



Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 11:29 am BST

PDB ID : 6FKJ
Title : Tubulin-TUB075 complex
Authors : Prota, A.E.; Steinmetz, M.O.; Priego, E.-M.
Deposited on : 2018-01-24
Resolution : 2.15 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

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)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

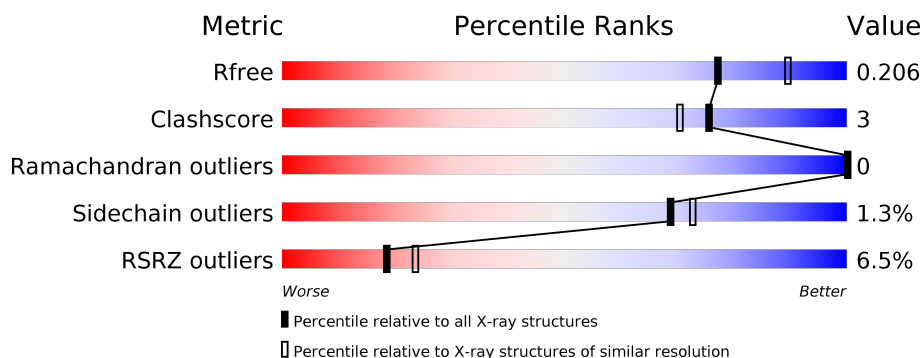
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	2523 (2.16-2.12)
Clashscore	141614	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)
RSRZ outliers	127900	2485 (2.16-2.12)

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 on the lower 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 $\leq 5\%$. 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	<div> <div>2%</div> <div> <div></div> <div>90%</div> <div>6%</div> <div>•</div> </div> </div>
1	C	451	<div> <div>0%</div> <div> <div></div> <div>91%</div> <div>6%</div> <div>•</div> </div> </div>
2	B	445	<div> <div>2%</div> <div> <div></div> <div>86%</div> <div>9%</div> <div>5%</div> </div> </div>
2	D	445	<div> <div>5%</div> <div> <div></div> <div>86%</div> <div>9%</div> <div>•</div> </div> </div>
3	E	143	<div> <div>7%</div> <div> <div></div> <div>80%</div> <div>6%</div> <div>15%</div> </div> </div>
4	F	384	<div> <div>23%</div> <div> <div></div> <div>78%</div> <div>12%</div> <div>•</div> <div>9%</div> </div> </div>

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 18235 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	438	Total	C	N	O	S	0	1	0
			3427	2169	582	653	23			
1	C	439	Total	C	N	O	S	0	2	0
			3435	2174	583	655	23			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	424	Total	C	N	O	S	0	0	0
			3339	2099	569	644	27			
2	D	425	Total	C	N	O	S	0	0	0
			3332	2092	569	645	26			

- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	122	Total	C	N	O	S	0	0	0
			1008	622	182	199	5			

There are 2 discrepancies between the modelled and reference sequences:

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

- Molecule 4 is a protein called Tubulin tyrosine ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	349	Total	C	N	O	S	0	1	0
			2854	1829	488	522	15			

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 (three-letter code: 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 (three-letter code: MG) (formula: Mg).

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

Continued on next page...

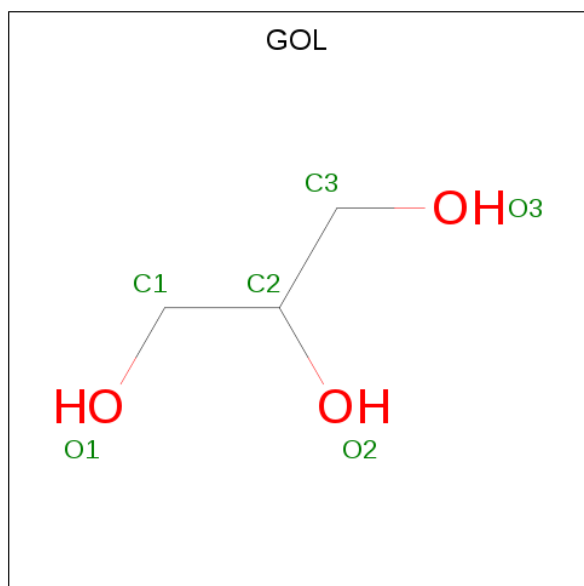
Continued from previous page...

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

- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

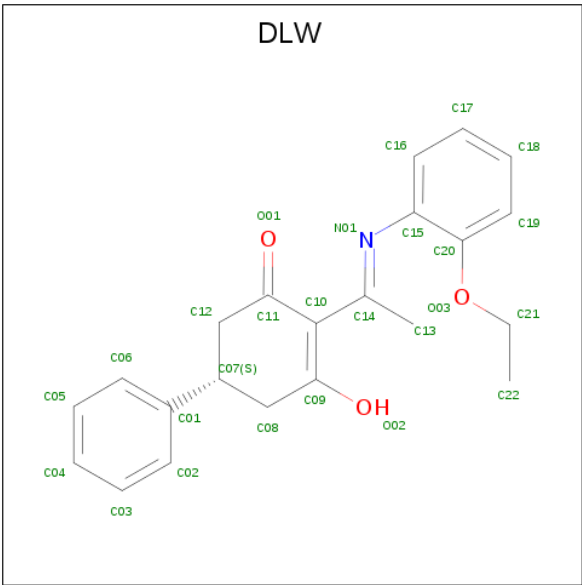
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	2	Total	Ca	0	0
			2	2		
7	A	1	Total	Ca	0	0
			1	1		
7	C	1	Total	Ca	0	0
			1	1		
7	E	1	Total	Ca	0	0
			1	1		

- Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



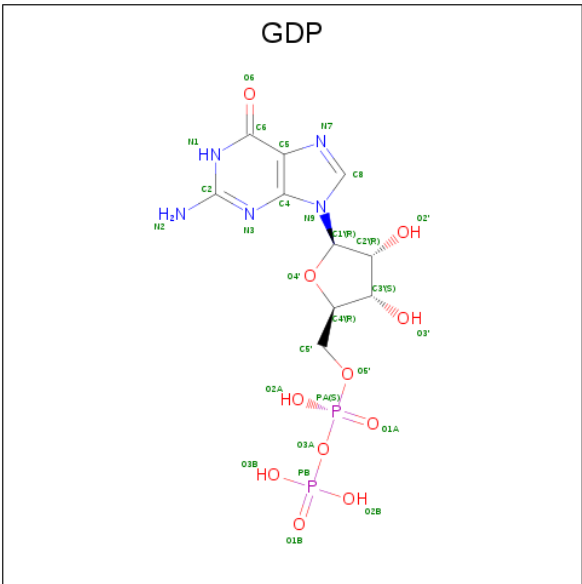
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			6	3	3		
8	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 9 is (5 {S})-2-[({E})- {N}-(2-ethoxyphenyl)- {C}-methyl-carbonimidoyl]-3-oxida nyl-5-phenyl-cyclohex-2-en-1-one (three-letter code: DLW) (formula: C₂₂H₂₃N O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	B	1	Total	C	N	O	0	0
			26	22	1	3		
9	D	1	Total	C	N	O	0	0
			26	22	1	3		

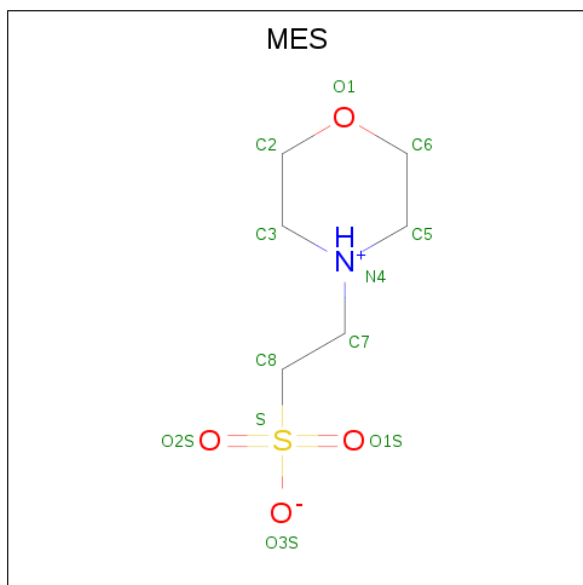
- Molecule 10 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Continued from previous page...

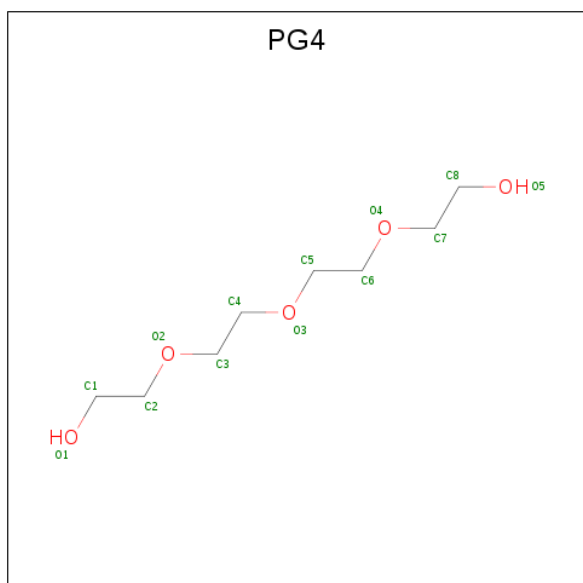
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	D	1	Total	C	N	O	P	
			28	10	5	11	2	
								0
								0

- Molecule 11 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).



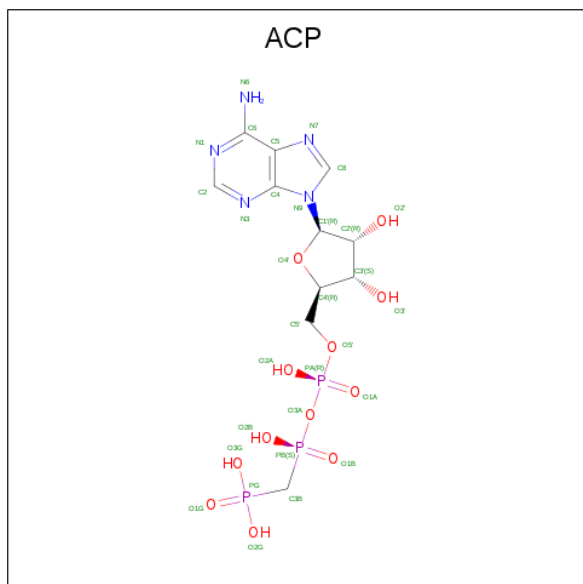
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	B	1	Total	C	N	O	S	
			12	6	1	4	1	
								0
								0

- Molecule 12 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	B	1	Total	C	O	0	0
			13	8	5		

- Molecule 13 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-letter code: ACP) (formula: $C_{11}H_{18}N_5O_{12}P_3$).



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

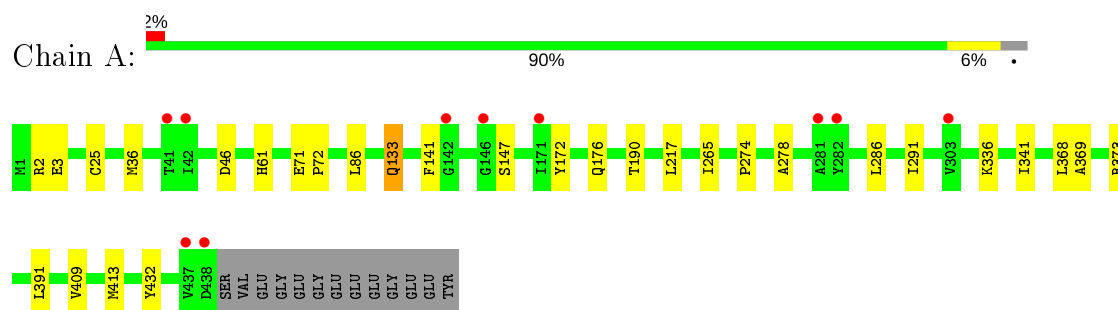
- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	127	Total	O	0	0
			127	127		
14	B	133	Total	O	0	0
			133	133		
14	C	219	Total	O	0	0
			219	219		
14	D	52	Total	O	0	0
			52	52		
14	E	17	Total	O	0	0
			17	17		
14	F	42	Total	O	0	0
			42	42		

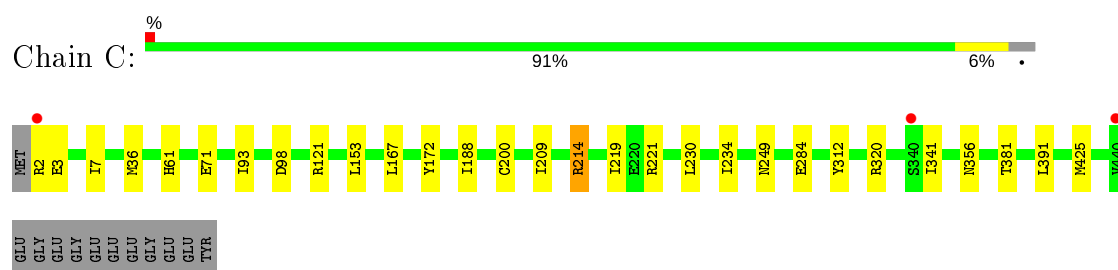
3 Residue-property plots [i](#)

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 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.

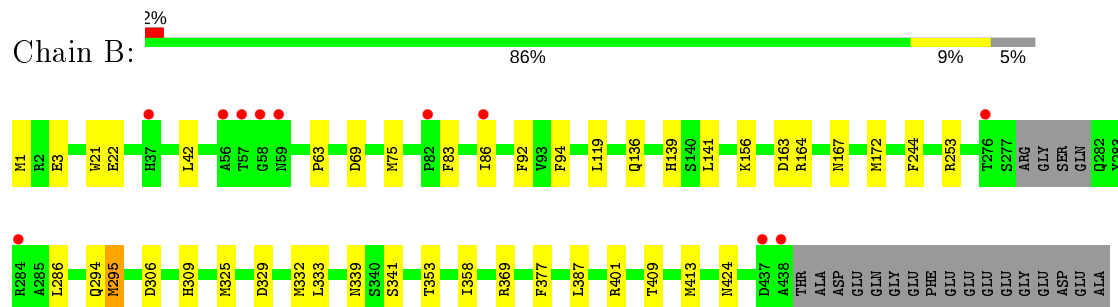
- Molecule 1: Tubulin alpha-1B chain



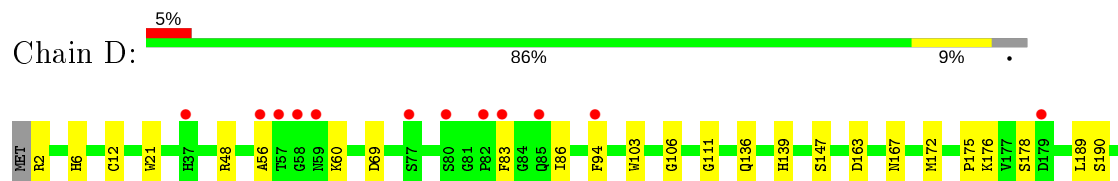
- Molecule 1: Tubulin alpha-1B chain

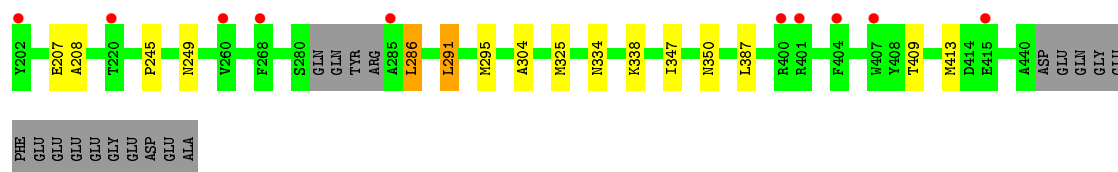


- Molecule 2: Tubulin beta-2B chain

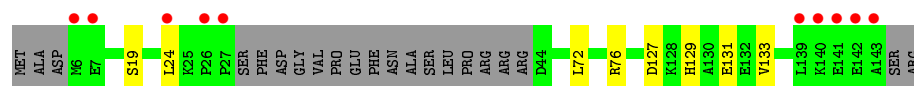
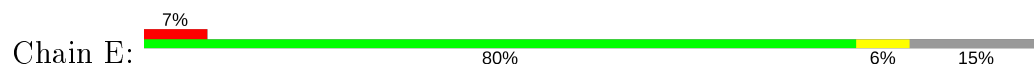


- Molecule 2: Tubulin beta-2B chain

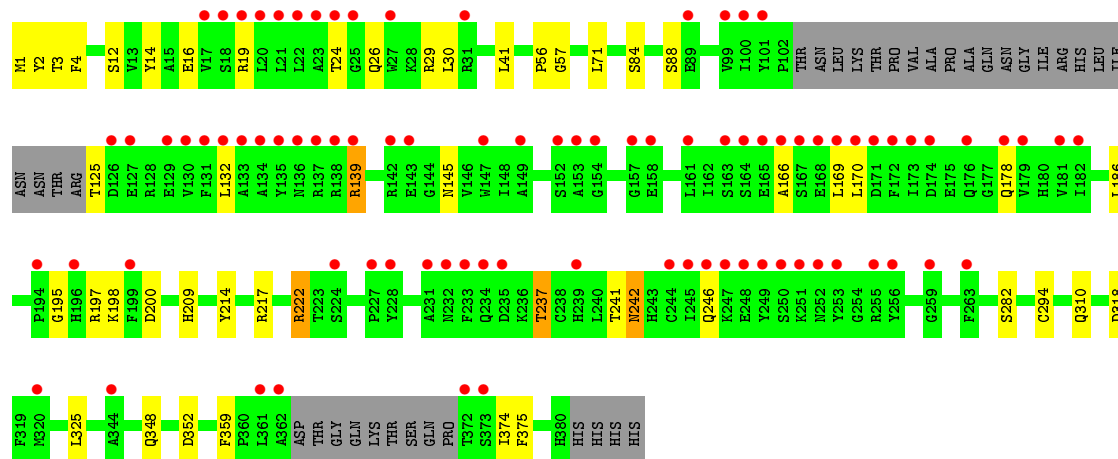
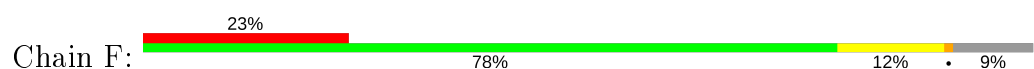




• Molecule 3: Stathmin-4



• 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, α , β , γ	104.67Å 157.56Å 180.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.45 – 2.15 49.45 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.2 (49.45-2.15) 99.4 (49.45-2.15)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.23 (at 2.14Å)	Xtriage
Refinement program	PHENIX (dev_2863: ???)	Depositor
R, R_{free}	0.175 , 0.206 0.175 , 0.206	Depositor DCC
R_{free} test set	8068 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	43.0	Xtriage
Anisotropy	0.066	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 47.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	18235	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.45% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: GDP, GOL, MG, CA, GTP, PG4, ACP, DLW, MES

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	0.30	0/3508	0.49	0/4762
1	C	0.34	0/3519	0.50	0/4779
2	B	0.31	0/3413	0.49	0/4622
2	D	0.28	0/3405	0.46	0/4612
3	E	0.29	0/1016	0.40	0/1348
4	F	0.27	0/2922	0.45	0/3946
All	All	0.30	0/17783	0.48	0/24069

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

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	3427	0	3339	18	0
1	C	3435	0	3346	15	0
2	B	3339	0	3220	25	0
2	D	3332	0	3211	22	0
3	E	1008	0	1024	4	0
4	F	2854	0	2825	27	0
5	A	32	0	12	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
7	C	1	0	0	0	0
7	E	1	0	0	0	0
8	A	6	0	8	0	0
8	B	6	0	8	0	0
9	B	26	0	0	0	0
9	D	26	0	0	0	0
10	B	28	0	12	0	0
10	D	28	0	12	1	0
11	B	12	0	12	1	0
12	B	13	0	18	1	0
13	F	31	0	14	3	0
14	A	127	0	0	0	0
14	B	133	0	0	2	0
14	C	219	0	0	0	0
14	D	52	0	0	0	0
14	E	17	0	0	0	0
14	F	42	0	0	0	0
All	All	18235	0	17073	106	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 3.

All (106) 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:249:ASN:OD1	1:C:356:ASN:ND2	2.24	0.70
4:F:139:ARG:HB2	4:F:145:ASN:HD22	1.62	0.65
2:B:119:LEU:HD11	2:B:156:LYS:HG2	1.80	0.63
4:F:241:THR:OG1	13:F:402:ACP:O3'	2.18	0.62
2:B:332:MET:HG3	2:B:353:THR:HG21	1.81	0.62
4:F:348:GLN:NE2	4:F:352:ASP:OD1	2.34	0.61
1:A:176:GLN:HG2	4:F:56:PRO:HB3	1.84	0.60
2:B:294:GLN:OE1	14:B:601:HOH:O	2.16	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:172:MET:HG3	2:D:387:LEU:HD11	1.85	0.57
1:A:36:MET:HB3	1:A:61:HIS:CE1	2.39	0.57
2:B:401:ARG:HA	12:B:508:PG4:H11	1.88	0.56
2:B:1:MET:N	2:B:3:GLU:OE1	2.26	0.55
2:D:147:SER:HG	2:D:190:SER:HG	1.54	0.54
2:D:56:ALA:HB3	2:D:60:LYS:HB3	1.90	0.54
2:B:83:PHE:O	2:B:86:ILE:HG12	2.08	0.53
4:F:16:GLU:OE2	4:F:19:ARG:NH1	2.31	0.52
4:F:71:LEU:HD11	4:F:294:CYS:HB3	1.92	0.52
2:D:12:CYS:HB2	10:D:501:GDP:C8	2.45	0.51
1:A:71:GLU:HG2	1:A:72:PRO:HD2	1.93	0.51
4:F:200:ASP:OD1	4:F:222:ARG:HB2	2.10	0.51
1:A:217:LEU:HD21	1:A:368:LEU:HD23	1.93	0.51
4:F:209:HIS:HB2	4:F:310:GLN:HE21	1.76	0.51
2:D:136:GLN:HA	2:D:167:ASN:O	2.11	0.51
2:B:329:ASP:O	2:B:333:LEU:HG	2.11	0.51
2:D:83:PHE:O	2:D:86:ILE:HG12	2.11	0.50
4:F:166:ALA:HA	4:F:169:LEU:HD12	1.93	0.50
2:D:176:LYS:HD2	2:D:207:GLU:HG3	1.94	0.50
4:F:139:ARG:HB2	4:F:145:ASN:ND2	2.26	0.50
2:B:295:MET:HG2	2:B:377:PHE:HB2	1.93	0.50
2:D:175:PRO:HA	2:D:178:SER:HB2	1.94	0.49
2:B:141:LEU:HD12	2:B:172:MET:SD	2.53	0.49
2:D:6:HIS:CD2	2:D:21:TRP:HE1	2.31	0.49
1:A:3:GLU:O	1:A:133:GLN:HG3	2.13	0.49
4:F:242:ASN:N	4:F:242:ASN:OD1	2.45	0.49
2:B:69:ASP:O	2:B:94:PHE:HA	2.13	0.48
1:C:312:TYR:CD1	1:C:341:ILE:HG23	2.48	0.48
2:D:347:ILE:HG22	2:D:350:ASN:HB3	1.96	0.48
4:F:318:ASP:OD2	13:F:402:ACP:O3G	2.32	0.48
4:F:214:TYR:HB3	4:F:375:PHE:HB3	1.95	0.47
2:B:172:MET:HG3	2:B:387:LEU:HD11	1.96	0.47
2:B:333:LEU:HD13	4:F:57:GLY:HA3	1.96	0.47
1:C:36:MET:HB3	1:C:61:HIS:CE1	2.49	0.47
1:C:230:LEU:O	1:C:234:ILE:HD12	2.14	0.46
1:C:188:ILE:HG13	1:C:425:MET:HG3	1.96	0.46
1:C:221:ARG:HG2	2:D:325:MET:HB3	1.97	0.46
1:C:320:ARG:HA	1:C:356:ASN:O	2.15	0.46
2:D:2:ARG:NH2	2:D:249:ASN:OD1	2.48	0.46
3:E:72:LEU:O	3:E:76:ARG:HG2	2.16	0.46
1:A:336:LYS:NZ	1:A:341:ILE:O	2.49	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:24:THR:HG22	4:F:26:GLN:HG3	1.99	0.45
1:C:7:ILE:HG21	1:C:153:LEU:HD21	1.99	0.45
1:C:93:ILE:HD11	1:C:121:ARG:HG3	1.98	0.45
1:A:265:ILE:HG23	1:A:432:TYR:CZ	2.52	0.44
1:A:291:ILE:HD13	1:A:373:ARG:HG3	1.98	0.44
2:D:334:ASN:HD21	2:D:338:LYS:HE3	1.82	0.44
2:D:208:ALA:HB2	2:D:304:ALA:HB2	1.99	0.44
1:A:172:TYR:CE2	1:A:391:LEU:HD22	2.53	0.44
1:C:172:TYR:CE2	1:C:391:LEU:HD22	2.53	0.44
4:F:2:TYR:CE1	4:F:359:PHE:HB3	2.53	0.43
1:A:147:SER:HB2	1:A:190:THR:HB	2.00	0.43
1:A:278:ALA:HA	1:A:369:ALA:HB2	2.00	0.43
1:A:274:PRO:HB3	1:A:286:LEU:HD22	2.00	0.43
2:B:163:ASP:O	2:B:253:ARG:NH2	2.51	0.43
2:B:409:THR:HA	2:B:413:MET:O	2.19	0.43
1:C:167:LEU:HG	1:C:200:CYS:HB3	1.99	0.43
1:A:265:ILE:HG23	1:A:432:TYR:CE1	2.54	0.43
1:C:209:ILE:HG23	1:C:230:LEU:HD23	2.01	0.43
1:A:25:CYS:SG	1:A:86:LEU:HD21	2.59	0.43
4:F:195:GLY:HA3	4:F:197:ARG:HD3	2.00	0.43
2:D:409:THR:HA	2:D:413:MET:O	2.19	0.43
4:F:132:LEU:HD21	4:F:170:LEU:HD11	2.01	0.43
2:D:48:ARG:NH2	2:D:245:PRO:HA	2.34	0.43
4:F:282:SER:HB2	4:F:325:LEU:HD13	2.01	0.43
2:B:22:GLU:HG2	2:B:83:PHE:CD1	2.55	0.42
2:D:286:LEU:HA	2:D:286:LEU:HD23	1.78	0.42
4:F:14:TYR:HB3	4:F:41:LEU:HD13	2.00	0.42
1:A:2:ARG:HB3	1:A:133:GLN:HG2	2.02	0.42
2:B:325:MET:HE3	2:B:325:MET:HB3	1.52	0.42
4:F:217:ARG:NH1	4:F:374:ILE:HG22	2.34	0.42
2:B:424:ASN:HB3	14:B:617:HOH:O	2.19	0.42
1:A:409:VAL:HA	1:A:413:MET:O	2.19	0.42
2:B:306:ASP:HB3	2:B:309:HIS:ND1	2.35	0.42
2:D:106:GLY:O	2:D:111:GLY:HA3	2.20	0.42
4:F:84:SER:O	4:F:88:SER:N	2.48	0.42
2:B:75:MET:HE3	2:B:92:PHE:HD2	1.85	0.41
1:C:71:GLU:HG2	1:C:98:ASP:HB3	2.01	0.41
2:B:164:ARG:O	11:B:507:MES:H31	2.19	0.41
4:F:198:LYS:HZ1	13:F:402:ACP:C2	2.33	0.41
4:F:237:THR:O	4:F:246:GLN:NE2	2.52	0.41
2:B:244:PHE:CD1	2:B:358:ILE:HD12	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2:ARG:HB3	1:C:3:GLU:H	1.64	0.41
3:E:127:ASP:O	3:E:131:GLU:HG2	2.21	0.41
2:D:163:ASP:N	2:D:163:ASP:OD1	2.53	0.41
2:D:69:ASP:O	2:D:94:PHE:HA	2.20	0.41
2:B:333:LEU:CD1	4:F:57:GLY:HA3	2.50	0.41
3:E:129:HIS:O	3:E:133:VAL:HG23	2.21	0.41
2:B:339:ASN:HD22	2:B:339:ASN:N	2.19	0.41
2:D:291:LEU:HD23	2:D:291:LEU:HA	1.89	0.41
2:D:103:TRP:CE3	2:D:189:LEU:HD13	2.56	0.40
4:F:3:THR:HB	4:F:30:LEU:HD11	2.02	0.40
1:A:336:LYS:HG2	3:E:24:LEU:HD13	2.03	0.40
1:A:141:PHE:O	1:A:147:SER:HB3	2.22	0.40
2:B:136:GLN:HA	2:B:167:ASN:O	2.21	0.40
4:F:4:PHE:CZ	4:F:29:ARG:HB2	2.56	0.40
2:B:21:TRP:CZ3	2:B:63:PRO:HB3	2.57	0.40
1:C:214:ARG:HG3	1:C:219:ILE:O	2.21	0.40

There are no symmetry-related clashes.

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	437/451 (97%)	431 (99%)	6 (1%)	0	100	100
1	C	439/451 (97%)	432 (98%)	7 (2%)	0	100	100
2	B	420/445 (94%)	412 (98%)	8 (2%)	0	100	100
2	D	421/445 (95%)	414 (98%)	7 (2%)	0	100	100
3	E	118/143 (82%)	116 (98%)	2 (2%)	0	100	100
4	F	344/384 (90%)	335 (97%)	9 (3%)	0	100	100
All	All	2179/2319 (94%)	2140 (98%)	39 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	370/379 (98%)	368 (100%)	2 (0%)	88	91
1	C	372/379 (98%)	369 (99%)	3 (1%)	81	85
2	B	367/383 (96%)	361 (98%)	6 (2%)	62	65
2	D	366/383 (96%)	362 (99%)	4 (1%)	73	76
3	E	109/127 (86%)	108 (99%)	1 (1%)	78	81
4	F	312/342 (91%)	303 (97%)	9 (3%)	42	40
All	All	1896/1993 (95%)	1871 (99%)	25 (1%)	69	73

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	ASP
1	A	133	GLN
2	B	42	LEU
2	B	139	HIS
2	B	286	LEU
2	B	295	MET
2	B	341	SER
2	B	369	ARG
1	C	214	ARG
1	C	284	GLU
1	C	381	THR
2	D	139	HIS
2	D	286	LEU
2	D	291	LEU
2	D	295	MET
3	E	19	SER
4	F	1	MET
4	F	12	SER
4	F	125	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	F	139	ARG
4	F	178	GLN
4	F	186	LEU
4	F	222	ARG
4	F	237	THR
4	F	242	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	256	GLN
2	B	247	GLN
2	B	339	ASN
4	F	243	HIS
4	F	306	HIS
4	F	310	GLN
4	F	348	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 21 ligands modelled in this entry, 10 are monoatomic - leaving 11 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	$\# Z > 2$
9	DLW	D	500	-	28,28,28	0.73	0	37,38,38	1.22	8 (21%)
10	GDP	B	502	6	24,30,30	1.15	2 (8%)	31,47,47	1.94	8 (25%)
11	MES	B	507	-	12,12,12	2.15	1 (8%)	14,16,16	1.85	3 (21%)
8	GOL	A	504	-	5,5,5	0.92	0	5,5,5	0.96	0
13	ACP	F	402	6	27,33,33	1.70	6 (22%)	32,52,52	1.31	4 (12%)
8	GOL	B	506	-	5,5,5	1.04	0	5,5,5	0.76	0
9	DLW	B	501	-	28,28,28	0.62	0	37,38,38	1.21	6 (16%)
5	GTP	A	501	6	26,34,34	0.97	1 (3%)	33,54,54	1.76	7 (21%)
5	GTP	C	501	6	26,34,34	0.94	1 (3%)	33,54,54	1.65	5 (15%)
10	GDP	D	501	6	24,30,30	1.21	2 (8%)	31,47,47	1.90	7 (22%)
12	PG4	B	508	-	12,12,12	0.42	0	11,11,11	0.45	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
9	DLW	D	500	-	-	6/15/31/31	0/3/3/3
10	GDP	B	502	6	-	5/12/32/32	0/3/3/3
11	MES	B	507	-	-	1/6/14/14	0/1/1/1
8	GOL	A	504	-	-	4/4/4/4	-
13	ACP	F	402	6	-	6/15/38/38	0/3/3/3
8	GOL	B	506	-	-	2/4/4/4	-
9	DLW	B	501	-	-	4/15/31/31	0/3/3/3
5	GTP	A	501	6	-	5/18/38/38	0/3/3/3
5	GTP	C	501	6	-	9/18/38/38	0/3/3/3
10	GDP	D	501	6	-	5/12/32/32	0/3/3/3
12	PG4	B	508	-	-	6/10/10/10	-

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	B	507	MES	C8-S	-7.15	1.67	1.77
10	D	501	GDP	C6-C5	4.21	1.48	1.41

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	F	402	ACP	PB-O1B	4.08	1.61	1.51
10	B	502	GDP	C6-C5	3.84	1.48	1.41
13	F	402	ACP	PB-O3A	3.35	1.62	1.58
13	F	402	ACP	PB-O2B	-3.21	1.48	1.56
13	F	402	ACP	PG-O2G	2.93	1.61	1.54
5	A	501	GTP	C6-N1	2.93	1.38	1.33
5	C	501	GTP	C6-N1	2.90	1.38	1.33
13	F	402	ACP	PG-O3G	2.88	1.61	1.54
13	F	402	ACP	C5-C4	2.60	1.47	1.40
10	D	501	GDP	C5-C4	2.38	1.47	1.40
10	B	502	GDP	C5-C4	2.04	1.46	1.40

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	501	GTP	N3-C2-N1	-5.38	120.04	127.22
5	C	501	GTP	N3-C2-N1	-5.13	120.38	127.22
10	D	501	GDP	C2-N3-C4	4.93	120.99	115.36
11	B	507	MES	C5-N4-C3	4.85	119.75	108.83
10	B	502	GDP	C6-C5-C4	-4.65	116.36	120.80
10	B	502	GDP	C2-N3-C4	4.58	120.59	115.36
10	B	502	GDP	C6-N1-C2	4.30	122.77	115.93
10	D	501	GDP	C6-N1-C2	4.11	122.46	115.93
10	D	501	GDP	C5-C6-N1	-4.10	117.82	123.43
5	C	501	GTP	C2-N3-C4	3.79	119.69	115.36
10	D	501	GDP	C6-C5-C4	-3.79	117.17	120.80
10	B	502	GDP	N3-C2-N1	-3.77	122.19	127.22
10	B	502	GDP	C5-C6-N1	-3.75	118.30	123.43
5	A	501	GTP	C2-N3-C4	3.66	119.54	115.36
10	D	501	GDP	N3-C2-N1	-3.35	122.75	127.22
5	A	501	GTP	C5-C6-N1	-3.29	118.93	123.43
13	F	402	ACP	PA-O3A-PB	-3.22	122.36	132.56
5	C	501	GTP	C5-C6-N1	-3.14	119.13	123.43
10	D	501	GDP	C4-C5-N7	-3.12	106.14	109.40
13	F	402	ACP	C3'-C2'-C1'	3.03	105.54	100.98
5	A	501	GTP	C6-N1-C2	3.01	120.71	115.93
13	F	402	ACP	N3-C2-N1	-2.85	124.22	128.68
11	B	507	MES	O1S-S-C8	2.84	110.33	106.92
5	C	501	GTP	C6-N1-C2	2.74	120.29	115.93
9	B	501	DLW	C07-C12-C11	-2.70	107.61	114.14
5	A	501	GTP	PA-O3A-PB	-2.70	123.58	132.83
13	F	402	ACP	C4-C5-N7	-2.69	106.59	109.40

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	501	GTP	PB-O3B-PG	-2.52	124.18	132.83
9	B	501	DLW	O03-C20-C19	-2.52	118.52	123.97
5	A	501	GTP	PB-O3B-PG	-2.36	124.73	132.83
10	B	502	GDP	C4-C5-N7	-2.35	106.95	109.40
10	D	501	GDP	PA-O3A-PB	-2.34	124.79	132.83
10	B	502	GDP	C1'-N9-C4	-2.31	122.59	126.64
11	B	507	MES	O3S-S-C8	2.30	109.49	105.77
9	D	500	DLW	C15-N01-C14	2.30	128.49	122.75
9	D	500	DLW	O03-C20-C19	-2.30	118.99	123.97
9	D	500	DLW	C07-C12-C11	-2.24	108.72	114.14
5	A	501	GTP	O2G-PG-O3B	2.21	112.04	104.64
9	B	501	DLW	C12-C11-C10	2.18	120.70	116.36
9	D	500	DLW	C13-C14-N01	-2.15	120.16	124.59
9	B	501	DLW	C15-N01-C14	2.14	128.10	122.75
9	B	501	DLW	C20-C15-N01	2.13	125.13	119.21
9	D	500	DLW	C16-C15-N01	-2.12	116.20	121.42
9	D	500	DLW	C11-C10-C09	-2.08	116.97	119.27
9	D	500	DLW	C20-C15-N01	2.08	124.99	119.21
9	D	500	DLW	C12-C11-C10	2.07	120.49	116.36
10	B	502	GDP	PA-O3A-PB	-2.06	125.76	132.83
9	B	501	DLW	C16-C15-N01	-2.05	116.38	121.42

There are no chirality outliers.

All (53) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	B	502	GDP	C5'-O5'-PA-O1A
10	B	502	GDP	C5'-O5'-PA-O2A
8	A	504	GOL	O1-C1-C2-C3
8	A	504	GOL	C1-C2-C3-O3
13	F	402	ACP	PG-C3B-PB-O1B
13	F	402	ACP	PG-C3B-PB-O2B
13	F	402	ACP	PG-C3B-PB-O3A
8	B	506	GOL	O1-C1-C2-C3
5	A	501	GTP	PB-O3B-PG-O2G
5	A	501	GTP	C5'-O5'-PA-O1A
5	A	501	GTP	C5'-O5'-PA-O2A
5	C	501	GTP	C5'-O5'-PA-O1A
5	C	501	GTP	C5'-O5'-PA-O2A
10	D	501	GDP	C5'-O5'-PA-O1A
10	D	501	GDP	C5'-O5'-PA-O2A
8	A	504	GOL	O2-C2-C3-O3

Continued on next page...

Continued from previous page...

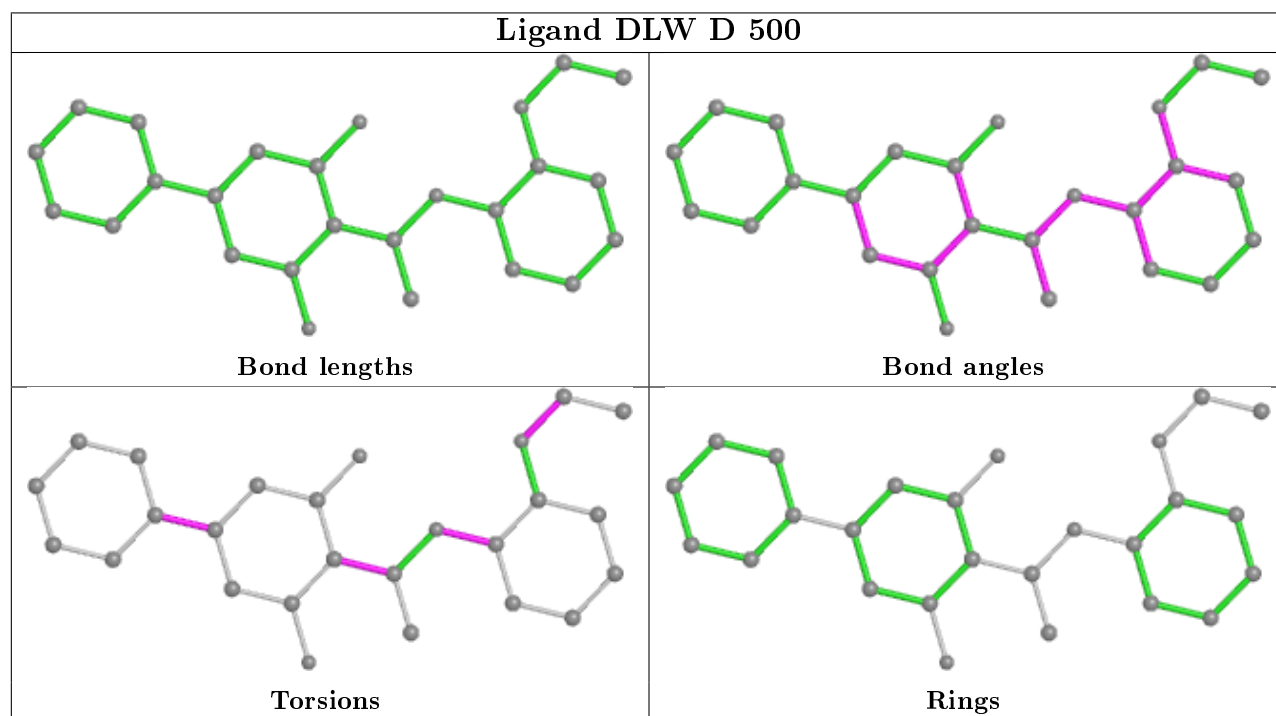
Mol	Chain	Res	Type	Atoms
8	B	506	GOL	O1-C1-C2-O2
12	B	508	PG4	O3-C5-C6-O4
12	B	508	PG4	O4-C7-C8-O5
9	D	500	DLW	C22-C21-O03-C20
5	C	501	GTP	PB-O3B-PG-O1G
10	D	501	GDP	C5'-O5'-PA-O3A
12	B	508	PG4	C8-C7-O4-C6
12	B	508	PG4	C3-C4-O3-C5
12	B	508	PG4	C5-C6-O4-C7
10	D	501	GDP	PB-O3A-PA-O2A
5	C	501	GTP	C4'-C5'-O5'-PA
11	B	507	MES	C8-C7-N4-C3
9	D	500	DLW	C09-C10-C14-C13
13	F	402	ACP	PB-O3A-PA-O2A
9	D	500	DLW	C06-C01-C07-C12
8	A	504	GOL	O1-C1-C2-O2
9	B	501	DLW	C06-C01-C07-C12
13	F	402	ACP	O4'-C4'-C5'-O5'
5	A	501	GTP	PB-O3B-PG-O1G
5	C	501	GTP	PB-O3B-PG-O2G
5	C	501	GTP	PB-O3B-PG-O3G
9	D	500	DLW	C20-C15-N01-C14
10	B	502	GDP	C5'-O5'-PA-O3A
5	A	501	GTP	C5'-O5'-PA-O3A
5	C	501	GTP	C5'-O5'-PA-O3A
10	B	502	GDP	PB-O3A-PA-O1A
10	B	502	GDP	PB-O3A-PA-O2A
9	B	501	DLW	C09-C10-C14-C13
5	C	501	GTP	PB-O3A-PA-O1A
5	C	501	GTP	PB-O3A-PA-O2A
10	D	501	GDP	PB-O3A-PA-O1A
9	D	500	DLW	C09-C10-C14-N01
9	B	501	DLW	C09-C10-C14-N01
9	D	500	DLW	C02-C01-C07-C12
13	F	402	ACP	C5'-O5'-PA-O1A
9	B	501	DLW	C02-C01-C07-C12
12	B	508	PG4	O2-C3-C4-O3

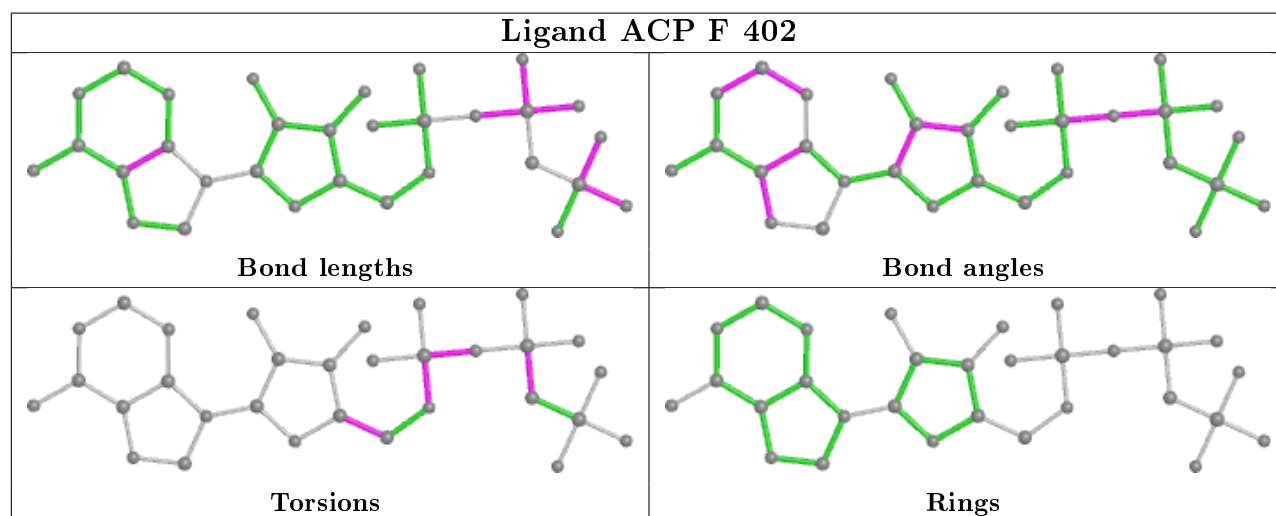
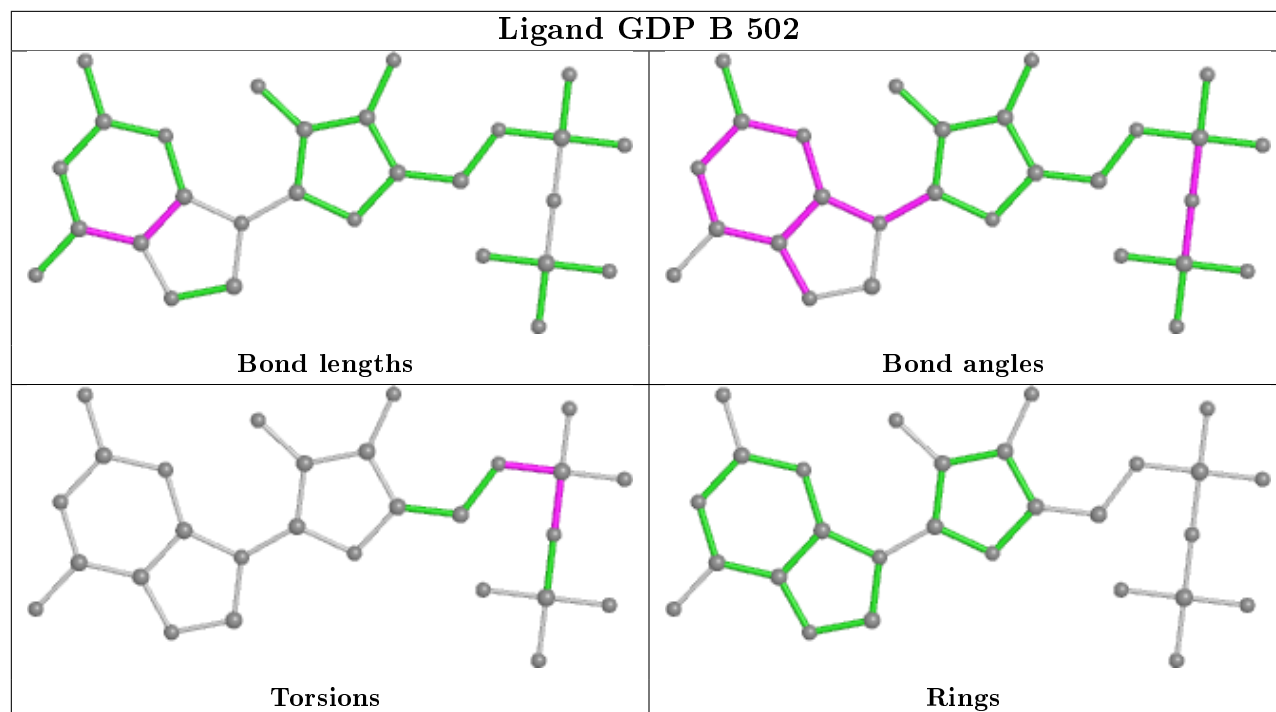
There are no ring outliers.

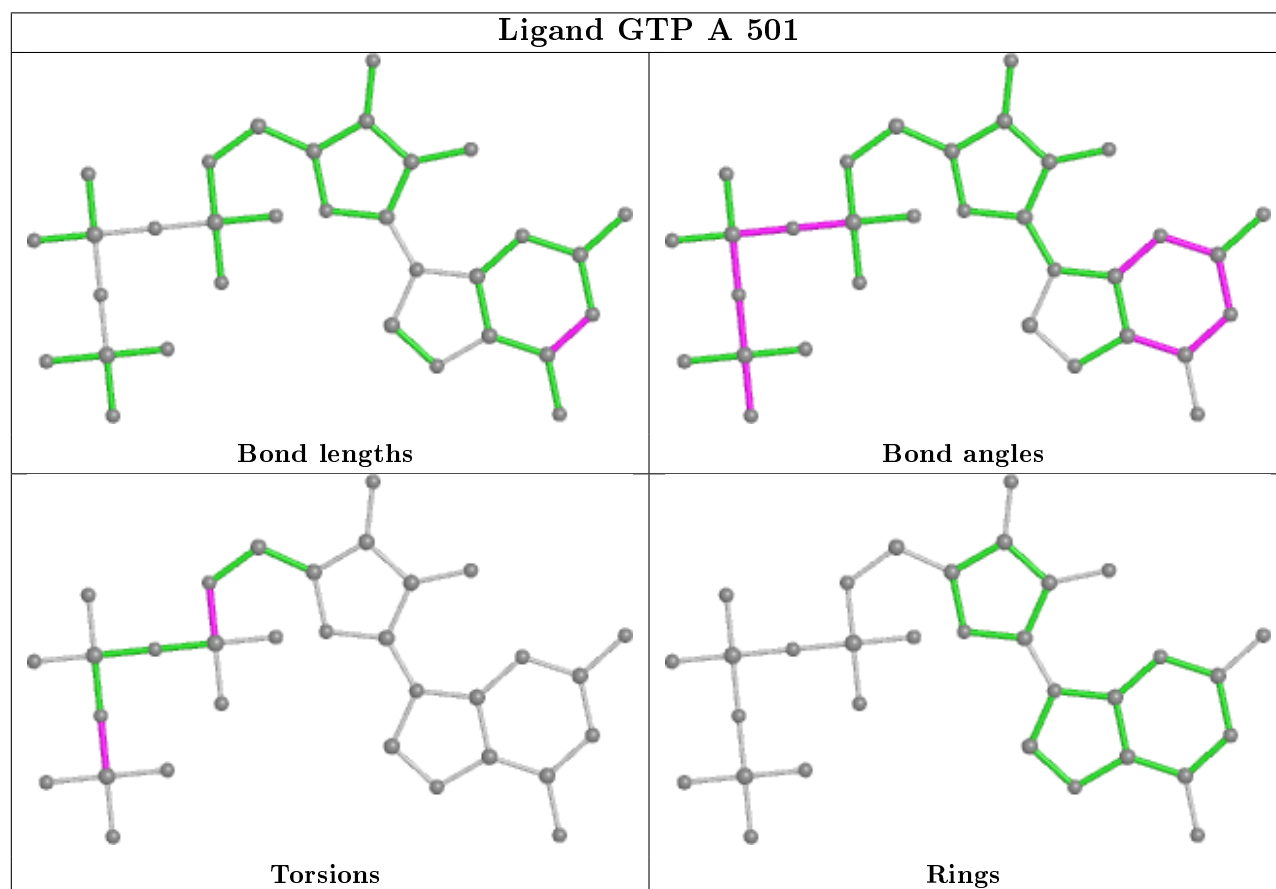
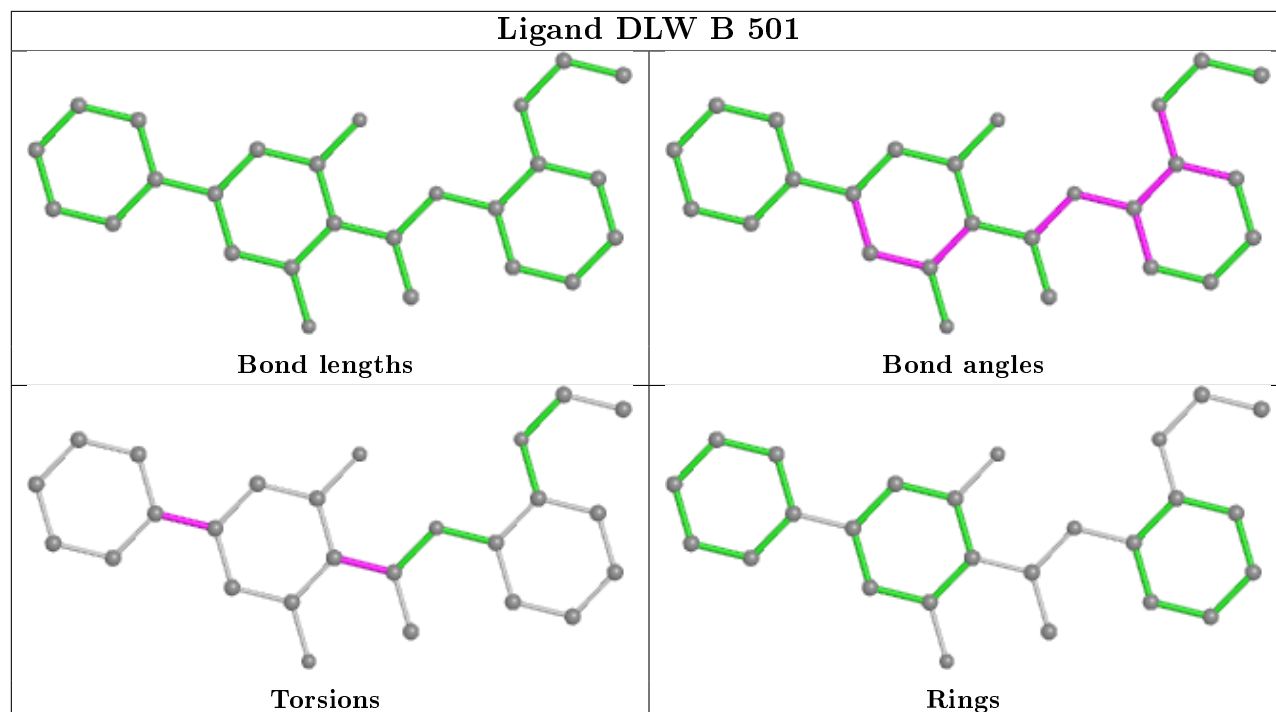
4 monomers are involved in 6 short contacts:

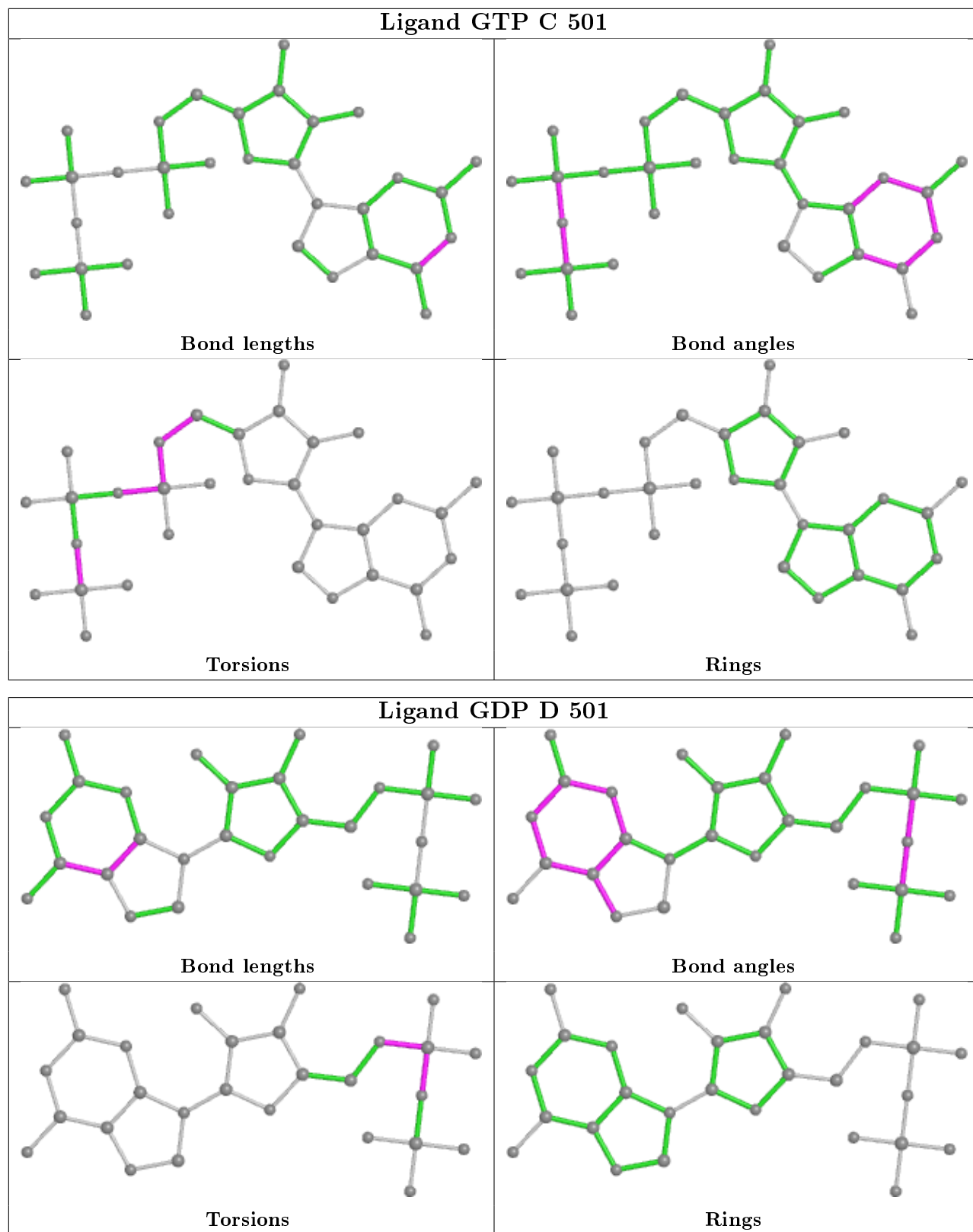
Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	B	507	MES	1	0
13	F	402	ACP	3	0
10	D	501	GDP	1	0
12	B	508	PG4	1	0

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 ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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, 95th 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 ²)	Q<0.9
1	A	438/451 (97%)	0.11	10 (2%) 60 67	35, 52, 85, 127	0
1	C	439/451 (97%)	-0.13	3 (0%) 87 90	29, 40, 68, 110	0
2	B	424/445 (95%)	0.04	11 (2%) 56 62	30, 48, 83, 118	0
2	D	425/445 (95%)	0.24	22 (5%) 27 33	36, 61, 94, 142	0
3	E	122/143 (85%)	0.29	10 (8%) 11 15	40, 70, 108, 134	0
4	F	349/384 (90%)	1.08	87 (24%) 0 0	42, 82, 144, 185	0
All	All	2197/2319 (94%)	0.24	143 (6%) 18 23	29, 55, 108, 185	0

All (143) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	F	173	ILE	8.7
4	F	170	LEU	7.4
2	D	57	THR	7.2
4	F	130	VAL	7.1
4	F	161	LEU	6.8
2	D	58	GLY	6.8
4	F	249	TYR	6.7
4	F	132	LEU	6.6
4	F	250	SER	6.3
4	F	101	TYR	6.0
4	F	251	LYS	6.0
4	F	233	PHE	5.6
4	F	372	THR	5.6
2	D	285	ALA	5.5
1	A	282	TYR	5.4
4	F	253	TYR	5.4
4	F	182	ILE	5.3
4	F	99	VAL	5.1
4	F	20	LEU	5.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	58	GLY	5.0
4	F	136	ASN	5.0
4	F	157	GLY	4.9
2	D	56	ALA	4.9
4	F	100	ILE	4.9
4	F	167	SER	4.8
4	F	178	GLN	4.7
4	F	231	ALA	4.7
1	A	281	ALA	4.5
3	E	139	LEU	4.4
2	D	400	ARG	4.4
4	F	158	GLU	4.4
4	F	166	ALA	4.3
4	F	234	GLN	4.3
4	F	176	GLN	4.2
4	F	134	ALA	4.1
4	F	361	LEU	4.1
4	F	21	LEU	4.1
1	C	340	SER	4.1
1	C	440	VAL	4.0
3	E	26	PRO	4.0
4	F	263	PHE	4.0
4	F	169	LEU	4.0
2	D	59	ASN	3.9
4	F	137	ARG	3.9
4	F	227	PRO	3.9
4	F	172	PHE	3.9
3	E	27	PRO	3.9
4	F	181	VAL	3.8
2	B	57	THR	3.8
4	F	362	ALA	3.7
4	F	259	GLY	3.7
2	D	37	HIS	3.6
4	F	133	ALA	3.6
4	F	256	TYR	3.6
4	F	154	GLY	3.6
3	E	24	LEU	3.5
4	F	252	ASN	3.5
2	B	59	ASN	3.4
4	F	131	PHE	3.4
4	F	244	CYS	3.4
2	B	276	THR	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
4	F	135	TYR	3.2
3	E	6	MET	3.2
1	A	438	ASP	3.2
4	F	17	VAL	3.2
4	F	23	ALA	3.2
4	F	179	VAL	3.2
2	B	37	HIS	3.2
4	F	139	ARG	3.1
4	F	255	ARG	3.1
4	F	232	ASN	3.1
4	F	248	GLU	3.1
4	F	24	THR	3.0
1	A	171	ILE	3.0
3	E	142	GLU	3.0
2	B	284	ARG	3.0
4	F	22	LEU	3.0
4	F	142	ARG	3.0
1	A	42	ILE	2.9
4	F	239	HIS	2.9
4	F	25	GLY	2.9
4	F	153	ALA	2.9
4	F	171	ASP	2.9
4	F	27	TRP	2.8
4	F	228	TYR	2.8
4	F	143	GLU	2.8
4	F	194	PRO	2.8
2	B	437	ASP	2.8
4	F	129	GLU	2.7
4	F	246	GLN	2.7
2	D	94	PHE	2.7
3	E	141	GLU	2.7
2	D	268	PHE	2.6
3	E	140	LYS	2.6
3	E	143	ALA	2.6
2	D	80	SER	2.6
4	F	373	SER	2.5
2	D	220	THR	2.5
2	D	407	TRP	2.5
2	B	56	ALA	2.5
3	E	7	GLU	2.5
4	F	89	GLU	2.4
4	F	224	SER	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
4	F	199	PHE	2.4
4	F	163	SER	2.4
2	D	404	PHE	2.4
2	B	438	ALA	2.4
2	D	179	ASP	2.4
2	B	82	PRO	2.4
2	D	85	GLN	2.3
4	F	174	ASP	2.3
4	F	168	GLU	2.3
4	F	247	LYS	2.3
2	B	86	ILE	2.3
4	F	127	GLU	2.3
4	F	149	ALA	2.3
4	F	152	SER	2.3
4	F	196	HIS	2.2
2	D	401	ARG	2.2
4	F	164	SER	2.2
4	F	31	ARG	2.2
1	A	142	GLY	2.2
4	F	320	MET	2.2
4	F	19	ARG	2.2
1	A	146	GLY	2.2
2	D	77	SER	2.2
4	F	165	GLU	2.1
4	F	126	ASP	2.1
2	D	83	PHE	2.1
4	F	138	ARG	2.1
4	F	18	SER	2.1
4	F	235	ASP	2.1
4	F	344	ALA	2.1
2	D	260	VAL	2.1
4	F	147	TRP	2.1
2	D	415	GLU	2.0
4	F	245	ILE	2.0
1	A	437	VAL	2.0
2	D	202	TYR	2.0
1	C	2	ARG	2.0
1	A	41	THR	2.0
2	D	82	PRO	2.0
1	A	303	VAL	2.0

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 carbohydrates in this entry.

6.4 Ligands [i](#)

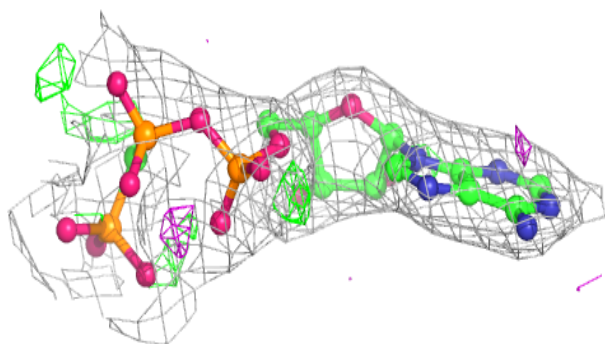
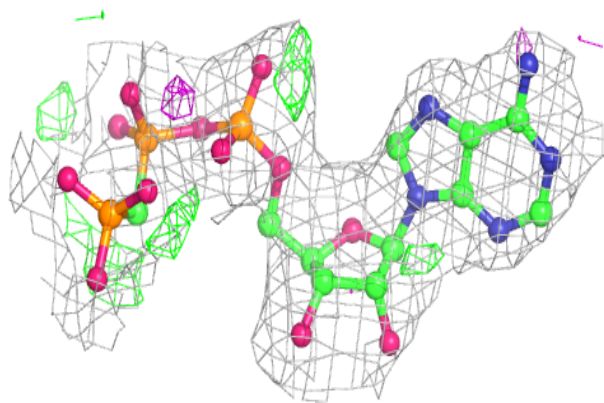
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
12	PG4	B	508	13/13	0.60	0.26	97,113,121,121	0
7	CA	E	201	1/1	0.75	0.10	99,99,99,99	0
6	MG	F	401	1/1	0.80	0.06	78,78,78,78	0
7	CA	B	505	1/1	0.83	0.14	132,132,132,132	0
6	MG	D	502	1/1	0.87	0.05	66,66,66,66	0
13	ACP	F	402	31/31	0.87	0.12	64,81,115,119	0
8	GOL	B	506	6/6	0.88	0.28	53,69,74,75	0
8	GOL	A	504	6/6	0.94	0.20	60,74,77,79	0
7	CA	B	504	1/1	0.95	0.08	98,98,98,98	0
6	MG	A	502	1/1	0.96	0.15	37,37,37,37	0
11	MES	B	507	12/12	0.96	0.12	49,54,73,82	0
10	GDP	D	501	28/28	0.97	0.10	47,53,60,65	0
9	DLW	D	500	26/26	0.97	0.13	35,50,56,60	0
7	CA	A	503	1/1	0.97	0.04	67,67,67,67	0
6	MG	C	502	1/1	0.98	0.12	31,31,31,31	0
9	DLW	B	501	26/26	0.98	0.14	30,38,45,50	0
7	CA	C	503	1/1	0.98	0.04	54,54,54,54	0
5	GTP	A	501	32/32	0.98	0.18	28,37,42,48	0
6	MG	B	503	1/1	0.99	0.23	27,27,27,27	0
5	GTP	C	501	32/32	0.99	0.14	27,31,34,39	0
10	GDP	B	502	28/28	0.99	0.17	28,34,38,39	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.

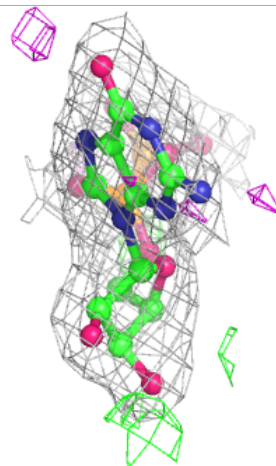
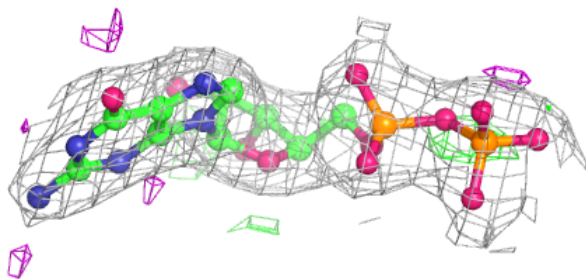
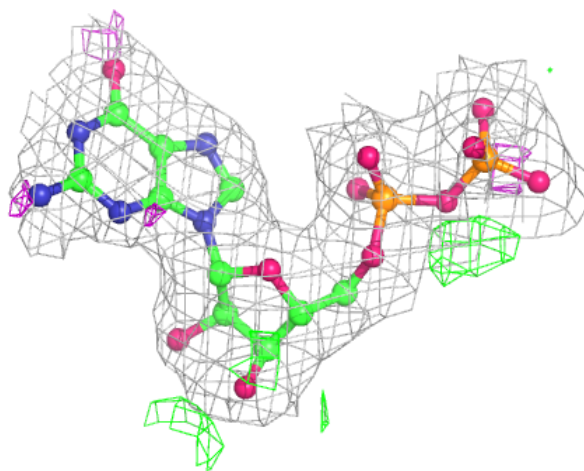
Electron density around ACP F 402:

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



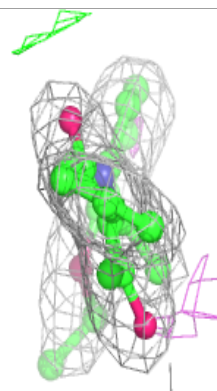
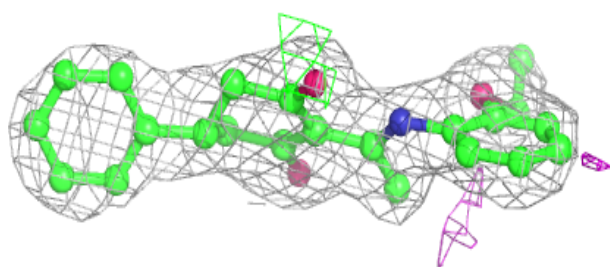
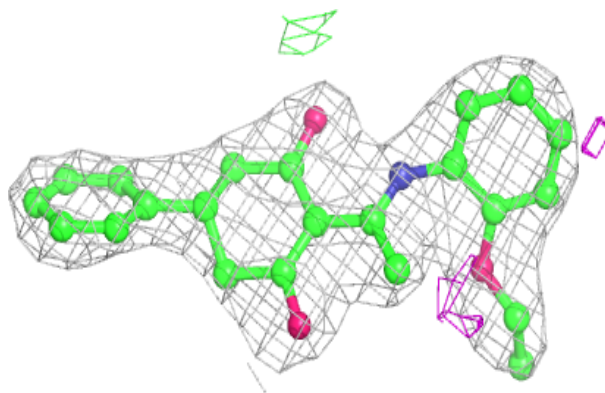
Electron density around GDP D 501:

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

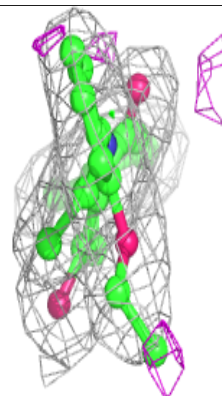
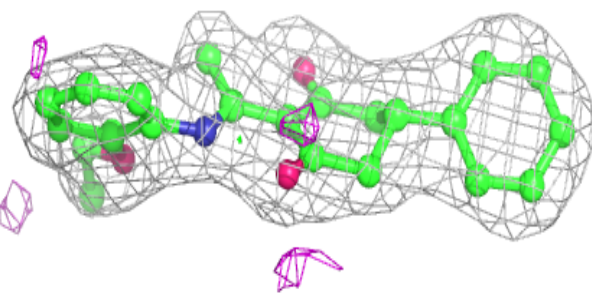
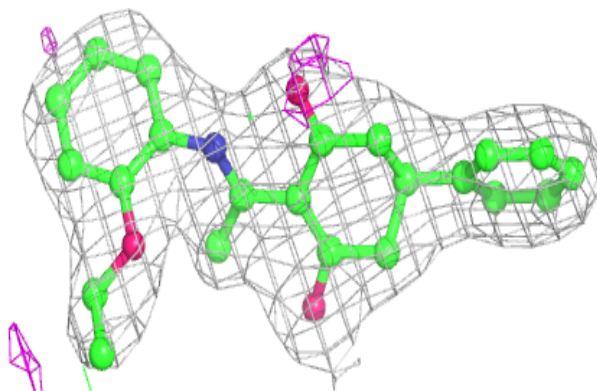


Electron density around DLW D 500:

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

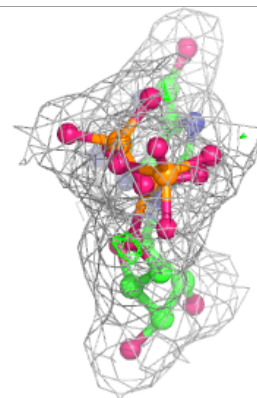
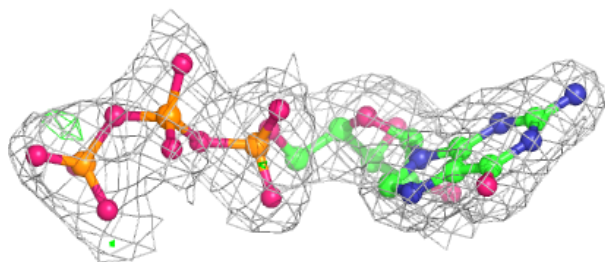
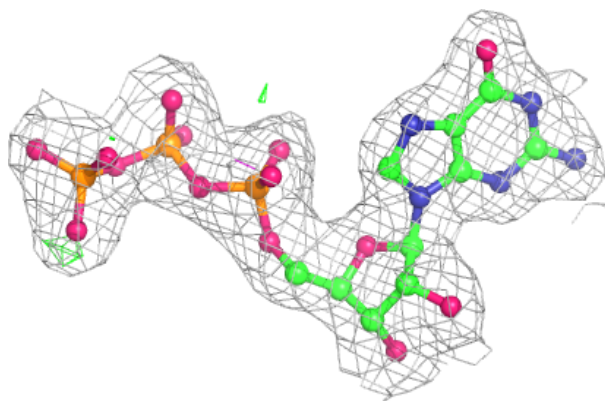
**Electron density around DLW B 501:**

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

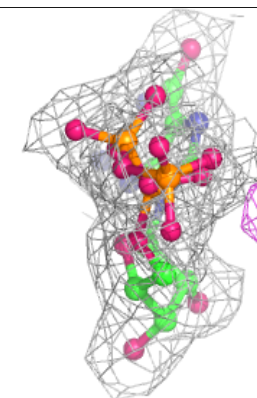
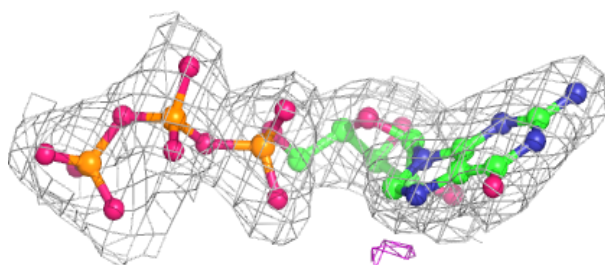
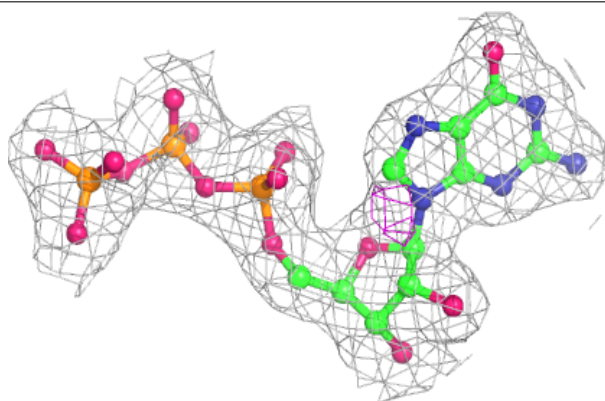


Electron density around GTP A 501:

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

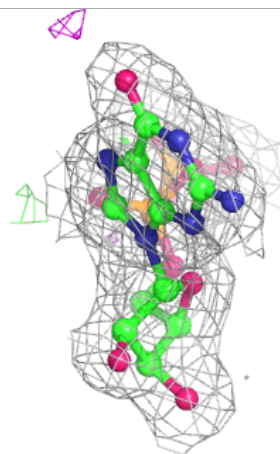
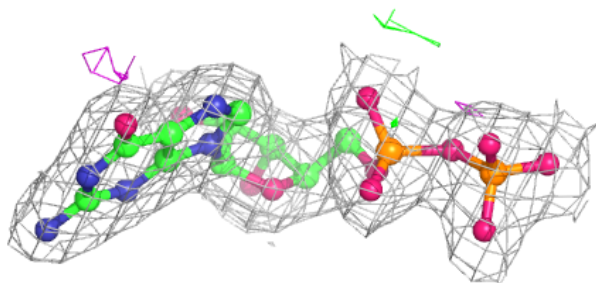
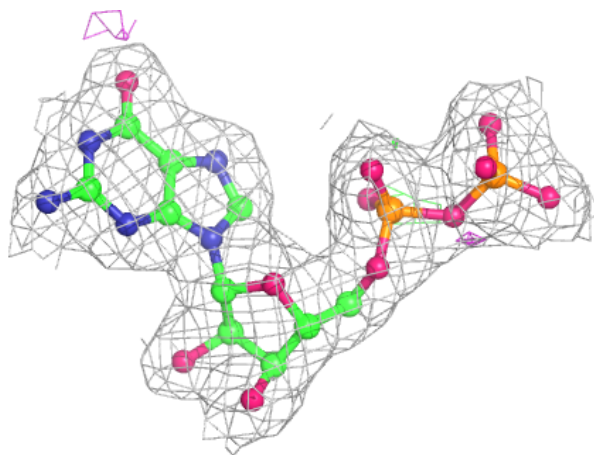
**Electron density around GTP C 501:**

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



Electron density around GDP B 502:

$2mF_o-DF_c$ (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.