



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:49 PM UTC

PDB ID : 5XI7 / pdb_00005xi7
Title : Crystal structure of T2R-TTL bound with PO-7
Authors : Chu, Y.; Wang, Y.; Yang, J.; Li, W.
Deposited on : 2017-04-26
Resolution : 2.99 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 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:

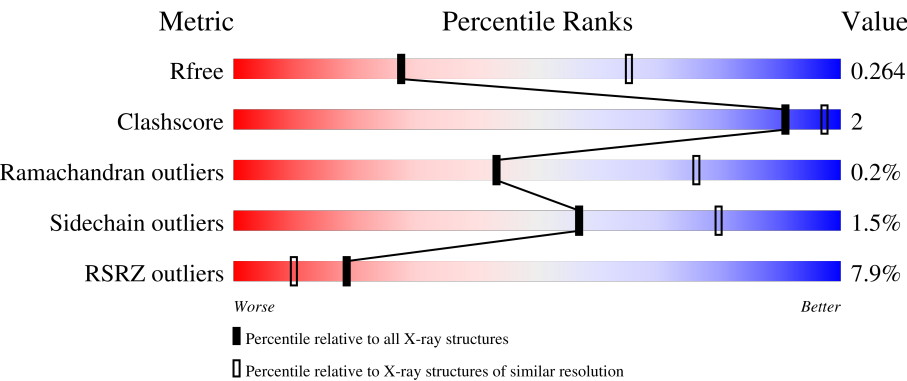
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal 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 i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.99 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	
1	C	450	
2	B	445	
2	D	445	
3	E	184	

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Mol	Chain	Length	Quality of chain
4	F	384	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: a red segment on the left labeled '16%', a green segment in the middle labeled '76%', and a yellow segment on the right labeled '20%'. The segments are separated by thin black lines.

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 17449 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Tubulin alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	437	Total	C	N	O	S	0	4	0
			3441	2179	586	652	24			
1	C	440	Total	C	N	O	S	0	9	0
			3482	2200	589	668	25			

- Molecule 2 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	424	Total	C	N	O	S	0	2	0
			3353	2107	574	645	27			
2	D	421	Total	C	N	O	S	0	1	0
			3306	2079	562	638	27			

- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	120	Total	C	N	O	S	0	2	0
			1004	621	181	196	6			

- Molecule 4 is a protein called Tubulin tyrosine ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	309	Total	C	N	O	S	0	3	0
			2553	1645	438	455	15			

There are 6 discrepancies between the modelled and reference sequences:

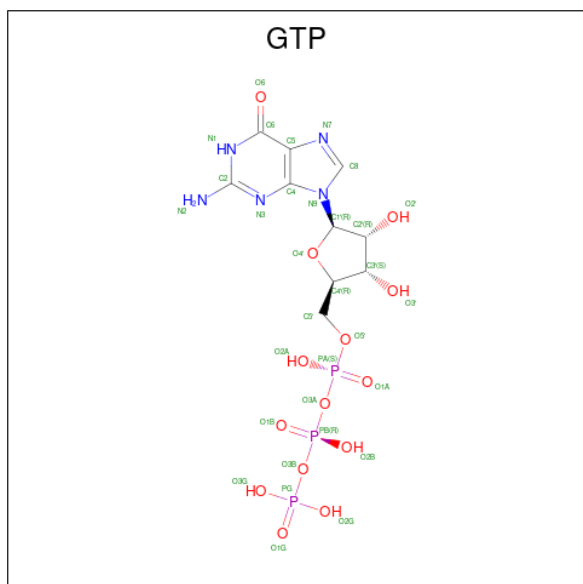
Chain	Residue	Modelled	Actual	Comment	Reference
F	379	HIS	-	expression tag	UNP E1BQ43
F	380	HIS	-	expression tag	UNP E1BQ43
F	381	HIS	-	expression tag	UNP E1BQ43
F	382	HIS	-	expression tag	UNP E1BQ43

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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 (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

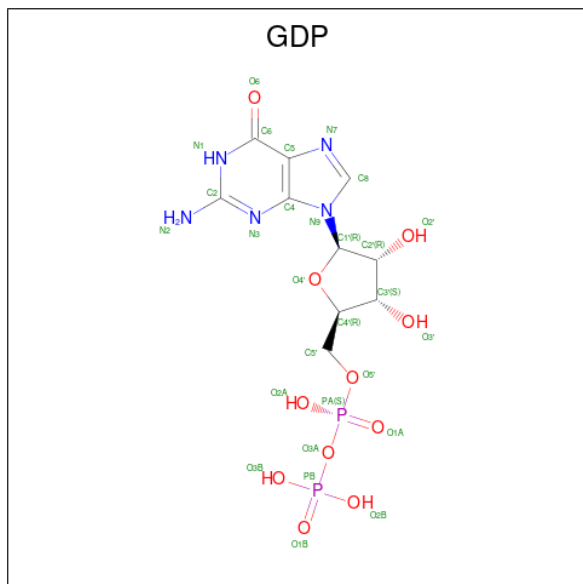
- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

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

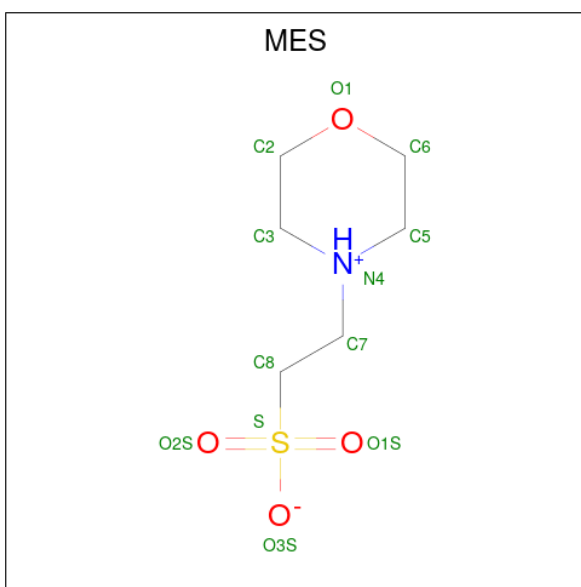
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Ca	0	0
			1	1		
7	B	1	Total	Ca	0	0
			1	1		
7	C	1	Total	Ca	0	0
			1	1		

- Molecule 8 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



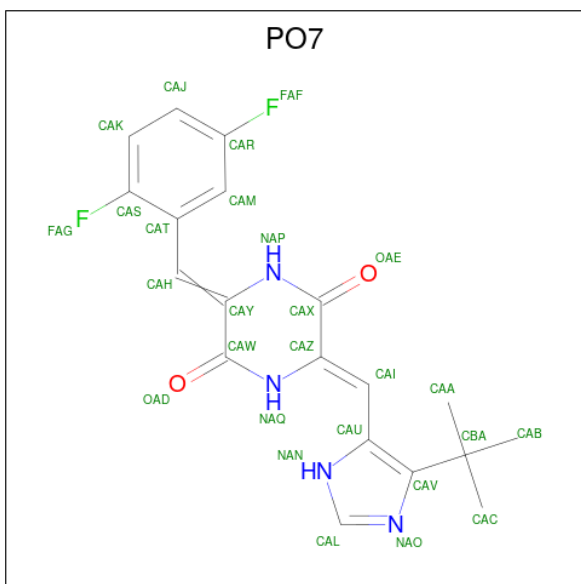
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	B	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

- Molecule 9 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



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

- Molecule 10 is (6Z)-3-[[2,5-bis(fluoranyl)phenyl]methylidene]-6-[(4-tert-butyl-1H-imidazol-5-yl)methylidene]piperazine-2,5-dione (CCD ID: PO7) (formula: C₁₉H₁₈F₂N₄O₂).



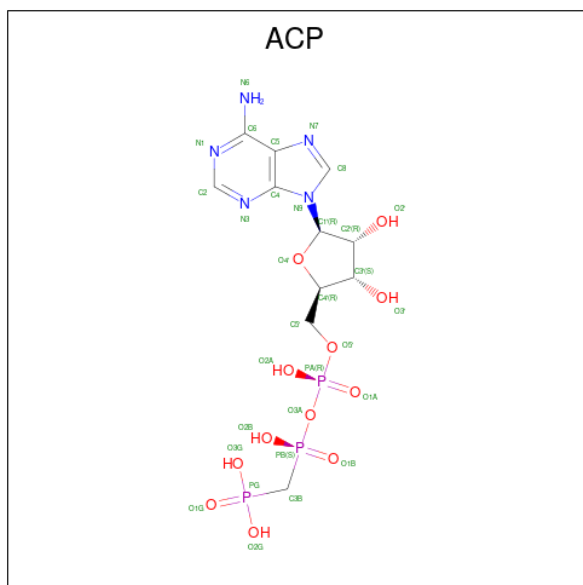
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	B	1	Total	C	F	N	O	0	0
			27	19	2	4	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	D	1	Total	C	F	N	O	0	0
			27	19	2	4	2		

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



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

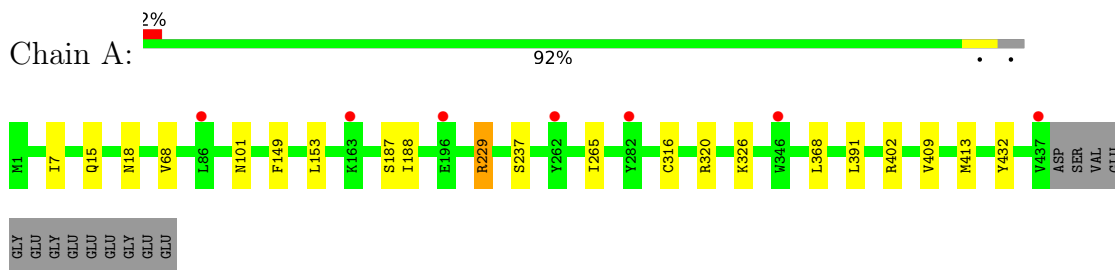
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	16	Total	O	0	0
			16	16		
12	B	15	Total	O	0	0
			15	15		
12	C	33	Total	O	0	0
			33	33		
12	E	2	Total	O	0	0
			2	2		
12	F	4	Total	O	0	0
			4	4		

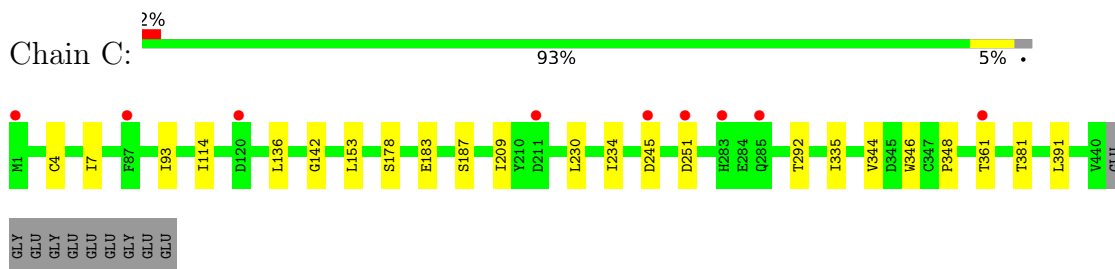
3 Residue-property plots [i](#)

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

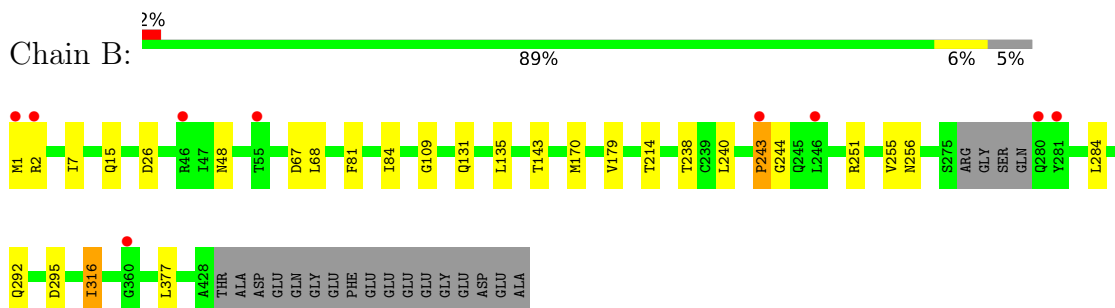
- Molecule 1: Tubulin alpha chain



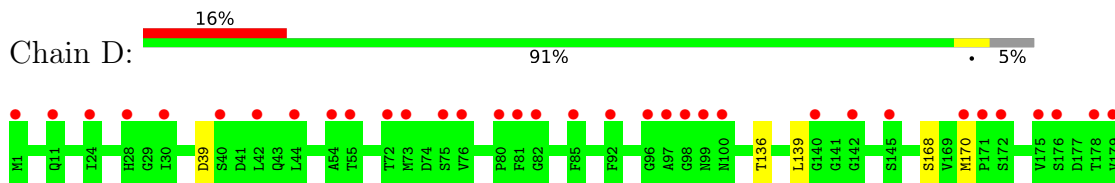
- Molecule 1: Tubulin alpha chain

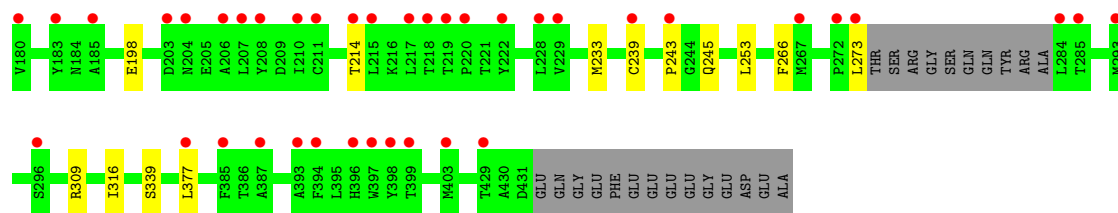


- Molecule 2: Tubulin beta chain

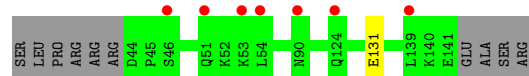
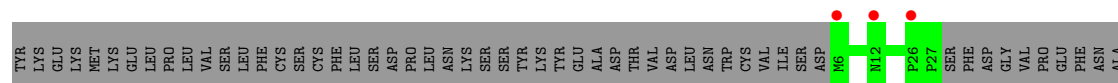


- Molecule 2: Tubulin beta chain

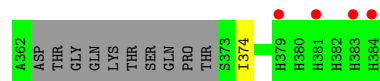
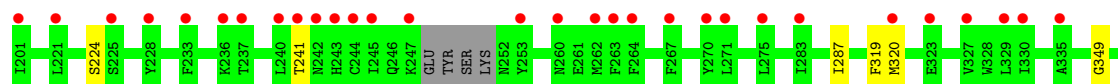
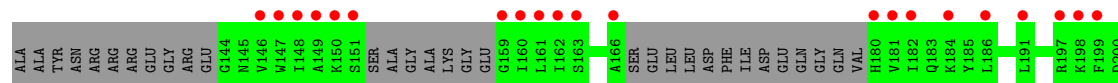
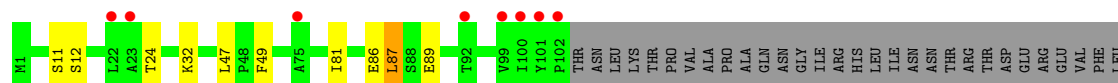
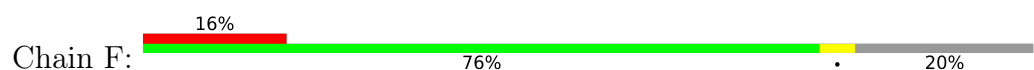




● Molecule 3: Stathmin-4



● 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	105.25Å 157.38Å 182.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	119.17 – 2.99 119.17 – 2.99	Depositor EDS
% Data completeness (in resolution range)	97.3 (119.17-2.99) 97.3 (119.17-2.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.222 , 0.266 0.221 , 0.264	Depositor DCC
R_{free} test set	3119 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	53.7	Xtriage
Anisotropy	0.017	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 27.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	17449	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 2.82% 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: CA, MES, GDP, ACP, GTP, MG, PO7

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	0.57	0/3525	0.83	0/4784
1	C	0.55	0/3572	0.81	0/4850
2	B	0.56	0/3427	0.81	0/4640
2	D	0.59	0/3379	0.84	0/4577
3	E	0.59	0/1018	0.82	0/1350
4	F	0.58	0/2618	0.74	0/3537
All	All	0.57	0/17539	0.81	0/23738

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 [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	3441	0	3363	15	0
1	C	3482	0	3384	11	0
2	B	3353	0	3228	17	0
2	D	3306	0	3181	9	0
3	E	1004	0	1028	0	0
4	F	2553	0	2519	6	0
5	A	32	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	32	0	12	0	0
5	D	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
7	A	1	0	0	0	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
8	B	28	0	12	0	0
9	B	24	0	26	2	0
10	B	27	0	0	1	0
10	D	27	0	0	2	0
11	F	31	0	14	1	0
12	A	16	0	0	0	0
12	B	15	0	0	0	0
12	C	33	0	0	0	0
12	E	2	0	0	0	0
12	F	4	0	0	0	0
All	All	17449	0	16791	57	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.

All (57) 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:A:229[A]:ARG:HG2	1:A:229[A]:ARG:HH11	1.09	1.08
1:A:229[A]:ARG:HH11	1:A:229[A]:ARG:CG	1.67	1.07
1:A:229[A]:ARG:HG2	1:A:229[A]:ARG:NH1	1.85	0.81
1:C:178:SER:OG	1:C:183:GLU:OE2	2.02	0.75
2:B:243:PRO:CB	2:B:244:GLY:HA2	2.19	0.73
2:B:295:ASP:HA	9:B:505:MES:O2S	1.95	0.66
2:B:243:PRO:HB2	2:B:244:GLY:HA2	1.80	0.63
1:A:368[B]:LEU:HD12	1:A:368[B]:LEU:N	2.15	0.61
1:A:229[A]:ARG:CG	1:A:229[A]:ARG:NH1	2.40	0.61
1:A:368[B]:LEU:HD12	1:A:368[B]:LEU:H	1.66	0.59
1:A:101:ASN:HD22	2:B:256:ASN:HD21	1.52	0.56
1:A:187:SER:HB3	1:A:391:LEU:HD21	1.87	0.55
1:C:187:SER:HB3	1:C:391:LEU:HD21	1.88	0.54
2:B:251:ARG:NH1	9:B:503:MES:O2S	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:238:THR:HB	2:B:316:ILE:HD11	1.90	0.52
1:A:68:VAL:HG11	1:A:149:PHE:CE2	2.45	0.51
1:A:187:SER:CB	1:A:391:LEU:HD21	2.41	0.50
2:B:179:VAL:HG12	1:C:348:PRO:HG2	1.94	0.48
4:F:224:SER:HB2	4:F:241:THR:HG22	1.94	0.48
4:F:349:GLY:HA3	4:F:374:ILE:HD11	1.94	0.48
2:D:170:MET:HE2	2:D:377:LEU:HD21	1.96	0.47
2:D:309:ARG:NH1	2:D:339:SER:O	2.48	0.46
4:F:81:ILE:O	4:F:87:LEU:O	2.33	0.46
2:B:7:ILE:HB	2:B:135:LEU:HD12	1.98	0.45
2:D:139:LEU:HD12	2:D:170:MET:SD	2.57	0.45
1:C:142:GLY:HA3	1:C:183:GLU:OE1	2.17	0.45
1:A:265:ILE:HG23	1:A:432:TYR:CE2	2.52	0.44
2:B:251:ARG:O	2:B:255:VAL:HG23	2.17	0.44
2:D:136:THR:CG2	2:D:233:MET:HE1	2.47	0.44
2:B:284:LEU:HD21	2:B:292:GLN:HE22	1.83	0.44
1:C:292:THR:HG22	1:C:335:ILE:CD1	2.48	0.44
10:D:503:PO7:NAN	10:D:503:PO7:NAQ	2.66	0.43
4:F:320:MET:HE2	11:F:401:ACP:C2	2.48	0.43
1:A:229[A]:ARG:HH11	1:A:229[A]:ARG:HG3	1.70	0.43
1:C:4[A]:CYS:SG	1:C:136:LEU:HG	2.59	0.43
2:D:139:LEU:HD11	2:D:168:SER:HB3	2.00	0.43
2:B:68:LEU:HD21	2:B:109:GLY:HA2	2.01	0.42
2:B:240:LEU:HD12	10:B:506:PO7:FAF	2.10	0.42
1:A:15:GLN:HA	1:A:18:ASN:HD22	1.84	0.42
4:F:47:LEU:HD22	4:F:49:PHE:CE1	2.54	0.42
2:B:67:ASP:HA	2:B:143:THR:HG21	2.01	0.42
2:B:170:MET:HG3	2:B:377:LEU:HD21	2.02	0.42
1:C:230:LEU:O	1:C:234:ILE:HD12	2.19	0.42
1:C:344:VAL:HG21	1:C:346:TRP:CE2	2.54	0.42
2:B:243:PRO:HB3	2:B:244:GLY:HA2	1.99	0.42
2:D:136:THR:HG21	2:D:233:MET:HE1	2.02	0.42
2:B:1:MET:HE3	2:B:131:GLN:HB2	2.02	0.41
1:C:7:ILE:HG21	1:C:153:LEU:HD21	2.03	0.41
2:D:239:CYS:SG	10:D:503:PO7:OAE	2.77	0.41
4:F:287:ILE:HG23	4:F:319:PHE:CE2	2.56	0.41
2:D:214:THR:HG21	2:D:273:LEU:HD12	2.03	0.41
1:A:409:VAL:HA	1:A:413:MET:O	2.20	0.40
1:C:209:ILE:HG23	1:C:230:LEU:HD23	2.03	0.40
2:D:198:GLU:HB2	2:D:266:PHE:CE2	2.56	0.40
2:B:81:PHE:O	2:B:84:ILE:HG22	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:ILE:HG21	1:A:153:LEU:HD21	2.03	0.40
1:C:93:ILE:HG22	1:C:114:ILE:HD11	2.04	0.40

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	439/450 (98%)	427 (97%)	12 (3%)	0	100	100
1	C	446/450 (99%)	437 (98%)	9 (2%)	0	100	100
2	B	422/445 (95%)	404 (96%)	17 (4%)	1 (0%)	43	76
2	D	417/445 (94%)	396 (95%)	19 (5%)	2 (0%)	24	60
3	E	118/184 (64%)	114 (97%)	4 (3%)	0	100	100
4	F	300/384 (78%)	286 (95%)	13 (4%)	1 (0%)	36	70
All	All	2142/2358 (91%)	2064 (96%)	74 (4%)	4 (0%)	43	76

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	243	PRO
2	D	243	PRO
4	F	11	SER
2	D	39	ASP

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	372/378 (98%)	363 (98%)	9 (2%)	43	73
1	C	379/378 (100%)	374 (99%)	5 (1%)	61	81
2	B	367/383 (96%)	361 (98%)	6 (2%)	55	79
2	D	362/383 (94%)	359 (99%)	3 (1%)	73	86
3	E	110/168 (66%)	109 (99%)	1 (1%)	70	85
4	F	281/342 (82%)	275 (98%)	6 (2%)	47	75
All	All	1871/2032 (92%)	1841 (98%)	30 (2%)	57	79

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	188	ILE
1	A	229[A]	ARG
1	A	229[B]	ARG
1	A	237	SER
1	A	316[A]	CYS
1	A	316[B]	CYS
1	A	320	ARG
1	A	326	LYS
1	A	402	ARG
2	B	2	ARG
2	B	15	GLN
2	B	26	ASP
2	B	48	ASN
2	B	214	THR
2	B	316	ILE
1	C	245	ASP
1	C	251[A]	ASP
1	C	251[B]	ASP
1	C	361	THR
1	C	381	THR
2	D	245	GLN
2	D	253	LEU
2	D	316	ILE
3	E	131	GLU
4	F	12	SER
4	F	24	THR
4	F	32	LYS

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Mol	Chain	Res	Type
4	F	86	GLU
4	F	87	LEU
4	F	89	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	GLN
1	A	35	GLN
1	A	61	HIS
1	A	233	GLN
1	A	258	ASN
1	A	309	HIS
1	A	393	HIS
2	B	11	GLN
2	B	37	HIS
2	B	83	GLN
2	B	256	ASN
2	B	292	GLN
2	B	375	GLN
1	C	11	GLN
1	C	133	GLN
1	C	249	ASN
1	C	283	HIS
1	C	356	ASN
1	C	358	GLN
1	C	393	HIS
2	D	15	GLN
2	D	99	ASN
3	E	18	GLN
3	E	90	ASN
3	E	115	HIS
3	E	124	GLN
3	E	136	ASN
4	F	242	ASN
4	F	333	ASN
4	F	382	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 7 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$
9	MES	B	505	-	12,12,12	2.10	2 (16%)	15,16,16	5.53	8 (53%)
8	GDP	B	501	6	29,30,30	1.22	3 (10%)	45,47,47	1.67	5 (11%)
11	ACP	F	401	-	31,33,33	2.20	11 (35%)	47,52,52	1.84	11 (23%)
5	GTP	C	501	6	33,34,34	1.28	4 (12%)	50,54,54	1.53	6 (12%)
5	GTP	A	501	6	33,34,34	1.33	5 (15%)	50,54,54	1.56	6 (12%)
5	GTP	D	501	6	33,34,34	1.22	3 (9%)	50,54,54	1.66	7 (14%)
9	MES	B	503	-	12,12,12	2.03	1 (8%)	15,16,16	6.11	9 (60%)
10	PO7	D	503	-	29,29,29	2.20	8 (27%)	39,43,43	2.00	11 (28%)
10	PO7	B	506	-	29,29,29	2.06	8 (27%)	39,43,43	1.96	11 (28%)

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	MES	B	505	-	-	2/6/14/14	0/1/1/1
8	GDP	B	501	6	-	3/16/32/32	0/3/3/3
11	ACP	F	401	-	-	6/19/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GTP	C	501	6	-	6/22/38/38	0/3/3/3
5	GTP	A	501	6	-	3/22/38/38	0/3/3/3
5	GTP	D	501	6	-	6/22/38/38	0/3/3/3
9	MES	B	503	-	-	3/6/14/14	0/1/1/1
10	PO7	D	503	-	-	2/14/14/14	0/3/3/3
10	PO7	B	506	-	-	4/14/14/14	0/3/3/3

All (45) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	503	MES	C8-S	-6.42	1.68	1.77
9	B	505	MES	C8-S	-6.42	1.68	1.77
10	D	503	PO7	FAF-CAR	-6.35	1.21	1.36
11	F	401	ACP	PG-O1G	5.63	1.61	1.50
11	F	401	ACP	C5-C4	4.86	1.47	1.39
10	B	506	PO7	CAY-CAW	-4.20	1.40	1.48
10	D	503	PO7	CAY-CAW	-4.17	1.40	1.48
11	F	401	ACP	PB-O1B	4.12	1.61	1.51
10	B	506	PO7	CAZ-CAX	-3.95	1.40	1.48
10	B	506	PO7	CAT-CAH	-3.71	1.40	1.46
10	D	503	PO7	CAH-CAY	3.66	1.42	1.34
5	A	501	GTP	PB-O3B	3.63	1.63	1.59
10	D	503	PO7	CAZ-CAX	-3.54	1.41	1.48
10	B	506	PO7	FAF-CAR	-3.47	1.28	1.36
11	F	401	ACP	PB-O3A	3.46	1.62	1.58
5	D	501	GTP	C5-C4	3.43	1.48	1.38
5	C	501	GTP	C5-C4	3.40	1.48	1.38
10	B	506	PO7	CAU-NAN	-3.35	1.33	1.37
10	B	506	PO7	CAH-CAY	3.34	1.41	1.34
5	A	501	GTP	C5-C4	3.28	1.47	1.38
8	B	501	GDP	C5-C4	3.21	1.47	1.38
10	D	503	PO7	CAU-NAN	-3.16	1.33	1.37
11	F	401	ACP	PB-O2B	-3.12	1.48	1.56
10	D	503	PO7	CAT-CAH	-3.07	1.41	1.46
10	B	506	PO7	CAU-CAV	-3.03	1.35	1.38
5	C	501	GTP	PB-O3B	3.00	1.62	1.59
11	F	401	ACP	PG-O2G	2.99	1.61	1.55
11	F	401	ACP	PG-O3G	-2.89	1.48	1.55
11	F	401	ACP	C5-C6	2.86	1.49	1.41
11	F	401	ACP	PA-O3A	2.69	1.62	1.59
5	C	501	GTP	C5-N7	-2.51	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	501	GTP	PB-O3B	2.48	1.62	1.59
11	F	401	ACP	C8-N7	2.43	1.36	1.31
5	A	501	GTP	C6-N1	-2.41	1.34	1.38
10	D	503	PO7	CAU-CAV	-2.33	1.35	1.38
11	F	401	ACP	C5-N7	-2.29	1.34	1.39
5	C	501	GTP	C6-N1	-2.26	1.34	1.38
9	B	505	MES	O2S-S	2.26	1.51	1.45
5	A	501	GTP	C5-N7	-2.21	1.34	1.39
10	B	506	PO7	CAI-CAU	-2.20	1.35	1.40
8	B	501	GDP	C6-N1	-2.20	1.34	1.38
8	B	501	GDP	PA-O3A	2.20	1.61	1.59
5	A	501	GTP	C4-N9	-2.16	1.32	1.38
10	D	503	PO7	CAV-NAO	-2.16	1.33	1.37
5	D	501	GTP	C5-N7	-2.06	1.34	1.39

All (74) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	B	503	MES	O1S-S-C8	-13.79	85.89	106.73
9	B	505	MES	O3S-S-O1S	-13.51	77.59	111.40
9	B	503	MES	O3S-S-O1S	-10.71	84.60	111.40
9	B	503	MES	O2S-S-O1S	-9.85	81.79	113.82
9	B	503	MES	O2S-S-C8	9.25	120.71	106.73
9	B	505	MES	O3S-S-C8	9.01	123.64	106.00
9	B	505	MES	O2S-S-O1S	-8.88	84.94	113.82
9	B	505	MES	O1S-S-C8	-7.40	95.54	106.73
9	B	505	MES	O3S-S-O2S	5.95	126.28	111.40
9	B	503	MES	O3S-S-C8	5.76	117.28	106.00
11	F	401	ACP	C5-C4-N3	-5.64	118.95	126.72
5	D	501	GTP	C5-C4-N3	-5.56	119.55	128.39
5	C	501	GTP	C5-C4-N3	-5.55	119.56	128.39
8	B	501	GDP	C5-C4-N3	-5.45	119.72	128.39
5	A	501	GTP	C5-C4-N3	-5.25	120.04	128.39
10	D	503	PO7	CAZ-CAX-NAP	5.13	121.06	116.02
8	B	501	GDP	C2-N3-C4	4.83	120.62	112.30
5	D	501	GTP	C2-N3-C4	4.66	120.32	112.30
10	D	503	PO7	CAY-CAW-NAQ	4.58	120.52	116.02
11	F	401	ACP	N3-C4-N9	4.44	134.72	127.17
10	B	506	PO7	CAZ-CAX-NAP	4.32	120.27	116.02
5	A	501	GTP	N9-C4-N3	4.22	134.39	125.95
5	D	501	GTP	N9-C4-N3	4.21	134.38	125.95
5	C	501	GTP	C2-N3-C4	4.21	119.55	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	501	GTP	N9-C4-N3	4.20	134.36	125.95
8	B	501	GDP	N9-C4-N3	4.19	134.34	125.95
10	B	506	PO7	CAY-CAW-NAQ	4.11	120.06	116.02
10	B	506	PO7	CBA-CAV-NAO	4.10	123.95	117.42
5	A	501	GTP	C2-N3-C4	4.09	119.35	112.30
10	B	506	PO7	NAN-CAL-NAO	-4.03	108.30	112.98
11	F	401	ACP	C2-N3-C4	3.93	121.42	111.83
11	F	401	ACP	N3-C2-N1	-3.88	122.71	128.58
9	B	503	MES	C2-C3-N4	3.86	115.98	110.12
10	D	503	PO7	NAN-CAL-NAO	-3.76	108.62	112.98
8	B	501	GDP	C6-C5-N7	3.68	136.99	130.29
10	B	506	PO7	FAG-CAS-CAT	3.66	122.97	118.11
11	F	401	ACP	C4-C5-N7	-3.59	106.48	110.58
5	D	501	GTP	C6-C5-N7	3.42	136.52	130.29
10	D	503	PO7	CBA-CAV-NAO	3.30	122.66	117.42
10	D	503	PO7	FAG-CAS-CAT	3.23	122.41	118.11
5	A	501	GTP	C6-C5-N7	3.15	136.02	130.29
10	D	503	PO7	CAY-NAP-CAX	-3.07	122.03	125.51
9	B	503	MES	O3S-S-O2S	2.98	118.86	111.40
10	B	506	PO7	CAU-CAI-CAZ	-2.89	122.49	130.82
10	D	503	PO7	CAU-CAI-CAZ	-2.85	122.62	130.82
11	F	401	ACP	C5-N7-C8	2.74	107.76	103.45
11	F	401	ACP	C4-N9-C8	2.74	108.62	105.74
10	D	503	PO7	CAL-NAO-CAV	2.65	107.95	104.97
10	B	506	PO7	CAY-NAP-CAX	-2.62	122.53	125.51
5	C	501	GTP	C6-C5-N7	2.57	134.97	130.29
10	B	506	PO7	CAL-NAO-CAV	2.54	107.83	104.97
9	B	503	MES	C6-C5-N4	2.51	113.93	110.12
9	B	505	MES	C6-C5-N4	2.45	113.85	110.12
8	B	501	GDP	C4-C5-N7	-2.44	106.81	110.67
10	D	503	PO7	CAZ-NAQ-CAW	-2.42	122.76	125.51
5	D	501	GTP	C4-C5-N7	-2.42	106.84	110.67
10	B	506	PO7	CAZ-NAQ-CAW	-2.39	122.80	125.51
11	F	401	ACP	C3'-C2'-C1'	2.37	105.94	101.46
5	A	501	GTP	C4-C5-N7	-2.35	106.94	110.67
11	F	401	ACP	C6-C5-N7	2.33	136.57	132.09
9	B	503	MES	C5-N4-C3	2.25	113.69	108.84
5	D	501	GTP	O6-C6-C5	-2.25	120.59	126.53
5	C	501	GTP	O6-C6-C5	-2.21	120.71	126.53
11	F	401	ACP	N9-C8-N7	-2.20	110.81	113.94
10	B	506	PO7	CBA-CAV-CAU	-2.18	128.20	131.26
5	C	501	GTP	C4-C5-N7	-2.09	107.36	110.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	F	401	ACP	C2-N1-C6	2.07	122.13	118.73
10	D	503	PO7	OAE-CAX-NAP	-2.05	116.26	120.11
5	D	501	GTP	O3B-PG-O1G	-2.05	100.26	111.04
10	B	506	PO7	CAU-CAV-NAO	-2.04	107.84	110.40
9	B	505	MES	C5-N4-C3	2.03	113.21	108.84
10	D	503	PO7	CAU-CAV-NAO	-2.02	107.87	110.40
5	A	501	GTP	O6-C6-C5	-2.02	121.21	126.53
9	B	505	MES	C7-N4-C5	-2.01	105.88	111.24

There are no chirality outliers.

All (35) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	501	GTP	C5'-O5'-PA-O3A
5	A	501	GTP	C5'-O5'-PA-O1A
5	A	501	GTP	C5'-O5'-PA-O2A
5	C	501	GTP	PB-O3B-PG-O3G
5	C	501	GTP	C5'-O5'-PA-O3A
5	C	501	GTP	C5'-O5'-PA-O1A
5	C	501	GTP	C5'-O5'-PA-O2A
5	D	501	GTP	C5'-O5'-PA-O3A
5	D	501	GTP	C5'-O5'-PA-O1A
5	D	501	GTP	C5'-O5'-PA-O2A
8	B	501	GDP	C5'-O5'-PA-O3A
8	B	501	GDP	C5'-O5'-PA-O1A
8	B	501	GDP	C5'-O5'-PA-O2A
9	B	503	MES	N4-C7-C8-S
10	B	506	PO7	CAT-CAH-CAY-CAW
10	B	506	PO7	CAT-CAH-CAY-NAP
10	D	503	PO7	CAT-CAH-CAY-CAW
10	D	503	PO7	CAT-CAH-CAY-NAP
11	F	401	ACP	O4'-C4'-C5'-O5'
9	B	503	MES	C7-C8-S-O3S
9	B	505	MES	C7-C8-S-O3S
10	B	506	PO7	CAZ-CAI-CAU-NAN
10	B	506	PO7	CAZ-CAI-CAU-CAV
11	F	401	ACP	C3'-C4'-C5'-O5'
9	B	503	MES	C7-C8-S-O2S
9	B	505	MES	C7-C8-S-O1S
11	F	401	ACP	PB-C3B-PG-O2G
11	F	401	ACP	PB-C3B-PG-O3G
5	C	501	GTP	C4'-C5'-O5'-PA

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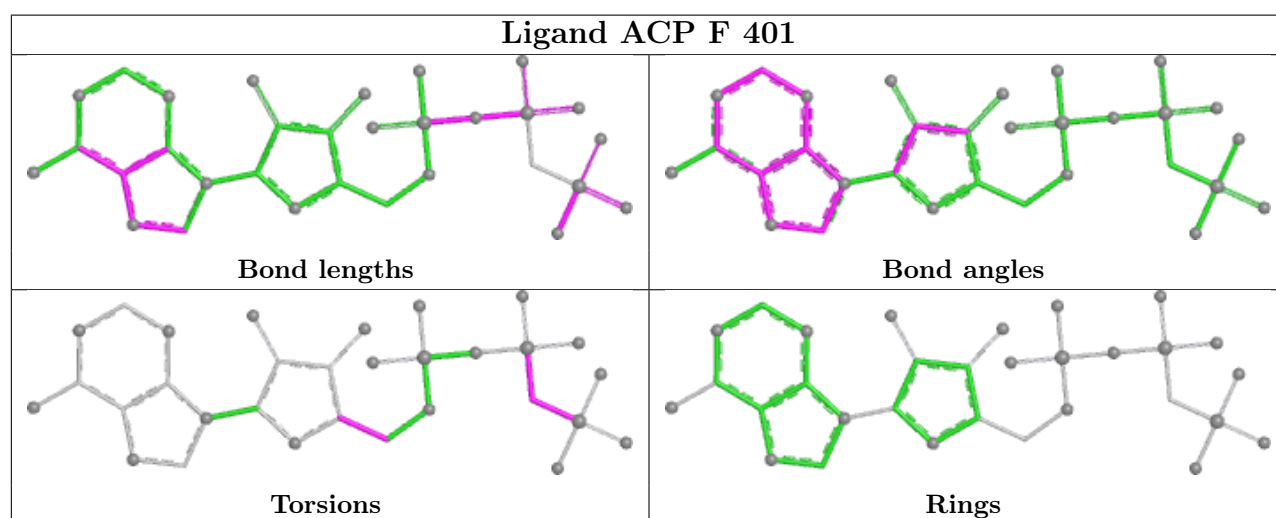
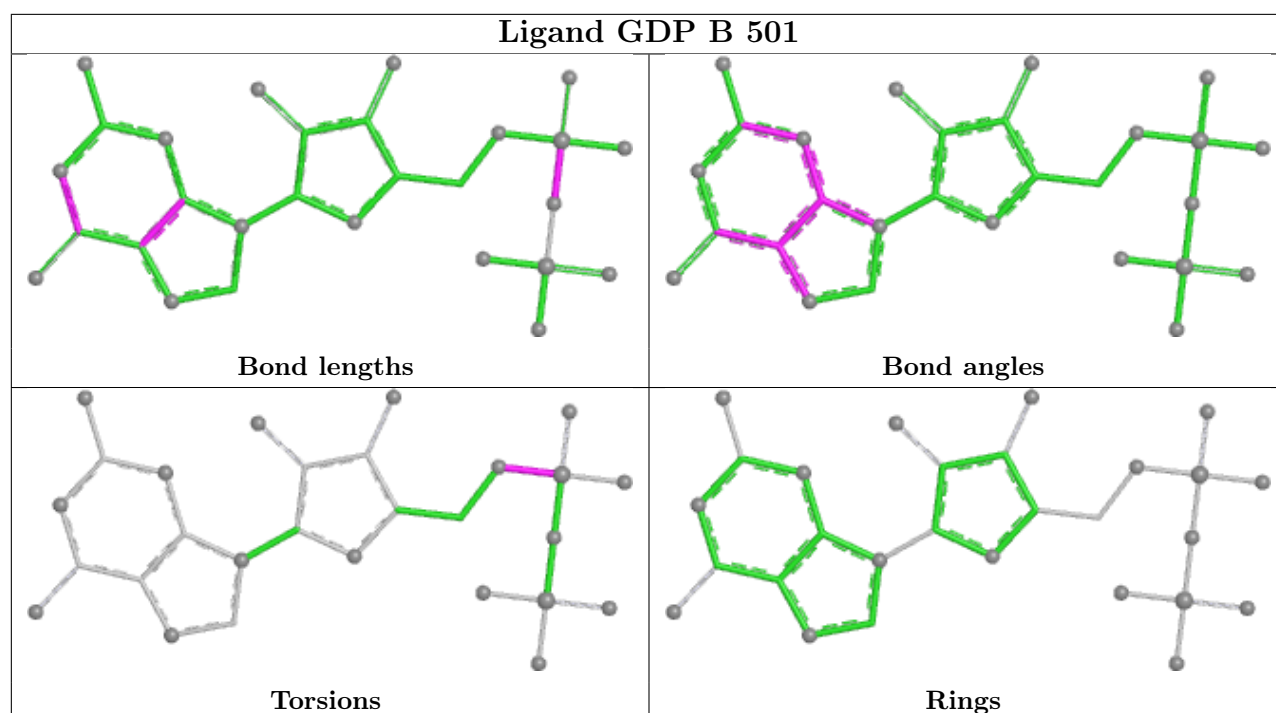
Mol	Chain	Res	Type	Atoms
5	D	501	GTP	C4'-C5'-O5'-PA
11	F	401	ACP	PG-C3B-PB-O1B
5	C	501	GTP	PB-O3B-PG-O2G
11	F	401	ACP	PB-C3B-PG-O1G
5	D	501	GTP	C3'-C4'-C5'-O5'
5	D	501	GTP	PB-O3A-PA-O2A

There are no ring outliers.

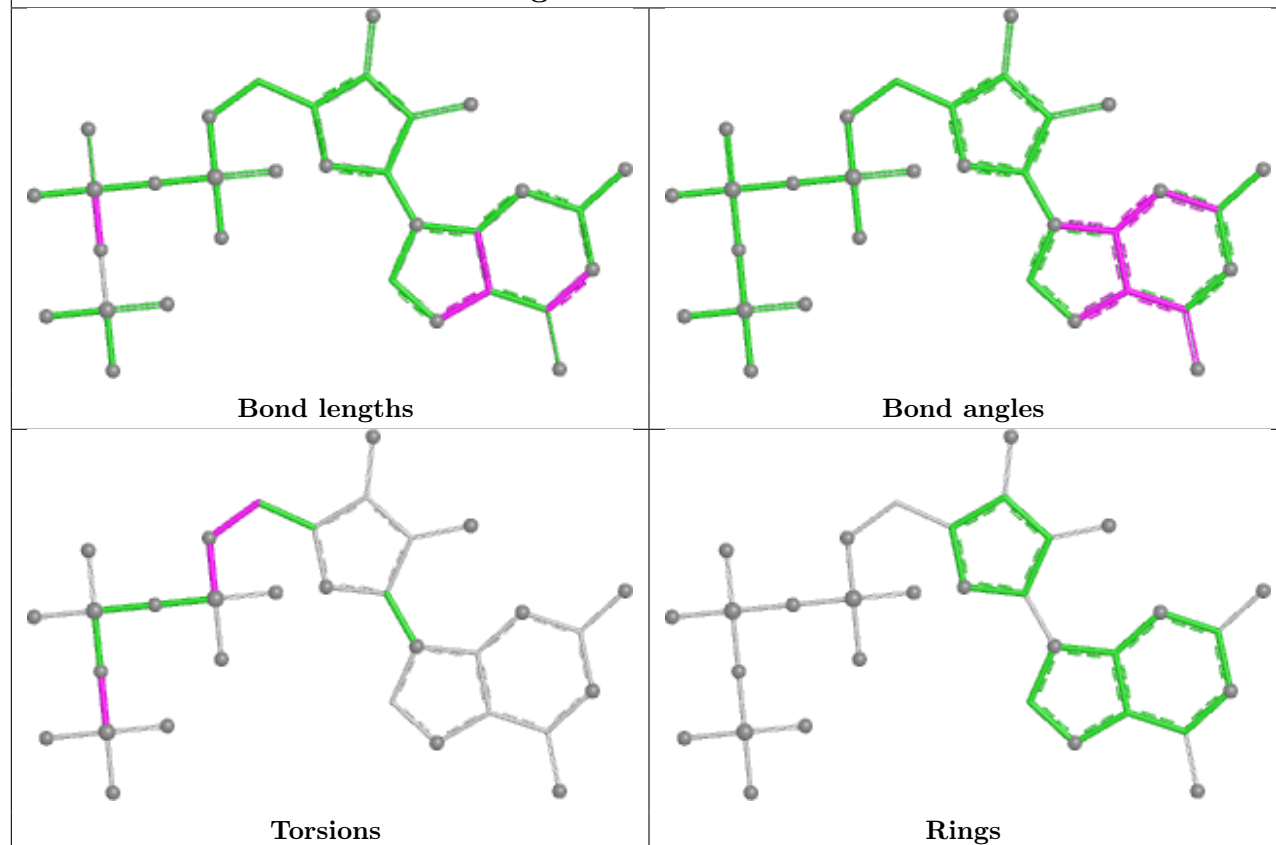
5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	B	505	MES	1	0
11	F	401	ACP	1	0
9	B	503	MES	1	0
10	D	503	PO7	2	0
10	B	506	PO7	1	0

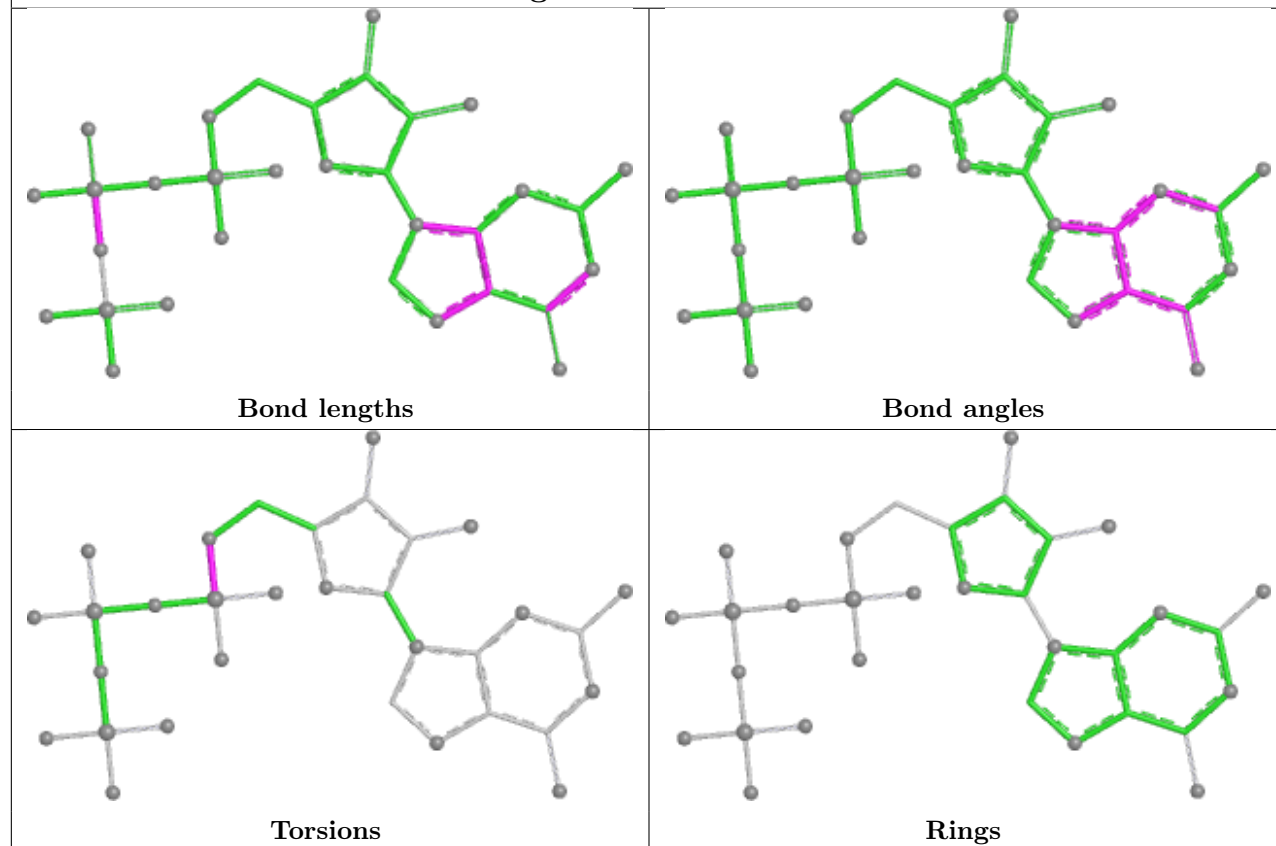
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

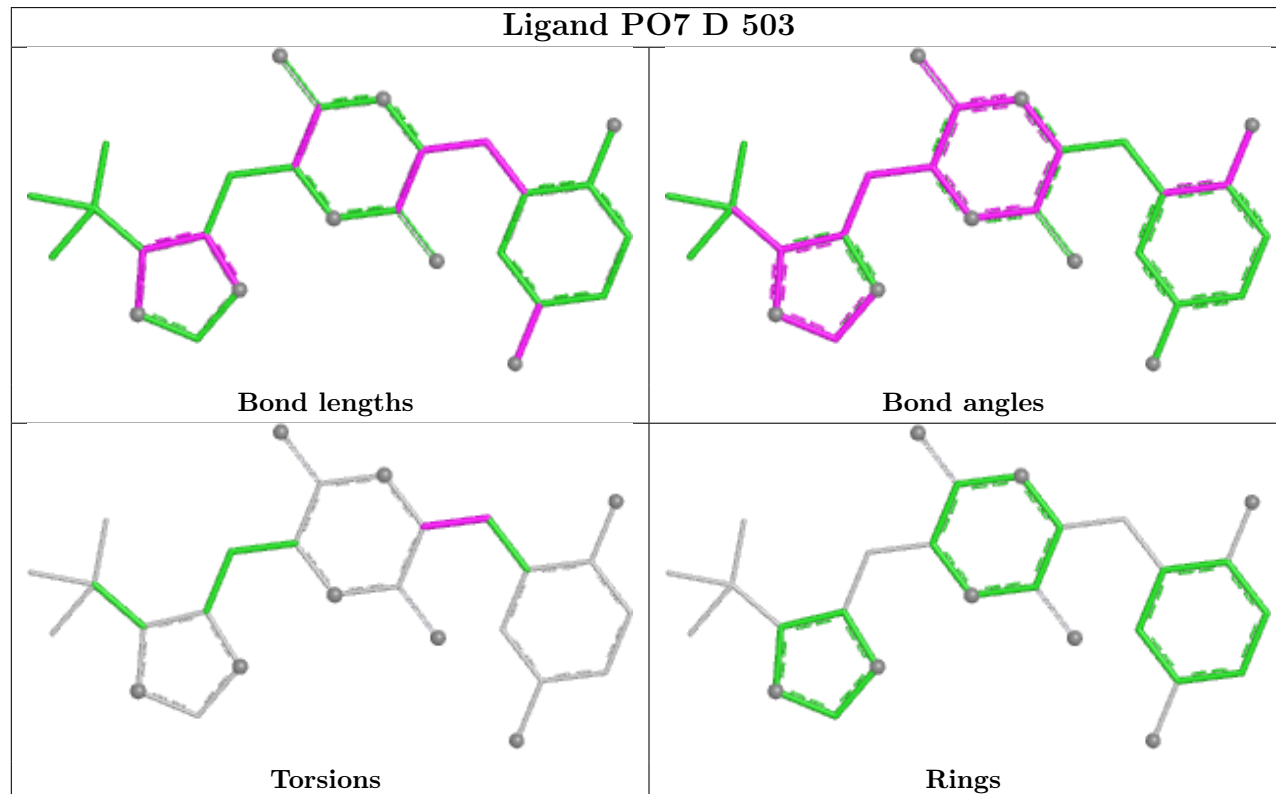
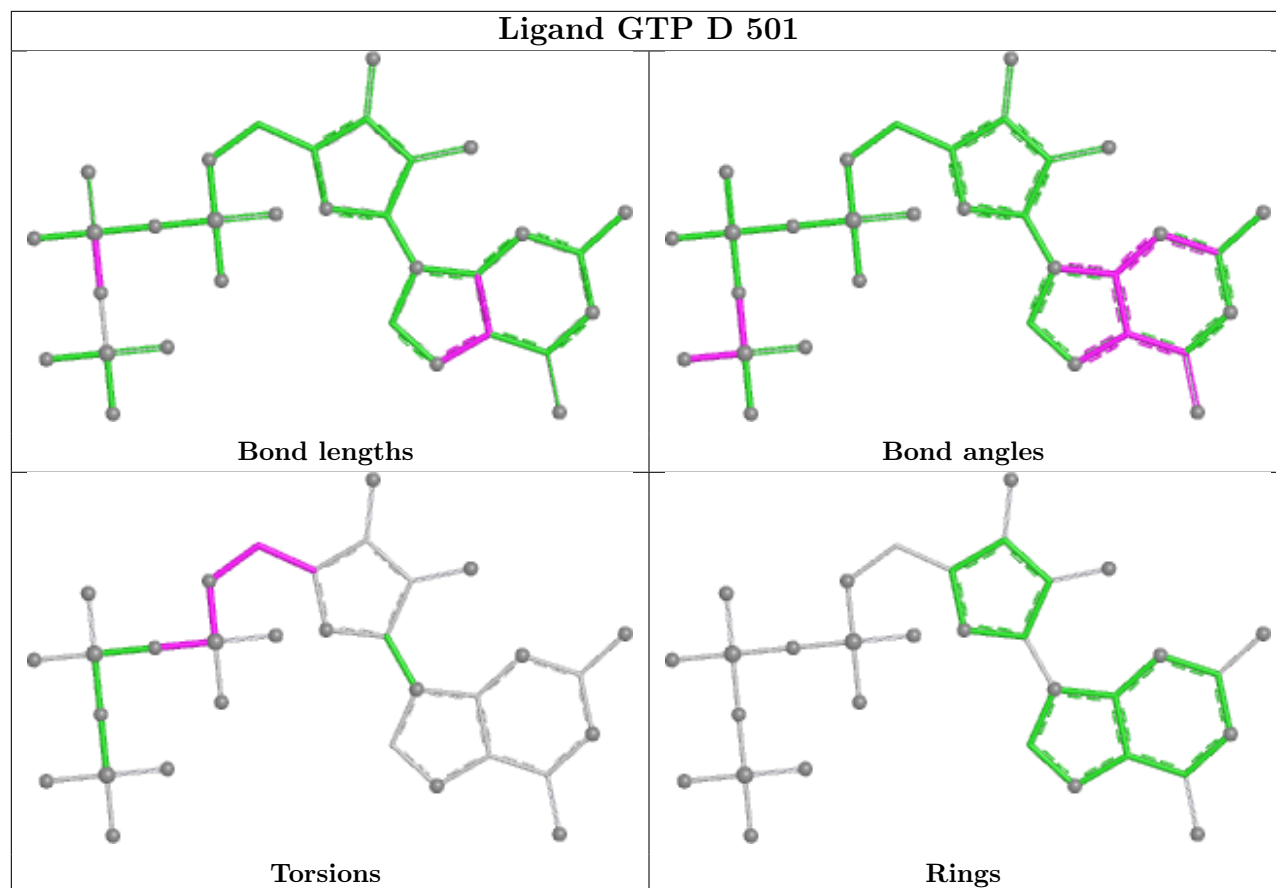


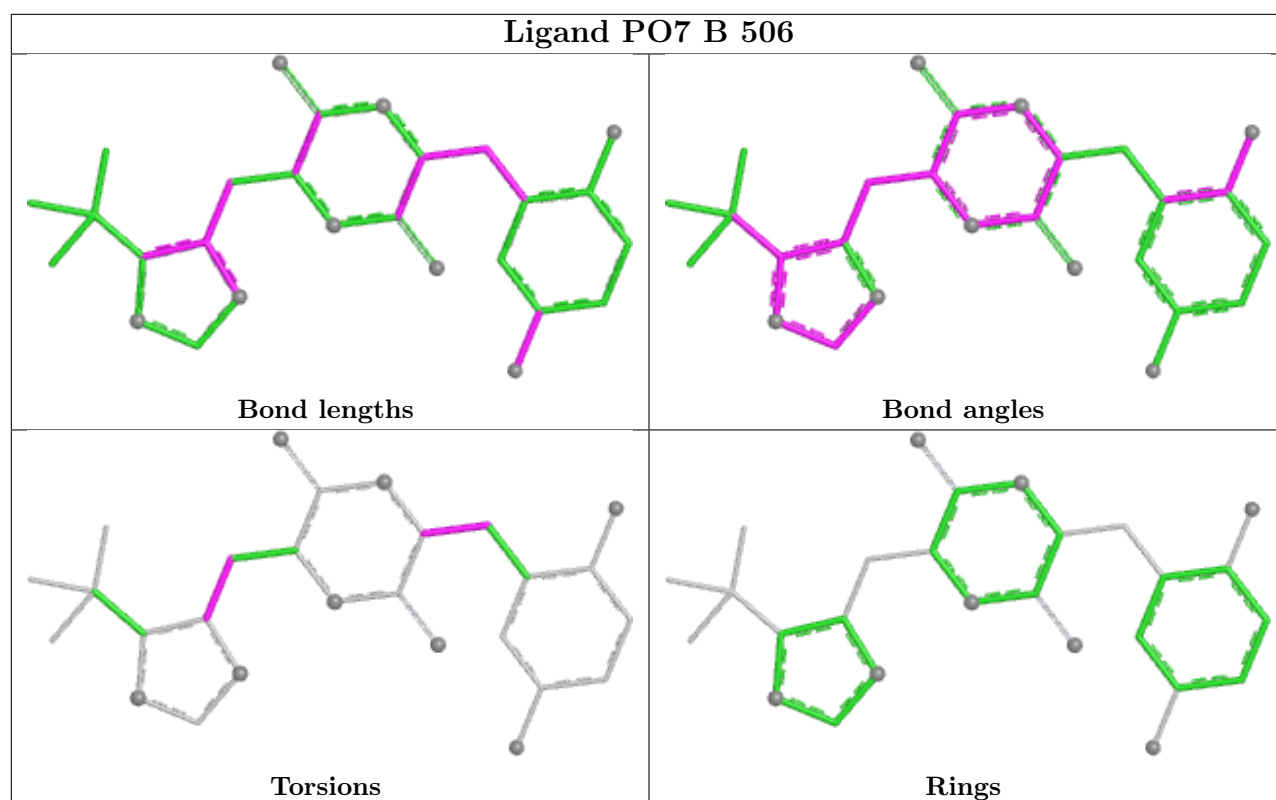
Ligand GTP C 501



Ligand GTP A 501







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 ⓘ

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	437/450 (97%)	0.12	7 (1%) 70 47	22, 48, 78, 98	4 (0%)
1	C	440/450 (97%)	-0.08	9 (2%) 65 41	17, 39, 66, 81	9 (2%)
2	B	424/445 (95%)	0.18	9 (2%) 63 40	19, 48, 77, 114	3 (0%)
2	D	421/445 (94%)	1.12	73 (17%) 4 3	37, 75, 111, 149	4 (0%)
3	E	120/184 (65%)	0.76	10 (8%) 17 9	35, 71, 104, 116	2 (1%)
4	F	309/384 (80%)	1.12	63 (20%) 3 2	20, 77, 120, 147	3 (0%)
All	All	2151/2358 (91%)	0.47	171 (7%) 18 10	17, 55, 104, 149	25 (1%)

All (171) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	F	161	LEU	6.5
4	F	182	ILE	6.4
4	F	166	ALA	6.3
2	D	99	ASN	5.9
4	F	100	ILE	5.3
4	F	149	ALA	4.6
3	E	12[A]	ASN	4.3
2	B	243	PRO	4.2
2	D	175	VAL	4.2
2	D	97	ALA	3.9
3	E	51	GLN	3.9
4	F	102	PRO	3.8
2	D	73	MET	3.8
2	D	215	LEU	3.7
4	F	199	PHE	3.6
2	D	170	MET	3.6
2	D	377	LEU	3.5
2	D	98	GLY	3.5
3	E	6	MET	3.5

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Mol	Chain	Res	Type	RSRZ
4	F	147	TRP	3.5
4	F	233	PHE	3.4
2	D	72	THR	3.4
1	A	262	TYR	3.4
2	D	222	TYR	3.4
2	D	243	PRO	3.3
2	D	273	LEU	3.3
1	A	346	TRP	3.3
2	D	396	HIS	3.3
4	F	237	THR	3.3
2	D	207	LEU	3.3
4	F	162	ILE	3.2
2	D	228	LEU	3.2
4	F	159	GLY	3.2
1	C	245	ASP	3.2
4	F	245	ILE	3.2
4	F	186	LEU	3.2
2	D	394	PHE	3.2
2	D	403	MET	3.2
2	D	211	CYS	3.1
2	D	81	PHE	3.1
4	F	247	LYS	3.1
4	F	253	TYR	3.1
2	D	11	GLN	3.1
2	B	360	GLY	3.1
2	B	2	ARG	3.1
2	D	296	SER	3.0
3	E	139	LEU	3.0
2	B	281	TYR	3.0
2	D	171	PRO	3.0
1	A	282	TYR	2.9
2	D	204	ASN	2.9
2	D	76	VAL	2.9
2	D	1	MET	2.9
2	D	54	ALA	2.9
4	F	184	LYS	2.9
4	F	225	SER	2.9
4	F	323	GLU	2.9
4	F	150	LYS	2.9
2	D	180	VAL	2.9
4	F	263	PHE	2.8
1	C	211[A]	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
2	D	217	LEU	2.8
2	B	246	LEU	2.8
2	D	239	CYS	2.7
4	F	198	LYS	2.7
2	D	145[A]	SER	2.7
4	F	160	ILE	2.7
2	B	1	MET	2.7
2	D	218	THR	2.7
4	F	264	PHE	2.7
2	D	55	THR	2.7
2	D	210	ILE	2.6
2	D	42	LEU	2.6
2	D	284	LEU	2.6
2	D	397	TRP	2.6
2	D	399	THR	2.6
2	D	44	LEU	2.6
2	D	185	ALA	2.6
4	F	23	ALA	2.6
4	F	243	HIS	2.6
2	D	82	GLY	2.6
2	D	178	THR	2.6
4	F	240	LEU	2.6
2	D	393	ALA	2.6
2	D	172	SER	2.6
2	D	80	PRO	2.6
4	F	163	SER	2.5
2	D	24	ILE	2.5
2	B	55	THR	2.5
2	D	219	THR	2.5
2	D	92	PHE	2.5
4	F	381	HIS	2.5
1	A	196	GLU	2.5
1	C	87	PHE	2.5
4	F	262	MET	2.5
2	D	28	HIS	2.4
4	F	275	LEU	2.4
4	F	228	TYR	2.4
4	F	242	ASN	2.4
2	D	272	PRO	2.4
2	D	208	TYR	2.4
4	F	270	TYR	2.4
4	F	283	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
2	B	46	ARG	2.4
3	E	53	LYS	2.4
1	C	361	THR	2.4
2	D	398	TYR	2.4
2	D	100	ASN	2.3
1	C	120[A]	ASP	2.3
2	D	229	VAL	2.3
2	D	293	MET	2.3
4	F	320	MET	2.3
2	D	75	SER	2.3
2	D	140	GLY	2.3
2	D	142	GLY	2.3
2	D	385	PHE	2.3
4	F	267	PHE	2.3
4	F	335	ALA	2.3
3	E	46	SER	2.3
4	F	201	ILE	2.3
4	F	101	TYR	2.3
1	C	251[A]	ASP	2.3
2	D	429	THR	2.3
4	F	327	VAL	2.3
2	D	85	PHE	2.2
4	F	260	ASN	2.2
4	F	151	SER	2.2
4	F	181	VAL	2.2
2	D	267	MET	2.2
2	D	387	ALA	2.2
3	E	54	LEU	2.2
4	F	197	ARG	2.2
2	D	176	SER	2.2
1	A	86	LEU	2.2
4	F	383	HIS	2.2
4	F	99	VAL	2.2
2	D	214	THR	2.2
4	F	241	THR	2.2
2	D	183	TYR	2.2
4	F	191	LEU	2.2
4	F	221	LEU	2.2
1	C	285	GLN	2.1
2	B	280	GLN	2.1
2	D	179	VAL	2.1
2	D	285	THR	2.1

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Mol	Chain	Res	Type	RSRZ
4	F	271	LEU	2.1
4	F	244	CYS	2.1
3	E	124	GLN	2.1
4	F	379	HIS	2.1
1	A	437	VAL	2.1
4	F	146	VAL	2.1
1	C	1	MET	2.1
2	D	220	PRO	2.1
4	F	236	LYS	2.1
2	D	203	ASP	2.1
2	D	30	ILE	2.1
1	C	283	HIS	2.1
3	E	26	PRO	2.1
4	F	22	LEU	2.1
4	F	329	LEU	2.1
2	D	96	GLY	2.1
4	F	92	THR	2.1
4	F	75	ALA	2.1
4	F	384	HIS	2.0
3	E	90	ASN	2.0
4	F	330	ILE	2.0
2	D	206	ALA	2.0
2	D	40	SER	2.0
4	F	180	HIS	2.0
4	F	148	ILE	2.0
1	A	163	LYS	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

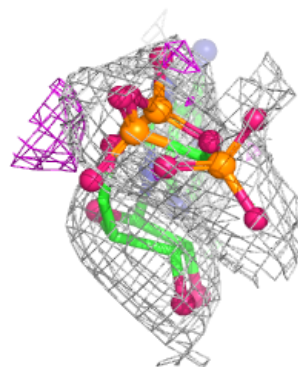
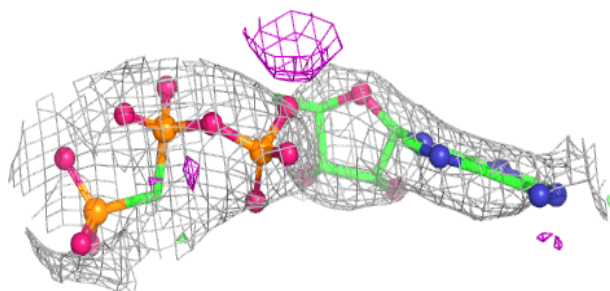
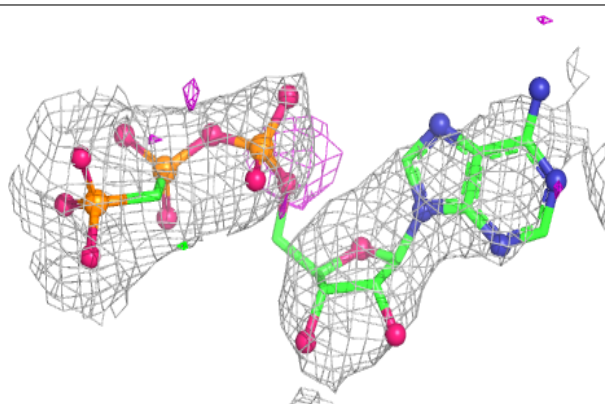
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
11	ACP	F	401	31/31	0.77	0.14	91,103,119,121	0
5	GTP	D	501	32/32	0.84	0.14	55,62,76,82	0
9	MES	B	503	12/12	0.86	0.21	77,83,87,90	0
6	MG	D	502	1/1	0.87	0.12	60,60,60,60	0
9	MES	B	505	12/12	0.89	0.16	91,93,97,97	0
7	CA	B	504	1/1	0.90	0.06	65,65,65,65	0
10	PO7	B	506	27/27	0.91	0.13	33,41,59,66	0
10	PO7	D	503	27/27	0.92	0.11	48,57,67,68	0
7	CA	C	503	1/1	0.95	0.06	56,56,56,56	0
5	GTP	C	501	32/32	0.97	0.06	26,30,31,32	0
7	CA	A	503	1/1	0.97	0.09	76,76,76,76	0
5	GTP	A	501	32/32	0.97	0.07	29,32,35,36	0
8	GDP	B	501	28/28	0.98	0.06	28,30,32,33	0
6	MG	A	502	1/1	0.99	0.04	25,25,25,25	0
6	MG	B	502	1/1	0.99	0.04	40,40,40,40	0
6	MG	C	502	1/1	1.00	0.02	31,31,31,31	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.

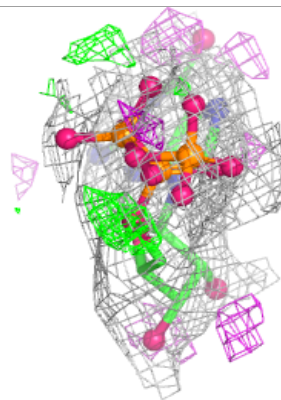
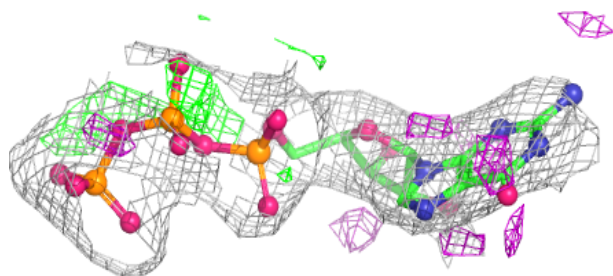
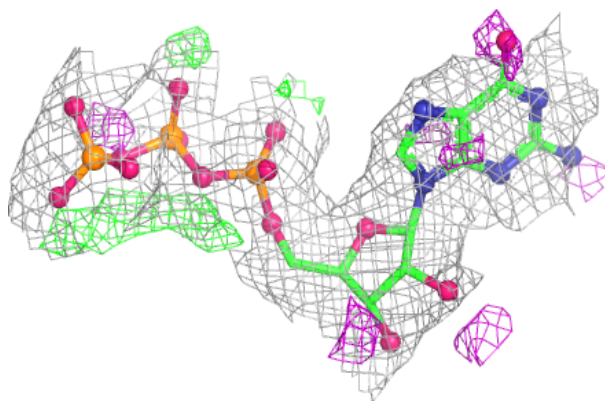
Electron density around ACP F 401:

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

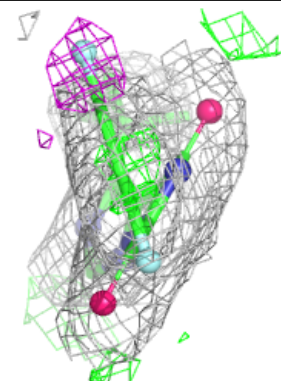
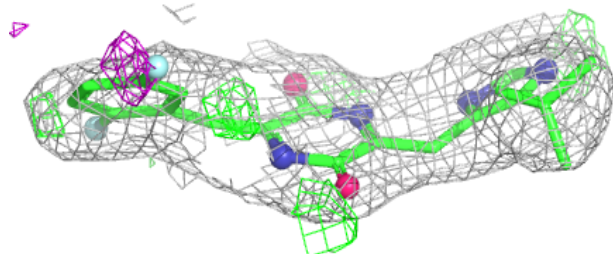
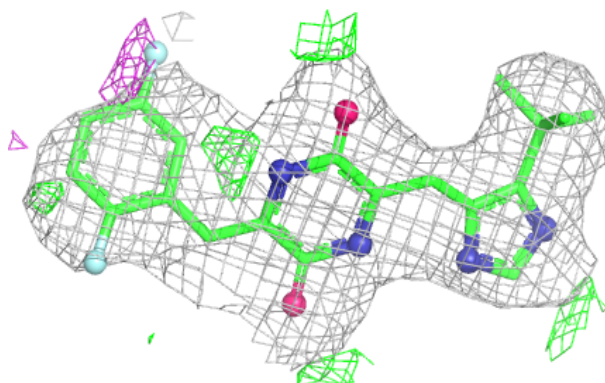


Electron density around GTP D 501:

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

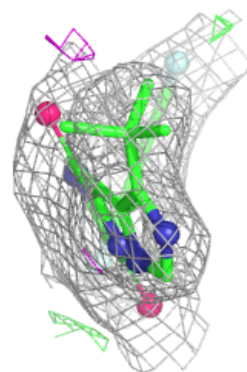
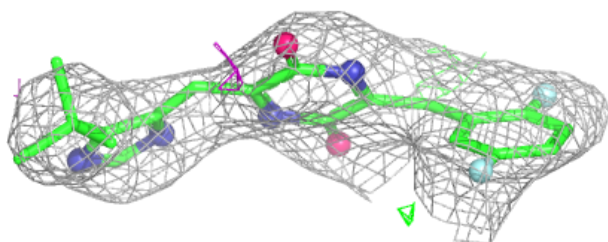
**Electron density around PO7 B 506:**

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

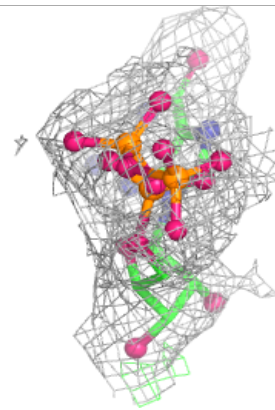
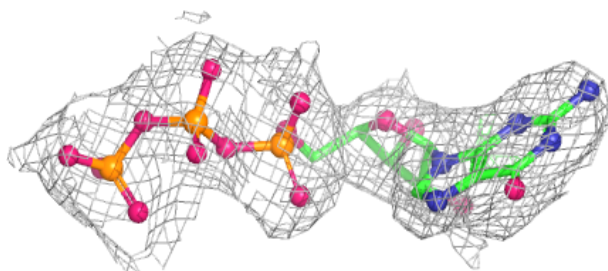
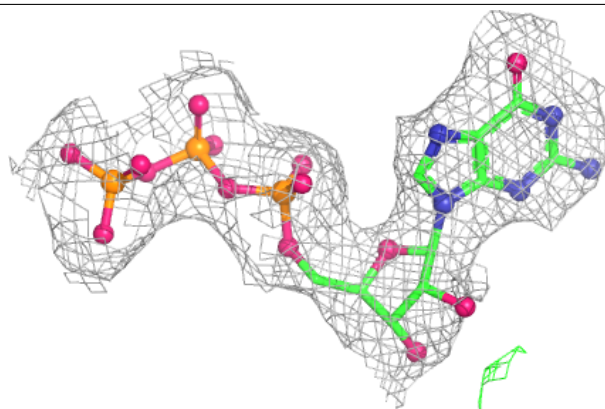


Electron density around PO7 D 503:

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

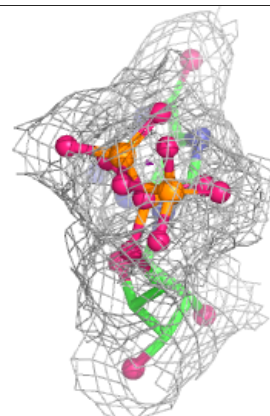
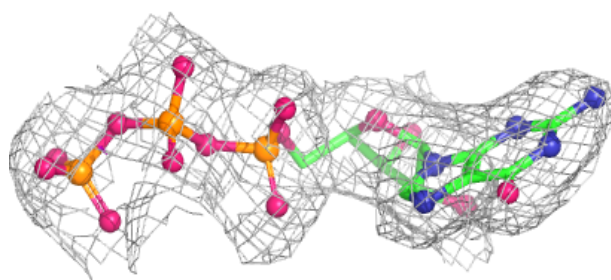
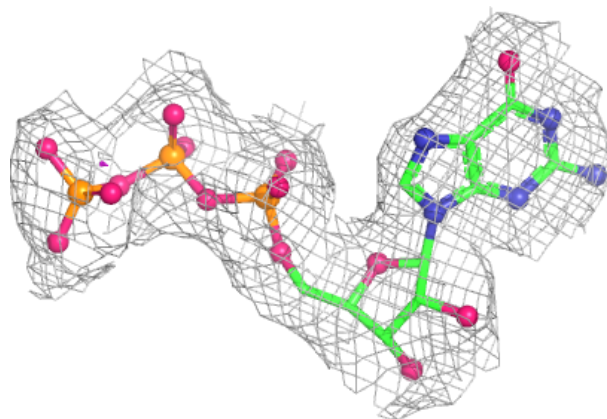
**Electron density around GTP C 501:**

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



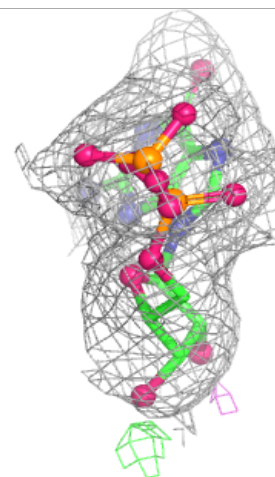
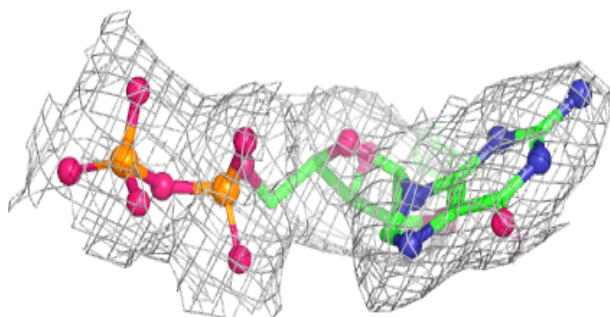
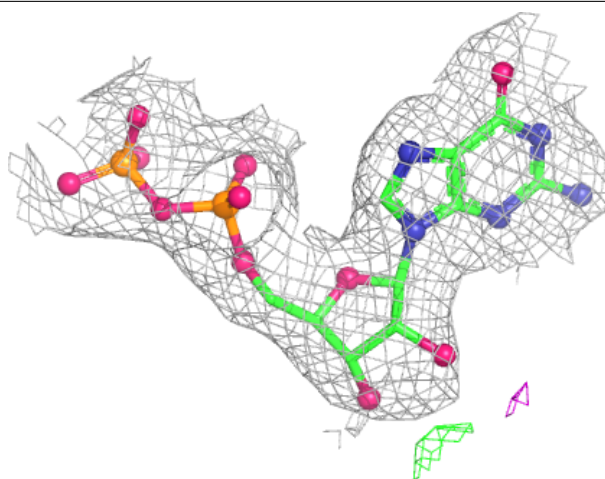
Electron density around GTP A 501:

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



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)



6.5 Other polymers [i](#)

There are no such residues in this entry.