



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 29, 2025 – 02:53 PM EDT

PDB ID : 4O4H / pdb\_00004o4h  
Title : Tubulin-Laulimalide complex  
Authors : Prota, A.E.; Bargsten, K.; Northcote, P.T.; Marsh, M.; Altmann, K.H.; Miller, J.H.; Diaz, J.F.; Steinmetz, M.O.  
Deposited on : 2013-12-18  
Resolution : 2.10 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

<http://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 : 4-5-2 with Phenix2.0rc1  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

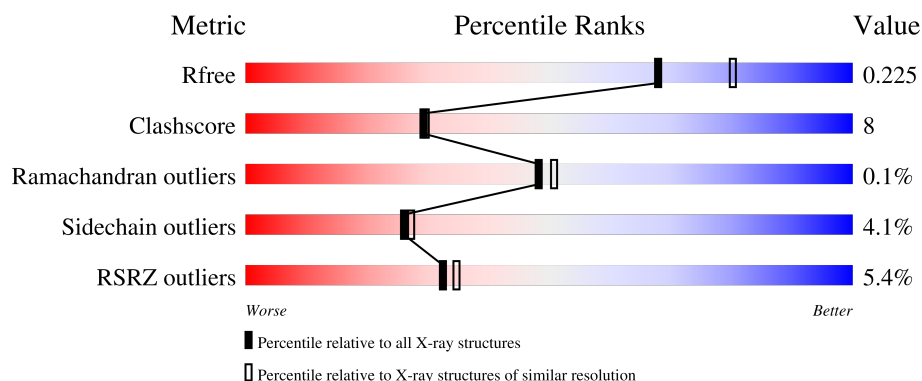
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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))
$R_{free}$	164625	6234 (2.10-2.10)
Clashscore	180529	6893 (2.10-2.10)
Ramachandran outliers	177936	6839 (2.10-2.10)
Sidechain outliers	177891	6840 (2.10-2.10)
RSRZ outliers	164620	6234 (2.10-2.10)

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	
1	C	451	
2	B	445	
2	D	445	
3	E	143	

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Mol	Chain	Length	Quality of chain
4	F	384	

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:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
10	GOL	B	504	-	-	X	-

## 2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 18548 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-1B chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	439	Total	C	N	O	S	0	12	0
			3481	2214	584	658	25			
1	C	440	Total	C	N	O	S	0	19	0
			3519	2235	586	672	26			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	426	Total	C	N	O	S	0	10	0
			3397	2137	573	660	27			
2	D	427	Total	C	N	O	S	0	6	0
			3370	2117	571	653	29			

- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	123	Total	C	N	O	S	0	5	0
			1039	642	187	205	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	3	MET	ILE	cloning artifact	UNP P63043
E	4	ALA	SER	cloning artifact	UNP P63043

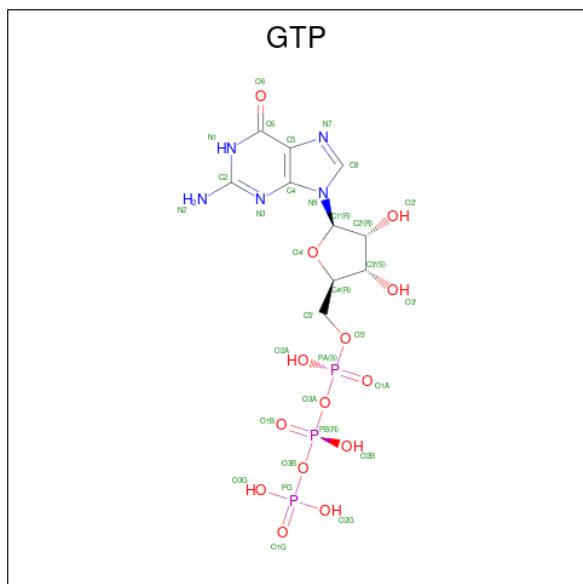
- Molecule 4 is a protein called Tubulin-tyrosine ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	348	Total	C	N	O	S	0	6	0
			2878	1852	487	525	14			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	379	HIS	-	expression tag	UNP E1BQ43
F	380	HIS	-	expression tag	UNP E1BQ43
F	381	HIS	-	expression tag	UNP E1BQ43
F	382	HIS	-	expression tag	UNP E1BQ43
F	383	HIS	-	expression tag	UNP E1BQ43
F	384	HIS	-	expression tag	UNP E1BQ43

- Molecule 5 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula:  $C_{10}H_{16}N_5O_{14}P_3$ ).



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

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

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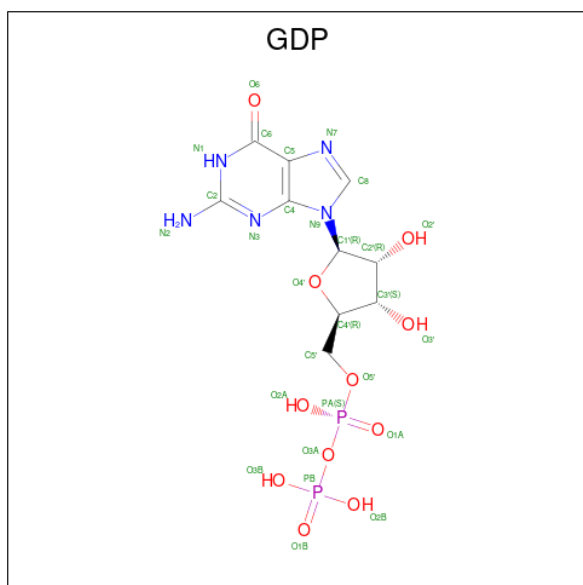
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	1	Total	Mg	0	0
			1	1		

- Molecule 7 is CALCIUM ION (CCD ID: CA) (formula: Ca).

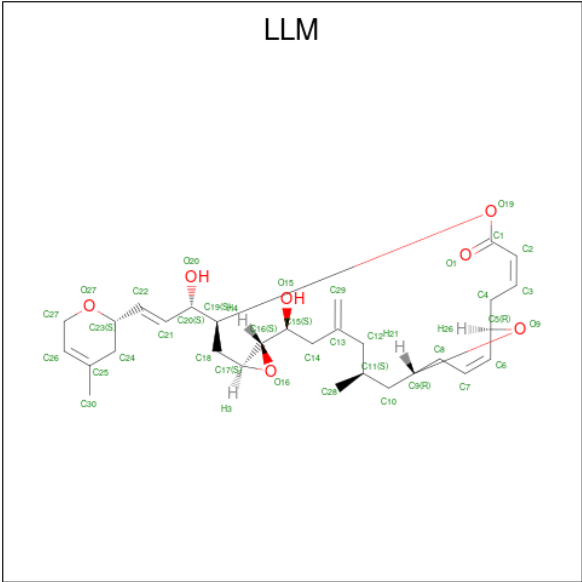
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Ca	0	0
			1	1		
7	B	2	Total	Ca	0	0
			2	2		

- Molecule 8 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>11</sub>P<sub>2</sub>).



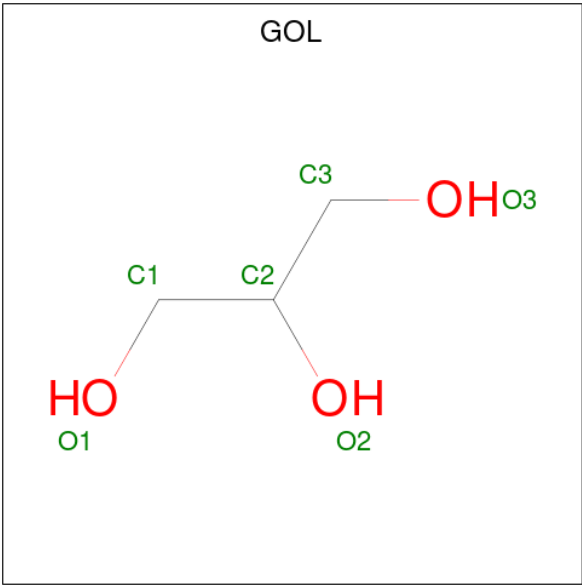
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	B	1	Total 28	C 10	N 5	O 11	P 2	0	0
8	D	1	Total 28	C 10	N 5	O 11	P 2	0	0

- Molecule 9 is Laulimalide (CCD ID: LLM) (formula: C<sub>30</sub>H<sub>42</sub>O<sub>7</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	C	O	0	0
			37	30	7		

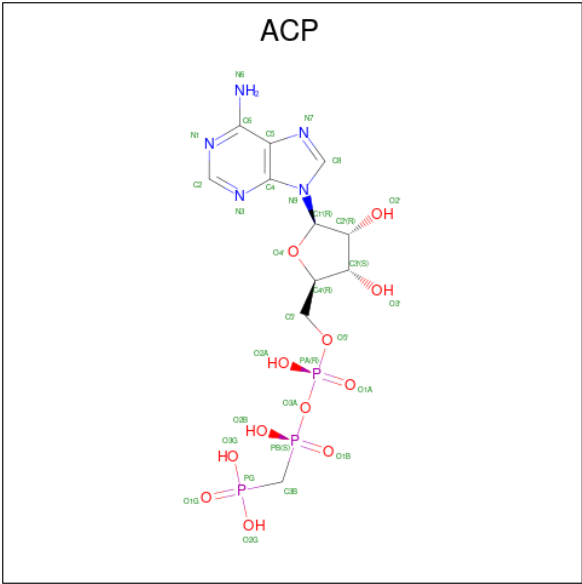
- Molecule 10 is GLYCEROL (CCD ID: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	B	1	Total	C	O	0	0
			6	3	3		
10	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 11 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (CCD

ID: ACP) (formula: C<sub>11</sub>H<sub>18</sub>N<sub>5</sub>O<sub>12</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
11	F	1	Total	C	N	O	P	0	0
			31	11	5	12	3		

- Molecule 12 is water.

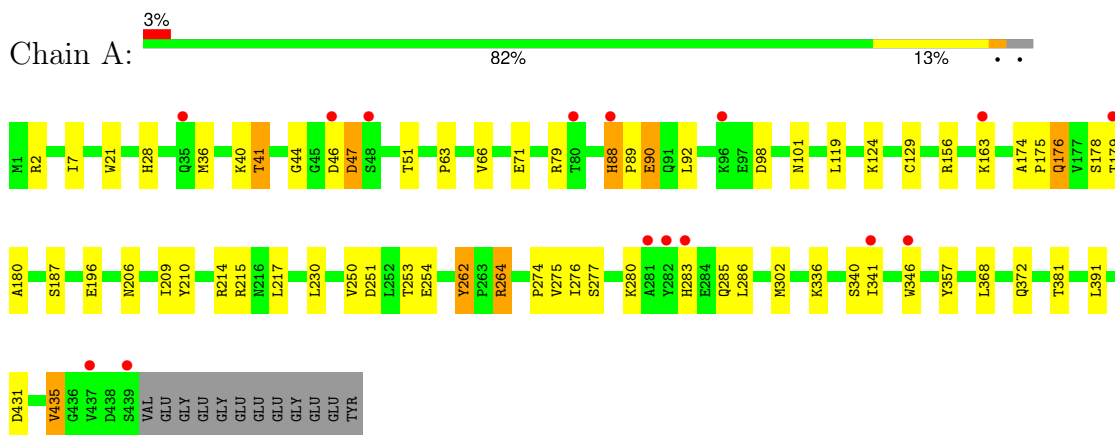
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	110	Total	O	0	0
			110	110		
12	B	142	Total	O	0	0
			142	142		
12	C	231	Total	O	0	0
			231	231		
12	D	102	Total	O	0	0
			102	102		
12	E	31	Total	O	0	0
			31	31		
12	F	40	Total	O	0	0
			40	40		



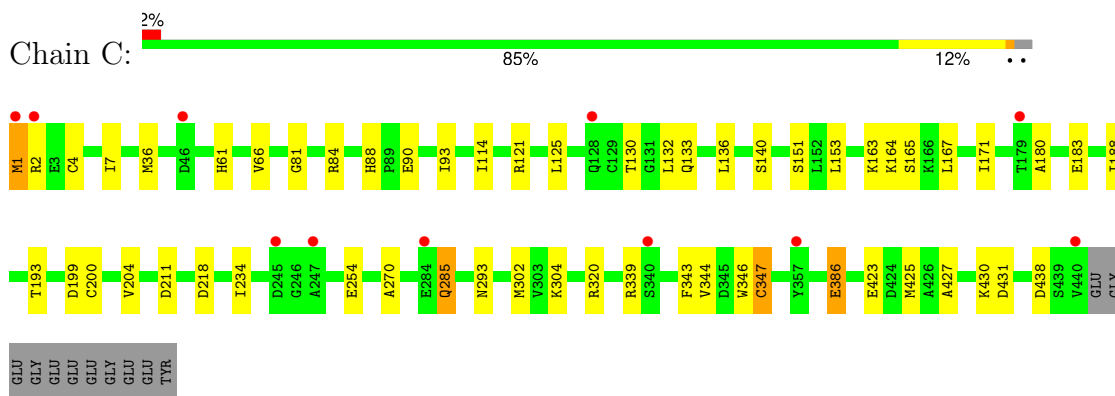
### 3 Residue-property plots [i](#)

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.

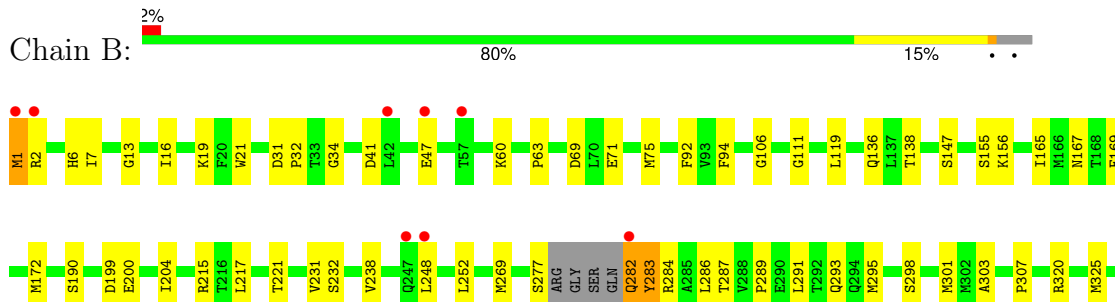
- Molecule 1: Tubulin alpha-1B chain



- Molecule 1: Tubulin alpha-1B chain

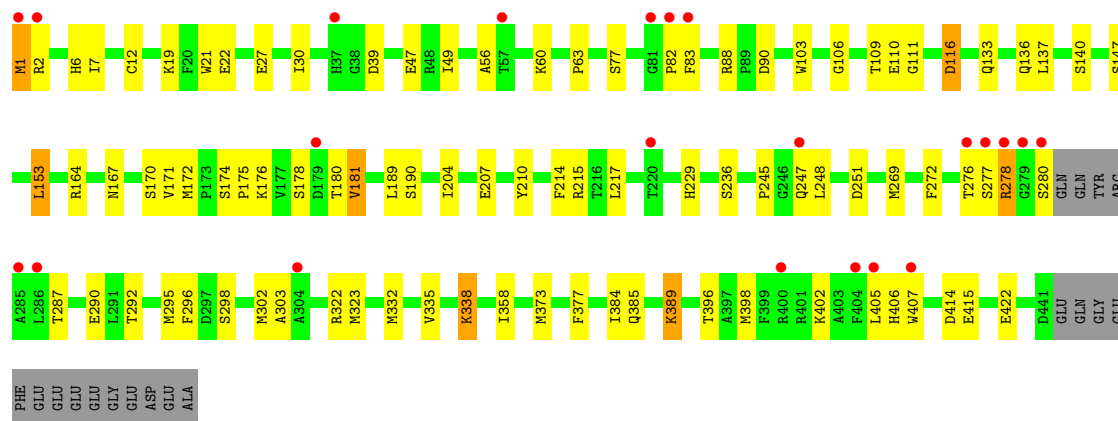
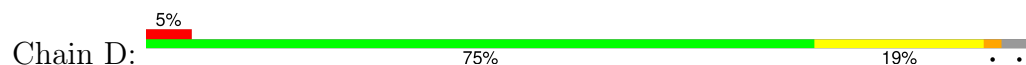


- Molecule 2: Tubulin beta-2B chain

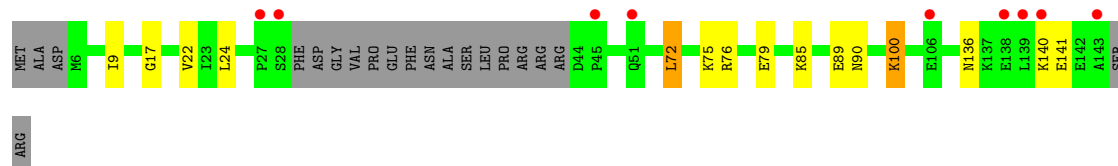
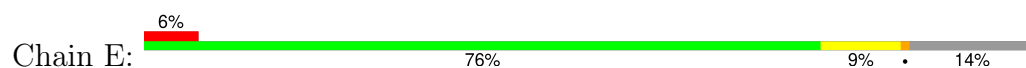




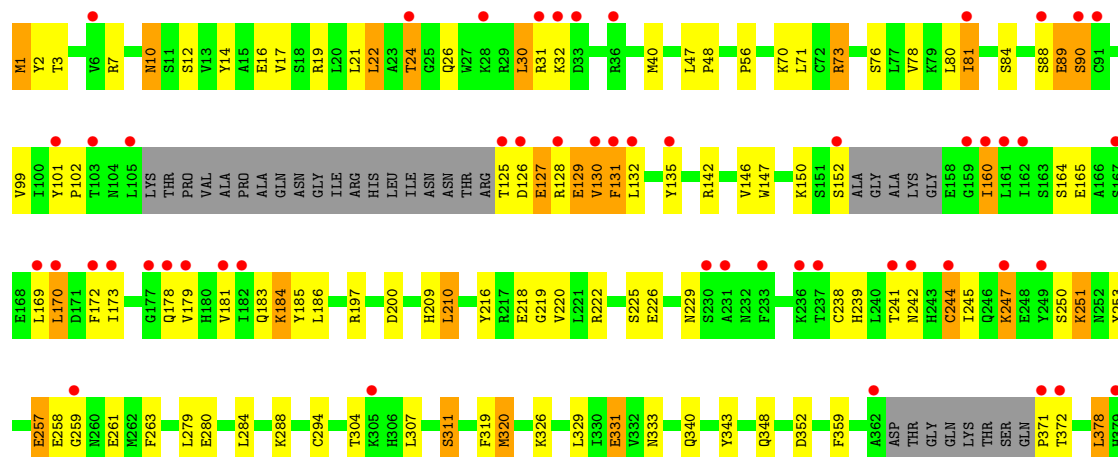
• Molecule 2: Tubulin beta-2B chain



• Molecule 3: Stathmin-4



• Molecule 4: Tubulin-tyrosine ligase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	104.69Å 156.87Å 180.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	71.90 – 2.10 71.90 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (71.90-2.10) 99.8 (71.90-2.10)	Depositor EDS
$R_{merge}$	0.18	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.62 (at 2.10Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, $R_{free}$	0.192 , 0.224 0.194 , 0.225	Depositor DCC
$R_{free}$ test set	8659 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	33.4	Xtriage
Anisotropy	0.217	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 56.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	18548	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.51% 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

### 5.1 Standard geometry

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

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	0.41	2/3596 (0.1%)	0.77	4/4883 (0.1%)
1	C	0.40	0/3655	0.74	0/4965
2	B	0.39	0/3498	0.75	0/4738
2	D	0.38	0/3461	0.78	2/4689 (0.0%)
3	E	0.36	0/1063	0.69	0/1412
4	F	0.41	1/2961 (0.0%)	0.75	0/4002
All	All	0.40	3/18234 (0.0%)	0.75	6/24689 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	90	SER	CB-OG	-8.32	1.25	1.42
1	A	89	PRO	N-CD	5.35	1.55	1.47
1	A	88	HIS	C-N	5.34	1.40	1.33

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	338	LYS	CD-CE-NZ	-8.77	83.83	111.90
1	A	88	HIS	CA-C-N	-5.37	113.37	119.28
1	A	88	HIS	C-N-CA	-5.37	113.37	119.28
2	D	358	ILE	N-CA-C	5.14	112.95	107.76
1	A	262	TYR	CA-C-N	5.03	124.47	119.24

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

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	3481	0	3437	53	2
1	C	3519	0	3469	43	0
2	B	3397	0	3291	52	0
2	D	3370	0	3265	51	1
3	E	1039	0	1062	11	0
4	F	2878	0	2872	88	3
5	A	32	0	12	0	0
5	C	32	0	12	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
6	F	1	0	0	0	0
7	A	1	0	0	0	0
7	B	2	0	0	0	0
8	B	28	0	12	0	0
8	D	28	0	12	0	0
9	B	37	0	42	7	0
10	B	6	0	8	5	0
10	D	6	0	8	0	0
11	F	31	0	14	6	0
12	A	110	0	0	6	0
12	B	142	0	0	6	0
12	C	231	0	0	5	0
12	D	102	0	0	6	0
12	E	31	0	0	0	0
12	F	40	0	0	3	0
All	All	18548	0	17516	300	3

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 8.

The worst 5 of 300 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)
9:B:503:LLM:H18	9:B:503:LLM:H11	1.29	1.14
1:A:88:HIS:CD2	1:A:90:GLU:HB2	1.99	0.96
4:F:19:ARG:HA	4:F:22:LEU:HD12	1.53	0.90
1:A:88:HIS:CD2	1:A:90:GLU:H	1.90	0.88
2:B:282:GLN:HG2	2:B:283:TYR:H	1.43	0.84

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:HIS:CE1	4:F:142:ARG:NH2[2_564]	1.14	1.06
1:A:88:HIS:ND1	4:F:142:ARG:NH2[2_564]	1.95	0.25
2:D:338:LYS:NZ	4:F:90:SER:OG[3_545]	2.05	0.15

## 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 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	449/451 (100%)	440 (98%)	9 (2%)	0	100	100
1	C	457/451 (101%)	447 (98%)	10 (2%)	0	100	100
2	B	432/445 (97%)	417 (96%)	14 (3%)	1 (0%)	44	45
2	D	429/445 (96%)	410 (96%)	18 (4%)	1 (0%)	44	45
3	E	124/143 (87%)	123 (99%)	1 (1%)	0	100	100
4	F	346/384 (90%)	327 (94%)	19 (6%)	0	100	100
All	All	2237/2319 (96%)	2164 (97%)	71 (3%)	2 (0%)	48	51

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	283	TYR
2	D	181	VAL

### 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 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	382/379 (101%)	373 (98%)	9 (2%)	44	49
1	C	390/379 (103%)	383 (98%)	7 (2%)	54	61
2	B	378/383 (99%)	366 (97%)	12 (3%)	34	37
2	D	374/383 (98%)	360 (96%)	14 (4%)	29	31
3	E	115/127 (91%)	110 (96%)	5 (4%)	25	25
4	F	320/342 (94%)	287 (90%)	33 (10%)	6	3
All	All	1959/1993 (98%)	1879 (96%)	80 (4%)	26	27

5 of 80 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	F	129	GLU
4	F	257	GLU
4	F	131	PHE
4	F	186	LEU
4	F	320	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
4	F	229	ASN
4	F	333	ASN
4	F	269	GLN
2	B	385	GLN
4	F	178	GLN

### 5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 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$
10	GOL	D	503	-	5,5,5	0.42	0	5,5,5	0.45	0
11	ACP	F	401	-	27,33,33	2.53	11 (40%)	33,52,52	4.64	14 (42%)
8	GDP	D	501	6	25,30,30	0.96	2 (8%)	30,47,47	1.16	2 (6%)
9	LLM	B	503	-	39,40,40	2.55	14 (35%)	41,55,55	1.95	8 (19%)
8	GDP	B	501	6	25,30,30	0.97	2 (8%)	30,47,47	1.29	5 (16%)
5	GTP	A	501	6	29,34,34	1.17	1 (3%)	35,54,54	1.22	4 (11%)
5	GTP	C	501	6	29,34,34	1.23	2 (6%)	35,54,54	1.35	8 (22%)
10	GOL	B	504	-	5,5,5	0.39	0	5,5,5	0.50	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
10	GOL	D	503	-	-	2/4/4/4	-
11	ACP	F	401	-	-	5/15/38/38	0/3/3/3
8	GDP	D	501	6	-	4/12/32/32	0/3/3/3
9	LLM	B	503	-	-	9/39/64/64	0/3/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	GDP	B	501	6	-	5/12/32/32	0/3/3/3
5	GTP	A	501	6	-	8/18/38/38	0/3/3/3
5	GTP	C	501	6	-	8/18/38/38	0/3/3/3
10	GOL	B	504	-	-	2/4/4/4	-

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	503	LLM	C22-C21	6.85	1.52	1.32
11	F	401	ACP	PG-O1G	5.68	1.61	1.50
9	B	503	LLM	C5-C6	-5.49	1.40	1.50
11	F	401	ACP	C2-N3	5.07	1.39	1.32
9	B	503	LLM	C30-C25	-5.04	1.38	1.50

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	F	401	ACP	O4'-C4'-C5'	12.84	150.47	109.33
11	F	401	ACP	O4'-C4'-C3'	-10.42	84.48	105.15
11	F	401	ACP	C4'-O4'-C1'	9.26	118.41	109.92
11	F	401	ACP	C1'-N9-C4	-8.71	111.34	126.64
11	F	401	ACP	N3-C2-N1	-7.91	117.93	128.67

There are no chirality outliers.

5 of 43 torsion outliers are listed below:

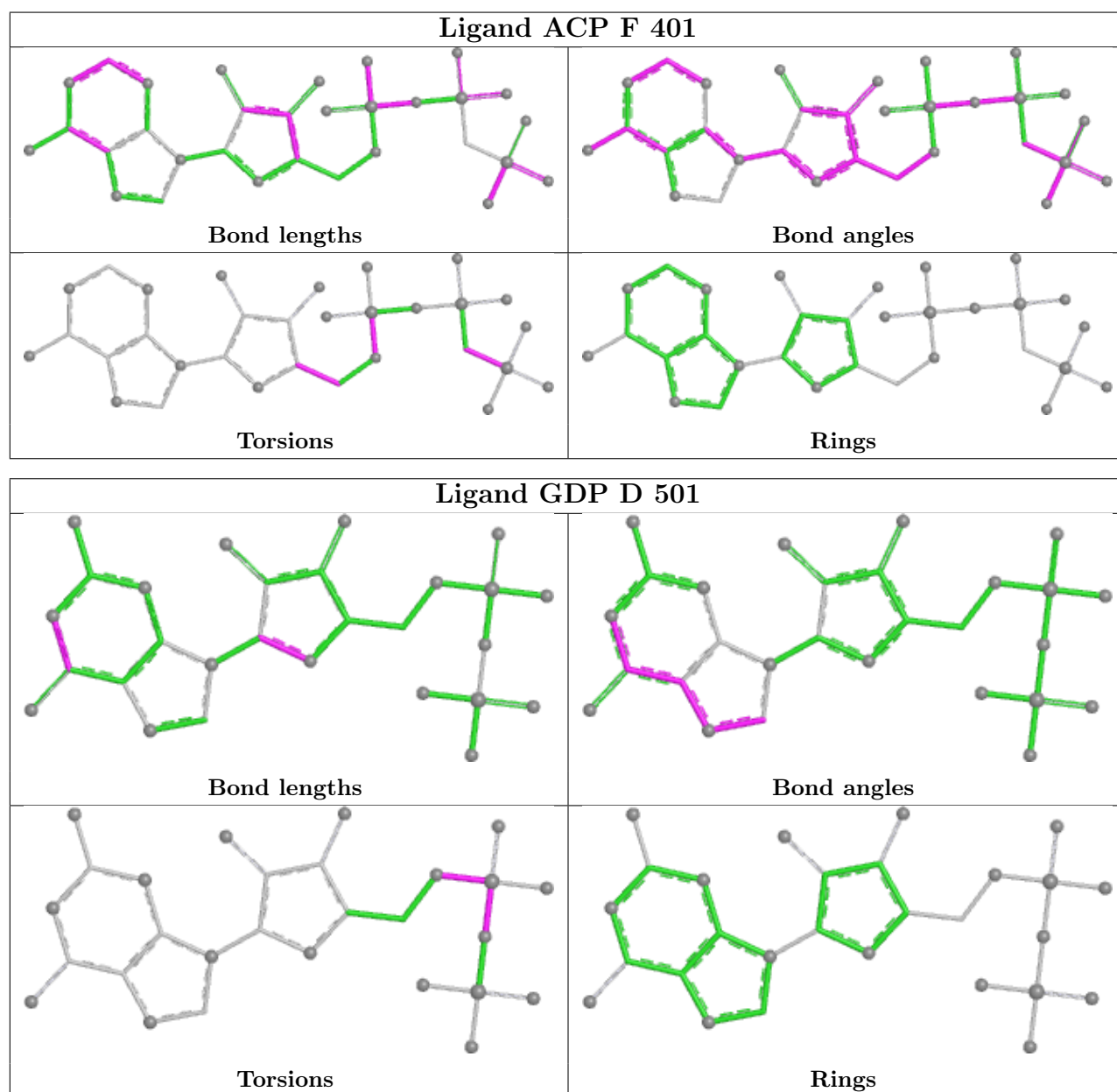
Mol	Chain	Res	Type	Atoms
5	A	501	GTP	C5'-O5'-PA-O3A
5	A	501	GTP	C5'-O5'-PA-O1A
5	A	501	GTP	C5'-O5'-PA-O2A
5	C	501	GTP	C5'-O5'-PA-O3A
5	C	501	GTP	C5'-O5'-PA-O1A

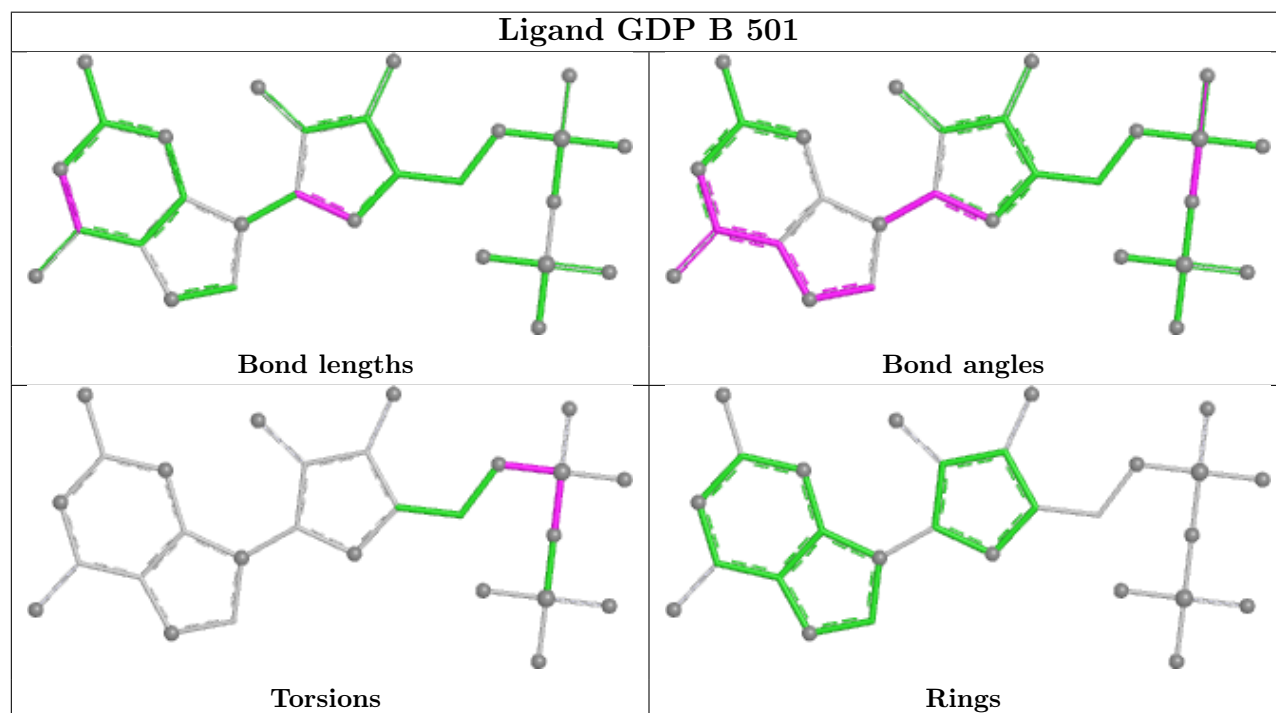
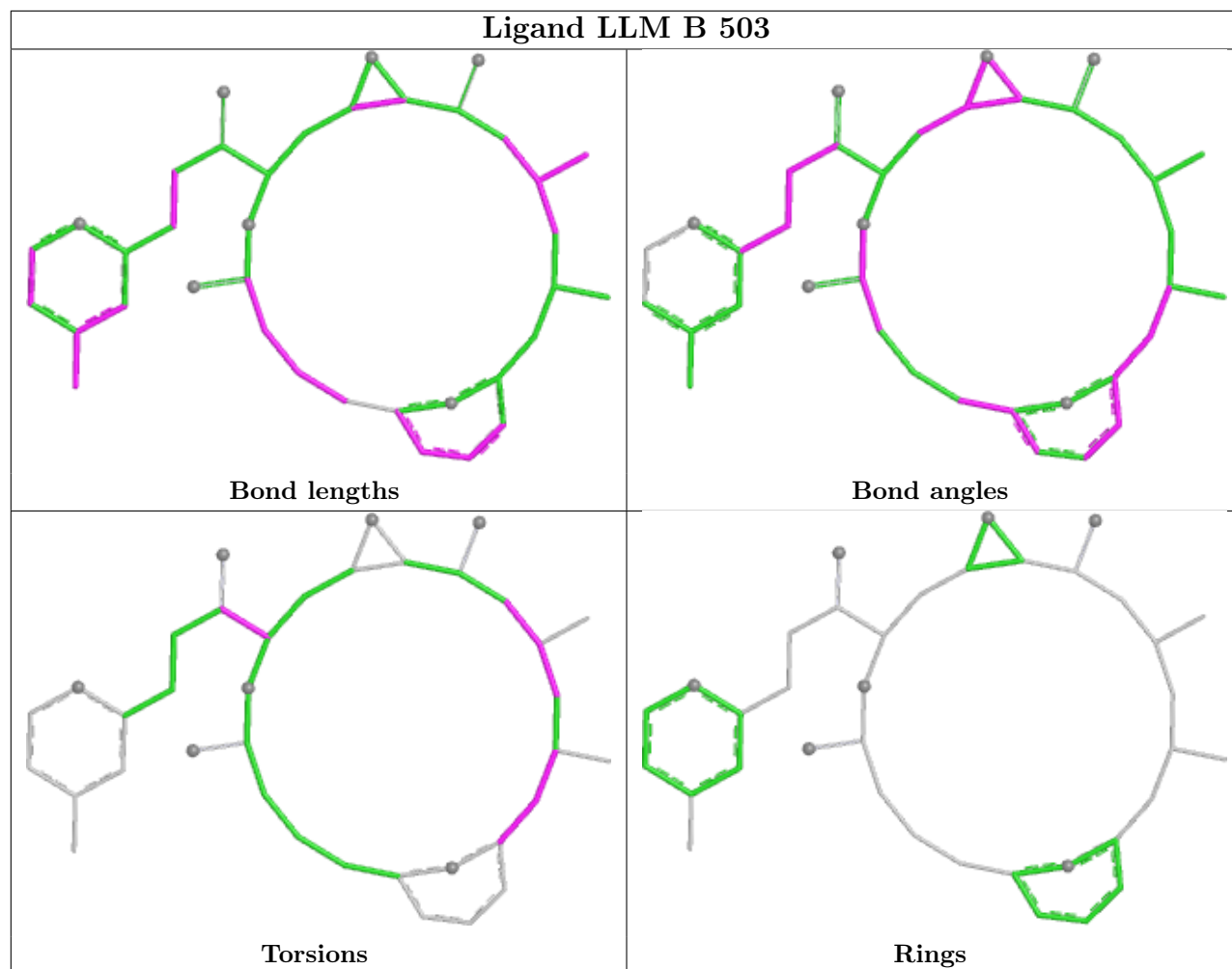
There are no ring outliers.

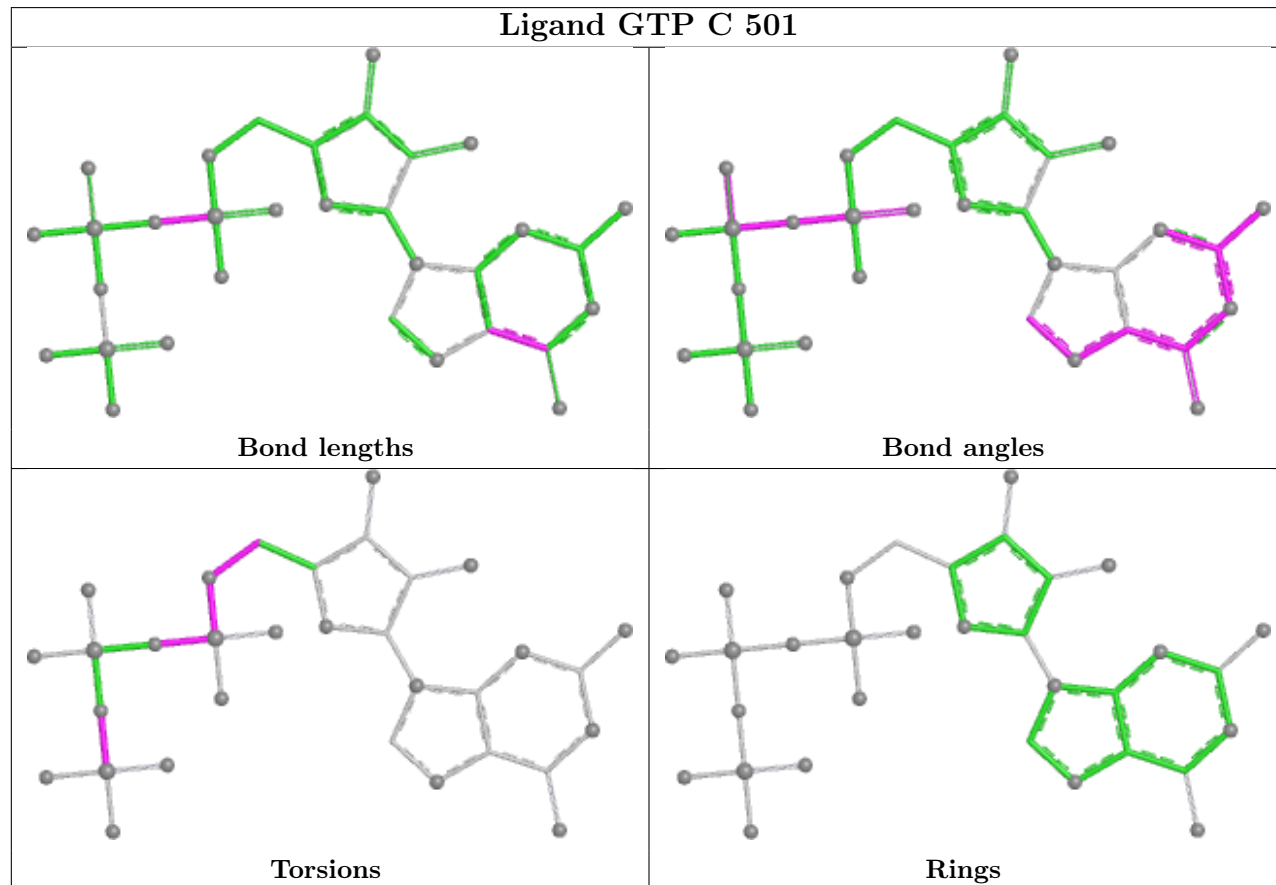
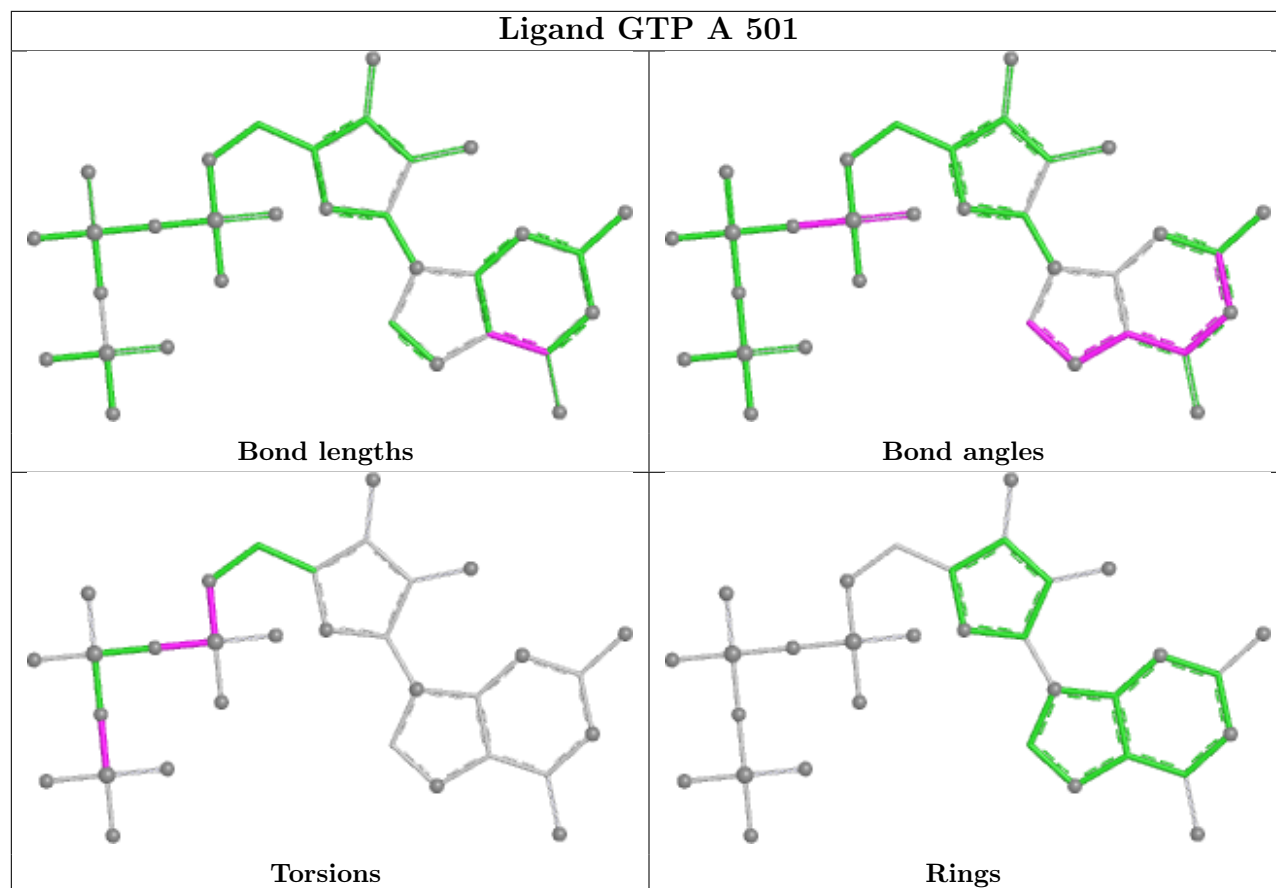
3 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	F	401	ACP	6	0
9	B	503	LLM	7	0
10	B	504	GOL	5	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	439/451 (97%)	0.01	15 (3%)	48	50	20, 44, 80, 131	12 (2%)
1	C	440/451 (97%)	-0.27	11 (2%)	58	60	17, 33, 58, 99	19 (4%)
2	B	426/445 (95%)	0.02	9 (2%)	63	65	18, 41, 71, 126	12 (2%)
2	D	427/445 (95%)	0.19	22 (5%)	34	36	23, 47, 78, 123	12 (2%)
3	E	123/143 (86%)	0.53	9 (7%)	22	24	23, 56, 93, 139	5 (4%)
4	F	348/384 (90%)	0.88	53 (15%)	6	7	30, 69, 131, 174	6 (1%)
All	All	2203/2319 (94%)	0.16	119 (5%)	32	35	17, 45, 96, 174	66 (2%)

The worst 5 of 119 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	1	MET	7.0
2	D	285	ALA	5.8
2	D	1	MET	5.6
4	F	105	LEU	5.0
3	E	143	ALA	5.0

### 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 ⓘ

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.

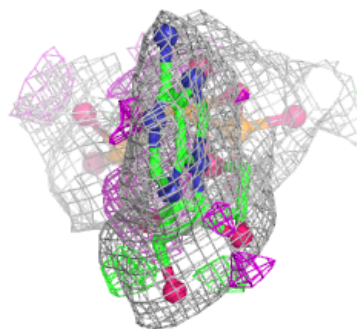
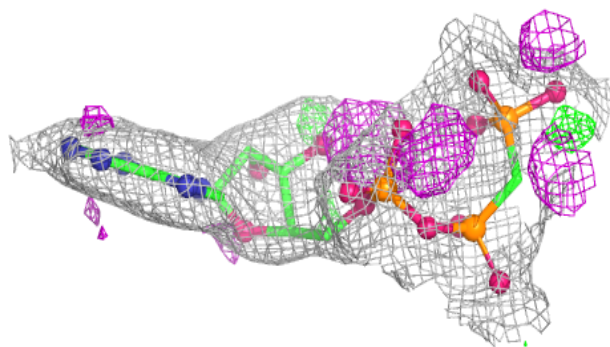
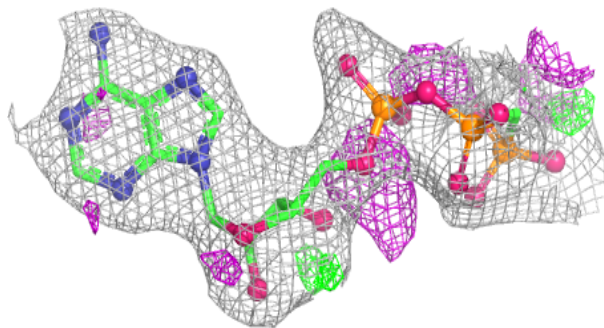
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
7	CA	B	505	1/1	0.66	0.17	109,109,109,109	0
10	GOL	D	503	6/6	0.75	0.26	63,74,92,100	0
7	CA	B	506	1/1	0.80	0.11	93,93,93,93	0
10	GOL	B	504	6/6	0.85	0.18	55,62,66,75	0
11	ACP	F	401	31/31	0.85	0.13	49,73,130,140	0
9	LLM	B	503	37/37	0.87	0.17	91,93,102,104	0
7	CA	A	503	1/1	0.90	0.13	80,80,80,80	0
6	MG	F	402	1/1	0.92	0.24	30,30,30,30	0
8	GDP	D	501	28/28	0.95	0.09	34,44,53,59	0
6	MG	B	502	1/1	0.98	0.07	22,22,22,22	0
6	MG	C	502	1/1	0.98	0.14	34,34,34,34	0
6	MG	D	502	1/1	0.98	0.05	44,44,44,44	0
6	MG	A	502	1/1	0.98	0.12	38,38,38,38	0
8	GDP	B	501	28/28	0.99	0.04	21,27,33,37	0
5	GTP	A	501	32/32	0.99	0.04	25,30,34,43	0
5	GTP	C	501	32/32	0.99	0.04	21,26,32,36	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.



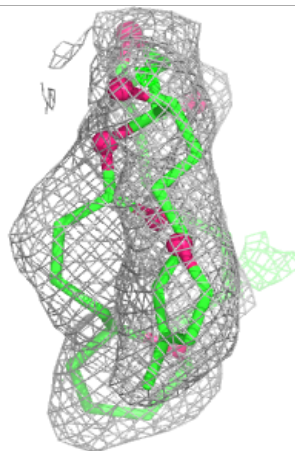
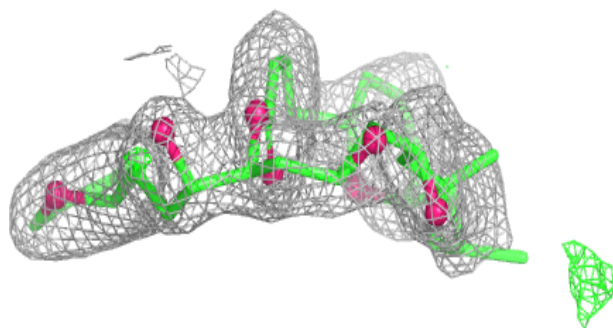
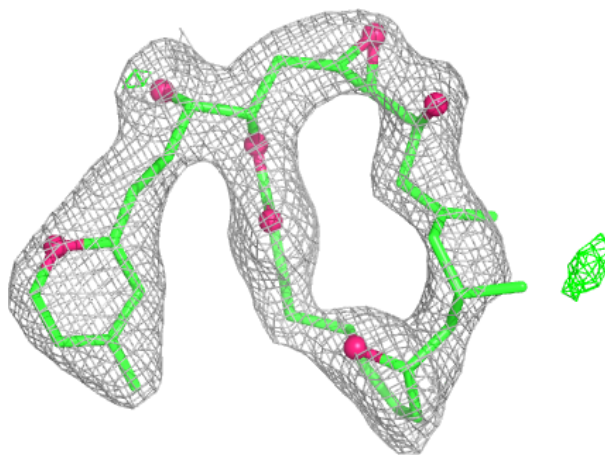
**Electron density around ACP F 401:**

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



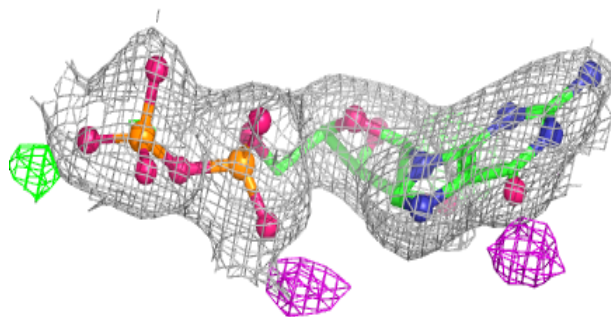
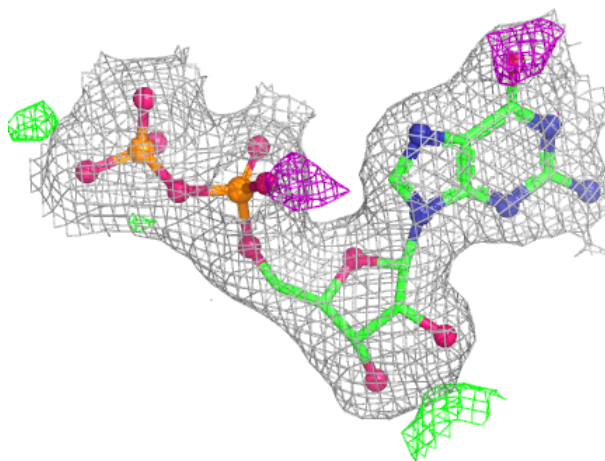
**Electron density around LLM B 503:**

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



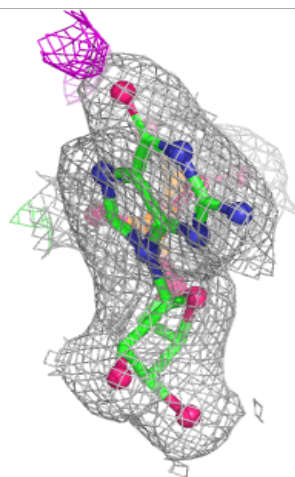
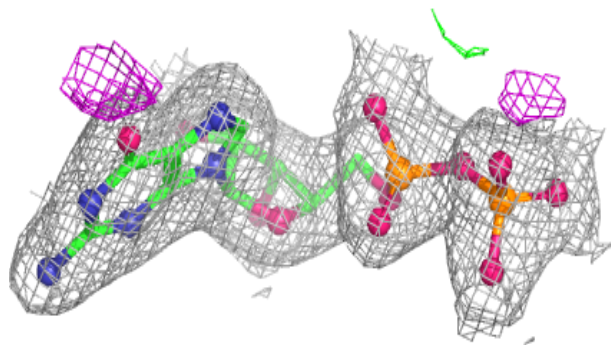
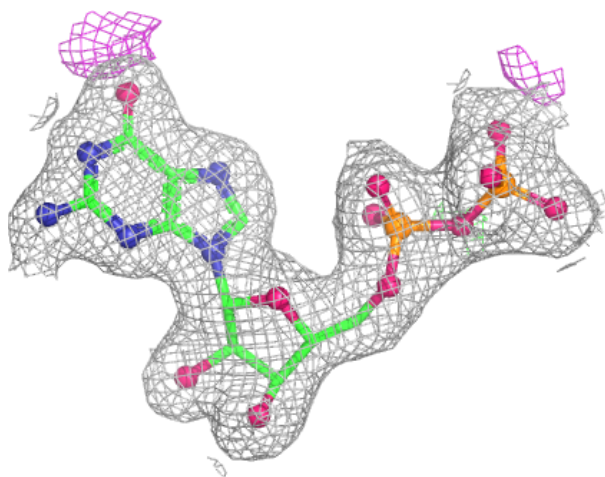
**Electron density around GDP D 501:**

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



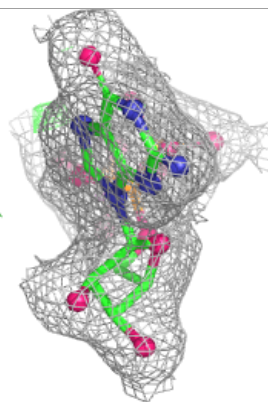
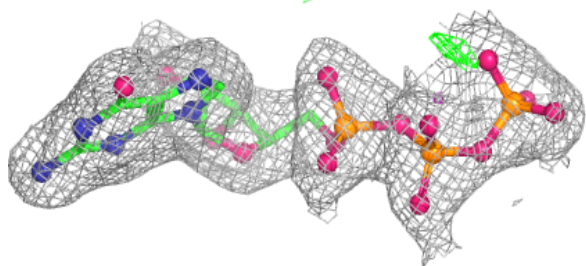
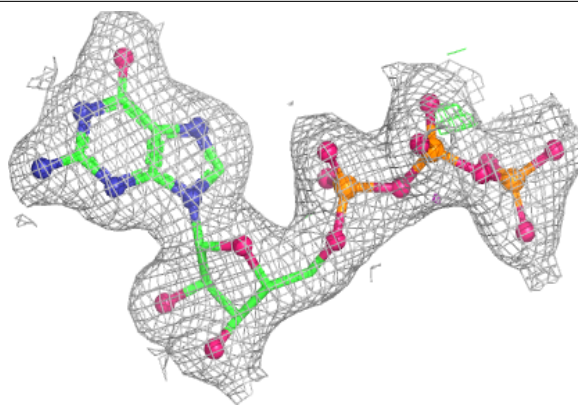
**Electron density around GDP B 501:**

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

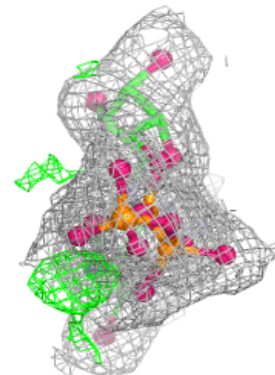
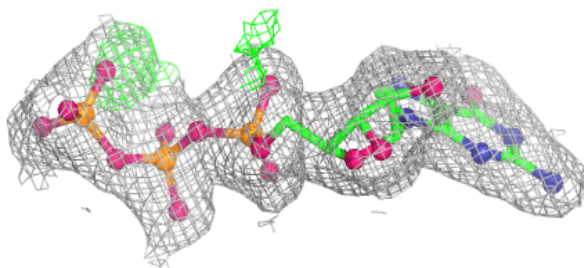
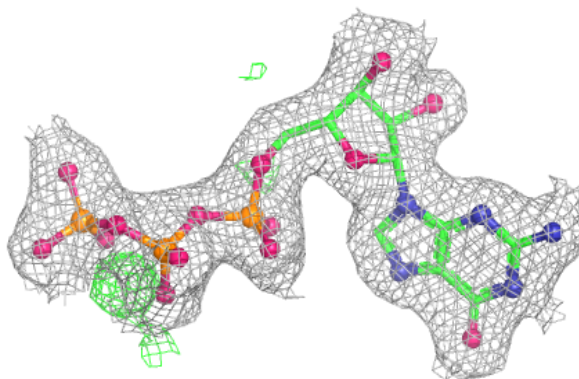


**Electron density around GTP A 501:**

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

**Electron density around GTP C 501:**

$2mF_o-DF_c$  (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.