



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 4, 2023 – 02:17 am GMT

PDB ID : 1W5E
Title : FtsZ W319Y mutant, P1 (M. jannaschii)
Authors : Oliva, M.A.; Cordell, S.C.; Lowe, J.
Deposited on : 2004-08-06
Resolution : 3.00 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

<https://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 : **FAILED**
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

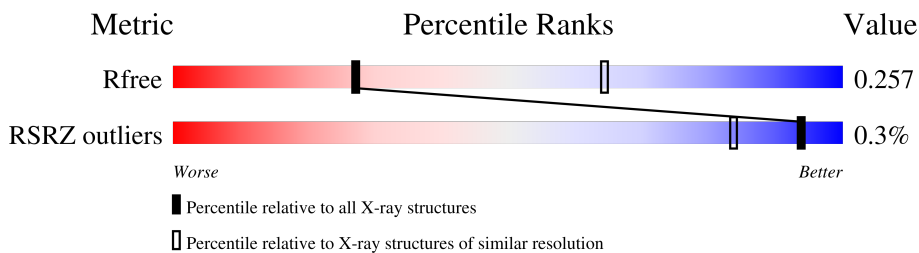
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 23131 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 FTSZ.

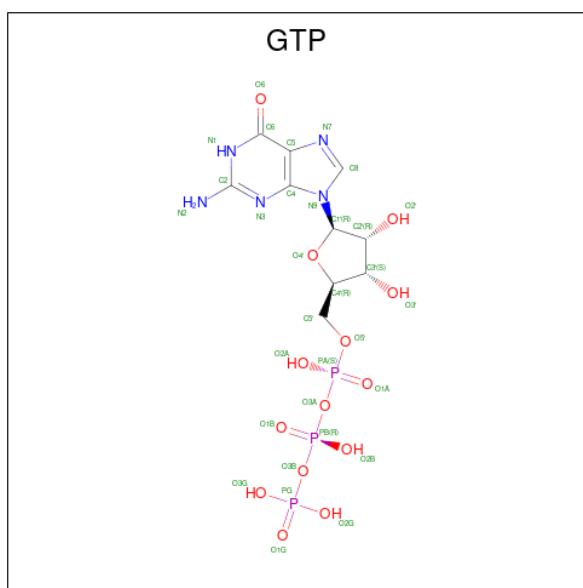
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	332	2460	1544	419	485	12	0	0	0
1	B	333	2469	1550	421	486	12	0	0	0
1	C	332	2460	1544	419	485	12	0	0	0
1	D	332	2460	1544	419	485	12	0	0	0
1	E	333	2469	1550	421	486	12	0	0	0
1	F	332	2460	1544	419	485	12	0	0	0
1	G	332	2460	1544	419	485	12	0	0	0
1	H	333	2469	1550	421	486	12	0	0	0
1	I	332	2460	1544	419	485	12	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	319	TYR	TRP	engineered mutation	UNP Q57816
B	319	TYR	TRP	engineered mutation	UNP Q57816
C	319	TYR	TRP	engineered mutation	UNP Q57816
D	319	TYR	TRP	engineered mutation	UNP Q57816
E	319	TYR	TRP	engineered mutation	UNP Q57816
F	319	TYR	TRP	engineered mutation	UNP Q57816
G	319	TYR	TRP	engineered mutation	UNP Q57816
H	319	TYR	TRP	engineered mutation	UNP Q57816
I	319	TYR	TRP	engineered mutation	UNP Q57816

- Molecule 2 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula:

C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
2	B	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
2	C	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
2	D	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
2	E	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
2	F	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
2	G	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
2	H	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
2	I	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	76	Total	O	0	0
			76	76		
3	B	46	Total	O	0	0
			46	46		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	88	Total 88	O 88	0	0
3	D	81	Total 81	O 81	0	0
3	E	52	Total 52	O 52	0	0
3	F	87	Total 87	O 87	0	0
3	G	80	Total 80	O 80	0	0
3	H	60	Total 60	O 60	0	0
3	I	106	Total 106	O 106	0	0

MolProbity failed to run properly - this section is therefore empty.

3 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	113.95Å 114.33Å 115.14Å 90.07° 90.19° 119.86°	Depositor
Resolution (Å)	50.00 – 3.00 115.13 – 3.00	Depositor EDS
% Data completeness (in resolution range)	94.7 (50.00-3.00) 92.8 (115.13-3.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.35 (at 3.01Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.264 , 0.298 0.258 , 0.257	Depositor DCC
R_{free} test set	5036 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	50.2	Xtrriage
Anisotropy	0.368	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 28.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.25$	Xtrriage
Estimated twinning fraction	0.000 for h+k,-h,l 0.000 for -k,h+k,l 0.398 for k,-h-k,l 0.398 for -h-k,h,l 0.034 for h,-h-k,-l 0.035 for -h-k,k,-l 0.000 for -h,-k,l 0.034 for k,h,-l 0.000 for -k,-h,-l 0.000 for -h,h+k,-l 0.000 for h+k,-k,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	23131	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 75.53 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2420e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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.

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

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

4.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

4.6 Ligand geometry [i](#)

9 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
2	GTP	C	500	-	26,34,34	1.20	4 (15%)	32,54,54	0.88	1 (3%)
2	GTP	H	500	-	26,34,34	1.01	2 (7%)	32,54,54	1.00	1 (3%)
2	GTP	I	500	-	26,34,34	1.13	3 (11%)	32,54,54	0.90	1 (3%)
2	GTP	A	500	-	26,34,34	1.16	3 (11%)	32,54,54	0.90	1 (3%)
2	GTP	G	500	-	26,34,34	1.04	2 (7%)	32,54,54	1.04	1 (3%)
2	GTP	F	500	-	26,34,34	1.13	2 (7%)	32,54,54	0.93	1 (3%)
2	GTP	B	500	-	26,34,34	1.19	3 (11%)	32,54,54	0.94	1 (3%)
2	GTP	E	500	-	26,34,34	1.12	2 (7%)	32,54,54	1.00	1 (3%)
2	GTP	D	500	-	26,34,34	1.08	2 (7%)	32,54,54	0.95	1 (3%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GTP	C	500	-	-	4/18/38/38	0/3/3/3
2	GTP	H	500	-	-	4/18/38/38	0/3/3/3
2	GTP	I	500	-	-	3/18/38/38	0/3/3/3
2	GTP	A	500	-	-	5/18/38/38	0/3/3/3
2	GTP	G	500	-	-	7/18/38/38	0/3/3/3
2	GTP	F	500	-	-	5/18/38/38	0/3/3/3
2	GTP	B	500	-	-	3/18/38/38	0/3/3/3
2	GTP	E	500	-	-	6/18/38/38	0/3/3/3
2	GTP	D	500	-	-	7/18/38/38	0/3/3/3

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	500	GTP	C5-C6	-3.18	1.40	1.47
2	A	500	GTP	C6-N1	3.16	1.42	1.37
2	D	500	GTP	C6-N1	3.16	1.42	1.37
2	C	500	GTP	C5-C6	-3.15	1.41	1.47
2	B	500	GTP	C5-C6	-3.05	1.41	1.47

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	500	GTP	O2G-PG-O3B	2.83	114.13	104.64
2	C	500	GTP	O2G-PG-O3B	2.52	113.08	104.64
2	B	500	GTP	O2G-PG-O3B	2.50	113.01	104.64
2	G	500	GTP	O2G-PG-O3B	2.48	112.96	104.64
2	A	500	GTP	O2G-PG-O3B	2.45	112.85	104.64

There are no chirality outliers.

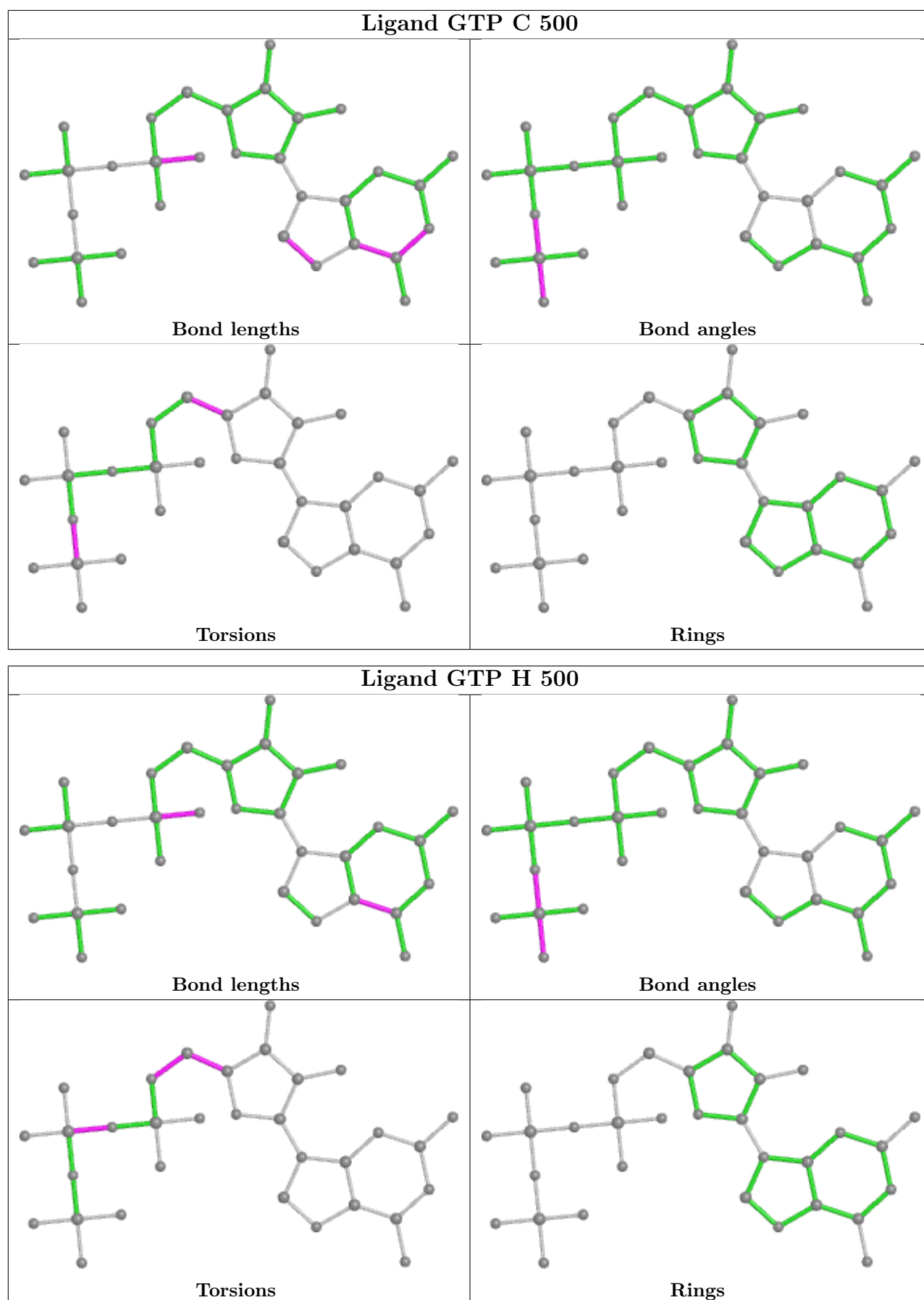
5 of 44 torsion outliers are listed below:

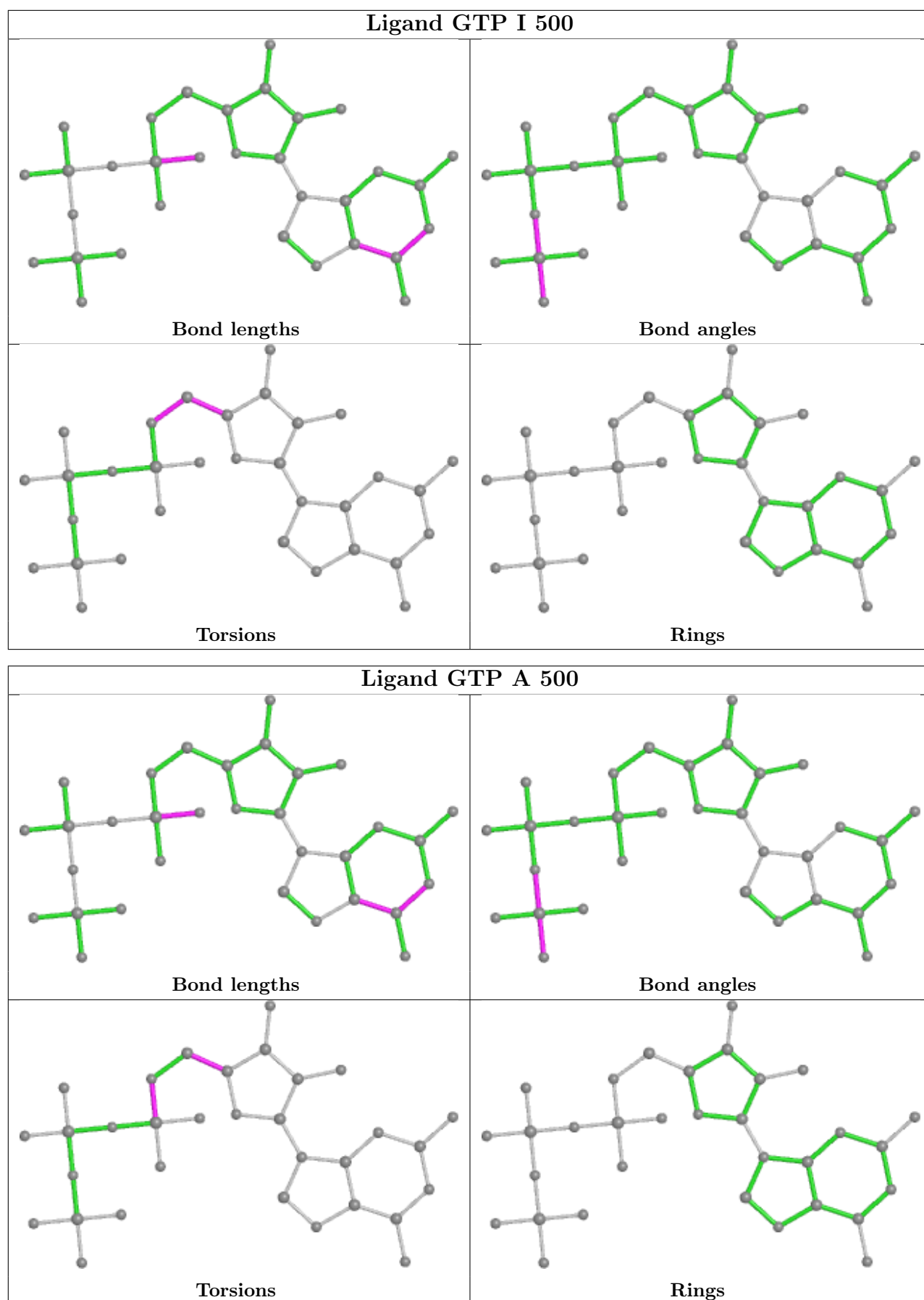
Mol	Chain	Res	Type	Atoms
2	A	500	GTP	C5'-O5'-PA-O1A
2	A	500	GTP	O4'-C4'-C5'-O5'
2	B	500	GTP	O4'-C4'-C5'-O5'
2	B	500	GTP	C3'-C4'-C5'-O5'
2	C	500	GTP	PB-O3B-PG-O3G

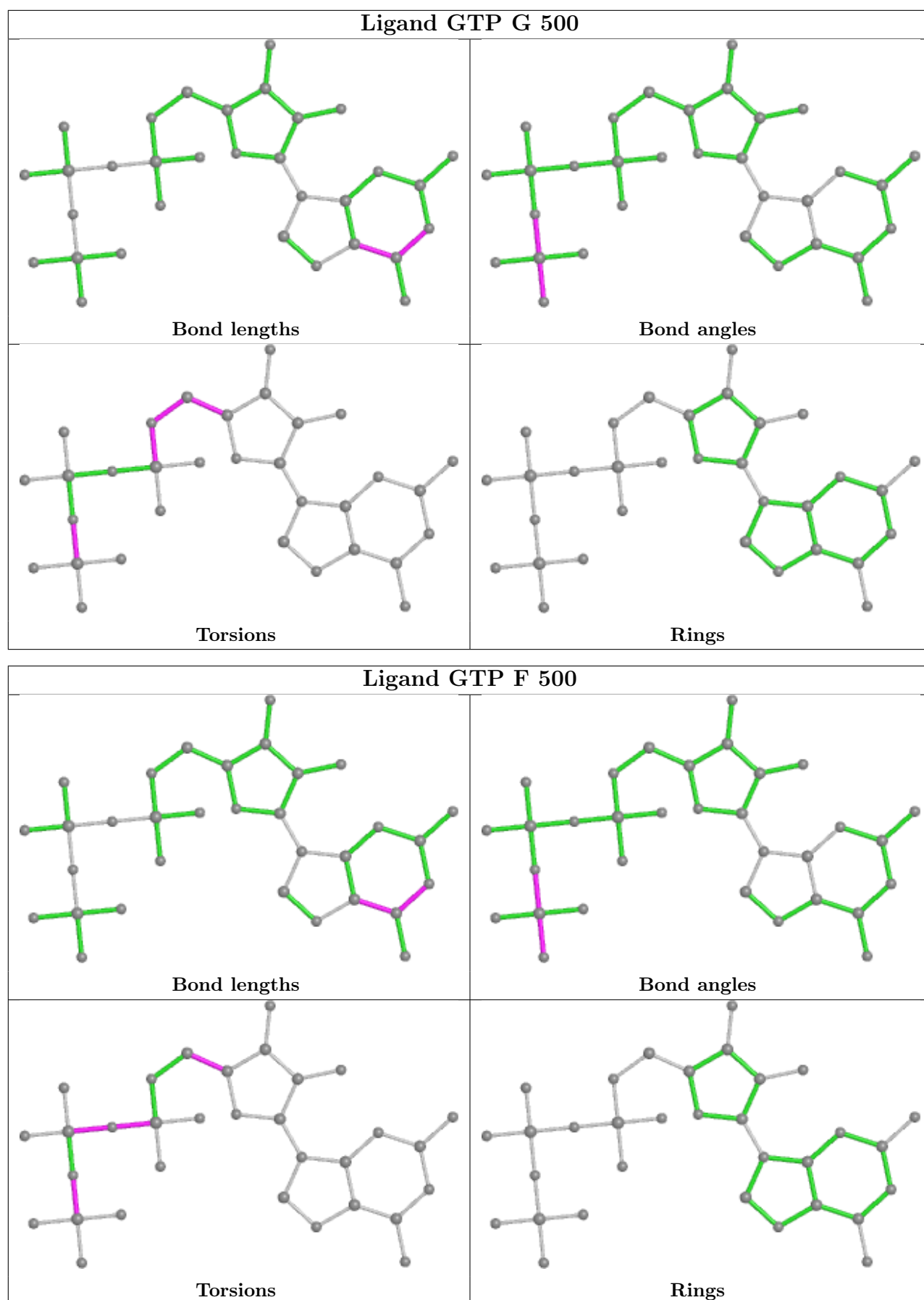
There are no ring outliers.

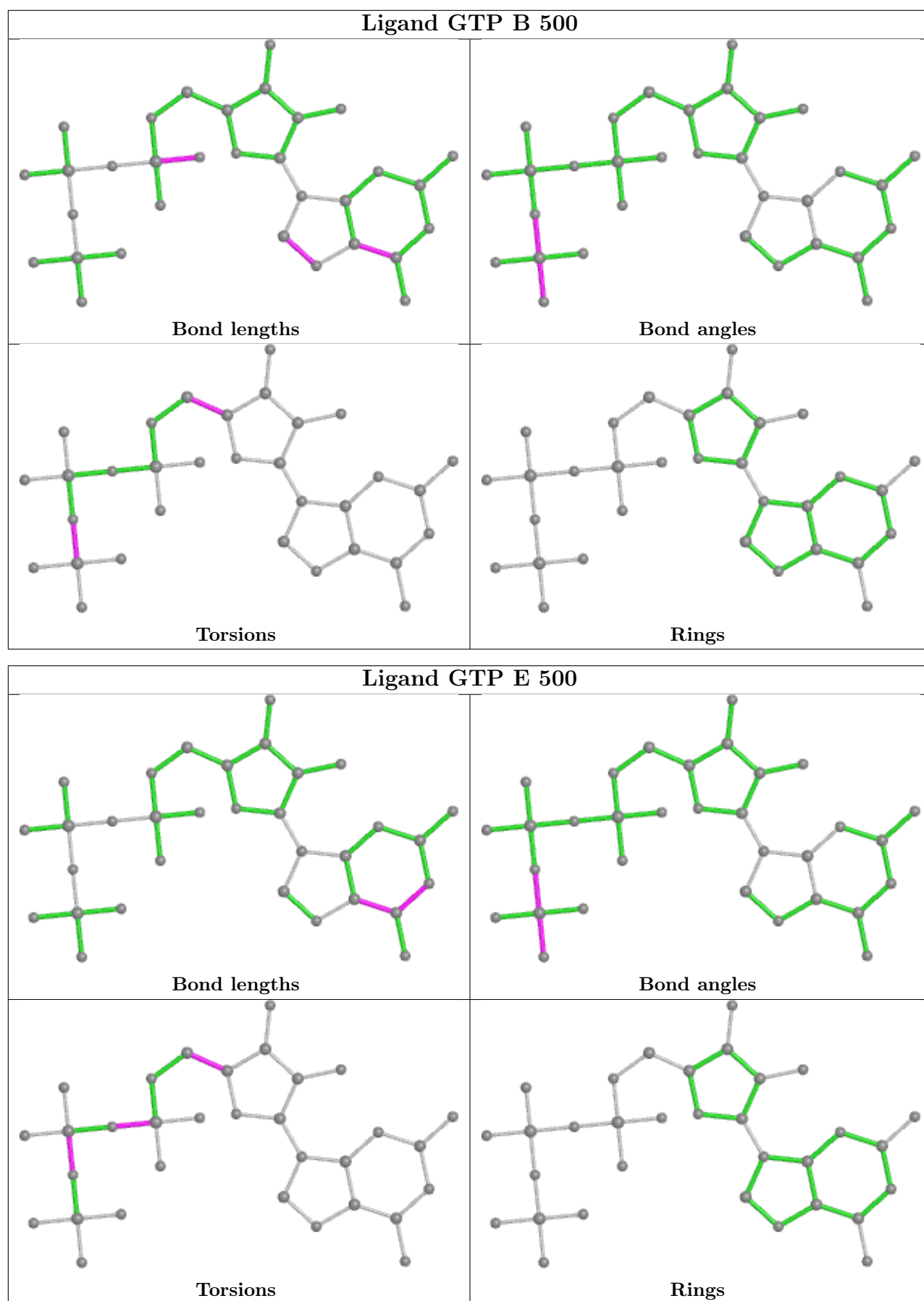
No monomer is involved in short contacts.

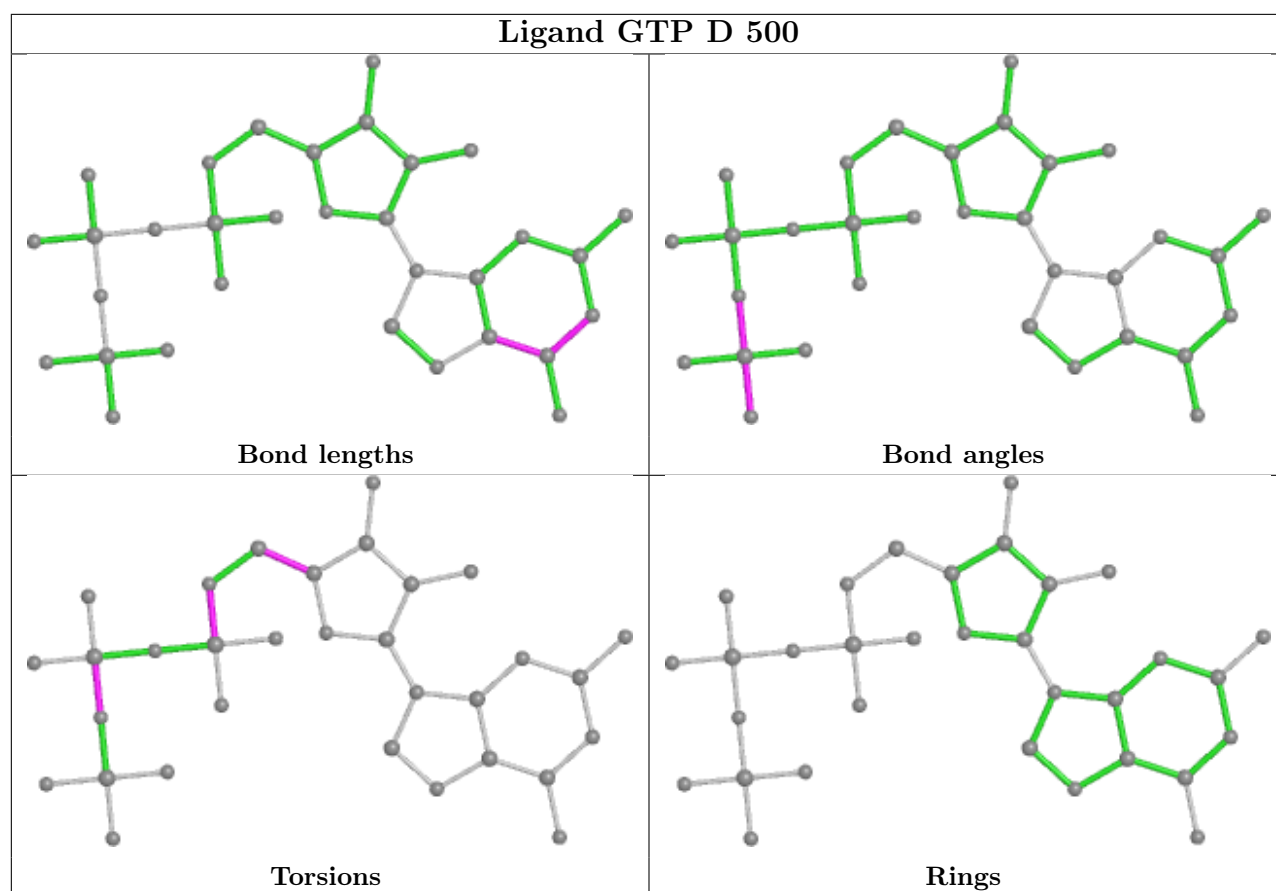
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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











4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

5.1 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	332/364 (91%)	-0.21	2 (0%) 89 72	17, 52, 82, 101	0
1	B	333/364 (91%)	-0.47	0 100 100	9, 33, 68, 99	0
1	C	332/364 (91%)	-0.21	2 (0%) 89 72	20, 52, 89, 125	0
1	D	332/364 (91%)	-0.20	2 (0%) 89 72	20, 52, 81, 102	0
1	E	333/364 (91%)	-0.47	0 100 100	10, 32, 70, 96	0
1	F	332/364 (91%)	-0.18	2 (0%) 89 72	20, 52, 89, 133	0
1	G	332/364 (91%)	-0.27	0 100 100	19, 51, 83, 103	0
1	H	333/364 (91%)	-0.49	0 100 100	9, 33, 71, 95	0
1	I	332/364 (91%)	-0.26	1 (0%) 94 84	20, 52, 87, 136	0
All	All	2991/3276 (91%)	-0.31	9 (0%) 94 84	9, 47, 82, 136	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	69	ILE	2.9
1	C	119	ILE	2.7
1	D	69	ILE	2.6
1	F	119	ILE	2.6
1	C	352	LYS	2.2

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

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

5.3 Carbohydrates [i](#)

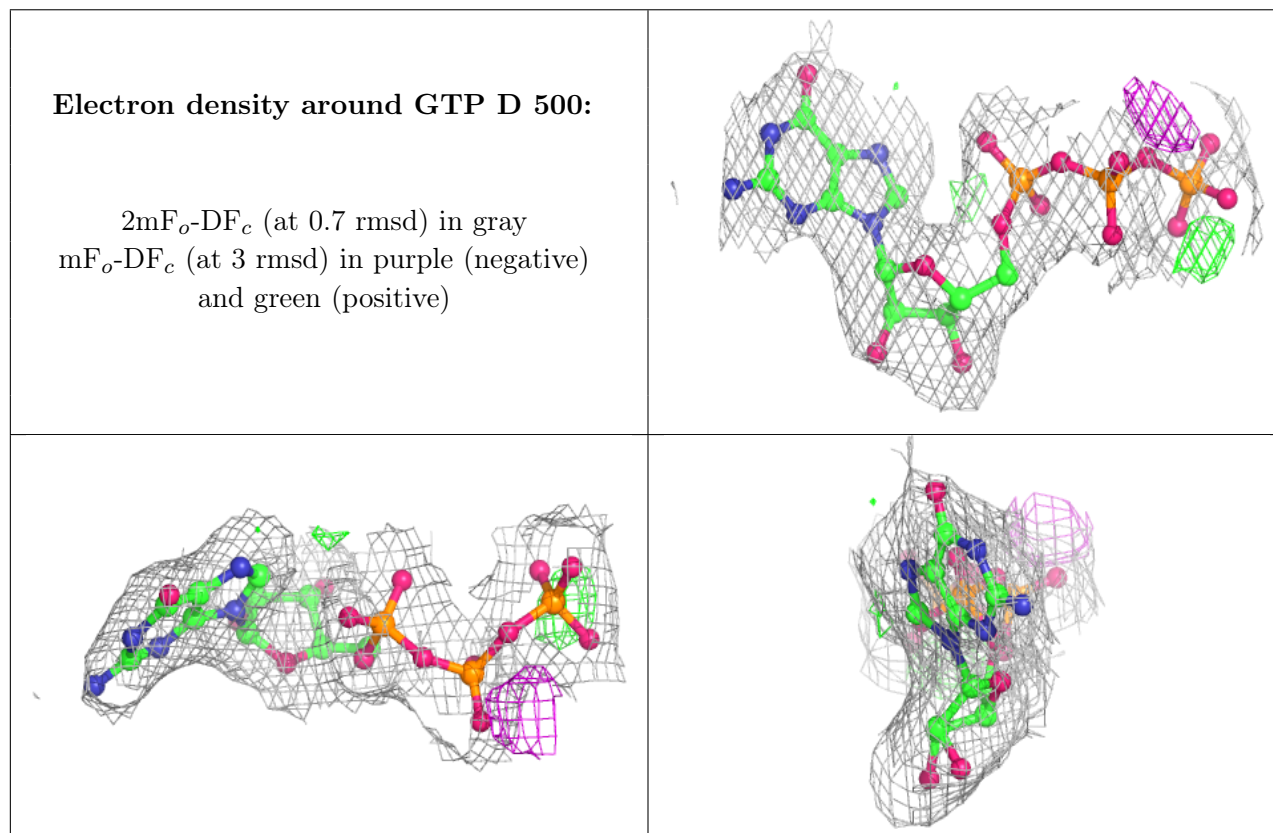
There are no monosaccharides in this entry.

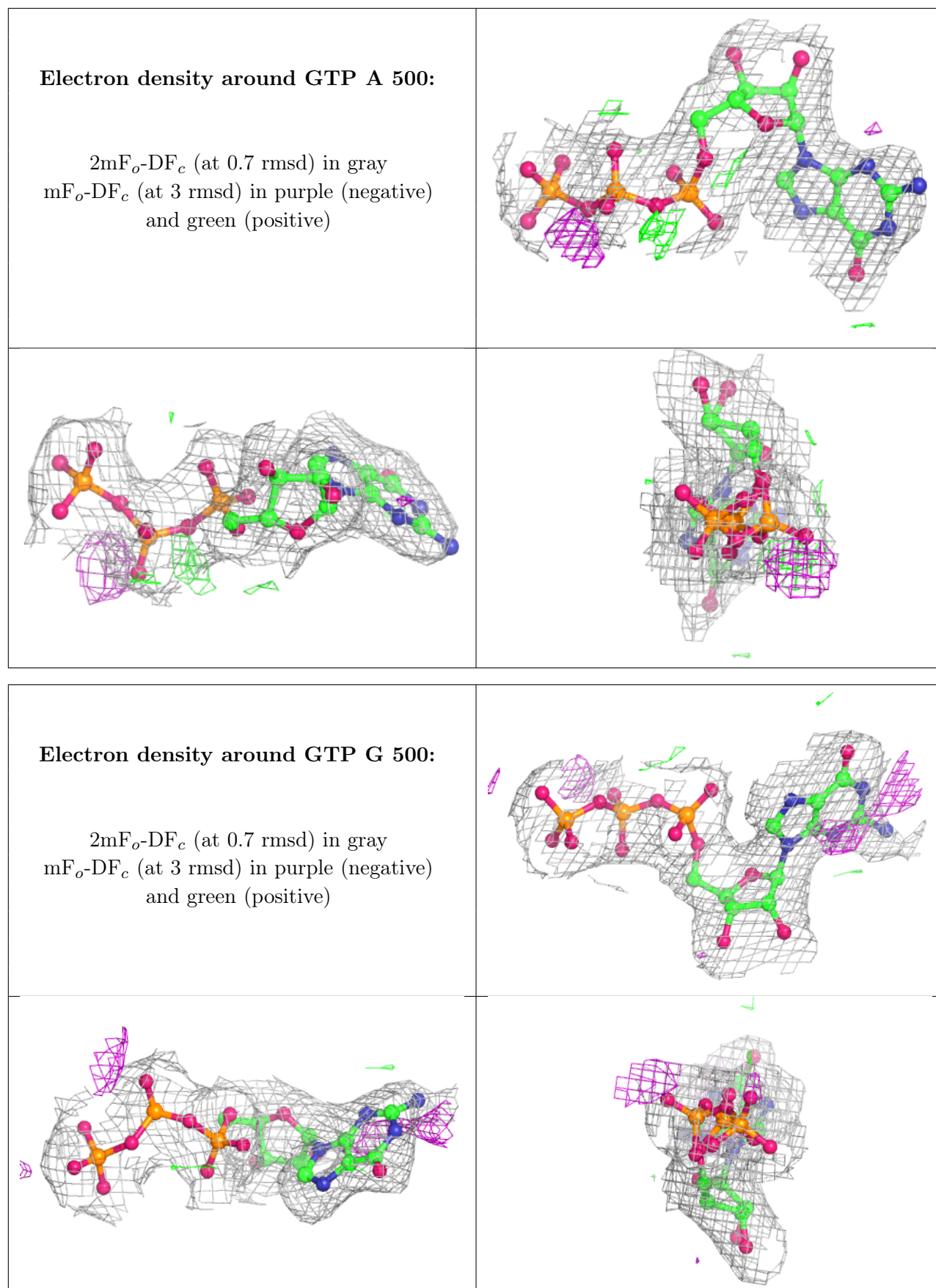
5.4 Ligands [i](#)

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(Å ²)	Q<0.9
2	GTP	D	500	32/32	0.94	0.17	21,48,64,67	0
2	GTP	A	500	32/32	0.95	0.18	29,51,64,71	0
2	GTP	G	500	32/32	0.95	0.17	12,49,58,65	0
2	GTP	F	500	32/32	0.96	0.17	34,50,61,65	0
2	GTP	E	500	32/32	0.97	0.17	5,28,39,46	0
2	GTP	C	500	32/32	0.97	0.17	43,51,65,67	0
2	GTP	B	500	32/32	0.97	0.18	20,33,46,49	0
2	GTP	I	500	32/32	0.97	0.16	35,46,57,64	0
2	GTP	H	500	32/32	0.98	0.18	13,25,42,45	0

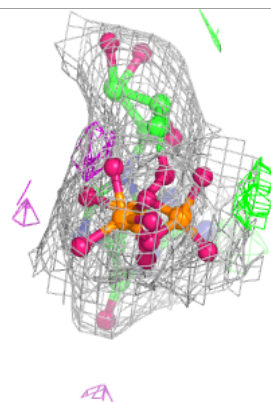
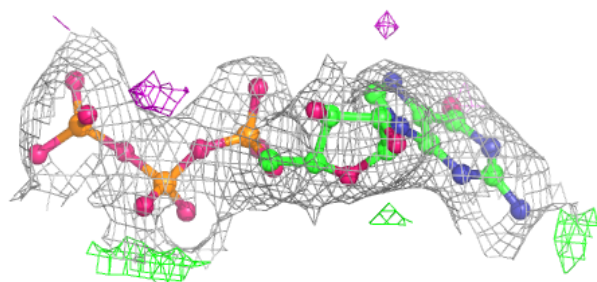
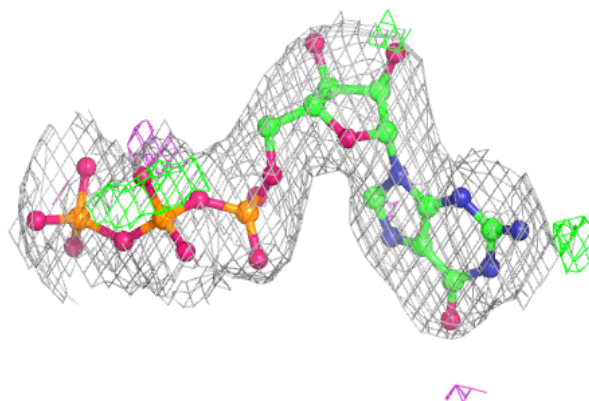
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



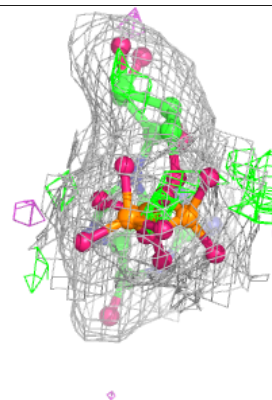
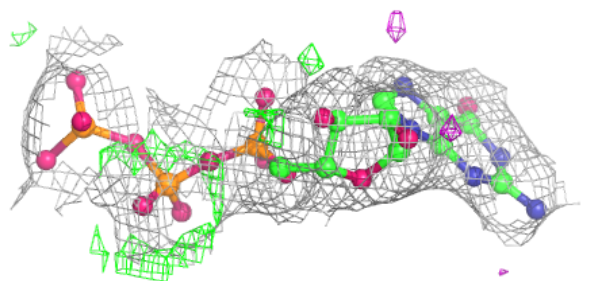
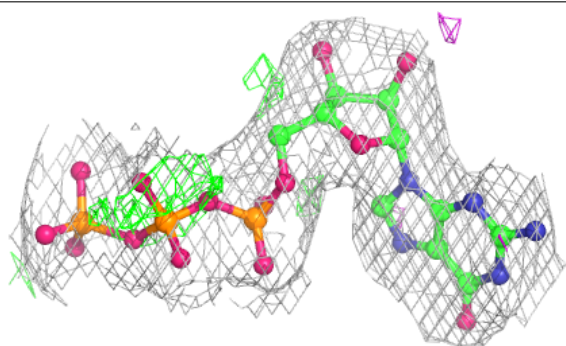


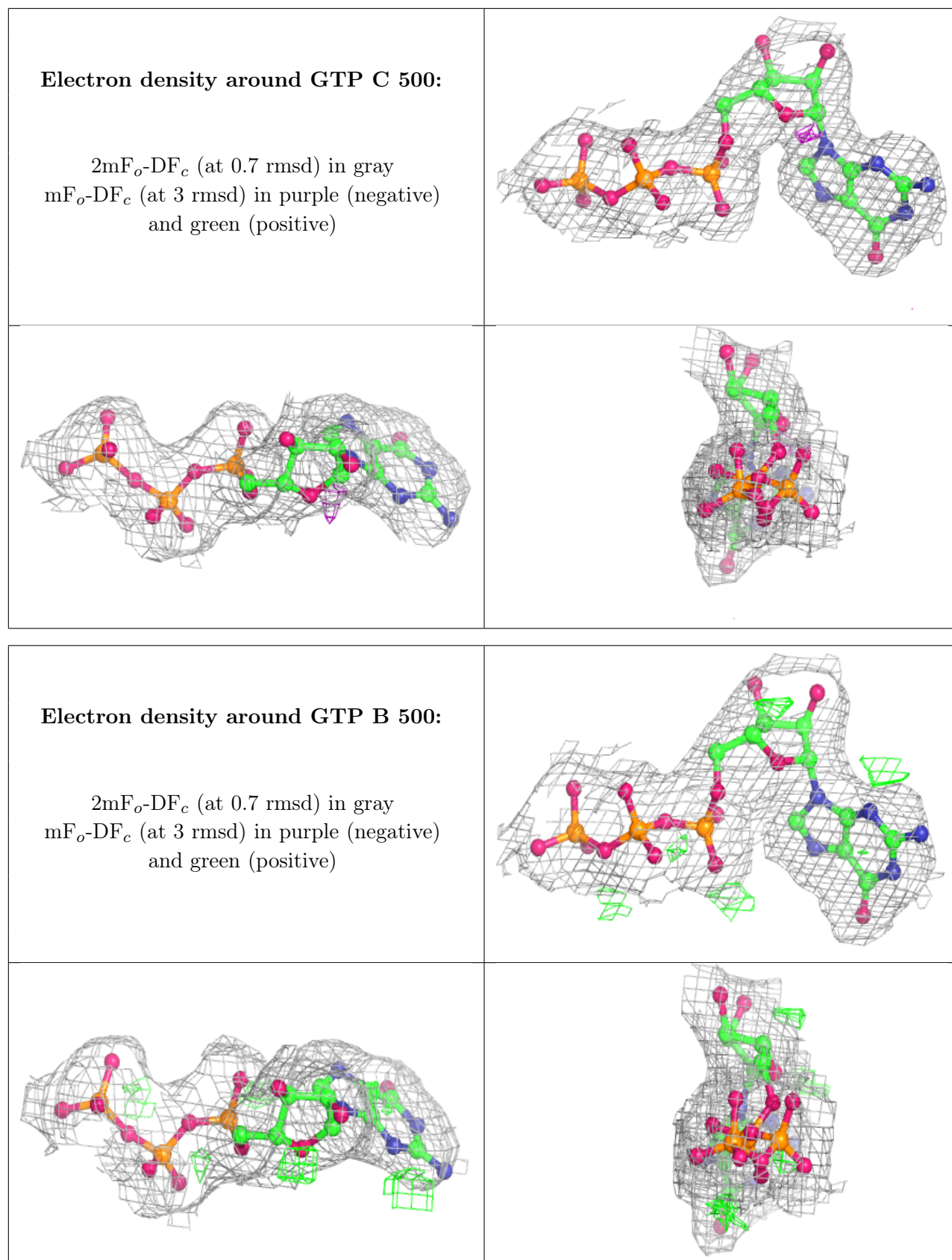
Electron density around GTP F 500:

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

**Electron density around GTP E 500:**

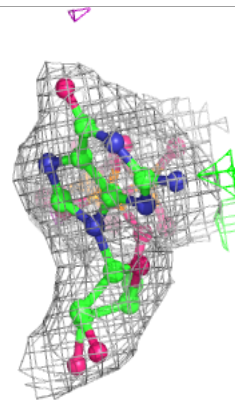
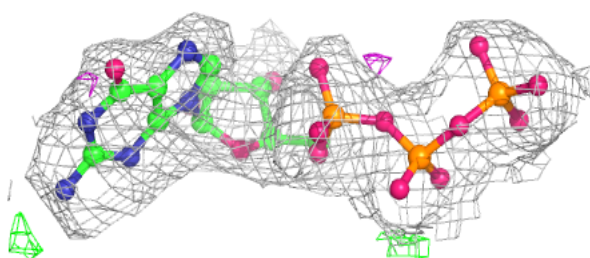
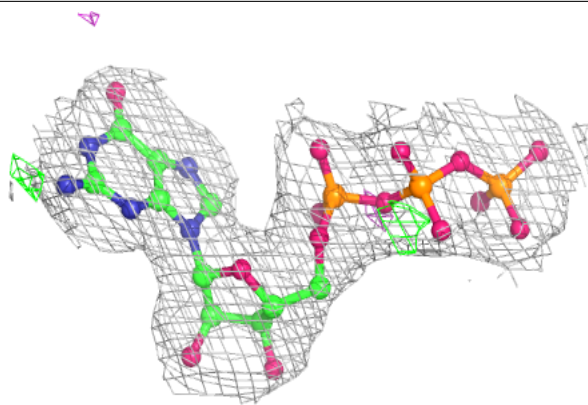
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



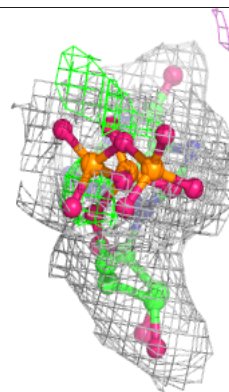
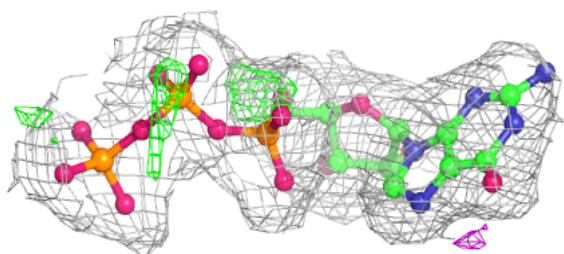
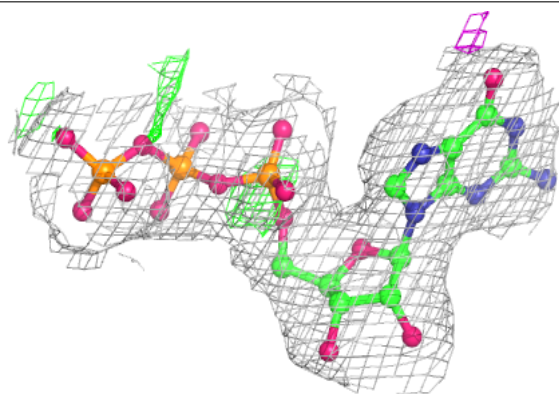


Electron density around GTP I 500:

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

**Electron density around GTP H 500:**

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



5.5 Other polymers [i](#)

There are no such residues in this entry.