



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 01:20 PM UTC

PDB ID : 7LZ8 / pdb_00007lz8
Title : Tubulin-RB3_SLD-TTL in complex with compound 5t
Authors : White, S.W.; Yun, M.
Deposited on : 2021-03-09
Resolution : 2.92 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

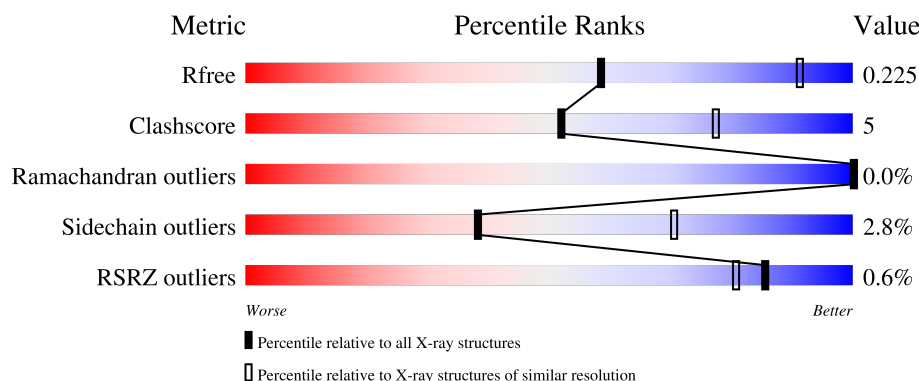
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.92 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}	180053	2995 (2.94-2.90)
Clashscore	190562	3213 (2.94-2.90)
Ramachandran outliers	187476	3128 (2.94-2.90)
Sidechain outliers	187428	3130 (2.94-2.90)
RSRZ outliers	180081	2995 (2.94-2.90)

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	450	83% 14% .
1	C	450	84% 12% ..
2	B	445	86% 9% 5%
2	D	445	75% 18% 6%
3	E	143	67% 17% 15%

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Mol	Chain	Length	Quality of chain
4	F	384	% 58%8%33%

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 16797 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	437	Total	C	N	O	S	0	0	0
			3406	2155	581	649	21			
1	C	438	Total	C	N	O	S	0	0	0
			3428	2170	582	654	22			

- 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
			3333	2093	571	643	26			
2	D	417	Total	C	N	O	S	0	0	0
			3278	2061	558	633	26			

- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	121	Total	C	N	O	S	0	0	0
			993	614	181	193	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	3	MET	-	initiating methionine	UNP P63043
E	4	ALA	-	expression tag	UNP P63043

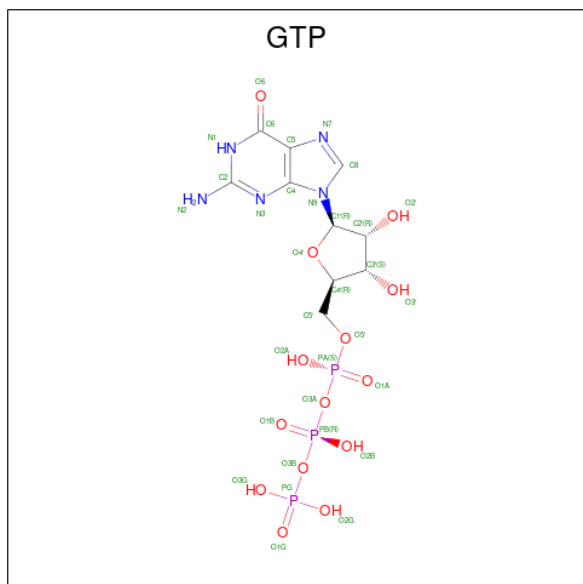
- Molecule 4 is a protein called Tubulin Tyrosine Ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	256	Total	C	N	O	S	0	0	0
			2095	1357	357	370	11			

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 32	C 10	N 5	O 14	P 3	0	0
5	C	1	Total 32	C 10	N 5	O 14	P 3	0	0
5	D	1	Total 32	C 10	N 5	O 14	P 3	0	0

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

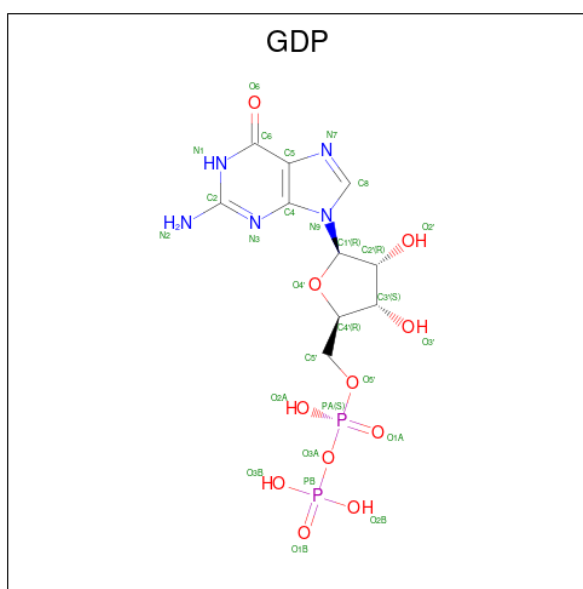
- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

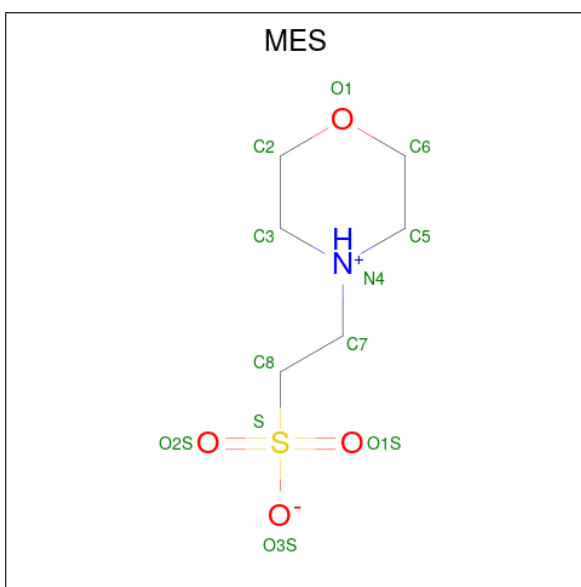
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Mg	0	0
			1	1		
7	B	1	Total	Mg	0	0
			1	1		
7	C	1	Total	Mg	0	0
			1	1		
7	D	1	Total	Mg	0	0
			1	1		

- Molecule 8 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

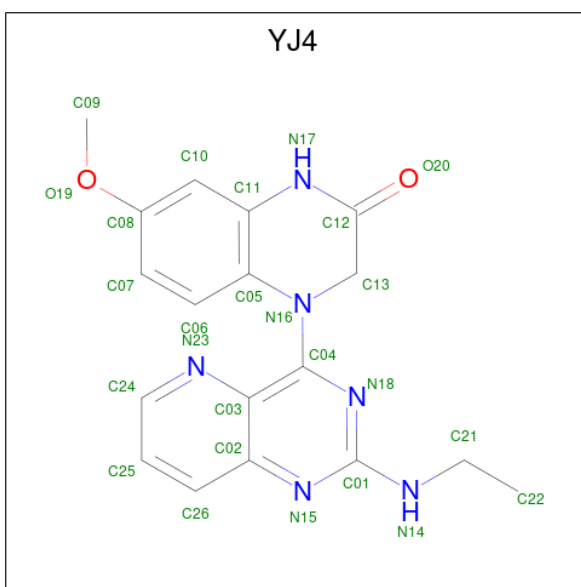
- Molecule 9 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).





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

- Molecule 11 is 4-[2-(ethylamino)pyrido[3,2-d]pyrimidin-4-yl]-7-methoxy-3,4-dihydroquinolin-2(1H)-one (CCD ID: YJ4) (formula: $C_{18}H_{18}N_6O_2$) (labeled as "Ligand of Interest" by depositor).



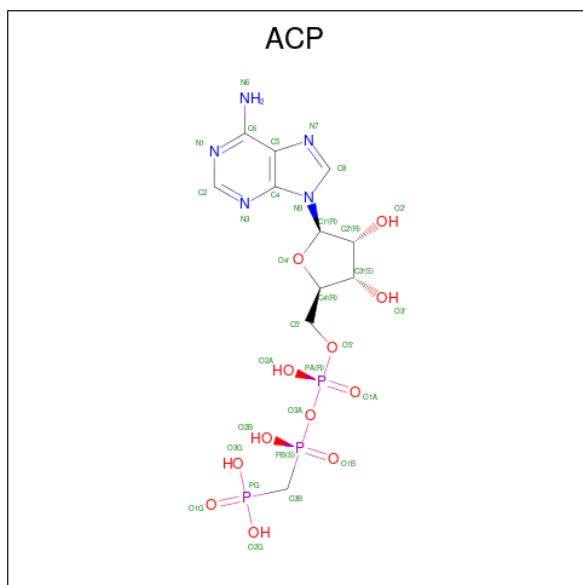
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
11	B	1	Total	C	N	O		0	0
			26	18	6	2			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	D	1	Total	C	N	O	0	0
			26	18	6	2		

- Molecule 12 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (CCD ID: ACP) (formula: $C_{11}H_{18}N_5O_{12}P_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	F	1	Total	C	N	O	0	0
			17	9	5	3		

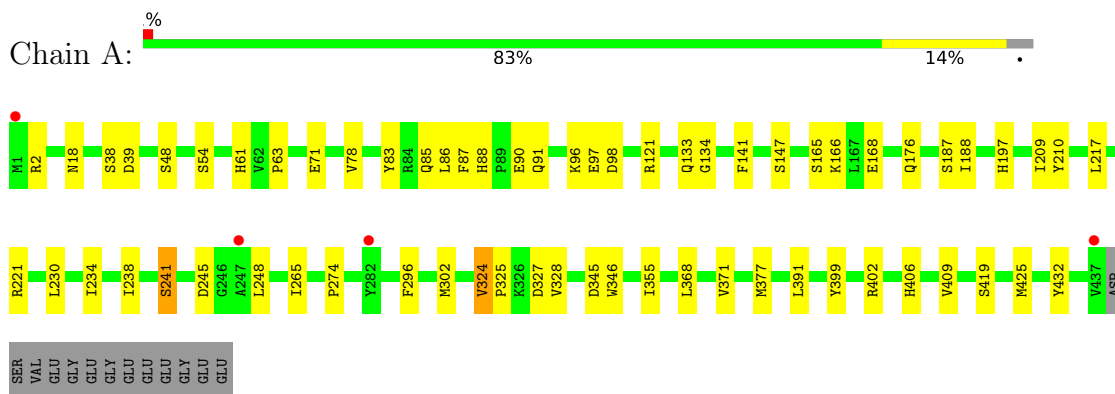
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	7	Total	O	0	0
			7	7		
13	B	10	Total	O	0	0
			10	10		
13	C	17	Total	O	0	0
			17	17		
13	D	3	Total	O	0	0
			3	3		

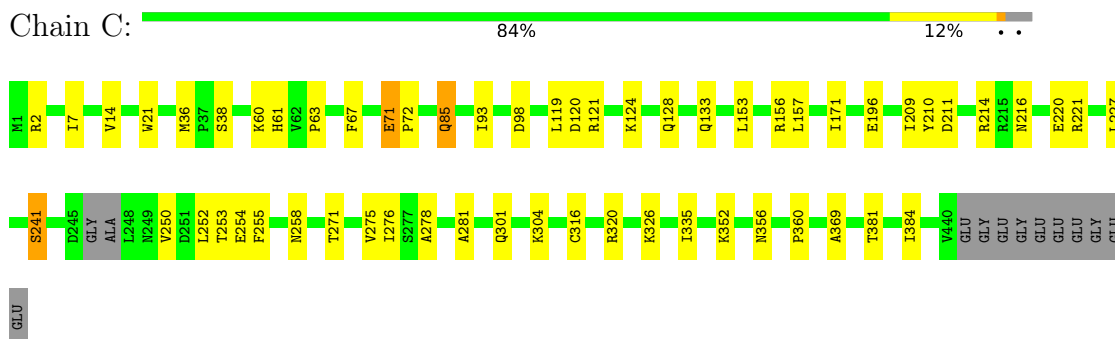
3 Residue-property plots

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.

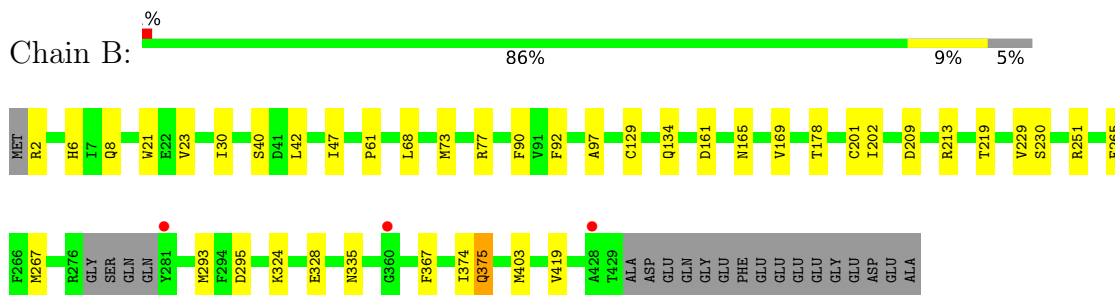
- Molecule 1: Tubulin alpha-1B chain



- Molecule 1: Tubulin alpha-1B chain



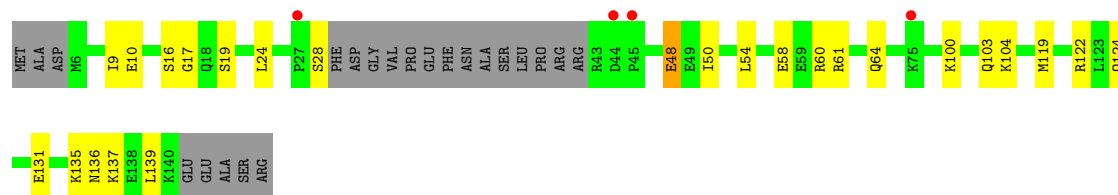
- Molecule 2: Tubulin beta-2B chain



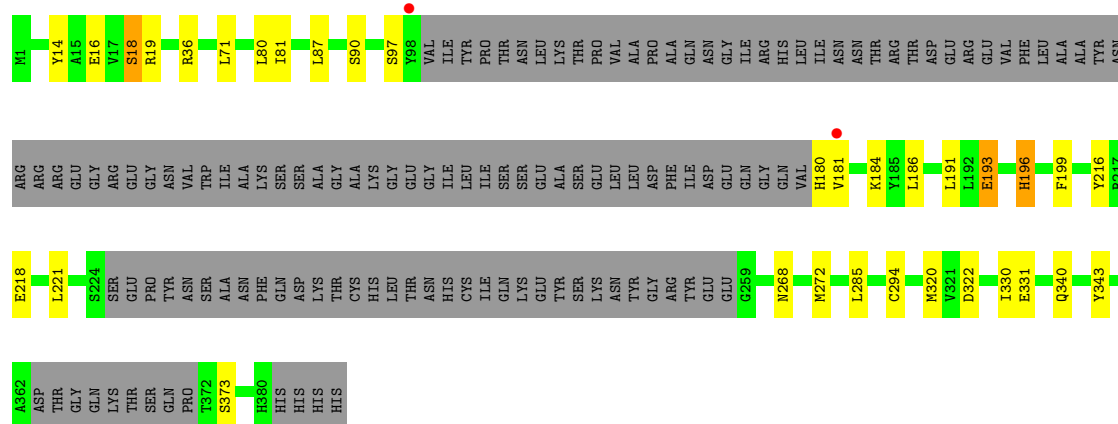
- Molecule 2: Tubulin beta-2B chain

GLY	GLN	SL24	MET
GLU	TYR	E125	R2
PHE	ARG	SL26	V5
GLU	ALA	L130	H6
GLU	T285	F133	I7
GLU	T286	Q134	Q8
GLU	P287	S138	C12
GLU	E288	T149	G13
ASP	L289	L150	N14
GLU	Q292	L151	K19
ALA	M293	I152	V23
	F294	T163	E27
	N298	M164	H28
	M299	N165	D31
	K300	V169	G34
	A301	M170	D41
	Y310	P171	E53
	A315	S172	ALA
	M323	D177	THR
	M330	E198	GLY
	M344	T202	N57
	T345	D203	T72
	N348	N204	M73
	T351	E205	D74
	P357	A206	S75
	L361	L207	V76
	F367	V208	R77
	Q375	P220	F81
	E376	V229	G82
	L377	T232	Q83
	S382	V236	I84
	M388	R241	A97
	Y398	A248	N100
	M403	D249	V101
	M415	L250	A102
	V419	M267	K103
	D431	L273	G104
GLU	GLN	THR	H105
		SER	Y106
		ARG	T107
		GLY	V113
		SER	V116
		GLN	V120

Chain E: 3% 67% 17% 15%



Chain F: 58% 8% 33%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.57Å 155.04Å 182.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.36 – 2.92 45.36 – 2.92	Depositor EDS
% Data completeness (in resolution range)	98.1 (45.36-2.92) 92.2 (45.36-2.92)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.184 , 0.228 0.187 , 0.225	Depositor DCC
R_{free} test set	2000 reflections (3.12%)	wwPDB-VP
Wilson B-factor (Å ²)	71.3	Xtriage
Anisotropy	0.198	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 50.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	16797	wwPDB-VP
Average B, all atoms (Å ²)	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.72% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, CL, ACP, MG, YJ4, GDP, CA, 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	0.14	0/3483	0.35	0/4729
1	C	0.15	0/3505	0.40	2/4757 (0.0%)
2	B	0.15	0/3406	0.34	0/4613
2	D	0.14	0/3350	0.35	0/4537
3	E	0.13	0/1001	0.35	0/1328
4	F	0.13	0/2144	0.38	0/2897
All	All	0.14	0/16889	0.36	2/22861 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	171	ILE	CA-C-N	5.23	127.68	120.67
1	C	171	ILE	C-N-CA	5.23	127.68	120.67

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3406	0	3316	35	0
1	C	3428	0	3339	33	0
2	B	3333	0	3213	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	3278	0	3148	51	0
3	E	993	0	1012	15	0
4	F	2095	0	2097	17	0
5	A	32	0	12	0	0
5	C	32	0	12	0	0
5	D	32	0	12	1	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	2	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	D	1	0	0	0	0
8	A	1	0	0	0	0
8	D	1	0	0	0	0
9	B	28	0	12	0	0
10	B	24	0	24	1	0
11	B	26	0	0	0	0
11	D	26	0	0	1	0
12	F	17	0	8	4	0
13	A	7	0	0	0	0
13	B	10	0	0	0	0
13	C	17	0	0	0	0
13	D	3	0	0	0	0
All	All	16797	0	16205	169	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 5.

The worst 5 of 169 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)
2:B:178:THR:HG22	1:C:258:ASN:HD21	1.53	0.74
2:D:170:MET:HE3	2:D:377:LEU:HD11	1.72	0.72
2:D:375:GLN:HB2	2:D:419:VAL:HG23	1.72	0.71
2:D:398:TYR:HB3	2:D:403:MET:HE3	1.75	0.69
1:C:252:LEU:HA	1:C:255:PHE:HD2	1.62	0.65

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	435/450 (97%)	422 (97%)	13 (3%)	0	100	100
1	C	434/450 (96%)	423 (98%)	11 (2%)	0	100	100
2	B	420/445 (94%)	413 (98%)	7 (2%)	0	100	100
2	D	411/445 (92%)	401 (98%)	10 (2%)	0	100	100
3	E	117/143 (82%)	116 (99%)	1 (1%)	0	100	100
4	F	248/384 (65%)	236 (95%)	11 (4%)	1 (0%)	30	58
All	All	2065/2317 (89%)	2011 (97%)	53 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	F	373	SER

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	366/378 (97%)	358 (98%)	8 (2%)	45	75
1	C	371/378 (98%)	361 (97%)	10 (3%)	39	71
2	B	366/383 (96%)	363 (99%)	3 (1%)	73	89
2	D	360/383 (94%)	347 (96%)	13 (4%)	31	63
3	E	107/127 (84%)	99 (92%)	8 (8%)	12	35
4	F	230/342 (67%)	221 (96%)	9 (4%)	28	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1800/1991 (90%)	1749 (97%)	51 (3%)	38 70

5 of 51 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	172	SER
3	E	24	LEU
4	F	285	LEU
2	D	177	ASP
2	D	388	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	100	ASN
4	F	333	ASN
1	C	15	GLN
1	C	61	HIS
1	C	133	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 19 ligands modelled in this entry, 10 are monoatomic - leaving 9 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	ACP	F	401	-	19,19,33	1.86	5 (26%)	27,28,52	2.19	10 (37%)
11	YJ4	D	504	-	29,29,29	0.94	1 (3%)	35,41,41	1.75	9 (25%)
9	GDP	B	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.74	6 (13%)
5	GTP	C	501	7	33,34,34	0.99	2 (6%)	50,54,54	1.62	9 (18%)
5	GTP	A	501	7	33,34,34	0.94	1 (3%)	50,54,54	1.64	9 (18%)
11	YJ4	B	506	-	29,29,29	0.95	1 (3%)	35,41,41	1.82	8 (22%)
5	GTP	D	501	7	33,34,34	0.97	2 (6%)	50,54,54	1.60	8 (16%)
10	MES	B	502	-	12,12,12	2.33	1 (8%)	15,16,16	1.90	3 (20%)
10	MES	B	503	-	12,12,12	2.30	1 (8%)	15,16,16	1.80	3 (20%)

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	ACP	F	401	-	-	0/4/17/38	0/3/3/3
11	YJ4	D	504	-	-	3/9/21/21	0/4/4/4
9	GDP	B	501	-	-	5/16/32/32	0/3/3/3
5	GTP	C	501	7	-	5/22/38/38	0/3/3/3
5	GTP	A	501	7	-	6/22/38/38	0/3/3/3
11	YJ4	B	506	-	-	3/9/21/21	0/4/4/4
5	GTP	D	501	7	-	3/22/38/38	0/3/3/3
10	MES	B	502	-	-	4/6/14/14	0/1/1/1
10	MES	B	503	-	-	0/6/14/14	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	B	502	MES	C8-S	-7.82	1.66	1.77
10	B	503	MES	C8-S	-7.72	1.66	1.77
12	F	401	ACP	C6-N6	4.43	1.45	1.34
12	F	401	ACP	O3'-C3'	-3.40	1.36	1.43
9	B	501	GDP	C5-C4	3.02	1.47	1.38

The worst 5 of 65 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	B	501	GDP	C5-C4-N3	-6.06	118.74	128.39
12	F	401	ACP	N3-C2-N1	-5.27	120.61	128.58
9	B	501	GDP	C2-N3-C4	5.08	121.05	112.30
5	A	501	GTP	C5-C4-N3	-5.07	120.32	128.39
5	A	501	GTP	C2-N3-C4	4.96	120.85	112.30

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

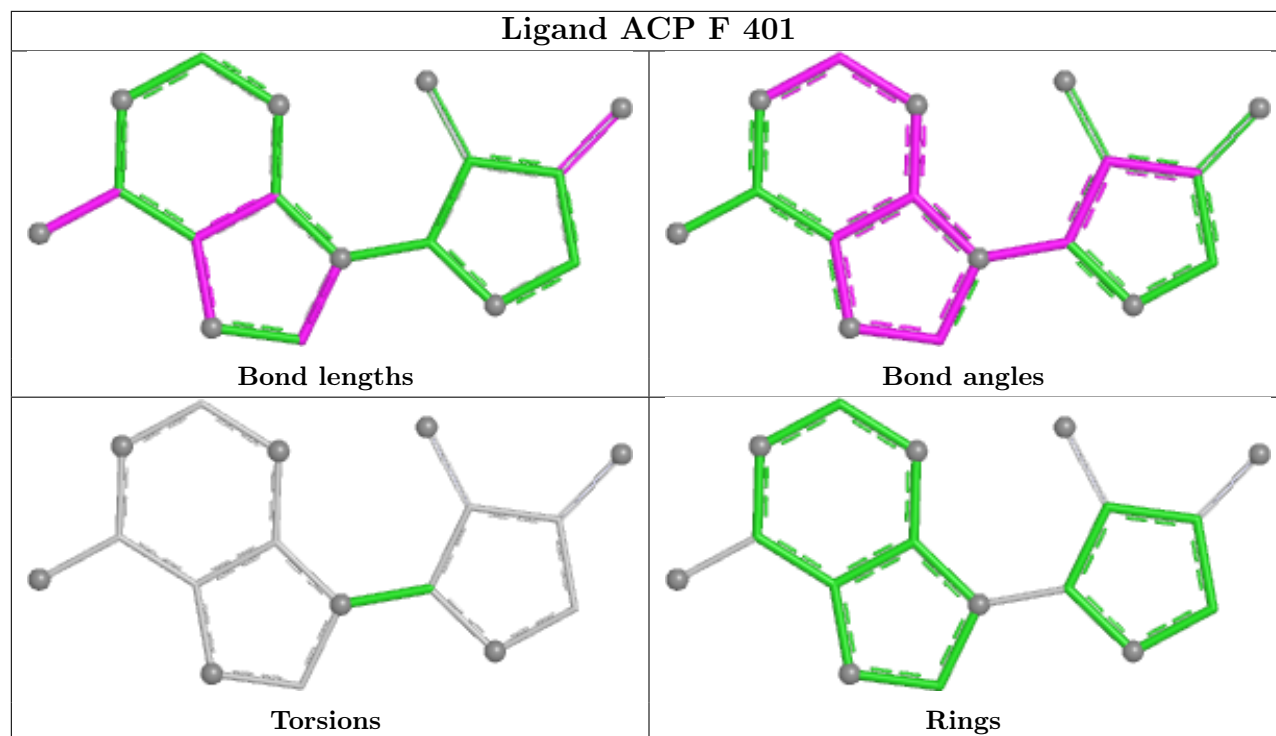
Mol	Chain	Res	Type	Atoms
5	A	501	GTP	PB-O3B-PG-O2G
5	A	501	GTP	C5'-O5'-PA-O3A
5	A	501	GTP	C5'-O5'-PA-O1A
5	A	501	GTP	C5'-O5'-PA-O2A
5	C	501	GTP	PB-O3B-PG-O3G

There are no ring outliers.

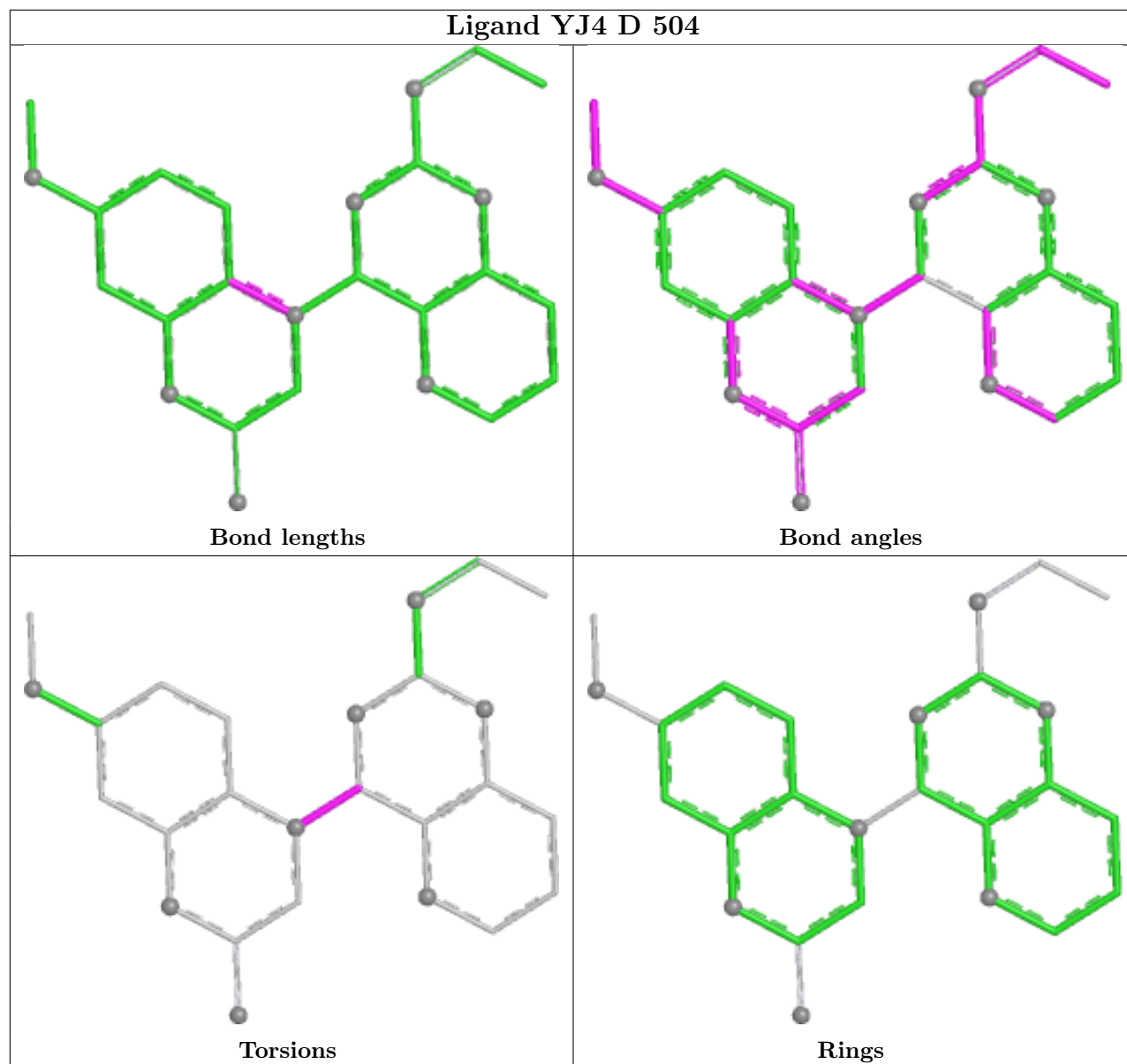
4 monomers are involved in 7 short contacts:

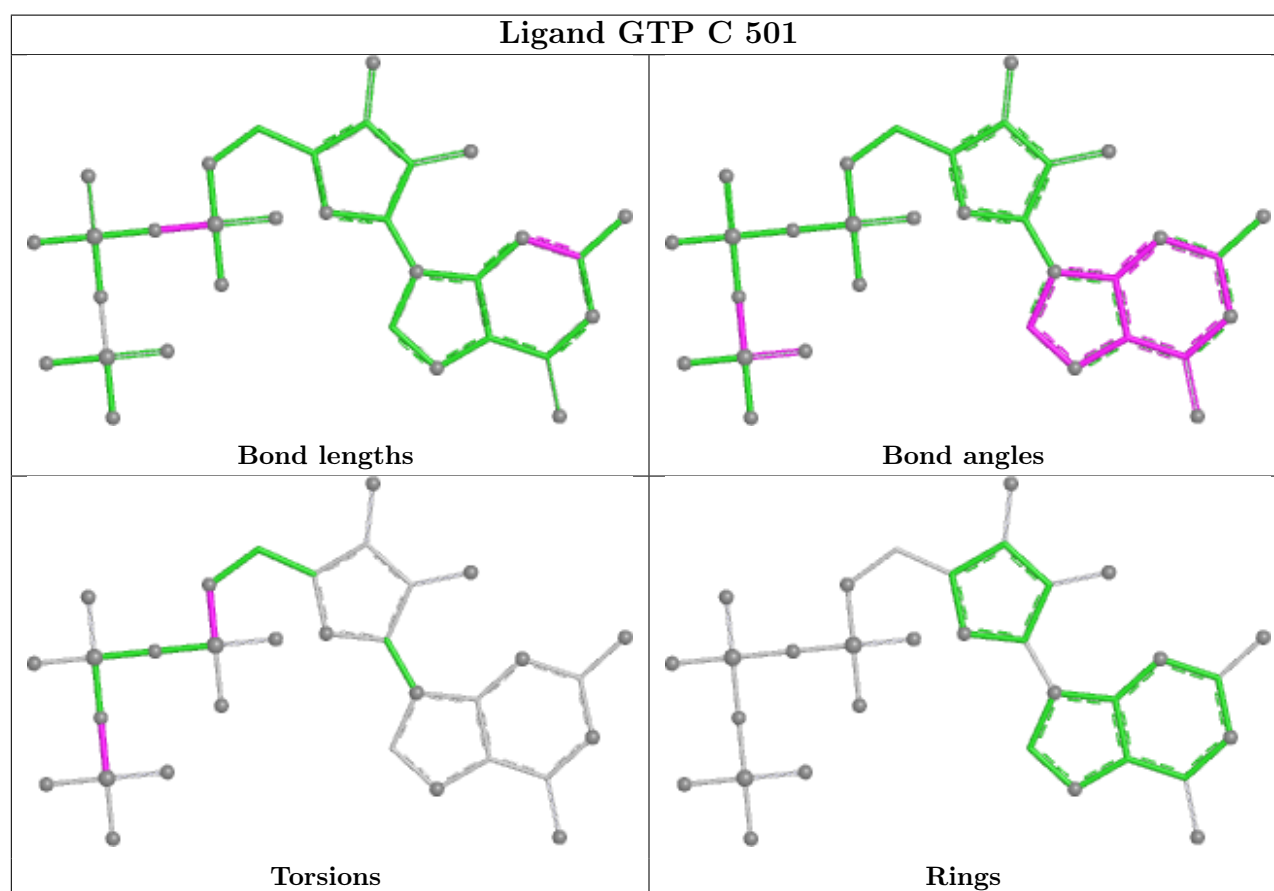
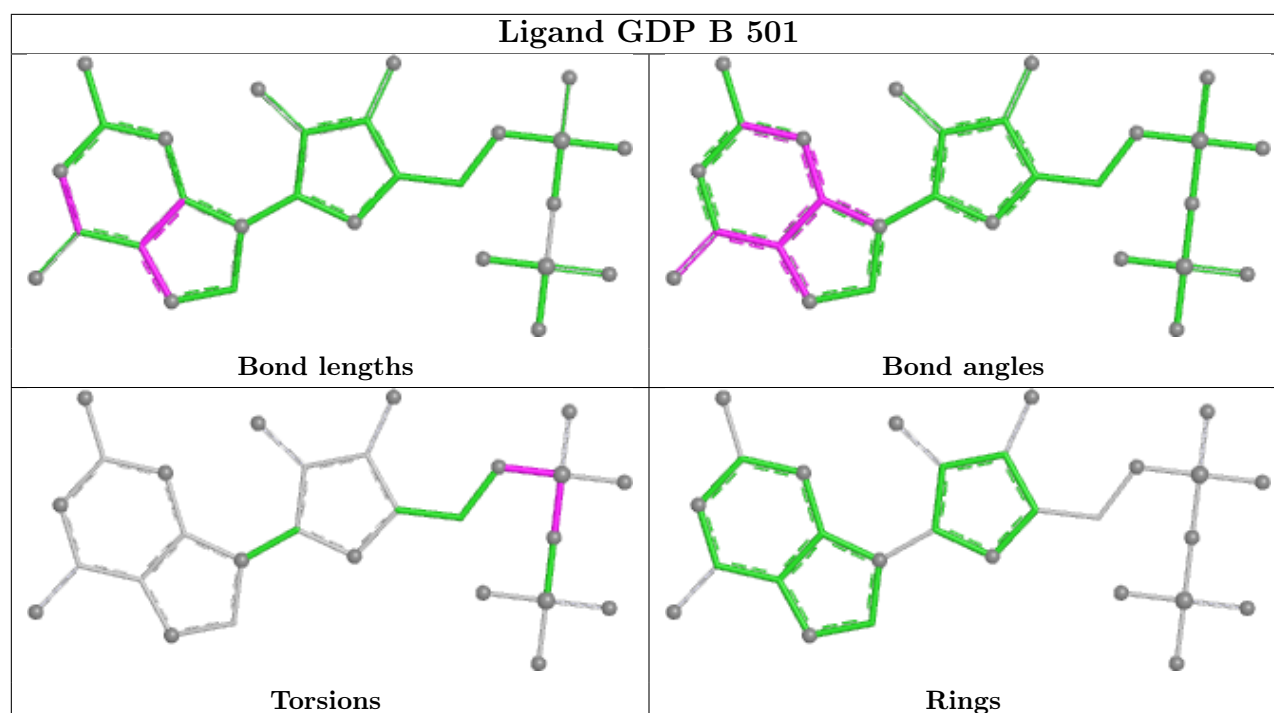
Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	F	401	ACP	4	0
11	D	504	YJ4	1	0
5	D	501	GTP	1	0
10	B	503	MES	1	0

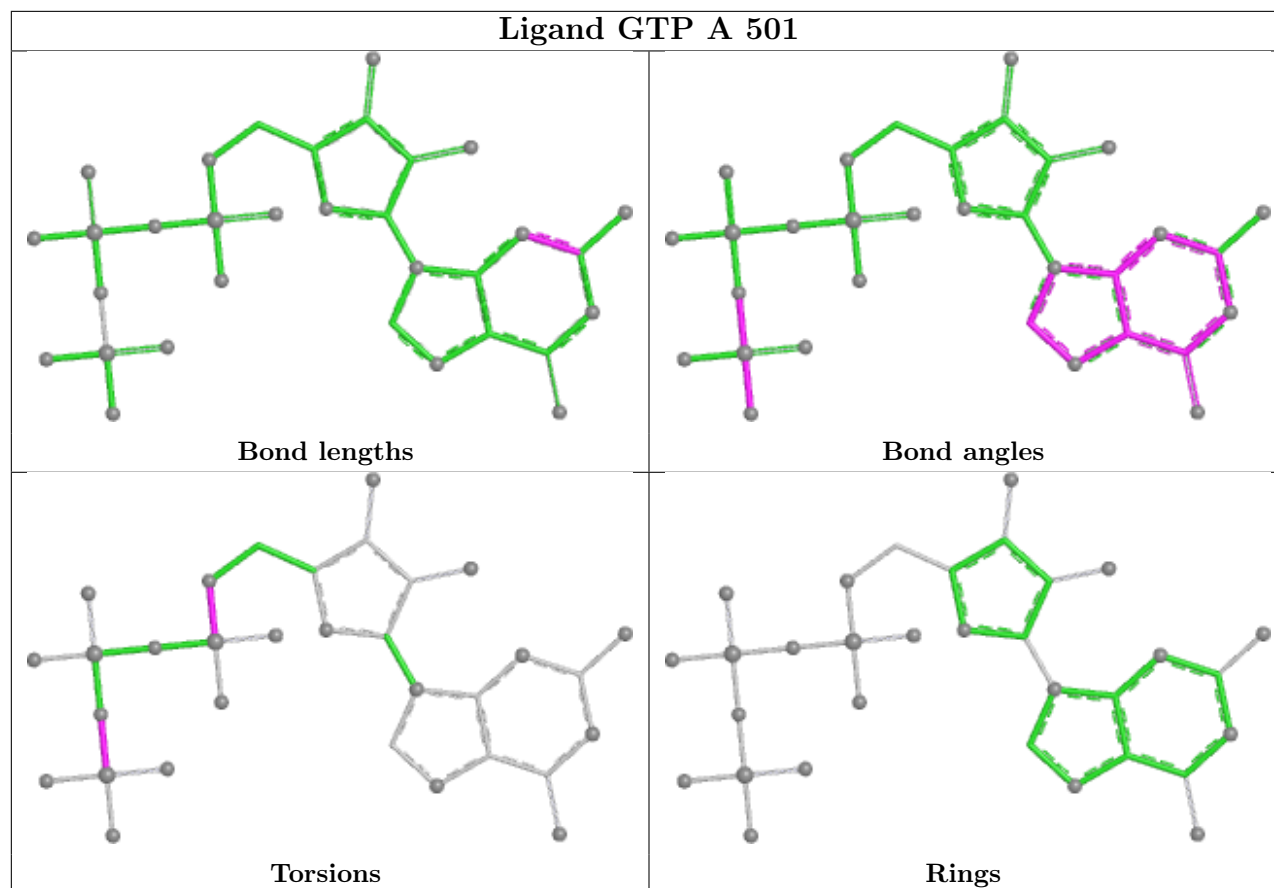
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



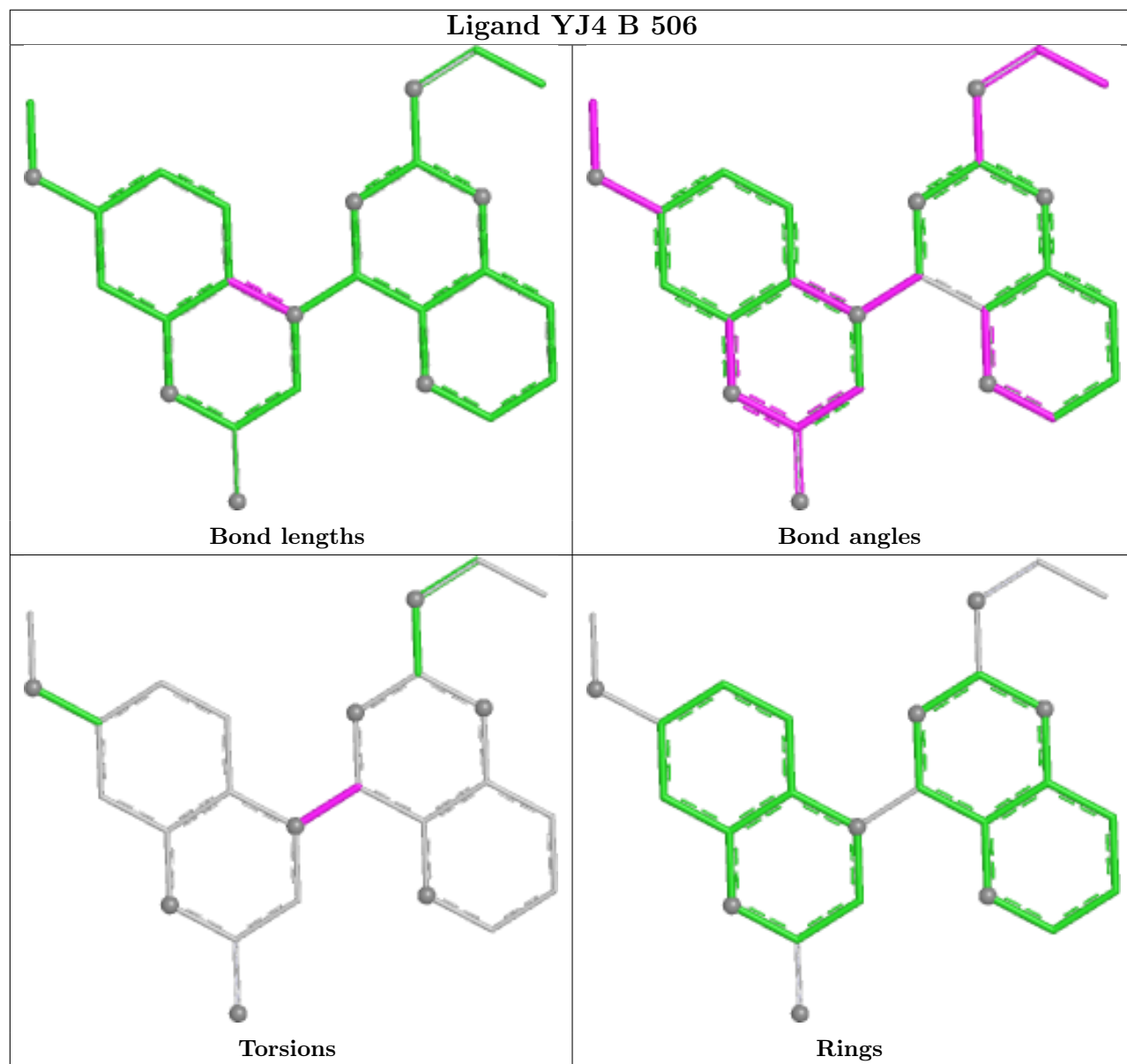
Ligand YJ4 D 504

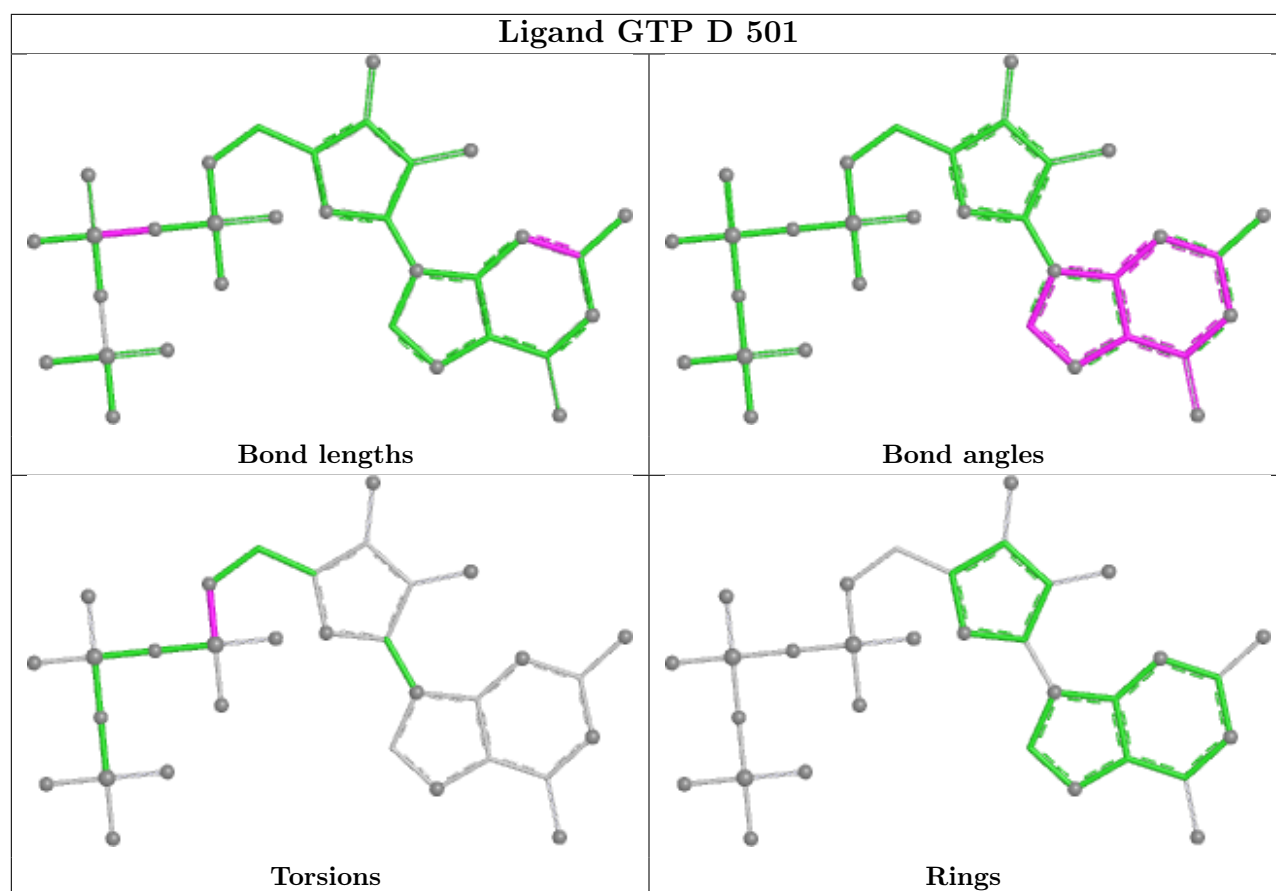






Ligand YJ4 B 506





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	437/450 (97%)	-0.17	4 (0%) 81 74	57, 81, 121, 164	0
1	C	438/450 (97%)	-0.25	0 100 100	50, 66, 99, 147	0
2	B	424/445 (95%)	-0.22	3 (0%) 84 79	48, 68, 111, 153	0
2	D	417/445 (93%)	-0.03	0 100 100	61, 95, 131, 156	0
3	E	121/143 (84%)	0.07	4 (3%) 49 39	57, 94, 136, 167	0
4	F	256/384 (66%)	0.05	2 (0%) 82 76	65, 103, 146, 177	0
All	All	2093/2317 (90%)	-0.13	13 (0%) 85 81	48, 82, 128, 177	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	281	TYR	3.5
4	F	181	VAL	2.8
1	A	1	MET	2.7
3	E	44	ASP	2.6
4	F	98	TYR	2.5

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 oligosaccharides in this entry.

6.4 Ligands ⓘ

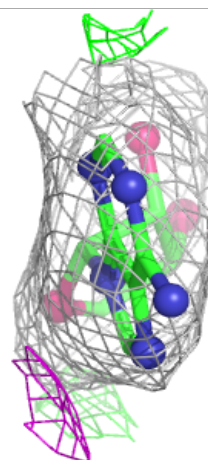
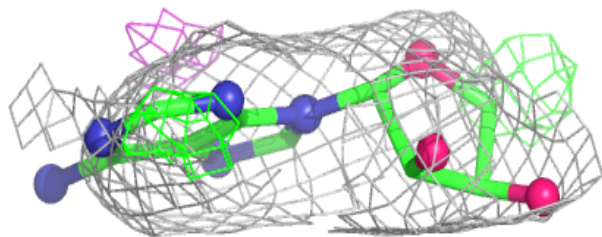
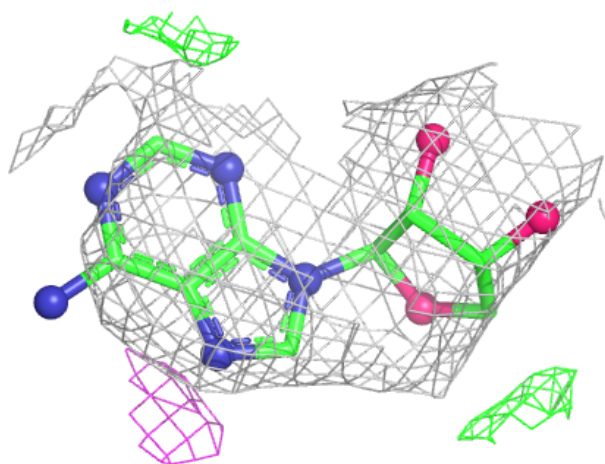
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
12	ACP	F	401	17/31	0.71	0.14	119,132,155,166	0
6	CA	C	504	1/1	0.76	0.23	124,124,124,124	0
6	CA	B	505	1/1	0.86	0.22	120,120,120,120	0
8	CL	A	504	1/1	0.88	0.15	102,102,102,102	0
7	MG	D	502	1/1	0.92	0.10	104,104,104,104	0
10	MES	B	503	12/12	0.94	0.11	89,103,134,147	0
8	CL	D	503	1/1	0.94	0.21	86,86,86,86	0
10	MES	B	502	12/12	0.95	0.09	61,73,90,103	0
7	MG	B	504	1/1	0.95	0.07	109,109,109,109	0
5	GTP	D	501	32/32	0.95	0.07	80,99,115,120	0
6	CA	A	502	1/1	0.96	0.06	133,133,133,133	0
7	MG	A	503	1/1	0.96	0.04	58,58,58,58	0
11	YJ4	D	504	26/26	0.96	0.08	58,69,89,93	0
9	GDP	B	501	28/28	0.96	0.06	47,56,64,81	0
11	YJ4	B	506	26/26	0.97	0.08	50,63,78,81	0
6	CA	C	502	1/1	0.97	0.05	97,97,97,97	0
5	GTP	C	501	32/32	0.97	0.06	54,58,77,82	0
5	GTP	A	501	32/32	0.98	0.05	56,60,75,83	0
7	MG	C	503	1/1	1.00	0.02	62,62,62,62	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.

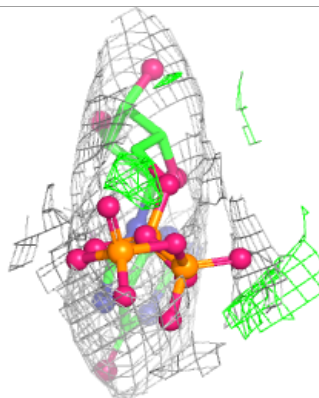
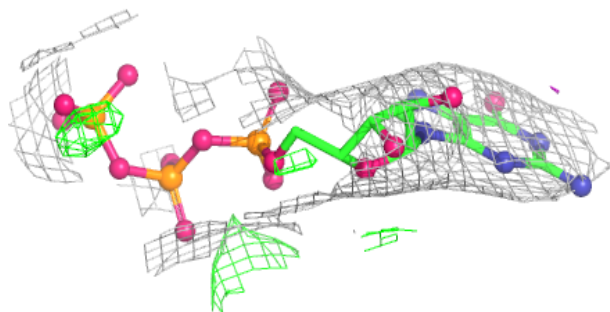
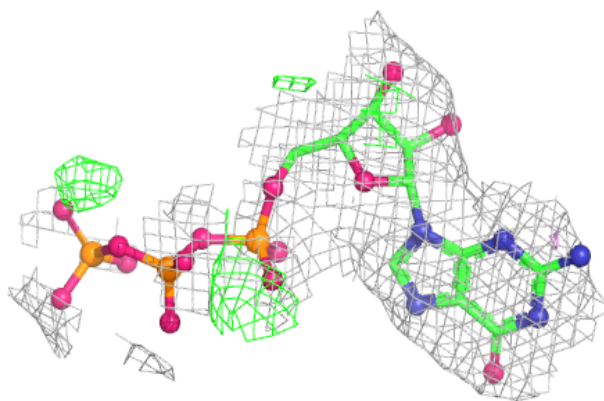
Electron density around ACP F 401:

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

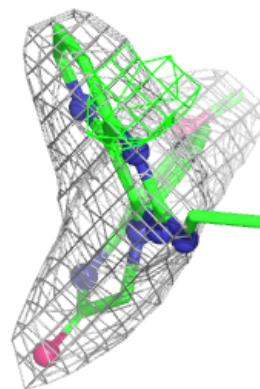
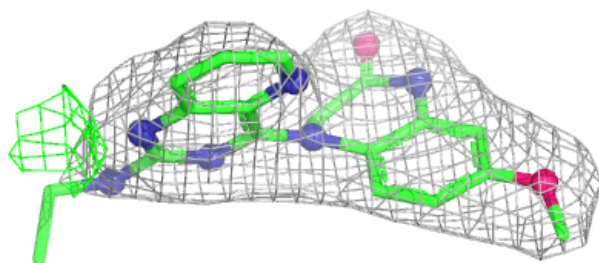
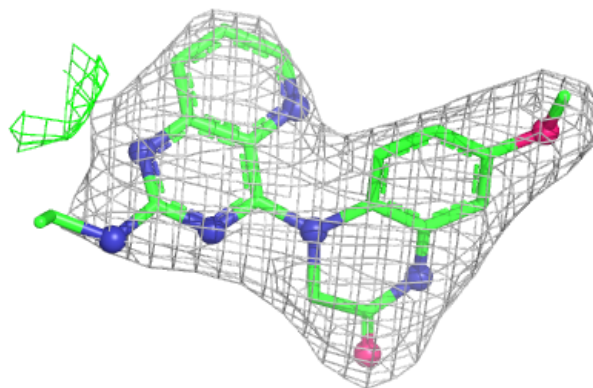


Electron density around GTP D 501:

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

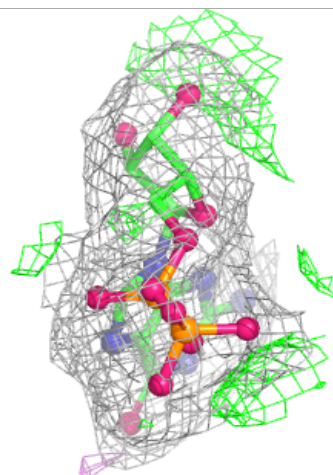
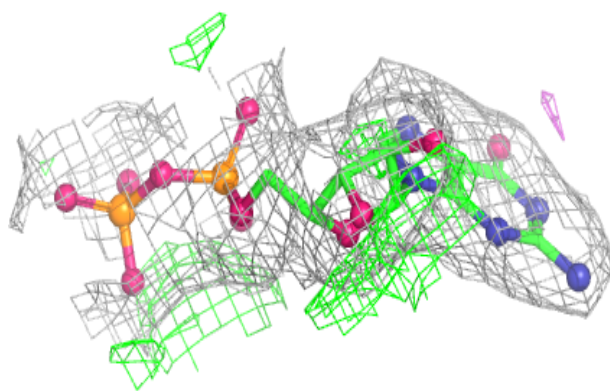
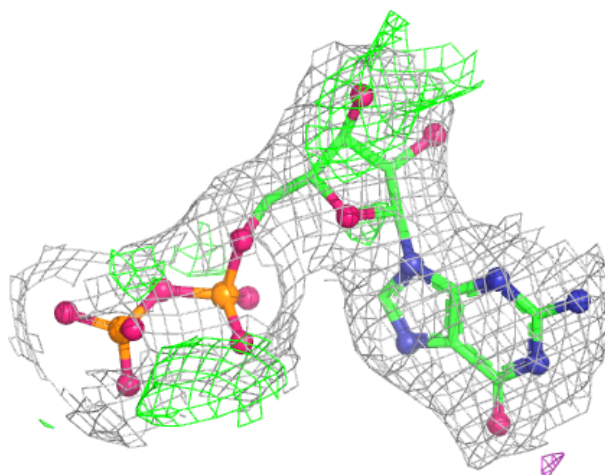
**Electron density around YJ4 D 504:**

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



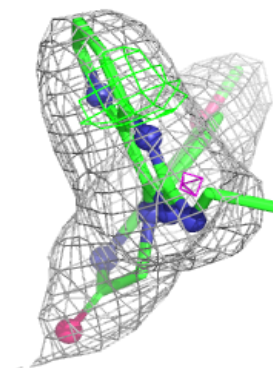
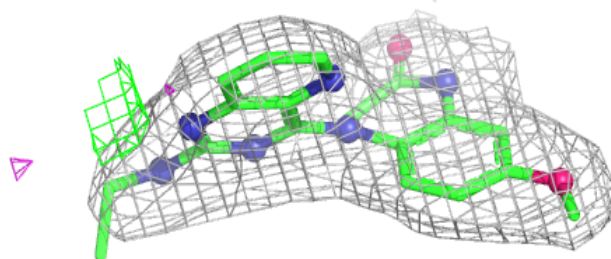
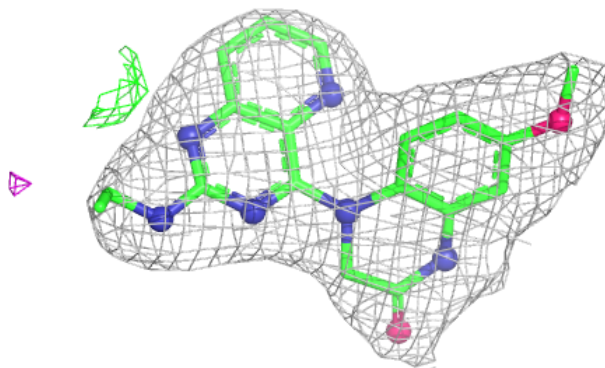
Electron density around GDP B 501:

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

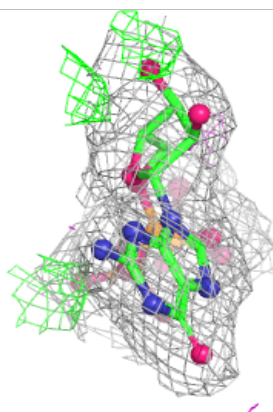
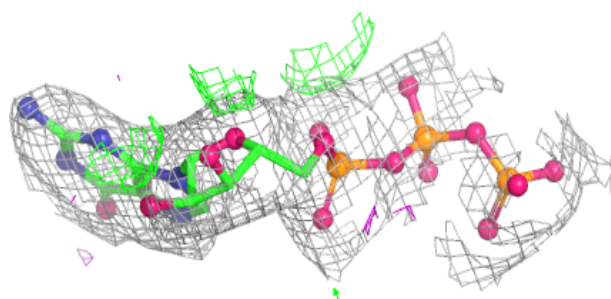
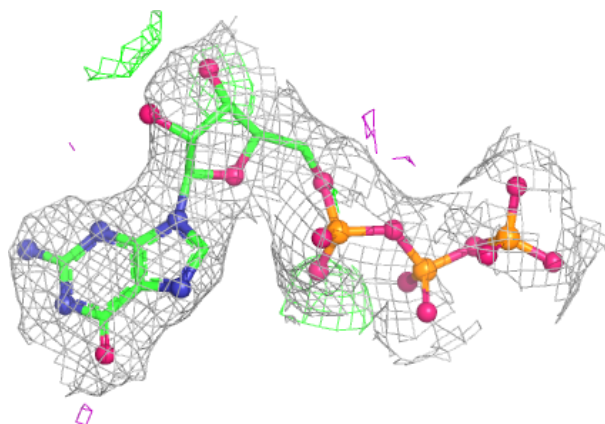


Electron density around YJ4 B 506:

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

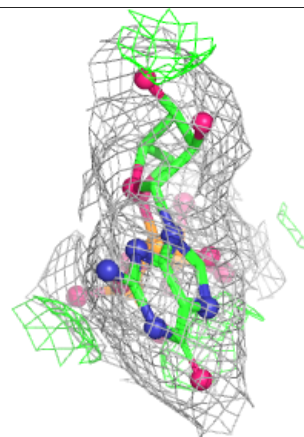
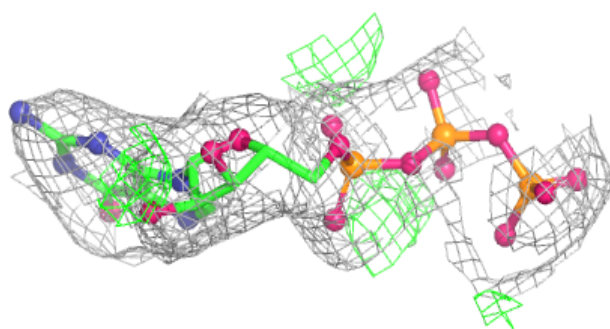
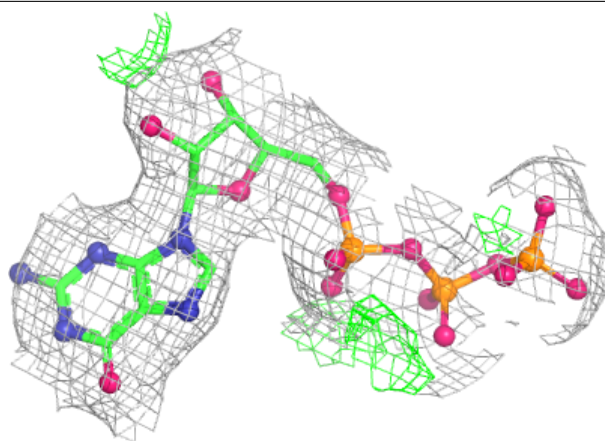
**Electron density around GTP C 501:**

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



Electron density around 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.