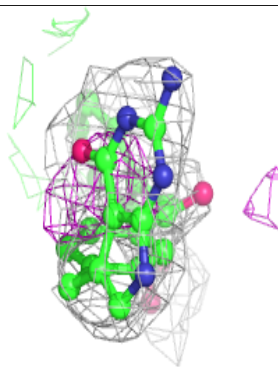
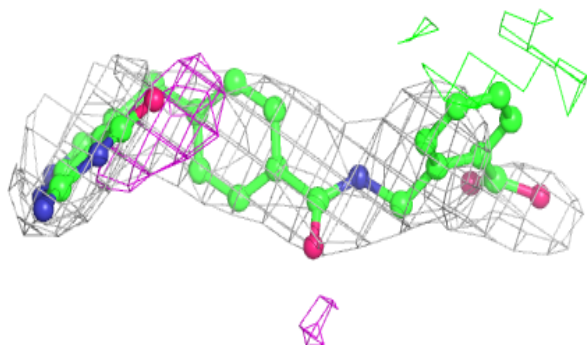
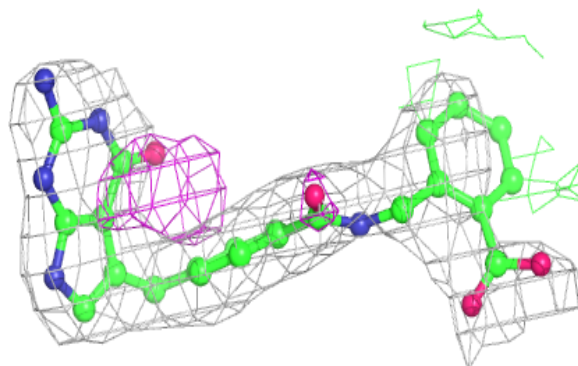


**Electron density around OF4 A 603:**

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and green (positive)

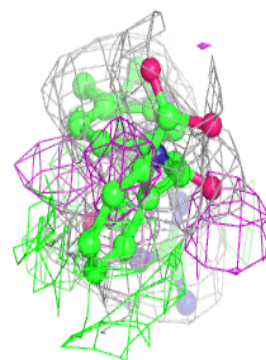
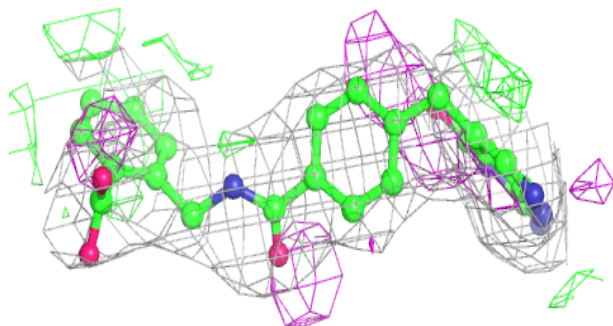
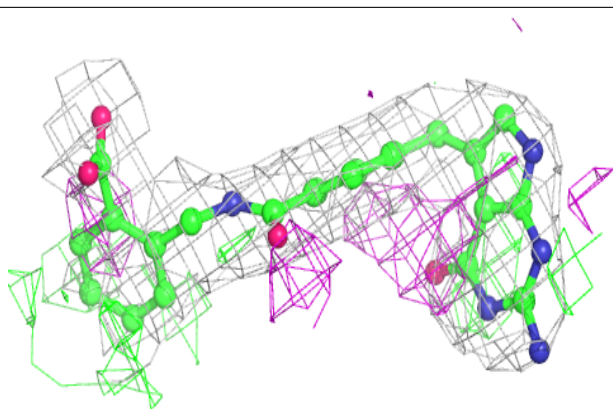
**Electron density around OF4 C 603:**

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and green (positive)

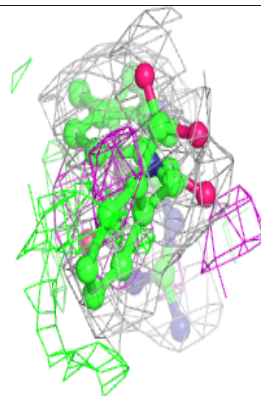
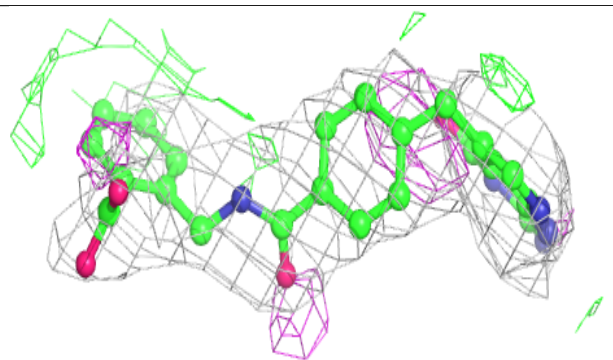
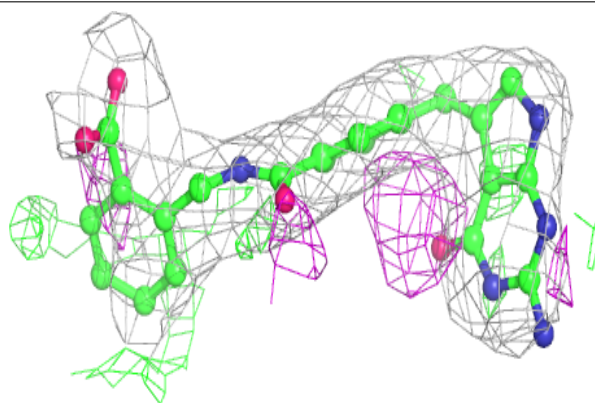


**Electron density around OF4 B 603:**

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and green (positive)

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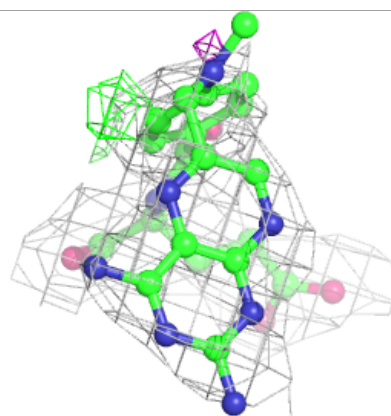
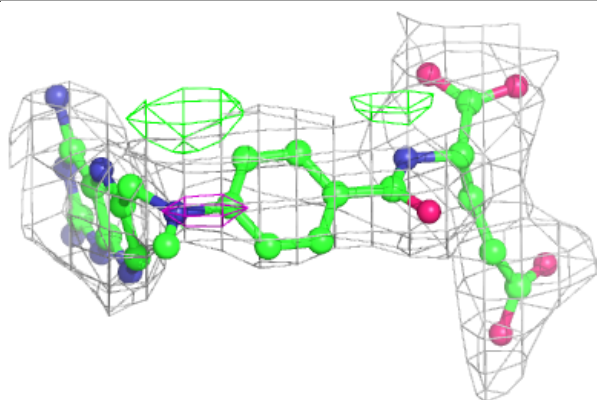
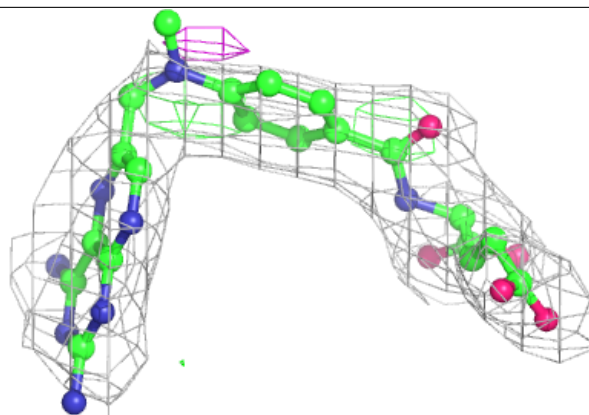
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and green (positive)



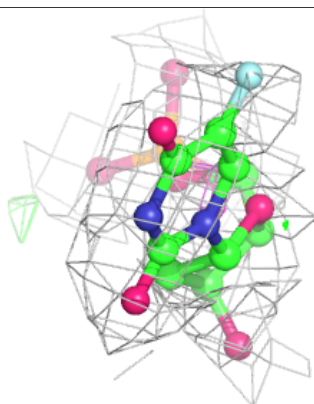
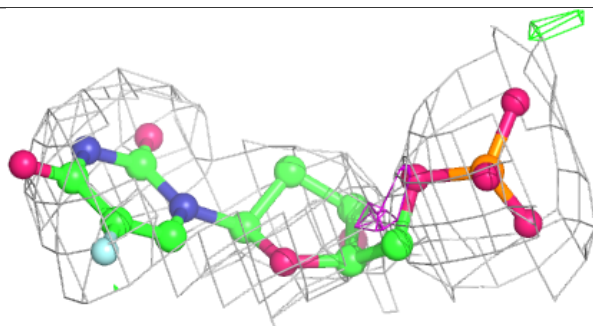
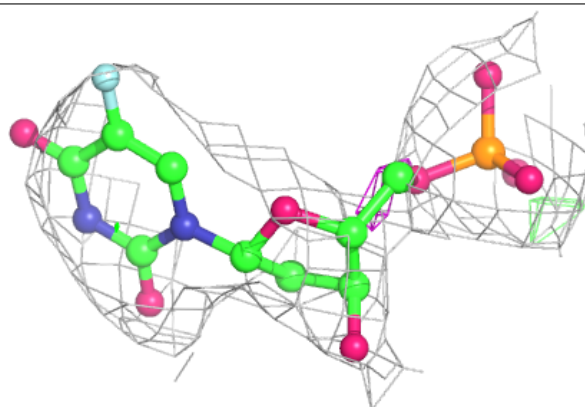


**Electron density around MTX E 604:**

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and green (positive)

**Electron density around UFP E 602:**

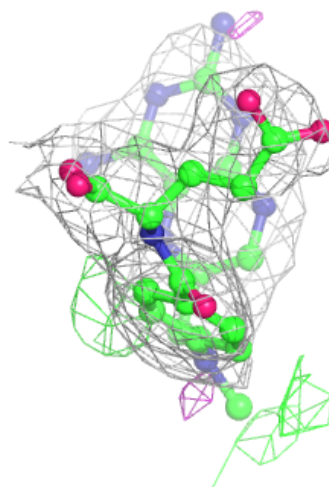
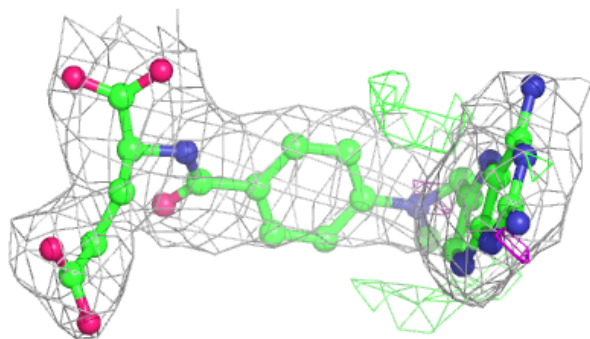
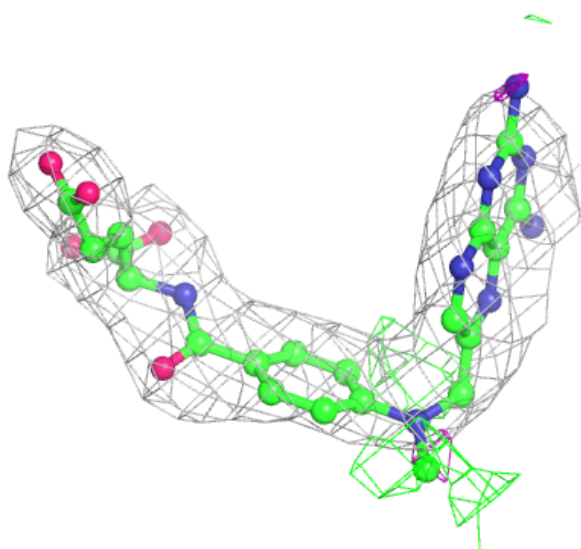
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and green (positive)





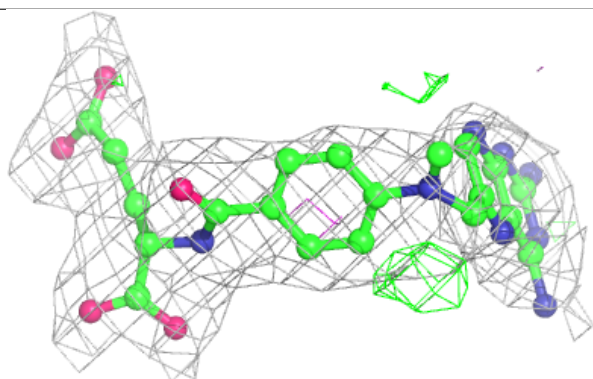
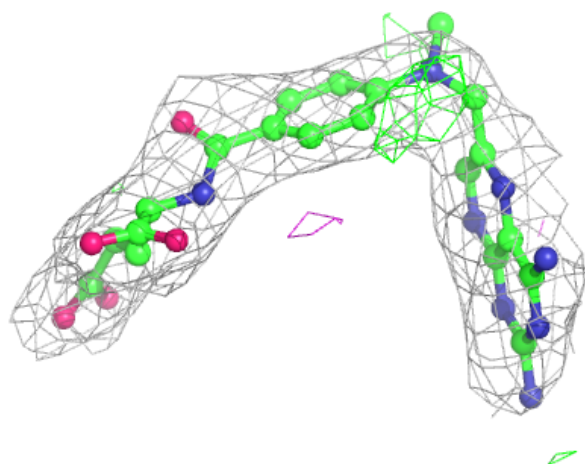
**Electron density around MTX C 604:**

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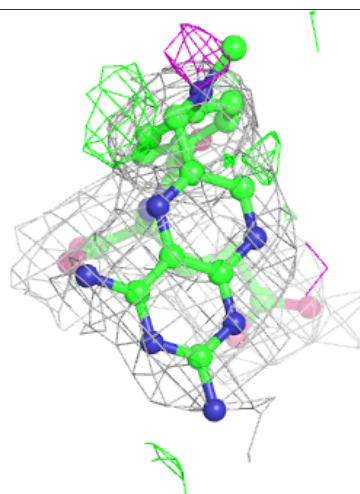
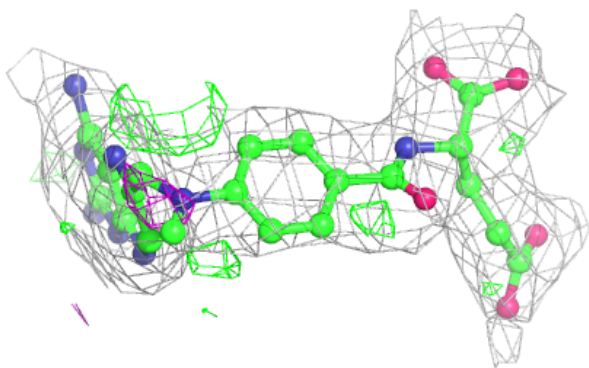
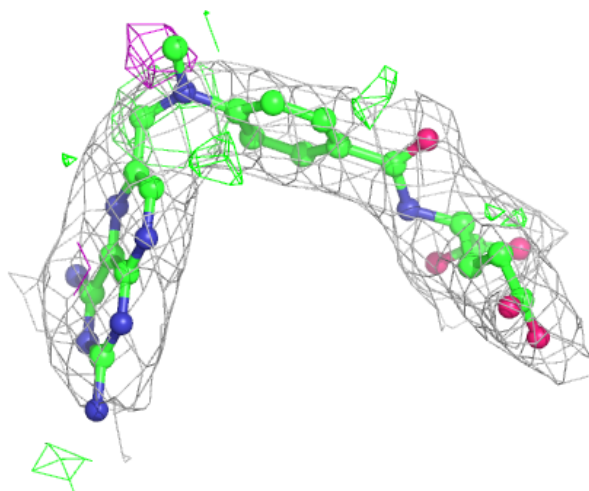
**Electron density around MTX D 604:**

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and green (positive)



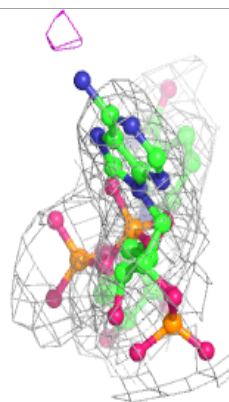
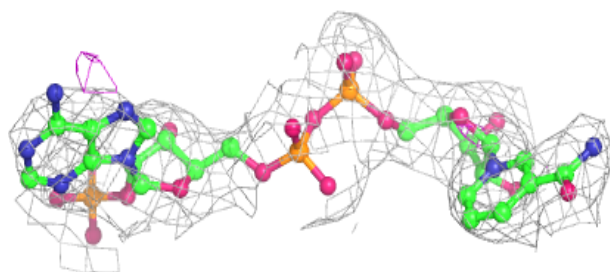
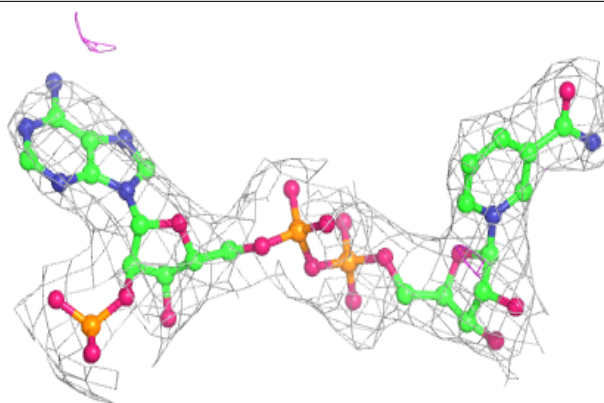
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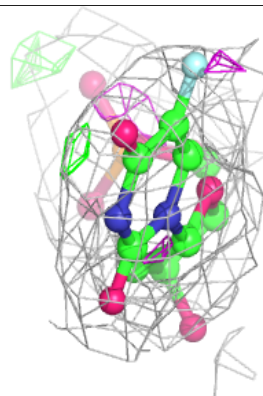
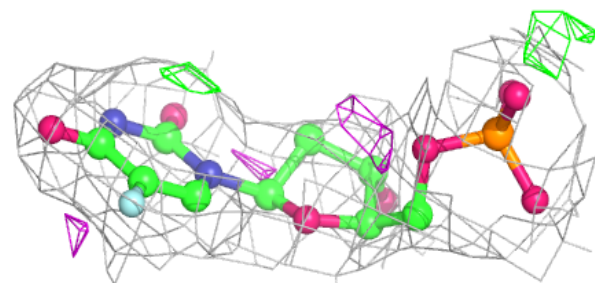
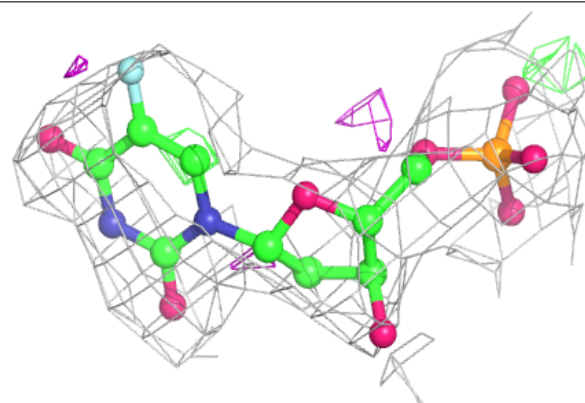


**Electron density around NDP D 601:**

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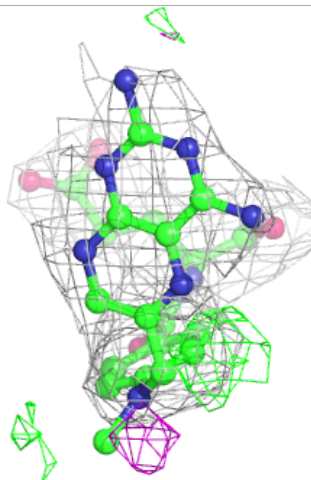
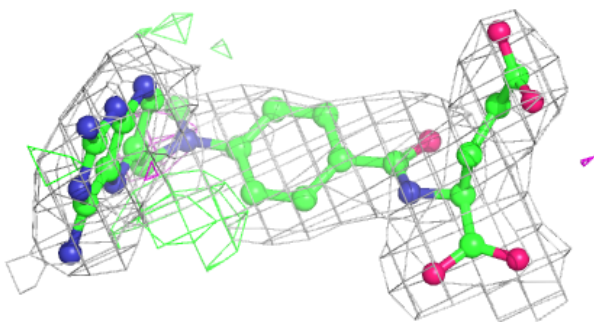
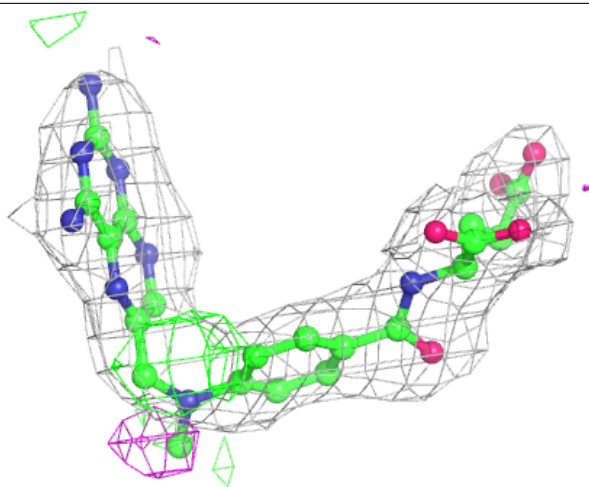
**Electron density around UFP C 602:**

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



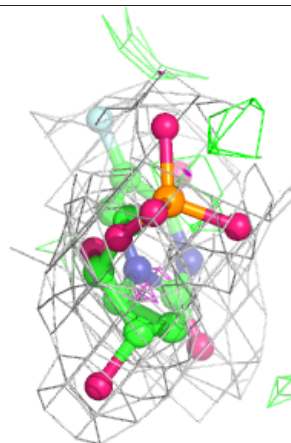
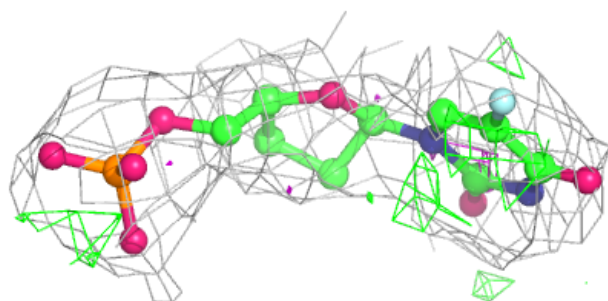
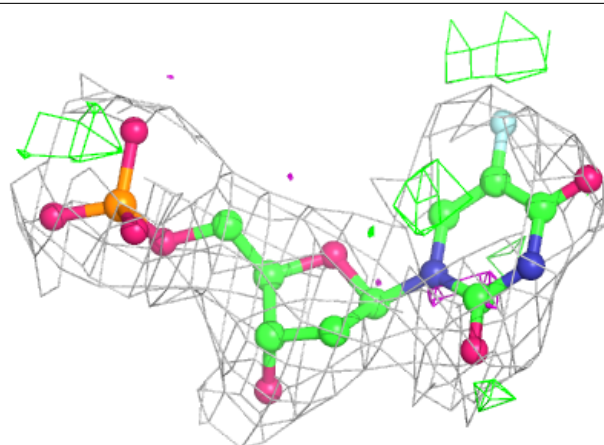
**Electron density around MTX A 604:**

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

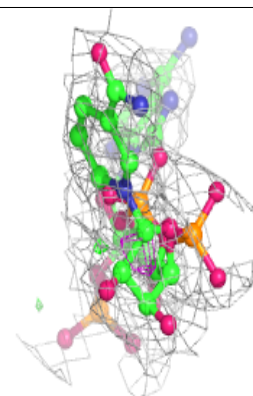
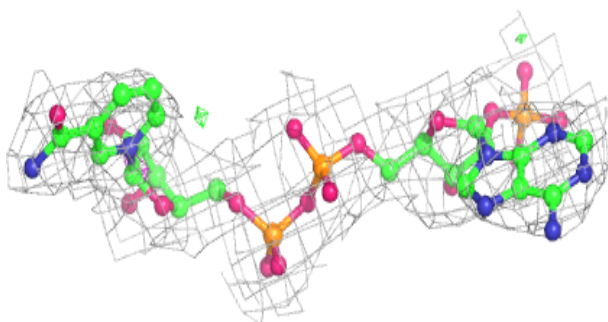
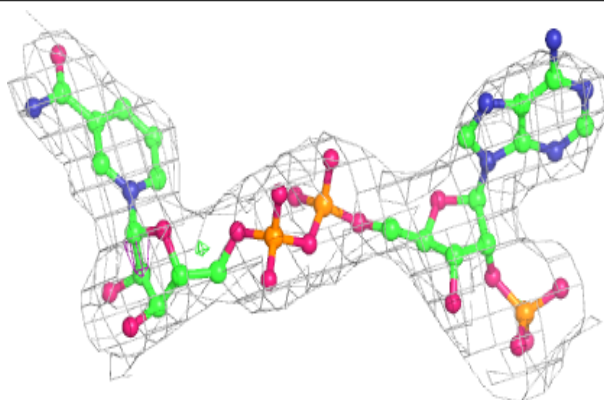


**Electron density around UFP A 602:**

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

**Electron density around NDP E 601:**

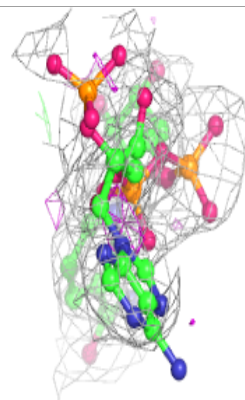
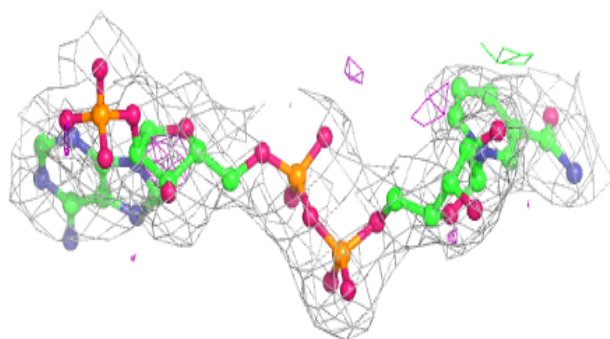
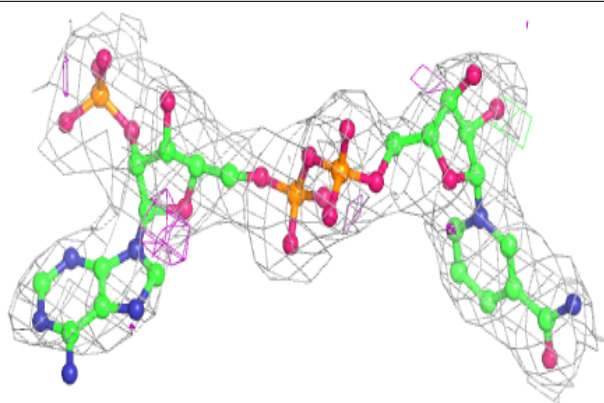
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



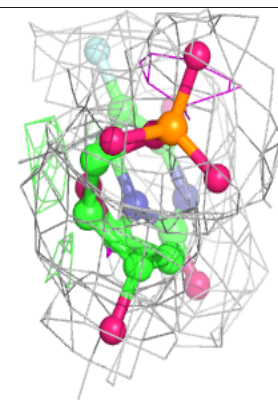
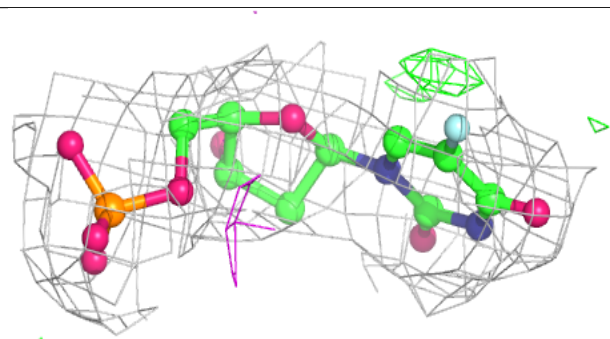
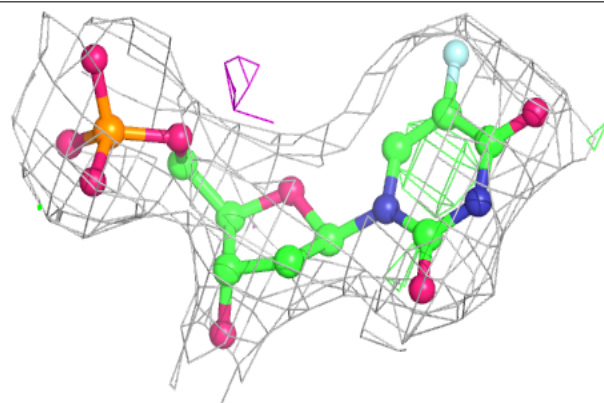


**Electron density around NDP C 601:**

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

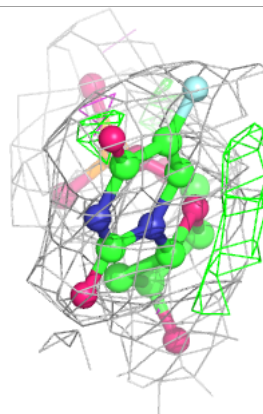
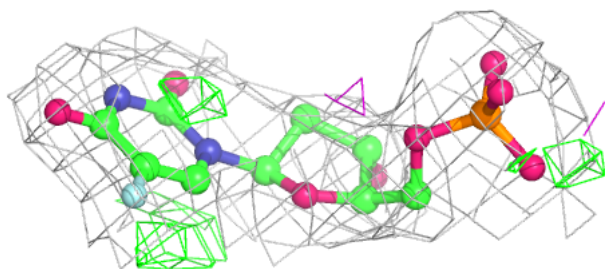
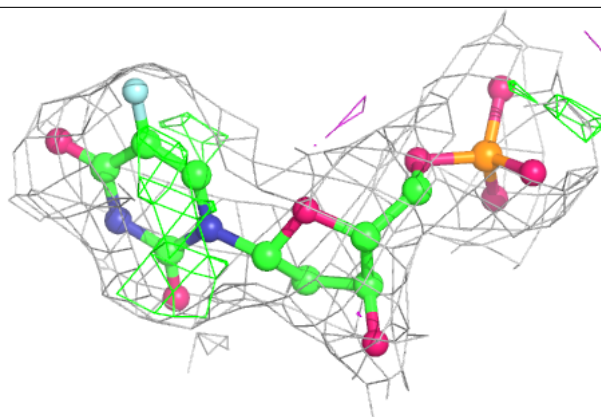
**Electron density around UFP D 602:**

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

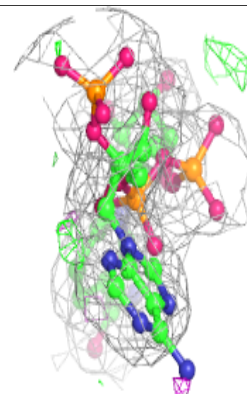
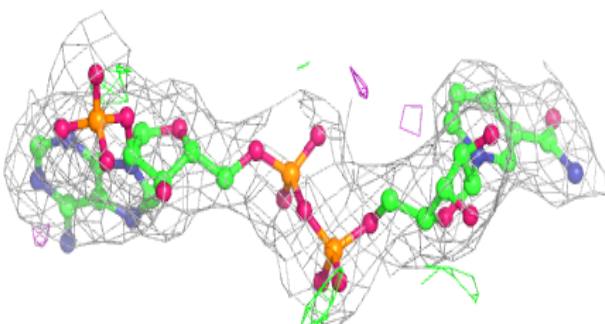
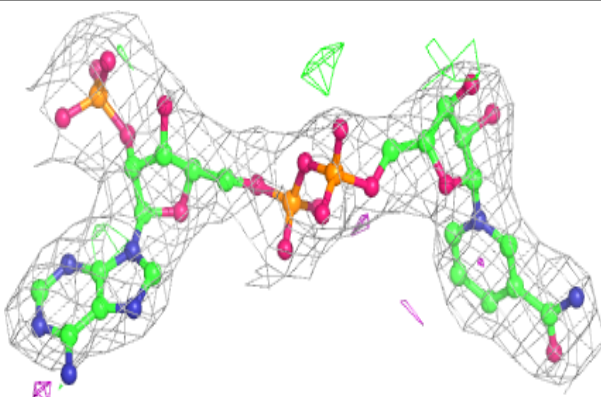


**Electron density around UFP B 602:**

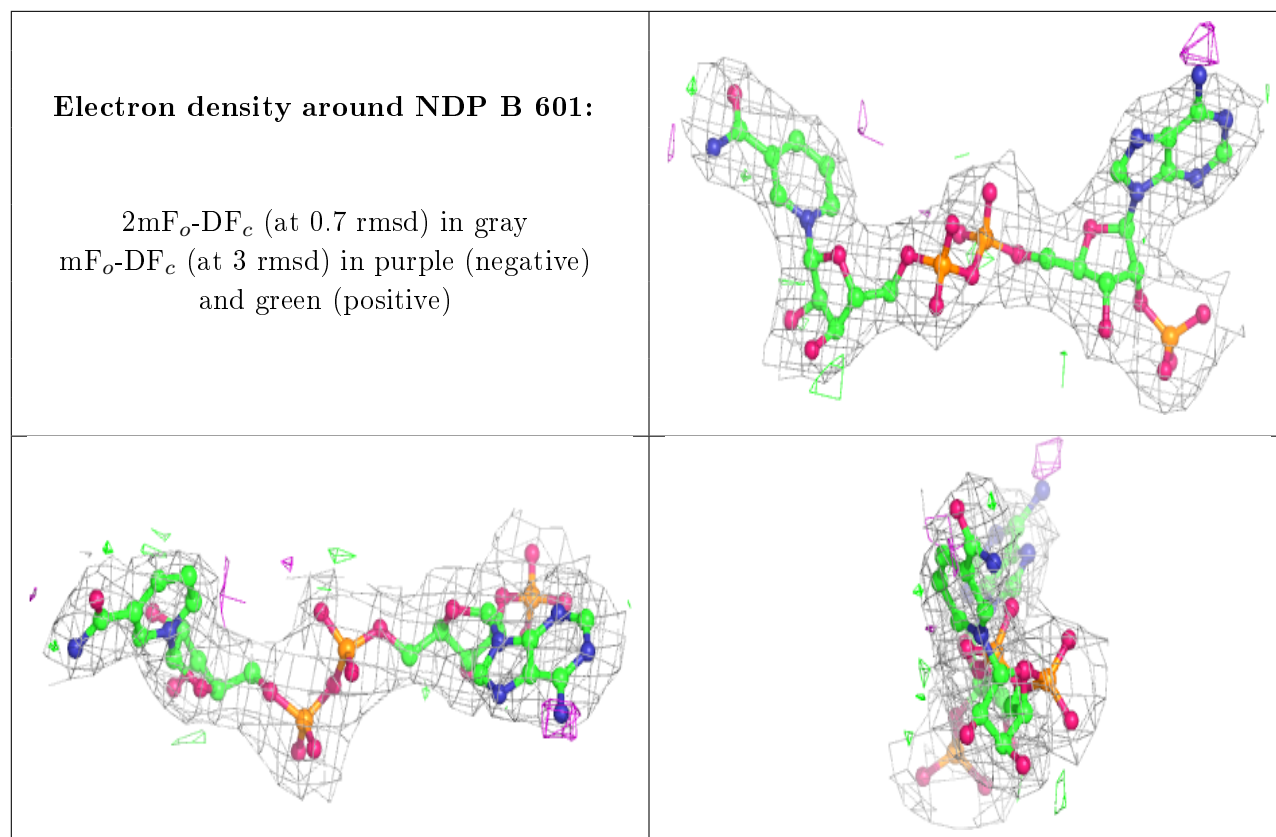
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around NDP A 601:**

$2mF_o-DF_c$  (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.