



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 3, 2023 – 07:41 AM EDT

PDB ID : 3RYI  
Title : GDP-Tubulin: rb3 stathmin-like domain complex  
Authors : Nawrotek, A.; Knossow, M.; Gigant, B.  
Deposited on : 2011-05-11  
Resolution : 2.40 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>.

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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 : 2.35  
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) : 2.35

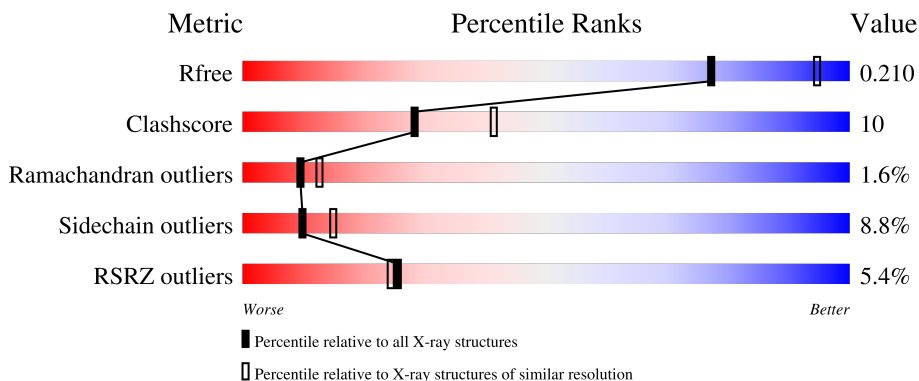
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

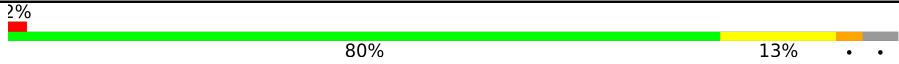
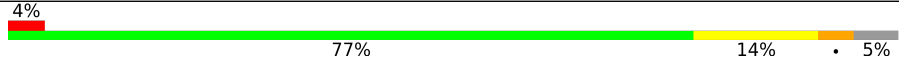



The reported resolution of this entry is 2.40 Å.

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)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	451	 2% 80% 13% • •
1	C	451	 4% 77% 14% • 5%
2	B	445	 8% 73% 20% • •
2	D	445	 3% 76% 18% • •
3	E	143	 17% 69% 24% • 5%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
6	SO4	C	454	-	-	-	X

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 15541 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	433	3389	2144	575	647	23	0	1	0
1	C	429	3333	2112	565	633	23	0	2	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	232	SER	GLY	SEE REMARK 999	UNP D0VWZ0
A	340	SER	THR	SEE REMARK 999	UNP D0VWZ0
C	232	SER	GLY	SEE REMARK 999	UNP D0VWZ0
C	340	SER	THR	SEE REMARK 999	UNP D0VWZ0

- Molecule 2 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	431	3428	2155	582	664	27	0	7	0
2	D	431	3449	2163	588	672	26	0	10	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	317	THR	ALA	SEE REMARK 999	UNP D0VWY9
B	318	ILE	VAL	SEE REMARK 999	UNP D0VWY9
B	335	ILE	VAL	SEE REMARK 999	UNP D0VWY9
B	375	SER	ALA	SEE REMARK 999	UNP D0VWY9
D	317	THR	ALA	SEE REMARK 999	UNP D0VWY9
D	318	ILE	VAL	SEE REMARK 999	UNP D0VWY9
D	335	ILE	VAL	SEE REMARK 999	UNP D0VWY9
D	375	SER	ALA	SEE REMARK 999	UNP D0VWY9

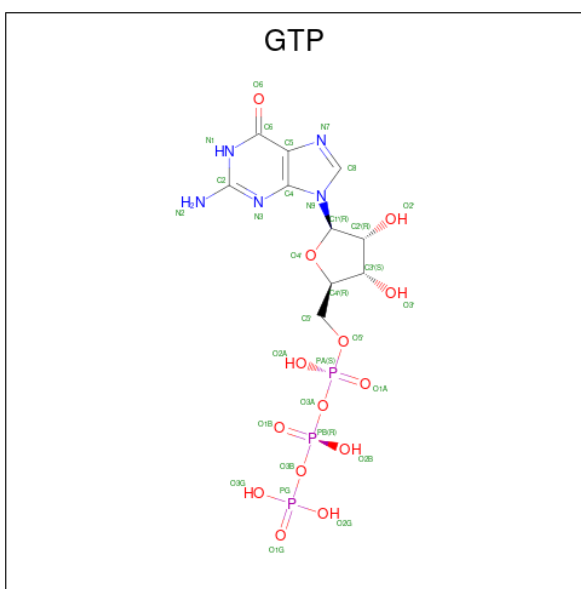
- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	136	1101	680	199	218	4	0	1	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	3	ACE	-	SEE REMARK 999	UNP P63043
E	4	ALA	-	SEE REMARK 999	UNP P63043
E	14	ALA	CYS	engineered mutation	UNP P63043
E	20	TRP	PHE	engineered mutation	UNP P63043

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



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).

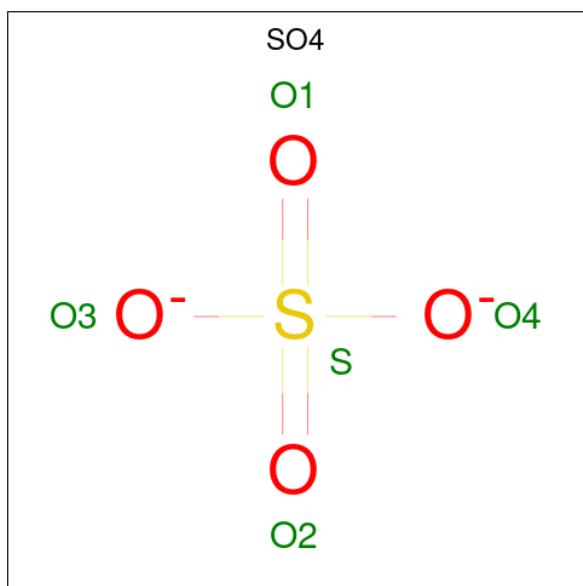
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		

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

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



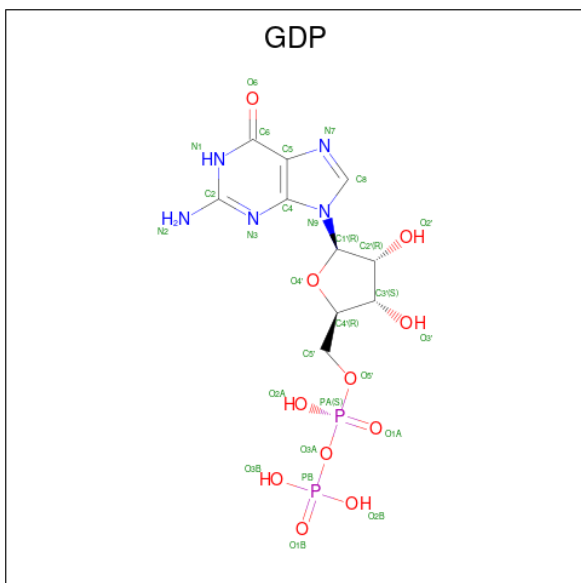
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
6	A	1	5	4	1	0	0
6	A	1	5	4	1	0	0
6	A	1	5	4	1	0	0
6	A	1	5	4	1	0	0
6	A	1	5	4	1	0	0
6	B	1	5	4	1	0	0
6	C	1	5	4	1	0	0
6	C	1	5	4	1	0	0
6	C	1	5	4	1	0	0
6	D	1	5	4	1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf		
6	D	1	Total	O	S	0	0
			5	4	1		
6	E	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula:  $C_{10}H_{15}N_5O_{11}P_2$ ).



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

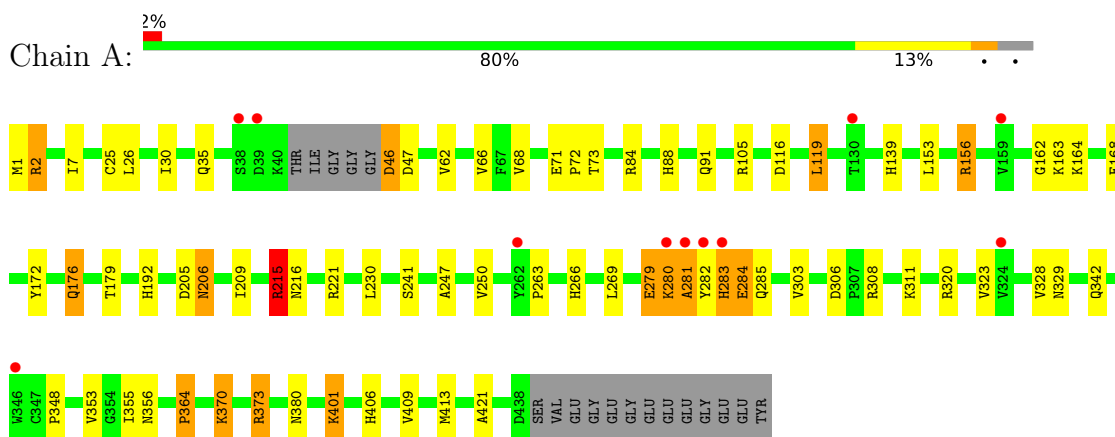
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf		
8	A	192	Total	O		0	0
			192	192			
8	B	128	Total	O		0	0
			128	128			
8	C	143	Total	O		0	0
			143	143			
8	D	161	Total	O		0	0
			161	161			
8	E	35	Total	O		0	0
			35	35			

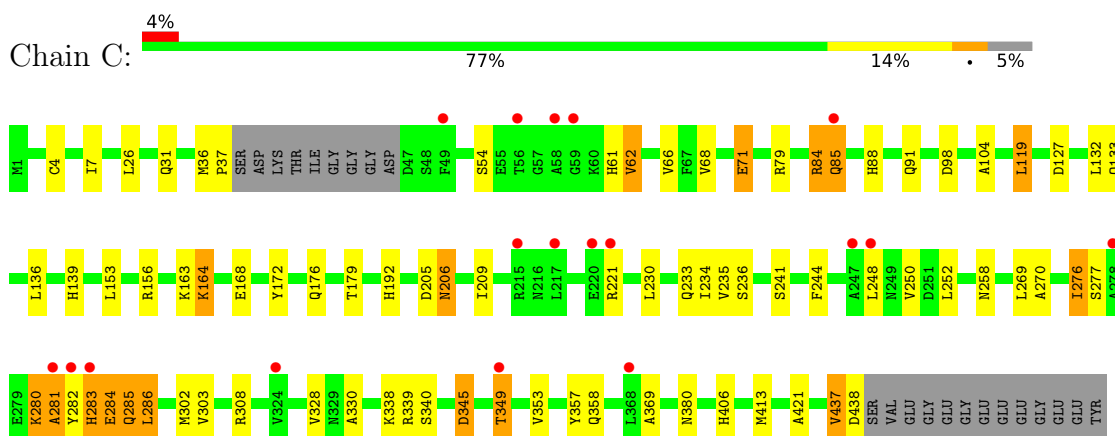
### 3 Residue-property plots [i](#)

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

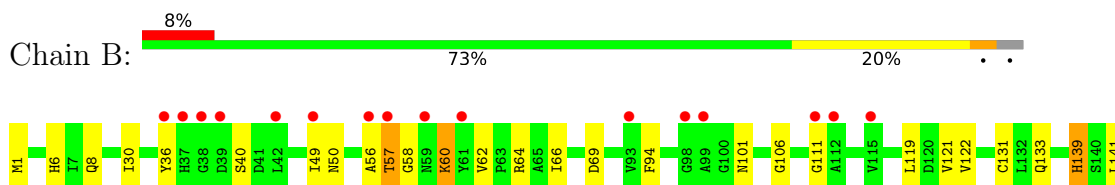
- Molecule 1: Tubulin alpha chain



- Molecule 1: Tubulin alpha chain



- Molecule 2: Tubulin beta chain







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	65.72Å 127.60Å 250.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.59 – 2.40 46.59 – 2.40	Depositor EDS
% Data completeness (in resolution range)	(Not available) (46.59-2.40) 97.6 (46.59-2.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.91 (at 2.39Å)	Xtrriage
Refinement program	BUSTER 2.8.0	Depositor
R, $R_{free}$	0.167 , 0.201 0.177 , 0.210	Depositor DCC
$R_{free}$ test set	4075 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	47.6	Xtrriage
Anisotropy	0.677	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 60.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	15541	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	67.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.23% 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, GDP, SO4, 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	0.46	0/3464	0.68	0/4702
1	C	0.48	0/3413	0.69	0/4636
2	B	0.48	0/3515	0.72	0/4761
2	D	0.47	0/3531	0.72	1/4782 (0.0%)
3	E	0.49	0/1116	0.71	0/1488
All	All	0.47	0/15039	0.70	1/20369 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	177	VAL	C-N-CA	5.50	135.46	121.70

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	3389	0	3292	71	0
1	C	3333	0	3236	61	0
2	B	3428	0	3279	91	0
2	D	3449	0	3304	58	0
3	E	1101	0	1083	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	32	0	12	1	0
4	C	32	0	12	1	0
5	A	1	0	0	0	0
5	C	1	0	0	0	0
6	A	25	0	0	0	0
6	B	5	0	0	0	0
6	C	15	0	0	0	0
6	D	10	0	0	0	0
6	E	5	0	0	0	0
7	B	28	0	12	2	0
7	D	28	0	12	2	0
8	A	192	0	0	3	0
8	B	128	0	0	5	0
8	C	143	0	0	4	0
8	D	161	0	0	2	0
8	E	35	0	0	2	0
All	All	15541	0	14242	285	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 10.

The worst 5 of 285 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:C:340:SER:HB2	8:C:609:HOH:O	1.42	1.18
1:A:46:ASP:N	1:A:47:ASP:HA	1.52	1.18
1:C:281:ALA:HB1	1:C:282:TYR:C	1.68	1.13
1:C:281:ALA:HB1	1:C:282:TYR:CB	1.82	1.09
1:A:283:HIS:CB	1:A:284:GLU:OE2	2.02	1.08

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	430/451 (95%)	404 (94%)	19 (4%)	7 (2%)	9	13
1	C	427/451 (95%)	407 (95%)	14 (3%)	6 (1%)	11	15
2	B	436/445 (98%)	415 (95%)	14 (3%)	7 (2%)	9	13
2	D	439/445 (99%)	420 (96%)	14 (3%)	5 (1%)	14	20
3	E	133/143 (93%)	121 (91%)	8 (6%)	4 (3%)	4	3
All	All	1865/1935 (96%)	1767 (95%)	69 (4%)	29 (2%)	9	13

5 of 29 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	ARG
1	A	281	ALA
2	B	60	LYS
2	B	220	THR
2	B	284	ARG

### 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	365/379 (96%)	341 (93%)	24 (7%)	16	26
1	C	357/379 (94%)	328 (92%)	29 (8%)	11	18
2	B	375/385 (97%)	345 (92%)	30 (8%)	12	18
2	D	379/385 (98%)	344 (91%)	35 (9%)	9	13
3	E	114/125 (91%)	91 (80%)	23 (20%)	1	1
All	All	1590/1653 (96%)	1449 (91%)	141 (9%)	10	14

5 of 141 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	373	MET

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Mol	Chain	Res	Type
3	E	24	LEU
3	E	96	MET
2	B	377[A]	PHE
2	B	373	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 61 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	350	ASN
2	D	350	ASN
1	C	91	GLN
2	D	300	ASN
2	D	436	GLN

### 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 [i](#)

Of 18 ligands modelled in this entry, 2 are monoatomic - leaving 16 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	SO4	D	456	-	4,4,4	0.21	0	6,6,6	0.17	0
6	SO4	C	454	-	4,4,4	0.15	0	6,6,6	0.08	0
7	GDP	D	600	-	24,30,30	1.19	3 (12%)	30,47,47	1.55	6 (20%)
7	GDP	B	600	-	24,30,30	1.01	1 (4%)	30,47,47	1.43	5 (16%)
6	SO4	A	452	-	4,4,4	0.16	0	6,6,6	0.13	0
6	SO4	A	455	-	4,4,4	0.16	0	6,6,6	0.07	0
6	SO4	E	146	-	4,4,4	0.12	0	6,6,6	0.08	0
6	SO4	A	453	-	4,4,4	0.18	0	6,6,6	0.08	0
6	SO4	A	456	-	4,4,4	0.12	0	6,6,6	0.08	0
6	SO4	A	454	-	4,4,4	0.19	0	6,6,6	0.17	0
4	GTP	C	600	5	26,34,34	1.33	4 (15%)	32,54,54	1.24	3 (9%)
4	GTP	A	600	5	26,34,34	1.13	3 (11%)	32,54,54	1.18	3 (9%)
6	SO4	D	457	-	4,4,4	0.22	0	6,6,6	0.13	0
6	SO4	C	452	-	4,4,4	0.16	0	6,6,6	0.12	0
6	SO4	C	453	-	4,4,4	0.17	0	6,6,6	0.10	0
6	SO4	B	456	-	4,4,4	0.14	0	6,6,6	0.21	0

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	C	600	5	-	6/18/38/38	0/3/3/3
4	GTP	A	600	5	-	6/18/38/38	0/3/3/3
7	GDP	B	600	-	-	5/12/32/32	0/3/3/3
7	GDP	D	600	-	-	5/12/32/32	0/3/3/3

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	600	GDP	C8-N7	-3.01	1.29	1.35
4	C	600	GTP	C2'-C1'	2.93	1.58	1.53
4	A	600	GTP	O4'-C1'	2.75	1.44	1.41
4	A	600	GTP	C8-N7	-2.44	1.30	1.35
4	C	600	GTP	C8-N7	-2.40	1.30	1.35

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	D	600	GDP	PA-O3A-PB	-4.00	119.09	132.83
7	B	600	GDP	PA-O3A-PB	-3.75	119.97	132.83
7	D	600	GDP	O4'-C1'-C2'	-3.43	101.91	106.93
4	C	600	GTP	PB-O3B-PG	-2.90	122.88	132.83
4	A	600	GTP	PB-O3B-PG	-2.85	123.06	132.83

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	600	GTP	C5'-O5'-PA-O1A
4	A	600	GTP	C5'-O5'-PA-O2A
4	C	600	GTP	C5'-O5'-PA-O1A
4	C	600	GTP	C5'-O5'-PA-O2A
7	B	600	GDP	C5'-O5'-PA-O1A

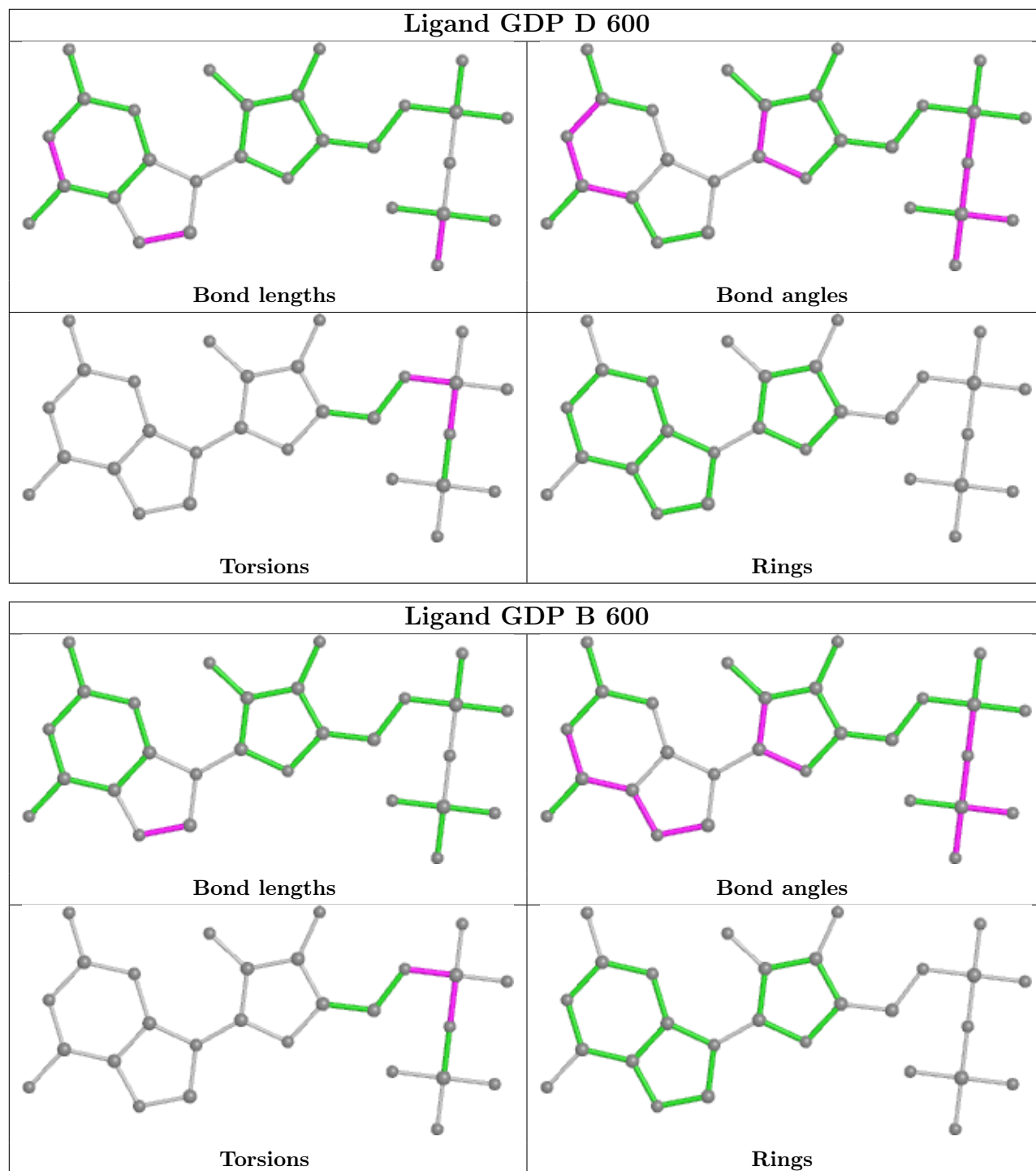
There are no ring outliers.

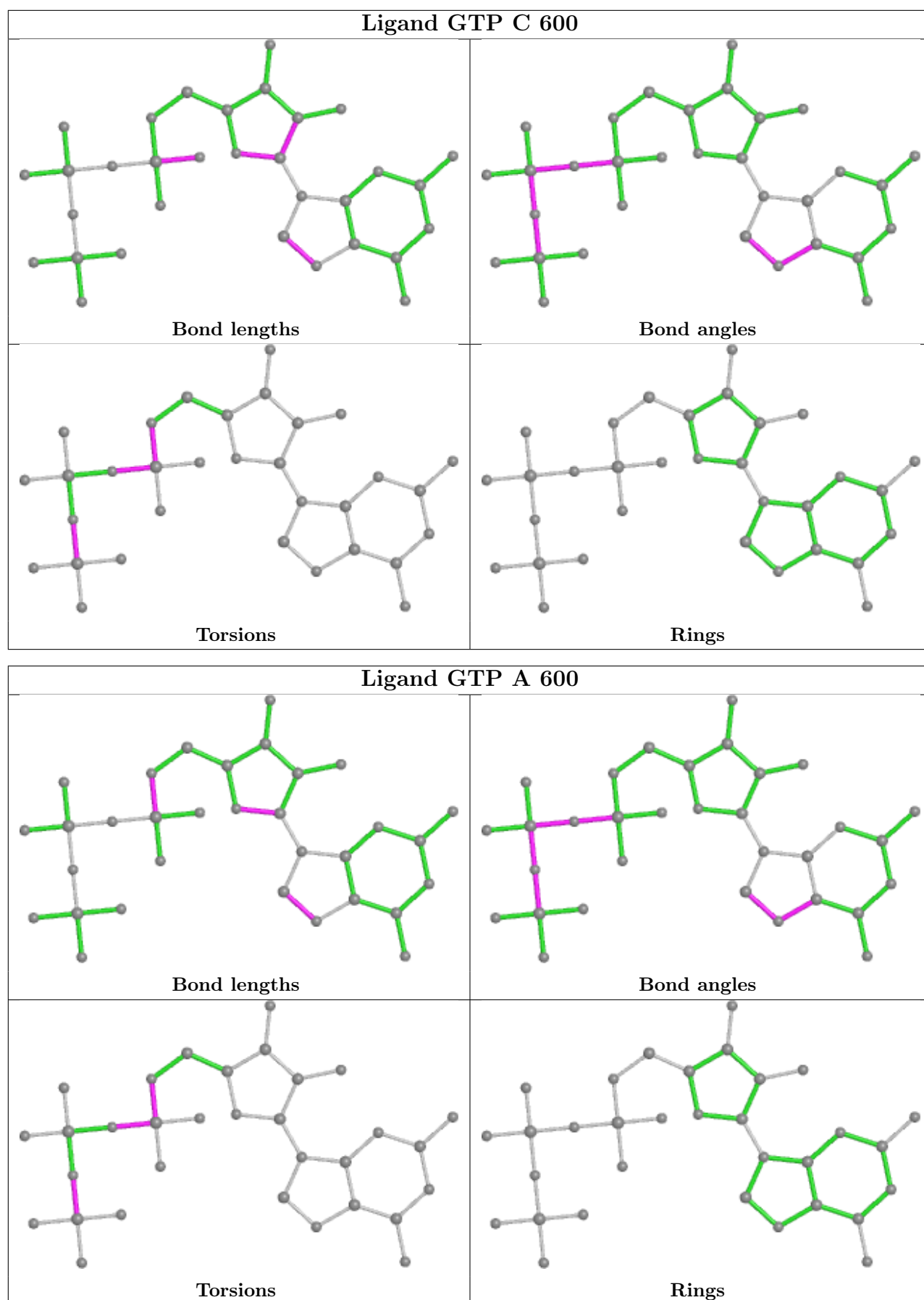
4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	D	600	GDP	2	0
7	B	600	GDP	2	0
4	C	600	GTP	1	0
4	A	600	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 [i](#)

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	433/451 (96%)	-0.13	11 (2%) 57 55	41, 60, 91, 133	0
1	C	429/451 (95%)	0.12	18 (4%) 36 35	44, 68, 106, 145	0
2	B	431/445 (96%)	0.33	34 (7%) 12 11	39, 63, 115, 171	1 (0%)
2	D	431/445 (96%)	-0.07	12 (2%) 53 51	38, 55, 99, 138	1 (0%)
3	E	136/143 (95%)	0.90	25 (18%) 1 1	60, 80, 128, 155	0
All	All	1860/1935 (96%)	0.13	100 (5%) 25 24	38, 63, 107, 171	2 (0%)

The worst 5 of 100 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	283	TYR	10.8
3	E	33	PRO	9.0
3	E	32	VAL	8.9
3	E	31	GLY	8.4
2	B	371	LEU	7.6

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

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

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

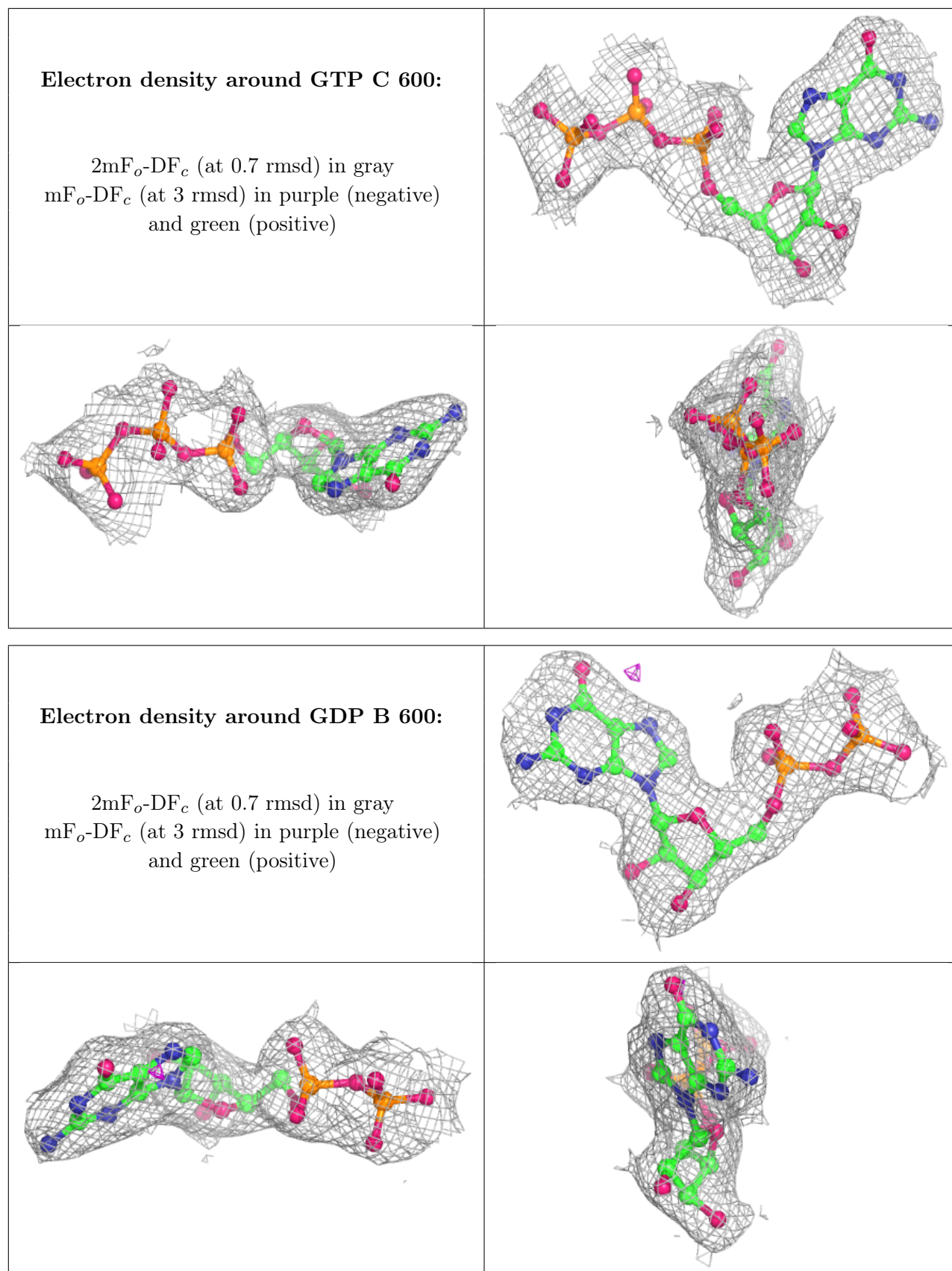
### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

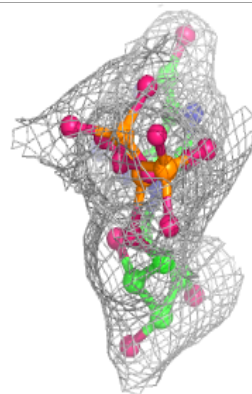
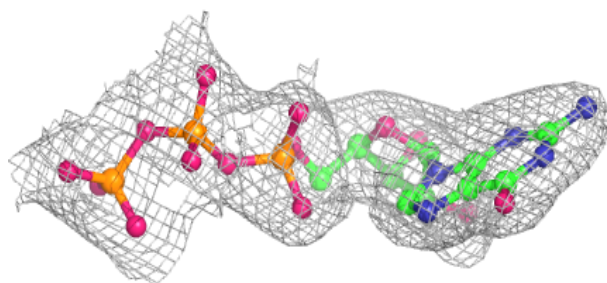
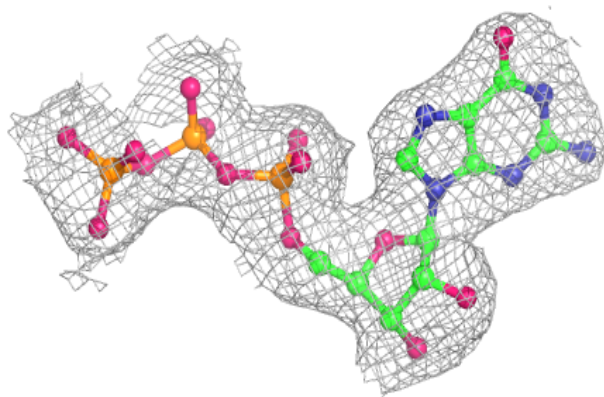
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
6	SO4	A	456	5/5	0.48	0.33	191,196,197,197	0
6	SO4	C	454	5/5	0.64	0.57	208,213,213,214	0
6	SO4	A	455	5/5	0.86	0.21	148,152,154,154	0
6	SO4	D	457	5/5	0.86	0.13	136,140,141,141	0
6	SO4	B	456	5/5	0.89	0.14	115,119,119,120	0
6	SO4	C	453	5/5	0.89	0.35	142,146,146,147	0
6	SO4	A	453	5/5	0.90	0.15	131,135,136,137	0
6	SO4	E	146	5/5	0.93	0.15	129,133,134,135	0
6	SO4	A	454	5/5	0.96	0.13	99,103,104,104	0
5	MG	C	601	1/1	0.97	0.13	61,61,61,61	0
6	SO4	C	452	5/5	0.97	0.10	96,100,101,101	0
6	SO4	A	452	5/5	0.97	0.18	90,94,95,96	0
4	GTP	C	600	32/32	0.98	0.14	49,55,58,60	0
5	MG	A	601	1/1	0.98	0.17	54,54,54,54	0
7	GDP	B	600	28/28	0.98	0.15	51,53,55,57	0
6	SO4	D	456	5/5	0.99	0.12	73,79,79,79	0
4	GTP	A	600	32/32	0.99	0.16	43,46,49,51	0
7	GDP	D	600	28/28	0.99	0.10	39,41,46,47	0

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

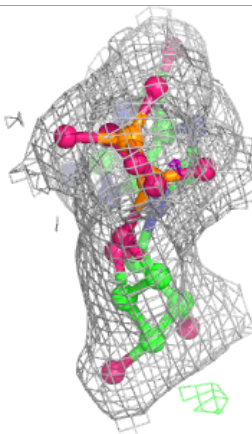
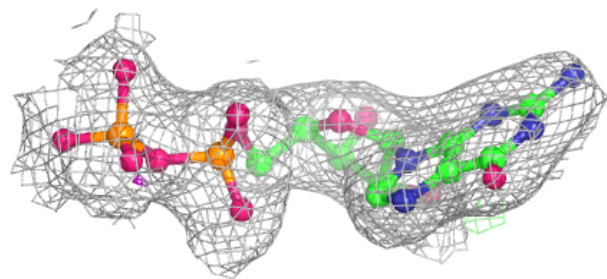
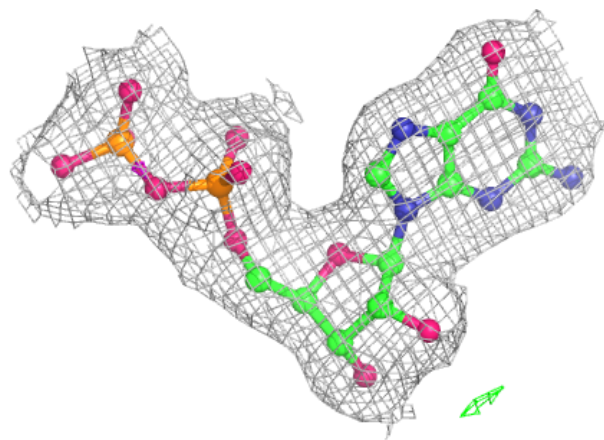


**Electron density around GTP A 600:**

$2mF_o-DF_c$  (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)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.