



Full wwPDB EM Validation Report ⓘ

Nov 14, 2022 – 02:27 AM EST

PDB ID : 7JU4
EMDB ID : EMD-22481
Title : Radial spoke 2 stalk, IDAc, and N-DRC attached with doublet microtubule
Authors : Gui, M.; Ma, M.; Sze-Tu, E.; Wang, X.; Koh, F.; Zhong, E.; Berger, B.; Davis, J.; Dutcher, S.; Zhang, R.; Brown, A.
Deposited on : 2020-08-19
Resolution : 3.40 Å(reported)

This is a Full wwPDB EM Validation 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/EMValidationReportHelp>
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:

EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

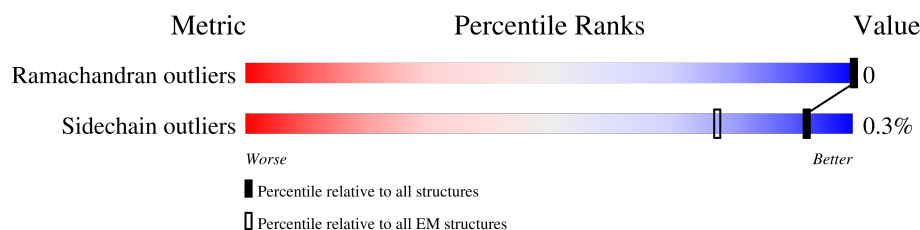
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY











The reported resolution of this entry is 3.40 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.



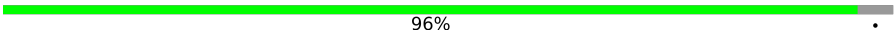
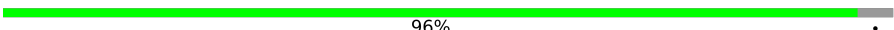
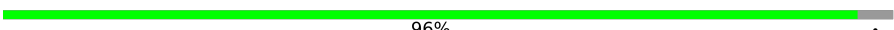
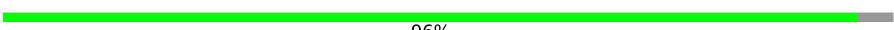
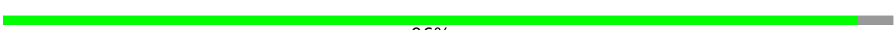





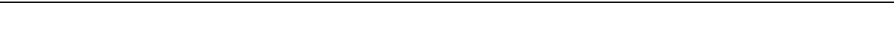

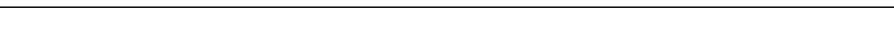
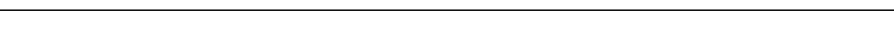
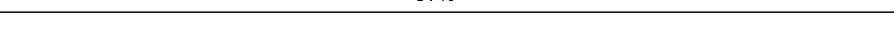
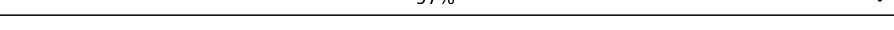
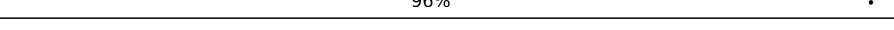
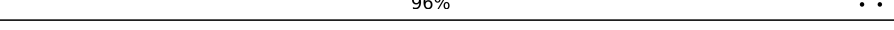
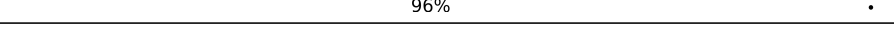
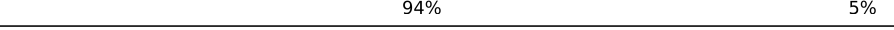
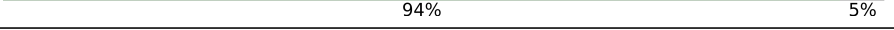
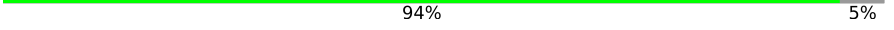
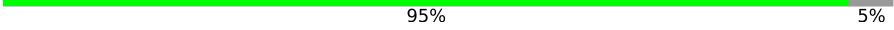


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	0	471	 37% 63%
1	4	471	 33% 67%
2	1	698	 24% 76%
3	2	573	 32% 68%
4	3	72	 100%
5	6	443	 96% .
5	8	443	 96% .
5	C	443	 96% .
5	G	443	 96% .
5	I	443	 96% .
















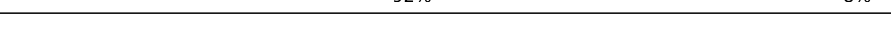
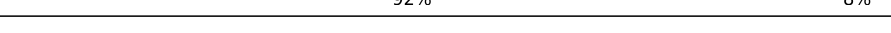
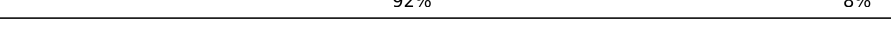

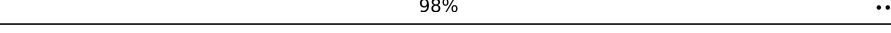



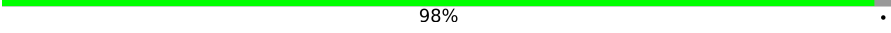

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	K	443	 96% .
5	O	443	 96% .
5	Q	443	 96% .
5	S	443	 96% .
5	W	443	 96% .
5	Y	443	 96% .
5	i	443	 96% .
5	k	443	 96% .
5	y	443	 96% .
6	7	451	 94% . 5%
6	9	451	 94% 5%
6	D	451	 96% .
6	H	451	 96% .
6	J	451	 97% .
6	L	451	 97% .
6	P	451	 96% .
6	R	451	 96% . .
6	T	451	 96% .
6	X	451	 94% 5%
6	Z	451	 94% 5%
6	j	451	 94% 5%
6	t	451	 95% 5%
6	z	451	 94% 5%
7	A	925	 47% 53%
8	B	904	 48% 52%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	E	516	
9	F	516	
10	M	500	
10	N	500	
11	U	204	
11	V	204	
12	a	91	
12	b	91	
12	c	91	
12	d	91	
12	e	91	
12	f	91	
12	g	91	
12	h	91	
12	o	91	
12	p	91	
12	q	91	
12	r	91	
13	l	331	
14	m	256	
15	n	378	
16	s	682	
17	u	377	
18	v	253	
18	w	253	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
19	x	1298	<div><div></div><div>17%</div><div>83%</div></div>

2 Entry composition [i](#)

There are 23 unique types of molecules in this entry. The entry contains 133504 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Dynein regulatory complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	173	Total	C	N	O	S	0	0
			1364	858	235	270	1		
1	4	154	Total	C	N	O	S	0	0
			1246	788	214	243	1		

- Molecule 2 is a protein called Dynein regulatory complex protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	168	Total	C	N	O	S	0	0
			1431	896	265	267	3		

- Molecule 3 is a protein called Dynein regulatory complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	183	Total	C	N	O	S	0	0
			1497	933	281	279	4		

- Molecule 4 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	3	72	Total	C	N	O	0	0
			360	216	72	72		

- Molecule 5 is a protein called Tubulin beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6	426	Total	C	N	O	S	0	0
			3346	2103	574	639	30		
5	8	426	Total	C	N	O	S	0	0
			3346	2103	574	639	30		
5	C	426	Total	C	N	O	S	0	0
			3346	2103	574	639	30		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	426	Total 3346	C 2103	N 574	O 639	S 30	0	0
5	I	426	Total 3346	C 2103	N 574	O 639	S 30	0	0
5	K	426	Total 3346	C 2103	N 574	O 639	S 30	0	0
5	O	426	Total 3346	C 2103	N 574	O 639	S 30	0	0
5	Q	426	Total 3346	C 2103	N 574	O 639	S 30	0	0
5	S	426	Total 3346	C 2103	N 574	O 639	S 30	0	0
5	W	426	Total 3346	C 2103	N 574	O 639	S 30	0	0
5	Y	426	Total 3346	C 2103	N 574	O 639	S 30	0	0
5	i	426	Total 3346	C 2103	N 574	O 639	S 30	0	0
5	k	426	Total 3346	C 2103	N 574	O 639	S 30	0	0
5	y	426	Total 3346	C 2103	N 574	O 639	S 30	0	0

- Molecule 6 is a protein called Tubulin alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	7	427	Total 3318	C 2103	N 565	O 629	S 21	0	0
6	9	427	Total 3318	C 2103	N 565	O 629	S 21	0	0
6	D	436	Total 3376	C 2136	N 575	O 644	S 21	0	0
6	H	436	Total 3376	C 2136	N 575	O 644	S 21	0	0
6	J	436	Total 3376	C 2136	N 575	O 644	S 21	0	0
6	L	436	Total 3376	C 2136	N 575	O 644	S 21	0	0
6	P	436	Total 3376	C 2136	N 575	O 644	S 21	0	0
6	R	436	Total 3376	C 2136	N 575	O 644	S 21	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
6	T	436	Total	C	N	O	S	0	0
			3376	2136	575	644	21		
6	X	427	Total	C	N	O	S	0	0
			3318	2103	565	629	21		
6	Z	427	Total	C	N	O	S	0	0
			3318	2103	565	629	21		
6	j	427	Total	C	N	O	S	0	0
			3318	2103	565	629	21		
6	t	427	Total	C	N	O	S	0	0
			3318	2103	565	629	21		
6	z	427	Total	C	N	O	S	0	0
			3318	2103	565	629	21		

- Molecule 7 is a protein called Flagellar-associated protein 59.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	435	Total	C	N	O	S	0	0
			3535	2170	665	686	14		

- Molecule 8 is a protein called Flagellar-associated protein 172.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	435	Total	C	N	O	S	0	0
			3479	2134	655	674	16		

- Molecule 9 is a protein called Radial spoke protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	86	Total	C	N	O	S	0	0
			685	432	109	142	2		
9	F	117	Total	C	N	O	S	0	0
			931	583	150	195	3		

- Molecule 10 is a protein called Radial spoke protein 7.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	M	44	Total	C	N	O	0	0
			353	232	59	62		
10	N	40	Total	C	N	O	0	0
			316	208	53	55		

- Molecule 11 is a protein called Radial spoke protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	U	49	Total	C	N	O	S	0	0
			391	255	65	70	1		
11	V	160	Total	C	N	O		0	0
			891	544	172	175			

- Molecule 12 is a protein called Dynein 8 kDa light chain, flagellar outer arm.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	a	84	Total	C	N	O	S	0	0
			686	442	115	125	4		
12	b	84	Total	C	N	O	S	0	0
			686	442	115	125	4		
12	c	84	Total	C	N	O	S	0	0
			686	442	115	125	4		
12	d	84	Total	C	N	O	S	0	0
			686	442	115	125	4		
12	e	84	Total	C	N	O	S	0	0
			686	442	115	125	4		
12	f	84	Total	C	N	O	S	0	0
			686	442	115	125	4		
12	g	84	Total	C	N	O	S	0	0
			686	442	115	125	4		
12	h	84	Total	C	N	O	S	0	0
			686	442	115	125	4		
12	o	84	Total	C	N	O	S	0	0
			686	442	115	125	4		
12	p	84	Total	C	N	O	S	0	0
			686	442	115	125	4		
12	q	84	Total	C	N	O	S	0	0
			686	442	115	125	4		
12	r	84	Total	C	N	O	S	0	0
			686	442	115	125	4		

- Molecule 13 is a protein called Radial spoke protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	l	327	Total	C	N	O	S	0	0
			2438	1529	434	465	10		

- Molecule 14 is a protein called FAP207.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	m	204	Total	C	N	O	S	0	0
			1639	1029	294	310	6		

- Molecule 15 is a protein called Radial spike protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	n	307	Total	C	N	O	S	0	0
			1516	902	307	307			

- Molecule 16 is a protein called FAP253.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	s	176	Total	C	N	O	S	0	0
			1465	924	265	273	3		

- Molecule 17 is a protein called Actin.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	u	370	Total	C	N	O	S	0	0
			2880	1828	487	542	23		

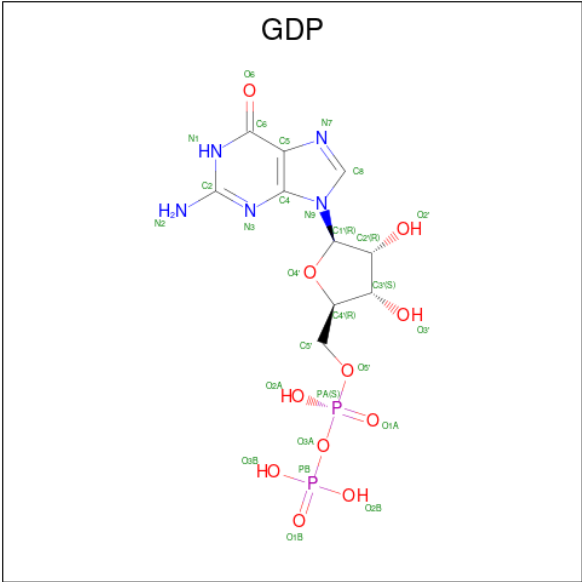
- Molecule 18 is a protein called 28 kDa inner dynein arm light chain, axonemal.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	v	152	Total	C	N	O	S	0	0
			1256	776	229	245	6		
18	w	143	Total	C	N	O	S	0	0
			1186	736	213	232	5		

- Molecule 19 is a protein called CFAP91 domain-containing protein.

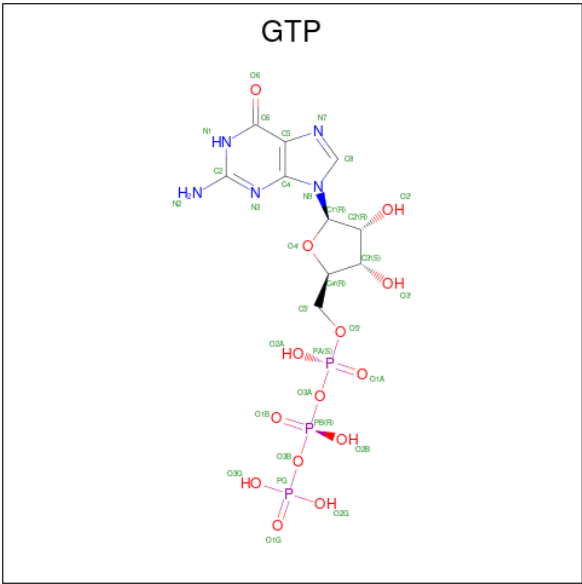
Mol	Chain	Residues	Atoms					AltConf	Trace
19	x	224	Total	C	N	O	S	0	0
			1826	1135	343	343	5		

- Molecule 20 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					AltConf
20	6	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	8	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	C	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	G	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	I	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	K	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	O	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	Q	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	S	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	W	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	Y	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	i	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	k	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	y	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 21 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms					AltConf
21	7	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	9	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	D	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	H	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	J	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	L	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	P	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	R	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	T	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	X	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	Z	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	j	1	Total	C	N	O	P	0
			32	10	5	14	3	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf
21	y	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	z	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 22 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
22	7	1	Total	Mg	0
			1	1	
22	9	1	Total	Mg	0
			1	1	
22	D	1	Total	Mg	0
			1	1	
22	H	1	Total	Mg	0
			1	1	
22	J	1	Total	Mg	0
			1	1	
22	L	1	Total	Mg	0
			1	1	
22	P	1	Total	Mg	0
			1	1	
22	R	1	Total	Mg	0
			1	1	
22	T	1	Total	Mg	0
			1	1	
22	X	1	Total	Mg	0
			1	1	
22	Z	1	Total	Mg	0
			1	1	
22	j	1	Total	Mg	0
			1	1	
22	t	1	Total	Mg	0
			1	1	
22	z	1	Total	Mg	0
			1	1	

- Molecule 23 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



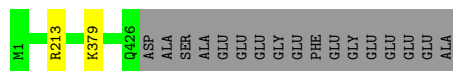
Mol	Chain	Residues	Atoms					AltConf
23	u	1	Total 31	C 10	N 5	O 13	P 3	0

Chain 3:  100%

There are no outlier residues recorded for this chain.

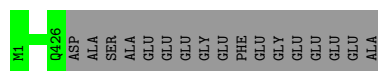
- Molecule 5: Tubulin beta

Chain 6:  96%



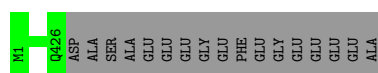
- Molecule 5: Tubulin beta

Chain 8:  96%



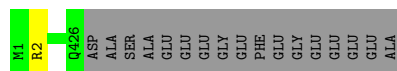
- Molecule 5: Tubulin beta

Chain C:  96%



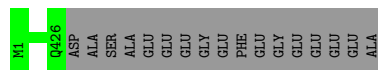
- Molecule 5: Tubulin beta

Chain G:  96%



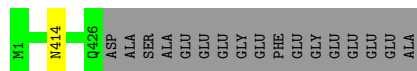
- Molecule 5: Tubulin beta

Chain I:  96%



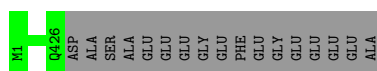
- Molecule 5: Tubulin beta

Chain K:  96%



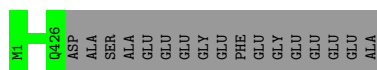
- Molecule 5: Tubulin beta

Chain O:  96%



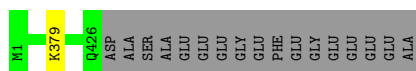
- Molecule 5: Tubulin beta

Chain Q:  96%



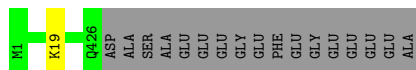
- Molecule 5: Tubulin beta

Chain S:  96%



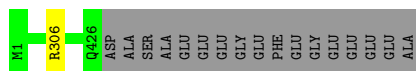
- Molecule 5: Tubulin beta

Chain W:  96%



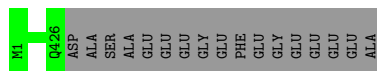
- Molecule 5: Tubulin beta

Chain Y:  96%



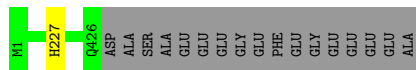
- Molecule 5: Tubulin beta

Chain i:  96%



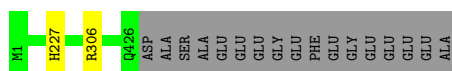
- Molecule 5: Tubulin beta

Chain k:  96%



- Molecule 5: Tubulin beta

Chain y:  96%



- Molecule 6: Tubulin alpha

Chain 7:  94% 5%



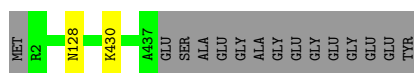
- Molecule 6: Tubulin alpha

Chain 9:  94% 5%



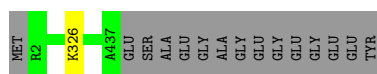
- Molecule 6: Tubulin alpha

Chain D:  96% .



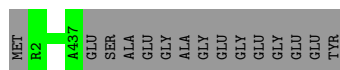
- Molecule 6: Tubulin alpha

Chain H:  96% .



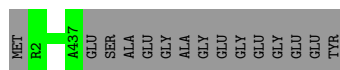
- Molecule 6: Tubulin alpha

Chain J:  97% .



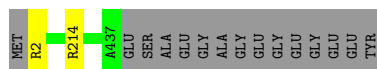
- Molecule 6: Tubulin alpha

Chain L:  97% .



- Molecule 6: Tubulin alpha

Chain P:  96% .



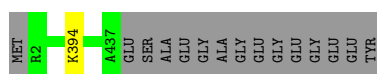
- Molecule 6: Tubulin alpha

Chain R:
96%



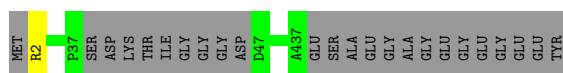
- Molecule 6: Tubulin alpha

Chain T:
96%



- Molecule 6: Tubulin alpha

Chain X:
94% 5%



- Molecule 6: Tubulin alpha

Chain Z:
94% 5%



- Molecule 6: Tubulin alpha

Chain j:
94% 5%



- Molecule 6: Tubulin alpha

Chain t:
95% 5%



- Molecule 6: Tubulin alpha

Chain z:
94% 5%



ILE	ASP	ILE	LEU	LEU	TYR	MET	ASP	LYS	GLY	ALA	ALA	ILE	THR	LYS	ASP	ALA	ILE	LYS	GLY	GLU	GLY	ALA
GLN	LYS	ALA	LEU	LEU	GLU	LEU	ALA	ALA	THR	ALA	ALA	ALA	ALA	LYS	ASP	GLY	GLY	VAL	GLU	VAL	VAL	THR

- Molecule 10: Radial spoke protein 7

Chain M: 9% 91%

[illegible]

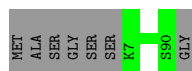
- Molecule 10: Radial spoke protein 7

Chain N: 8% 92%


[illegible]

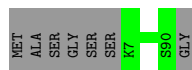
- Molecule 12: Dynein 8 kDa light chain, flagellar outer arm

Chain e:  92% 8%



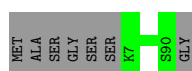
- Molecule 12: Dynein 8 kDa light chain, flagellar outer arm

Chain f:  92% 8%



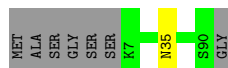
- Molecule 12: Dynein 8 kDa light chain, flagellar outer arm

Chain g:  92% 8%



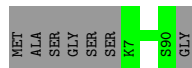
- Molecule 12: Dynein 8 kDa light chain, flagellar outer arm

Chain h:  91% 8%



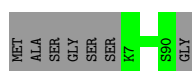
- Molecule 12: Dynein 8 kDa light chain, flagellar outer arm

Chain o:  92% 8%



- Molecule 12: Dynein 8 kDa light chain, flagellar outer arm

Chain p:  92% 8%



- Molecule 12: Dynein 8 kDa light chain, flagellar outer arm

Chain q:  92% 8%



GLN
ILE
VAL
PRO
MET
ASP
PHE
GLU
ALA
TYR
LEU
TYR
GLU
GLN
VAL
GLY
LYS
ALA
THR
ALA
LYS
ALA
GLY
THR
SER
SER
VAL
GLY
THR
ARG
THR
LEU
SER

- Molecule 17: Actin

Chain u:  98%

MET		
ALA		
ASP		
GLU		
GLY		
GLU		
VAL		
S8		
F377		

- Molecule 18: 28 kDa inner dynein arm light chain, axonemal

Chain v: 60% 40%

GLU
TRP
THR
GLU
ASP
GLY
GLN
LEU
TRP
VAL
GLN
TYP
VAL
SER
SER
THR
PRO
A78
K215
-
Q229
LEU
LYS
GLN
GLN
LEU
GLU
THR
PHE
LEU
VAL
PRO
ALA
LYS
LYS
GLY
ALA
PRO
GLY
ALA
PRO
ALA
ALA
ALA
THR

- Molecule 18: 28 kDa inner dynein arm light chain, axonemal

Chain w:  56% 43%

[illegible]

- Molecule 19: CFAP91 domain-containing protein

Chain x:  17% 83%

[illegible]



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	202168	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	38.9	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

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: GDP, MG, ATP, GTP

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	0	0.28	0/1379	0.50	0/1860
1	4	0.27	0/1258	0.49	0/1690
2	1	0.27	0/1458	0.45	0/1962
3	2	0.33	0/1517	0.51	0/2038
5	6	0.28	0/3420	0.47	0/4628
5	8	0.29	0/3420	0.47	0/4628
5	C	0.28	0/3420	0.46	0/4628
5	G	0.29	0/3420	0.46	0/4628
5	I	0.29	0/3420	0.47	0/4628
5	K	0.32	0/3420	0.47	0/4628
5	O	0.30	0/3420	0.48	0/4628
5	Q	0.29	0/3420	0.47	0/4628
5	S	0.29	0/3420	0.47	0/4628
5	W	0.27	0/3420	0.46	0/4628
5	Y	0.28	0/3420	0.47	0/4628
5	i	0.28	0/3420	0.45	0/4628
5	k	0.29	0/3420	0.46	0/4628
5	y	0.29	0/3420	0.47	0/4628
6	7	0.29	0/3389	0.48	0/4595
6	9	0.28	0/3389	0.47	0/4595
6	D	0.30	0/3448	0.47	0/4675
6	H	0.30	0/3448	0.48	0/4675
6	J	0.29	0/3448	0.48	0/4675
6	L	0.31	0/3448	0.49	0/4675
6	P	0.29	0/3448	0.46	0/4675
6	R	0.29	0/3448	0.48	0/4675
6	T	0.28	0/3448	0.47	0/4675
6	X	0.29	0/3389	0.47	0/4595
6	Z	0.28	0/3389	0.46	0/4595
6	j	0.28	0/3389	0.48	0/4595
6	t	0.28	0/3389	0.49	0/4595
6	z	0.30	0/3389	0.49	0/4595

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
7	A	0.28	0/3562	0.42	0/4763
8	B	0.29	0/3499	0.46	0/4674
9	E	0.32	0/698	0.54	0/948
9	F	0.30	0/946	0.56	0/1287
10	M	0.33	0/363	0.48	0/491
10	N	0.29	0/325	0.46	0/439
11	U	0.29	0/399	0.48	0/543
11	V	0.27	0/891	0.43	0/1221
12	a	0.35	0/702	0.48	0/945
12	b	0.36	0/702	0.52	0/945
12	c	0.36	0/702	0.54	0/945
12	d	0.35	0/702	0.51	0/945
12	e	0.33	0/702	0.50	0/945
12	f	0.38	0/702	0.53	0/945
12	g	0.33	0/702	0.50	0/945
12	h	0.32	0/702	0.49	0/945
12	o	0.27	0/702	0.47	0/945
12	p	0.27	0/702	0.49	0/945
12	q	0.25	0/702	0.46	0/945
12	r	0.27	0/702	0.50	0/945
13	l	0.28	0/2469	0.54	0/3363
14	m	0.32	0/1688	0.54	0/2273
15	n	0.24	0/1515	0.39	0/2108
16	s	0.24	0/1487	0.41	0/2004
17	u	0.27	0/2942	0.48	0/3985
18	v	0.27	0/1267	0.48	0/1696
18	w	0.27	0/1196	0.42	0/1599
19	x	0.28	0/1847	0.43	0/2473
All	All	0.29	0/134869	0.47	0/182439

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

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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 PDB entries followed by that with respect to all EM entries.

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	0	171/471 (36%)	166 (97%)	5 (3%)	0	100	100
1	4	150/471 (32%)	148 (99%)	2 (1%)	0	100	100
2	1	164/698 (24%)	157 (96%)	7 (4%)	0	100	100
3	2	179/573 (31%)	176 (98%)	3 (2%)	0	100	100
5	6	424/443 (96%)	398 (94%)	26 (6%)	0	100	100
5	8	424/443 (96%)	399 (94%)	25 (6%)	0	100	100
5	C	424/443 (96%)	410 (97%)	14 (3%)	0	100	100
5	G	424/443 (96%)	393 (93%)	31 (7%)	0	100	100
5	I	424/443 (96%)	398 (94%)	26 (6%)	0	100	100
5	K	424/443 (96%)	396 (93%)	28 (7%)	0	100	100
5	O	424/443 (96%)	401 (95%)	23 (5%)	0	100	100
5	Q	424/443 (96%)	396 (93%)	28 (7%)	0	100	100
5	S	424/443 (96%)	398 (94%)	26 (6%)	0	100	100
5	W	424/443 (96%)	405 (96%)	19 (4%)	0	100	100
5	Y	424/443 (96%)	405 (96%)	19 (4%)	0	100	100
5	i	424/443 (96%)	404 (95%)	20 (5%)	0	100	100
5	k	424/443 (96%)	398 (94%)	26 (6%)	0	100	100
5	y	424/443 (96%)	400 (94%)	24 (6%)	0	100	100
6	7	423/451 (94%)	396 (94%)	27 (6%)	0	100	100
6	9	423/451 (94%)	393 (93%)	30 (7%)	0	100	100
6	D	434/451 (96%)	413 (95%)	21 (5%)	0	100	100
6	H	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
6	J	434/451 (96%)	402 (93%)	32 (7%)	0	100	100
6	L	434/451 (96%)	404 (93%)	30 (7%)	0	100	100
6	P	434/451 (96%)	405 (93%)	29 (7%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	R	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
6	T	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
6	X	423/451 (94%)	407 (96%)	16 (4%)	0	100	100
6	Z	423/451 (94%)	401 (95%)	22 (5%)	0	100	100
6	j	423/451 (94%)	402 (95%)	21 (5%)	0	100	100
6	t	423/451 (94%)	399 (94%)	24 (6%)	0	100	100
6	z	423/451 (94%)	398 (94%)	25 (6%)	0	100	100
7	A	429/925 (46%)	428 (100%)	1 (0%)	0	100	100
8	B	429/904 (48%)	428 (100%)	1 (0%)	0	100	100
9	E	84/516 (16%)	81 (96%)	3 (4%)	0	100	100
9	F	115/516 (22%)	105 (91%)	10 (9%)	0	100	100
10	M	42/500 (8%)	38 (90%)	4 (10%)	0	100	100
10	N	38/500 (8%)	33 (87%)	5 (13%)	0	100	100
11	U	47/204 (23%)	42 (89%)	5 (11%)	0	100	100
11	V	150/204 (74%)	133 (89%)	17 (11%)	0	100	100
12	a	82/91 (90%)	72 (88%)	10 (12%)	0	100	100
12	b	82/91 (90%)	76 (93%)	6 (7%)	0	100	100
12	c	82/91 (90%)	79 (96%)	3 (4%)	0	100	100
12	d	82/91 (90%)	76 (93%)	6 (7%)	0	100	100
12	e	82/91 (90%)	76 (93%)	6 (7%)	0	100	100
12	f	82/91 (90%)	75 (92%)	7 (8%)	0	100	100
12	g	82/91 (90%)	77 (94%)	5 (6%)	0	100	100
12	h	82/91 (90%)	79 (96%)	3 (4%)	0	100	100
12	o	82/91 (90%)	73 (89%)	9 (11%)	0	100	100
12	p	82/91 (90%)	73 (89%)	9 (11%)	0	100	100
12	q	82/91 (90%)	73 (89%)	9 (11%)	0	100	100
12	r	82/91 (90%)	78 (95%)	4 (5%)	0	100	100
13	l	325/331 (98%)	285 (88%)	40 (12%)	0	100	100
14	m	202/256 (79%)	174 (86%)	28 (14%)	0	100	100
15	n	305/378 (81%)	270 (88%)	35 (12%)	0	100	100
16	s	172/682 (25%)	160 (93%)	12 (7%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	u	368/377 (98%)	350 (95%)	18 (5%)	0	100	100
18	v	150/253 (59%)	144 (96%)	6 (4%)	0	100	100
18	w	139/253 (55%)	138 (99%)	1 (1%)	0	100	100
19	x	216/1298 (17%)	206 (95%)	10 (5%)	0	100	100
All	All	16794/23918 (70%)	15820 (94%)	974 (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 PDB entries followed by that with respect to all EM entries.

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	0	146/418 (35%)	145 (99%)	1 (1%)	84	92
1	4	135/418 (32%)	135 (100%)	0	100	100
2	1	153/573 (27%)	153 (100%)	0	100	100
3	2	158/470 (34%)	156 (99%)	2 (1%)	69	84
5	6	367/379 (97%)	365 (100%)	2 (0%)	88	94
5	8	367/379 (97%)	367 (100%)	0	100	100
5	C	367/379 (97%)	367 (100%)	0	100	100
5	G	367/379 (97%)	366 (100%)	1 (0%)	92	97
5	I	367/379 (97%)	367 (100%)	0	100	100
5	K	367/379 (97%)	366 (100%)	1 (0%)	92	97
5	O	367/379 (97%)	367 (100%)	0	100	100
5	Q	367/379 (97%)	367 (100%)	0	100	100
5	S	367/379 (97%)	366 (100%)	1 (0%)	92	97
5	W	367/379 (97%)	366 (100%)	1 (0%)	92	97
5	Y	367/379 (97%)	366 (100%)	1 (0%)	92	97
5	i	367/379 (97%)	367 (100%)	0	100	100
5	k	367/379 (97%)	366 (100%)	1 (0%)	92	97

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	y	367/379 (97%)	365 (100%)	2 (0%)	88	94
6	7	359/374 (96%)	356 (99%)	3 (1%)	81	91
6	9	359/374 (96%)	358 (100%)	1 (0%)	92	97
6	D	365/374 (98%)	363 (100%)	2 (0%)	88	94
6	H	365/374 (98%)	364 (100%)	1 (0%)	92	97
6	J	365/374 (98%)	365 (100%)	0	100	100
6	L	365/374 (98%)	365 (100%)	0	100	100
6	P	365/374 (98%)	363 (100%)	2 (0%)	88	94
6	R	365/374 (98%)	360 (99%)	5 (1%)	67	83
6	T	365/374 (98%)	364 (100%)	1 (0%)	92	97
6	X	359/374 (96%)	358 (100%)	1 (0%)	92	97
6	Z	359/374 (96%)	358 (100%)	1 (0%)	92	97
6	j	359/374 (96%)	358 (100%)	1 (0%)	92	97
6	t	359/374 (96%)	359 (100%)	0	100	100
6	z	359/374 (96%)	358 (100%)	1 (0%)	92	97
7	A	368/766 (48%)	367 (100%)	1 (0%)	92	97
8	B	362/742 (49%)	361 (100%)	1 (0%)	92	97
9	E	76/406 (19%)	76 (100%)	0	100	100
9	F	102/406 (25%)	101 (99%)	1 (1%)	76	88
10	M	36/406 (9%)	36 (100%)	0	100	100
10	N	32/406 (8%)	32 (100%)	0	100	100
11	U	42/162 (26%)	42 (100%)	0	100	100
11	V	28/162 (17%)	28 (100%)	0	100	100
12	a	72/76 (95%)	72 (100%)	0	100	100
12	b	72/76 (95%)	72 (100%)	0	100	100
12	c	72/76 (95%)	72 (100%)	0	100	100
12	d	72/76 (95%)	72 (100%)	0	100	100
12	e	72/76 (95%)	72 (100%)	0	100	100
12	f	72/76 (95%)	72 (100%)	0	100	100
12	g	72/76 (95%)	72 (100%)	0	100	100
12	h	72/76 (95%)	71 (99%)	1 (1%)	67	83

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	o	72/76 (95%)	72 (100%)	0	100	100
12	p	72/76 (95%)	72 (100%)	0	100	100
12	q	72/76 (95%)	72 (100%)	0	100	100
12	r	72/76 (95%)	71 (99%)	1 (1%)	67	83
13	l	259/263 (98%)	256 (99%)	3 (1%)	71	85
14	m	159/197 (81%)	159 (100%)	0	100	100
16	s	162/553 (29%)	162 (100%)	0	100	100
17	u	313/318 (98%)	313 (100%)	0	100	100
18	v	134/218 (62%)	133 (99%)	1 (1%)	84	92
18	w	127/218 (58%)	126 (99%)	1 (1%)	81	91
19	x	191/884 (22%)	190 (100%)	1 (0%)	88	94
All	All	14053/19440 (72%)	14010 (100%)	43 (0%)	92	97

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	404	ARG
3	2	280	HIS
3	2	291	GLU
5	6	213	ARG
5	6	379	LYS
6	7	2	ARG
6	7	133	GLN
6	7	329	ASN
6	9	128	ASN
7	A	58	ASN
8	B	63	GLN
6	D	128	ASN
6	D	430	LYS
9	F	127	ARG
5	G	2	ARG
6	H	326	LYS
5	K	414	ASN
6	P	2	ARG
6	P	214	ARG
6	R	2	ARG
6	R	40	LYS
6	R	221	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	R	308	ARG
6	R	339	ARG
5	S	379	LYS
6	T	394	LYS
5	W	19	LYS
6	X	2	ARG
5	Y	306	ARG
6	Z	308	ARG
12	h	35	ASN
6	j	233	GLN
5	k	227	HIS
13	l	36	ARG
13	l	130	ARG
13	l	309	ARG
12	r	38	LYS
18	v	215	LYS
18	w	161	ARG
19	x	327	ARG
5	y	227	HIS
5	y	306	ARG
6	z	228	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (59) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	430	HIS
3	2	288	ASN
1	4	383	GLN
5	8	195	ASN
5	8	332	ASN
7	A	58	ASN
5	C	6	HIS
5	C	8	GLN
9	E	198	ASN
5	G	105	HIS
5	G	190	HIS
6	H	101	ASN
6	H	258	ASN
5	I	347	ASN
5	K	426	GLN
5	O	6	HIS
5	O	8	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	O	11	GLN
5	O	15	GLN
5	O	99	ASN
5	O	298	ASN
6	P	258	ASN
6	P	358	GLN
6	R	256	GLN
5	S	8	GLN
5	S	190	HIS
5	S	347	ASN
5	S	414	ASN
6	T	176	GLN
5	W	8	GLN
5	W	14	ASN
6	X	329	ASN
5	Y	334	GLN
5	Y	347	ASN
5	Y	348	ASN
12	d	70	HIS
12	f	53	ASN
12	h	63	ASN
12	h	70	HIS
5	i	190	HIS
5	i	334	GLN
6	j	8	HIS
6	j	88	HIS
5	k	99	ASN
5	k	105	HIS
13	l	52	ASN
12	p	63	ASN
16	s	502	GLN
6	t	101	ASN
6	t	258	ASN
18	v	216	HIS
18	w	216	HIS
5	y	256	ASN
5	y	347	ASN
5	y	414	ASN
6	z	11	GLN
6	z	197	HIS
6	z	256	GLN
6	z	293	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 43 ligands modelled in this entry, 14 are monoatomic - leaving 29 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$
23	ATP	u	401	-	26,33,33	0.92	1 (3%)	31,52,52	1.49	5 (16%)
20	GDP	K	501	-	24,30,30	1.01	1 (4%)	30,47,47	1.22	2 (6%)
21	GTP	z	501	22	26,34,34	1.14	2 (7%)	32,54,54	1.61	8 (25%)
20	GDP	6	501	-	24,30,30	0.93	1 (4%)	30,47,47	1.42	4 (13%)
21	GTP	J	501	22	26,34,34	1.17	2 (7%)	32,54,54	1.79	7 (21%)
20	GDP	i	501	-	24,30,30	0.93	1 (4%)	30,47,47	1.44	4 (13%)
20	GDP	y	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.34	4 (13%)
21	GTP	7	501	22	26,34,34	1.16	2 (7%)	32,54,54	1.62	7 (21%)
21	GTP	L	501	22	26,34,34	1.09	1 (3%)	32,54,54	1.55	6 (18%)
20	GDP	I	501	-	24,30,30	0.98	1 (4%)	30,47,47	1.40	5 (16%)
20	GDP	C	501	-	24,30,30	0.96	1 (4%)	30,47,47	1.36	5 (16%)
20	GDP	G	501	-	24,30,30	0.95	1 (4%)	30,47,47	1.36	4 (13%)
20	GDP	k	501	-	24,30,30	0.89	1 (4%)	30,47,47	1.50	6 (20%)
20	GDP	W	501	-	24,30,30	0.94	1 (4%)	30,47,47	1.42	5 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
21	GTP	y	501	22	26,34,34	1.17	2 (7%)	32,54,54	1.61	7 (21%)
20	GDP	Y	501	-	24,30,30	0.94	1 (4%)	30,47,47	1.36	4 (13%)
21	GTP	Z	501	22	26,34,34	1.18	2 (7%)	32,54,54	1.69	7 (21%)
21	GTP	R	501	22	26,34,34	1.21	2 (7%)	32,54,54	1.74	7 (21%)
20	GDP	8	501	-	24,30,30	0.96	1 (4%)	30,47,47	1.42	4 (13%)
21	GTP	D	501	22	26,34,34	1.20	2 (7%)	32,54,54	1.65	7 (21%)
21	GTP	9	501	22	26,34,34	1.17	2 (7%)	32,54,54	1.77	7 (21%)
20	GDP	Q	501	-	24,30,30	0.95	1 (4%)	30,47,47	1.39	4 (13%)
20	GDP	S	501	-	24,30,30	0.96	1 (4%)	30,47,47	1.39	4 (13%)
21	GTP	T	501	22	26,34,34	1.19	2 (7%)	32,54,54	1.70	7 (21%)
21	GTP	H	501	22	26,34,34	1.19	1 (3%)	32,54,54	1.59	8 (25%)
21	GTP	X	501	22	26,34,34	1.21	2 (7%)	32,54,54	1.69	7 (21%)
21	GTP	P	501	22	26,34,34	1.19	2 (7%)	32,54,54	1.52	7 (21%)
21	GTP	j	501	22	26,34,34	1.16	2 (7%)	32,54,54	1.67	7 (21%)
20	GDP	O	501	-	24,30,30	0.98	1 (4%)	30,47,47	1.41	4 (13%)

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
23	ATP	u	401	-	-	4/18/38/38	0/3/3/3
20	GDP	K	501	-	-	4/12/32/32	0/3/3/3
21	GTP	z	501	22	-	8/18/38/38	0/3/3/3
20	GDP	6	501	-	-	3/12/32/32	0/3/3/3
21	GTP	J	501	22	-	9/18/38/38	0/3/3/3
20	GDP	i	501	-	-	3/12/32/32	0/3/3/3
20	GDP	y	502	-	-	4/12/32/32	0/3/3/3
21	GTP	7	501	22	-	4/18/38/38	0/3/3/3
21	GTP	L	501	22	-	5/18/38/38	0/3/3/3
20	GDP	I	501	-	-	5/12/32/32	0/3/3/3
20	GDP	C	501	-	-	2/12/32/32	0/3/3/3
20	GDP	G	501	-	-	5/12/32/32	0/3/3/3
20	GDP	k	501	-	-	1/12/32/32	0/3/3/3
20	GDP	W	501	-	-	7/12/32/32	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
21	GTP	y	501	22	-	4/18/38/38	0/3/3/3
20	GDP	Y	501	-	-	1/12/32/32	0/3/3/3
21	GTP	Z	501	22	-	4/18/38/38	0/3/3/3
21	GTP	R	501	22	-	6/18/38/38	0/3/3/3
20	GDP	8	501	-	-	4/12/32/32	0/3/3/3
21	GTP	D	501	22	-	6/18/38/38	0/3/3/3
21	GTP	9	501	22	-	6/18/38/38	0/3/3/3
20	GDP	Q	501	-	-	7/12/32/32	0/3/3/3
20	GDP	S	501	-	-	0/12/32/32	0/3/3/3
21	GTP	T	501	22	-	4/18/38/38	0/3/3/3
21	GTP	H	501	22	-	5/18/38/38	0/3/3/3
21	GTP	X	501	22	-	5/18/38/38	0/3/3/3
21	GTP	P	501	22	-	4/18/38/38	0/3/3/3
21	GTP	j	501	22	-	4/18/38/38	0/3/3/3
20	GDP	O	501	-	-	3/12/32/32	0/3/3/3

All (41) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	X	501	GTP	C5-C6	-4.33	1.38	1.47
21	D	501	GTP	C5-C6	-4.31	1.38	1.47
21	y	501	GTP	C5-C6	-4.28	1.38	1.47
21	P	501	GTP	C5-C6	-4.27	1.38	1.47
21	R	501	GTP	C5-C6	-4.25	1.38	1.47
21	T	501	GTP	C5-C6	-4.24	1.38	1.47
21	Z	501	GTP	C5-C6	-4.20	1.38	1.47
21	H	501	GTP	C5-C6	-4.20	1.38	1.47
21	9	501	GTP	C5-C6	-4.12	1.39	1.47
21	j	501	GTP	C5-C6	-4.12	1.39	1.47
21	7	501	GTP	C5-C6	-4.10	1.39	1.47
21	J	501	GTP	C5-C6	-4.09	1.39	1.47
21	z	501	GTP	C5-C6	-3.97	1.39	1.47
21	L	501	GTP	C5-C6	-3.64	1.40	1.47
20	S	501	GDP	C6-N1	-2.76	1.33	1.37
20	I	501	GDP	C6-N1	-2.70	1.33	1.37
20	O	501	GDP	C6-N1	-2.70	1.33	1.37
20	W	501	GDP	C6-N1	-2.57	1.34	1.37
20	G	501	GDP	C6-N1	-2.55	1.34	1.37
20	Q	501	GDP	C6-N1	-2.55	1.34	1.37

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	8	501	GDP	C6-N1	-2.54	1.34	1.37
20	6	501	GDP	C6-N1	-2.52	1.34	1.37
20	K	501	GDP	C6-N1	-2.51	1.34	1.37
20	y	502	GDP	C6-N1	-2.50	1.34	1.37
20	i	501	GDP	C6-N1	-2.48	1.34	1.37
20	Y	501	GDP	C6-N1	-2.47	1.34	1.37
20	C	501	GDP	C6-N1	-2.47	1.34	1.37
23	u	401	ATP	C5-C4	2.40	1.47	1.40
21	9	501	GTP	C2-N3	2.21	1.38	1.33
21	z	501	GTP	C2-N3	2.15	1.38	1.33
21	T	501	GTP	C2-N3	2.13	1.38	1.33
21	X	501	GTP	C2-N3	2.13	1.38	1.33
21	j	501	GTP	C2-N3	2.10	1.38	1.33
21	y	501	GTP	C2-N3	2.10	1.38	1.33
21	D	501	GTP	C2-N3	2.08	1.38	1.33
21	Z	501	GTP	C2-N3	2.05	1.38	1.33
21	J	501	GTP	C2-N3	2.03	1.38	1.33
21	R	501	GTP	C2-N3	2.03	1.38	1.33
20	k	501	GDP	C6-N1	-2.02	1.34	1.37
21	P	501	GTP	C2-N3	2.01	1.38	1.33
21	7	501	GTP	C2-N3	2.01	1.38	1.33

All (163) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	J	501	GTP	PA-O3A-PB	-4.53	117.28	132.83
20	8	501	GDP	PA-O3A-PB	-4.53	117.29	132.83
21	R	501	GTP	PA-O3A-PB	-4.49	117.41	132.83
21	9	501	GTP	PA-O3A-PB	-4.46	117.52	132.83
20	6	501	GDP	PA-O3A-PB	-4.44	117.61	132.83
21	X	501	GTP	PA-O3A-PB	-4.42	117.67	132.83
20	S	501	GDP	PA-O3A-PB	-4.38	117.81	132.83
21	D	501	GTP	PB-O3B-PG	-4.34	117.92	132.83
21	j	501	GTP	PA-O3A-PB	-4.34	117.95	132.83
21	Z	501	GTP	PA-O3A-PB	-4.32	118.00	132.83
20	I	501	GDP	PA-O3A-PB	-4.29	118.09	132.83
21	y	501	GTP	PA-O3A-PB	-4.29	118.11	132.83
20	G	501	GDP	PA-O3A-PB	-4.28	118.13	132.83
20	O	501	GDP	PA-O3A-PB	-4.27	118.16	132.83
21	T	501	GTP	PB-O3B-PG	-4.26	118.21	132.83
21	T	501	GTP	PA-O3A-PB	-4.17	118.53	132.83
21	J	501	GTP	PB-O3B-PG	-4.13	118.67	132.83

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	i	501	GDP	PA-O3A-PB	-4.12	118.68	132.83
20	W	501	GDP	PA-O3A-PB	-4.11	118.71	132.83
20	Y	501	GDP	PA-O3A-PB	-4.11	118.73	132.83
20	y	502	GDP	PA-O3A-PB	-4.09	118.80	132.83
21	z	501	GTP	PA-O3A-PB	-4.07	118.87	132.83
21	7	501	GTP	PA-O3A-PB	-4.04	118.97	132.83
21	9	501	GTP	PB-O3B-PG	-4.03	119.01	132.83
21	R	501	GTP	PB-O3B-PG	-3.99	119.13	132.83
20	C	501	GDP	PA-O3A-PB	-3.95	119.27	132.83
21	Z	501	GTP	PB-O3B-PG	-3.94	119.30	132.83
20	Q	501	GDP	PA-O3A-PB	-3.90	119.45	132.83
21	L	501	GTP	PA-O3A-PB	-3.86	119.58	132.83
20	K	501	GDP	PA-O3A-PB	-3.85	119.63	132.83
20	k	501	GDP	PA-O3A-PB	-3.85	119.63	132.83
21	X	501	GTP	PB-O3B-PG	-3.78	119.84	132.83
21	j	501	GTP	PB-O3B-PG	-3.74	119.98	132.83
21	H	501	GTP	PB-O3B-PG	-3.74	119.99	132.83
21	H	501	GTP	PA-O3A-PB	-3.68	120.20	132.83
20	Q	501	GDP	C3'-C2'-C1'	3.47	106.21	100.98
21	9	501	GTP	C5-C6-N1	3.47	120.07	113.95
21	J	501	GTP	C5-C6-N1	3.46	120.07	113.95
23	u	401	ATP	PA-O3A-PB	-3.45	121.00	132.83
21	Z	501	GTP	C5-C6-N1	3.44	120.03	113.95
21	y	501	GTP	C5-C6-N1	3.41	119.98	113.95
20	i	501	GDP	C3'-C2'-C1'	3.41	106.11	100.98
21	D	501	GTP	PA-O3A-PB	-3.40	121.17	132.83
21	z	501	GTP	C5-C6-N1	3.39	119.93	113.95
21	P	501	GTP	PB-O3B-PG	-3.39	121.21	132.83
21	L	501	GTP	PB-O3B-PG	-3.38	121.22	132.83
21	9	501	GTP	C3'-C2'-C1'	3.34	106.01	100.98
21	R	501	GTP	C5-C6-N1	3.34	119.85	113.95
21	X	501	GTP	C5-C6-N1	3.34	119.85	113.95
21	7	501	GTP	C5-C6-N1	3.33	119.84	113.95
21	T	501	GTP	C5-C6-N1	3.33	119.83	113.95
21	7	501	GTP	PB-O3B-PG	-3.32	121.44	132.83
21	L	501	GTP	C8-N7-C5	3.30	109.28	102.99
20	6	501	GDP	C3'-C2'-C1'	3.30	105.95	100.98
21	D	501	GTP	C5-C6-N1	3.28	119.75	113.95
21	j	501	GTP	C5-C6-N1	3.25	119.70	113.95
21	P	501	GTP	C5-C6-N1	3.24	119.68	113.95
21	H	501	GTP	C5-C6-N1	3.23	119.65	113.95
20	8	501	GDP	C3'-C2'-C1'	3.22	105.82	100.98

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	W	501	GDP	C3'-C2'-C1'	3.16	105.74	100.98
20	k	501	GDP	C3'-C2'-C1'	3.16	105.74	100.98
20	O	501	GDP	C3'-C2'-C1'	3.15	105.73	100.98
21	H	501	GTP	C8-N7-C5	3.14	108.97	102.99
21	7	501	GTP	C8-N7-C5	3.13	108.95	102.99
21	J	501	GTP	C8-N7-C5	3.11	108.91	102.99
21	z	501	GTP	C8-N7-C5	3.11	108.91	102.99
23	u	401	ATP	PB-O3B-PG	-3.10	122.20	132.83
21	9	501	GTP	C8-N7-C5	3.08	108.86	102.99
20	Y	501	GDP	C3'-C2'-C1'	3.07	105.60	100.98
21	9	501	GTP	C2-N1-C6	-3.07	119.44	125.10
23	u	401	ATP	N3-C2-N1	-3.02	123.95	128.68
21	J	501	GTP	C3'-C2'-C1'	3.02	105.53	100.98
21	X	501	GTP	C2-N1-C6	-3.02	119.54	125.10
21	j	501	GTP	C8-N7-C5	3.01	108.73	102.99
21	z	501	GTP	C2-N1-C6	-3.01	119.55	125.10
21	J	501	GTP	C2-N1-C6	-3.01	119.56	125.10
21	7	501	GTP	C2-N1-C6	-3.01	119.56	125.10
21	X	501	GTP	C3'-C2'-C1'	3.01	105.50	100.98
21	P	501	GTP	C8-N7-C5	3.00	108.70	102.99
21	Z	501	GTP	C8-N7-C5	2.99	108.68	102.99
21	y	501	GTP	C2-N1-C6	-2.98	119.60	125.10
21	D	501	GTP	C3'-C2'-C1'	2.98	105.47	100.98
21	Z	501	GTP	C2-N1-C6	-2.97	119.62	125.10
21	X	501	GTP	C8-N7-C5	2.96	108.63	102.99
21	Z	501	GTP	C3'-C2'-C1'	2.96	105.43	100.98
21	j	501	GTP	C2-N1-C6	-2.96	119.65	125.10
20	S	501	GDP	C3'-C2'-C1'	2.96	105.43	100.98
21	j	501	GTP	C3'-C2'-C1'	2.96	105.43	100.98
21	T	501	GTP	C8-N7-C5	2.95	108.62	102.99
21	R	501	GTP	C3'-C2'-C1'	2.94	105.40	100.98
21	D	501	GTP	C8-N7-C5	2.93	108.58	102.99
20	k	501	GDP	C5-C6-N1	2.93	119.13	113.95
21	R	501	GTP	C8-N7-C5	2.92	108.55	102.99
21	y	501	GTP	C8-N7-C5	2.92	108.55	102.99
21	P	501	GTP	C2-N1-C6	-2.91	119.75	125.10
21	T	501	GTP	C2-N1-C6	-2.91	119.75	125.10
21	D	501	GTP	C2-N1-C6	-2.91	119.75	125.10
20	C	501	GDP	C3'-C2'-C1'	2.88	105.31	100.98
20	I	501	GDP	C3'-C2'-C1'	2.86	105.29	100.98
21	y	501	GTP	PB-O3B-PG	-2.86	123.02	132.83
21	R	501	GTP	C2-N1-C6	-2.85	119.84	125.10

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	u	401	ATP	C3'-C2'-C1'	2.83	105.24	100.98
21	T	501	GTP	C3'-C2'-C1'	2.80	105.20	100.98
23	u	401	ATP	C4-C5-N7	-2.74	106.55	109.40
21	L	501	GTP	N2-C2-N1	2.72	122.51	116.71
21	z	501	GTP	C3'-C2'-C1'	2.70	105.04	100.98
21	H	501	GTP	C2-N1-C6	-2.70	120.13	125.10
21	P	501	GTP	C3'-C2'-C1'	2.69	105.03	100.98
20	k	501	GDP	C2-N1-C6	-2.60	120.31	125.10
21	L	501	GTP	C5-C6-N1	2.59	118.53	113.95
20	K	501	GDP	C8-N7-C5	2.58	107.91	102.99
21	y	501	GTP	C3'-C2'-C1'	2.58	104.87	100.98
20	k	501	GDP	O6-C6-C5	-2.53	119.43	124.37
21	y	501	GTP	O6-C6-C5	-2.51	119.46	124.37
20	y	502	GDP	C3'-C2'-C1'	2.46	104.68	100.98
20	i	501	GDP	C5-C6-N1	2.43	118.24	113.95
21	z	501	GTP	PB-O3B-PG	-2.42	124.53	132.83
20	W	501	GDP	C5-C6-N1	2.39	118.18	113.95
20	O	501	GDP	C5-C6-N1	2.38	118.16	113.95
20	G	501	GDP	C8-N7-C5	2.38	107.52	102.99
20	S	501	GDP	C8-N7-C5	2.37	107.51	102.99
20	S	501	GDP	C5-C6-N1	2.36	118.11	113.95
20	I	501	GDP	C8-N7-C5	2.35	107.48	102.99
20	k	501	GDP	C8-N7-C5	2.35	107.47	102.99
20	Q	501	GDP	C8-N7-C5	2.35	107.46	102.99
21	R	501	GTP	O6-C6-C5	-2.34	119.79	124.37
20	C	501	GDP	C5-C6-N1	2.34	118.09	113.95
20	6	501	GDP	C8-N7-C5	2.34	107.45	102.99
20	I	501	GDP	C5-C6-N1	2.34	118.09	113.95
20	y	502	GDP	C5-C6-N1	2.34	118.09	113.95
20	G	501	GDP	C3'-C2'-C1'	2.33	104.49	100.98
21	X	501	GTP	O6-C6-C5	-2.33	119.82	124.37
20	G	501	GDP	C5-C6-N1	2.33	118.07	113.95
20	Y	501	GDP	C8-N7-C5	2.33	107.42	102.99
21	L	501	GTP	C2-N1-C6	-2.32	120.82	125.10
20	6	501	GDP	C5-C6-N1	2.32	118.05	113.95
20	y	502	GDP	C8-N7-C5	2.32	107.40	102.99
20	W	501	GDP	C8-N7-C5	2.30	107.38	102.99
20	Q	501	GDP	C5-C6-N1	2.30	118.01	113.95
20	i	501	GDP	C8-N7-C5	2.29	107.36	102.99
20	8	501	GDP	C8-N7-C5	2.29	107.36	102.99
20	Y	501	GDP	C5-C6-N1	2.28	117.98	113.95
21	P	501	GTP	PA-O3A-PB	-2.28	125.00	132.83

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	8	501	GDP	C5-C6-N1	2.27	117.96	113.95
21	7	501	GTP	C3'-C2'-C1'	2.27	104.39	100.98
21	P	501	GTP	O6-C6-C5	-2.27	119.94	124.37
21	D	501	GTP	O6-C6-C5	-2.23	120.01	124.37
21	z	501	GTP	O3G-PG-O3B	2.23	112.12	104.64
20	O	501	GDP	C8-N7-C5	2.23	107.23	102.99
21	j	501	GTP	O6-C6-C5	-2.23	120.03	124.37
20	C	501	GDP	C8-N7-C5	2.22	107.22	102.99
21	T	501	GTP	O6-C6-C5	-2.21	120.06	124.37
21	7	501	GTP	O6-C6-C5	-2.19	120.10	124.37
21	H	501	GTP	N2-C2-N1	2.18	121.36	116.71
21	Z	501	GTP	O6-C6-C5	-2.18	120.12	124.37
21	z	501	GTP	O6-C6-C5	-2.10	120.26	124.37
21	9	501	GTP	O6-C6-C5	-2.09	120.29	124.37
21	J	501	GTP	O6-C6-C5	-2.06	120.35	124.37
21	H	501	GTP	O6-C6-C5	-2.02	120.42	124.37
20	I	501	GDP	C2'-C3'-C4'	2.02	106.57	102.64
20	C	501	GDP	C2'-C3'-C4'	2.01	106.56	102.64
20	W	501	GDP	C2'-C3'-C4'	2.01	106.54	102.64
21	H	501	GTP	N1-C2-N3	-2.01	119.57	123.32

There are no chirality outliers.

All (127) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
20	6	501	GDP	C5'-O5'-PA-O2A
20	8	501	GDP	C5'-O5'-PA-O3A
20	8	501	GDP	C5'-O5'-PA-O1A
20	C	501	GDP	C5'-O5'-PA-O3A
20	C	501	GDP	C5'-O5'-PA-O1A
20	G	501	GDP	C5'-O5'-PA-O3A
20	G	501	GDP	C5'-O5'-PA-O2A
20	G	501	GDP	O4'-C4'-C5'-O5'
20	I	501	GDP	C5'-O5'-PA-O1A
20	I	501	GDP	C5'-O5'-PA-O2A
20	K	501	GDP	C5'-O5'-PA-O3A
20	O	501	GDP	C5'-O5'-PA-O1A
20	O	501	GDP	C5'-O5'-PA-O2A
20	Q	501	GDP	PA-O3A-PB-O3B
20	Q	501	GDP	C5'-O5'-PA-O1A
20	W	501	GDP	PA-O3A-PB-O2B
20	W	501	GDP	PA-O3A-PB-O3B

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
20	W	501	GDP	C5'-O5'-PA-O3A
20	W	501	GDP	O4'-C4'-C5'-O5'
20	W	501	GDP	C3'-C4'-C5'-O5'
20	Y	501	GDP	C5'-O5'-PA-O1A
20	i	501	GDP	C5'-O5'-PA-O3A
20	i	501	GDP	C5'-O5'-PA-O2A
20	k	501	GDP	C5'-O5'-PA-O1A
20	y	502	GDP	C5'-O5'-PA-O3A
21	7	501	GTP	C5'-O5'-PA-O3A
21	9	501	GTP	C5'-O5'-PA-O1A
21	9	501	GTP	C5'-O5'-PA-O2A
21	9	501	GTP	O4'-C4'-C5'-O5'
21	9	501	GTP	C3'-C4'-C5'-O5'
21	D	501	GTP	C5'-O5'-PA-O1A
21	D	501	GTP	C3'-C4'-C5'-O5'
21	H	501	GTP	PB-O3B-PG-O3G
21	H	501	GTP	O4'-C4'-C5'-O5'
21	J	501	GTP	C5'-O5'-PA-O1A
21	J	501	GTP	C5'-O5'-PA-O2A
21	J	501	GTP	O4'-C4'-C5'-O5'
21	L	501	GTP	C5'-O5'-PA-O3A
21	R	501	GTP	C5'-O5'-PA-O3A
21	R	501	GTP	C5'-O5'-PA-O1A
21	R	501	GTP	C4'-C5'-O5'-PA
21	R	501	GTP	C3'-C4'-C5'-O5'
21	X	501	GTP	C5'-O5'-PA-O3A
21	X	501	GTP	C5'-O5'-PA-O1A
21	X	501	GTP	C5'-O5'-PA-O2A
21	Z	501	GTP	C5'-O5'-PA-O1A
21	j	501	GTP	C5'-O5'-PA-O1A
21	y	501	GTP	PB-O3B-PG-O2G
21	z	501	GTP	PB-O3B-PG-O3G
21	z	501	GTP	C5'-O5'-PA-O1A
21	z	501	GTP	O4'-C4'-C5'-O5'
21	z	501	GTP	C3'-C4'-C5'-O5'
20	8	501	GDP	C3'-C4'-C5'-O5'
20	G	501	GDP	C3'-C4'-C5'-O5'
21	H	501	GTP	C3'-C4'-C5'-O5'
21	T	501	GTP	C4'-C5'-O5'-PA
21	J	501	GTP	C3'-C4'-C5'-O5'
20	K	501	GDP	C3'-C4'-C5'-O5'
21	y	501	GTP	C3'-C4'-C5'-O5'

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
20	y	502	GDP	C3'-C4'-C5'-O5'
20	K	501	GDP	O4'-C4'-C5'-O5'
21	D	501	GTP	O4'-C4'-C5'-O5'
21	P	501	GTP	C3'-C4'-C5'-O5'
21	R	501	GTP	O4'-C4'-C5'-O5'
21	T	501	GTP	C3'-C4'-C5'-O5'
20	8	501	GDP	O4'-C4'-C5'-O5'
21	L	501	GTP	C4'-C5'-O5'-PA
21	9	501	GTP	C4'-C5'-O5'-PA
21	D	501	GTP	C4'-C5'-O5'-PA
21	H	501	GTP	C4'-C5'-O5'-PA
21	X	501	GTP	C4'-C5'-O5'-PA
21	H	501	GTP	PB-O3A-PA-O5'
21	y	501	GTP	O4'-C4'-C5'-O5'
21	J	501	GTP	PB-O3B-PG-O1G
21	z	501	GTP	PB-O3B-PG-O1G
21	Z	501	GTP	C4'-C5'-O5'-PA
20	6	501	GDP	C5'-O5'-PA-O3A
20	Q	501	GDP	C5'-O5'-PA-O3A
21	D	501	GTP	C5'-O5'-PA-O3A
21	J	501	GTP	C5'-O5'-PA-O3A
21	Z	501	GTP	C5'-O5'-PA-O3A
21	P	501	GTP	O4'-C4'-C5'-O5'
21	L	501	GTP	PB-O3A-PA-O2A
23	u	401	ATP	PB-O3A-PA-O2A
21	P	501	GTP	C4'-C5'-O5'-PA
21	j	501	GTP	C4'-C5'-O5'-PA
21	y	501	GTP	C4'-C5'-O5'-PA
20	6	501	GDP	C5'-O5'-PA-O1A
20	K	501	GDP	C5'-O5'-PA-O1A
20	Q	501	GDP	C5'-O5'-PA-O2A
20	W	501	GDP	C5'-O5'-PA-O2A
20	y	502	GDP	C5'-O5'-PA-O1A
21	7	501	GTP	C5'-O5'-PA-O1A
21	7	501	GTP	C5'-O5'-PA-O2A
21	D	501	GTP	C5'-O5'-PA-O2A
21	L	501	GTP	C5'-O5'-PA-O2A
21	Z	501	GTP	C5'-O5'-PA-O2A
21	j	501	GTP	C5'-O5'-PA-O2A
23	u	401	ATP	C3'-C4'-C5'-O5'
21	J	501	GTP	C4'-C5'-O5'-PA
20	y	502	GDP	O4'-C4'-C5'-O5'

Continued on next page...

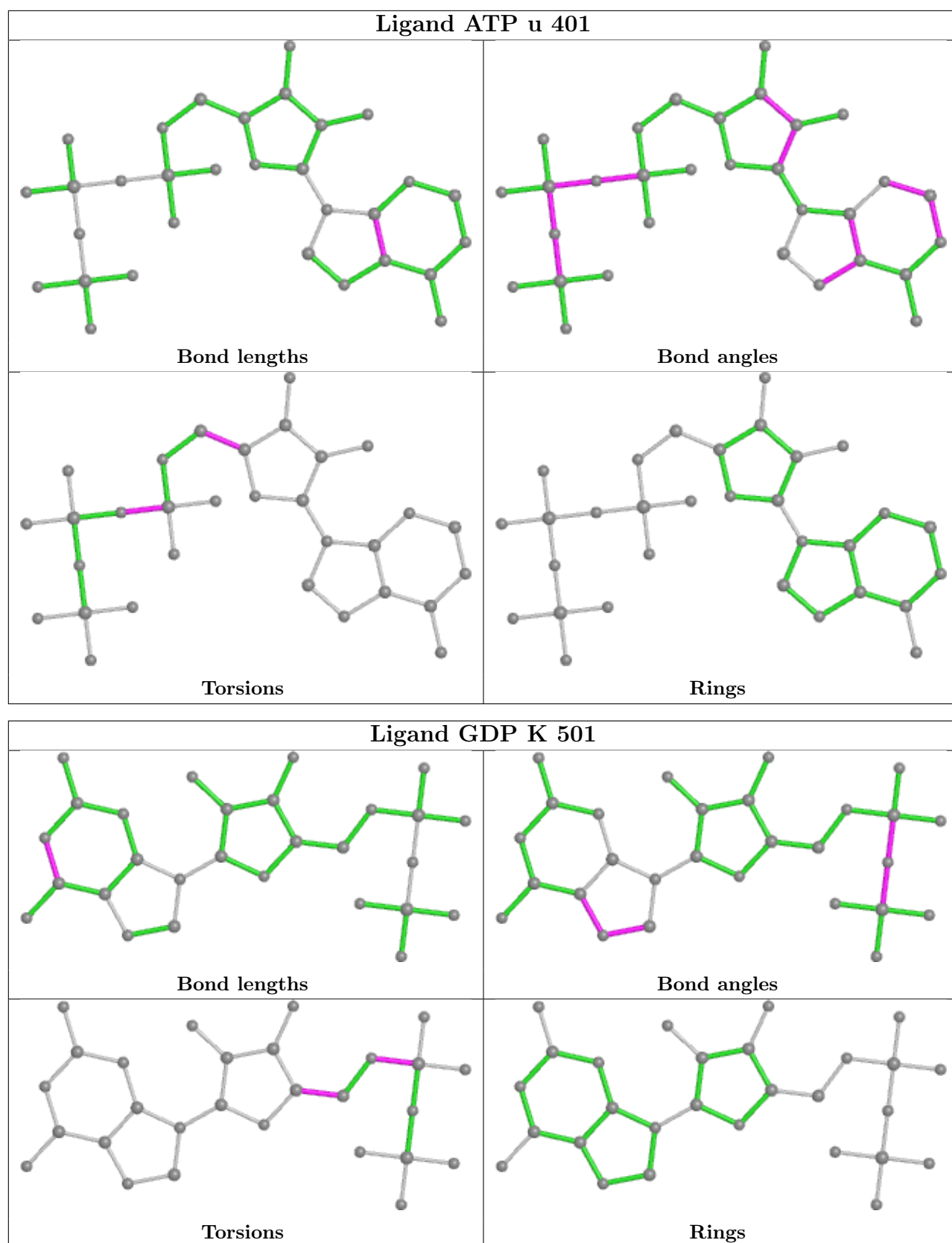
Continued from previous page...

Mol	Chain	Res	Type	Atoms
21	T	501	GTP	O4'-C4'-C5'-O5'
23	u	401	ATP	O4'-C4'-C5'-O5'
21	R	501	GTP	PB-O3A-PA-O2A
21	z	501	GTP	C4'-C5'-O5'-PA
20	I	501	GDP	C3'-C4'-C5'-O5'
21	z	501	GTP	PG-O3B-PB-O1B
23	u	401	ATP	PB-O3A-PA-O1A
20	G	501	GDP	PA-O3A-PB-O1B
21	X	501	GTP	C3'-C4'-C5'-O5'
20	Q	501	GDP	PA-O3A-PB-O2B
21	J	501	GTP	PB-O3B-PG-O2G
21	J	501	GTP	PB-O3B-PG-O3G
20	I	501	GDP	C5'-O5'-PA-O3A
20	O	501	GDP	C5'-O5'-PA-O3A
21	9	501	GTP	C5'-O5'-PA-O3A
21	T	501	GTP	C5'-O5'-PA-O3A
21	j	501	GTP	C5'-O5'-PA-O3A
21	z	501	GTP	C5'-O5'-PA-O3A
20	Q	501	GDP	O4'-C4'-C5'-O5'
20	I	501	GDP	PB-O3A-PA-O2A
21	L	501	GTP	PB-O3A-PA-O1A
21	P	501	GTP	PG-O3B-PB-O1B
20	Q	501	GDP	C4'-C5'-O5'-PA
20	i	501	GDP	O4'-C4'-C5'-O5'
21	7	501	GTP	C3'-C4'-C5'-O5'
20	W	501	GDP	PA-O3A-PB-O1B

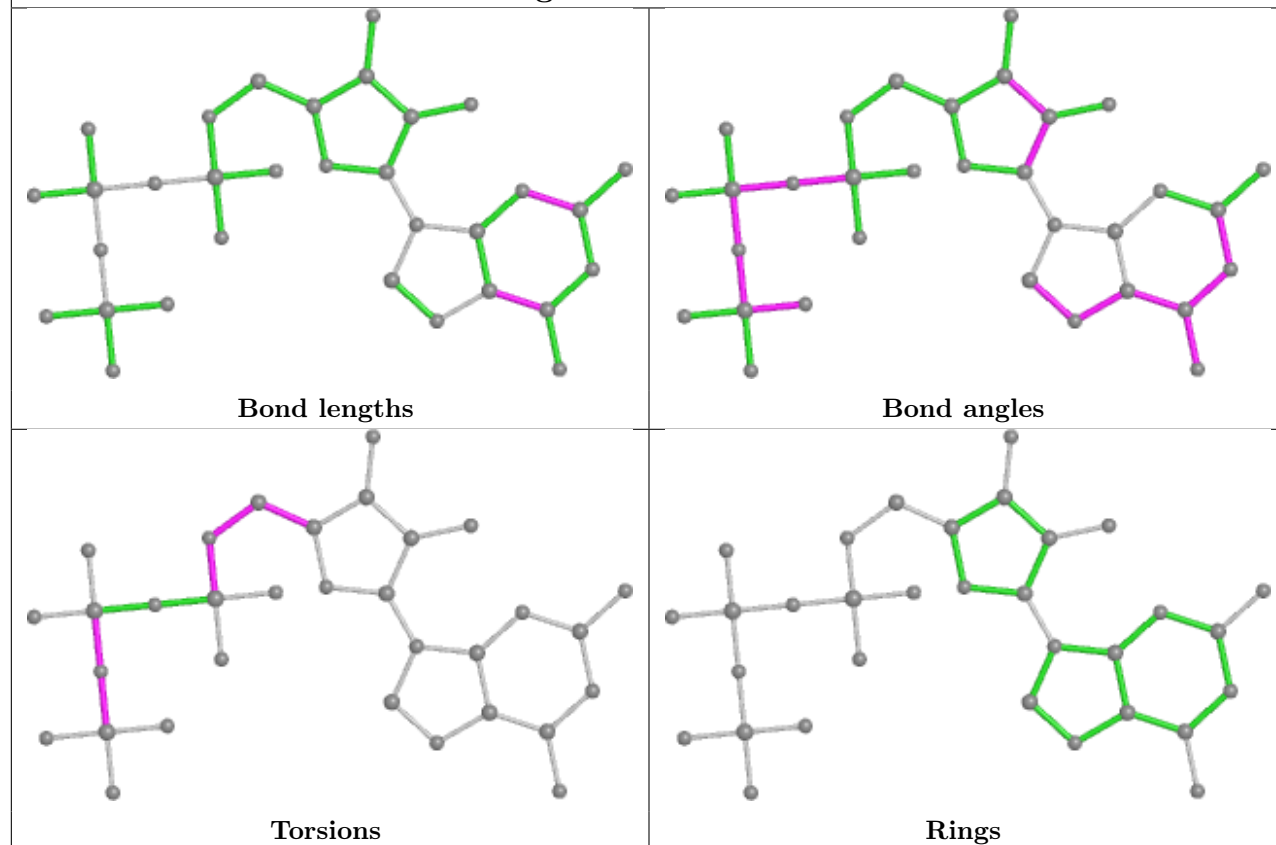
There are no ring outliers.

No monomer is involved in short contacts.

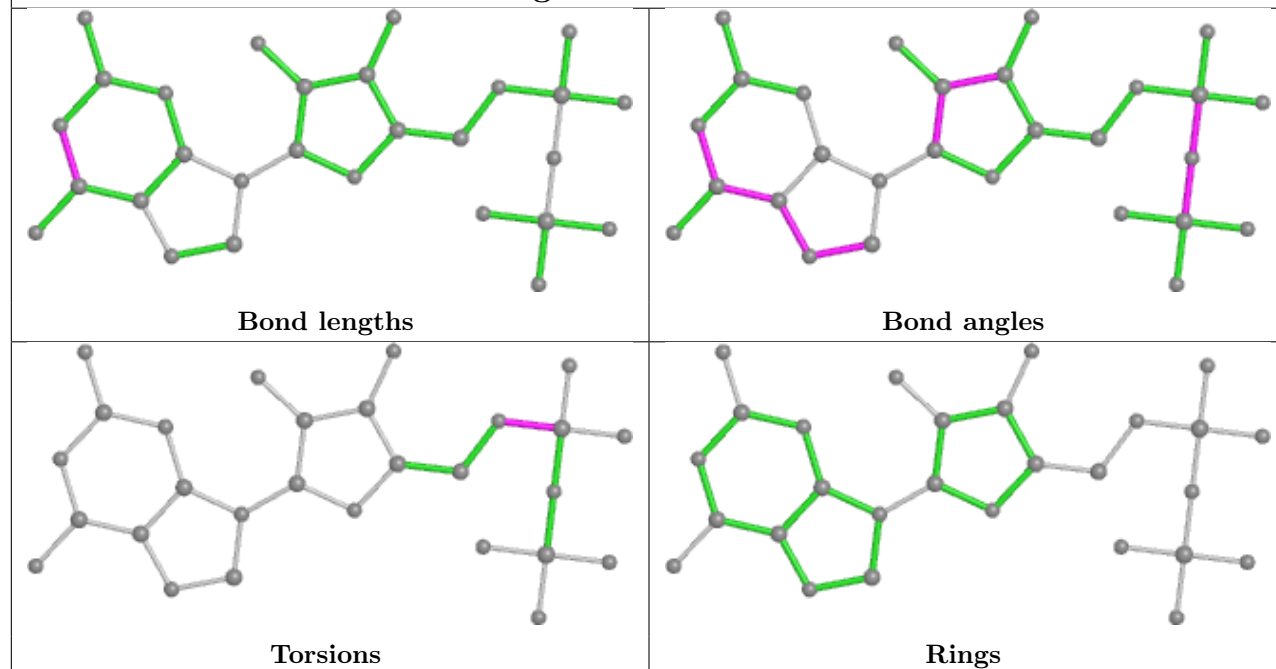
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



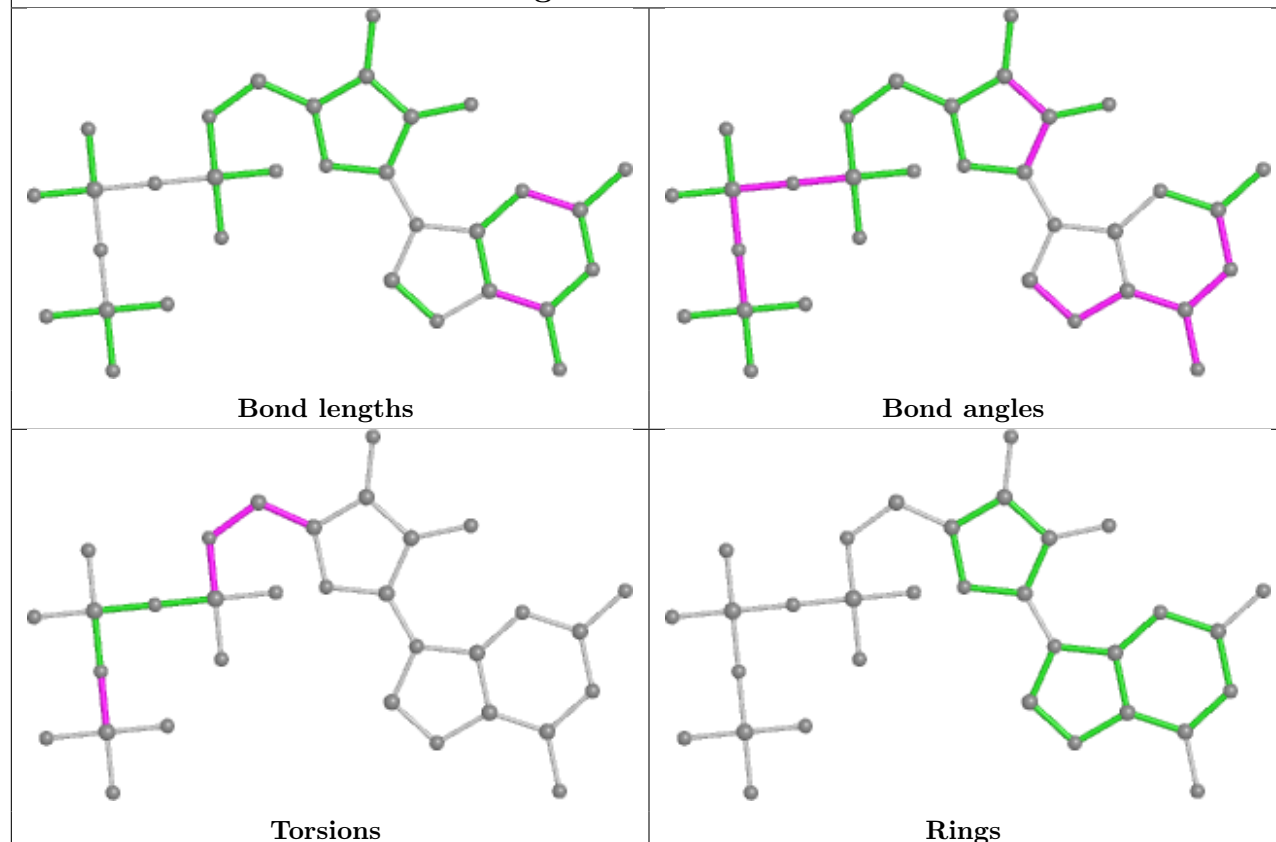
Ligand GTP z 501



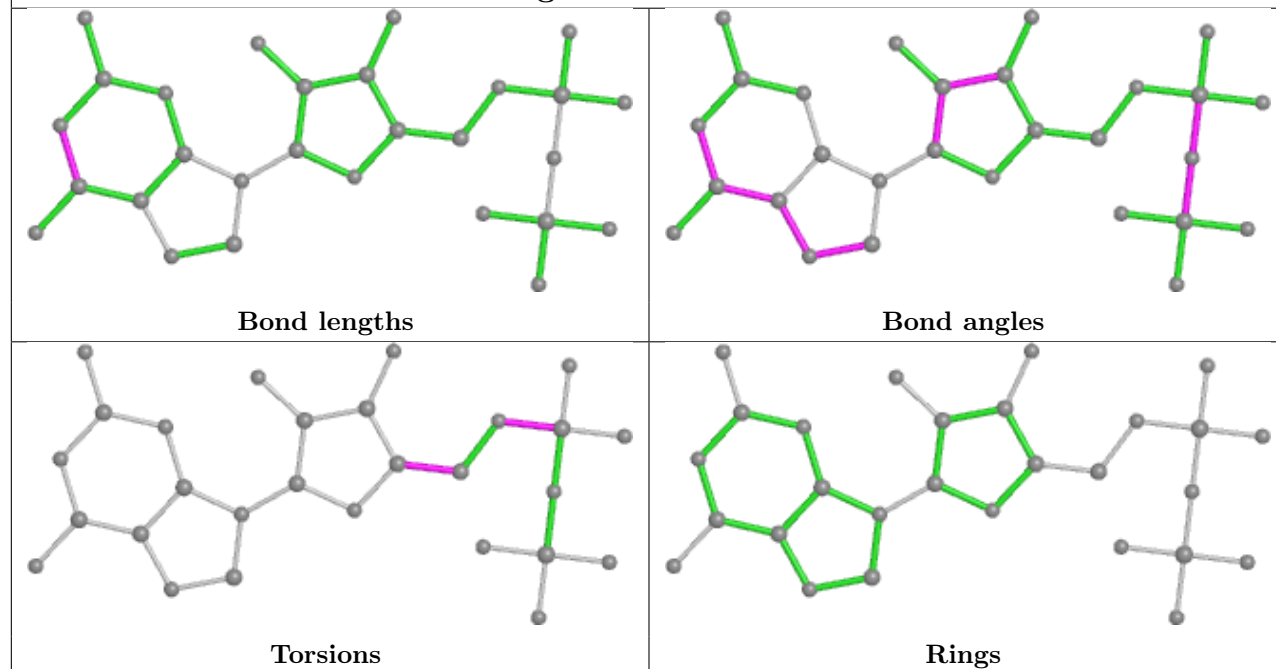
Ligand GDP 6 501

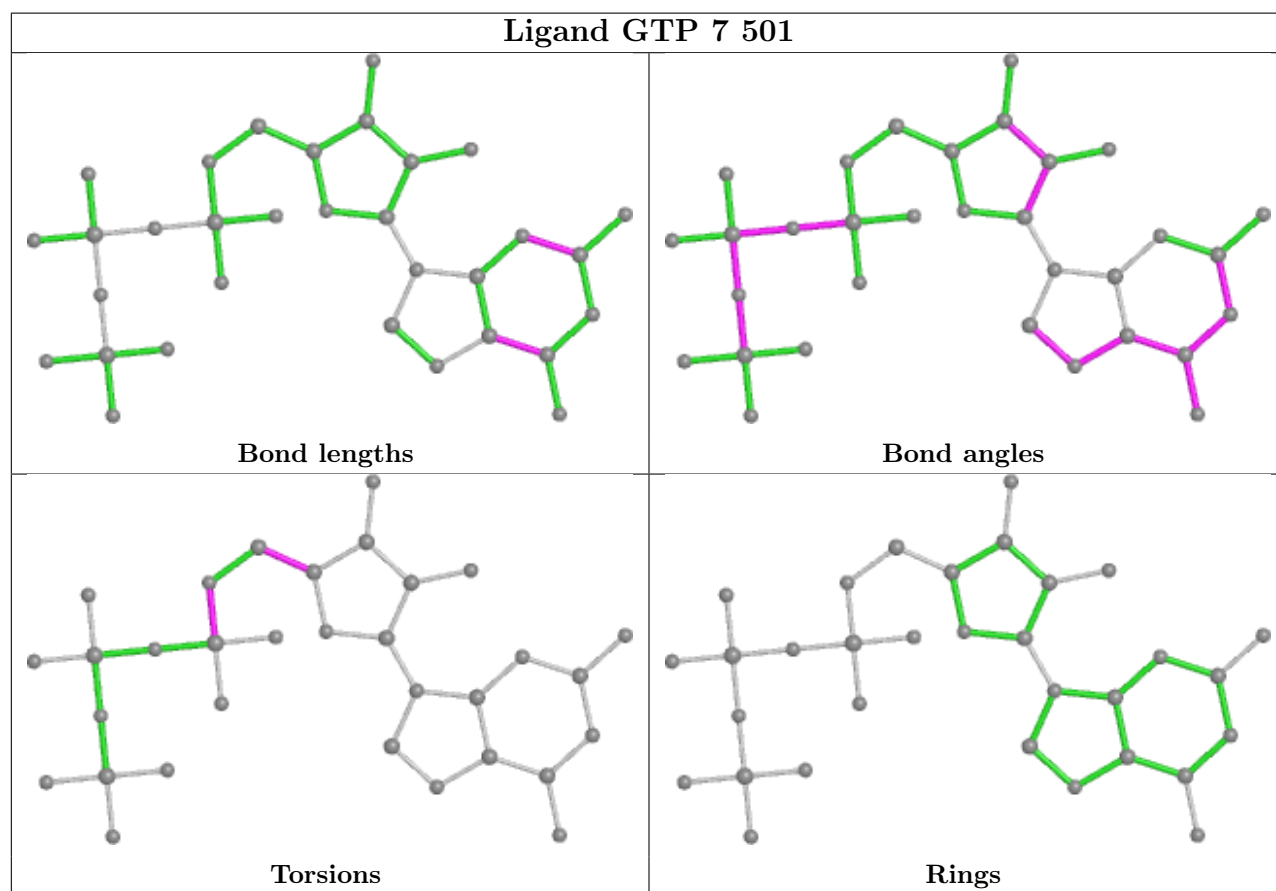
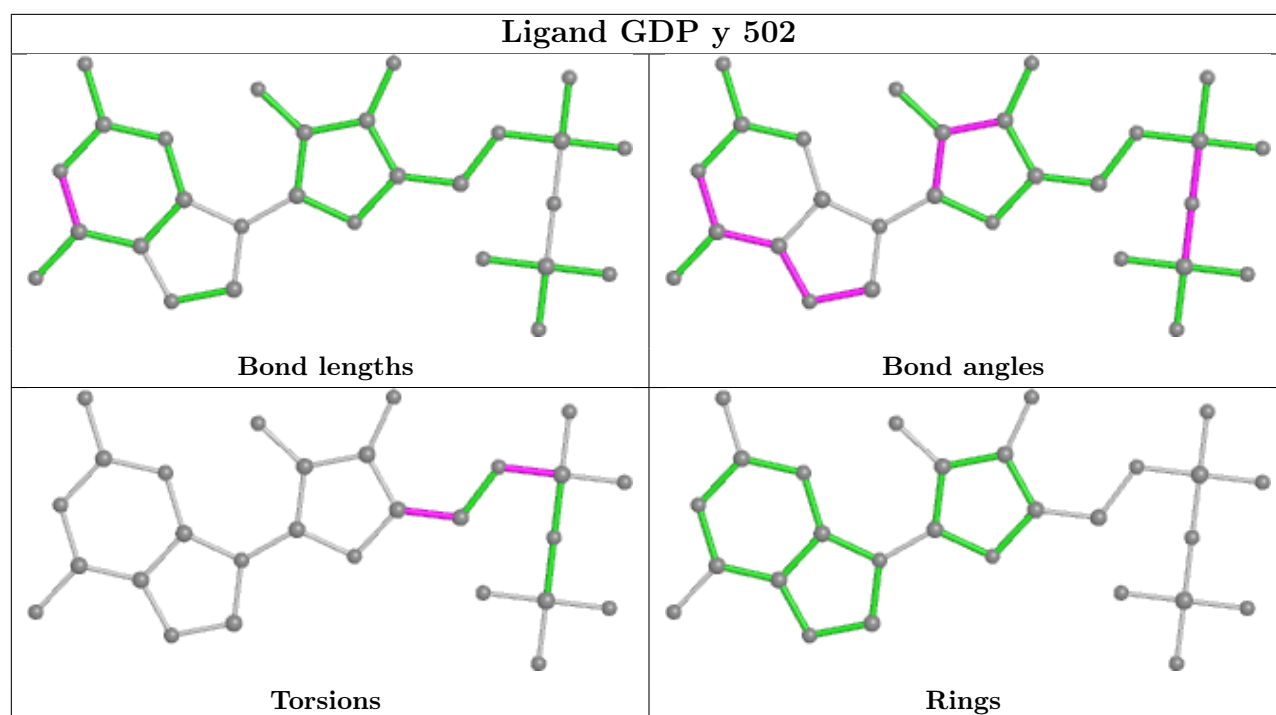


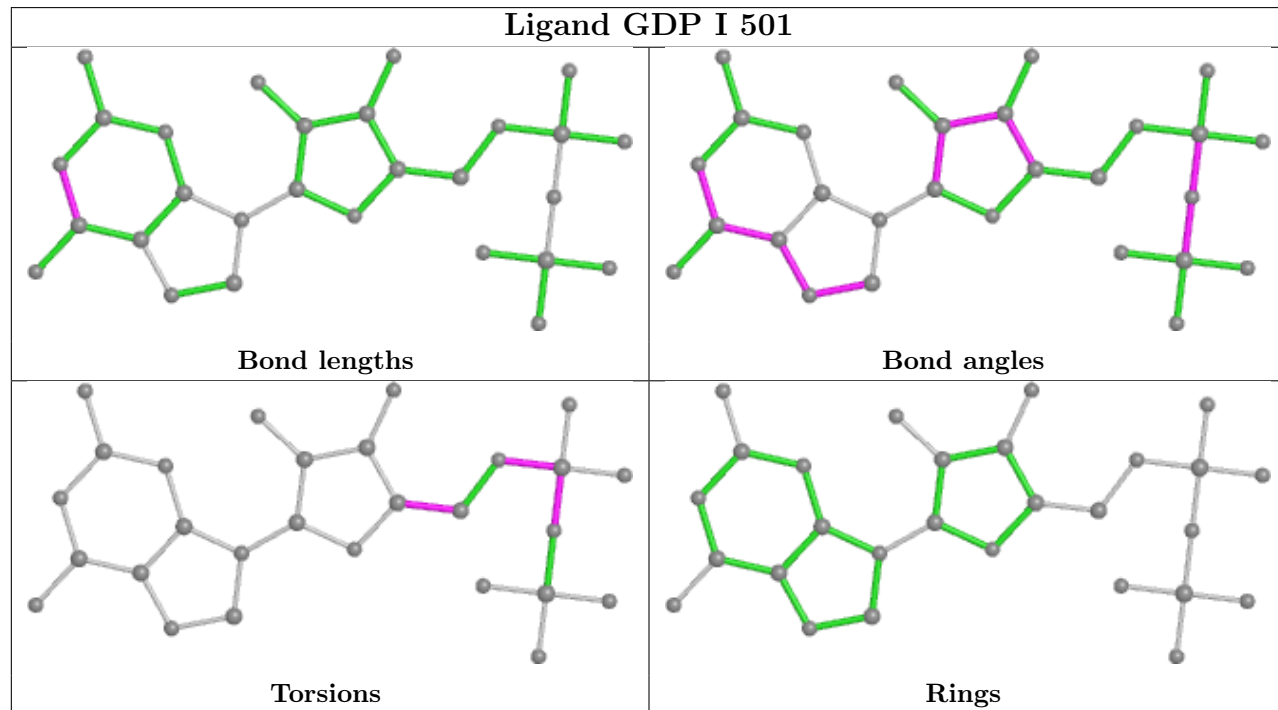
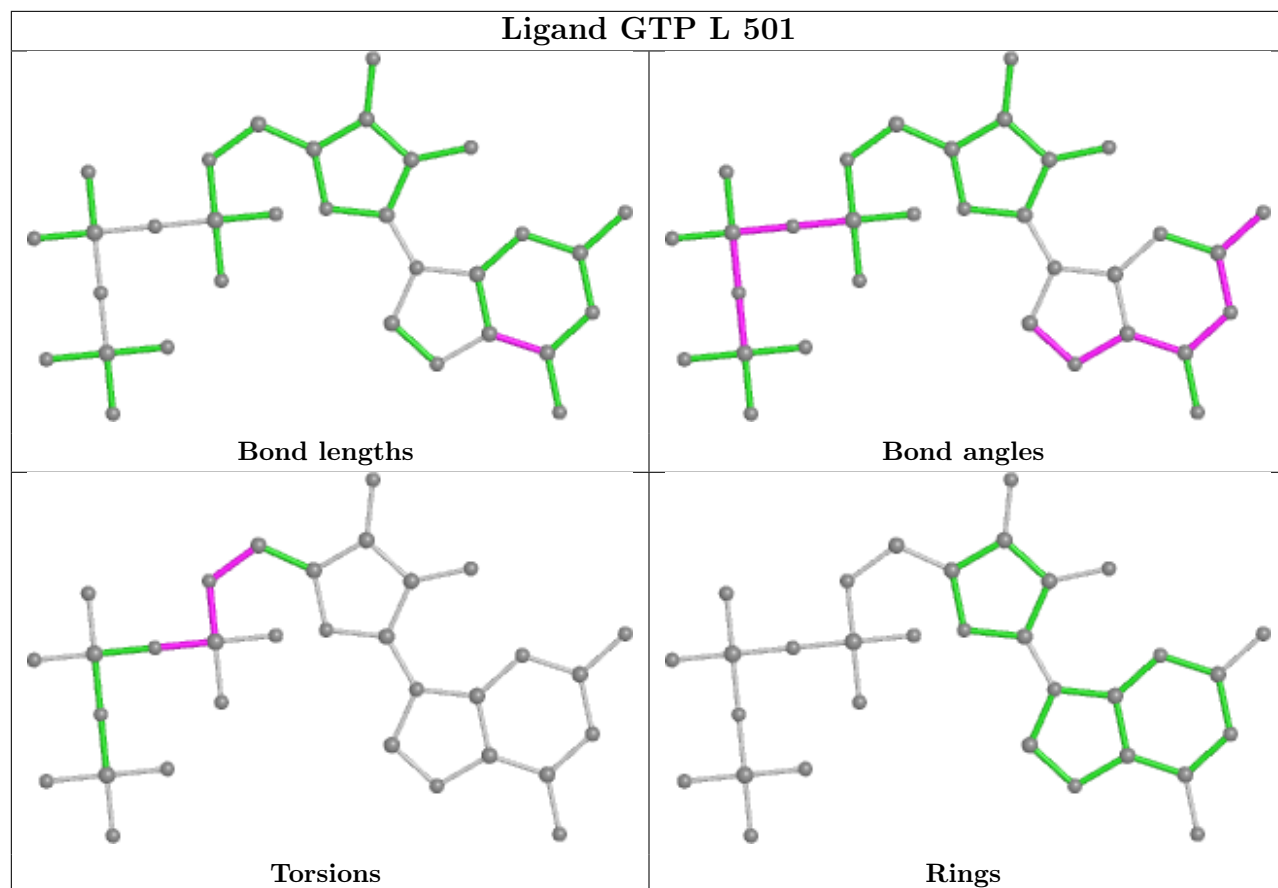
Ligand GTP J 501

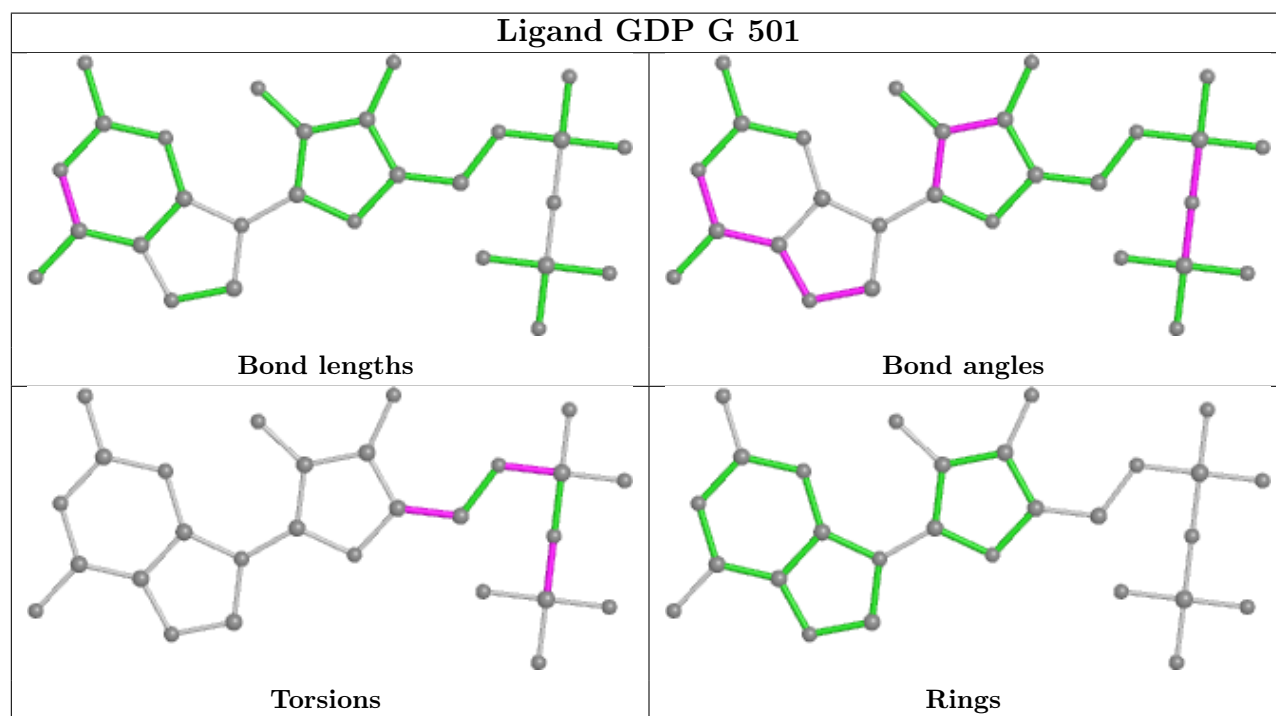
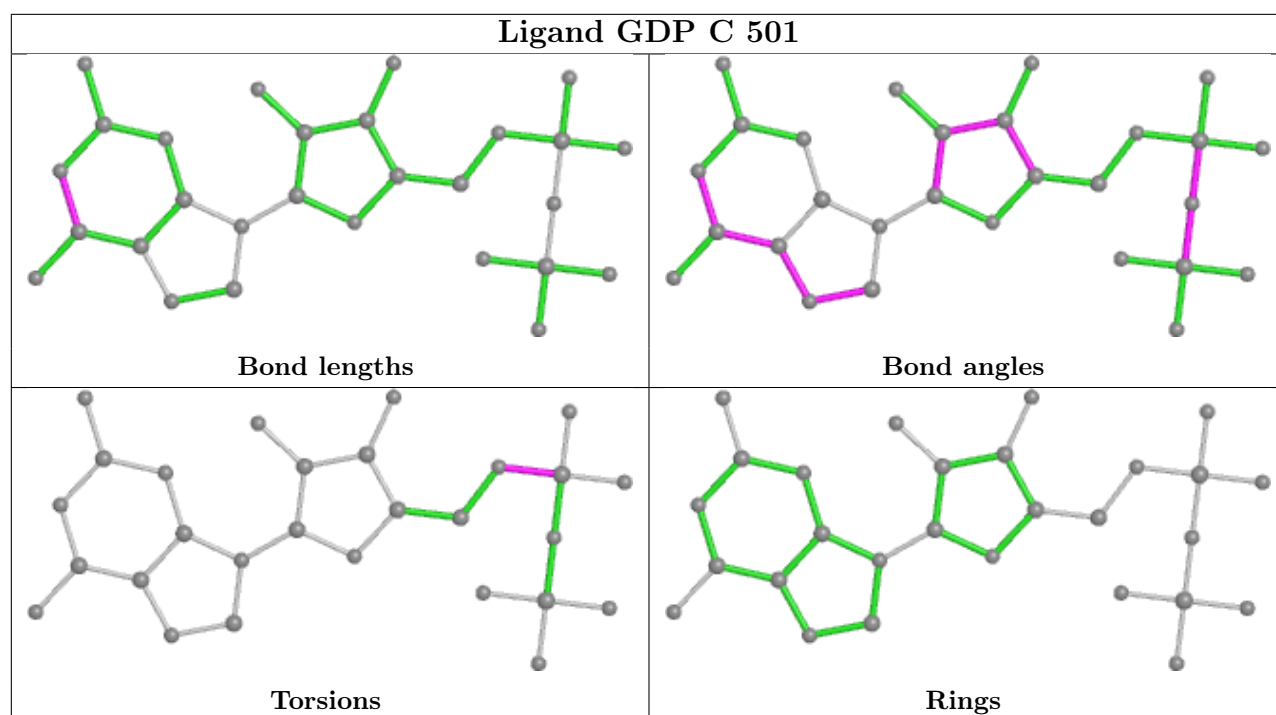


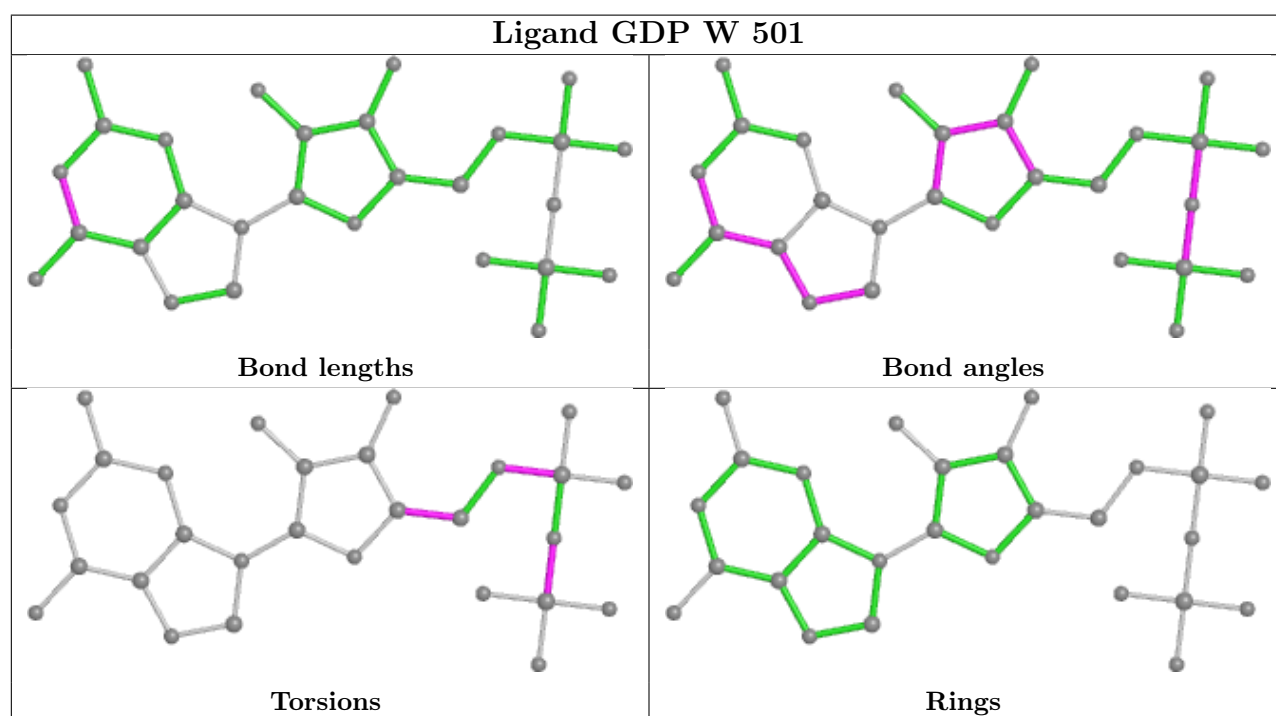
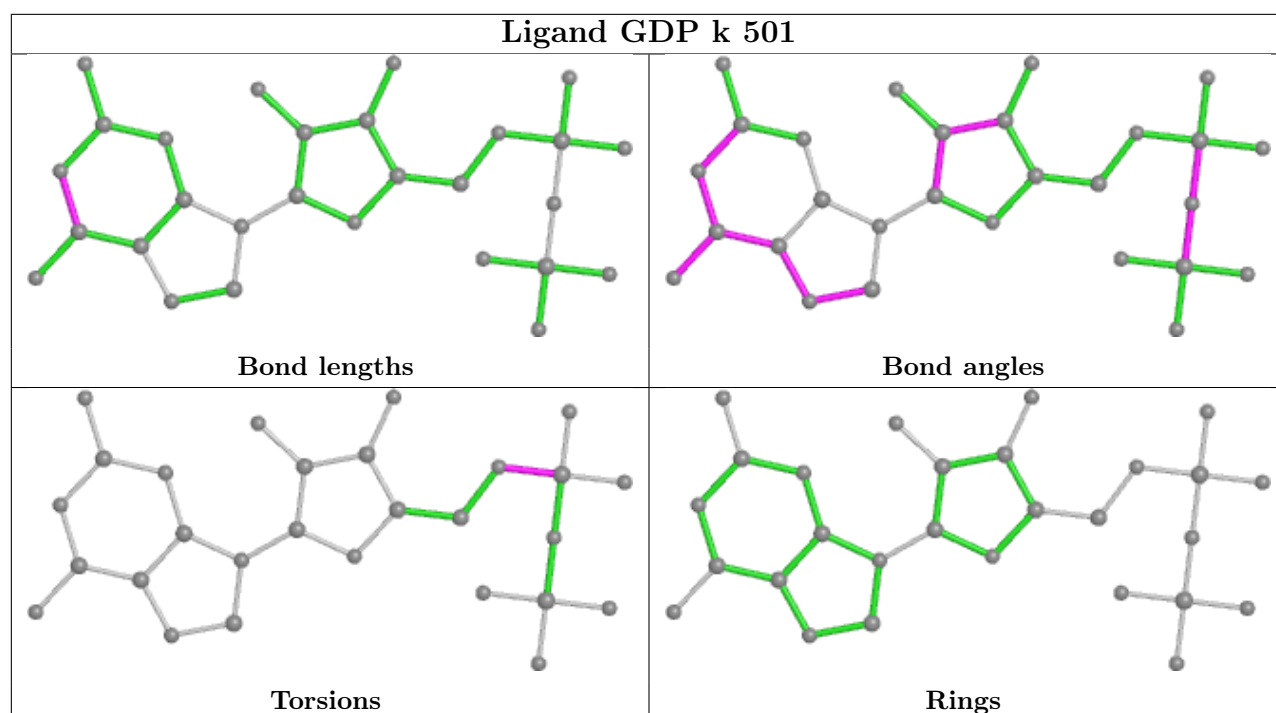
Ligand GDP i 501

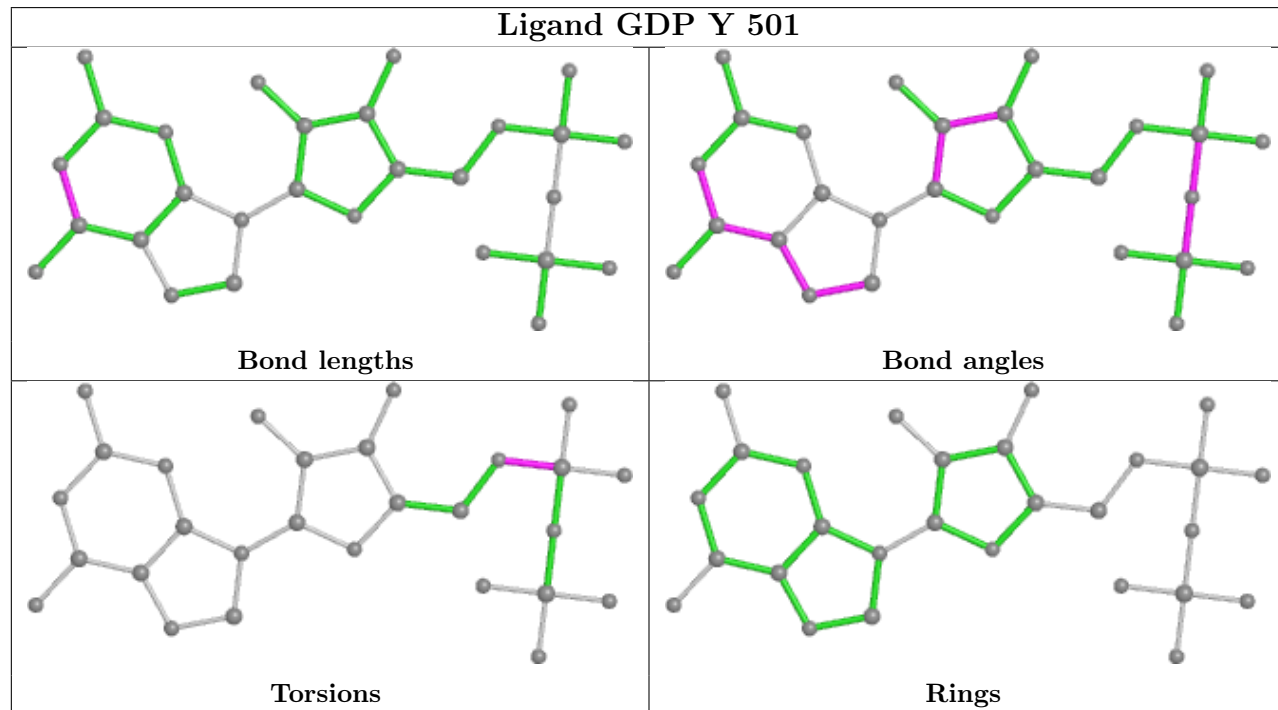
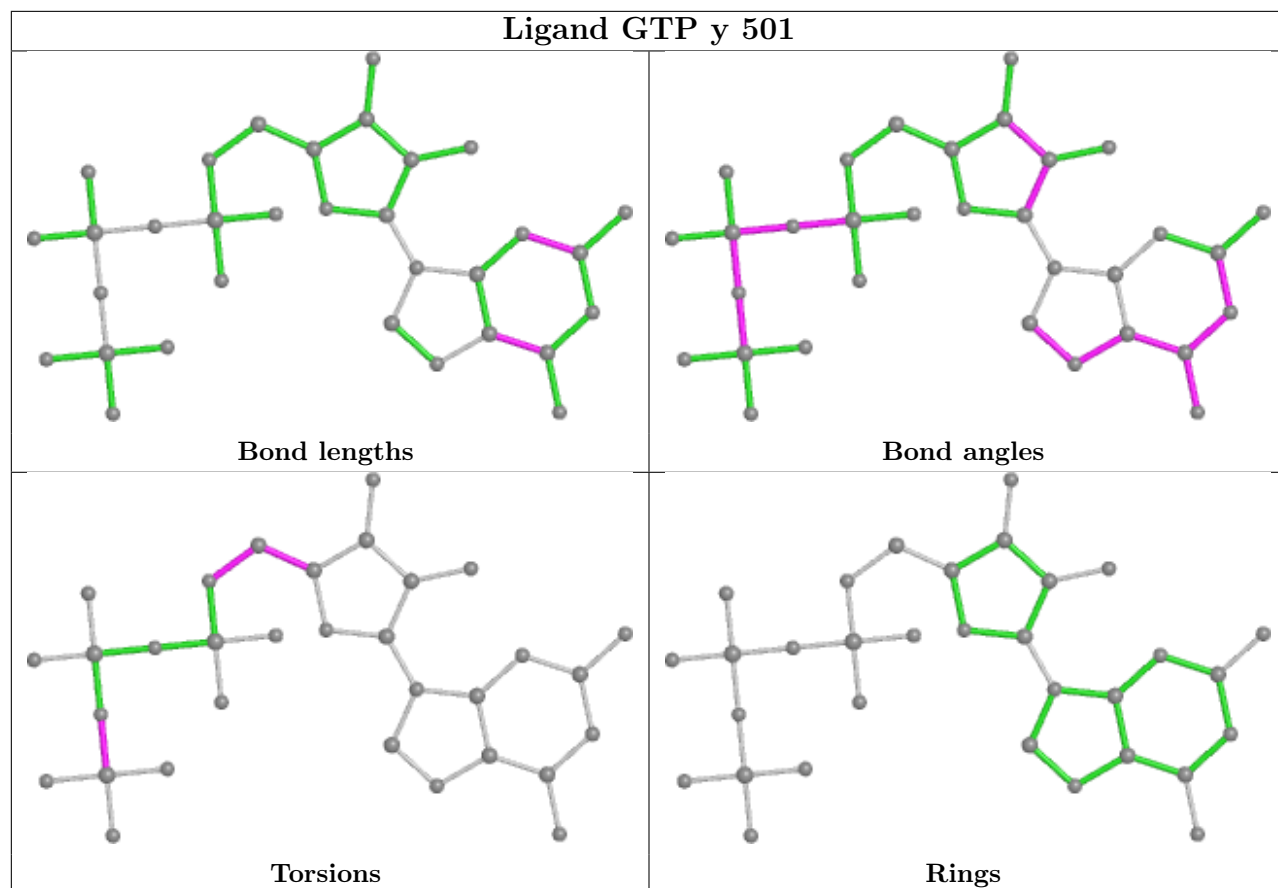




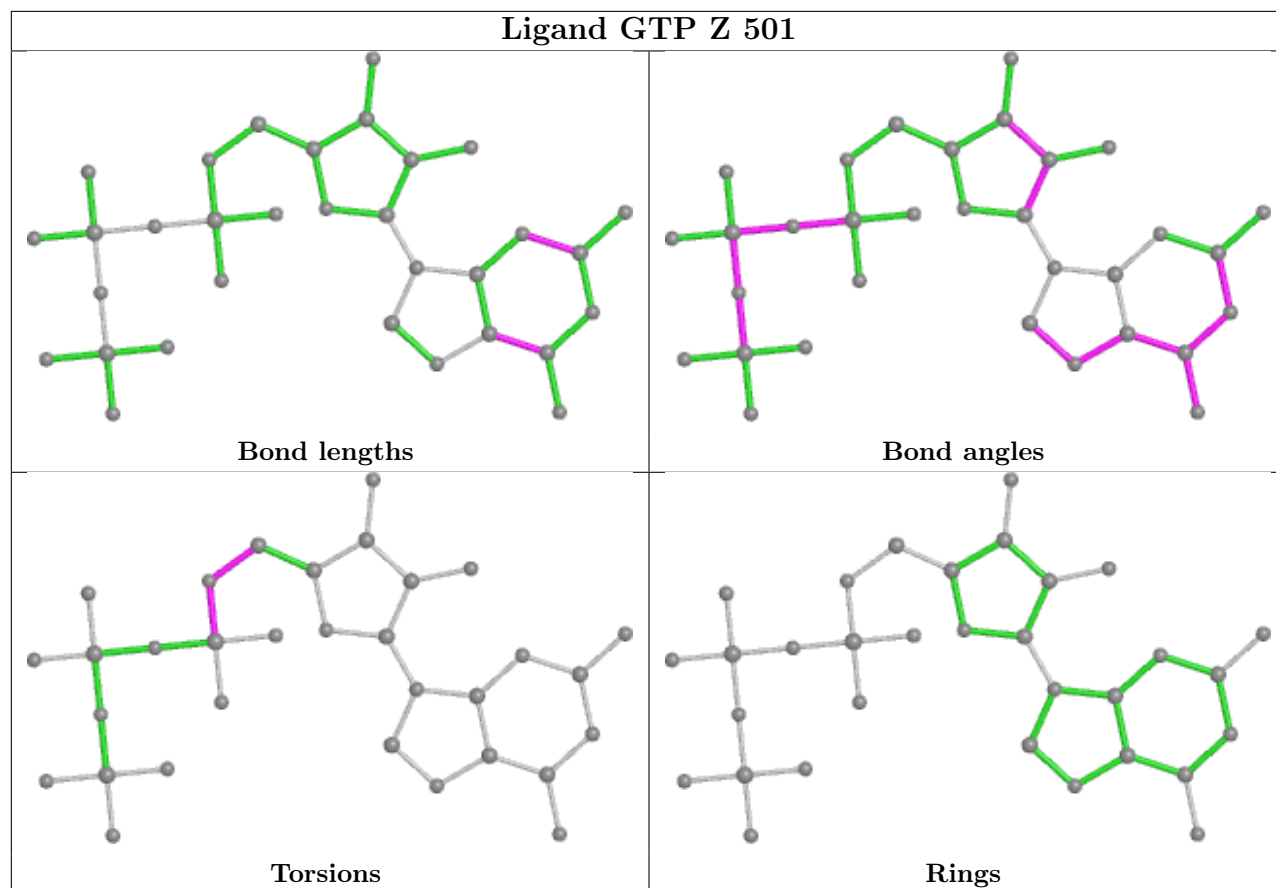




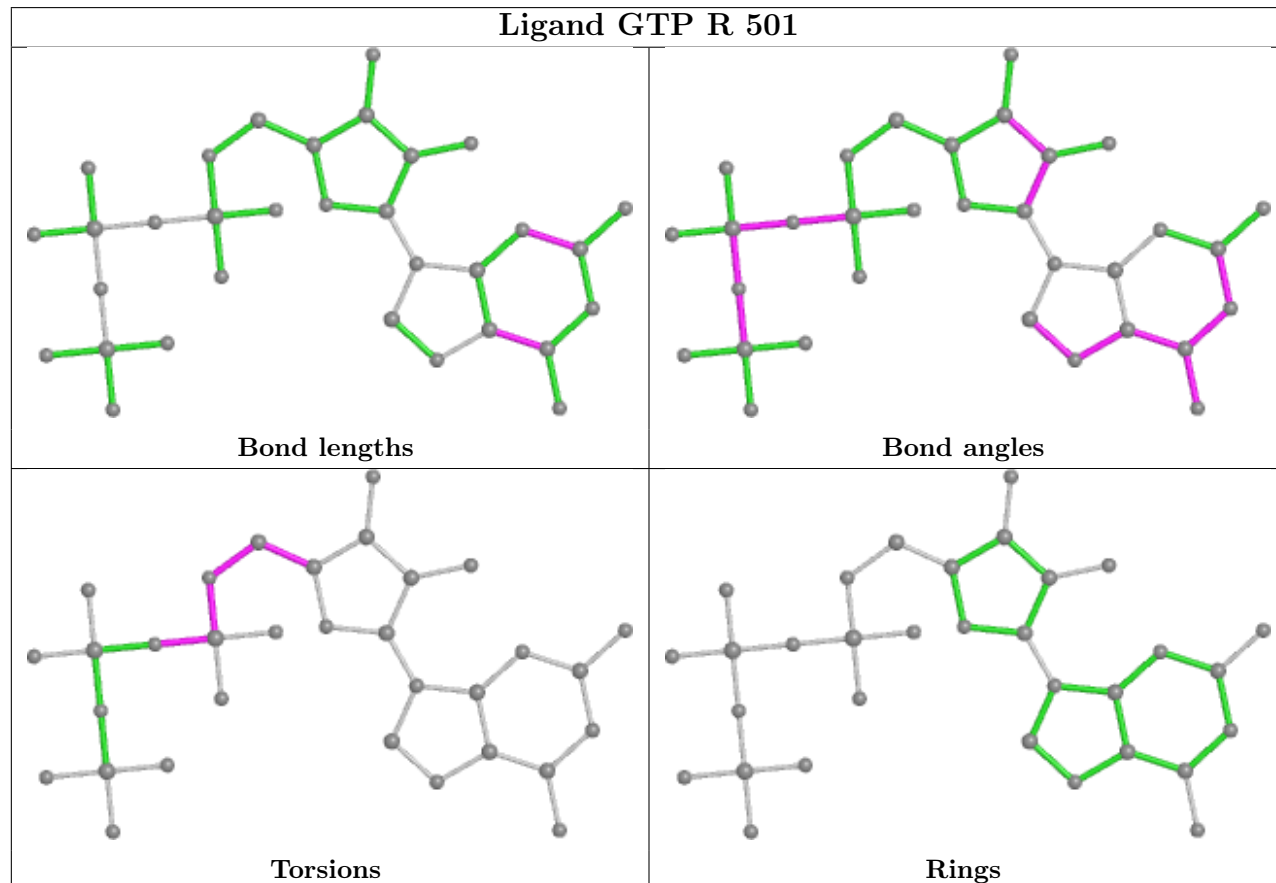


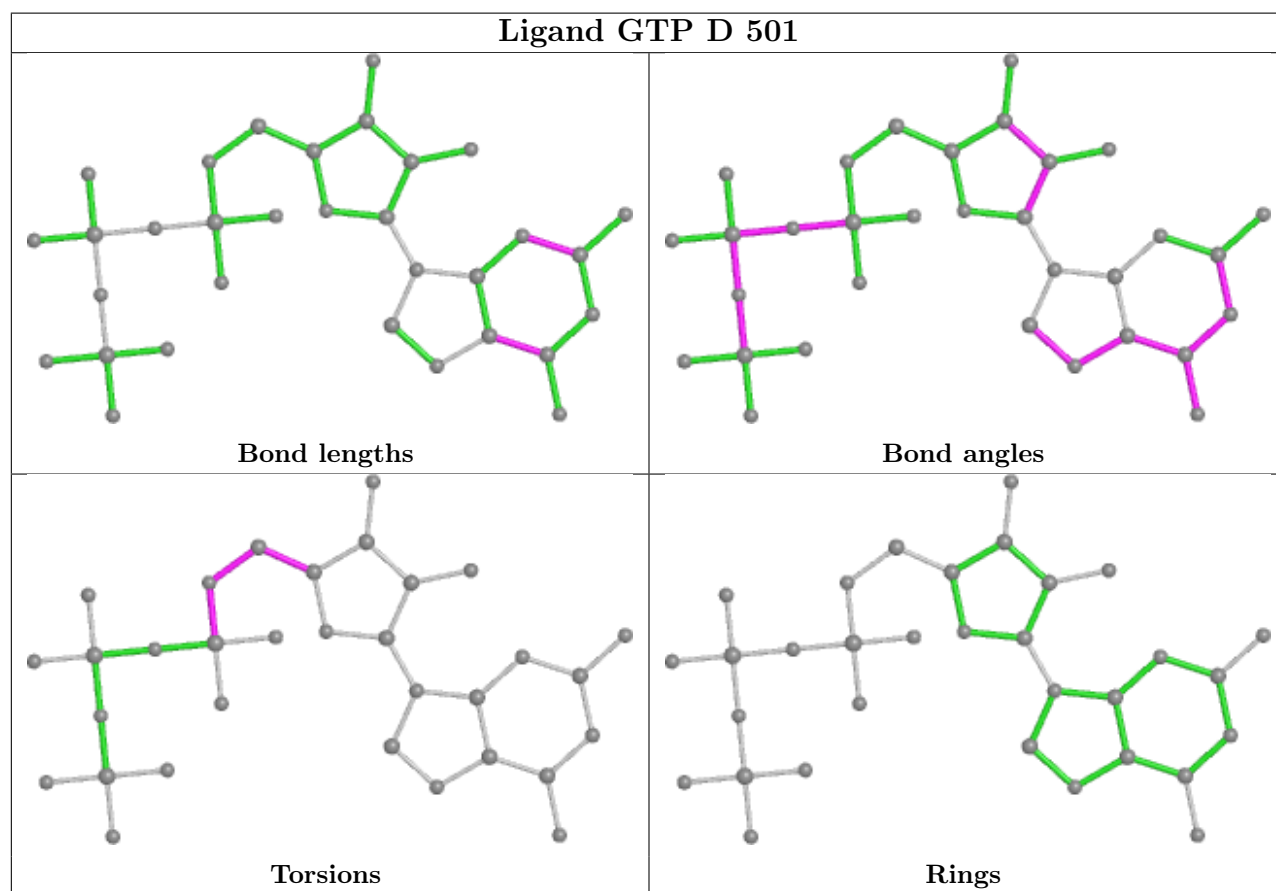
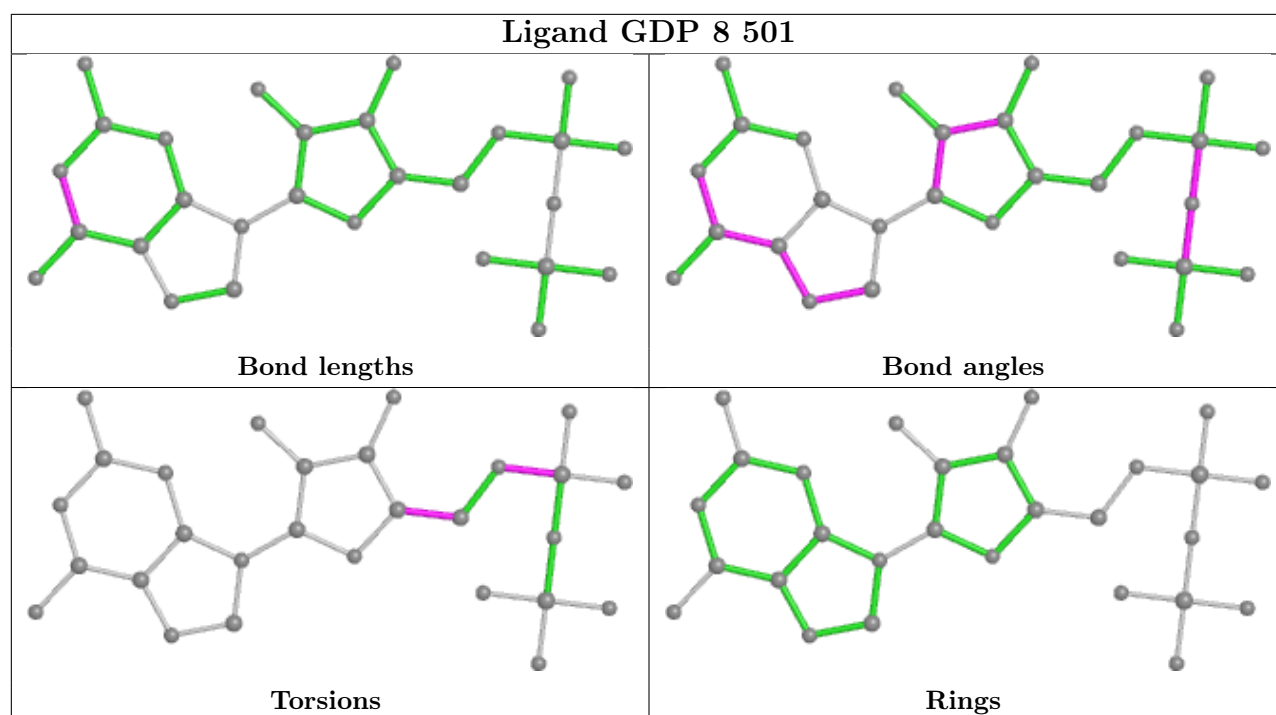


Ligand GTP Z 501

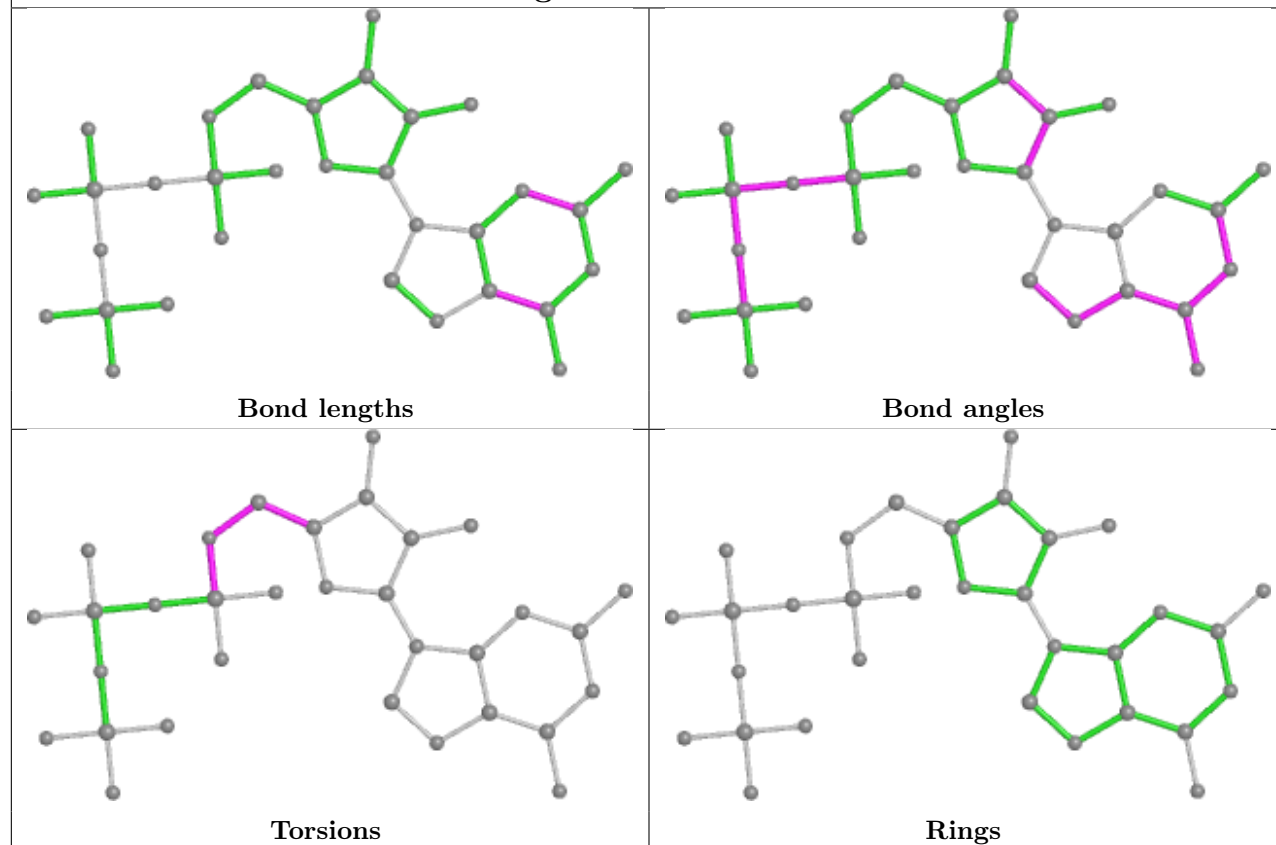


Ligand GTP R 501

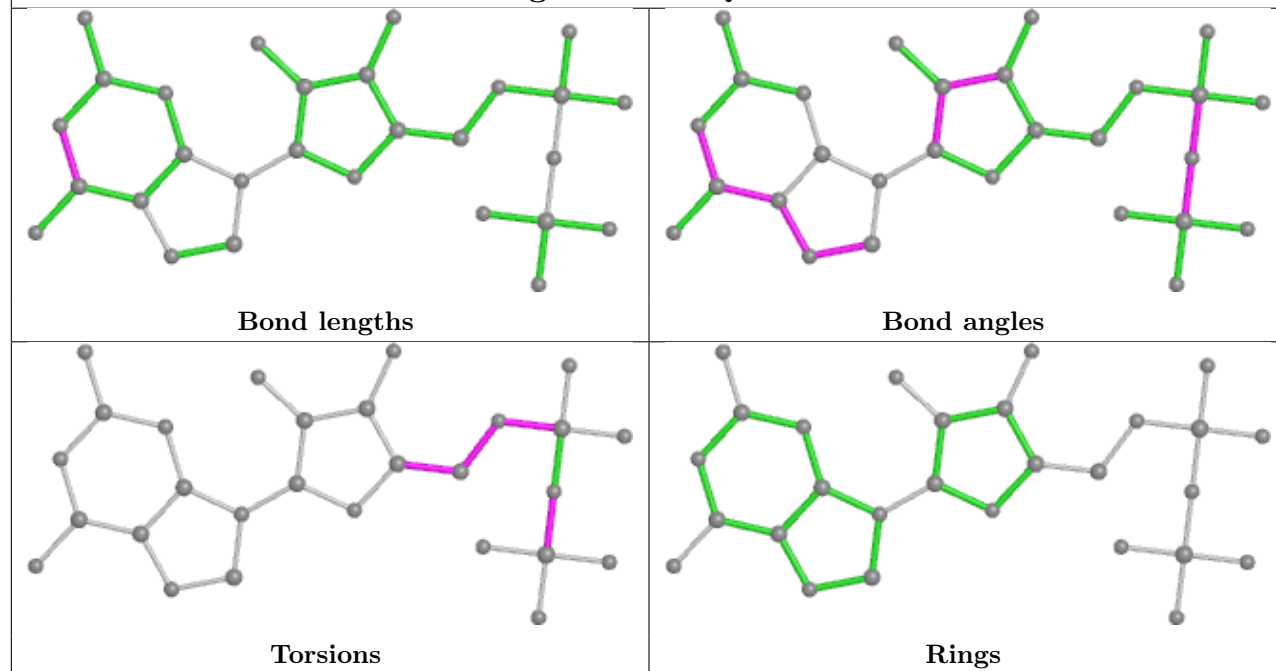


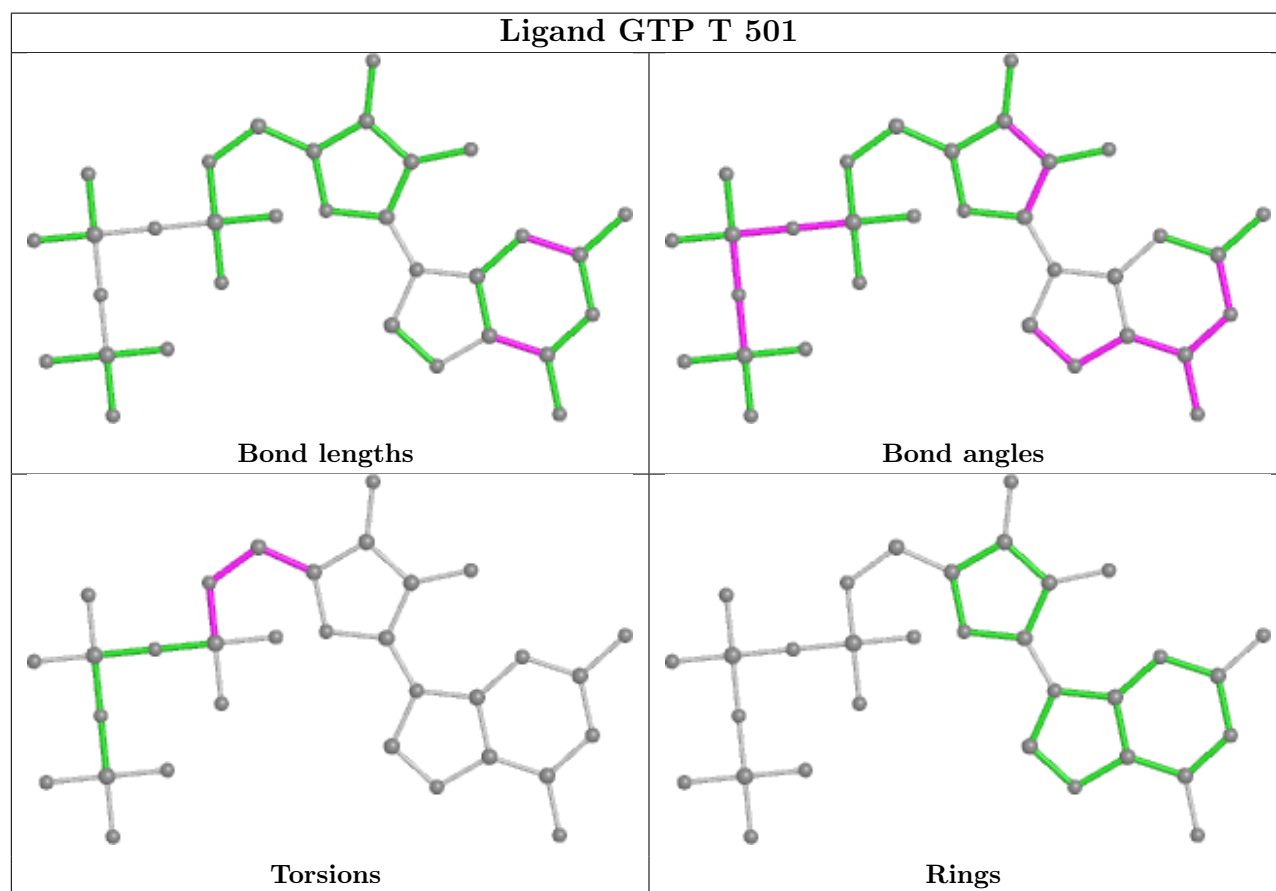
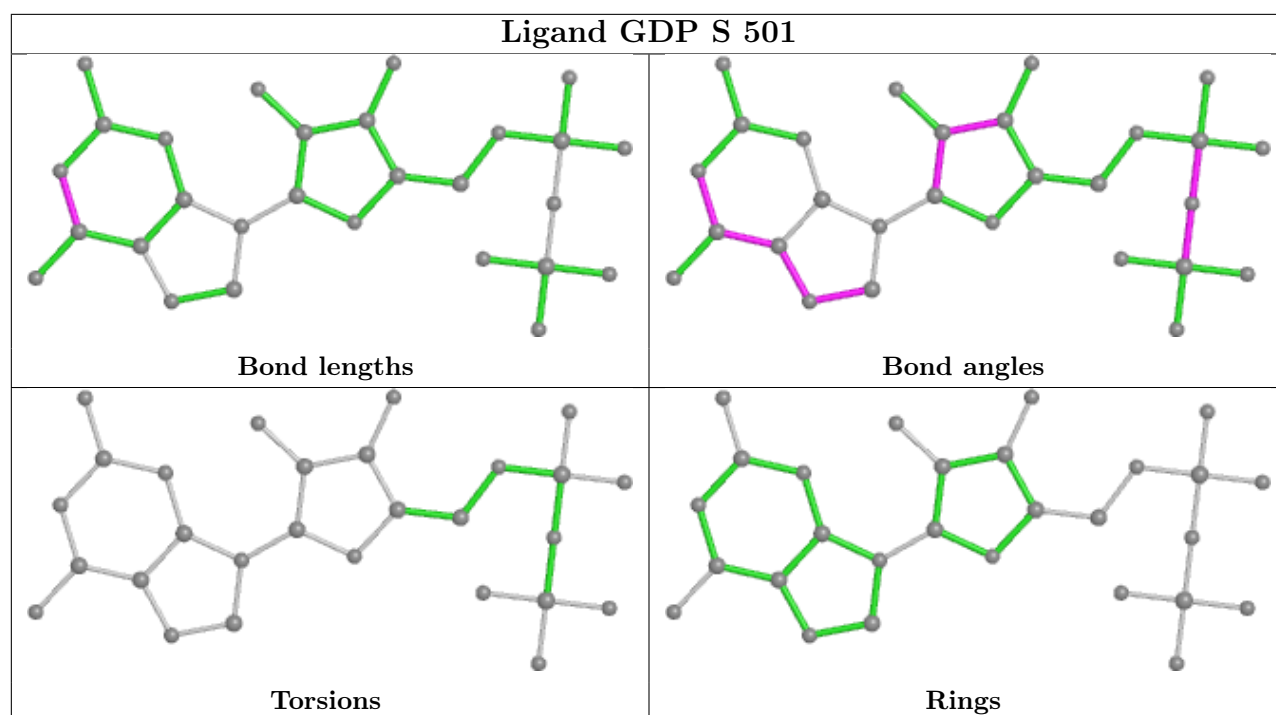


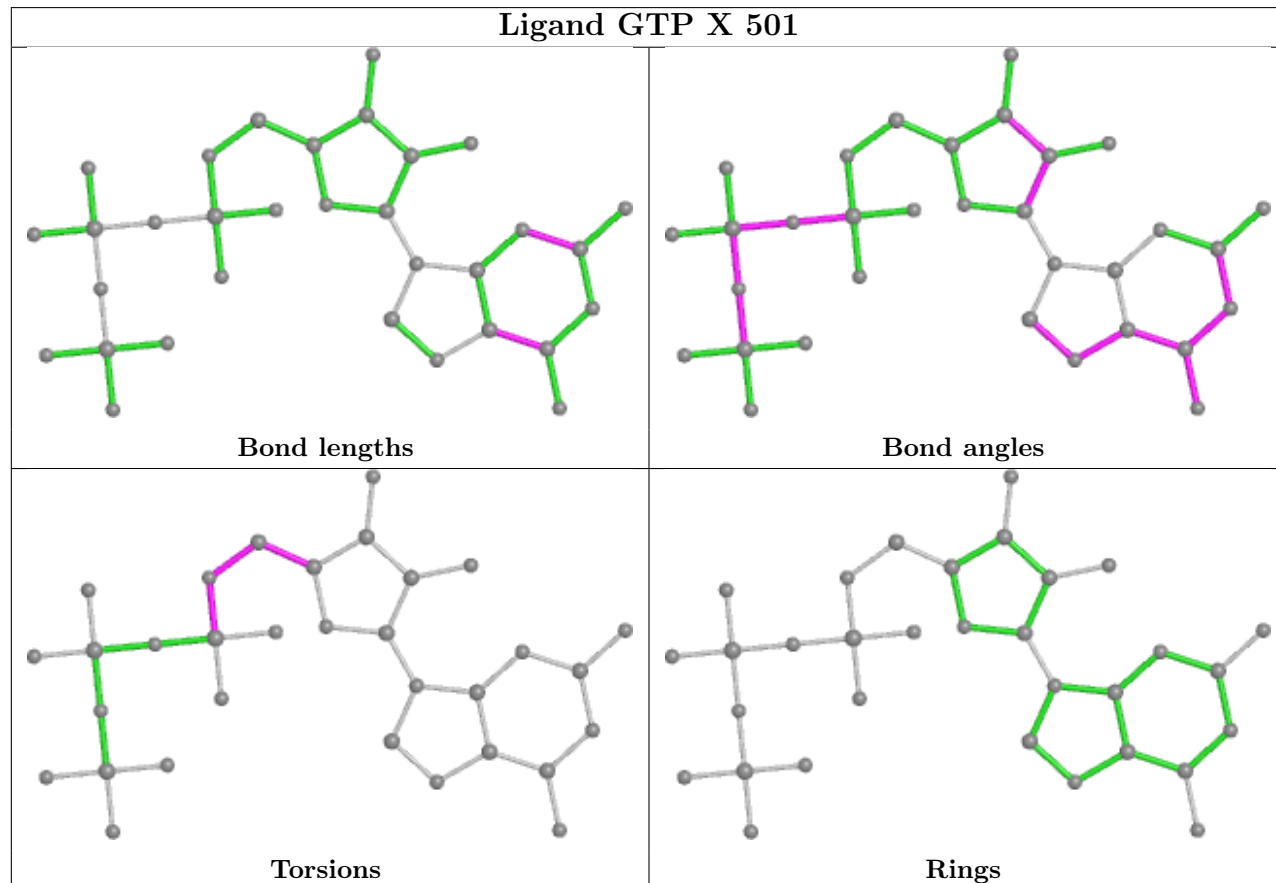
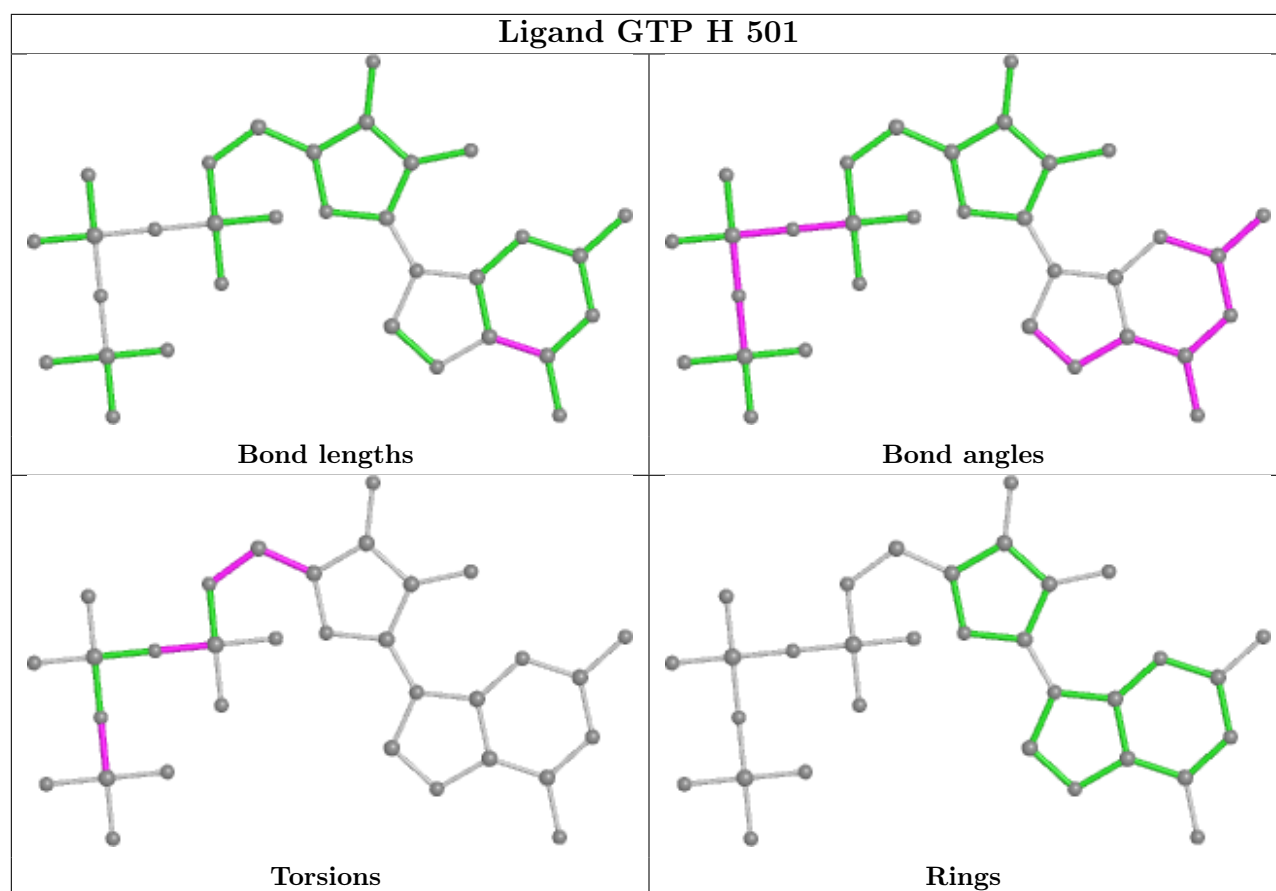
Ligand GTP 9 501

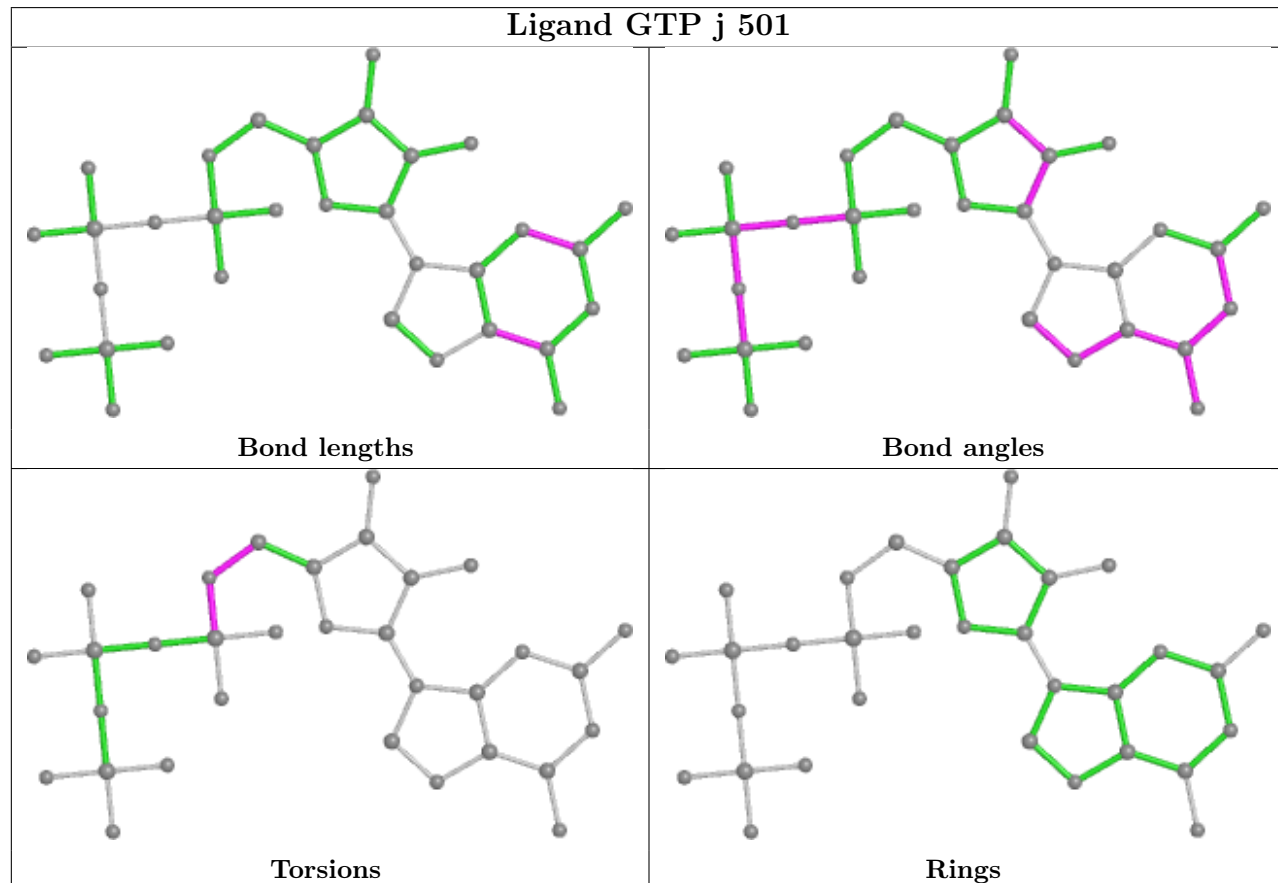
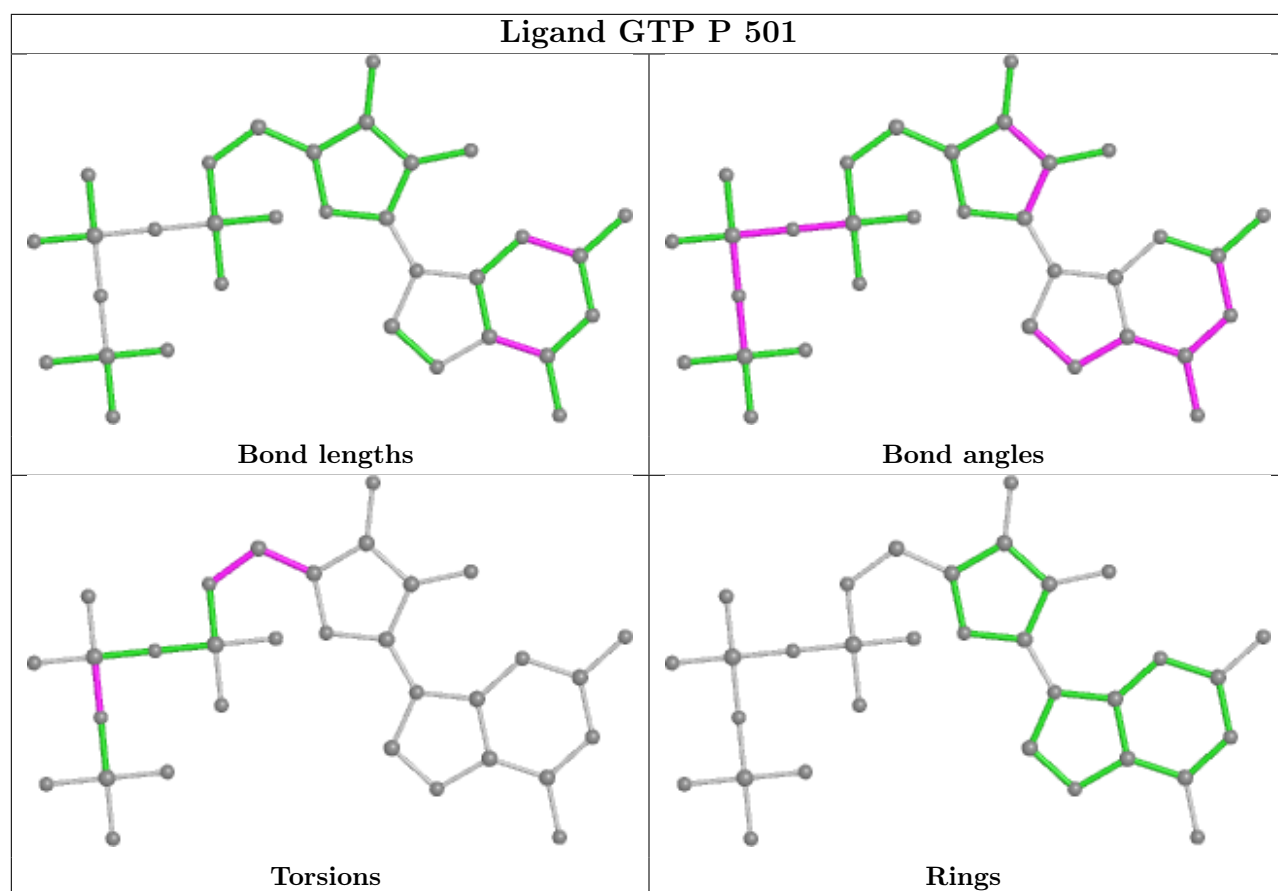


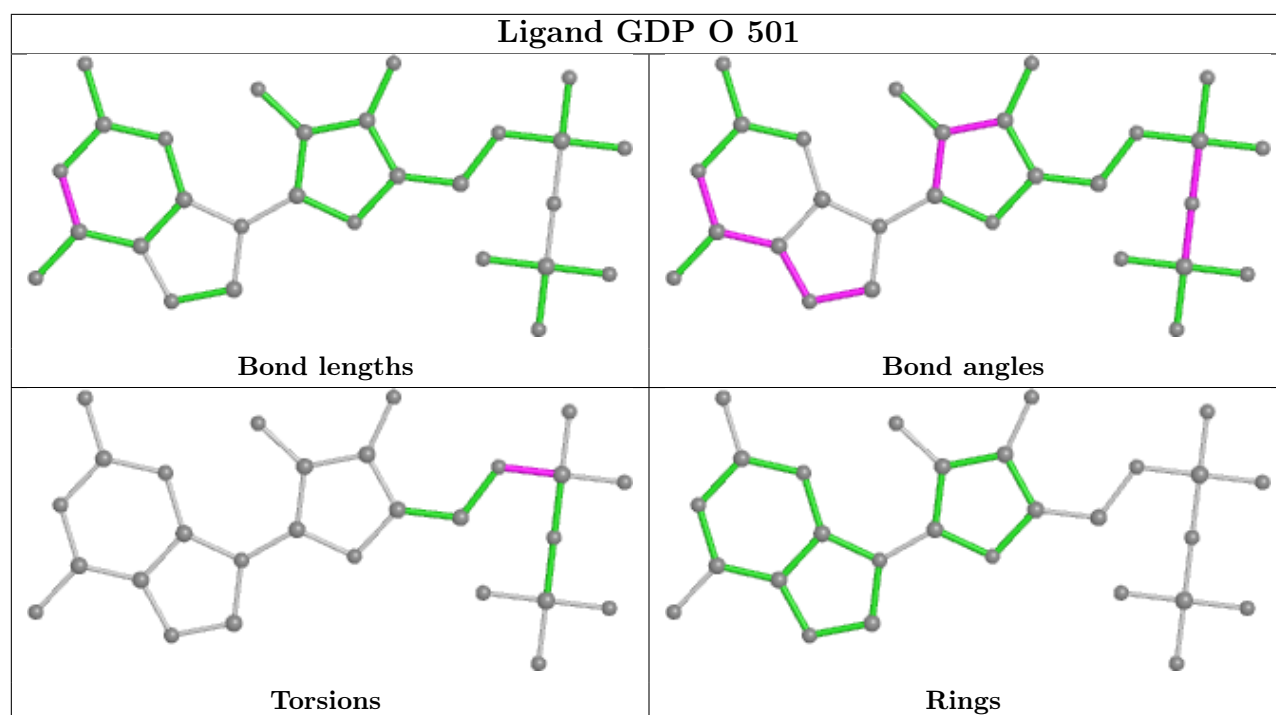
Ligand GDP Q 501











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 Map visualisation

This section contains visualisations of the EMDB entry EMD-22481. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal surface views

This section was not generated.

6.5 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.