



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 24, 2023 – 10:52 PM EDT

PDB ID : 3HKC  
Title : Tubulin-ABT751: RB3 stathmin-like domain complex  
Authors : Dorleans, A.; Gigant, B.; Ravelli, R.B.G.; Mailliet, P.; Mikol, V.; Knossow, M.  
Deposited on : 2009-05-23  
Resolution : 3.80 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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 : 4.02b-467  
Mogul : 1.8.5 (274361), 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

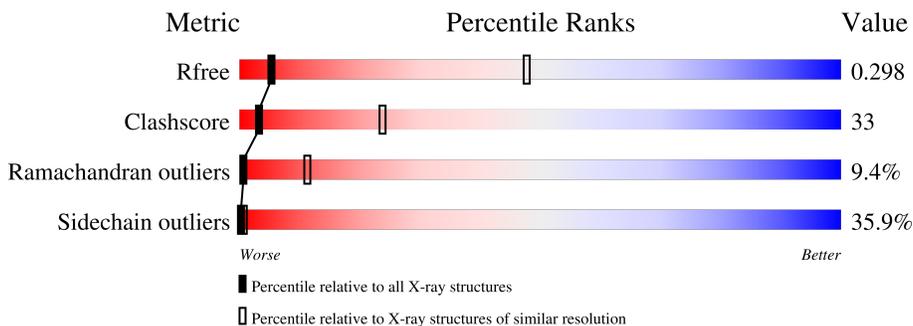
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.80 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	1212 (4.00-3.60)
Clashscore	141614	1288 (4.00-3.60)
Ramachandran outliers	138981	1243 (4.00-3.60)
Sidechain outliers	138945	1237 (4.00-3.60)

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

Mol	Chain	Length	Quality of chain
1	A	451	
1	C	451	
2	B	445	
2	D	445	
3	E	142	

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 14145 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 Tubulin alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	427	3300	2097	558	624	21	0	0	0
1	C	428	3270	2078	553	619	20	0	0	0

- Molecule 2 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	419	3240	2038	546	632	24	0	0	0
2	D	419	3239	2038	545	632	24	0	0	0

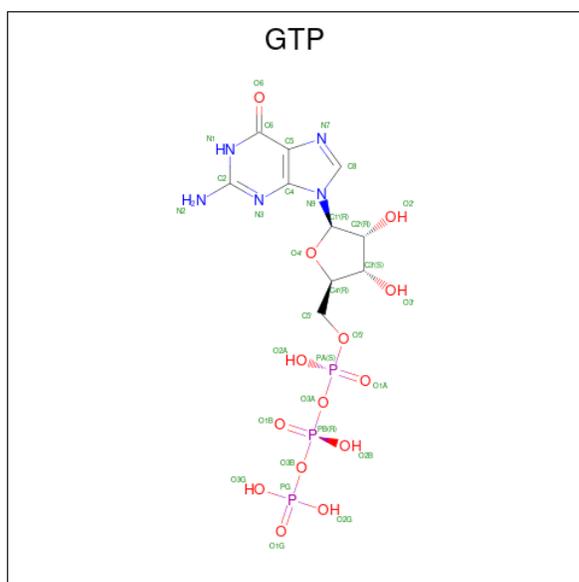
- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	124	921	558	175	183	5	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	4	ALA	-	expression tag	UNP P63043

- Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>14</sub>P<sub>3</sub>).

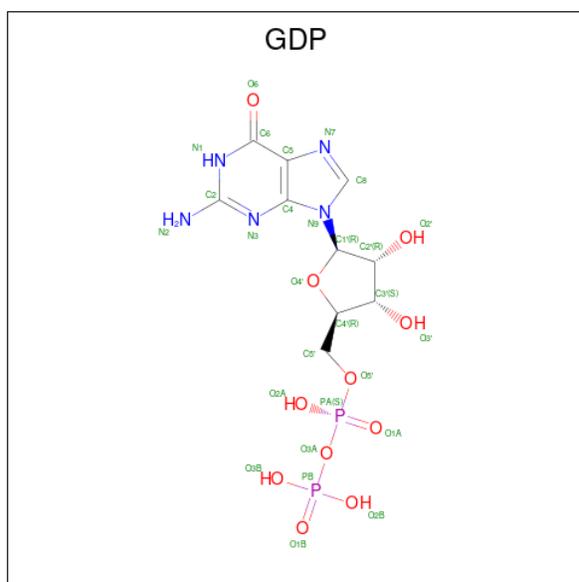


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
4	A	1	32	10	5	14	3	0	0
4	C	1	32	10	5	14	3	0	0

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

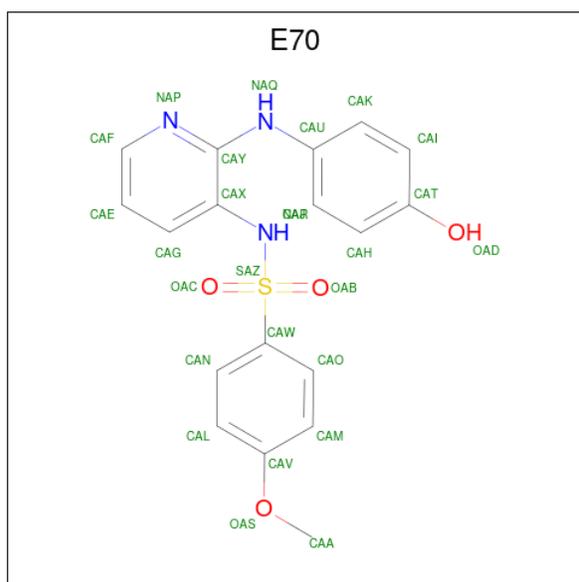
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
5	A	1	1	1	0	0
5	B	1	1	1	0	0
5	C	1	1	1	0	0

- Molecule 6 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>11</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
6	B	1	28	10	5	11	2	0	0
6	D	1	28	10	5	11	2	0	0

- Molecule 7 is N-{2-[(4-hydroxyphenyl)amino]pyridin-3-yl}-4-methoxybenzenesulfonamide (three-letter code: E70) (formula: C<sub>18</sub>H<sub>17</sub>N<sub>3</sub>O<sub>4</sub>S).



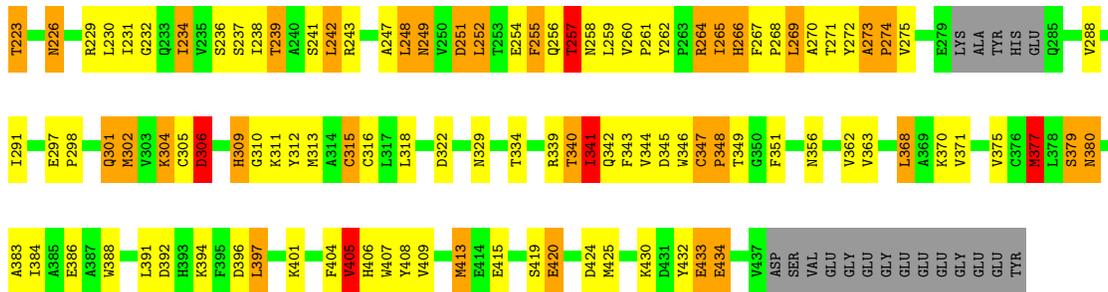
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
7	B	1	26	18	3	4	1	0	0

*Continued on next page...*

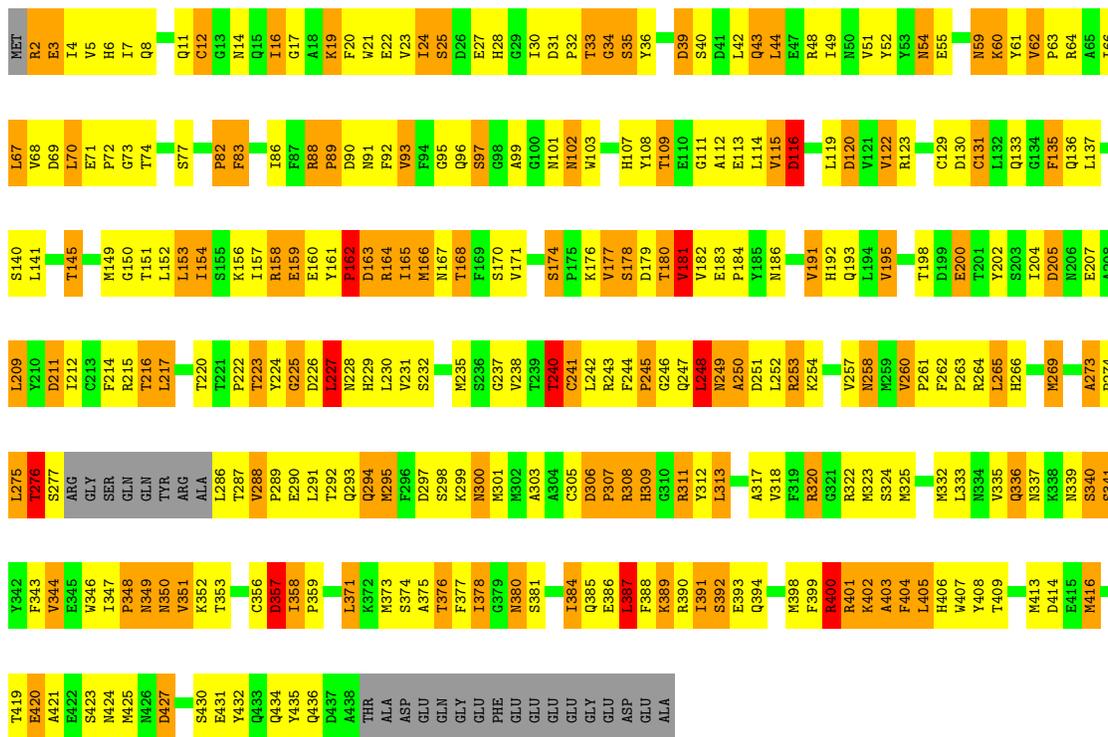
*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
7	D	1	26	18	3	4	1	0	0

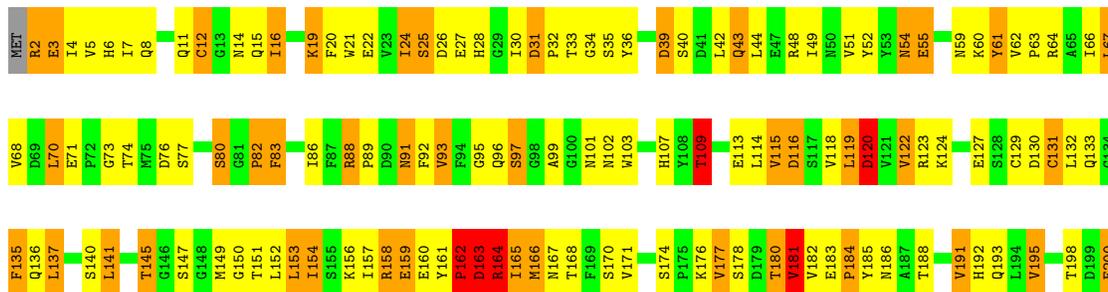




• Molecule 2: Tubulin beta chain



• Molecule 2: Tubulin beta chain





## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	329.24Å 329.24Å 53.87Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 3.80 48.19 – 3.80	Depositor EDS
% Data completeness (in resolution range)	99.3 (20.00-3.80) 97.6 (48.19-3.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.74 (at 3.77Å)	Xtrriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.203 , 0.252 0.261 , 0.298	Depositor DCC
$R_{free}$ test set	1674 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	172.4	Xtrriage
Anisotropy	0.047	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , -10.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.41$ , $\langle L^2 \rangle = 0.24$	Xtrriage
Estimated twinning fraction	0.068 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	14145	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.98% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, MG, GDP, E70

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	0.79	0/3376	0.99	17/4588 (0.4%)
1	C	0.67	0/3344	0.91	11/4552 (0.2%)
2	B	0.68	0/3312	0.94	11/4498 (0.2%)
2	D	0.71	0/3311	0.95	10/4495 (0.2%)
3	E	0.75	0/929	0.92	2/1245 (0.2%)
All	All	0.72	0/14272	0.95	51/19378 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
2	B	0	2
2	D	0	2
3	E	0	2
All	All	0	8

There are no bond length outliers.

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	427	ASP	CB-CG-OD2	8.56	126.00	118.30
1	C	211	ASP	CB-CG-OD2	8.46	125.91	118.30
1	A	76	ASP	CB-CG-OD2	8.07	125.56	118.30
1	A	120	ASP	CB-CG-OD2	7.62	125.16	118.30
1	C	120	ASP	CB-CG-OD2	7.48	125.03	118.30

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	283	HIS	Peptide
1	A	82	THR	Peptide
2	B	162	PRO	Peptide
2	B	248	LEU	Peptide
2	D	162	PRO	Peptide

## 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	3300	0	3169	185	0
1	C	3270	0	3122	180	0
2	B	3240	0	3056	269	0
2	D	3239	0	3058	269	0
3	E	921	0	814	41	0
4	A	32	0	12	4	0
4	C	32	0	12	4	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
6	B	28	0	12	3	0
6	D	28	0	12	4	0
7	B	26	0	17	5	0
7	D	26	0	17	5	0
All	All	14145	0	13301	912	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 33.

The worst 5 of 912 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)
3:E:105:MET:SD	3:E:105:MET:CE	2.03	1.44
2:D:273:ALA:CB	2:D:274:PRO:HD3	1.74	1.16
2:B:165:ILE:HD11	2:B:252:LEU:HG	1.25	1.15

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:273:ALA:HB3	1:C:274:PRO:HD3	1.22	1.15
1:A:99:ALA:HB2	1:A:145:THR:HG22	1.17	1.15

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 X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	422/451 (94%)	319 (76%)	70 (17%)	33 (8%)	1	15
1	C	422/451 (94%)	316 (75%)	70 (17%)	36 (8%)	1	12
2	B	415/445 (93%)	315 (76%)	58 (14%)	42 (10%)	0	9
2	D	415/445 (93%)	308 (74%)	64 (15%)	43 (10%)	0	9
3	E	120/142 (84%)	82 (68%)	24 (20%)	14 (12%)	0	6
All	All	1794/1934 (93%)	1340 (75%)	286 (16%)	168 (9%)	0	11

5 of 168 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	48	SER
1	A	73	THR
1	A	164	LYS
1	A	191	THR
1	A	247	ALA

### 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 X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	347/378 (92%)	229 (66%)	118 (34%)	0	1
1	C	340/378 (90%)	228 (67%)	112 (33%)	0	2
2	B	348/383 (91%)	221 (64%)	127 (36%)	0	0
2	D	348/383 (91%)	220 (63%)	128 (37%)	0	0
3	E	81/126 (64%)	41 (51%)	40 (49%)	0	0
All	All	1464/1648 (89%)	939 (64%)	525 (36%)	0	1

5 of 525 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	374	SER
2	D	398	MET
2	D	373	MET
3	E	119	MET
2	B	276	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 75 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	136	GLN
2	D	380	ASN
2	D	193	GLN
2	D	294	GLN
2	B	206	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 monosaccharides in this entry.

## 5.6 Ligand geometry

Of 9 ligands modelled in this entry, 3 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
4	GTP	A	600	-	26,34,34	1.12	2 (7%)	32,54,54	1.60	7 (21%)
4	GTP	C	600	-	26,34,34	1.09	3 (11%)	32,54,54	1.83	9 (28%)
7	E70	B	700	-	27,28,28	2.64	5 (18%)	38,39,39	1.92	6 (15%)
7	E70	D	700	-	27,28,28	3.46	7 (25%)	38,39,39	2.04	7 (18%)
6	GDP	D	600	-	24,30,30	1.16	1 (4%)	30,47,47	1.71	9 (30%)
6	GDP	B	600	-	24,30,30	1.17	2 (8%)	30,47,47	1.74	8 (26%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GTP	A	600	-	-	5/18/38/38	0/3/3/3
4	GTP	C	600	-	-	6/18/38/38	0/3/3/3
7	E70	B	700	-	-	7/17/17/17	0/3/3/3
7	E70	D	700	-	-	6/17/17/17	0/3/3/3
6	GDP	D	600	-	-	7/12/32/32	0/3/3/3
6	GDP	B	600	-	-	7/12/32/32	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	D	700	E70	OAB-SAZ	13.17	1.58	1.43
7	B	700	E70	OAB-SAZ	9.96	1.54	1.43
7	D	700	E70	OAC-SAZ	8.43	1.53	1.43
7	B	700	E70	OAC-SAZ	6.44	1.50	1.43
7	D	700	E70	CAX-NAR	-5.06	1.34	1.42

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	700	E70	OAC-SAZ-OAB	-8.38	109.25	119.55
7	D	700	E70	OAC-SAZ-OAB	-7.72	110.06	119.55
7	B	700	E70	OAB-SAZ-CAW	5.20	114.37	107.97
7	D	700	E70	OAB-SAZ-CAW	5.07	114.21	107.97
4	C	600	GTP	PB-O3B-PG	-4.11	118.72	132.83

There are no chirality outliers.

5 of 38 torsion outliers are listed below:

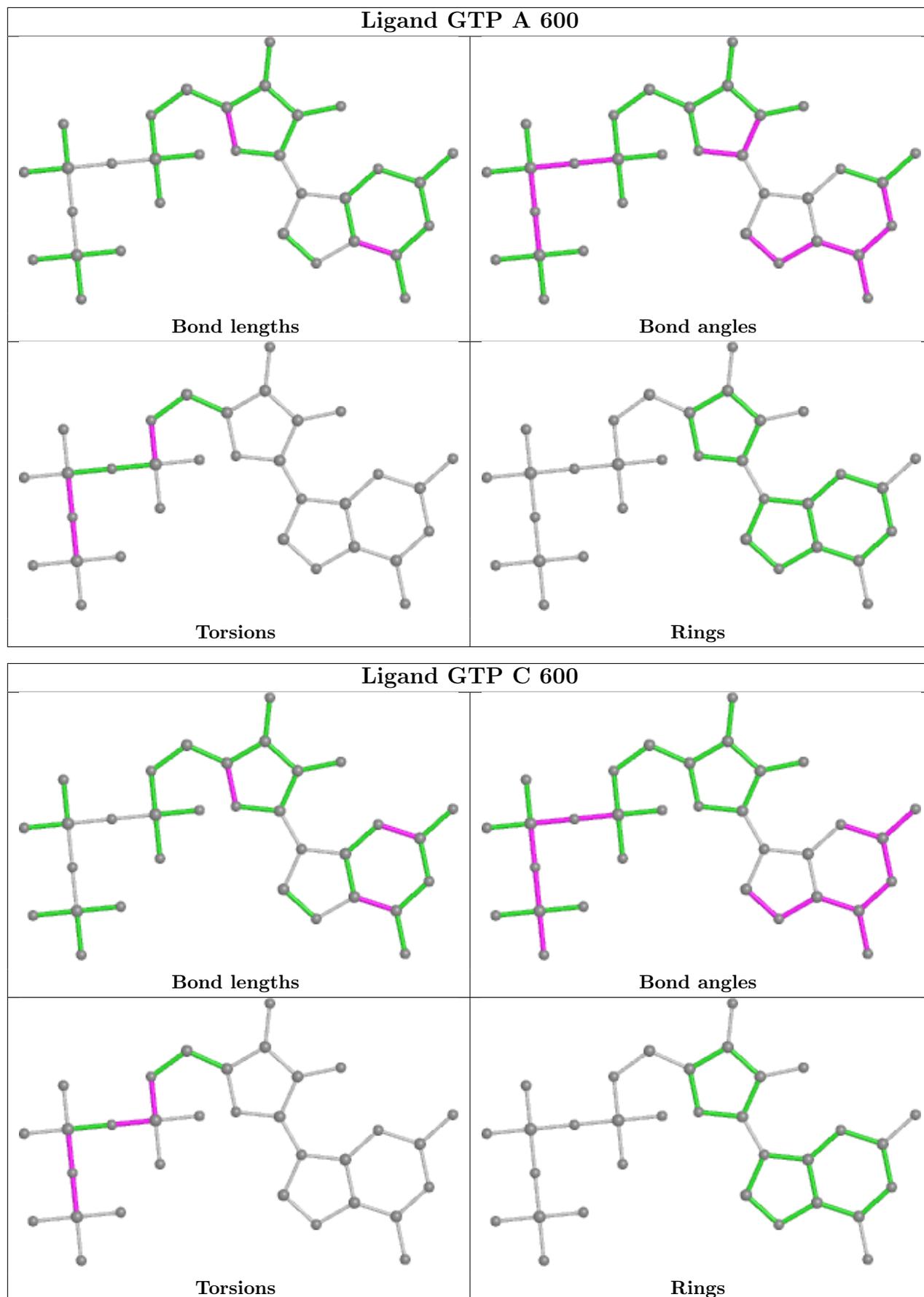
Mol	Chain	Res	Type	Atoms
4	A	600	GTP	C5'-O5'-PA-O1A
4	C	600	GTP	C5'-O5'-PA-O1A
6	B	600	GDP	PA-O3A-PB-O2B
6	B	600	GDP	O4'-C4'-C5'-O5'
6	B	600	GDP	C3'-C4'-C5'-O5'

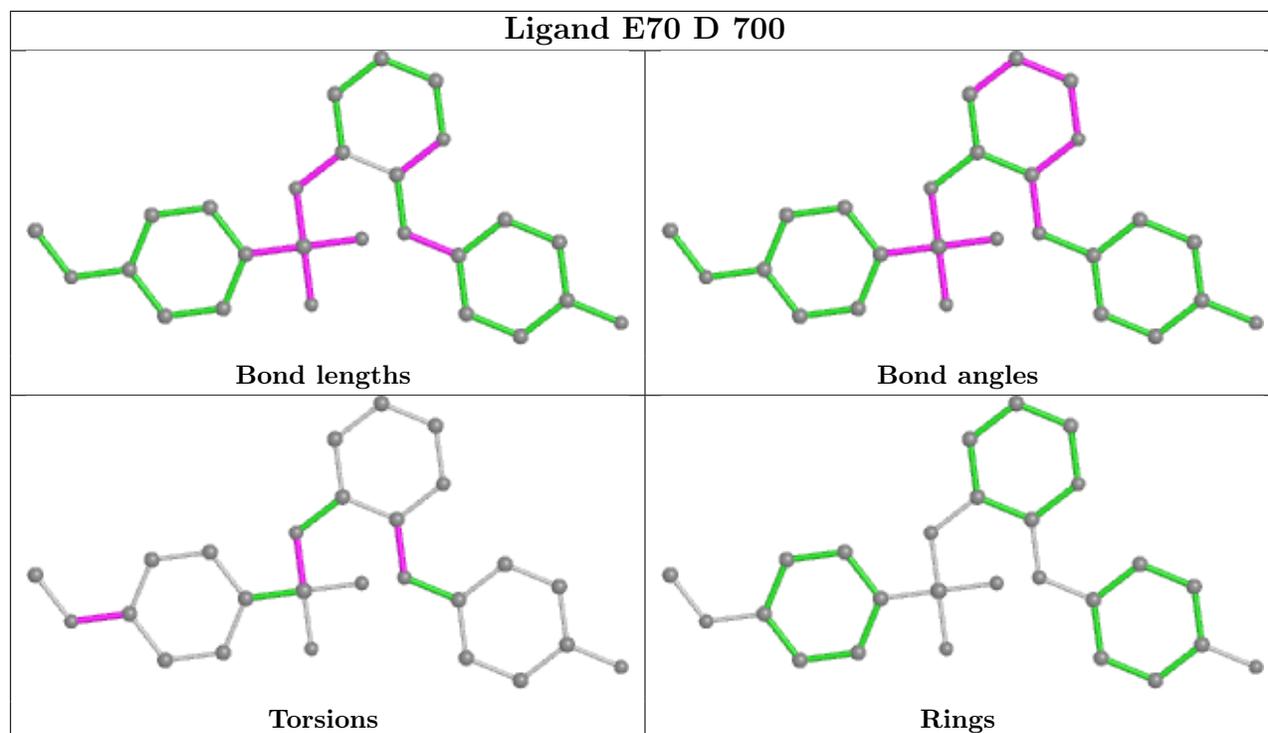
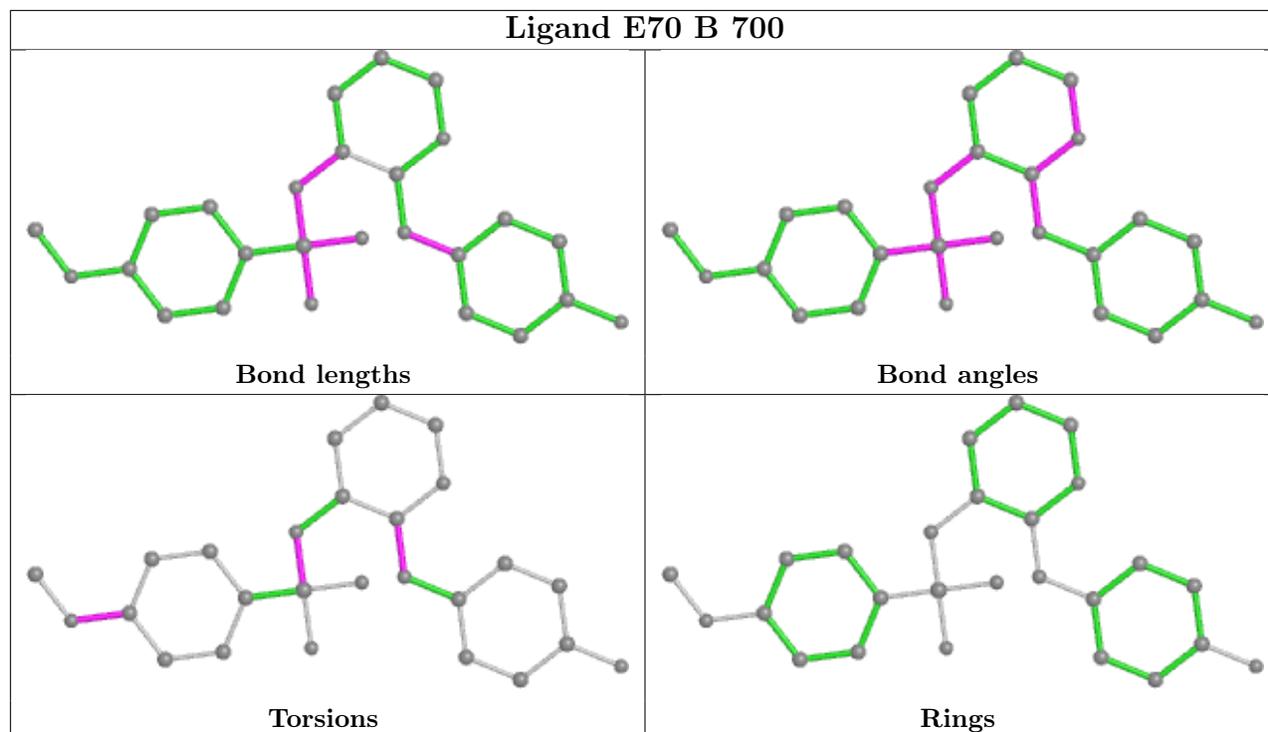
There are no ring outliers.

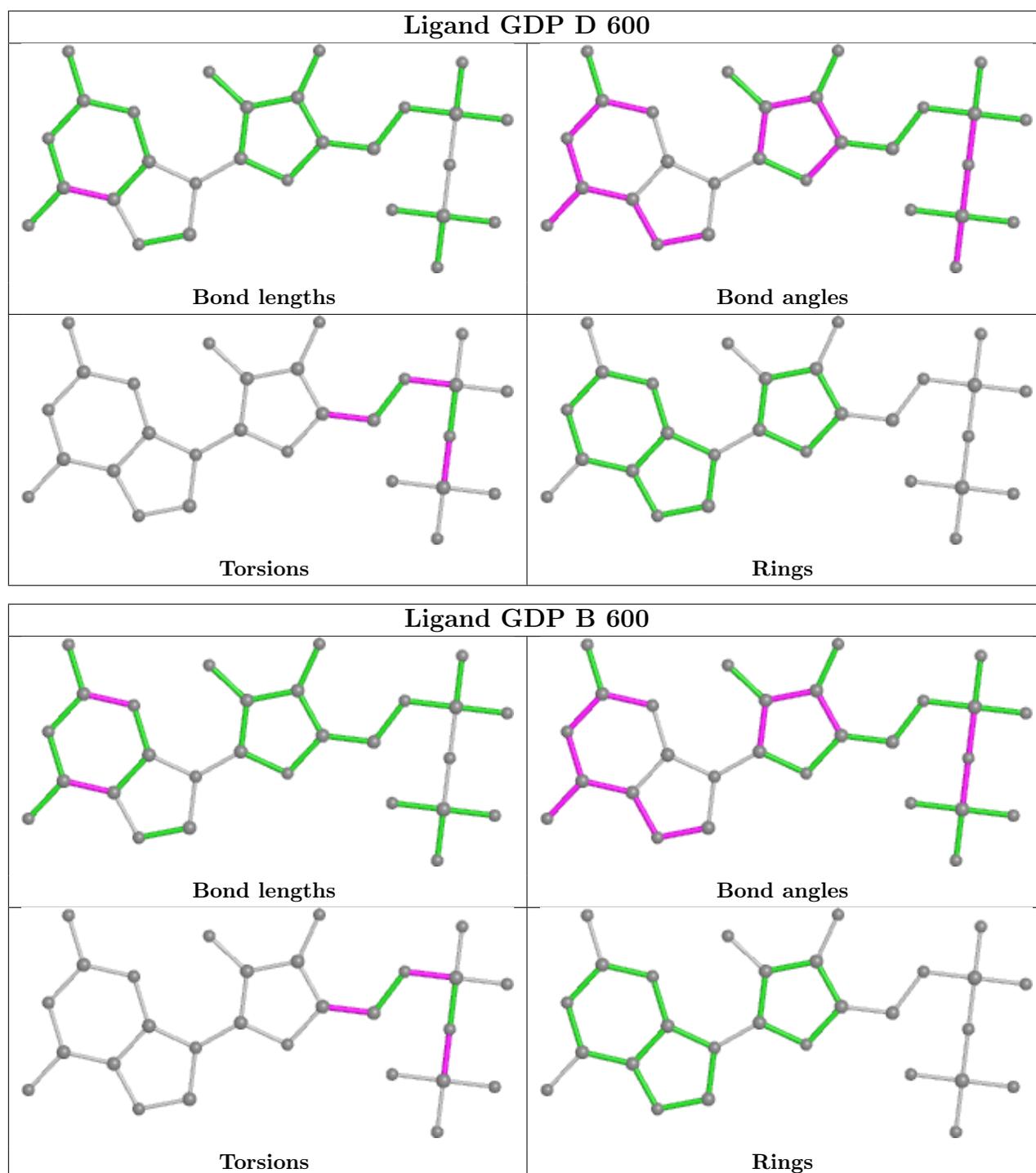
6 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	600	GTP	4	0
4	C	600	GTP	4	0
7	B	700	E70	5	0
7	D	700	E70	5	0
6	D	600	GDP	4	0
6	B	600	GDP	3	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 [i](#)

There are no chain breaks in this entry.

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

### 6.1 Protein, DNA and RNA chains [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

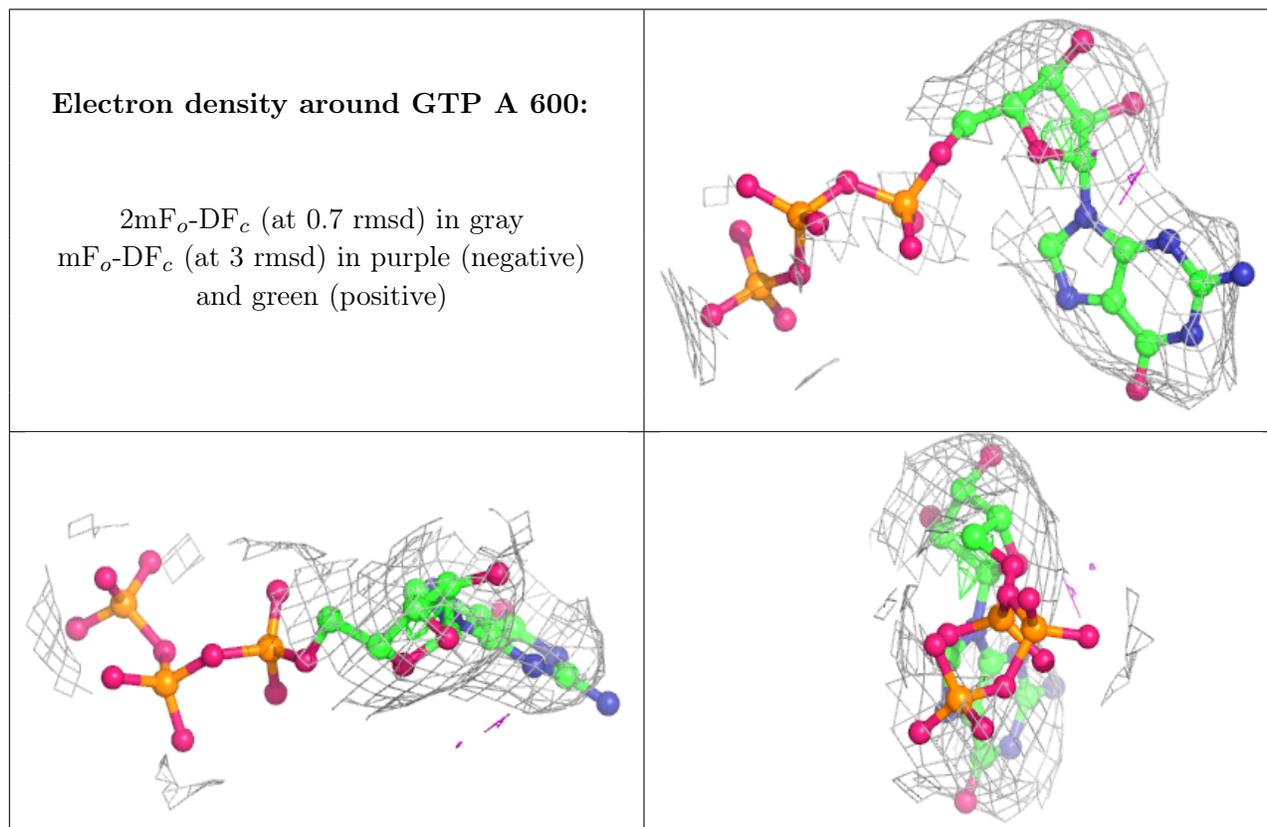
### 6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands [i](#)

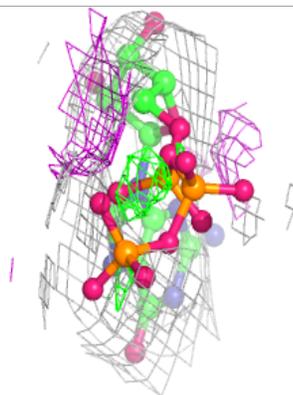
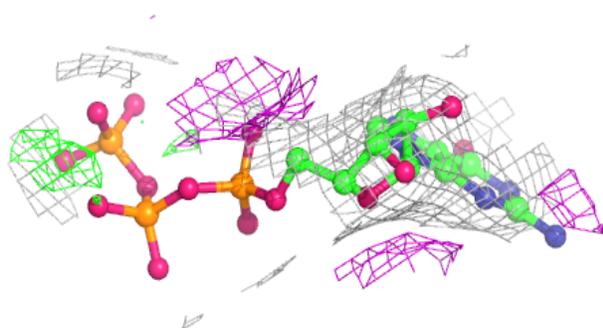
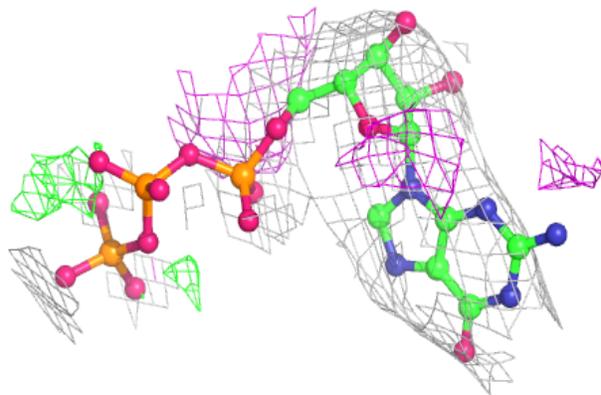
Unable to reproduce the depositors R factor - this section is therefore empty.

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.

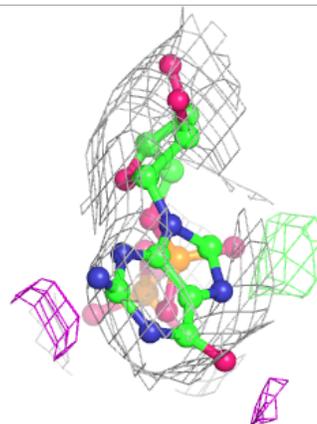
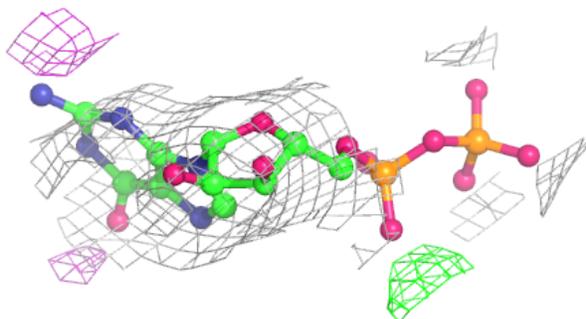
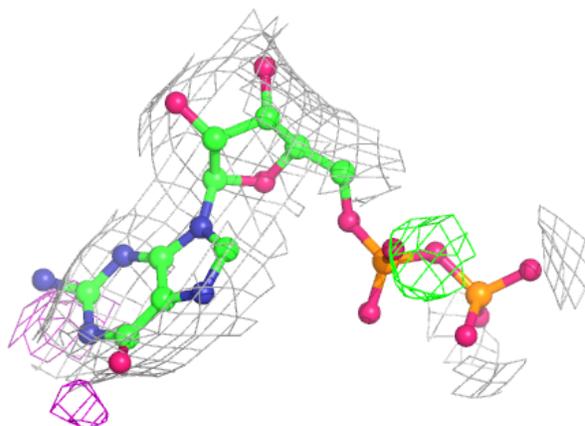


**Electron density around GTP C 600:**

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

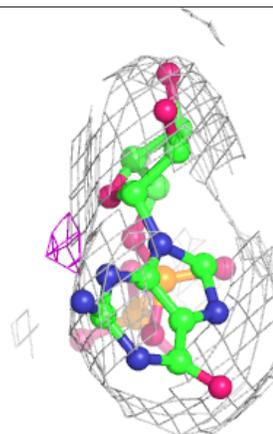
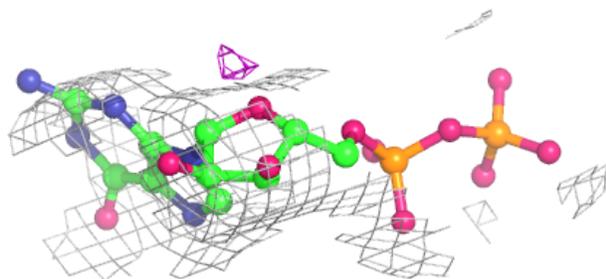
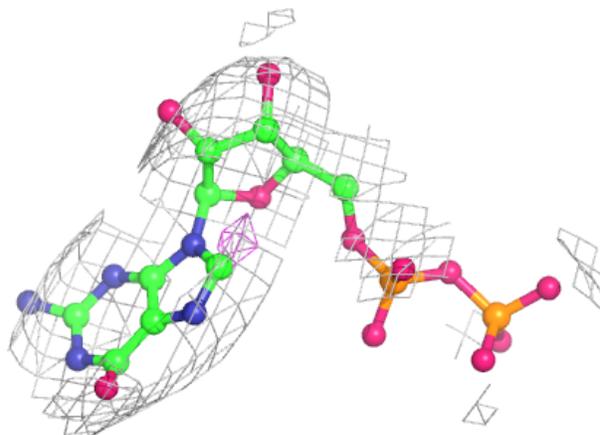
**Electron density around GDP B 600:**

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



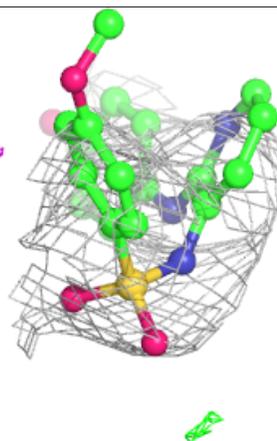
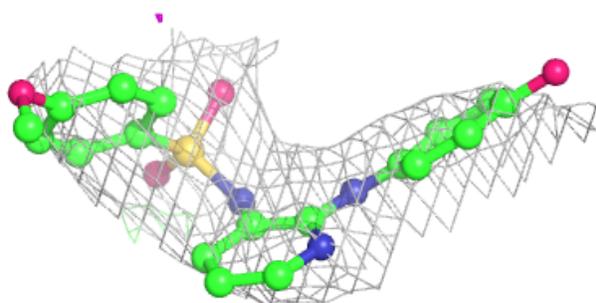
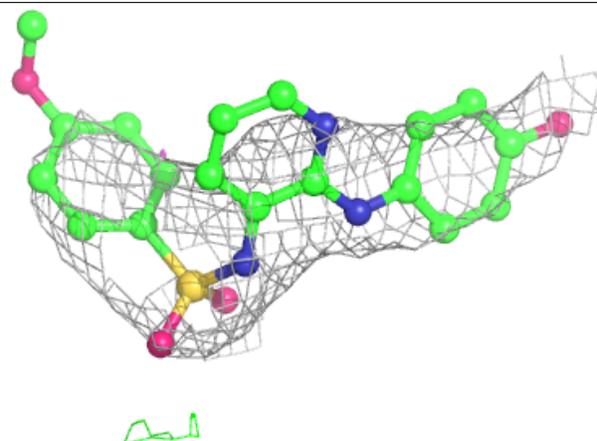
**Electron density around GDP D 600:**

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

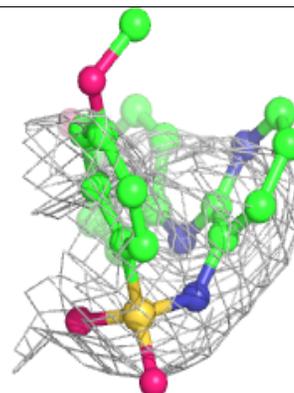
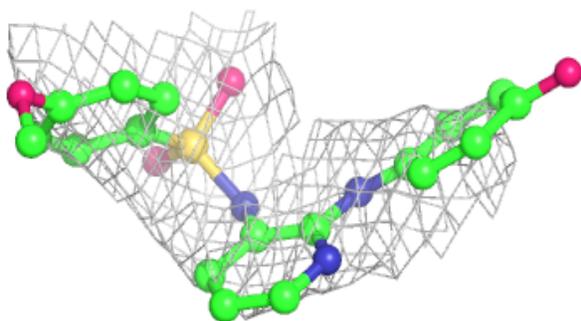
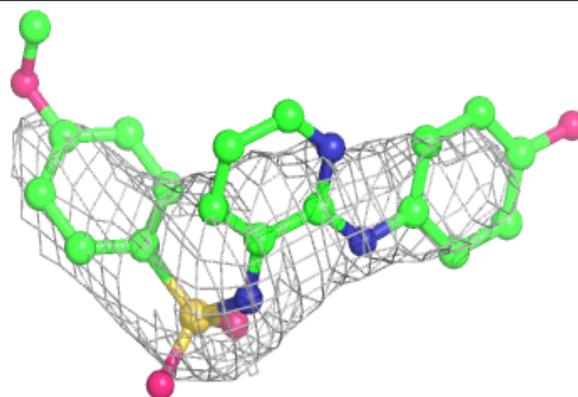


**Electron density around E70 B 700:**

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

**Electron density around E70 D 700:**

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



## 6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.