wwPDB X-ray Structure Validation Summary Report (i)

Mar 9, 2026 – 05:35 AM UTC

PDB ID	:	5IYZ / pdb_00005iyz
Title	:	Tubulin-MMAE complex
Authors	:	Waight, A.B.; Bargsten, K.; Doronina, S.; Steinmetz, M.O.; Sussman, D.; Prota, A.E.
Deposited on	:	2016-03-24
Resolution	:	1.80 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 (i) 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 (i)) were used in the production of this report:

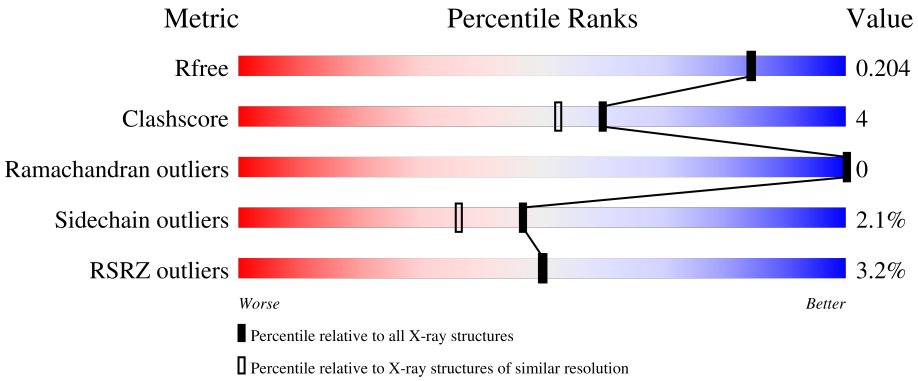
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 1.80 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.



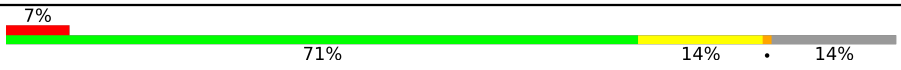
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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 <=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	91% 6%
1	C	451	89% 9%
2	B	445	86% 11%
2	D	445	4% 85% 10% 5%
3	E	143	3% 73% 12% 14%

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Mol	Chain	Length	Quality of chain
4	F	384	

2 Entry composition (i)

There are 12 unique types of molecules in this entry. The entry contains 19140 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	12	0
			3467	2206	582	654	25			
1	C	440	Total	C	N	O	S	0	11	0
			3482	2208	585	664	25			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	430	Total	C	N	O	S	3	14	0
			3447	2169	586	663	29			
2	D	424	Total	C	N	O	S	0	3	0
			3347	2101	570	648	28			

- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	123	Total	C	N	O	S	0	6	0
			1047	646	189	207	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

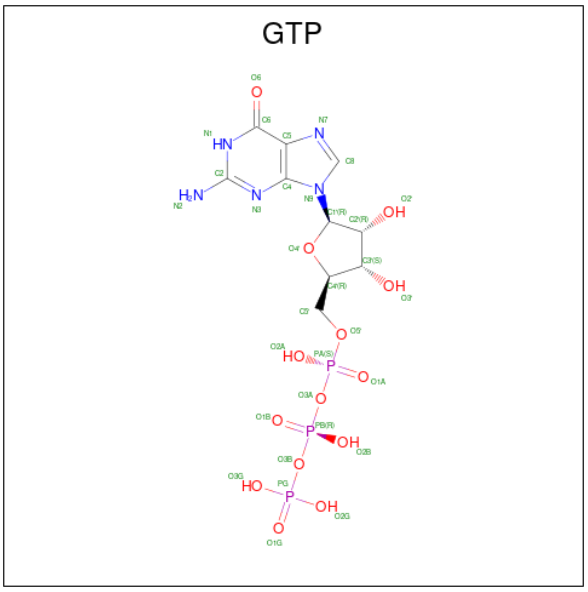
- Molecule 4 is a protein called TUBULIN-TYROSINE LIGASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	331	Total	C	N	O	S	0	3	0
			2725	1757	461	493	14			

There are 6 discrepancies between the modelled and reference sequences:

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

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



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

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

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

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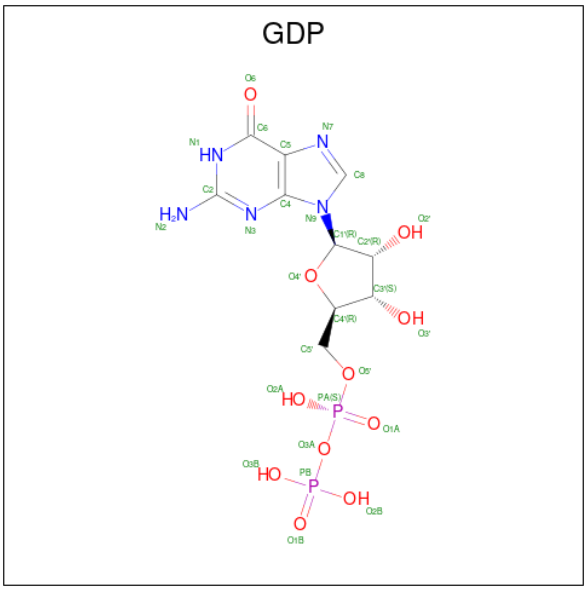
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	F	1	Total Mg 1 1	0	0

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

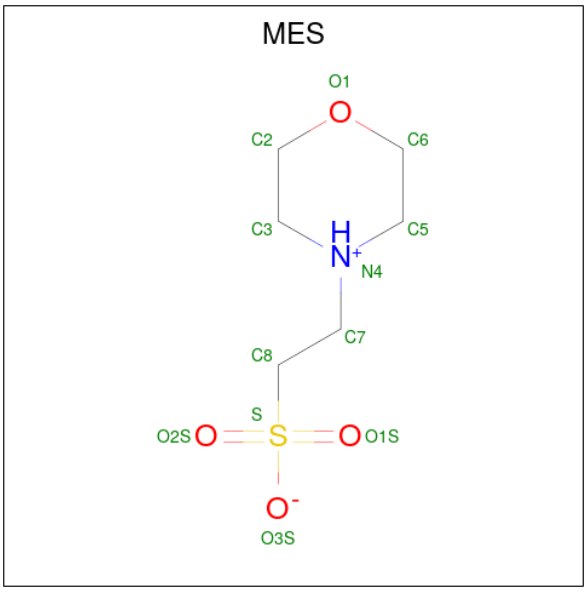
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Ca 1 1	0	0
7	C	1	Total Ca 1 1	0	0

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



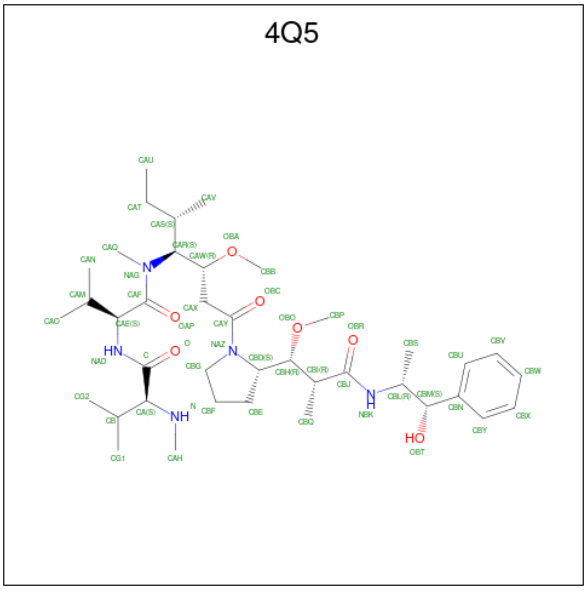
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	B	1	Total C N O P 28 10 5 11 2	0	0
8	D	1	Total C N O P 28 10 5 11 2	0	0

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



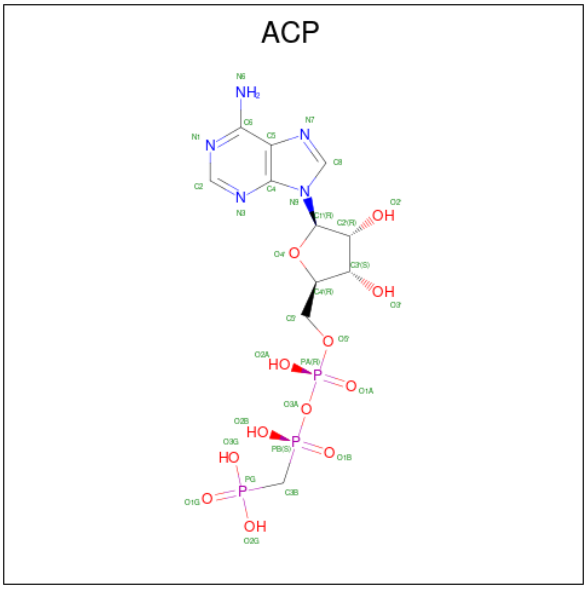
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 10 is N-methyl-L-valyl-N-[(3R,4S,5S)-1-{(2S)-2-[(1R,2R)-3-{[(1S,2R)-1-hydroxy-1-phenylpropan-2-yl]amino}-1-methoxy-2-methyl-3-oxopropyl]pyrrolidin-1-yl}-3-methoxy-5-methyl-1-oxoheptan-4-yl]-N-methyl-L-valinamide (CCD ID: 4Q5) (formula: $C_{39}H_{67}N_5O_7$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	B	1	Total	C	N	O	0	0
			51	39	5	7		
10	D	1	Total	C	N	O	0	0
			51	39	5	7		

- 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		

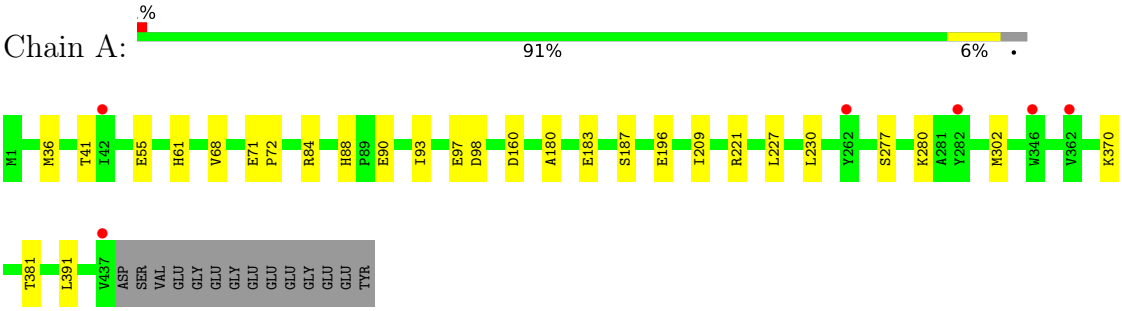
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	259	Total	O	0	0
			259	259		
12	B	314	Total	O	0	0
			314	314		
12	C	434	Total	O	0	0
			434	434		
12	D	178	Total	O	0	0
			178	178		
12	E	67	Total	O	0	0
			67	67		
12	F	101	Total	O	0	0
			101	101		

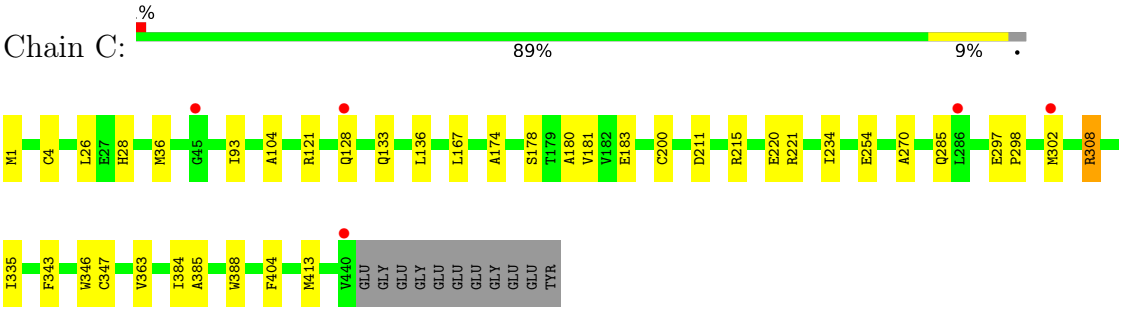
3 Residue-property plots (i)

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.

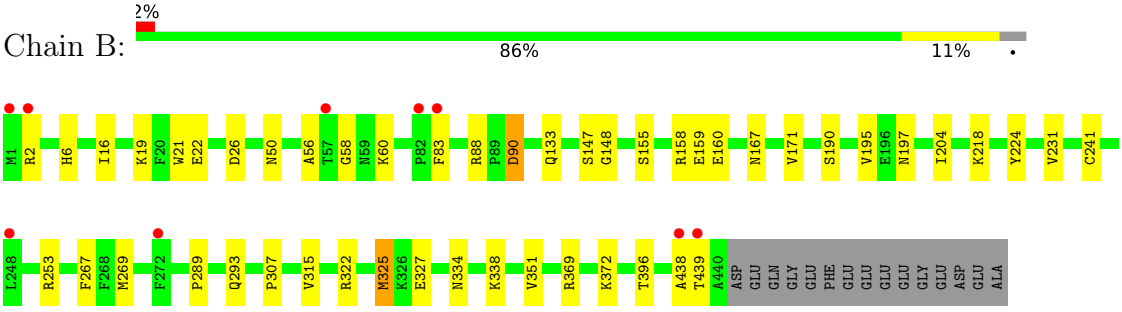
• Molecule 1: Tubulin alpha-1B chain



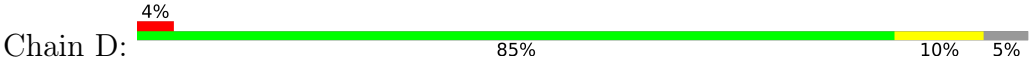
• Molecule 1: Tubulin alpha-1B chain

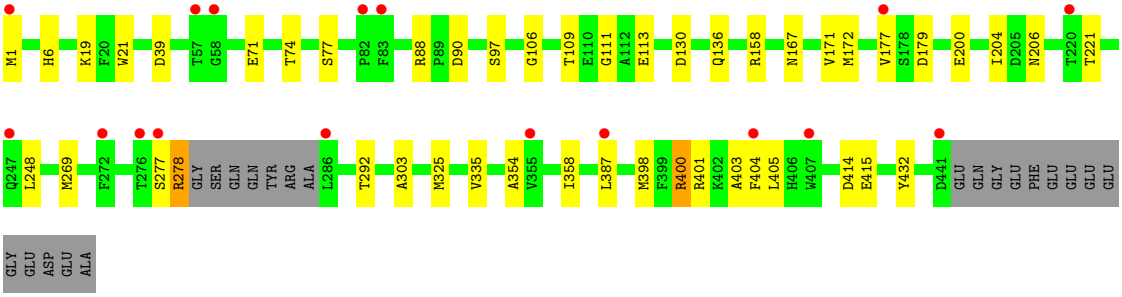


• Molecule 2: Tubulin beta-2B chain



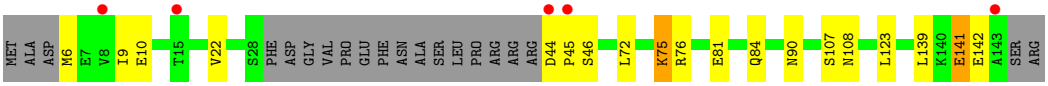
• Molecule 2: Tubulin beta-2B chain





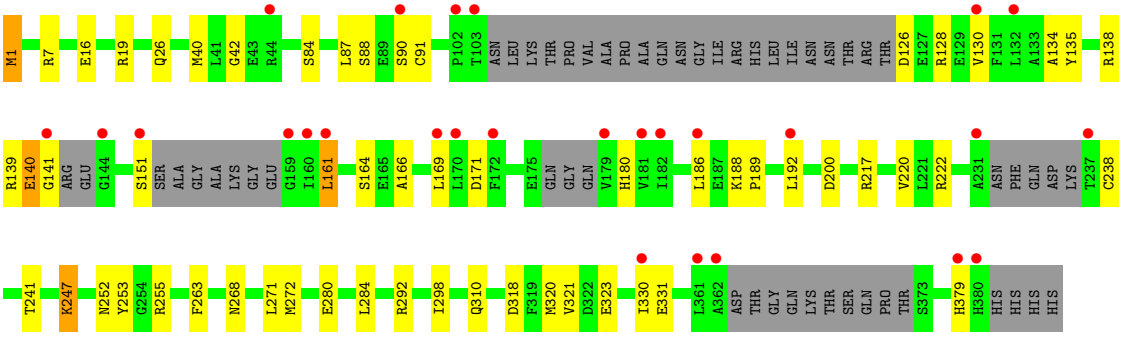
• Molecule 3: Stathmin-4





• Molecule 4: TUBULIN-TYROSINE LIGASE





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	104.51Å 156.61Å 182.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	71.96 – 1.80 71.96 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (71.96-1.80) 99.9 (71.96-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	1.00 (at 1.80Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.167 , 0.202 0.172 , 0.204	Depositor DCC
R_{free} test set	13782 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	37.2	Xtriage
Anisotropy	0.162	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 49.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	19140	wwPDB-VP
Average B, all atoms (Å^2)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.59% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: MES, GTP, ACP, MG, 4Q5, CA, GDP

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	0.49	0/3582	0.79	0/4864
1	C	0.63	0/3590	0.79	0/4877
2	B	0.58	0/3559	0.74	1/4817 (0.0%)
2	D	0.46	0/3426	0.74	3/4640 (0.1%)
3	E	0.47	0/1071	0.67	1/1423 (0.1%)
4	F	0.38	0/2794	0.75	0/3772
All	All	0.52	0/18022	0.76	5/24393 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	58	GLY	N-CA-C	-6.43	106.37	115.43
2	D	358	ILE	N-CA-C	5.53	112.59	107.56
3	E	141	GLU	N-CA-C	5.40	116.85	111.07
2	D	71	GLU	CA-C-N	-5.18	114.93	120.47
2	D	71	GLU	C-N-CA	-5.18	114.93	120.47

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	3467	0	3426	17	0
1	C	3482	0	3416	25	0
2	B	3447	0	3364	36	0
2	D	3347	0	3229	31	0
3	E	1047	0	1067	12	0
4	F	2725	0	2712	35	0
5	A	32	0	12	0	0
5	C	32	0	12	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
6	F	1	0	0	0	0
7	A	1	0	0	0	0
7	C	1	0	0	0	0
8	B	28	0	12	0	0
8	D	28	0	12	0	0
9	B	12	0	12	4	0
10	B	51	0	0	0	0
10	D	51	0	0	0	0
11	F	31	0	14	3	0
12	A	259	0	0	2	0
12	B	314	0	0	10	0
12	C	434	0	0	5	0
12	D	178	0	0	6	0
12	E	67	0	0	3	0
12	F	101	0	0	3	0
All	All	19140	0	17288	150	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 4.

The worst 5 of 150 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)
4:F:320:MET:HG2	4:F:330:ILE:HD11	1.60	0.83
1:C:128:GLN:NE2	12:C:601:HOH:O	2.11	0.83
4:F:40:MET:SD	12:F:595:HOH:O	2.40	0.78
1:C:270:ALA:HB3	1:C:302:MET:HE2	1.68	0.75
4:F:200:ASP:OD2	4:F:241:THR:OG1	2.05	0.74

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	447/451 (99%)	439 (98%)	8 (2%)	0	100	100
1	C	449/451 (100%)	437 (97%)	12 (3%)	0	100	100
2	B	440/445 (99%)	435 (99%)	5 (1%)	0	100	100
2	D	423/445 (95%)	417 (99%)	6 (1%)	0	100	100
3	E	125/143 (87%)	125 (100%)	0	0	100	100
4	F	320/384 (83%)	314 (98%)	6 (2%)	0	100	100
All	All	2204/2319 (95%)	2167 (98%)	37 (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	380/379 (100%)	375 (99%)	5 (1%)	61	54
1	C	382/379 (101%)	377 (99%)	5 (1%)	61	54
2	B	385/383 (100%)	381 (99%)	4 (1%)	68	64
2	D	370/383 (97%)	363 (98%)	7 (2%)	50	41
3	E	116/127 (91%)	111 (96%)	5 (4%)	26	13
4	F	301/342 (88%)	286 (95%)	15 (5%)	22	10
All	All	1934/1993 (97%)	1893 (98%)	41 (2%)	47	36

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	F	139	ARG
4	F	247	LYS
4	F	140	GLU
4	F	171	ASP
4	F	271[B]	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
4	F	269	GLN
3	E	136	ASN
2	D	11	GLN
1	C	393	HIS
2	D	167	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 15 ligands modelled in this entry, 7 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
8	GDP	D	501	6	29,30,30	1.17	5 (17%)	45,47,47	1.71	7 (15%)
5	GTP	A	501	6	33,34,34	1.31	4 (12%)	50,54,54	1.65	8 (16%)
9	MES	B	503	-	12,12,12	2.35	1 (8%)	15,16,16	2.43	7 (46%)
10	4Q5	D	503	-	52,52,52	1.30	2 (3%)	56,72,72	1.93	10 (17%)
11	ACP	F	402	6	31,33,33	1.73	8 (25%)	47,52,52	1.79	9 (19%)
5	GTP	C	501	6	33,34,34	1.24	4 (12%)	50,54,54	1.79	10 (20%)
10	4Q5	B	504	-	52,52,52	1.49	5 (9%)	56,72,72	1.77	9 (16%)
8	GDP	B	501	6	29,30,30	1.20	3 (10%)	45,47,47	1.77	9 (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
8	GDP	D	501	6	-	5/16/32/32	0/3/3/3
5	GTP	A	501	6	-	6/22/38/38	0/3/3/3
9	MES	B	503	-	-	2/6/14/14	0/1/1/1
10	4Q5	D	503	-	-	2/76/86/86	0/2/2/2
11	ACP	F	402	6	-	4/19/38/38	0/3/3/3
5	GTP	C	501	6	-	5/22/38/38	0/3/3/3
10	4Q5	B	504	-	-	1/76/86/86	0/2/2/2
8	GDP	B	501	6	-	5/16/32/32	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	D	503	4Q5	CBN-CBM	-8.00	1.40	1.51
9	B	503	MES	C8-S	-7.86	1.66	1.77
10	B	504	4Q5	CBN-CBM	-6.39	1.42	1.51
11	F	402	ACP	C5-C4	4.64	1.47	1.39
10	B	504	4Q5	CBH-CBD	4.22	1.58	1.52

The worst 5 of 69 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
10	B	504	4Q5	CAW-CAX-CAY	-6.50	102.76	112.38
9	B	503	MES	C5-N4-C3	6.41	122.64	108.84
10	D	503	4Q5	CBF-CBE-CBD	-6.06	94.09	104.21

Continued on next page...

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	C	501	GTP	C5-C4-N3	-5.71	119.31	128.39
10	D	503	4Q5	CBG-NAZ-CBD	-5.68	102.72	111.69

There are no chirality outliers.

5 of 30 torsion outliers are listed below:

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

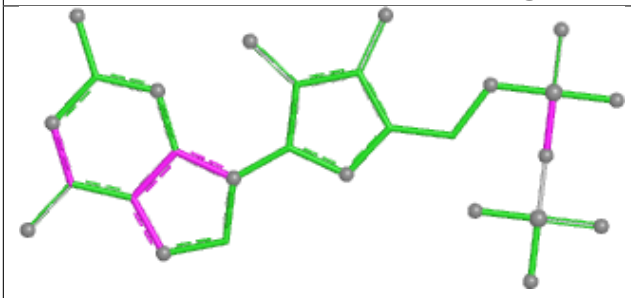
There are no ring outliers.

2 monomers are involved in 7 short contacts:

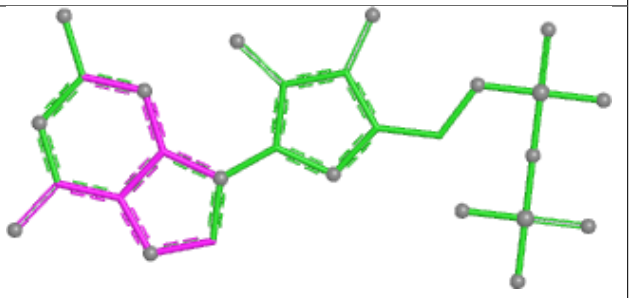
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	B	503	MES	4	0
11	F	402	ACP	3	0

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 then 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.

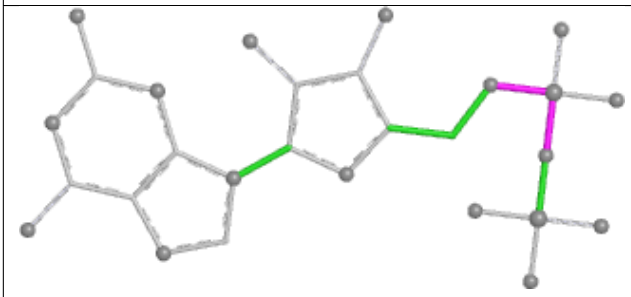
Ligand GDP D 501



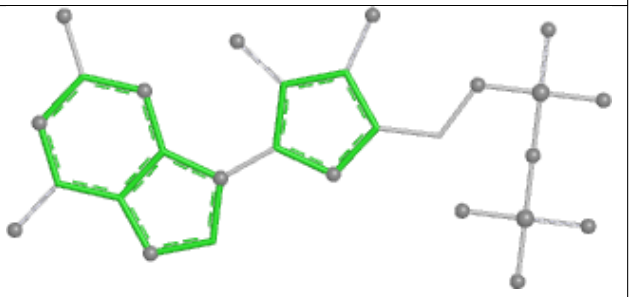
Bond lengths



Bond angles

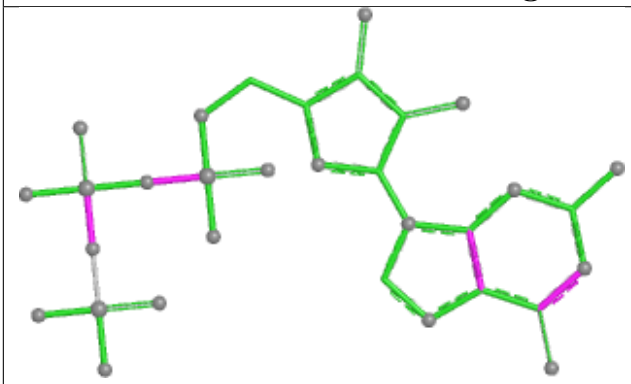


Torsions

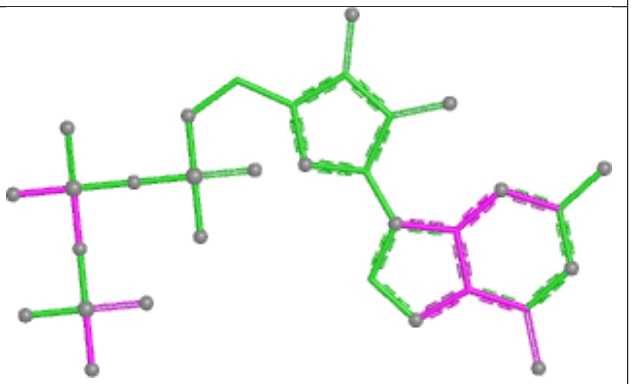


Rings

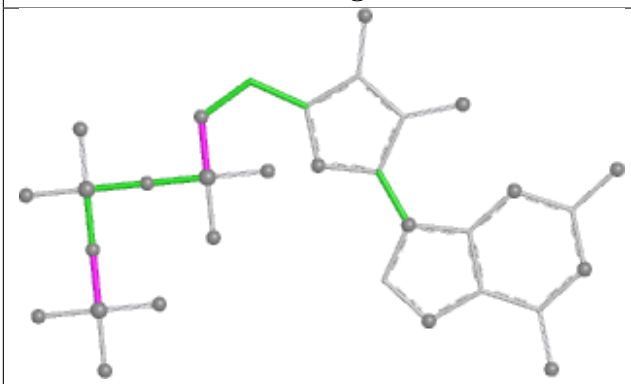
Ligand GTP A 501



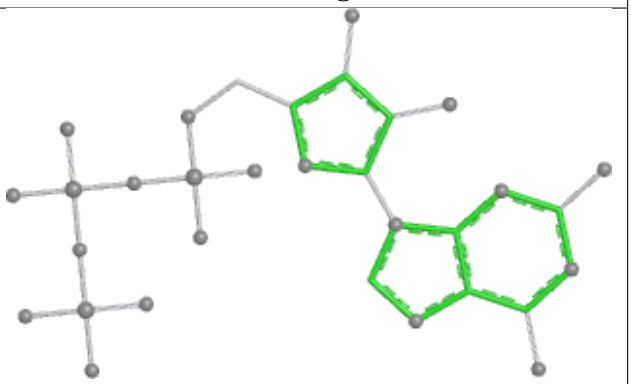
Bond lengths



Bond angles

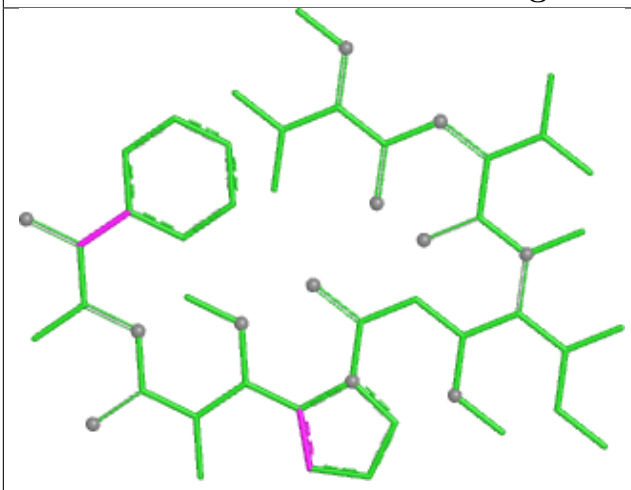


Torsions

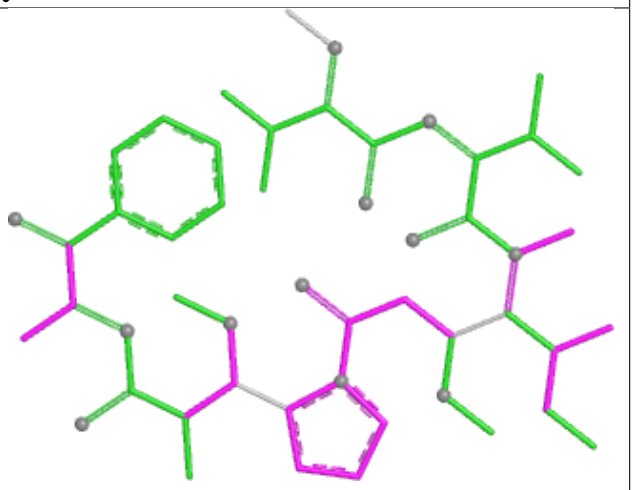


Rings

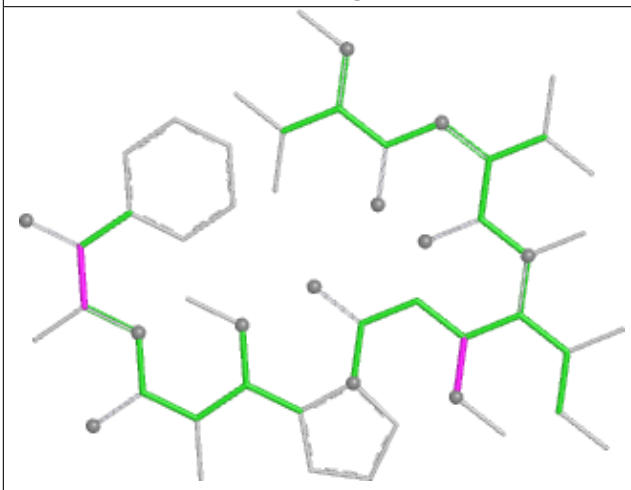
Ligand 4Q5 D 503



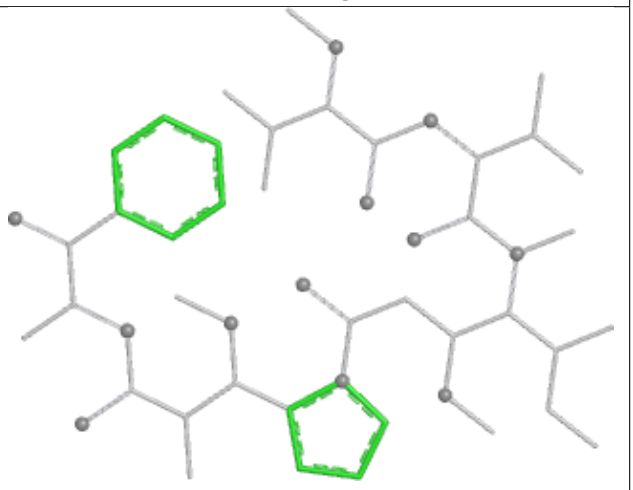
Bond lengths



Bond angles

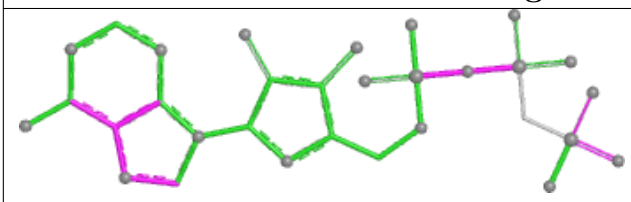


Torsions

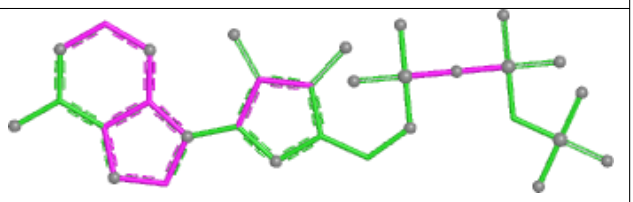


Rings

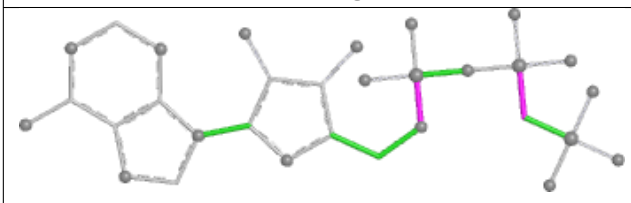
Ligand ACP F 402



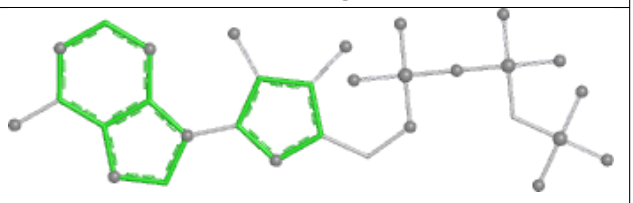
Bond lengths



Bond angles

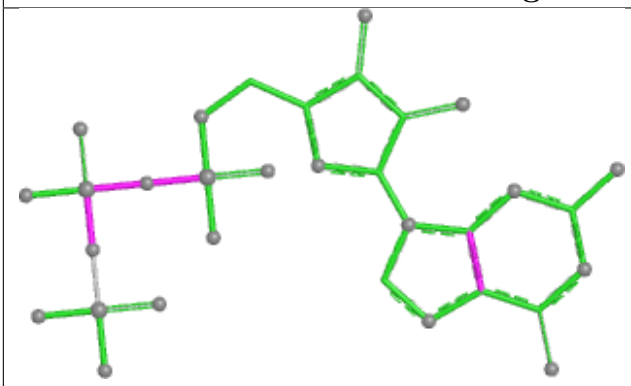


Torsions

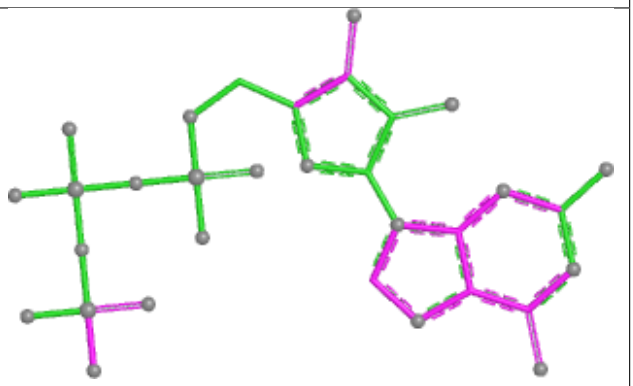


Rings

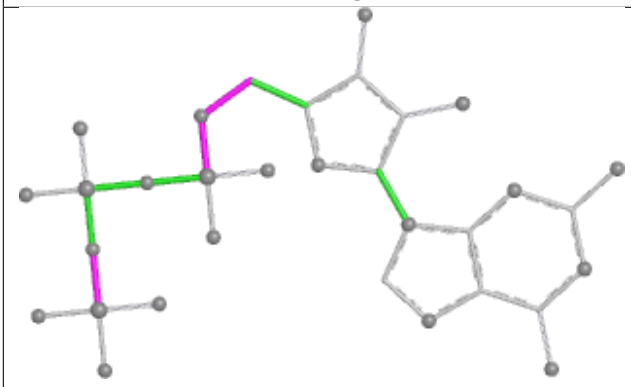
Ligand GTP C 501



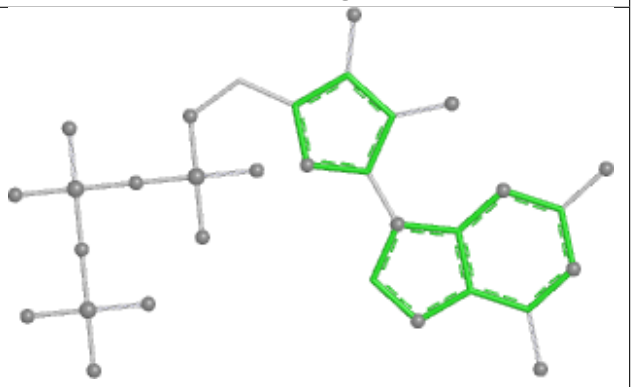
Bond lengths



Bond angles

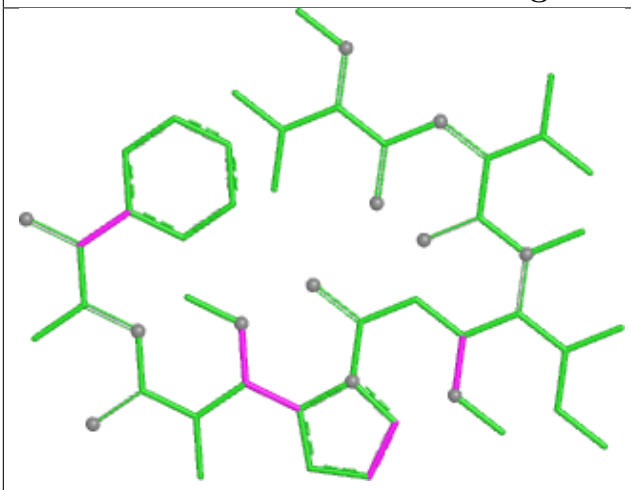


Torsions

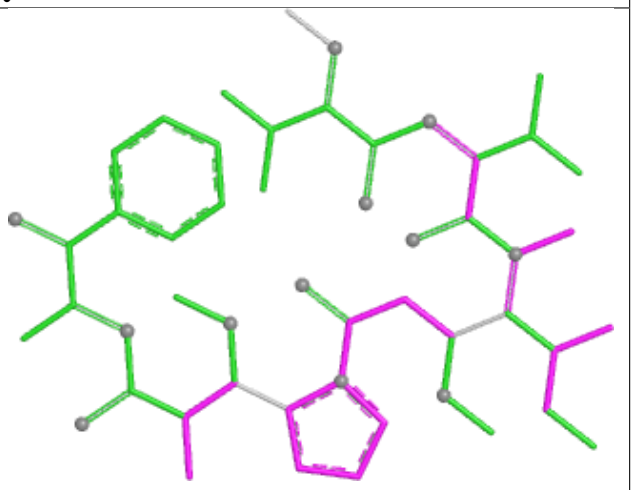


Rings

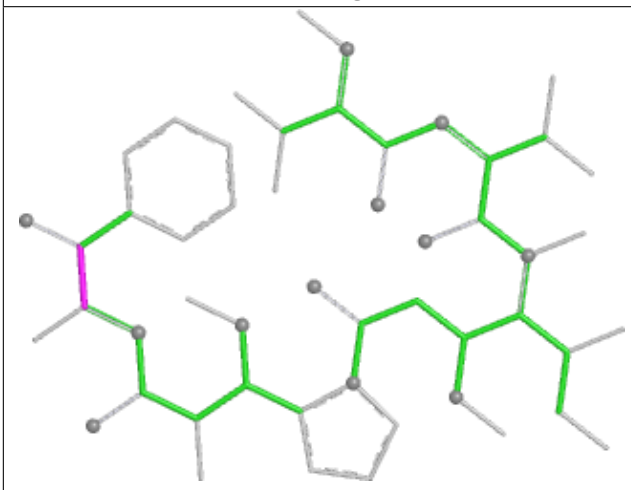
Ligand 4Q5 B 504



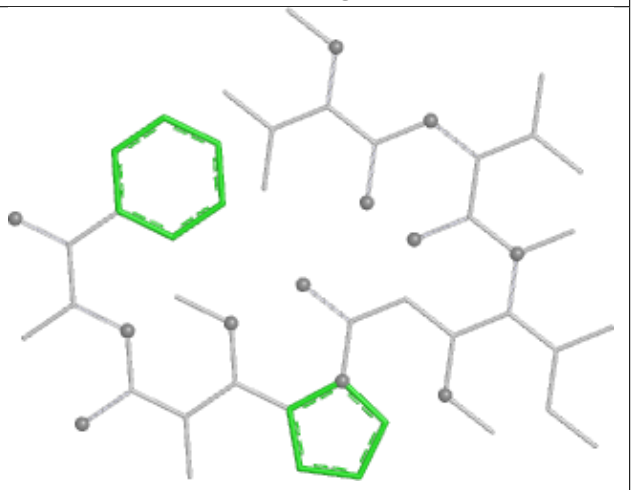
Bond lengths



Bond angles

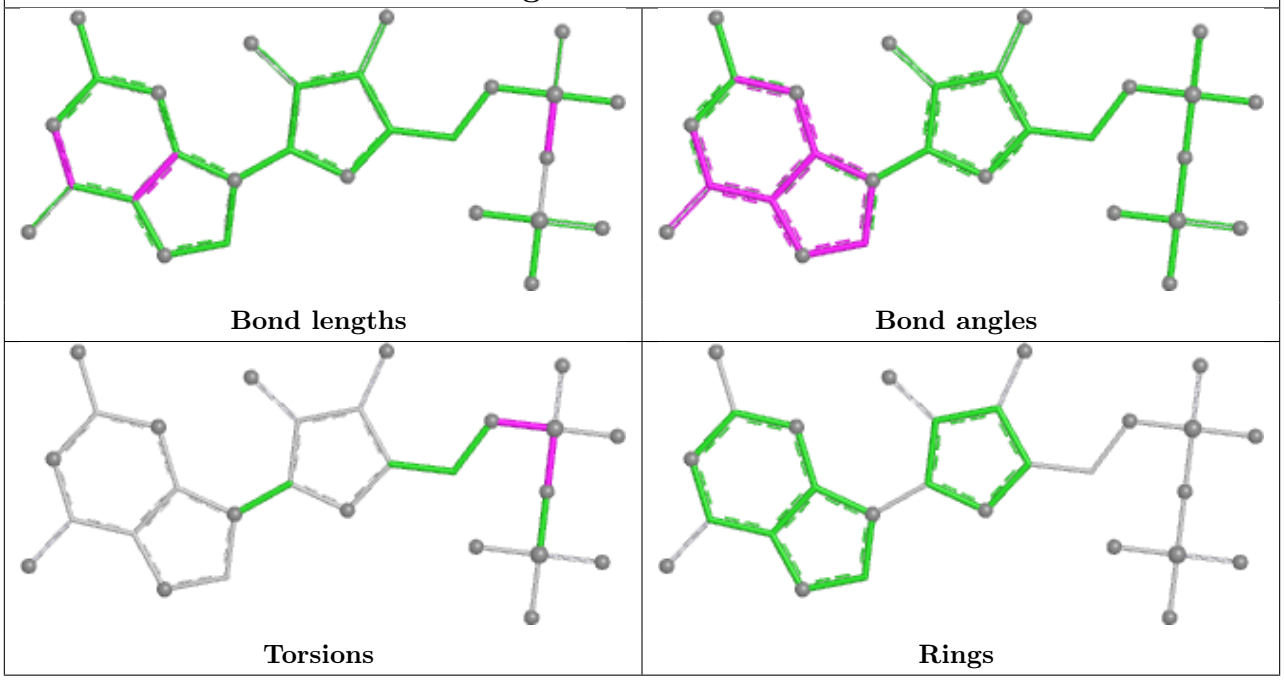


Torsions



Rings

Ligand GDP B 501



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	438:ALA	C	439:THR	N	2.74

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, 95^{th} 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	437/451 (96%)	0.03	6 (1%)	73	73	20, 49, 82, 104	12 (2%)
1	C	440/451 (97%)	-0.22	5 (1%)	78	78	16, 37, 61, 103	11 (2%)
2	B	430/445 (96%)	-0.09	9 (2%)	63	64	18, 40, 79, 132	16 (3%)
2	D	424/445 (95%)	0.24	17 (4%)	42	41	25, 54, 86, 121	6 (1%)
3	E	123/143 (86%)	0.50	5 (4%)	41	41	23, 61, 96, 132	6 (4%)
4	F	331/384 (86%)	0.57	27 (8%)	17	15	37, 69, 125, 156	3 (0%)
All	All	2185/2319 (94%)	0.10	69 (3%)	50	50	16, 49, 95, 156	54 (2%)

The worst 5 of 69 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	E	143	ALA	5.5
4	F	237	THR	5.0
1	C	440	VAL	5.0
4	F	231	ALA	4.3
4	F	103	THR	4.1

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no oligosaccharides in this entry.

6.4 Ligands (i)

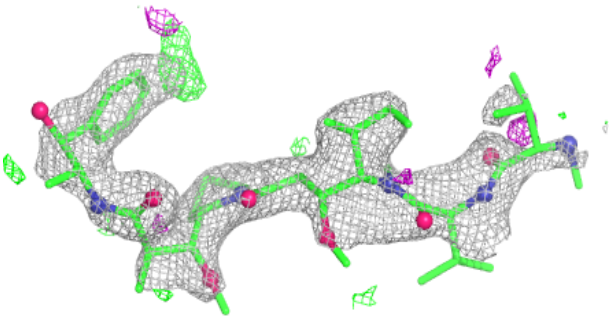
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

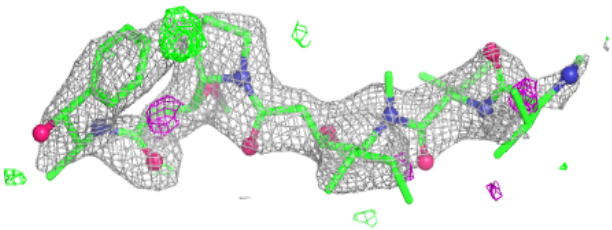
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
10	4Q5	D	503	51/51	0.78	0.19	73,106,125,133	0
9	MES	B	503	12/12	0.85	0.16	55,86,118,124	0
6	MG	B	502	1/1	0.85	0.12	63,63,63,63	0
6	MG	D	502	1/1	0.86	0.17	64,64,64,64	0
6	MG	F	401	1/1	0.89	0.13	78,78,78,78	0
11	ACP	F	402	31/31	0.90	0.10	61,70,108,130	0
7	CA	A	503	1/1	0.94	0.08	67,67,67,67	0
8	GDP	D	501	28/28	0.95	0.08	42,47,57,60	0
7	CA	C	503	1/1	0.96	0.17	86,86,86,86	0
10	4Q5	B	504	51/51	0.97	0.06	26,32,39,42	0
6	MG	A	502	1/1	0.98	0.09	37,37,37,37	0
5	GTP	A	501	32/32	0.98	0.04	30,33,38,39	0
6	MG	C	502	1/1	0.98	0.07	32,32,32,32	0
8	GDP	B	501	28/28	0.99	0.04	25,28,30,31	0
5	GTP	C	501	32/32	0.99	0.04	25,30,32,33	0

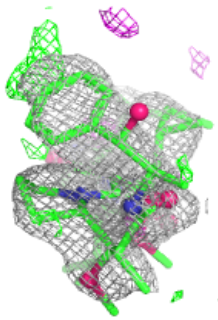
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 4Q5 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)

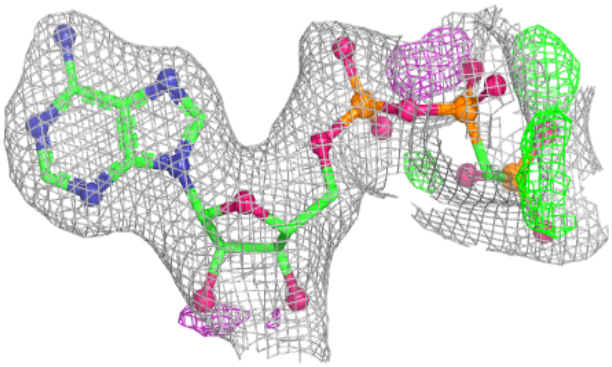


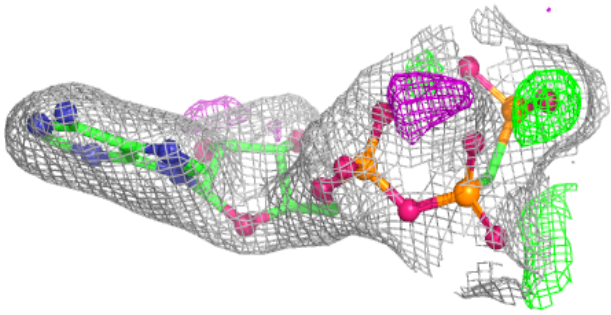


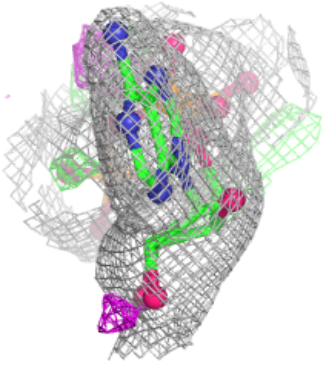


Electron density around ACP F 402:

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

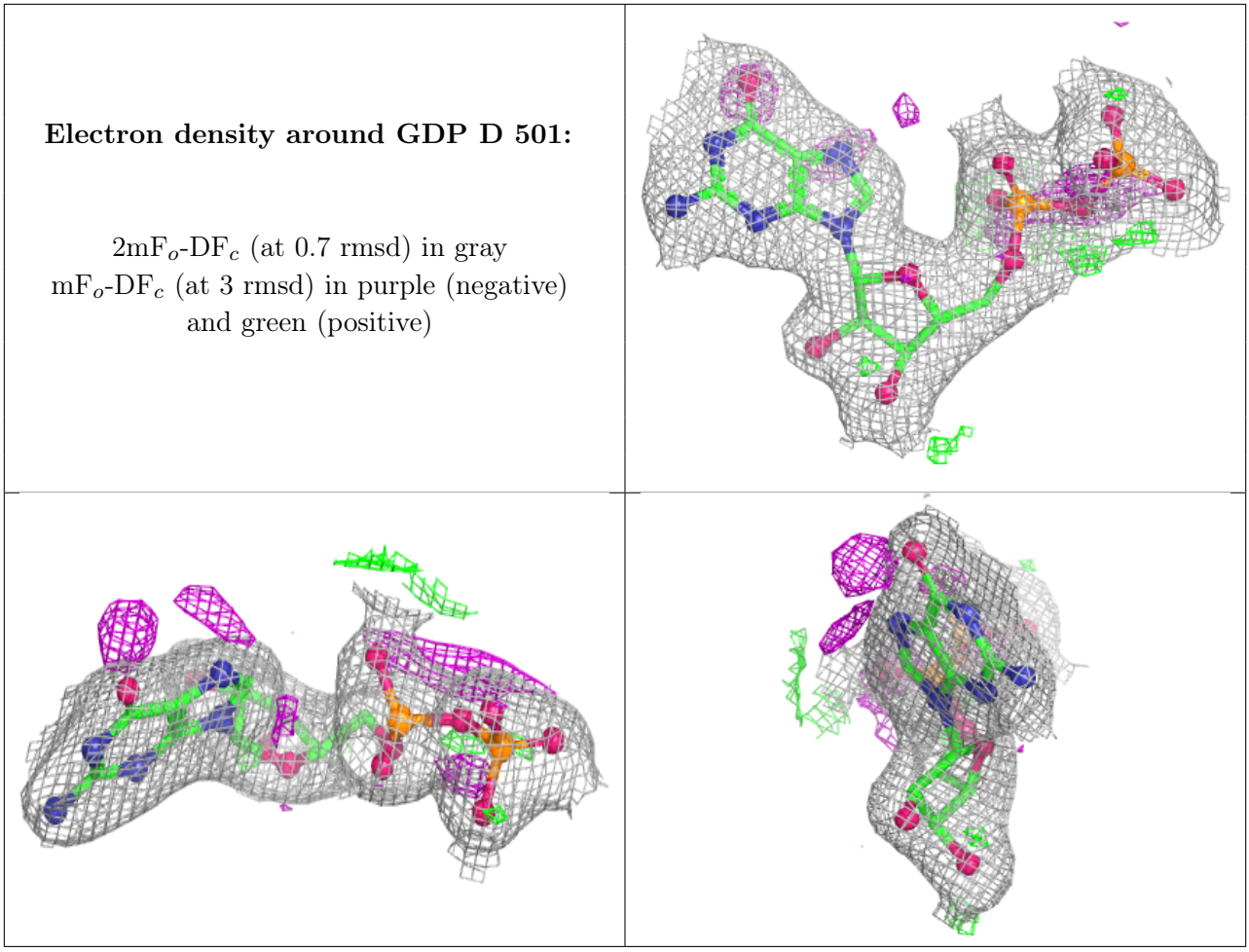






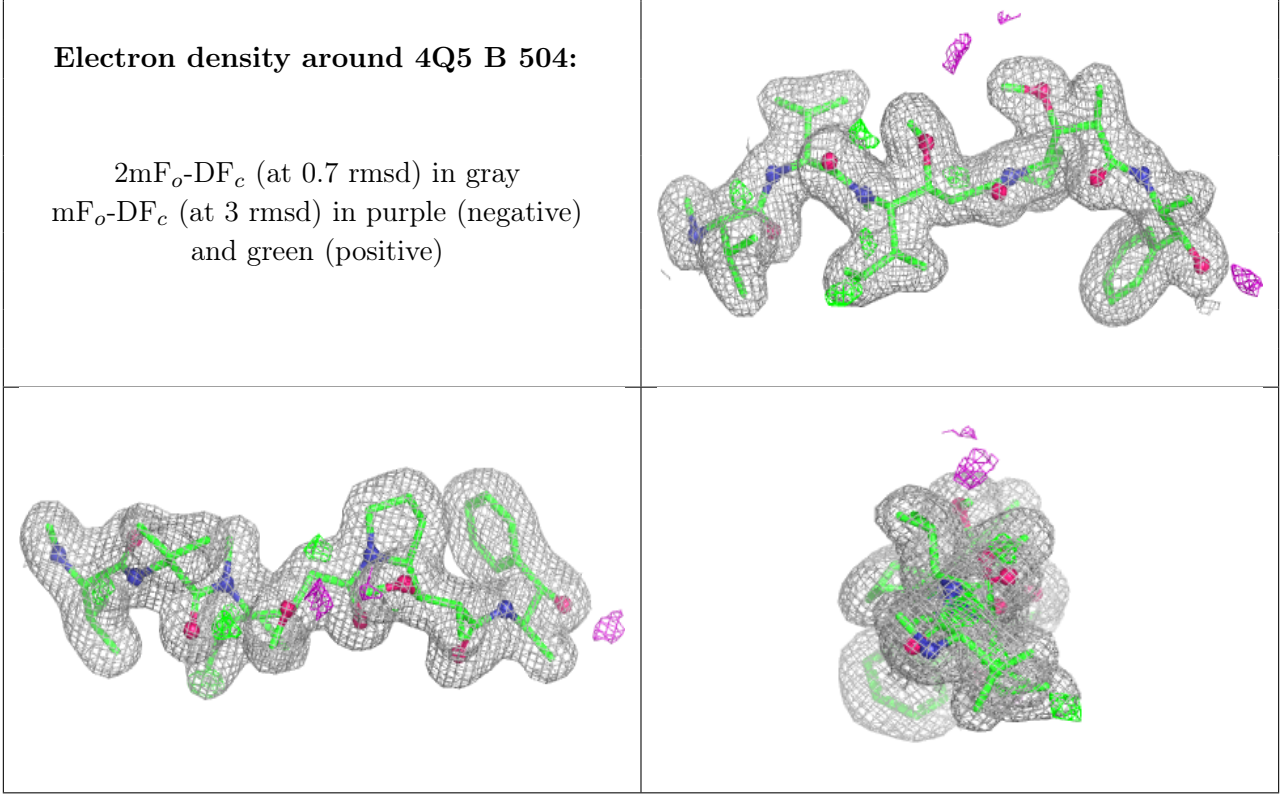
Electron density around GDP D 501:

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



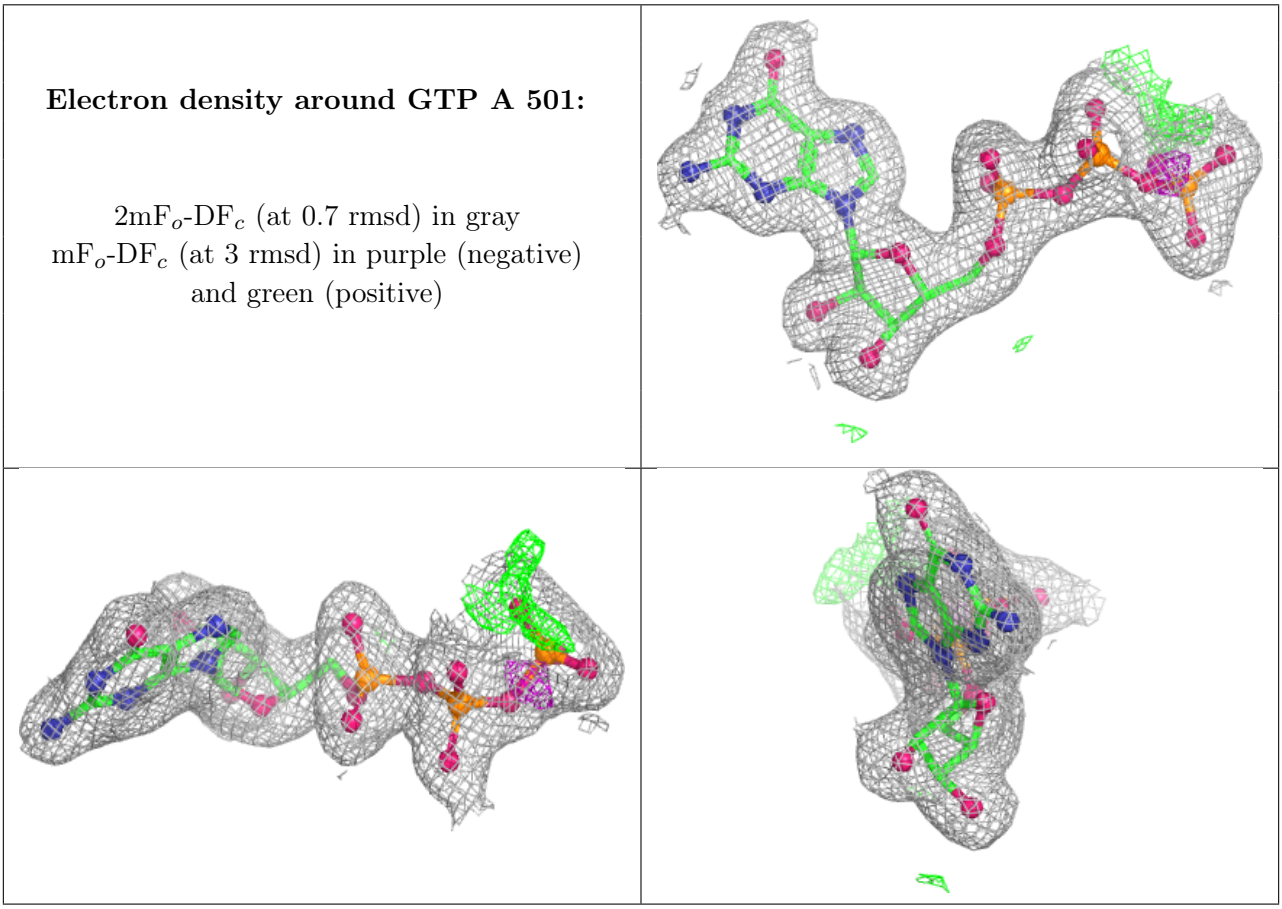
Electron density around 4Q5 B 504:

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



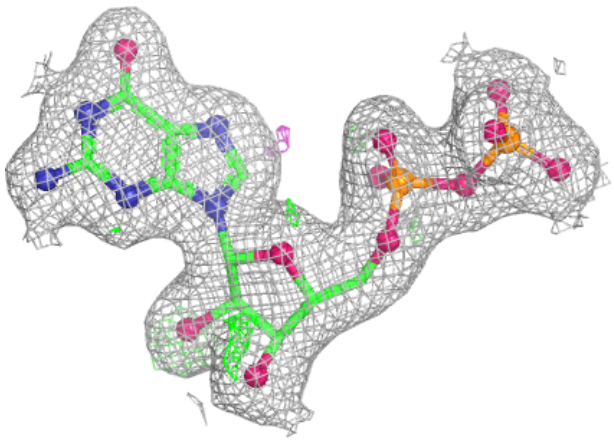
Electron density around GTP A 501:

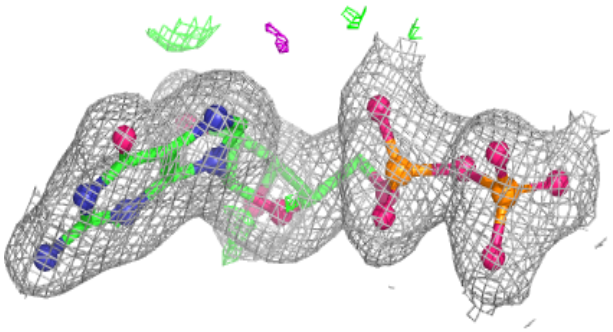
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

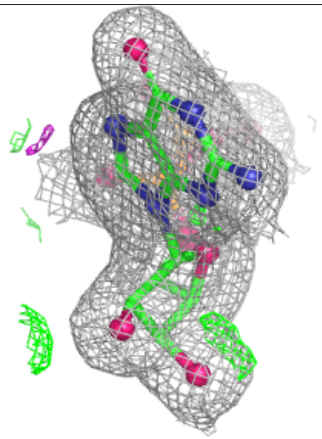


Electron density around GDP B 501:

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

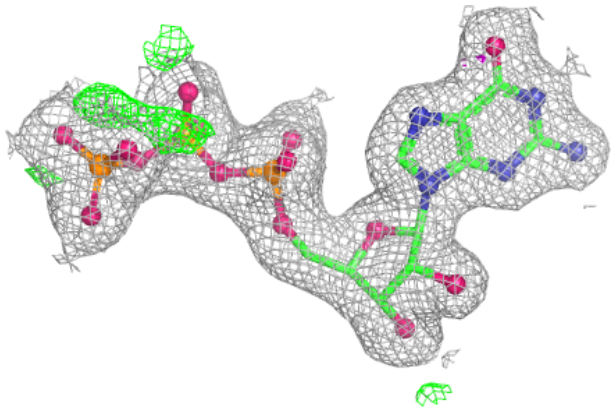


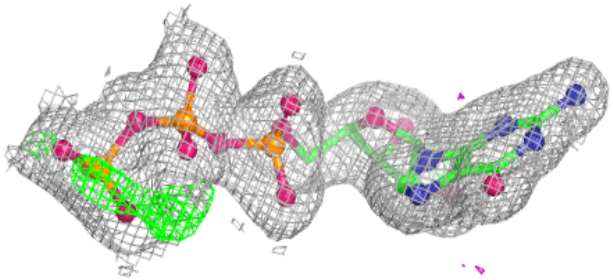


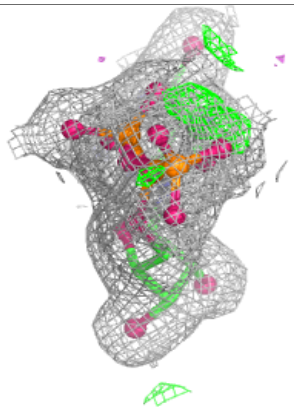


Electron density around GTP C 501:

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







6.5 Other polymers (i)

There are no such residues in this entry.