



wwPDB EM Model Validation Summary Report ⓘ

May 4, 2020 – 09:48 PM EDT

PDB ID : 6RF2
EMDB ID : EMD-4861
Title : Cryo-EM structure of the C-terminal DC repeat (CDC) of human doublecortin (DCX) bound to 13-protofilament GDP.Pi-microtubule
Authors : Manka, S.W.
Deposited on : 2019-04-12
Resolution : 4.20 Å (reported)
Based on initial model : 5IP4

This is a wwPDB EM Model Validation Summary Report for a publicly released PDB/EMDB 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
buster-report : 1.1.7 (2018)
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.10.1

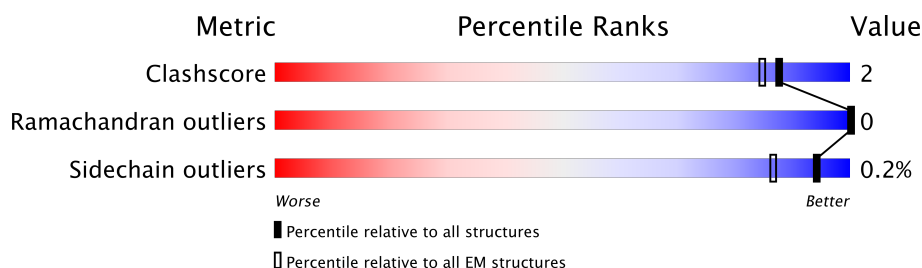
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 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)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

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 on 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	A	432	89% 11%
1	a	432	100%
2	B	429	90% 10%
2	b	429	100%
3	C	87	86% 14%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 14328 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 Tubulin alpha-1B chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	432	Total	C	N	O	S	0	0
			3382	2144	575	642	21		
1	A	432	Total	C	N	O	S	0	0
			3382	2144	575	642	21		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	?	-	SER	deletion	UNP P81947
a	?	-	ASP	deletion	UNP P81947
a	?	-	LYS	deletion	UNP P81947
a	?	-	THR	deletion	UNP P81947
a	?	-	ILE	deletion	UNP P81947
a	?	-	GLY	deletion	UNP P81947
a	?	-	GLY	deletion	UNP P81947
a	?	-	GLY	deletion	UNP P81947
a	?	-	ASP	deletion	UNP P81947
A	?	-	SER	deletion	UNP P81947
A	?	-	ASP	deletion	UNP P81947
A	?	-	LYS	deletion	UNP P81947
A	?	-	THR	deletion	UNP P81947
A	?	-	ILE	deletion	UNP P81947
A	?	-	GLY	deletion	UNP P81947
A	?	-	GLY	deletion	UNP P81947
A	?	-	GLY	deletion	UNP P81947
A	?	-	ASP	deletion	UNP P81947

- Molecule 2 is a protein called Tubulin beta-2B chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	429	Total	C	N	O	S	0	0
			3368	2115	578	650	25		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	429	Total	C	N	O	S	0	0
			3368	2115	578	650	25		

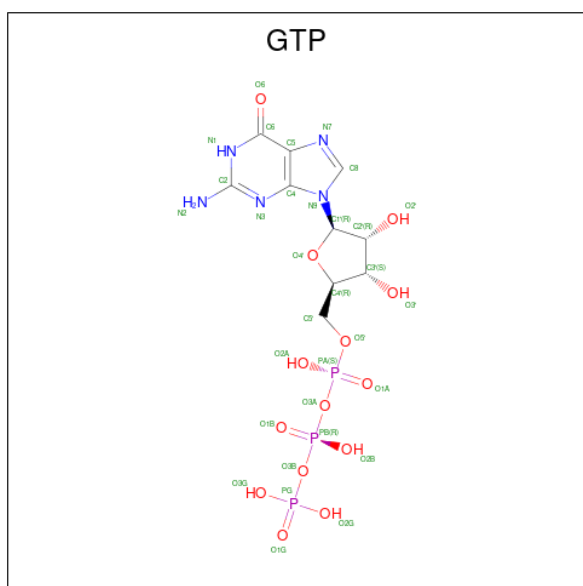
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	55	ALA	THR	conflict	UNP Q6B856
B	170	VAL	MET	conflict	UNP Q6B856
B	296	ALA	SER	conflict	UNP Q6B856
B	316	VAL	ILE	conflict	UNP Q6B856
b	55	ALA	THR	conflict	UNP Q6B856
b	170	VAL	MET	conflict	UNP Q6B856
b	296	ALA	SER	conflict	UNP Q6B856
b	316	VAL	ILE	conflict	UNP Q6B856

- Molecule 3 is a protein called Neuronal migration protein doublecortin.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	87	Total	C	N	O	S	0	0
			696	448	120	126	2		

- Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

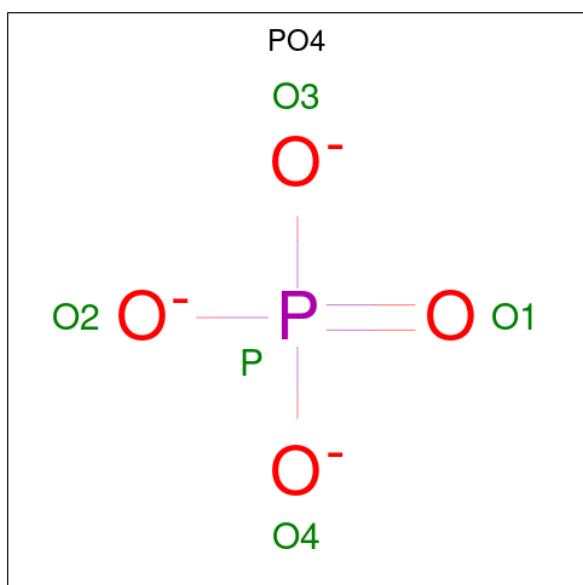


Mol	Chain	Residues	Atoms					AltConf
4	a	1	Total	C	N	O	P	0
			32	10	5	14	3	
4	A	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

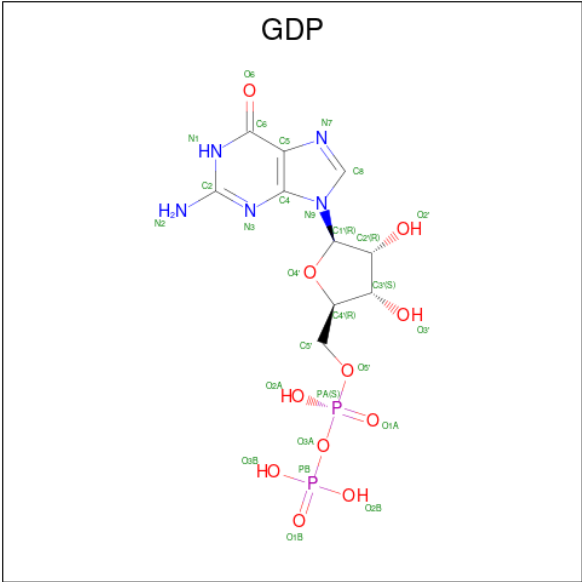
Mol	Chain	Residues	Atoms		AltConf
5	A	1	Total	Mg	0
			1	1	
5	a	1	Total	Mg	0
			1	1	

- Molecule 6 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			AltConf
6	a	1	Total	O	P	0
			5	4	1	
6	A	1	Total	O	P	0
			5	4	1	

- Molecule 7 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					AltConf
7	B	1	Total	C	N	O	P	0
			28	10	5	11	2	
7	b	1	Total	C	N	O	P	0
			28	10	5	11	2	

3 Residue-property plots


These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

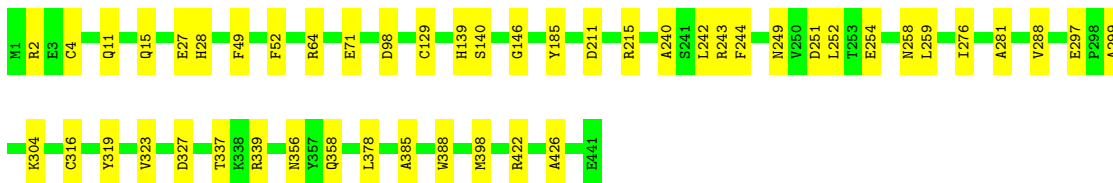
- Molecule 1: Tubulin alpha-1B chain

Chain a:  100%




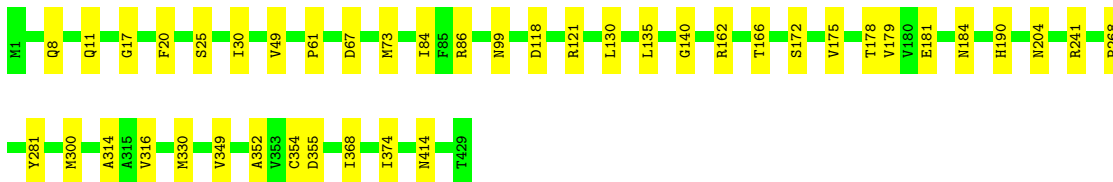
- Molecule 1: Tubulin alpha-1B chain

Chain A:  89% 11%



- Molecule 2: Tubulin beta-2B chain

Chain B:  90% 10%



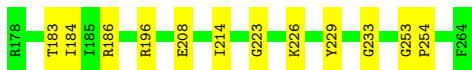
- Molecule 2: Tubulin beta-2B chain

Chain b:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Neuronal migration protein doublecortin

Chain C:  86% 14%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	6591	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
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, GTP, PO4, MG

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	0.28	0/3459	0.47	0/4697
1	a	0.28	0/3459	0.47	0/4697
2	B	0.29	0/3443	0.48	0/4666
2	b	0.29	0/3443	0.48	0/4666
3	C	0.31	0/708	0.59	0/953
All	All	0.28	0/14512	0.48	0/19679

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	3382	0	3292	30	0
1	a	3382	0	3292	0	0
2	B	3368	0	3246	24	0
2	b	3368	0	3246	0	0
3	C	696	0	720	7	0
4	A	32	0	12	1	0
4	a	32	0	12	0	0
5	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	a	1	0	0	0	0
6	A	5	0	0	0	0
6	a	5	0	0	0	0
7	B	28	0	12	1	0
7	b	28	0	12	0	0
All	All	14328	0	13844	57	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 2.

The worst 5 of 57 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:339:ARG:HH22	3:C:208:GLU:HB3	60.67	0.71
1:A:71:GLU:HB3	1:A:98:ASP:HB3	1.72	0.69
2:B:11:GLN:HE22	1:A:249:ASN:H	1.47	0.65
1:A:288:VAL:HG21	1:A:327:ASP:HB3	1.81	0.61
2:B:86:ARG:HG2	2:B:281:TYR:HB3	46.61	0.61

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	A	428/432 (99%)	409 (96%)	19 (4%)	0	100	100
1	a	428/432 (99%)	409 (96%)	19 (4%)	0	100	100
2	B	427/429 (100%)	413 (97%)	14 (3%)	0	100	100
2	b	427/429 (100%)	413 (97%)	14 (3%)	0	100	100
3	C	85/87 (98%)	69 (81%)	16 (19%)	0	100	100
All	All	1795/1809 (99%)	1713 (95%)	82 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	A	364/366 (100%)	363 (100%)	1 (0%)	93	95
1	a	364/366 (100%)	363 (100%)	1 (0%)	93	95
2	B	368/369 (100%)	368 (100%)	0	100	100
2	b	368/369 (100%)	368 (100%)	0	100	100
3	C	77/77 (100%)	76 (99%)	1 (1%)	71	86
All	All	1541/1547 (100%)	1538 (100%)	3 (0%)	94	96

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	a	2	ARG
1	A	2	ARG
3	C	186	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	226	ASN
2	b	11	GLN
1	A	88	HIS
2	B	204	ASN
1	A	101	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 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	$\# Z > 2$
6	PO4	a	503	-	4,4,4	0.96	0	6,6,6	0.54	0
7	GDP	B	501	-	24,30,30	0.90	1 (4%)	31,47,47	2.01	5 (16%)
4	GTP	a	501	5	26,34,34	0.99	1 (3%)	33,54,54	1.81	7 (21%)
6	PO4	A	501	-	4,4,4	0.97	0	6,6,6	0.49	0
4	GTP	A	502	5	26,34,34	1.01	1 (3%)	33,54,54	1.83	7 (21%)
7	GDP	b	501	-	24,30,30	0.90	1 (4%)	31,47,47	2.02	5 (16%)

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
7	GDP	B	501	-	-	4/12/32/32	0/3/3/3
4	GTP	a	501	5	-	8/18/38/38	0/3/3/3
4	GTP	A	502	5	-	8/18/38/38	0/3/3/3
7	GDP	b	501	-	-	4/12/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	501	GDP	C6-N1	3.08	1.38	1.33
7	b	501	GDP	C6-N1	3.07	1.38	1.33
4	a	501	GTP	C6-N1	2.74	1.37	1.33
4	A	502	GTP	C6-N1	2.74	1.37	1.33

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	b	501	GDP	C5-C6-N1	-8.14	112.30	123.43
7	B	501	GDP	C5-C6-N1	-8.12	112.32	123.43
7	b	501	GDP	C6-N1-C2	5.76	125.09	115.93
7	B	501	GDP	C6-N1-C2	5.73	125.04	115.93
4	A	502	GTP	N3-C2-N1	-5.26	120.20	127.22

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

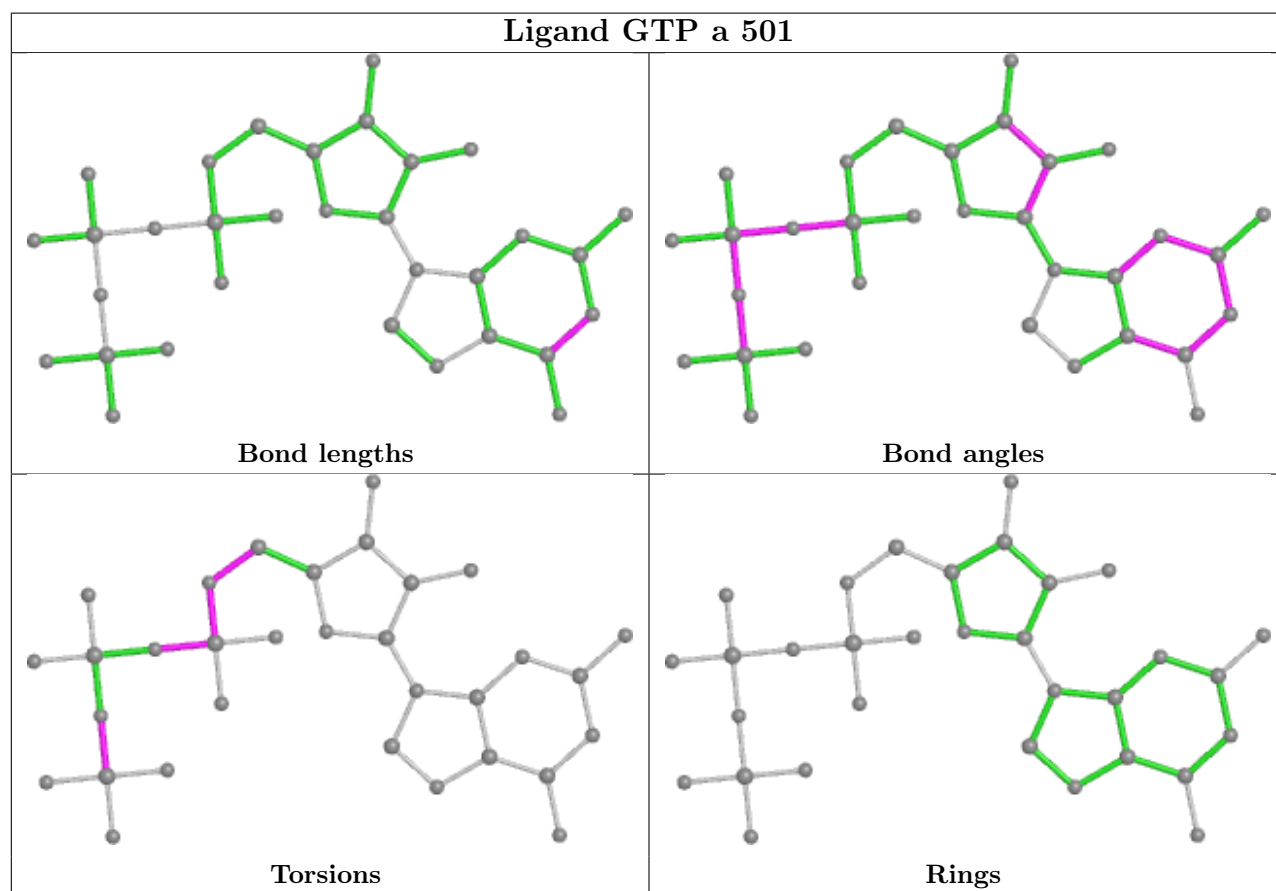
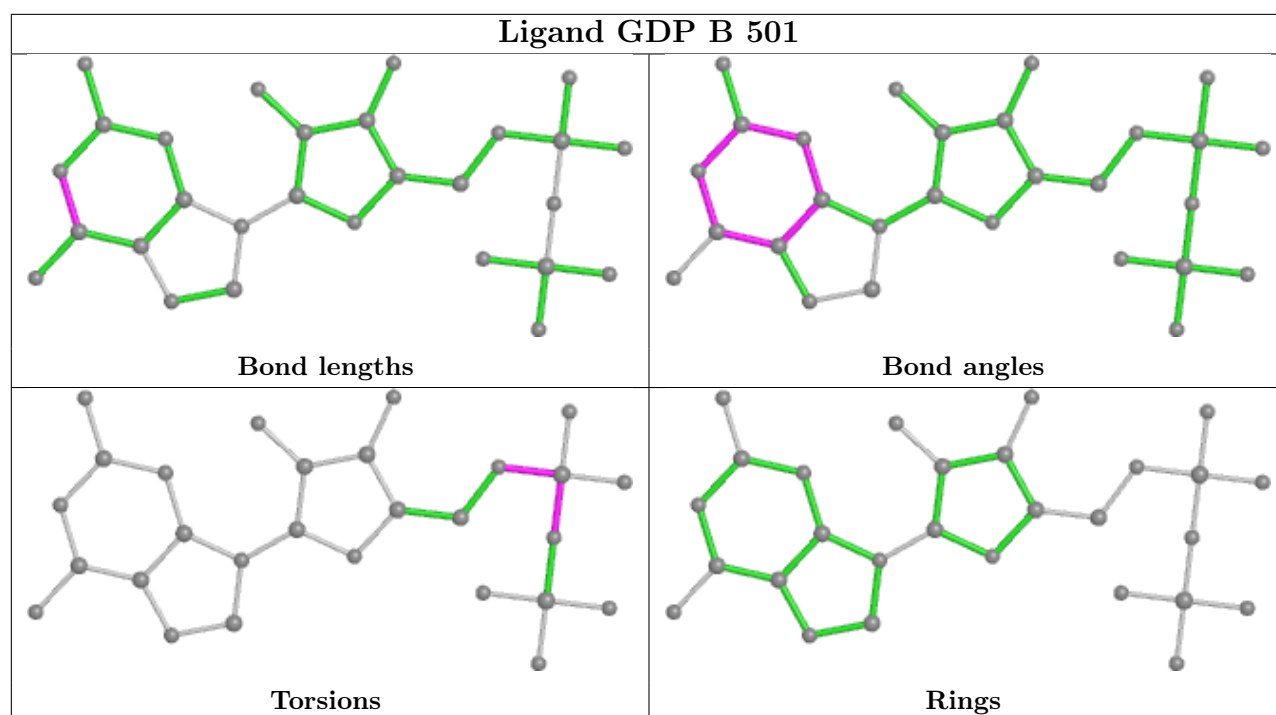
Mol	Chain	Res	Type	Atoms
7	B	501	GDP	C5'-O5'-PA-O2A
4	a	501	GTP	C5'-O5'-PA-O1A
4	a	501	GTP	C5'-O5'-PA-O2A
4	A	502	GTP	C5'-O5'-PA-O3A
4	A	502	GTP	C3'-C4'-C5'-O5'

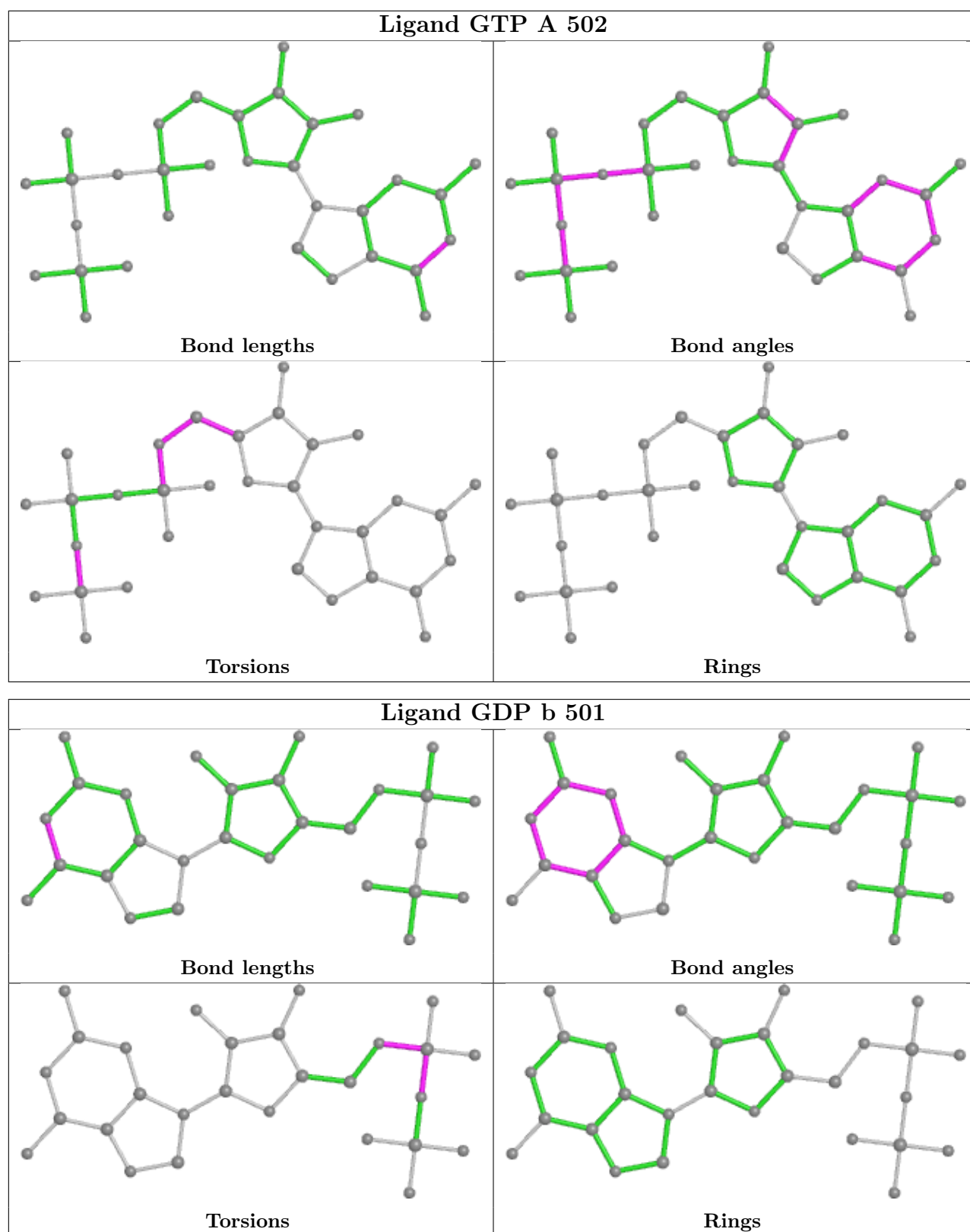
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	501	GDP	1	0
4	A	502	GTP	1	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1
1	a	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	a	37:PRO	C	47:ASP	N	14.27
1	A	37:PRO	C	47:ASP	N	14.27