



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 10, 2026 – 12:12 PM JST

PDB ID : 9M6E / pdb_00009m6e
Title : Crystal structure of xanthine/guanine RNA aptamer (P1-12bp) with hypoxanthine
Authors : Li, M.; Huang, L.
Deposited on : 2025-03-07
Resolution : 2.95 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

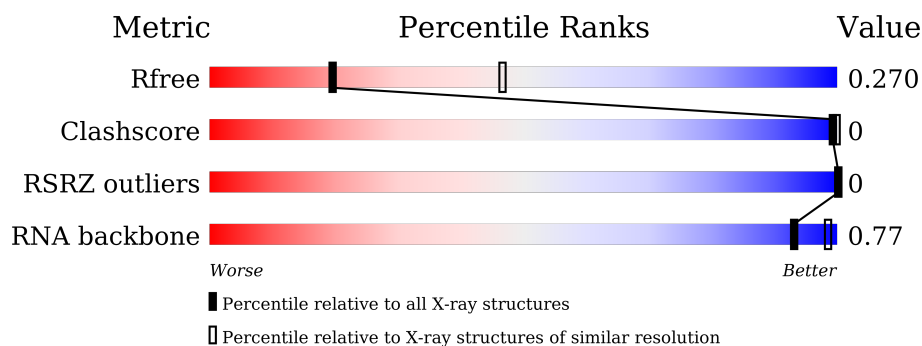
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

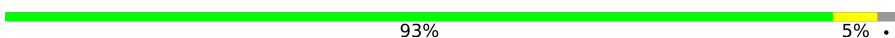
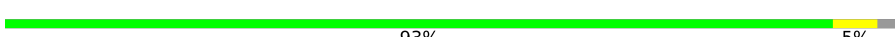
The reported resolution of this entry is 2.95 Å.

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}	180053	1130 (2.98-2.94)
Clashscore	190562	1157 (2.98-2.94)
RSRZ outliers	180081	1130 (2.98-2.94)
RNA backbone	3983	1046 (3.16-2.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	42	 90% 7%
1	B	42	 93% 5%
1	C	42	 93% 5%
1	D	42	 93% 5%
1	E	42	 93% 5%
1	F	42	 93% 5%

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Mol	Chain	Length	Quality of chain
1	G	42	 90% 7% •
1	H	42	 93% 5% •

2 Entry composition

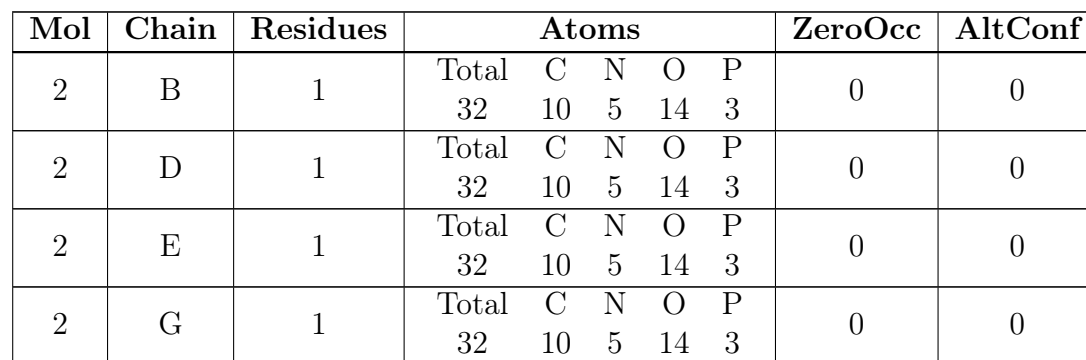
There are 5 unique types of molecules in this entry. The entry contains 10761 atoms, of which 3480 are hydrogens and 0 are deuteriums.

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 RNA chain called RNA (42-MER).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	41	Total	C	H	N	O	P	0	0	0
			1301	388	431	151	290	41			
1	A	41	Total	C	H	N	O	P	0	0	0
			1301	388	431	151	290	41			
1	D	41	Total	C	H	N	O	P	0	0	0
			1301	388	431	151	290	41			
1	C	41	Total	C	H	N	O	P	0	0	0
			1301	388	431	151	290	41			
1	E	41	Total	C	H	N	O	P	0	0	0
			1301	388	431	151	290	41			
1	F	41	Total	C	H	N	O	P	0	0	0
			1301	388	431	151	290	41			
1	G	41	Total	C	H	N	O	P	0	0	0
			1301	388	431	151	290	41			
1	H	41	Total	C	H	N	O	P	0	0	0
			1301	388	431	151	290	41			

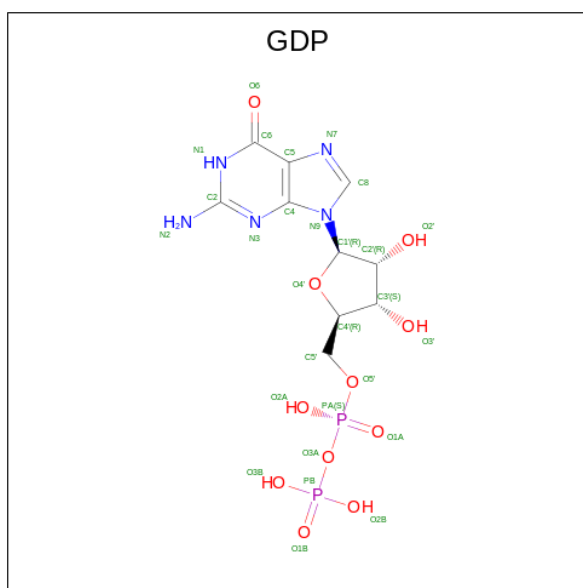
- Molecule 2 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



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- Chemical structure of Hypoxanthine (HPA) is shown. The structure is a purine derivative, consisting of a fused bicyclic system (a pyrimidine ring fused to an imidazole ring). The atoms are labeled as follows:
- N1: Nitrogen atom at the top left of the pyrimidine ring.
 - C2: Carbon atom at the bottom left of the pyrimidine ring.
 - N3: Nitrogen atom at the bottom of the pyrimidine ring.
 - C4: Carbon atom at the bottom right of the pyrimidine ring.
 - C5: Carbon atom at the top right of the pyrimidine ring.
 - C6: Carbon atom at the top of the pyrimidine ring, bonded to the carbonyl group (O6).
 - O6: Oxygen atom of the carbonyl group.
 - C7: Carbon atom at the top of the imidazole ring.
 - N7: Nitrogen atom at the top right of the imidazole ring.
 - C8: Carbon atom at the bottom right of the imidazole ring.
 - N9: Nitrogen atom at the bottom of the imidazole ring.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	H	N	O	0	0
			14	5	4	4	1		
3	A	1	Total	C	H	N	O	0	0
			14	5	4	4	1		
3	D	1	Total	C	H	N	O	0	0
			14	5	4	4	1		
3	C	1	Total	C	H	N	O	0	0
			14	5	4	4	1		
3	E	1	Total	C	H	N	O	0	0
			14	5	4	4	1		
3	F	1	Total	C	H	N	O	0	0
			14	5	4	4	1		
3	G	1	Total	C	H	N	O	0	0
			14	5	4	4	1		
3	H	1	Total	C	H	N	O	0	0
			14	5	4	4	1		

- Molecule 4 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	E	1	Total	Na	0	0
			1	1		

3 Residue-property plots [i](#)

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

- Molecule 1: RNA (42-MER)

Chain B:  93% 5% .



- Molecule 1: RNA (42-MER)

Chain A:  90% 7% .

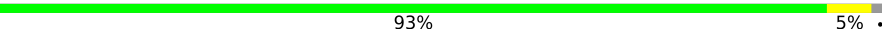


- Molecule 1: RNA (42-MER)

Chain D:  93% 5% .

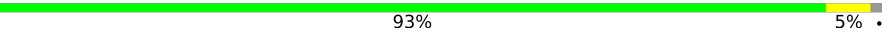


- Molecule 1: RNA (42-MER)

Chain C:  93% 5% .

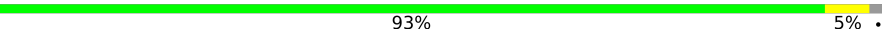


- Molecule 1: RNA (42-MER)

Chain E:  93% 5% .



- Molecule 1: RNA (42-MER)

Chain F:  93% 5% .



- Molecule 1: RNA (42-MER)

Chain G:  90% 7% .



- Molecule 1: RNA (42-MER)

Chain H:  93% 5% .



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	22.77Å 44.91Å 209.56Å 89.91° 89.90° 89.95°	Depositor
Resolution (Å)	34.93 – 2.95 34.93 – 2.95	Depositor EDS
% Data completeness (in resolution range)	96.9 (34.93-2.95) 97.6 (34.93-2.95)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 2.96Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.246 , 0.272 0.246 , 0.270	Depositor DCC
R_{free} test set	905 reflections (5.17%)	wwPDB-VP
Wilson B-factor (Å ²)	44.1	Xtriage
Anisotropy	0.536	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 30.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.359 for h,-k,-l 0.338 for -h,k,-l 0.360 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10761	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.35% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, NA, GDP, HPA

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	0.12	0/970	0.30	0/1509
1	B	0.12	0/970	0.28	0/1509
1	C	0.11	0/970	0.28	0/1509
1	D	0.11	0/970	0.27	0/1509
1	E	0.12	0/970	0.26	0/1509
1	F	0.12	0/970	0.28	0/1509
1	G	0.12	0/970	0.27	0/1509
1	H	0.11	0/970	0.28	0/1509
All	All	0.12	0/7760	0.28	0/12072

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	870	431	442	1	0
1	B	870	431	442	0	0
1	C	870	431	442	0	0
1	D	870	431	442	0	0
1	E	870	431	442	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	870	431	442	0	0
1	G	870	431	442	1	0
1	H	870	431	442	0	0
2	B	32	0	11	0	0
2	D	32	0	11	0	0
2	E	32	0	11	0	0
2	G	32	0	11	0	0
3	A	10	4	4	0	0
3	B	10	4	4	0	0
3	C	10	4	4	0	0
3	D	10	4	4	0	0
3	E	10	4	4	0	0
3	F	10	4	4	0	0
3	G	10	4	4	0	0
3	H	10	4	4	0	0
4	A	28	0	11	0	0
4	C	28	0	11	0	0
4	F	28	0	11	0	0
4	H	28	0	11	0	0
5	E	1	0	0	0	0
All	All	7281	3480	3656	1	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 0.

All (1) 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:18:A:O2'	1:G:18:A:O2'	2.32	0.46

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	40/42 (95%)	2 (5%)	0
1	B	40/42 (95%)	2 (5%)	0
1	C	40/42 (95%)	2 (5%)	0
1	D	40/42 (95%)	2 (5%)	0
1	E	40/42 (95%)	2 (5%)	0
1	F	40/42 (95%)	2 (5%)	0
1	G	40/42 (95%)	2 (5%)	0
1	H	40/42 (95%)	2 (5%)	0
All	All	320/336 (95%)	16 (5%)	0

5 of 16 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	B	12	U
1	B	20	U
1	A	12	U
1	A	20	U
1	D	12	U

There are no RNA pucker outliers to report.

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 1 is monoatomic - leaving 16 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GTP	D	101	1	30,34,34	0.84	1 (3%)	46,54,54	1.74	11 (23%)
3	HPA	G	102	-	10,11,11	1.72	1 (10%)	11,15,15	3.40	8 (72%)
2	GTP	B	101	1	30,34,34	0.84	1 (3%)	46,54,54	1.77	11 (23%)
4	GDP	F	101	1	28,30,30	0.88	1 (3%)	44,47,47	1.69	9 (20%)
3	HPA	E	102	-	10,11,11	1.74	2 (20%)	11,15,15	3.41	8 (72%)
3	HPA	H	102	-	10,11,11	1.76	2 (20%)	11,15,15	3.41	8 (72%)
4	GDP	C	101	1	28,30,30	0.87	1 (3%)	44,47,47	1.66	9 (20%)
3	HPA	C	102	-	10,11,11	1.76	1 (10%)	11,15,15	3.39	8 (72%)
3	HPA	F	102	-	10,11,11	1.74	2 (20%)	11,15,15	3.43	8 (72%)
2	GTP	E	101	1	30,34,34	0.80	1 (3%)	46,54,54	1.73	12 (26%)
3	HPA	A	102	-	10,11,11	1.75	1 (10%)	11,15,15	3.42	8 (72%)
4	GDP	A	101	1	28,30,30	0.89	1 (3%)	44,47,47	1.70	9 (20%)
2	GTP	G	101	1	30,34,34	0.82	1 (3%)	46,54,54	1.78	11 (23%)
3	HPA	B	102	-	10,11,11	1.77	1 (10%)	11,15,15	3.85	8 (72%)
3	HPA	D	102	-	10,11,11	1.73	2 (20%)	11,15,15	3.44	8 (72%)
4	GDP	H	101	1	28,30,30	0.89	1 (3%)	44,47,47	1.68	9 (20%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HPA	F	102	-	-	-	0/2/2/2
2	GTP	D	101	1	-	0/22/38/38	0/3/3/3
3	HPA	G	102	-	-	-	0/2/2/2
2	GTP	B	101	1	-	0/22/38/38	0/3/3/3
4	GDP	F	101	1	-	0/16/32/32	0/3/3/3
3	HPA	E	102	-	-	-	0/2/2/2
3	HPA	H	102	-	-	-	0/2/2/2
4	GDP	A	101	1	-	2/16/32/32	0/3/3/3
4	GDP	C	101	1	-	1/16/32/32	0/3/3/3
2	GTP	E	101	1	-	2/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GDP	H	101	1	-	1/16/32/32	0/3/3/3
3	HPA	A	102	-	-	-	0/2/2/2
2	GTP	G	101	1	-	1/22/38/38	0/3/3/3
3	HPA	B	102	-	-	-	0/2/2/2
3	HPA	D	102	-	-	-	0/2/2/2
3	HPA	C	102	-	-	-	0/2/2/2

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	102	HPA	C2-N3	4.82	1.39	1.30
3	C	102	HPA	C2-N3	4.62	1.38	1.30
3	A	102	HPA	C2-N3	4.59	1.38	1.30
3	H	102	HPA	C2-N3	4.55	1.38	1.30
3	E	102	HPA	C2-N3	4.50	1.38	1.30

The worst 5 of 145 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	102	HPA	C5-C6-N1	6.16	120.55	110.57
3	A	102	HPA	C5-C6-N1	5.70	119.80	110.57
3	C	102	HPA	C5-C6-N1	5.64	119.71	110.57
3	D	102	HPA	C5-C6-N1	5.61	119.67	110.57
3	E	102	HPA	C5-C6-N1	5.56	119.59	110.57

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

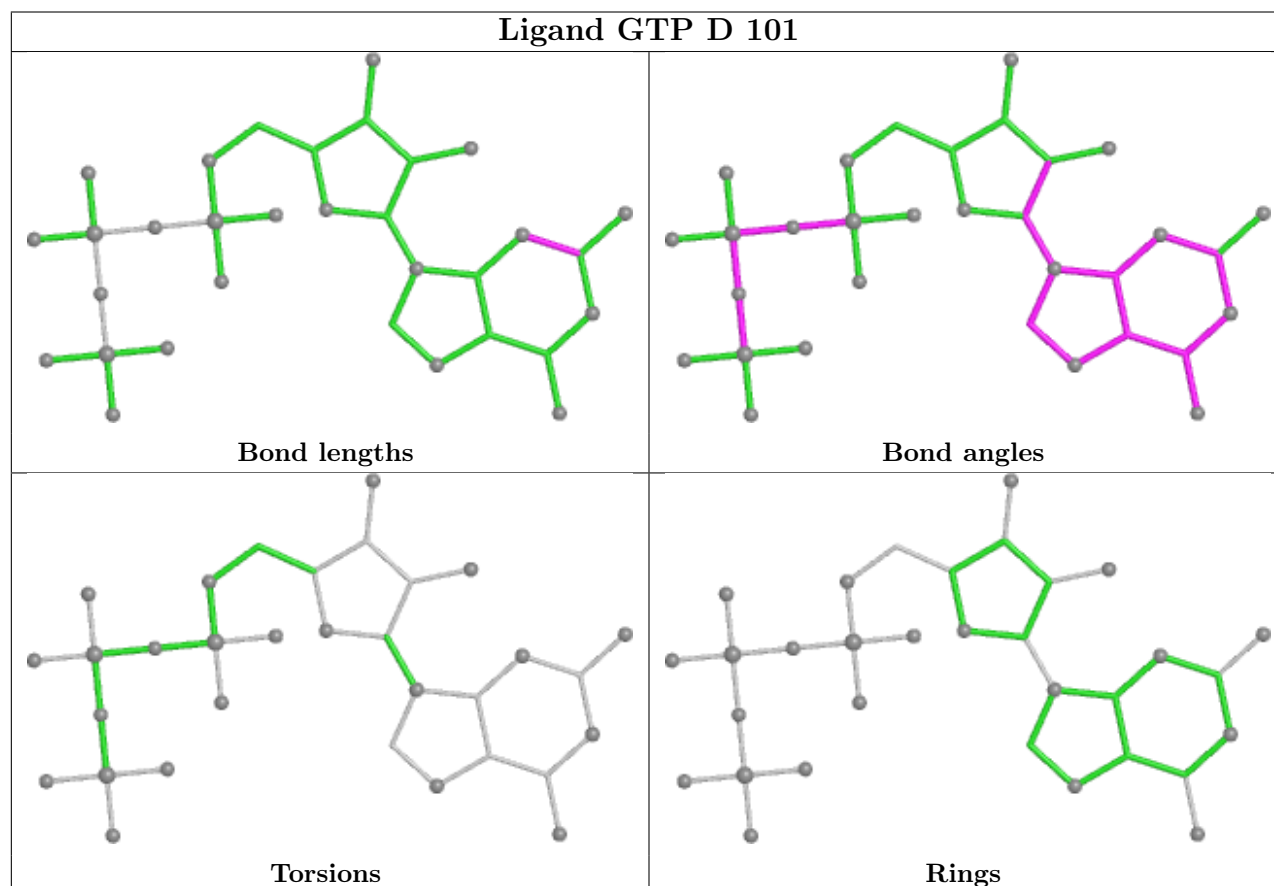
Mol	Chain	Res	Type	Atoms
2	E	101	GTP	PB-O3B-PG-O2G
2	E	101	GTP	PB-O3B-PG-O3G
4	C	101	GDP	PA-O3A-PB-O3B
4	H	101	GDP	PA-O3A-PB-O3B
2	G	101	GTP	PA-O3A-PB-O1B

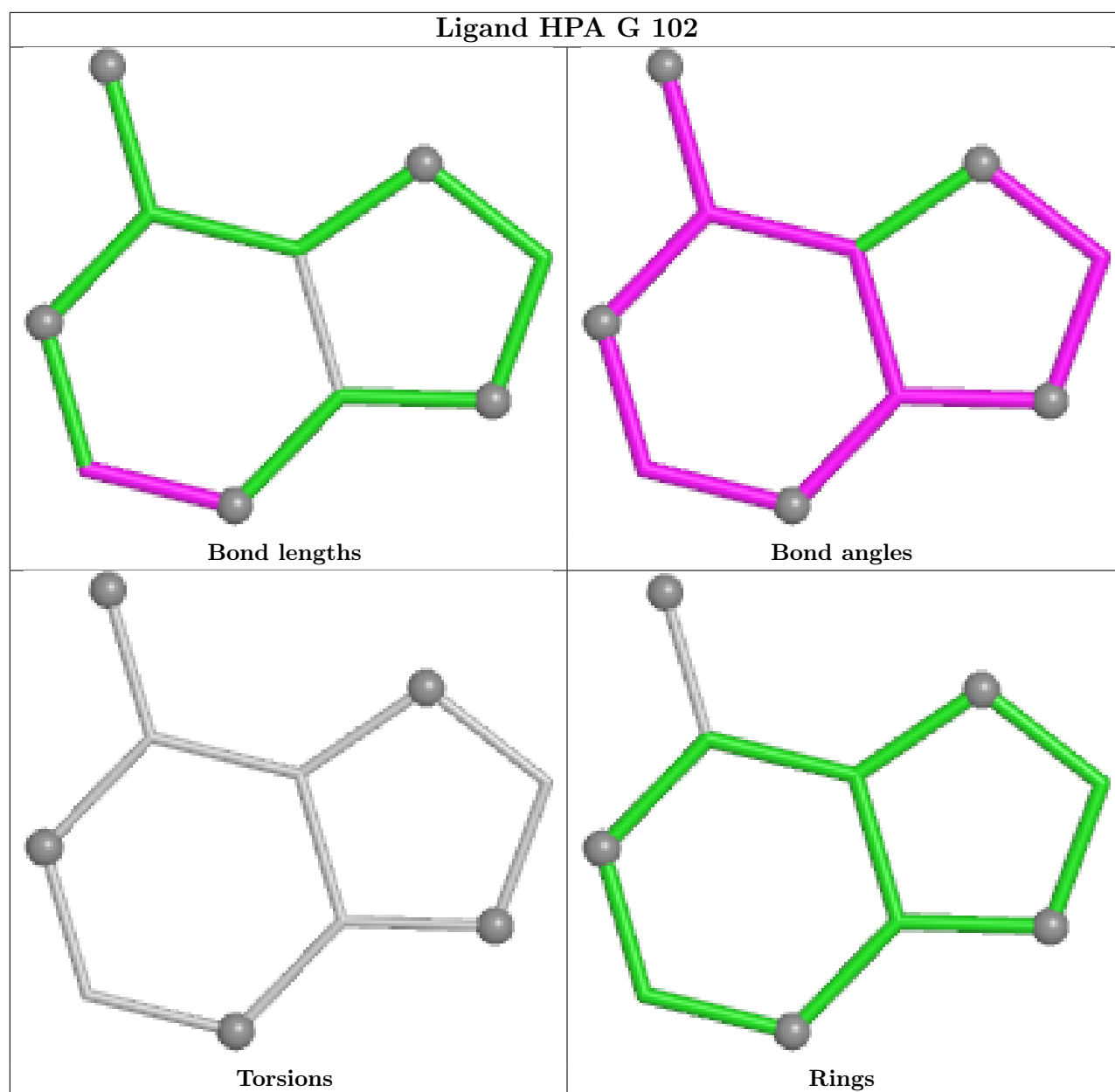
There are no ring outliers.

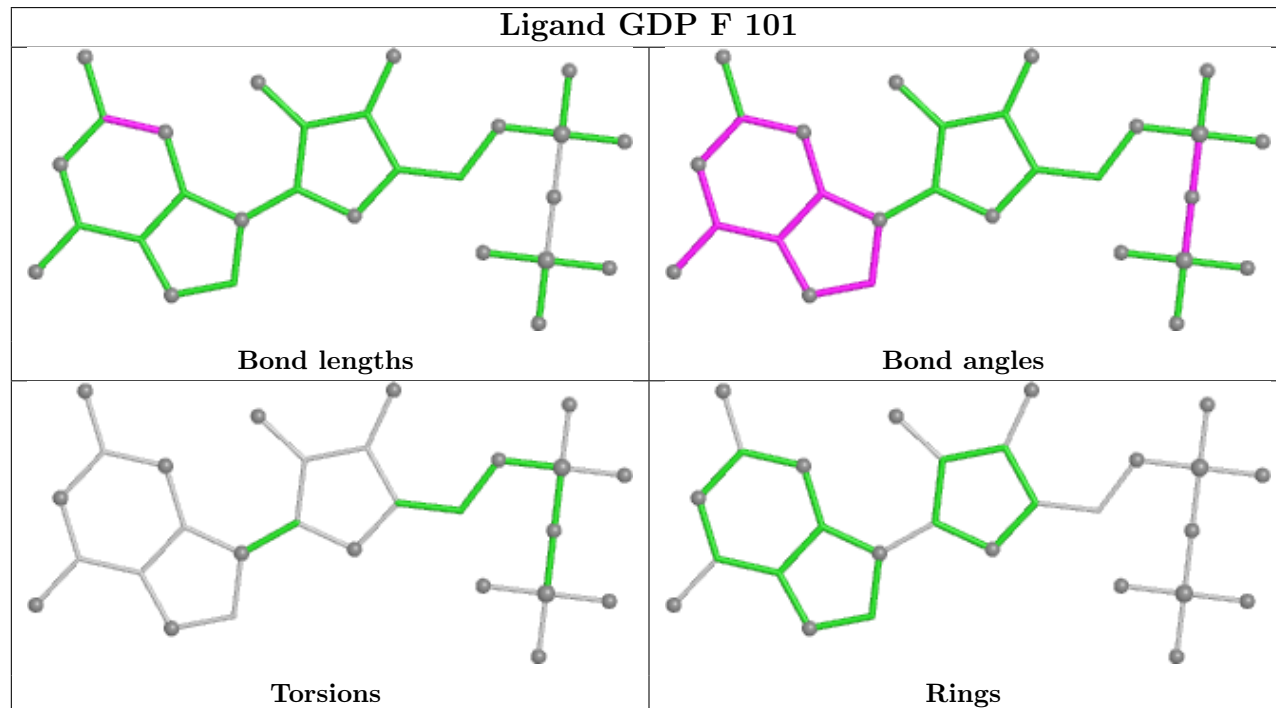
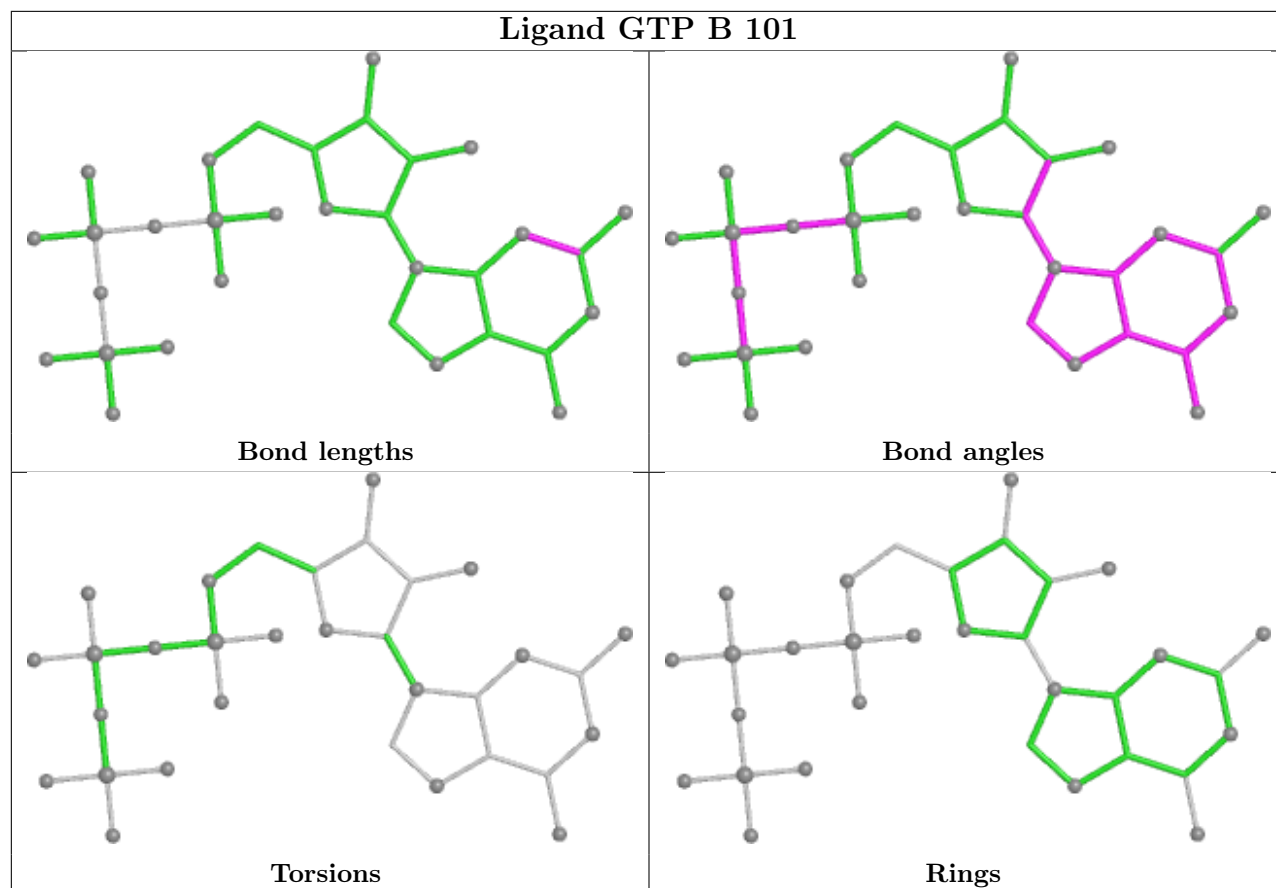
No monomer is involved in short contacts.

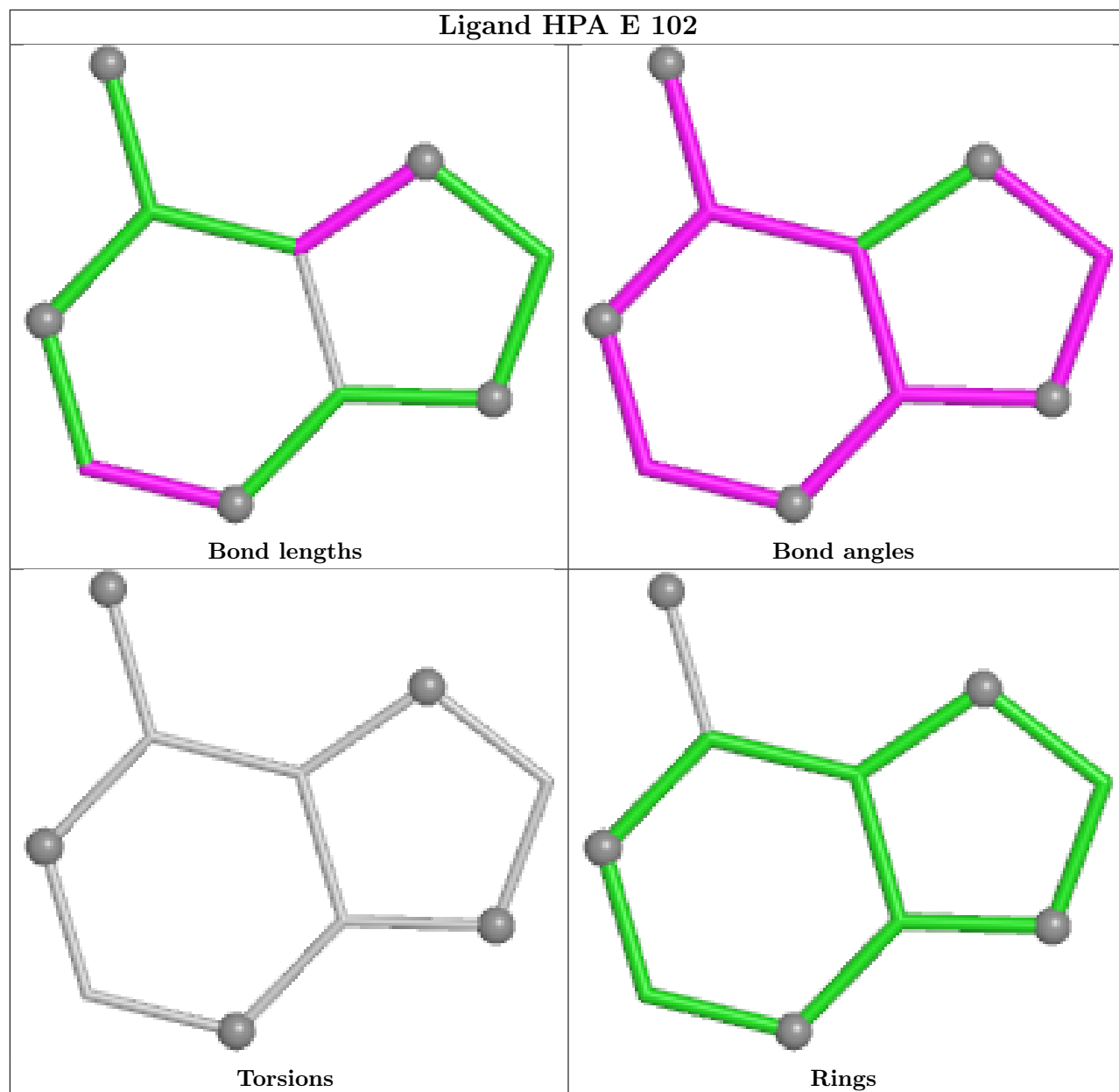
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

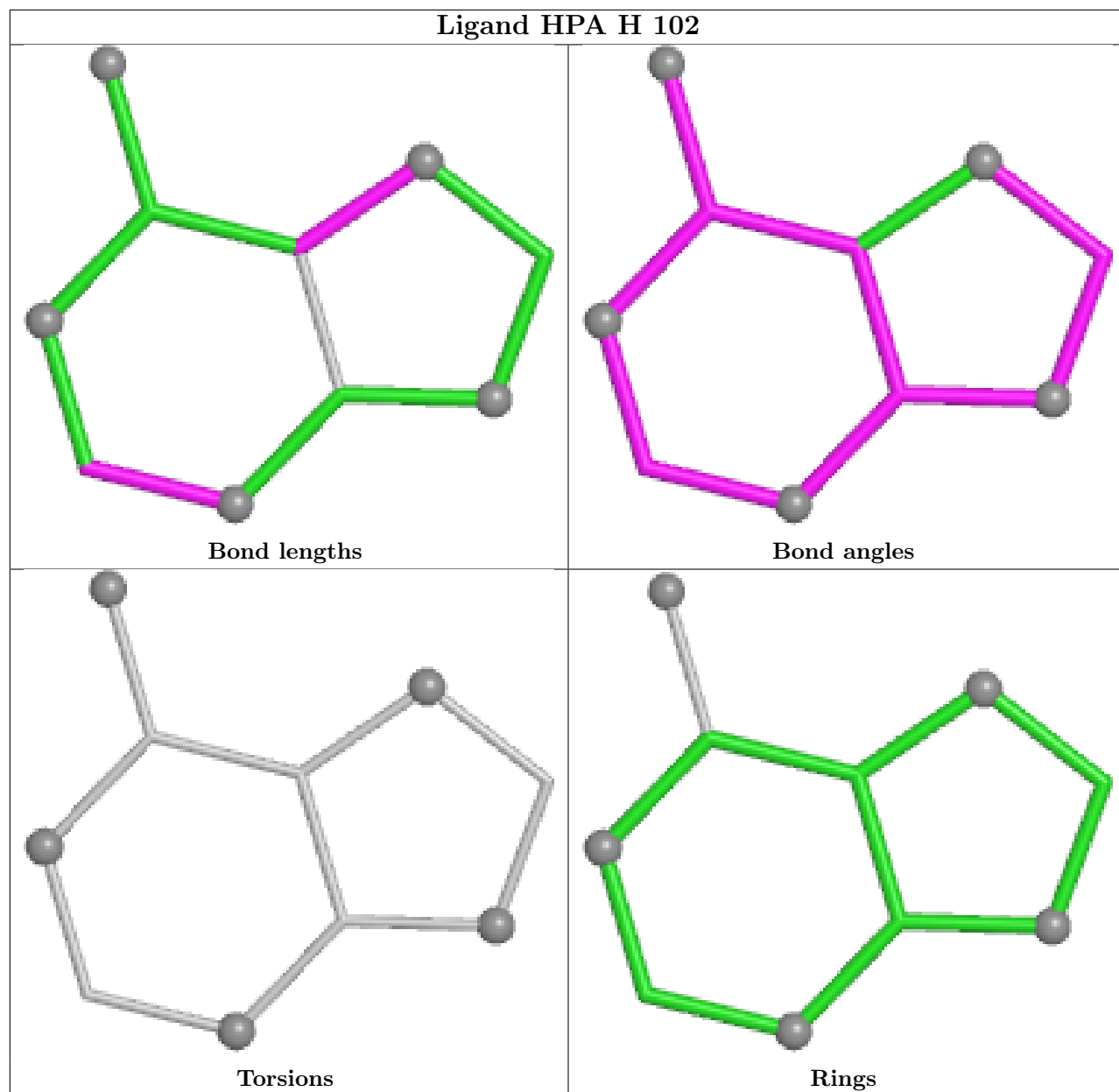
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question 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.

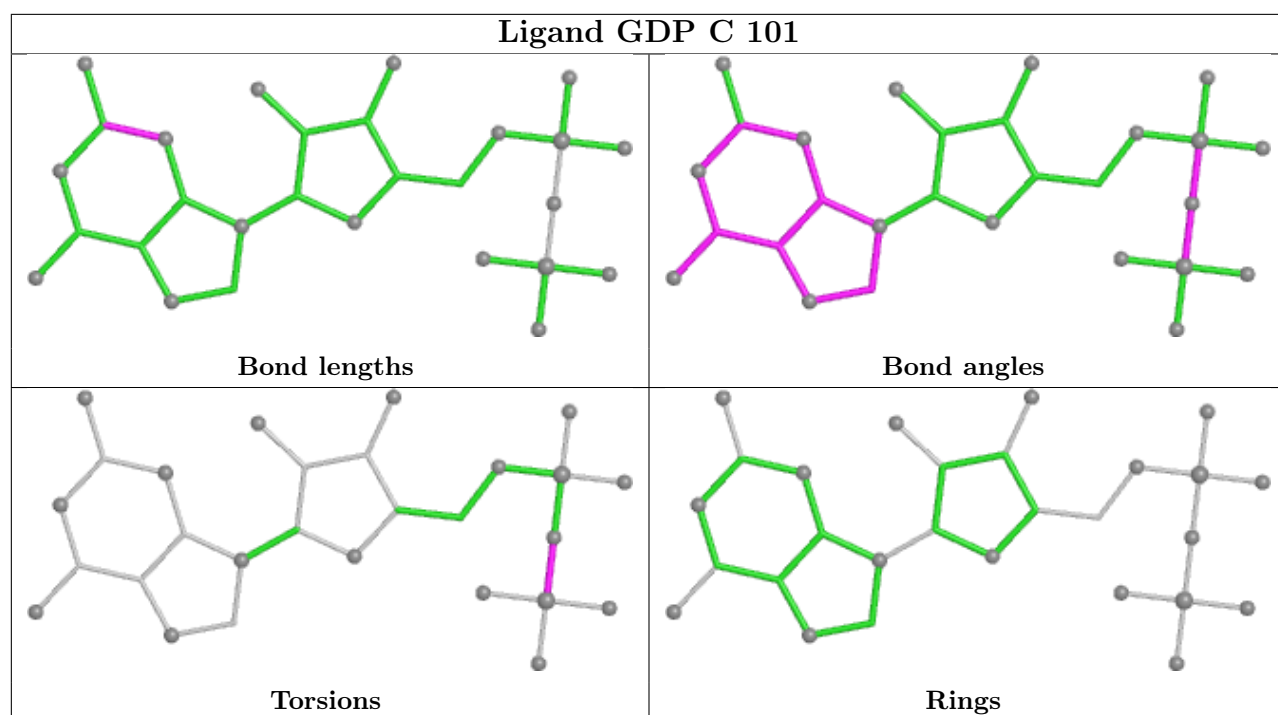


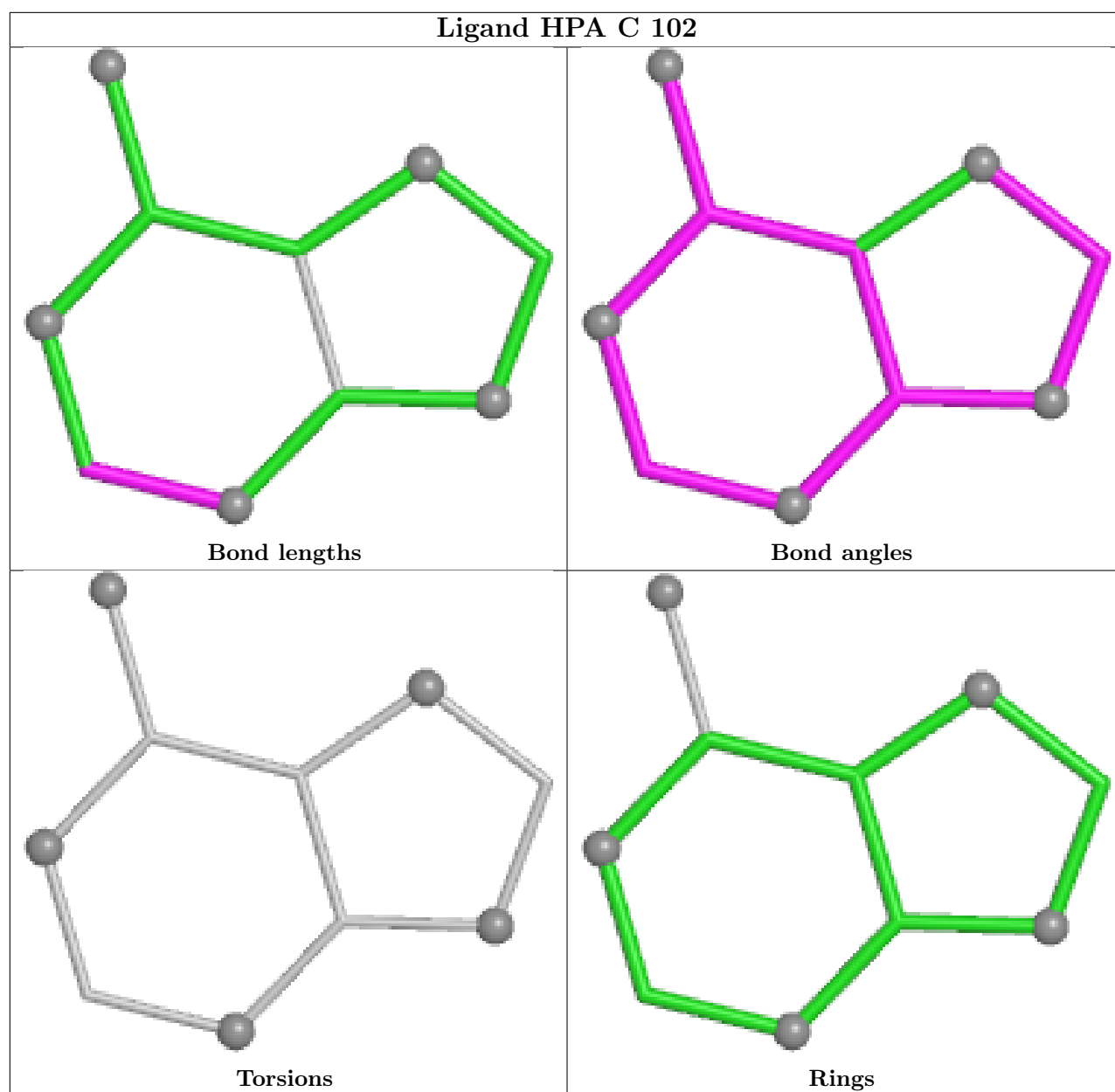




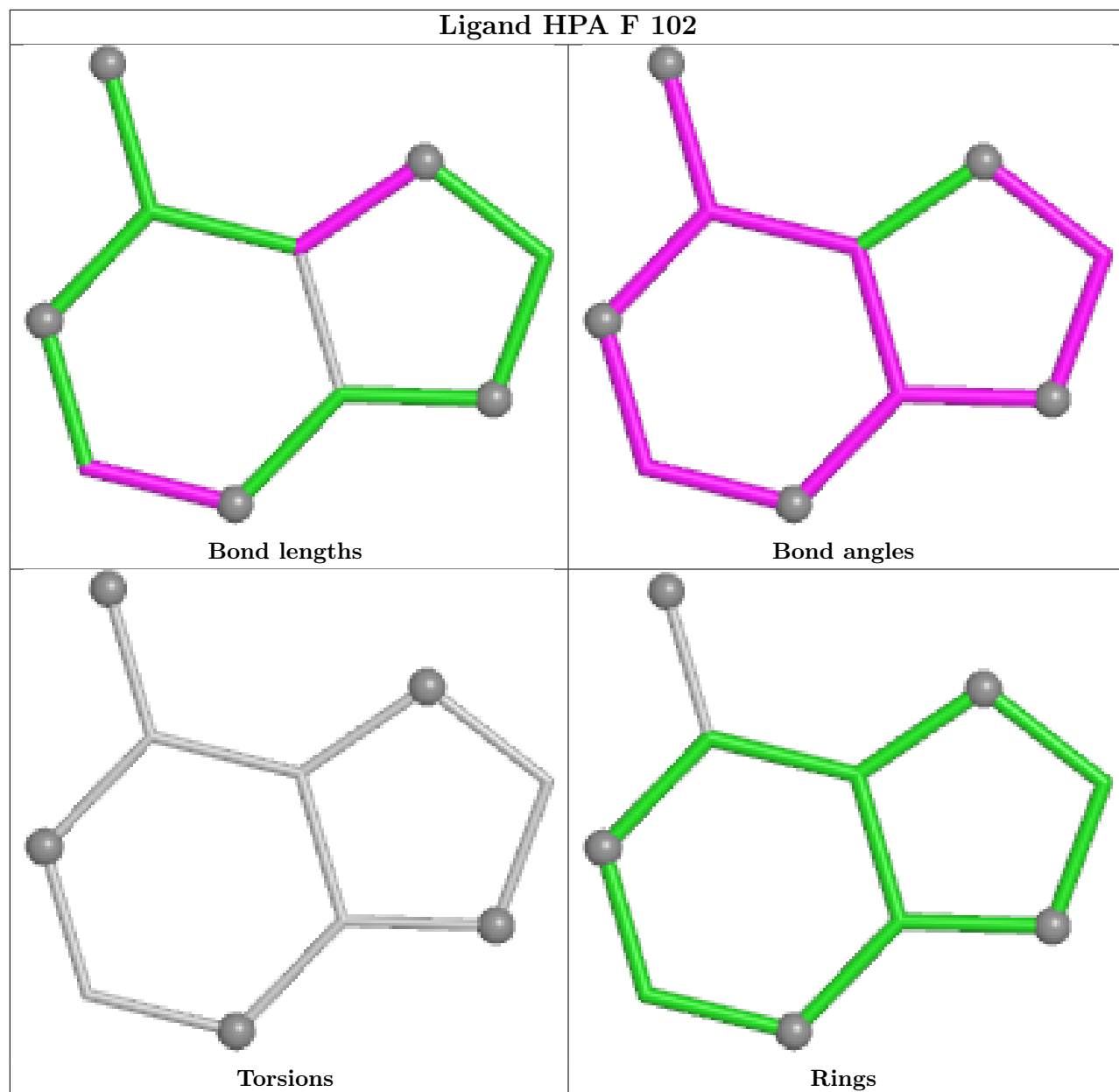


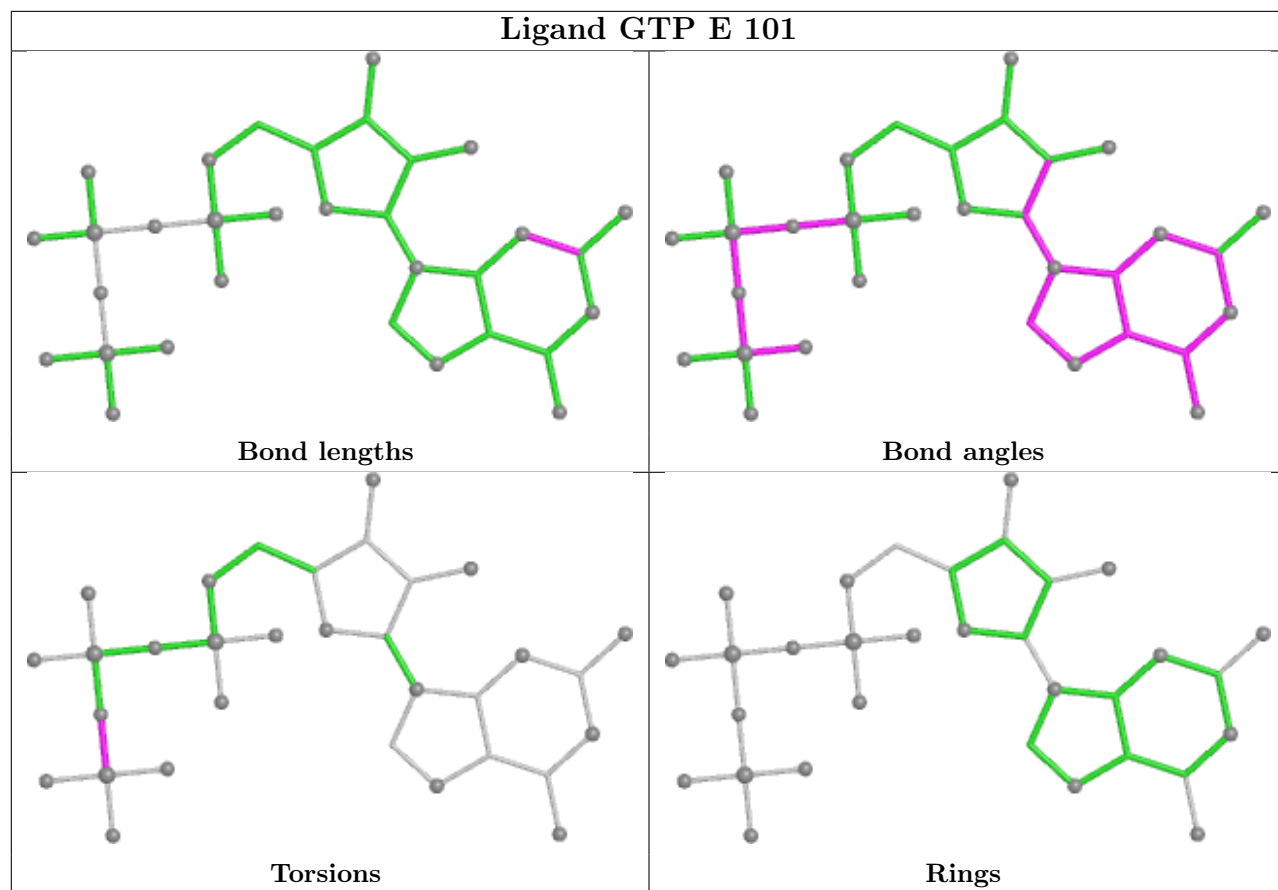


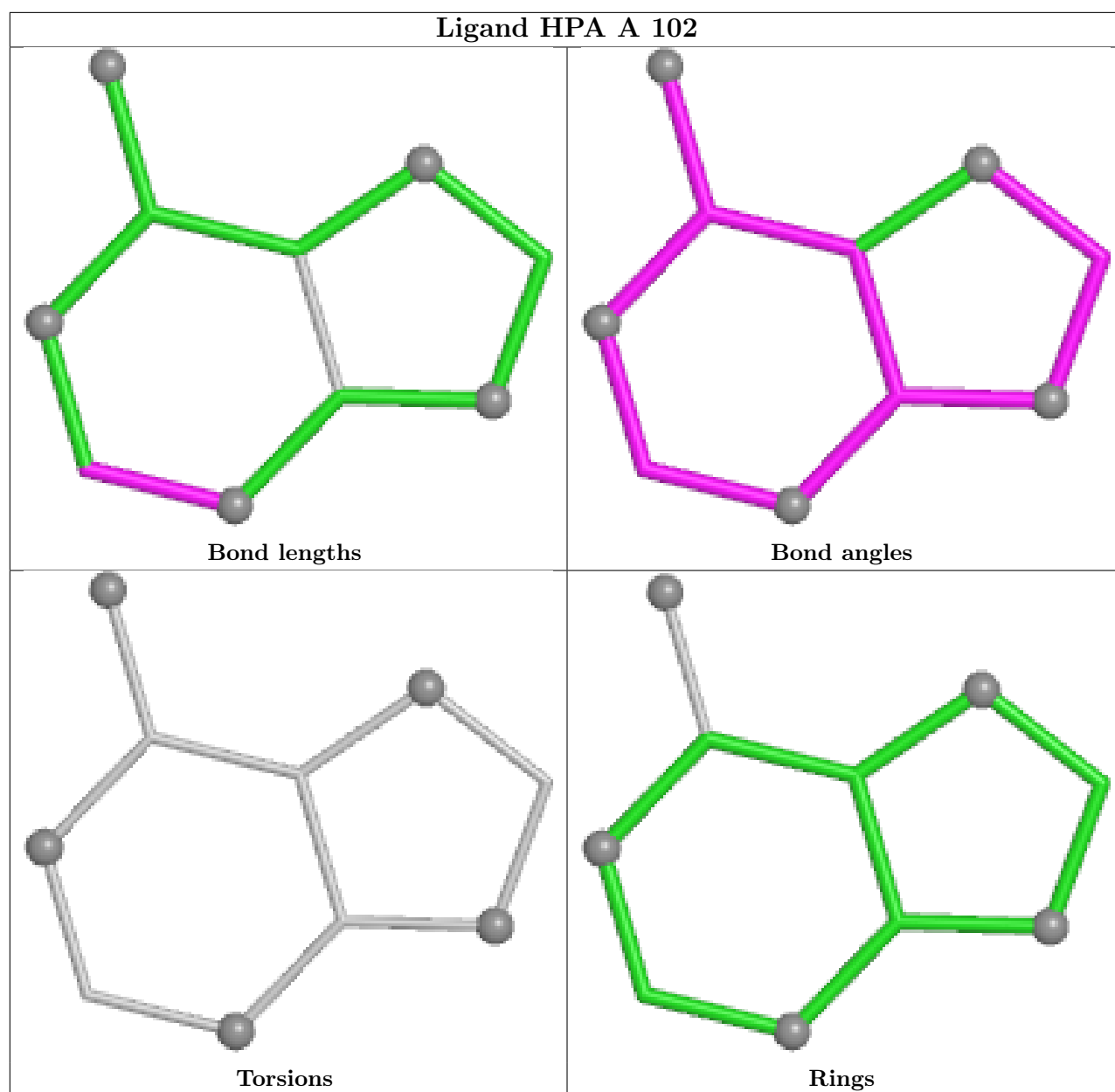


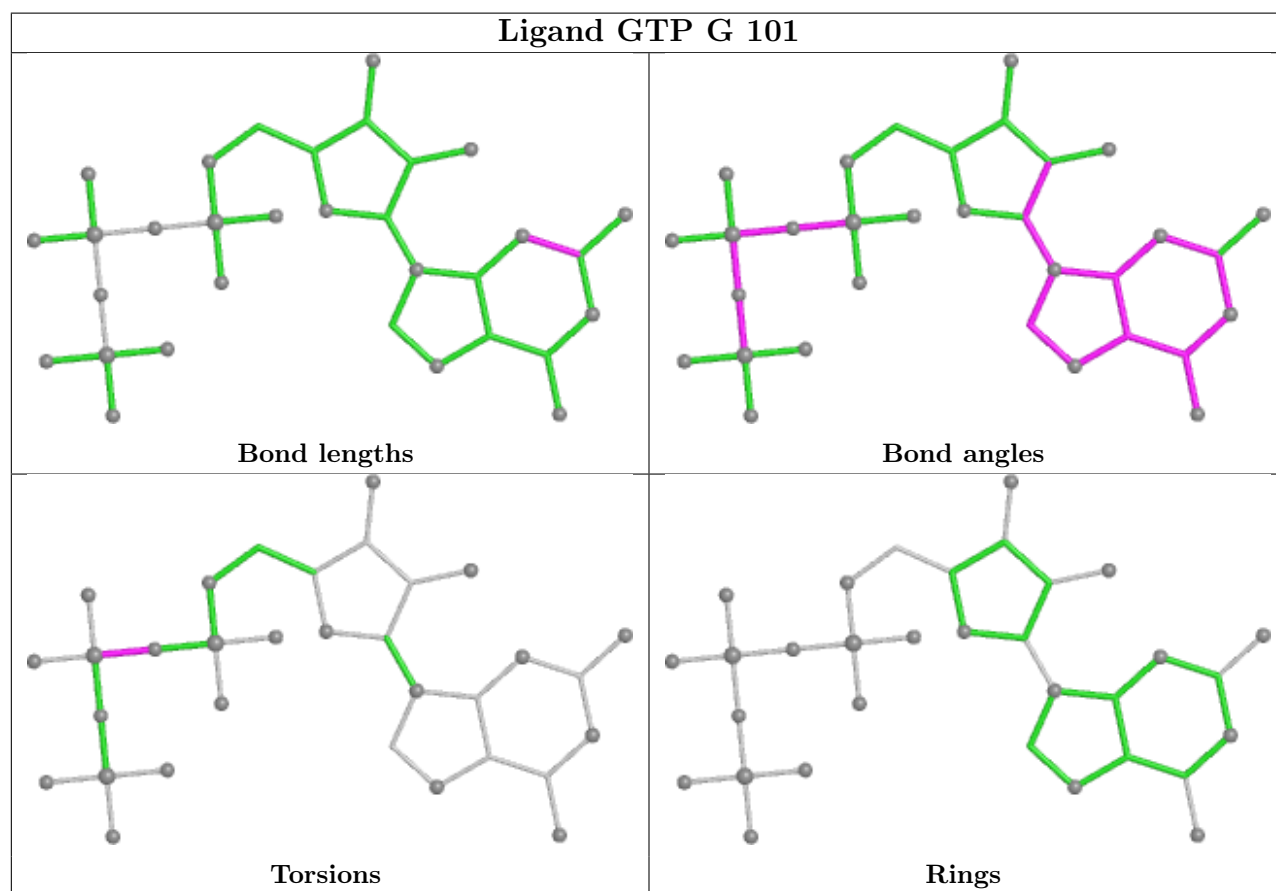
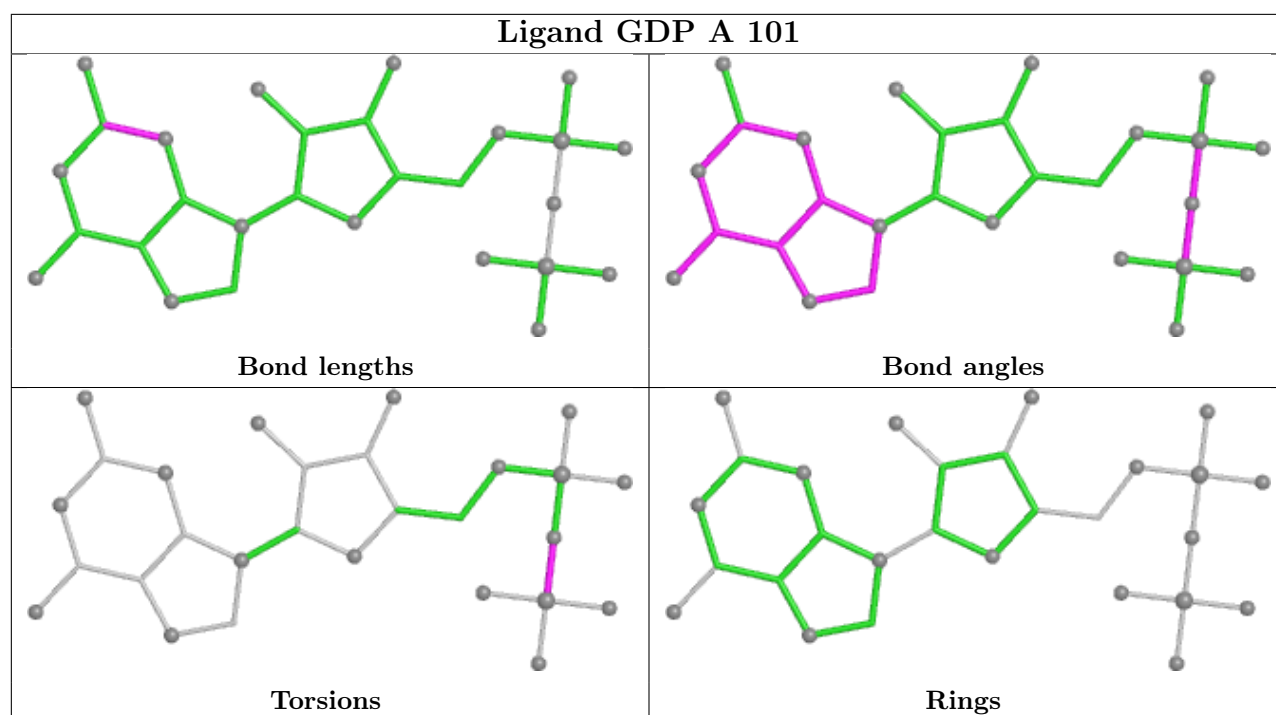


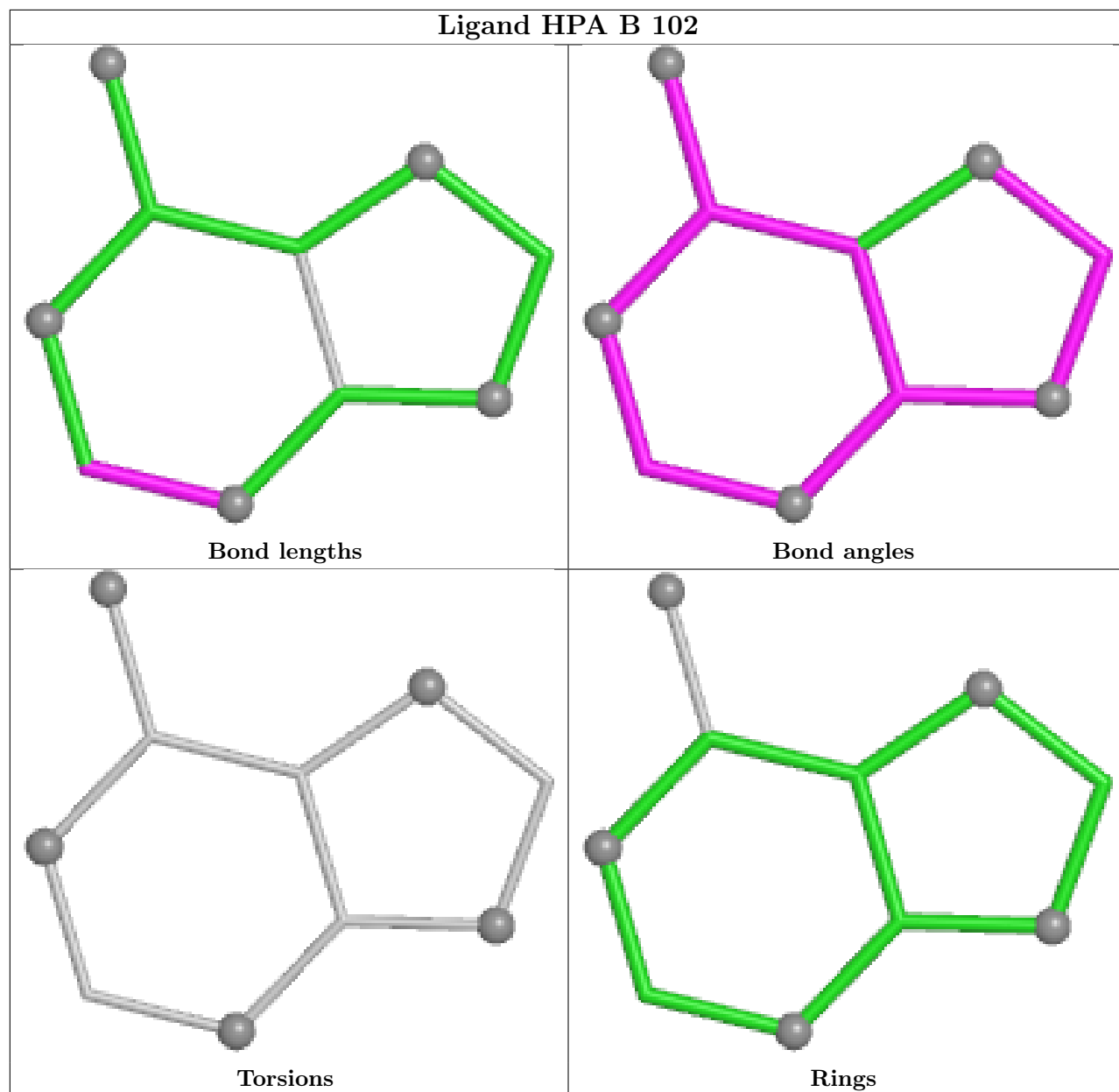
Ligand HPA F 102

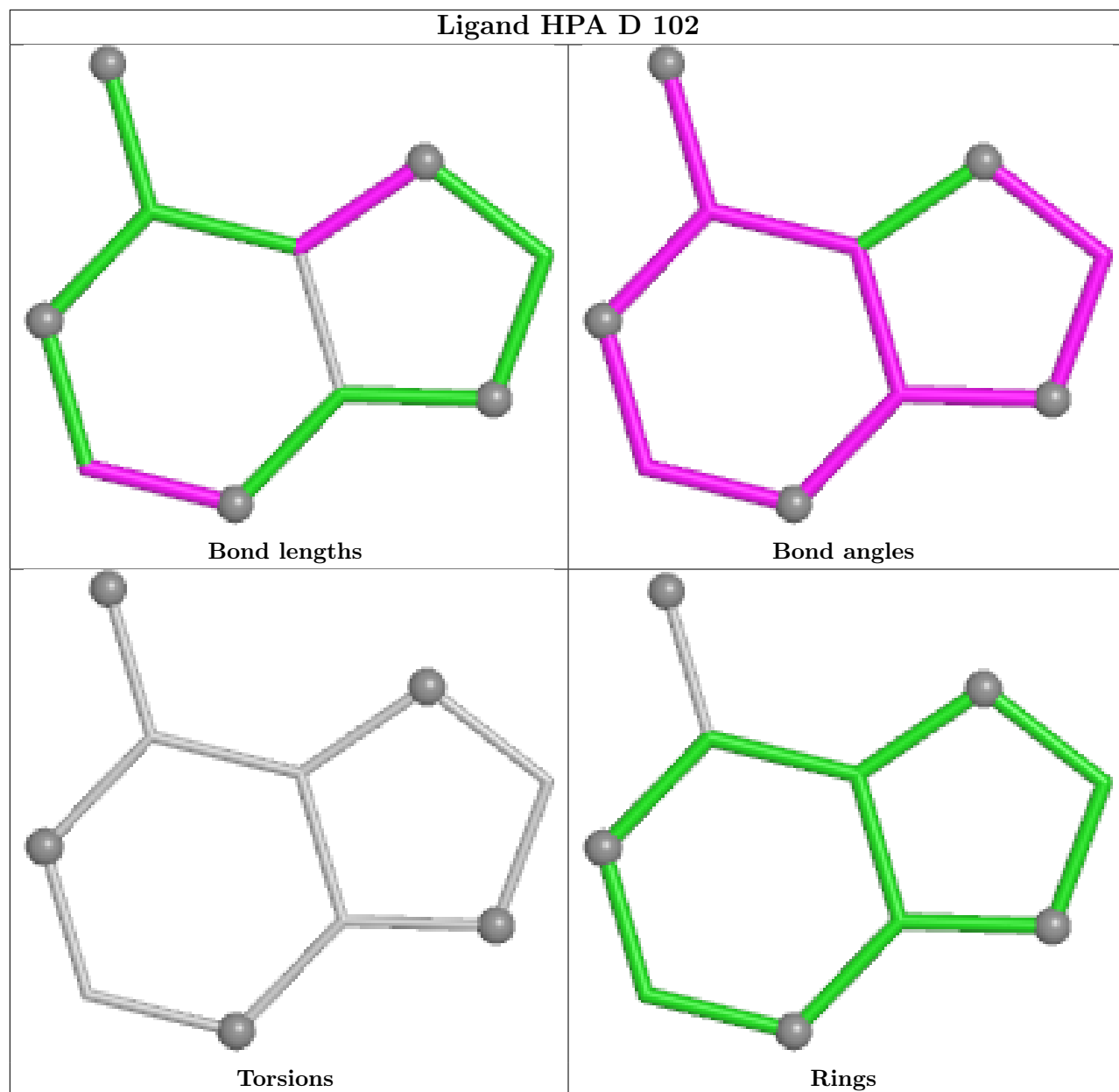


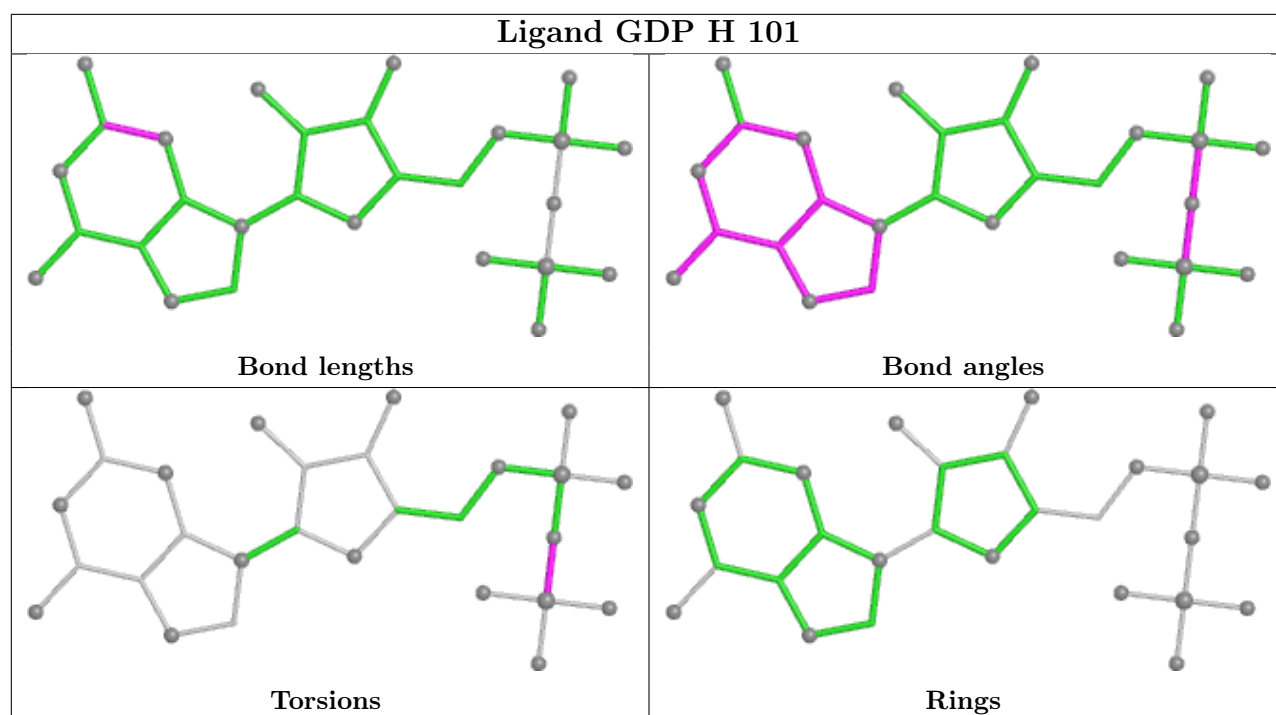












5.7 Other polymers [i](#)

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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	41/42 (97%)	-1.92	0 100 100	26, 50, 58, 73	0
1	B	41/42 (97%)	-1.94	0 100 100	29, 49, 63, 82	0
1	C	41/42 (97%)	-1.90	0 100 100	32, 49, 60, 84	0
1	D	41/42 (97%)	-1.96	0 100 100	30, 49, 63, 83	0
1	E	41/42 (97%)	-1.92	0 100 100	31, 52, 61, 85	0
1	F	41/42 (97%)	-1.90	0 100 100	23, 53, 58, 78	0
1	G	41/42 (97%)	-1.92	0 100 100	29, 51, 60, 79	0
1	H	41/42 (97%)	-1.92	0 100 100	29, 51, 59, 82	0
All	All	328/336 (97%)	-1.92	0 100 100	23, 51, 63, 85	0

There are no RSRZ outliers to report.

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

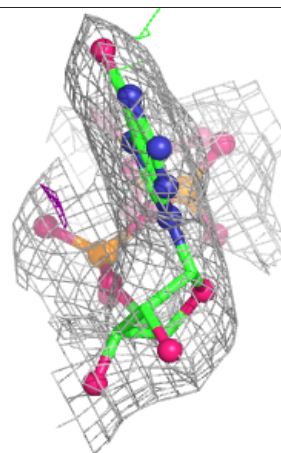
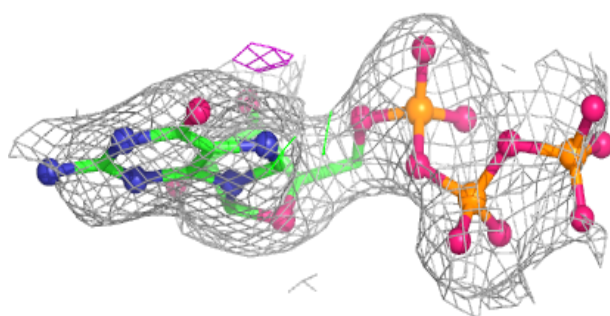
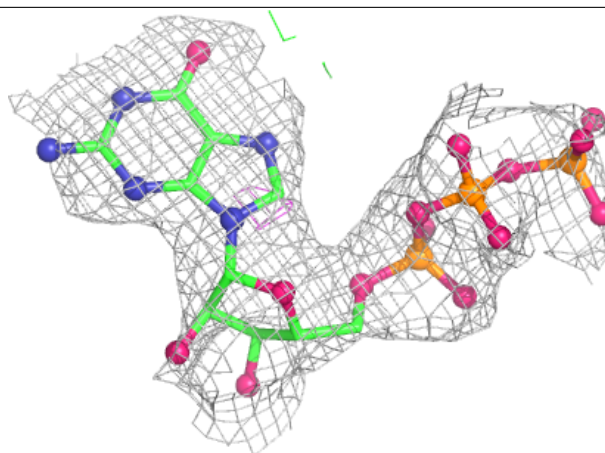
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GTP	B	101	32/32	0.99	0.03	21,33,86,94	0
2	GTP	D	101	32/32	0.99	0.03	26,34,67,76	0
2	GTP	E	101	32/32	0.99	0.03	23,31,65,71	0
2	GTP	G	101	32/32	0.99	0.03	23,34,73,75	0
3	HPA	A	102	10/10	0.99	0.04	40,42,53,53	0
3	HPA	D	102	10/10	0.99	0.06	39,42,52,55	0
3	HPA	C	102	10/10	0.99	0.05	40,44,54,54	0
3	HPA	E	102	10/10	0.99	0.04	39,44,54,59	0
3	HPA	F	102	10/10	0.99	0.04	46,48,58,59	0
3	HPA	G	102	10/10	0.99	0.05	37,39,48,49	0
3	HPA	H	102	10/10	0.99	0.04	48,50,62,62	0
4	GDP	A	101	28/28	0.99	0.03	22,28,57,68	0
4	GDP	C	101	28/28	0.99	0.03	23,35,53,57	0
4	GDP	F	101	28/28	0.99	0.04	21,25,49,54	0
4	GDP	H	101	28/28	0.99	0.03	27,30,47,55	0
5	NA	E	103	1/1	0.99	0.04	26,26,26,26	0
3	HPA	B	102	10/10	1.00	0.05	38,41,49,52	0

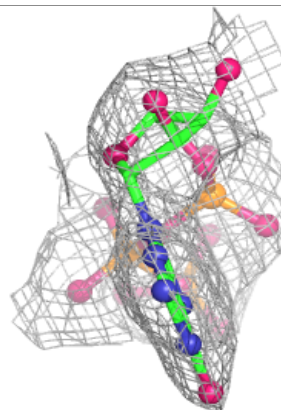
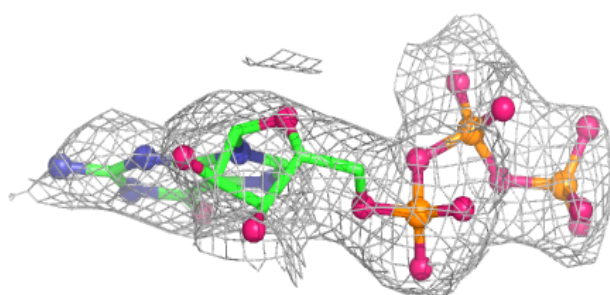
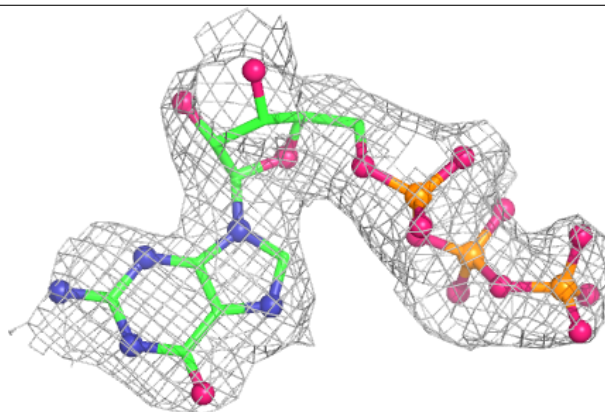
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around GTP B 101:

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

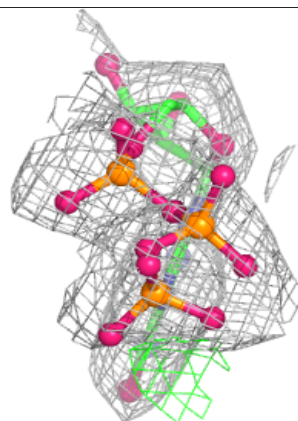
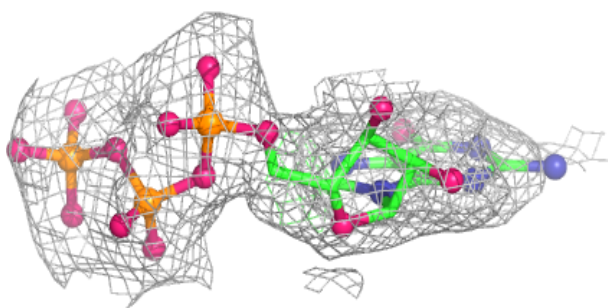
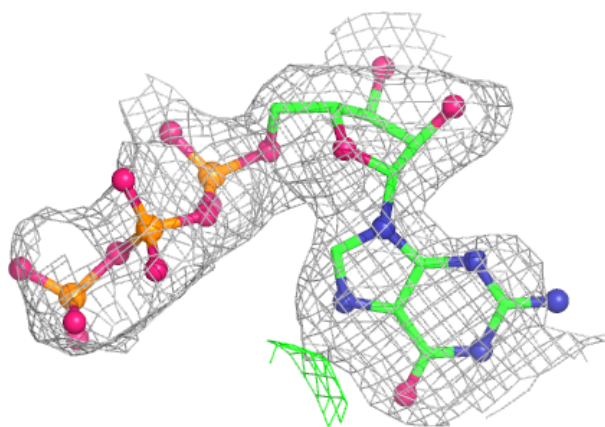
**Electron density around GTP D 101:**

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



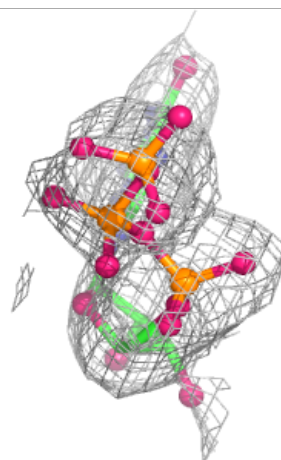
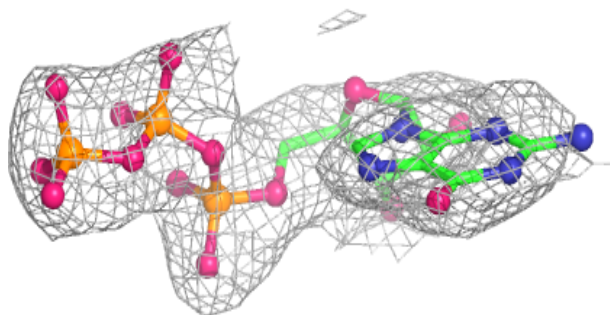
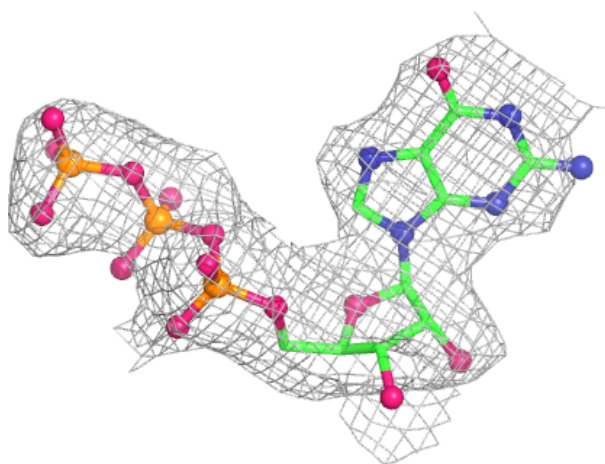
Electron density around GTP E 101:

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



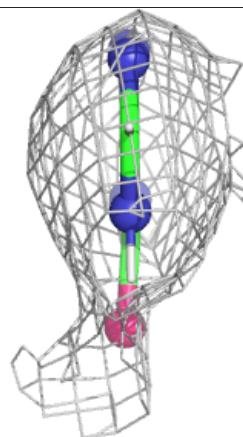
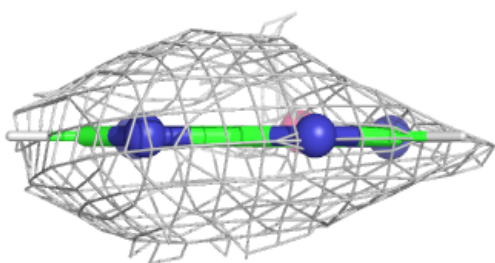
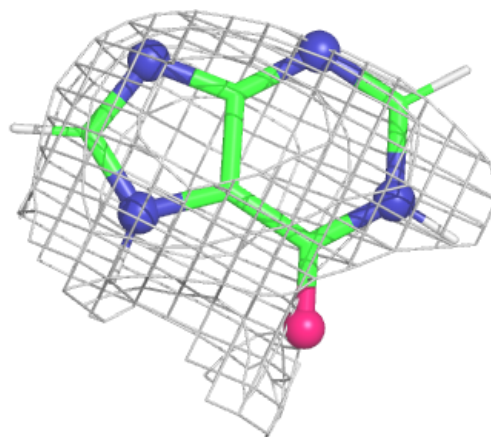
Electron density around GTP G 101:

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



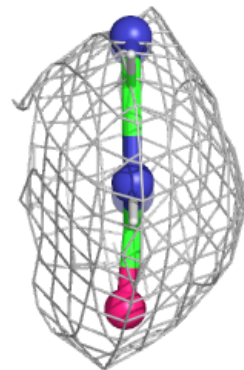
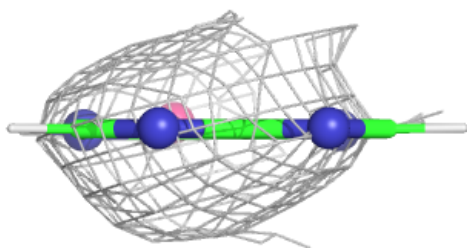
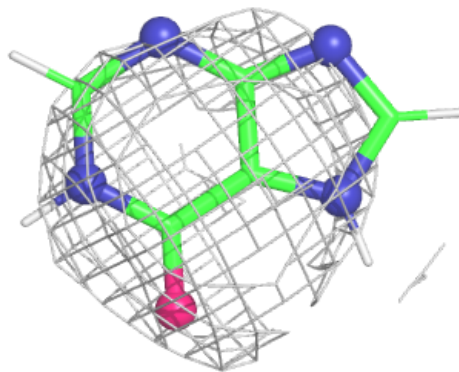
Electron density around HPA A 102:

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

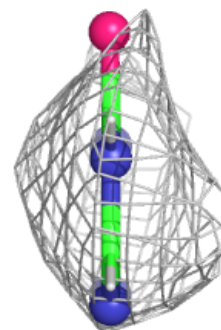
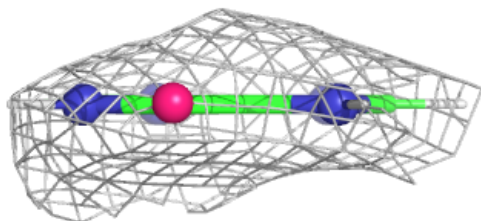
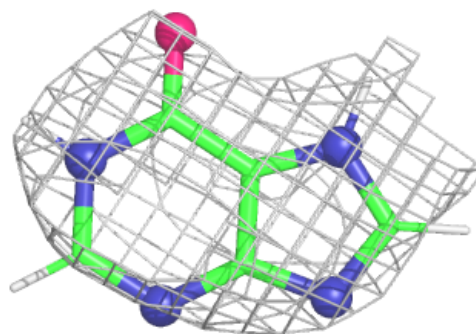


Electron density around HPA D 102:

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

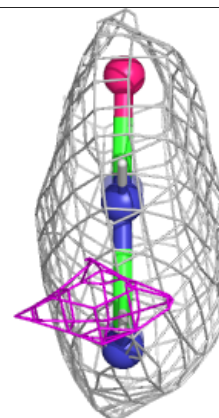
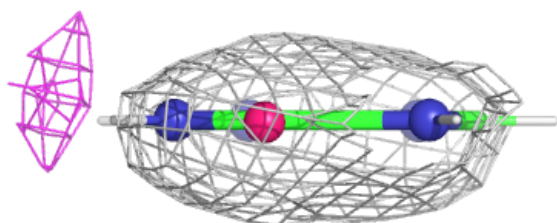
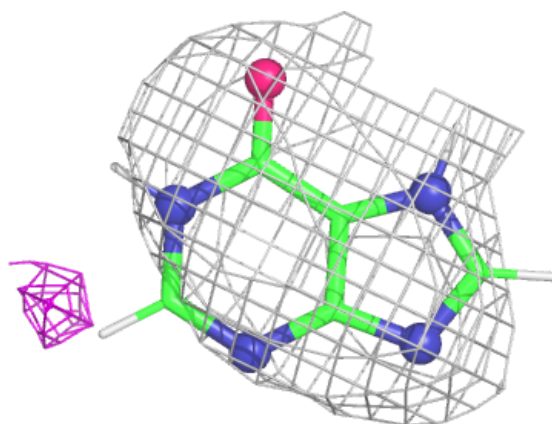
**Electron density around HPA C 102:**

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

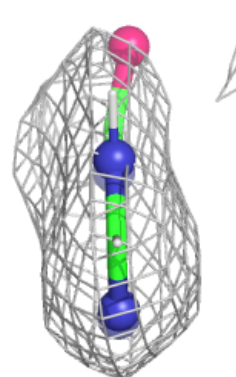
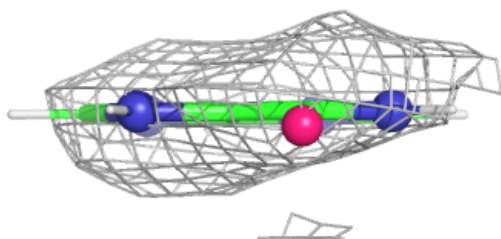
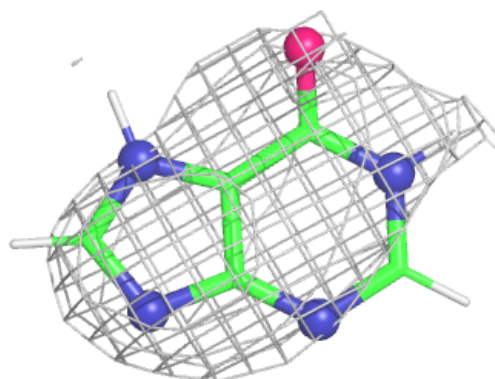


Electron density around HPA E 102:

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

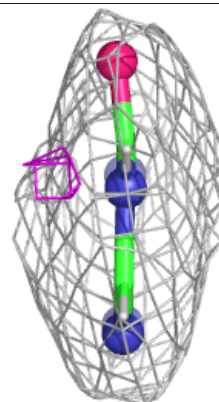
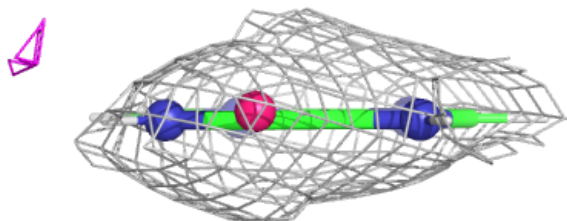
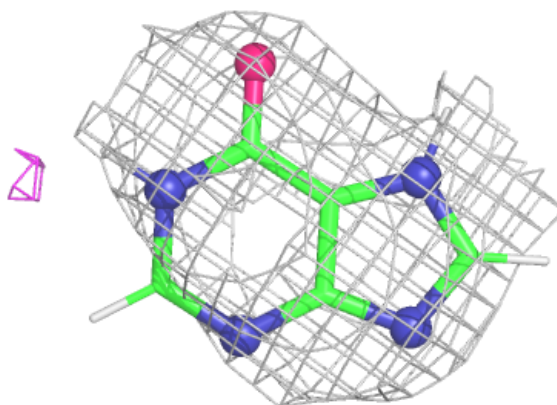
**Electron density around HPA F 102:**

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

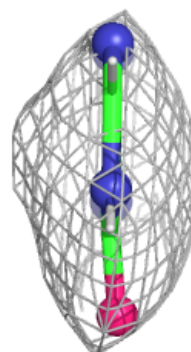
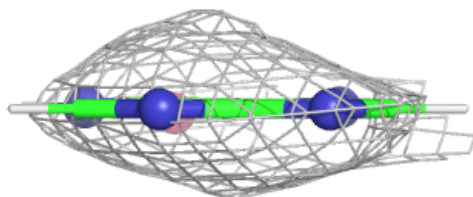
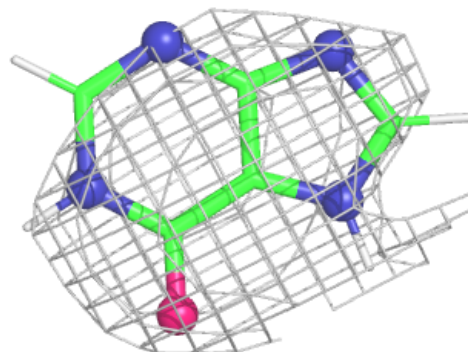


Electron density around HPA G 102:

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

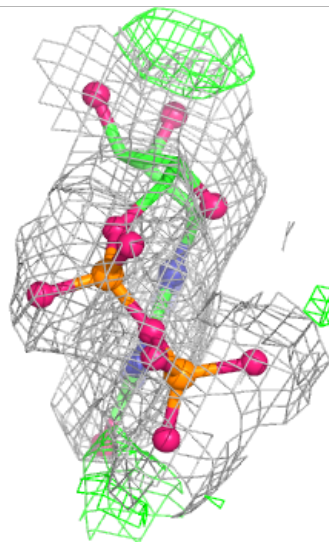
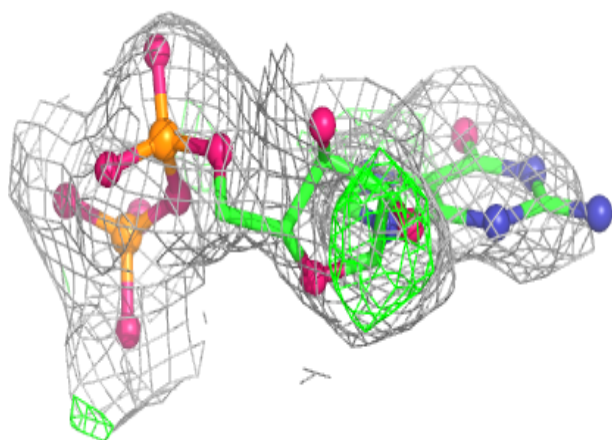
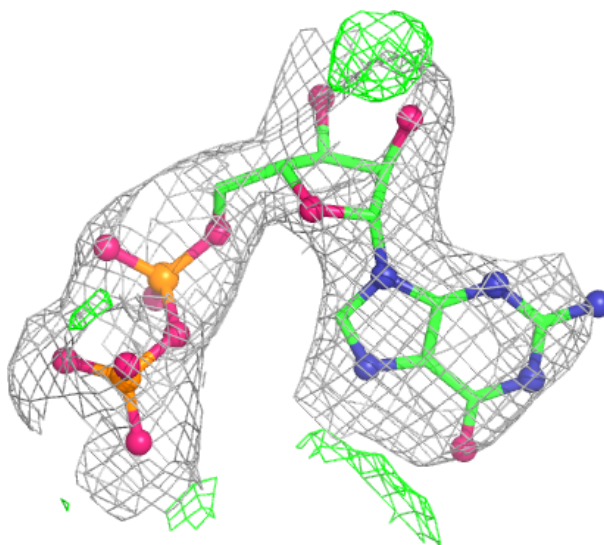
**Electron density around HPA H 102:**

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



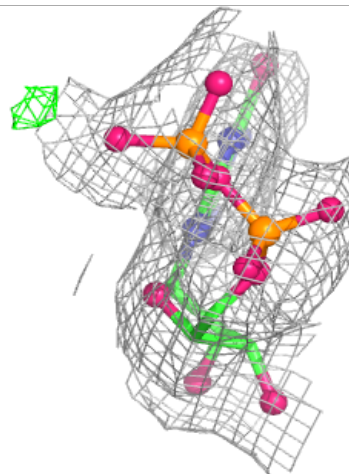
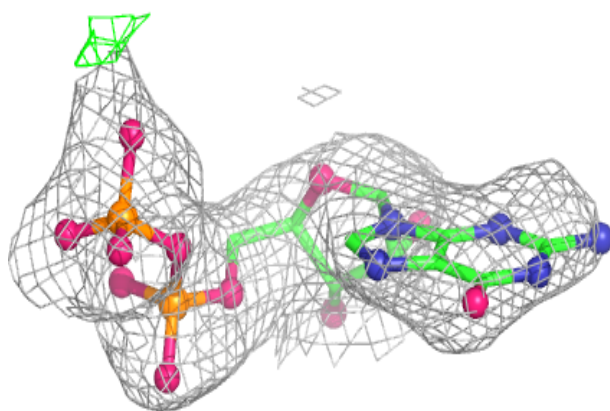
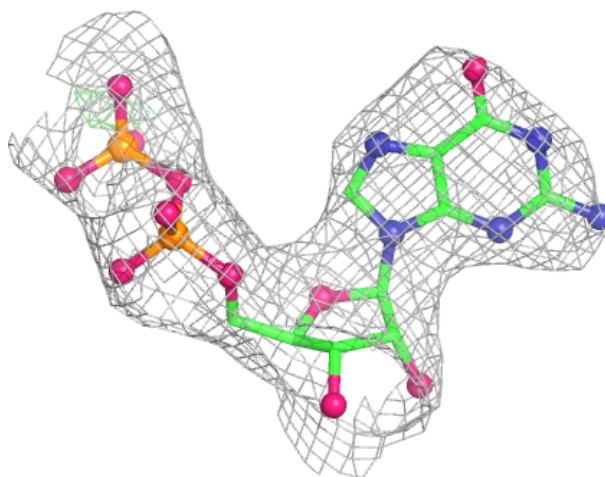
Electron density around GDP A 101:

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



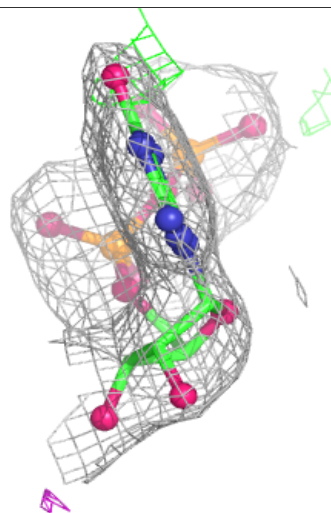
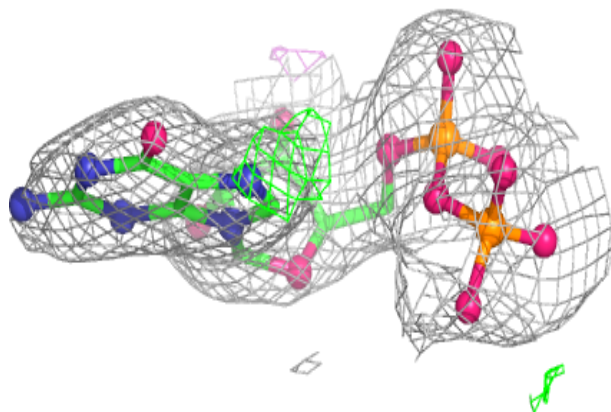
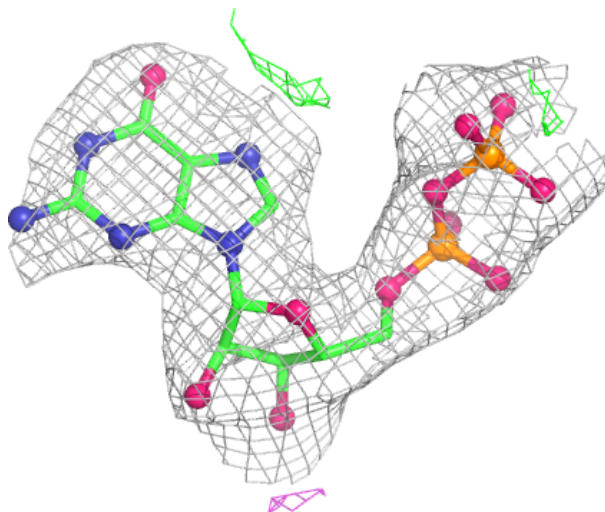
Electron density around GDP C 101:

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



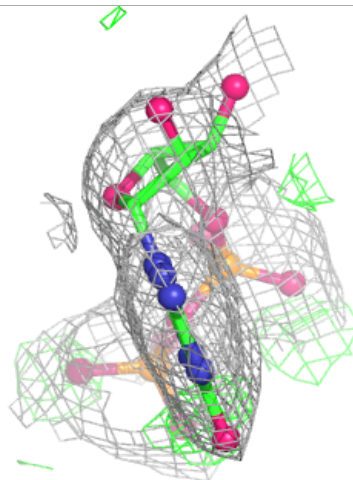
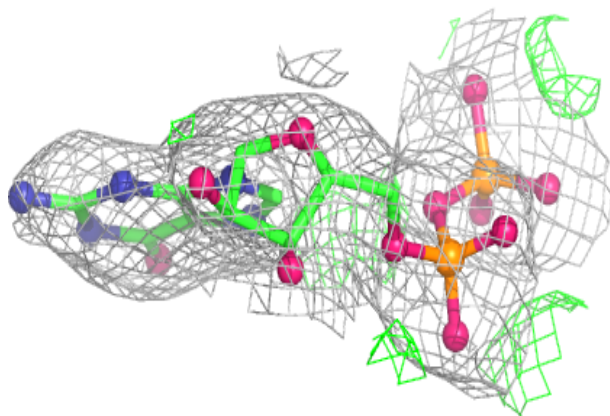
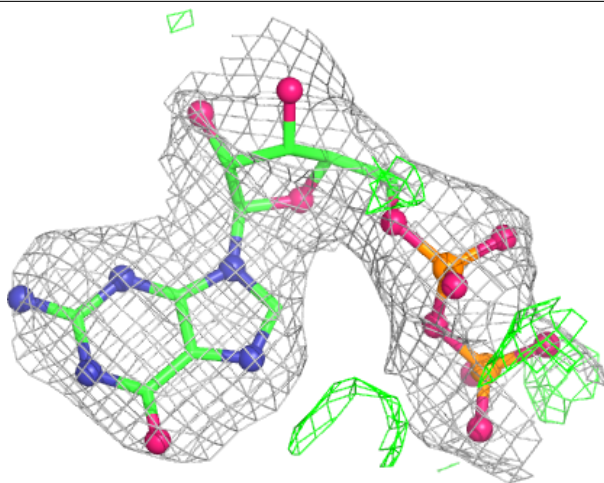
Electron density around GDP F 101:

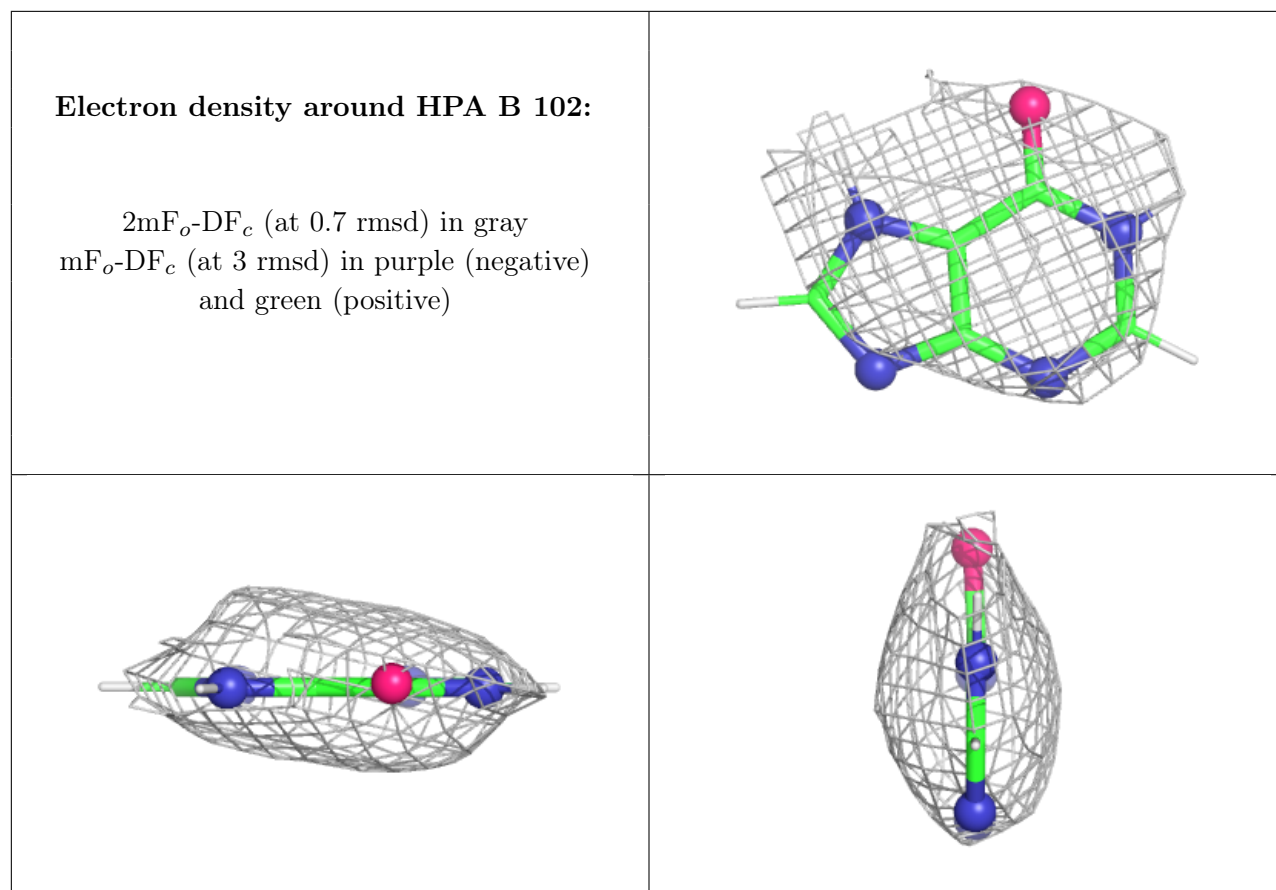
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around GDP H 101:

$2mF_o-DF_c$ (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.