



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 28, 2022 – 07:16 pm BST

PDB ID : 7OGN
Title : Crystal structure of T2R-TTL -mebendazole complex
Authors : Oliva, M.A.; Bonato, F.; Diaz, J.F.
Deposited on : 2021-05-07
Resolution : 2.20 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

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 : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.27
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.27

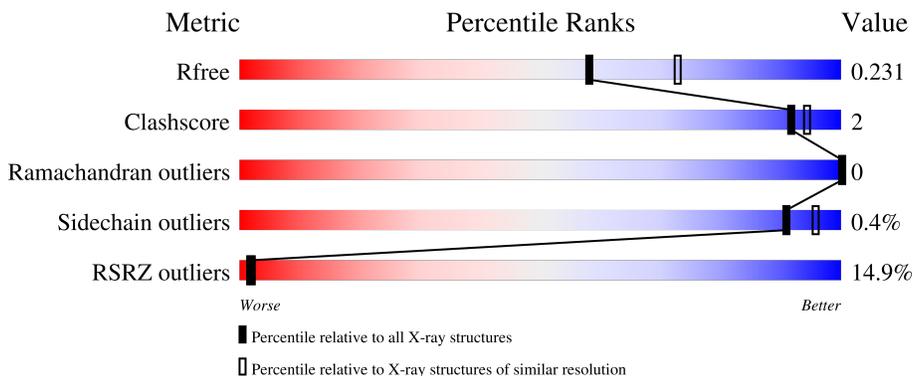
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 ≥ 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	189	

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Mol	Chain	Length	Quality of chain
4	F	384	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a red segment on the left labeled '29%', a green segment in the middle labeled '82%', and a yellow segment on the right labeled '14%'. A small black dot is visible at the end of the bar.</p>

2 Entry composition [i](#)

There are 15 unique types of molecules in this entry. The entry contains 34985 atoms, of which 17129 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	
			Total	C	H	N	O				S
1	A	439	Total	C	H	N	O	S	0	7	0
			6858	2196	3390	587	661	24			
1	C	440	Total	C	H	N	O	S	0	15	0
			6928	2216	3426	592	669	25			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
2	B	421	Total	C	H	N	O	S	0	6	0
			6580	2103	3235	571	642	29			
2	D	422	Total	C	H	N	O	S	0	9	0
			6600	2108	3242	570	653	27			

- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
3	E	120	Total	C	H	N	O	S	0	0	0
			2007	614	1013	180	195	5			

- Molecule 4 is a protein called Tubulin-Tyrosine Ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
4	F	329	Total	C	H	N	O	S	0	4	0
			5426	1750	2707	464	490	15			

There are 6 discrepancies between the modelled and reference sequences:

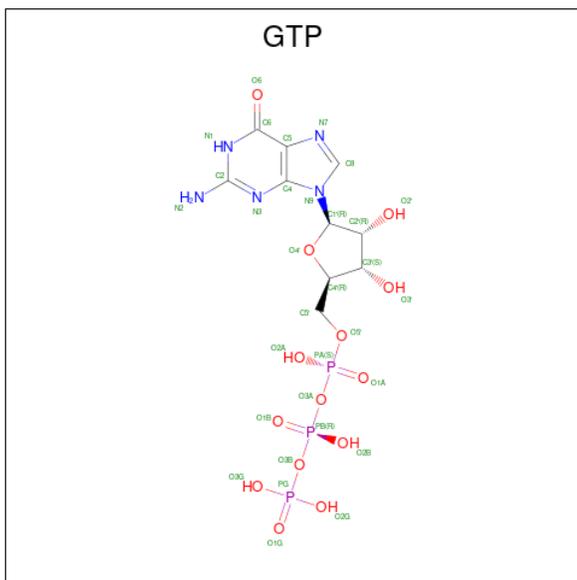
Chain	Residue	Modelled	Actual	Comment	Reference
F	379	HIS	-	expression tag	UNP E1BQ43
F	380	HIS	-	expression tag	UNP E1BQ43
F	381	HIS	-	expression tag	UNP E1BQ43
F	382	HIS	-	expression tag	UNP E1BQ43

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Chain	Residue	Modelled	Actual	Comment	Reference
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	
			Total	C	H	N	O			P
5	A	1	Total	C	H	N	O	P	0	0
			41	10	9	5	14	3		
5	C	1	Total	C	H	N	O	P	0	0
			41	10	9	5	14	3		

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	2	Total	Mg	0	0
			2	2		
6	B	2	Total	Mg	0	0
			2	2		
6	C	1	Total	Mg	0	0
			1	1		
6	D	1	Total	Mg	0	0
			1	1		
6	F	1	Total	Mg	0	0
			1	1		

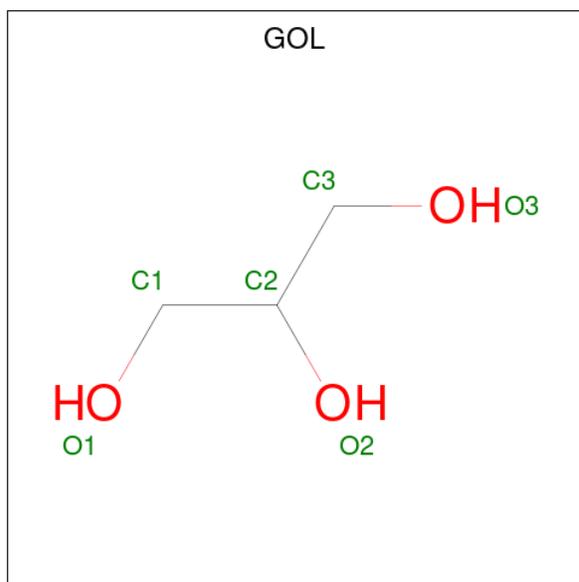
- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Ca	0	0
			1	1		
7	B	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 CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	Cl	0	0
			1	1		
8	C	1	Total	Cl	0	0
			1	1		

- Molecule 9 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



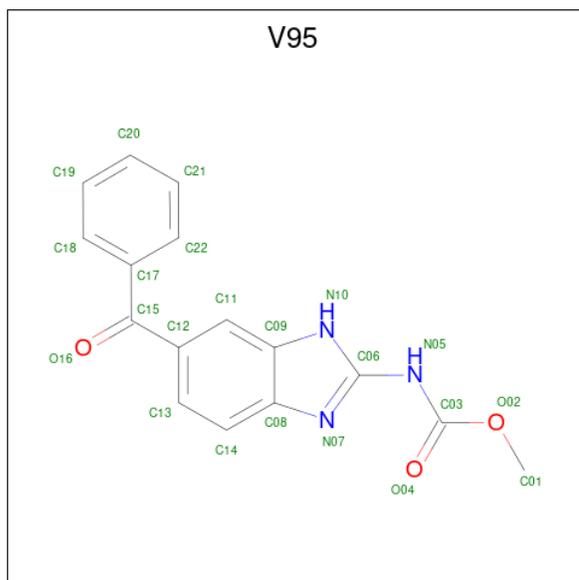
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
9	A	1	Total	C	H	O	0	0
			14	3	8	3		

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

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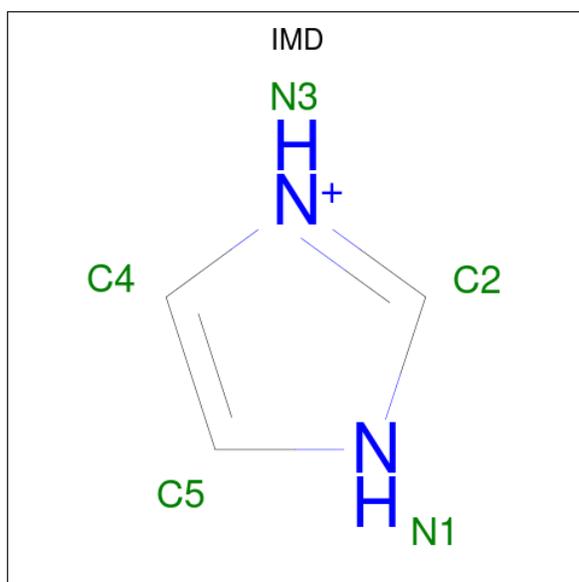
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	H	N	O			S
11	D	1	25	6	13	1	4	1	0	0

- Molecule 12 is methyl N-(6-benzoyl-1H-benzimidazol-2-yl)carbamate (three-letter code: V95) (formula: C₁₆H₁₃N₃O₃) (labeled as "Ligand of Interest" by depositor).



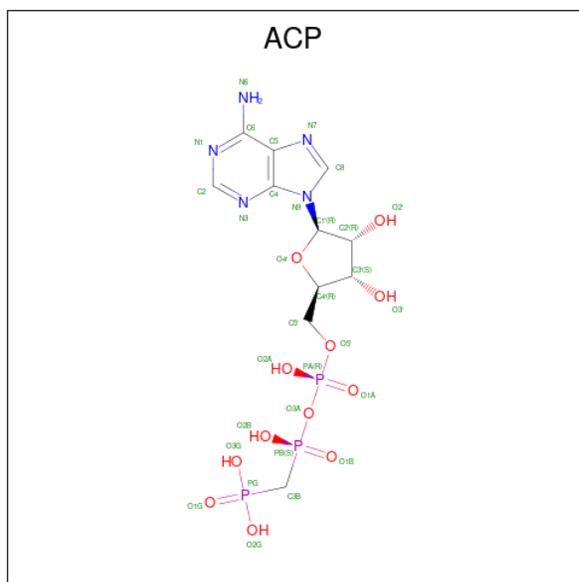
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
12	B	1	35	16	13	3	3	0	0
12	D	1	35	16	13	3	3	0	0

- Molecule 13 is IMIDAZOLE (three-letter code: IMD) (formula: C₃H₅N₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	N		
13	C	1	10	3	5	2	0	0

- Molecule 14 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	
			Total	C	H	N	O			P
14	F	1	44	11	13	5	12	3	0	0

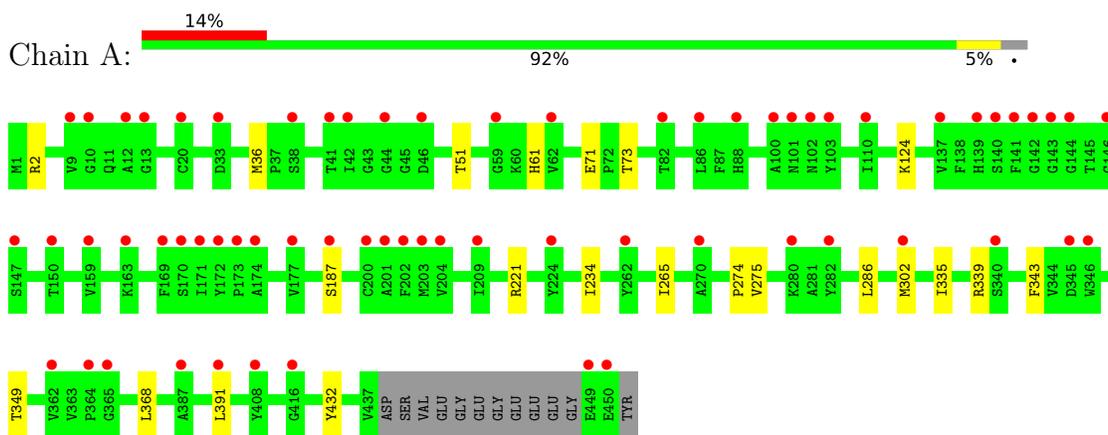
- Molecule 15 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	A	46	Total 46	O 46	0	0
15	B	49	Total 49	O 49	0	0
15	C	114	Total 114	O 114	0	0
15	D	14	Total 14	O 14	0	0
15	E	1	Total 1	O 1	0	0
15	F	3	Total 3	O 3	0	0

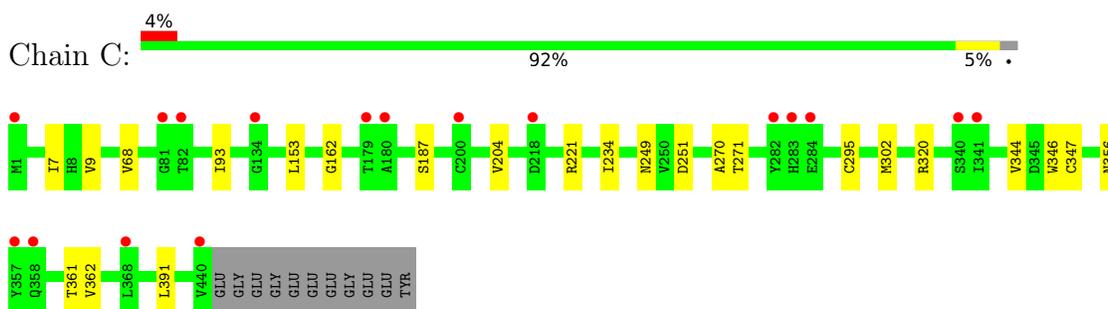
3 Residue-property plots [i](#)

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.

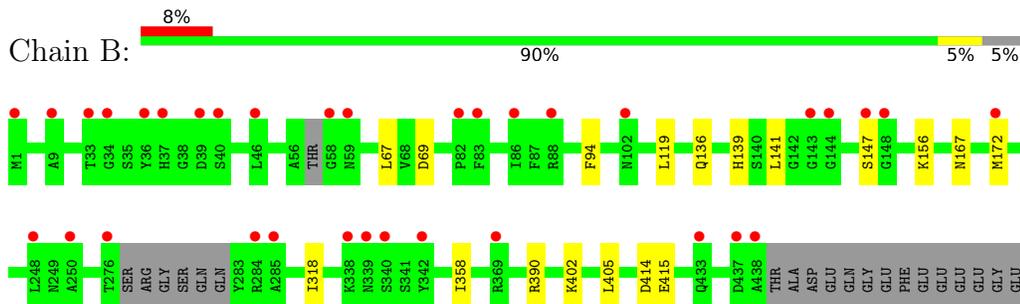
- Molecule 1: Tubulin alpha-1B chain



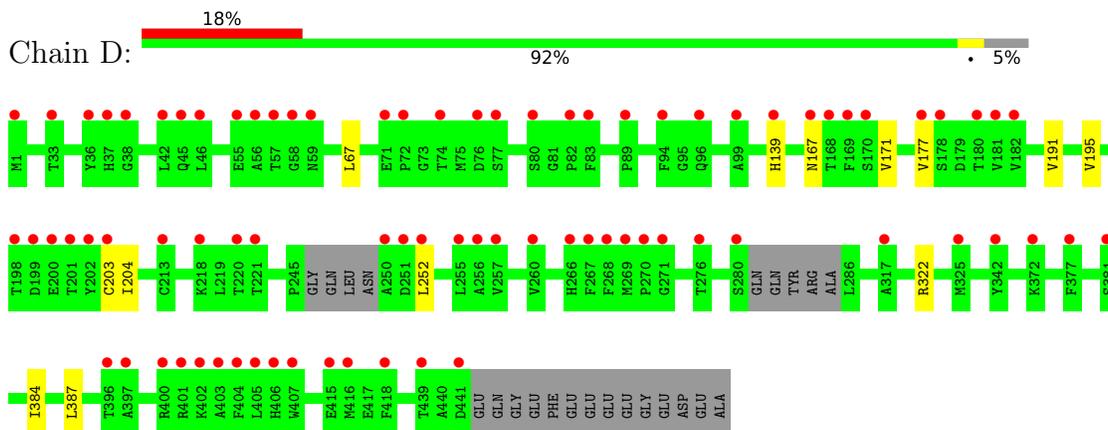
- Molecule 1: Tubulin alpha-1B chain



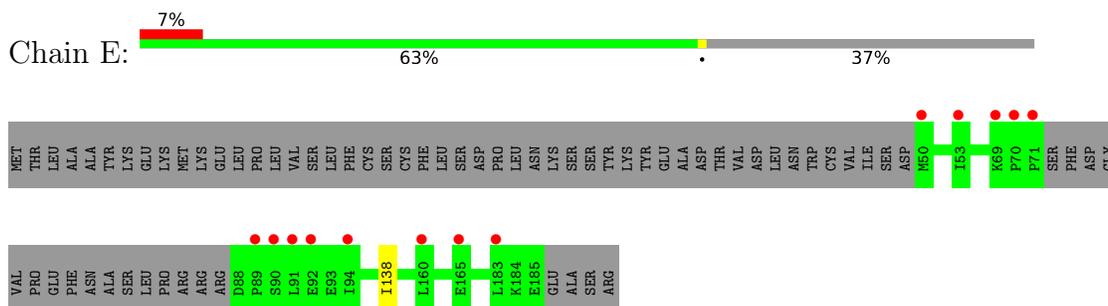
- Molecule 2: Tubulin beta-2B chain



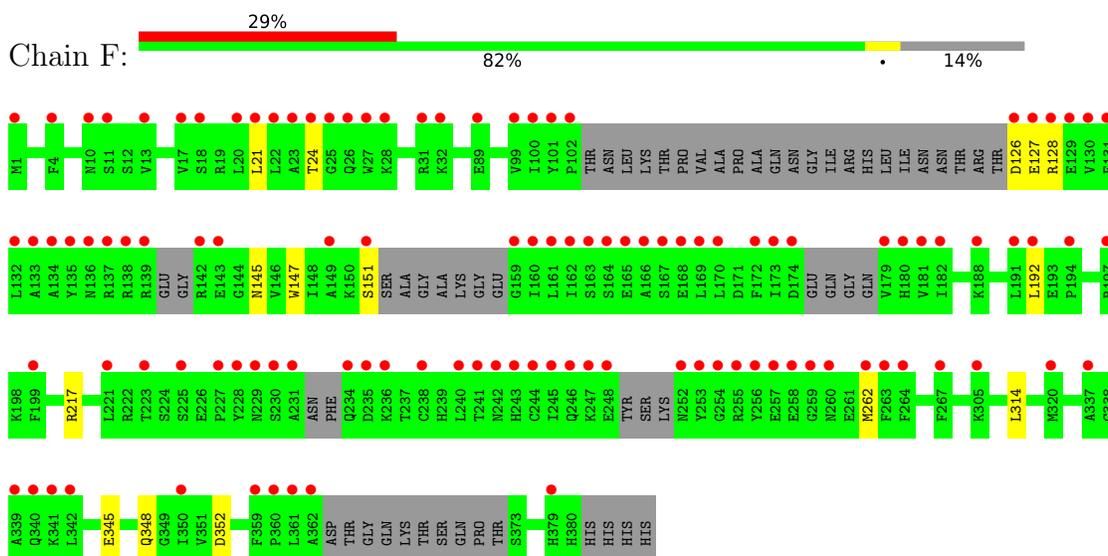
- Molecule 2: Tubulin beta-2B chain



• 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, α , β , γ	104.90Å 158.01Å 179.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.35 – 2.20 50.35 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.5 (50.35-2.20) 99.5 (50.35-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.209 , 0.234 0.206 , 0.231	Depositor DCC
R_{free} test set	7565 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	48.5	Xtriage
Anisotropy	0.135	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	34985	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.40% 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: ACP, GOL, GTP, GDP, MG, V95, CA, IMD, CL, 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	0.25	0/3563	0.47	0/4835
1	C	0.25	0/3630	0.48	0/4929
2	B	0.25	0/3437	0.48	0/4651
2	D	0.25	0/3450	0.47	0/4673
3	E	0.25	0/1002	0.43	0/1329
4	F	0.24	0/2789	0.47	0/3761
All	All	0.25	0/17871	0.48	0/24178

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	3468	3390	3389	12	0
1	C	3502	3426	3387	16	0
2	B	3345	3235	3211	11	0
2	D	3358	3242	3224	7	0
3	E	994	1013	1013	1	0
4	F	2719	2707	2701	9	0
5	A	32	9	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	32	9	12	0	0
6	A	2	0	0	0	0
6	B	2	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	1	0	0	0	0
7	C	1	0	0	0	0
7	E	1	0	0	0	0
8	A	1	0	0	0	0
8	C	1	0	0	0	0
9	A	6	8	8	0	0
10	B	28	10	12	0	0
10	D	28	10	12	0	0
11	B	12	13	13	0	0
11	D	12	13	13	0	0
12	B	22	13	0	0	0
12	D	22	13	0	0	0
13	C	5	5	5	0	0
14	F	31	13	13	0	0
15	A	46	0	0	0	0
15	B	49	0	0	0	0
15	C	114	0	0	0	0
15	D	14	0	0	0	0
15	E	1	0	0	0	0
15	F	3	0	0	0	0
All	All	17856	17129	17025	55	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 55 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:234:ILE:HG21	1:C:302[B]:MET:SD	2.11	0.91
1:C:204:VAL:HG22	1:C:302[B]:MET:CE	2.19	0.72
1:A:234:ILE:HD13	1:A:302:MET:SD	2.32	0.70
2:B:147[A]:SER:HG	2:B:190:SER:HG	1.47	0.61
1:A:275:VAL:HG13	1:A:368:LEU:HD21	1.82	0.60

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	442/451 (98%)	431 (98%)	11 (2%)	0	100	100
1	C	453/451 (100%)	445 (98%)	8 (2%)	0	100	100
2	B	421/445 (95%)	413 (98%)	8 (2%)	0	100	100
2	D	425/445 (96%)	416 (98%)	9 (2%)	0	100	100
3	E	116/189 (61%)	116 (100%)	0	0	100	100
4	F	317/384 (83%)	309 (98%)	8 (2%)	0	100	100
All	All	2174/2365 (92%)	2130 (98%)	44 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	377/379 (100%)	375 (100%)	2 (0%)	88	94
1	C	385/379 (102%)	383 (100%)	2 (0%)	88	94
2	B	370/383 (97%)	369 (100%)	1 (0%)	92	97
2	D	374/383 (98%)	372 (100%)	2 (0%)	88	94
3	E	108/171 (63%)	108 (100%)	0	100	100
4	F	301/342 (88%)	300 (100%)	1 (0%)	92	97

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1915/2037 (94%)	1907 (100%)	8 (0%)	91 96

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	F	314	LEU
2	D	322	ARG
1	C	251	ASP
1	C	221	ARG
2	D	139	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 24 ligands modelled in this entry, 13 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
12	V95	B	505	-	24,24,24	1.87	7 (29%)	26,33,33	1.89	4 (15%)
5	GTP	A	501	6	26,34,34	0.99	1 (3%)	33,54,54	1.82	7 (21%)
10	GDP	B	501	6	24,30,30	1.09	2 (8%)	31,47,47	1.93	7 (22%)
13	IMD	C	501	-	3,5,5	0.42	0	4,5,5	0.57	0
14	ACP	F	500	6	27,33,33	4.50	11 (40%)	32,52,52	1.81	5 (15%)
10	GDP	D	500	6	24,30,30	1.14	2 (8%)	31,47,47	1.91	7 (22%)
12	V95	D	503	-	24,24,24	1.92	7 (29%)	26,33,33	2.10	4 (15%)
9	GOL	A	505	-	5,5,5	0.91	0	5,5,5	1.01	0
11	MES	D	502	-	12,12,12	2.10	1 (8%)	14,16,16	1.57	4 (28%)
11	MES	B	504	-	12,12,12	2.03	1 (8%)	14,16,16	1.61	3 (21%)
5	GTP	C	502	6	26,34,34	0.97	1 (3%)	33,54,54	1.65	6 (18%)

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
12	V95	B	505	-	-	2/12/14/14	0/3/3/3
5	GTP	A	501	6	-	7/18/38/38	0/3/3/3
10	GDP	B	501	6	-	3/12/32/32	0/3/3/3
13	IMD	C	501	-	-	-	0/1/1/1
14	ACP	F	500	6	-	1/15/38/38	0/3/3/3
10	GDP	D	500	6	-	3/12/32/32	0/3/3/3
12	V95	D	503	-	-	2/12/14/14	0/3/3/3
9	GOL	A	505	-	-	0/4/4/4	-
11	MES	D	502	-	-	1/6/14/14	0/1/1/1
11	MES	B	504	-	-	0/6/14/14	0/1/1/1
5	GTP	C	502	6	-	5/18/38/38	0/3/3/3

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	F	500	ACP	O4'-C1'	15.48	1.62	1.41
14	F	500	ACP	C2'-C1'	-13.13	1.33	1.53
11	D	502	MES	C8-S	-7.00	1.67	1.77
11	B	504	MES	C8-S	-6.77	1.67	1.77
14	F	500	ACP	O4'-C4'	-5.63	1.32	1.45

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	D	503	V95	O02-C03-N05	7.63	119.93	109.25
12	B	505	V95	O02-C03-N05	6.76	118.71	109.25
14	F	500	ACP	C5-C6-N6	5.75	129.09	120.35
14	F	500	ACP	N3-C2-N1	-5.72	119.75	128.68
12	D	503	V95	C06-N05-C03	-5.55	119.47	127.67

There are no chirality outliers.

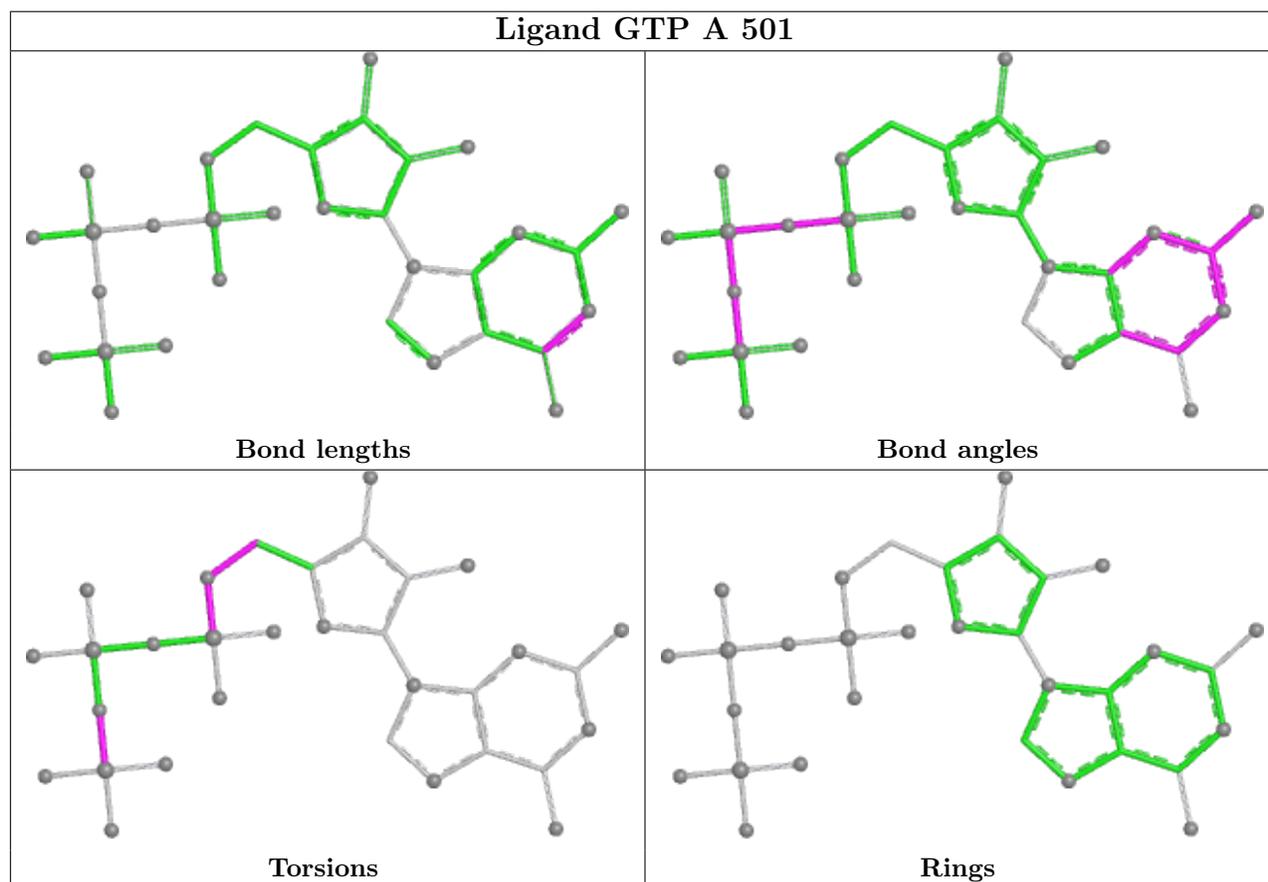
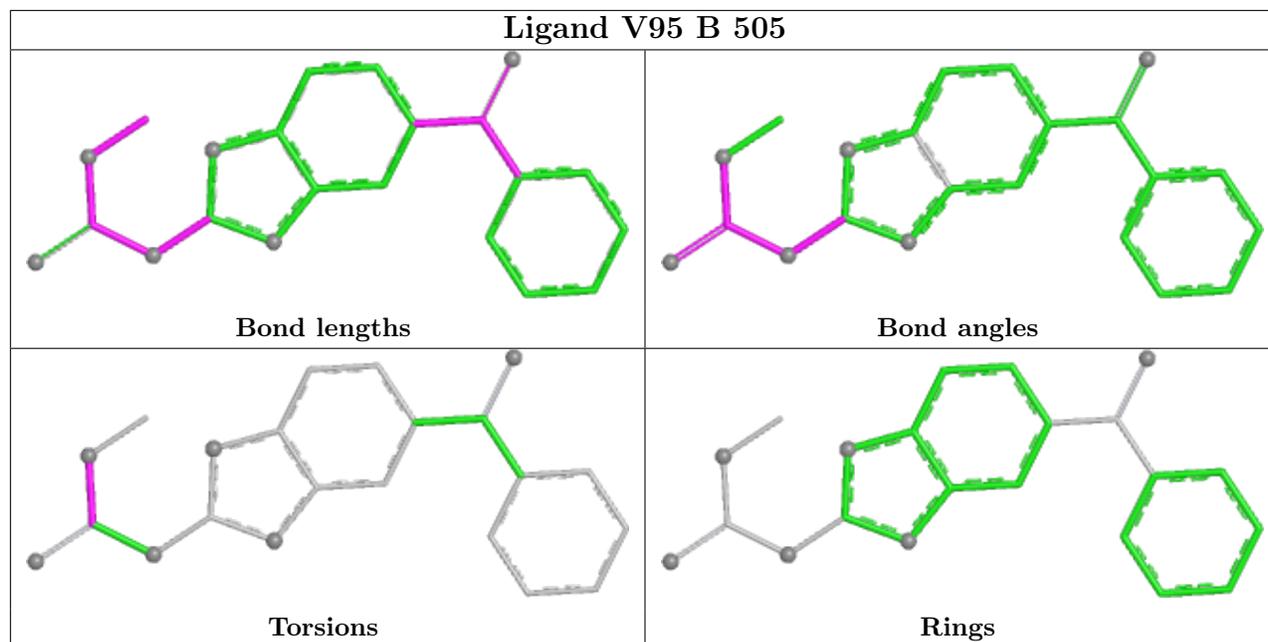
5 of 24 torsion outliers are listed below:

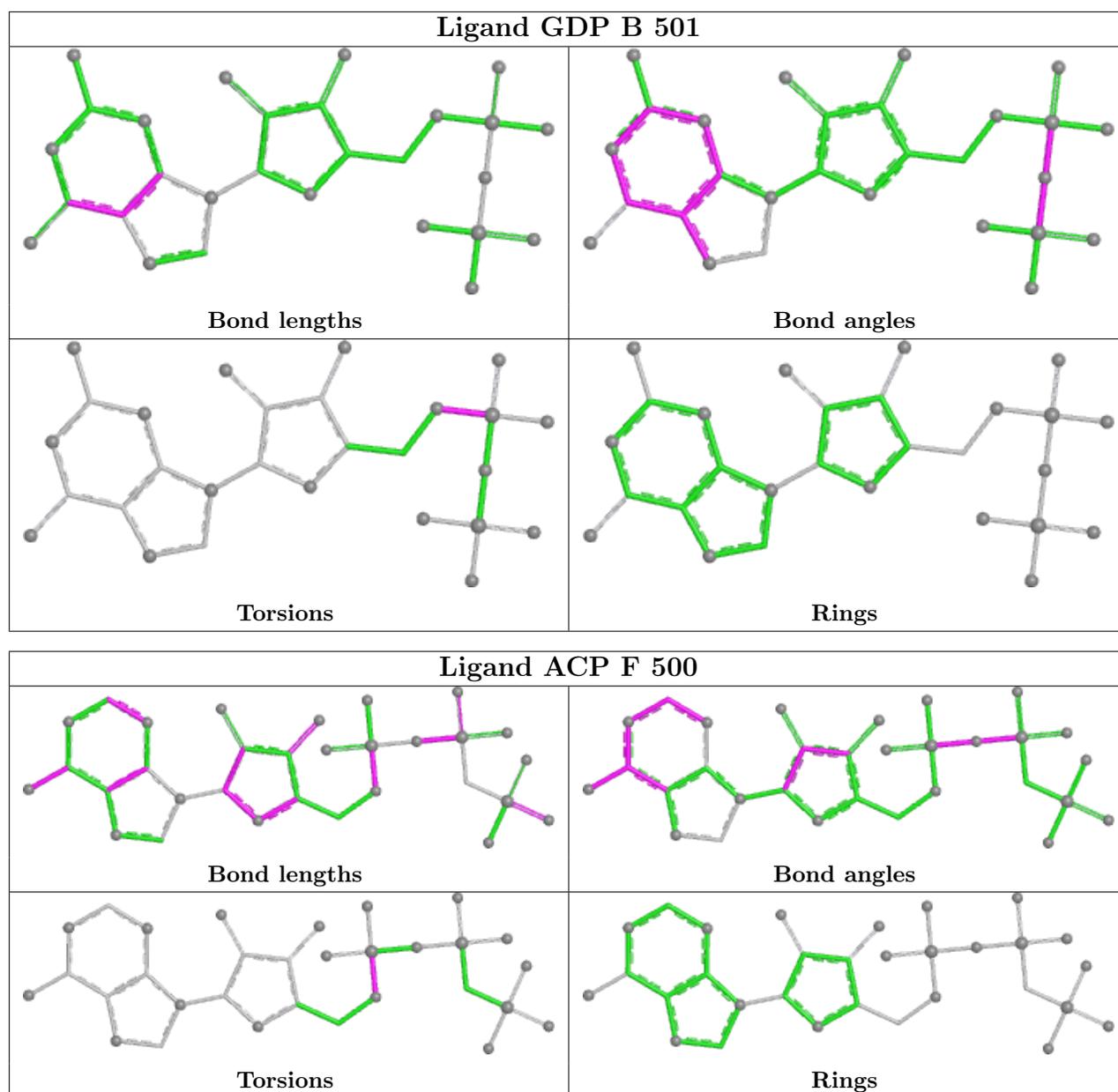
Mol	Chain	Res	Type	Atoms
5	A	501	GTP	PB-O3B-PG-O3G
5	A	501	GTP	C5'-O5'-PA-O1A
5	A	501	GTP	C5'-O5'-PA-O2A
5	C	502	GTP	PB-O3B-PG-O2G
5	C	502	GTP	C5'-O5'-PA-O1A

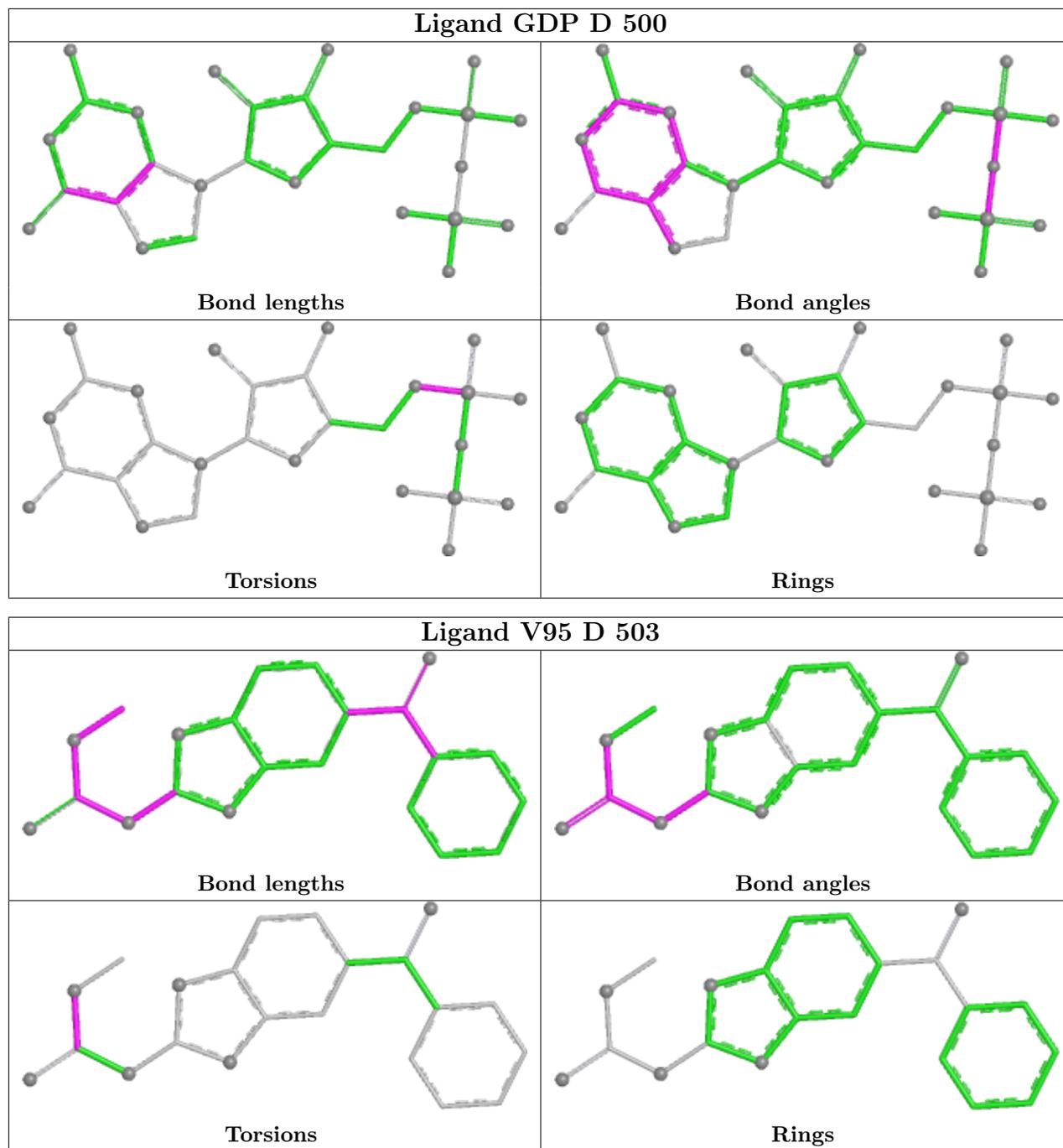
There are no ring outliers.

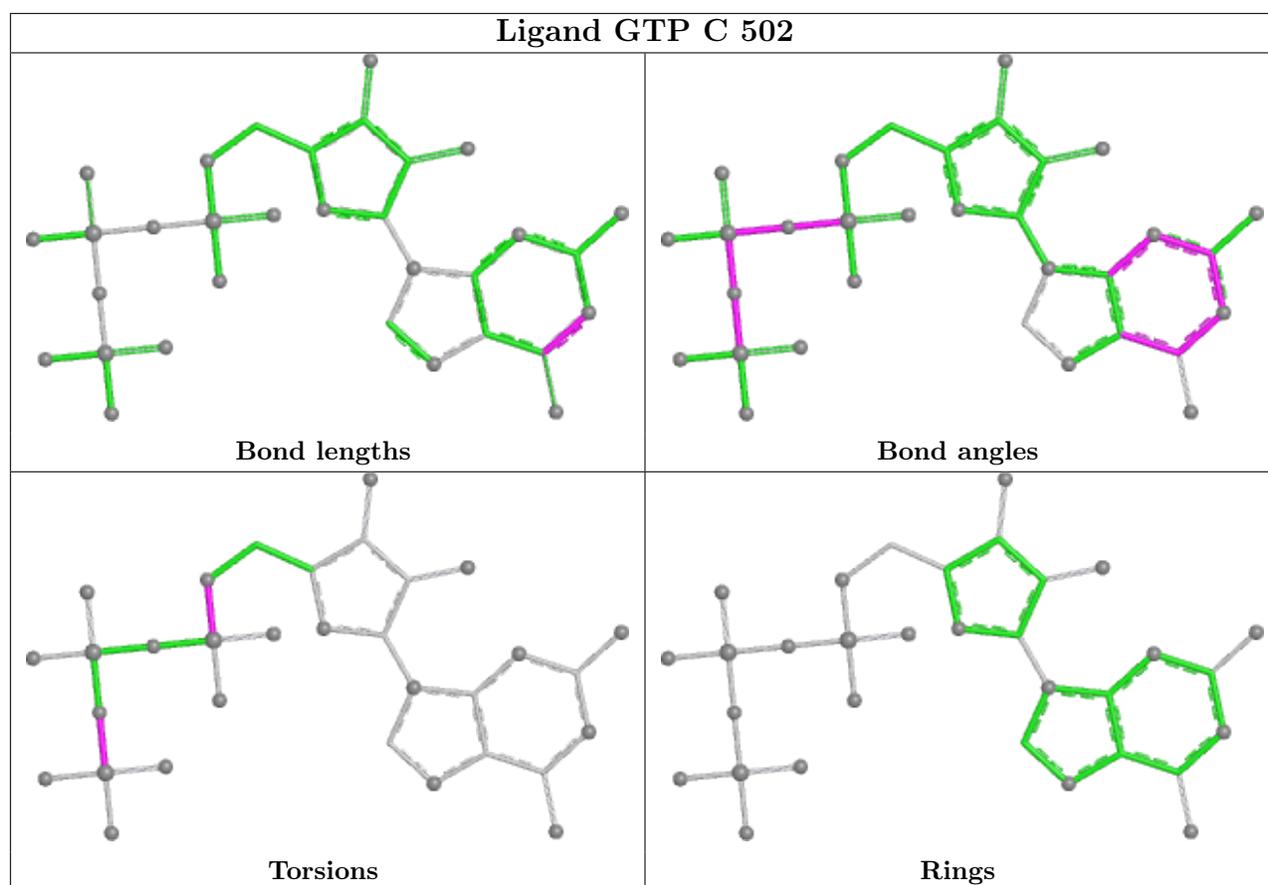
No monomer is involved in short contacts.

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, 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	439/451 (97%)	0.96	65 (14%) 2 2	37, 58, 91, 161	0
1	C	440/451 (97%)	0.49	17 (3%) 39 37	32, 46, 75, 115	0
2	B	421/445 (94%)	0.74	34 (8%) 12 10	32, 54, 88, 121	2 (0%)
2	D	422/445 (94%)	1.07	81 (19%) 1 1	44, 66, 100, 141	4 (0%)
3	E	120/189 (63%)	1.00	13 (10%) 5 5	44, 70, 114, 132	0
4	F	329/384 (85%)	1.72	113 (34%) 0 0	48, 83, 138, 174	0
All	All	2171/2365 (91%)	0.96	323 (14%) 2 2	32, 60, 107, 174	6 (0%)

The worst 5 of 323 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	F	169	LEU	12.8
4	F	132	LEU	11.4
4	F	135	TYR	9.1
4	F	166	ALA	8.1
3	E	70	PRO	7.9

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

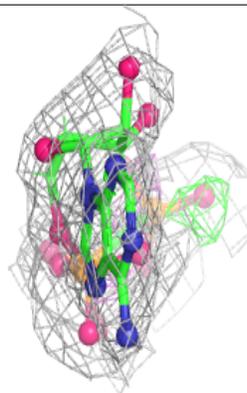
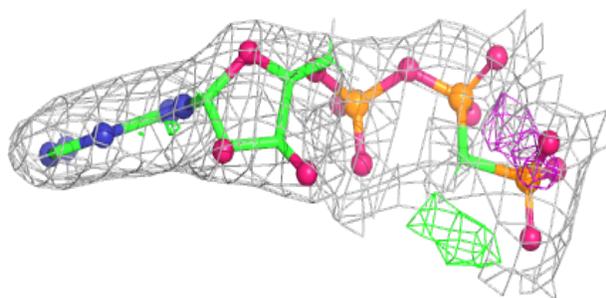
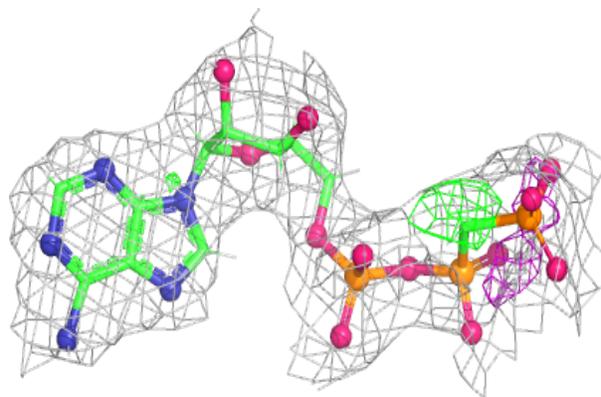
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	MG	A	506	1/1	0.41	0.24	71,71,71,71	0
6	MG	D	501	1/1	0.63	0.12	72,72,72,72	0
6	MG	B	506	1/1	0.64	0.16	79,79,79,79	0
6	MG	F	501	1/1	0.65	0.12	113,113,113,113	0
8	CL	C	505	1/1	0.68	0.13	69,69,69,69	0
7	CA	B	503	1/1	0.72	0.17	76,76,76,76	0
14	ACP	F	500	31/31	0.72	0.22	89,96,105,108	0
8	CL	A	504	1/1	0.79	0.13	73,73,73,73	0
9	GOL	A	505	6/6	0.80	0.19	64,70,82,82	14
12	V95	D	503	22/22	0.81	0.32	53,56,60,62	35
7	CA	A	503	1/1	0.82	0.09	68,68,68,68	0
13	IMD	C	501	5/5	0.85	0.14	49,53,56,56	10
6	MG	C	503	1/1	0.85	0.15	37,37,37,37	0
11	MES	D	502	12/12	0.90	0.30	49,59,65,65	25
10	GDP	D	500	28/28	0.90	0.14	55,62,66,75	0
6	MG	A	502	1/1	0.91	0.18	39,39,39,39	0
6	MG	B	502	1/1	0.91	0.22	30,30,30,30	0
7	CA	E	201	1/1	0.92	0.04	83,83,83,83	0
5	GTP	A	501	32/32	0.94	0.25	34,40,43,43	0
12	V95	B	505	22/22	0.95	0.12	39,42,48,48	0
5	GTP	C	502	32/32	0.95	0.17	32,36,42,44	0
11	MES	B	504	12/12	0.95	0.17	36,42,50,53	0
10	GDP	B	501	28/28	0.95	0.21	34,40,44,45	0
7	CA	C	504	1/1	0.98	0.04	56,56,56,56	0

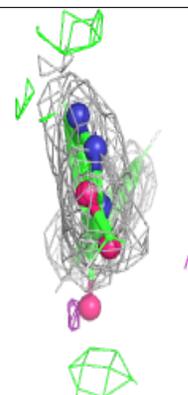
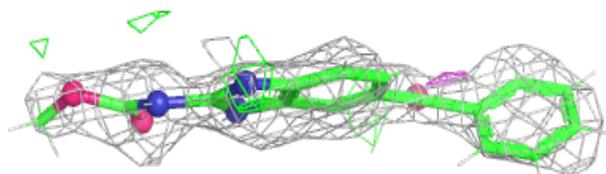
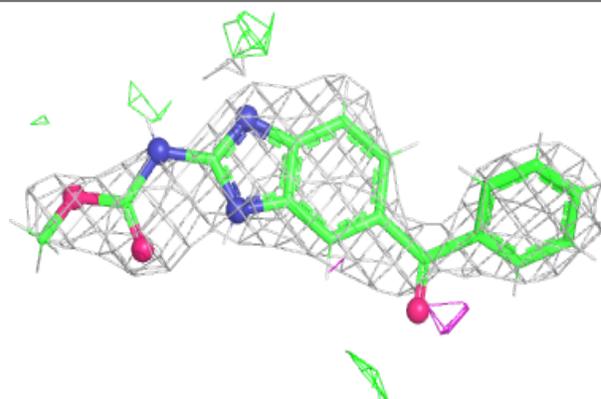
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ACP F 500:

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

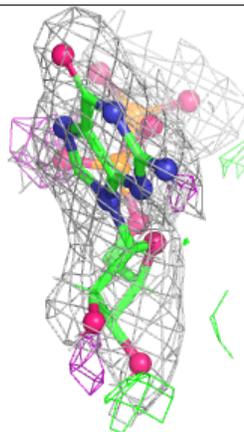
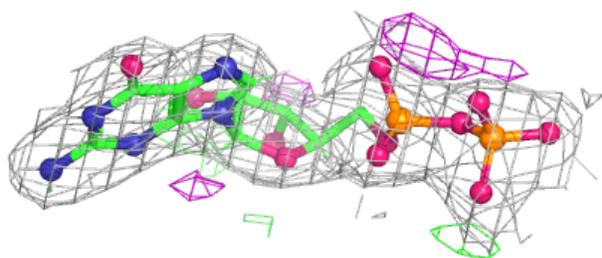
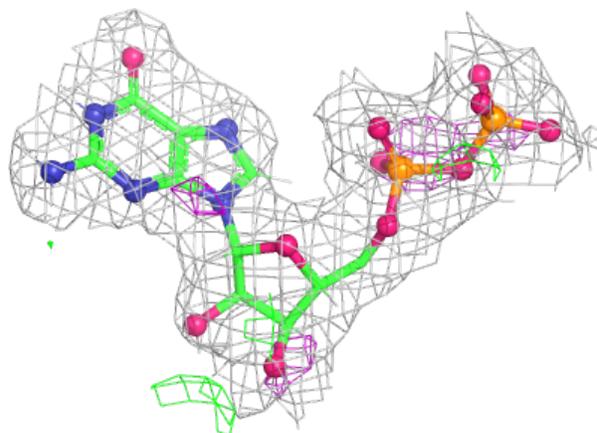
**Electron density around V95 D 503:**

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

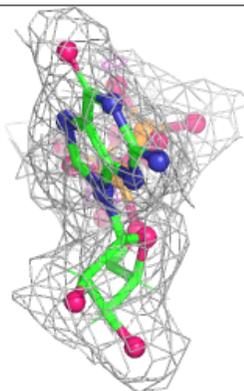
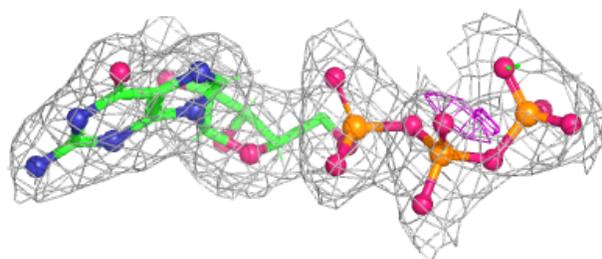
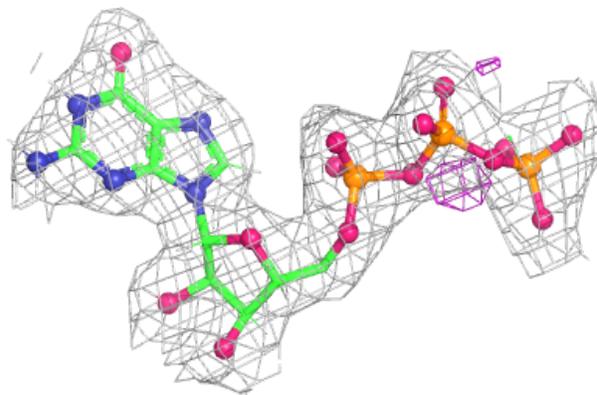


Electron density around GDP D 500:

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

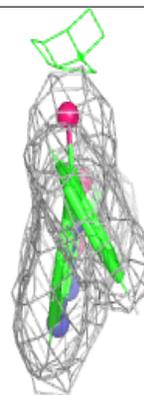
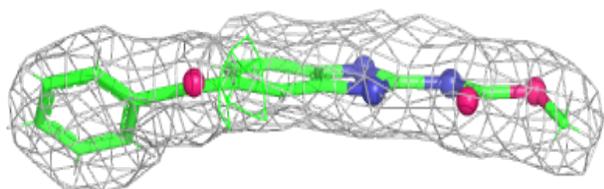
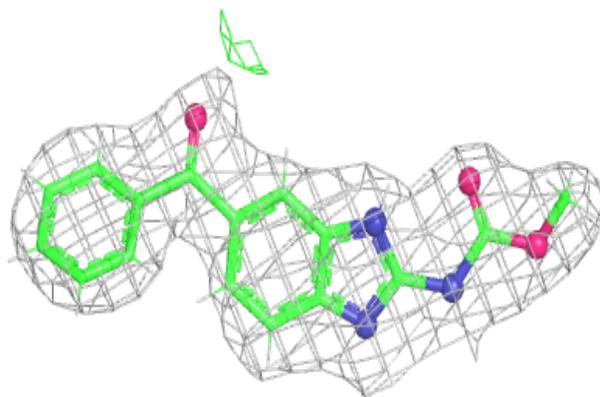
**Electron density around GTP A 501:**

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

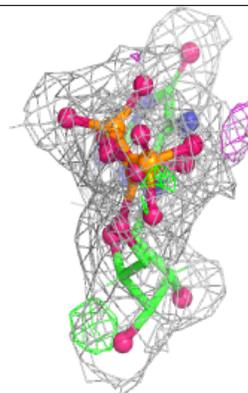
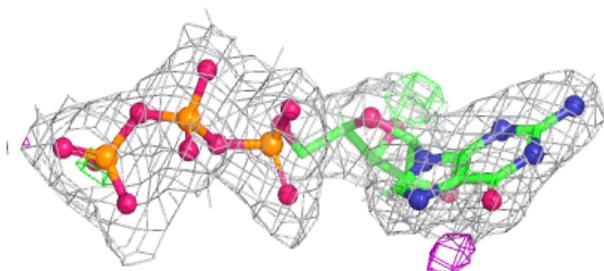
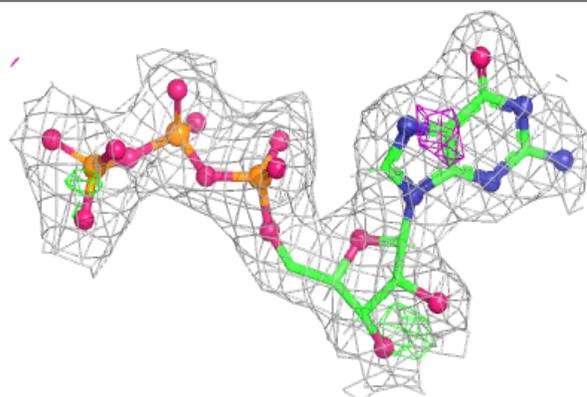


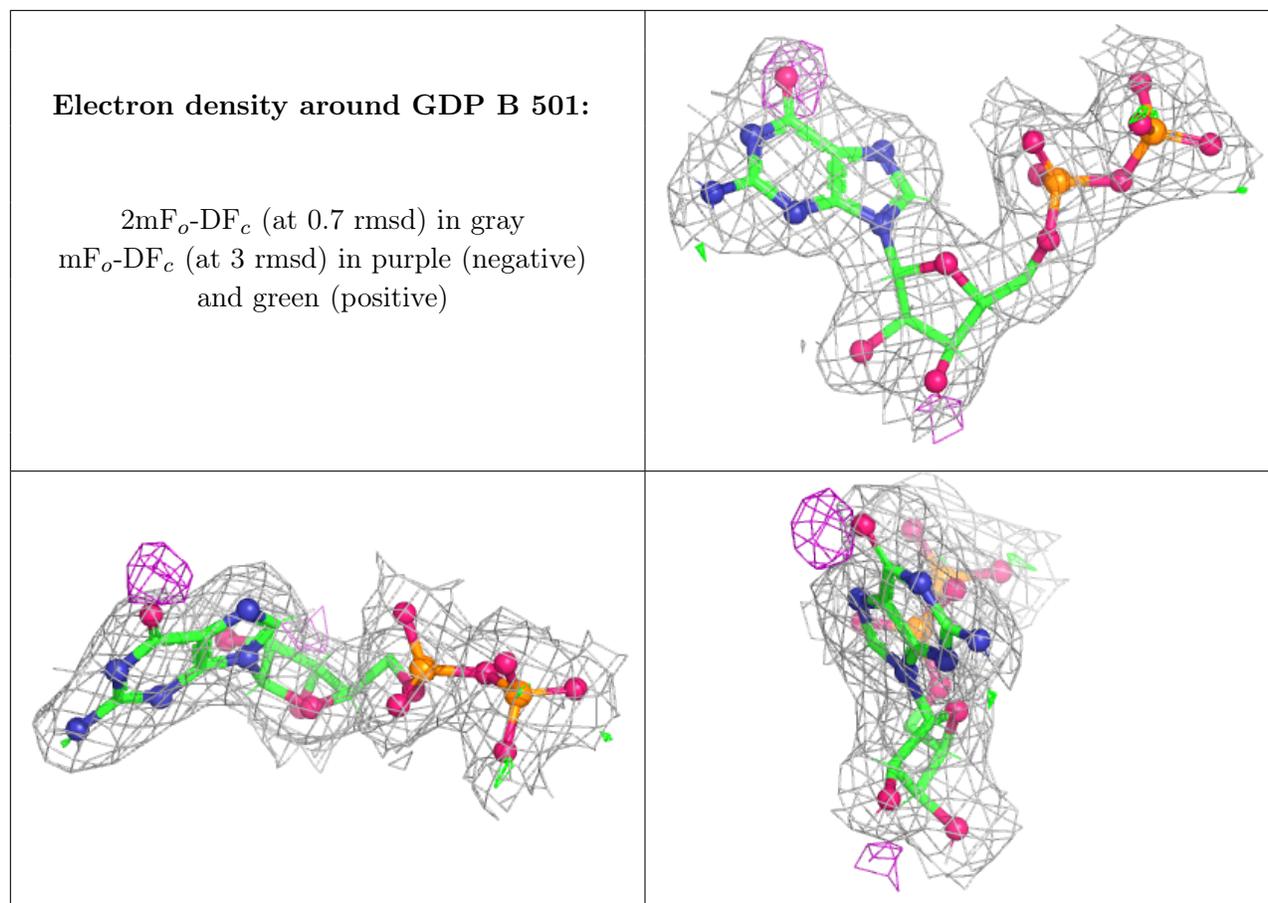
Electron density around V95 B 505:

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

**Electron density around GTP C 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.