



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 11:04 AM UTC

PDB ID : 9HG3 / pdb_00009hg3
Title : Crystal structure of M. smegmatis GMP reductase in complex with GMP and GTP.
Authors : Dolezal, M.; Pichova, I.
Deposited on : 2024-11-18
Resolution : 2.30 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

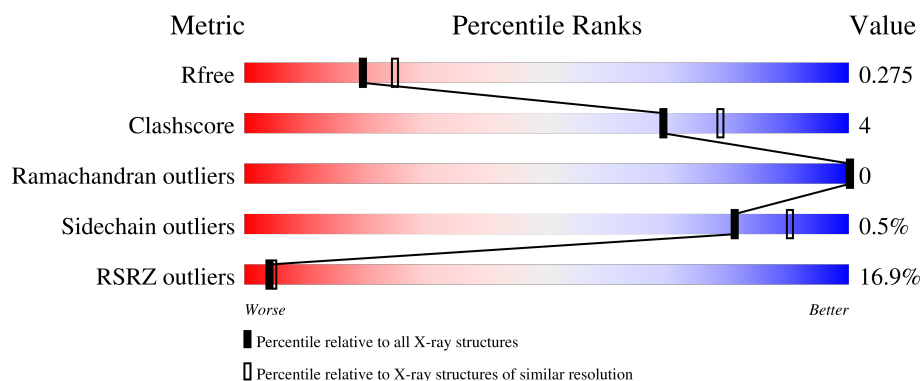
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	496	<div> <div>6%</div> <div> <div></div> <div>85%</div> <div>7%</div> <div>7%</div> </div> </div>
1	B	496	<div> <div>6%</div> <div> <div></div> <div>85%</div> <div>8%</div> <div>7%</div> </div> </div>
1	C	496	<div> <div>6%</div> <div> <div></div> <div>87%</div> <div>6%</div> <div>7%</div> </div> </div>
1	D	496	<div> <div>5%</div> <div> <div></div> <div>85%</div> <div>8%</div> <div>7%</div> </div> </div>
1	E	496	<div> <div>27%</div> <div> <div></div> <div>82%</div> <div>10%</div> <div>7%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	496	<div><div></div><div>36%</div><div></div><div>78%</div><div></div><div>14%</div><div></div><div>7%</div></div>
1	G	496	<div><div></div><div>24%</div><div></div><div>85%</div><div></div><div>8%</div><div></div><div>7%</div></div>
1	H	496	<div><div></div><div>14%</div><div></div><div>84%</div><div></div><div>8%</div><div></div><div>7%</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 27456 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 GMP reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	460	Total	C	N	O	S	0	0	0
			3344	2086	597	647	14			
1	B	460	Total	C	N	O	S	0	0	0
			3344	2086	597	647	14			
1	C	460	Total	C	N	O	S	0	0	0
			3344	2086	597	647	14			
1	D	460	Total	C	N	O	S	0	0	0
			3344	2086	597	647	14			
1	E	460	Total	C	N	O	S	0	0	0
			3344	2086	597	647	14			
1	F	460	Total	C	N	O	S	0	0	0
			3344	2086	597	647	14			
1	G	460	Total	C	N	O	S	0	0	0
			3344	2086	597	647	14			
1	H	460	Total	C	N	O	S	0	0	0
			3344	2086	597	647	14			

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	VAL	-	insertion	UNP A0QYE8
A	480	THR	-	expression tag	UNP A0QYE8
A	481	ALA	-	expression tag	UNP A0QYE8
A	482	ALA	-	expression tag	UNP A0QYE8
A	483	ALA	-	expression tag	UNP A0QYE8
A	484	LYS	-	expression tag	UNP A0QYE8
A	485	GLU	-	expression tag	UNP A0QYE8
A	486	ASP	-	expression tag	UNP A0QYE8
A	487	LEU	-	expression tag	UNP A0QYE8
A	488	GLU	-	expression tag	UNP A0QYE8
A	489	HIS	-	expression tag	UNP A0QYE8
A	490	HIS	-	expression tag	UNP A0QYE8
A	491	HIS	-	expression tag	UNP A0QYE8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	492	HIS	-	expression tag	UNP A0QYE8
A	493	HIS	-	expression tag	UNP A0QYE8
A	494	HIS	-	expression tag	UNP A0QYE8
A	495	HIS	-	expression tag	UNP A0QYE8
A	496	HIS	-	expression tag	UNP A0QYE8
B	2	VAL	-	insertion	UNP A0QYE8
B	480	THR	-	expression tag	UNP A0QYE8
B	481	ALA	-	expression tag	UNP A0QYE8
B	482	ALA	-	expression tag	UNP A0QYE8
B	483	ALA	-	expression tag	UNP A0QYE8
B	484	LYS	-	expression tag	UNP A0QYE8
B	485	GLU	-	expression tag	UNP A0QYE8
B	486	ASP	-	expression tag	UNP A0QYE8
B	487	LEU	-	expression tag	UNP A0QYE8
B	488	GLU	-	expression tag	UNP A0QYE8
B	489	HIS	-	expression tag	UNP A0QYE8
B	490	HIS	-	expression tag	UNP A0QYE8
B	491	HIS	-	expression tag	UNP A0QYE8
B	492	HIS	-	expression tag	UNP A0QYE8
B	493	HIS	-	expression tag	UNP A0QYE8
B	494	HIS	-	expression tag	UNP A0QYE8
B	495	HIS	-	expression tag	UNP A0QYE8
B	496	HIS	-	expression tag	UNP A0QYE8
C	2	VAL	-	insertion	UNP A0QYE8
C	480	THR	-	expression tag	UNP A0QYE8
C	481	ALA	-	expression tag	UNP A0QYE8
C	482	ALA	-	expression tag	UNP A0QYE8
C	483	ALA	-	expression tag	UNP A0QYE8
C	484	LYS	-	expression tag	UNP A0QYE8
C	485	GLU	-	expression tag	UNP A0QYE8
C	486	ASP	-	expression tag	UNP A0QYE8
C	487	LEU	-	expression tag	UNP A0QYE8
C	488	GLU	-	expression tag	UNP A0QYE8
C	489	HIS	-	expression tag	UNP A0QYE8
C	490	HIS	-	expression tag	UNP A0QYE8
C	491	HIS	-	expression tag	UNP A0QYE8
C	492	HIS	-	expression tag	UNP A0QYE8
C	493	HIS	-	expression tag	UNP A0QYE8
C	494	HIS	-	expression tag	UNP A0QYE8
C	495	HIS	-	expression tag	UNP A0QYE8
C	496	HIS	-	expression tag	UNP A0QYE8
D	2	VAL	-	insertion	UNP A0QYE8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	480	THR	-	expression tag	UNP A0QYE8
D	481	ALA	-	expression tag	UNP A0QYE8
D	482	ALA	-	expression tag	UNP A0QYE8
D	483	ALA	-	expression tag	UNP A0QYE8
D	484	LYS	-	expression tag	UNP A0QYE8
D	485	GLU	-	expression tag	UNP A0QYE8
D	486	ASP	-	expression tag	UNP A0QYE8
D	487	LEU	-	expression tag	UNP A0QYE8
D	488	GLU	-	expression tag	UNP A0QYE8
D	489	HIS	-	expression tag	UNP A0QYE8
D	490	HIS	-	expression tag	UNP A0QYE8
D	491	HIS	-	expression tag	UNP A0QYE8
D	492	HIS	-	expression tag	UNP A0QYE8
D	493	HIS	-	expression tag	UNP A0QYE8
D	494	HIS	-	expression tag	UNP A0QYE8
D	495	HIS	-	expression tag	UNP A0QYE8
D	496	HIS	-	expression tag	UNP A0QYE8
E	2	VAL	-	insertion	UNP A0QYE8
E	480	THR	-	expression tag	UNP A0QYE8
E	481	ALA	-	expression tag	UNP A0QYE8
E	482	ALA	-	expression tag	UNP A0QYE8
E	483	ALA	-	expression tag	UNP A0QYE8
E	484	LYS	-	expression tag	UNP A0QYE8
E	485	GLU	-	expression tag	UNP A0QYE8
E	486	ASP	-	expression tag	UNP A0QYE8
E	487	LEU	-	expression tag	UNP A0QYE8
E	488	GLU	-	expression tag	UNP A0QYE8
E	489	HIS	-	expression tag	UNP A0QYE8
E	490	HIS	-	expression tag	UNP A0QYE8
E	491	HIS	-	expression tag	UNP A0QYE8
E	492	HIS	-	expression tag	UNP A0QYE8
E	493	HIS	-	expression tag	UNP A0QYE8
E	494	HIS	-	expression tag	UNP A0QYE8
E	495	HIS	-	expression tag	UNP A0QYE8
E	496	HIS	-	expression tag	UNP A0QYE8
F	2	VAL	-	insertion	UNP A0QYE8
F	480	THR	-	expression tag	UNP A0QYE8
F	481	ALA	-	expression tag	UNP A0QYE8
F	482	ALA	-	expression tag	UNP A0QYE8
F	483	ALA	-	expression tag	UNP A0QYE8
F	484	LYS	-	expression tag	UNP A0QYE8
F	485	GLU	-	expression tag	UNP A0QYE8

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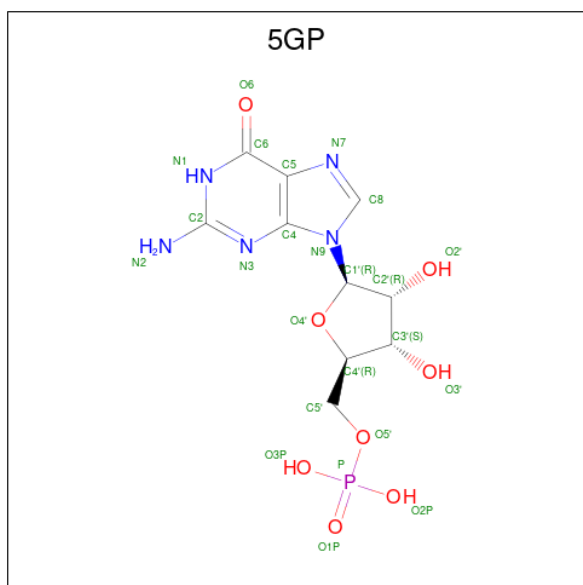
Chain	Residue	Modelled	Actual	Comment	Reference
F	486	ASP	-	expression tag	UNP A0QYE8
F	487	LEU	-	expression tag	UNP A0QYE8
F	488	GLU	-	expression tag	UNP A0QYE8
F	489	HIS	-	expression tag	UNP A0QYE8
F	490	HIS	-	expression tag	UNP A0QYE8
F	491	HIS	-	expression tag	UNP A0QYE8
F	492	HIS	-	expression tag	UNP A0QYE8
F	493	HIS	-	expression tag	UNP A0QYE8
F	494	HIS	-	expression tag	UNP A0QYE8
F	495	HIS	-	expression tag	UNP A0QYE8
F	496	HIS	-	expression tag	UNP A0QYE8
G	2	VAL	-	insertion	UNP A0QYE8
G	480	THR	-	expression tag	UNP A0QYE8
G	481	ALA	-	expression tag	UNP A0QYE8
G	482	ALA	-	expression tag	UNP A0QYE8
G	483	ALA	-	expression tag	UNP A0QYE8
G	484	LYS	-	expression tag	UNP A0QYE8
G	485	GLU	-	expression tag	UNP A0QYE8
G	486	ASP	-	expression tag	UNP A0QYE8
G	487	LEU	-	expression tag	UNP A0QYE8
G	488	GLU	-	expression tag	UNP A0QYE8
G	489	HIS	-	expression tag	UNP A0QYE8
G	490	HIS	-	expression tag	UNP A0QYE8
G	491	HIS	-	expression tag	UNP A0QYE8
G	492	HIS	-	expression tag	UNP A0QYE8
G	493	HIS	-	expression tag	UNP A0QYE8
G	494	HIS	-	expression tag	UNP A0QYE8
G	495	HIS	-	expression tag	UNP A0QYE8
G	496	HIS	-	expression tag	UNP A0QYE8
H	2	VAL	-	insertion	UNP A0QYE8
H	480	THR	-	expression tag	UNP A0QYE8
H	481	ALA	-	expression tag	UNP A0QYE8
H	482	ALA	-	expression tag	UNP A0QYE8
H	483	ALA	-	expression tag	UNP A0QYE8
H	484	LYS	-	expression tag	UNP A0QYE8
H	485	GLU	-	expression tag	UNP A0QYE8
H	486	ASP	-	expression tag	UNP A0QYE8
H	487	LEU	-	expression tag	UNP A0QYE8
H	488	GLU	-	expression tag	UNP A0QYE8
H	489	HIS	-	expression tag	UNP A0QYE8
H	490	HIS	-	expression tag	UNP A0QYE8
H	491	HIS	-	expression tag	UNP A0QYE8

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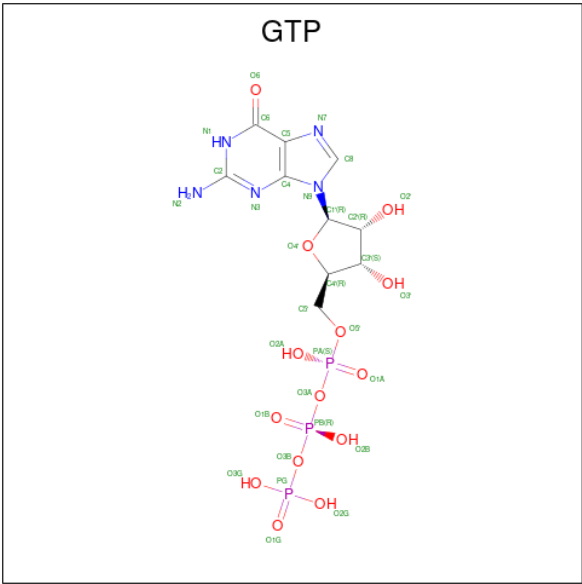
Chain	Residue	Modelled	Actual	Comment	Reference
H	492	HIS	-	expression tag	UNP A0QYE8
H	493	HIS	-	expression tag	UNP A0QYE8
H	494	HIS	-	expression tag	UNP A0QYE8
H	495	HIS	-	expression tag	UNP A0QYE8
H	496	HIS	-	expression tag	UNP A0QYE8

- Molecule 2 is GUANOSINE-5'-MONOPHOSPHATE (CCD ID: 5GP) (formula: $C_{10}H_{14}N_5O_8P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			24	10	5	8	1		
2	B	1	Total	C	N	O	P	0	0
			24	10	5	8	1		
2	C	1	Total	C	N	O	P	0	0
			24	10	5	8	1		
2	D	1	Total	C	N	O	P	0	0
			24	10	5	8	1		
2	E	1	Total	C	N	O	P	0	0
			24	10	5	8	1		
2	F	1	Total	C	N	O	P	0	0
			24	10	5	8	1		
2	G	1	Total	C	N	O	P	0	0
			24	10	5	8	1		
2	H	1	Total	C	N	O	P	0	0
			24	10	5	8	1		

- Molecule 3 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃) (labeled as "Ligand of Interest" by depositor).

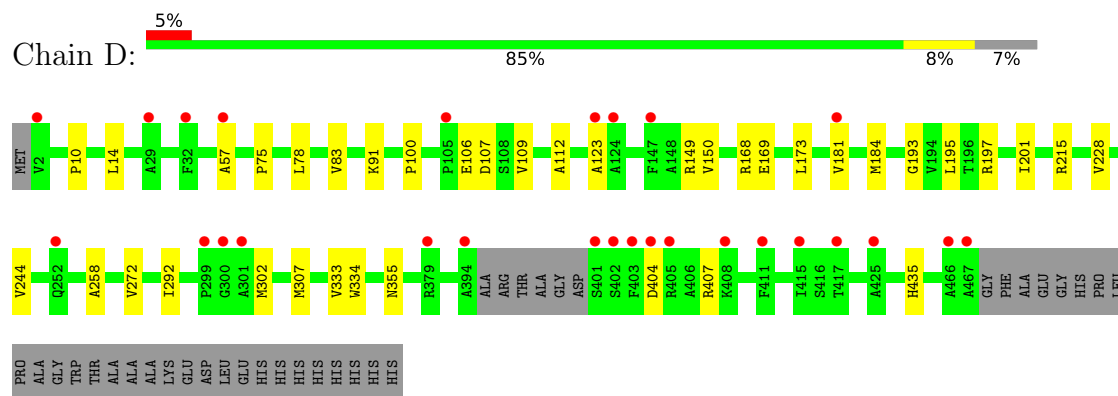


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	1
			64	20	10	28	6		
3	B	1	Total	C	N	O	P	0	1
			64	20	10	28	6		
3	C	1	Total	C	N	O	P	0	1
			64	20	10	28	6		
3	D	1	Total	C	N	O	P	0	1
			64	20	10	28	6		
3	E	1	Total	C	N	O	P	0	1
			64	20	10	28	6		
3	F	1	Total	C	N	O	P	0	1
			64	20	10	28	6		
3	G	1	Total	C	N	O	P	0	1
			64	20	10	28	6		
3	H	1	Total	C	N	O	P	0	1
			64	20	10	28	6		

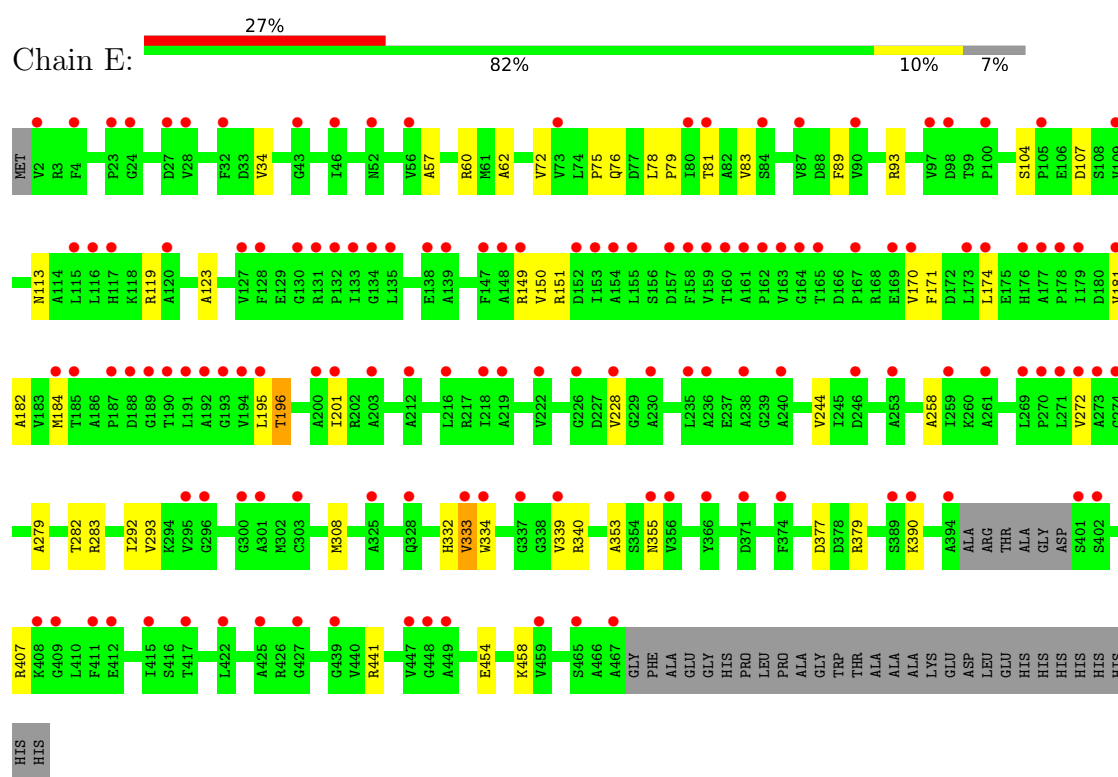
- Molecule 1: GMP reductase



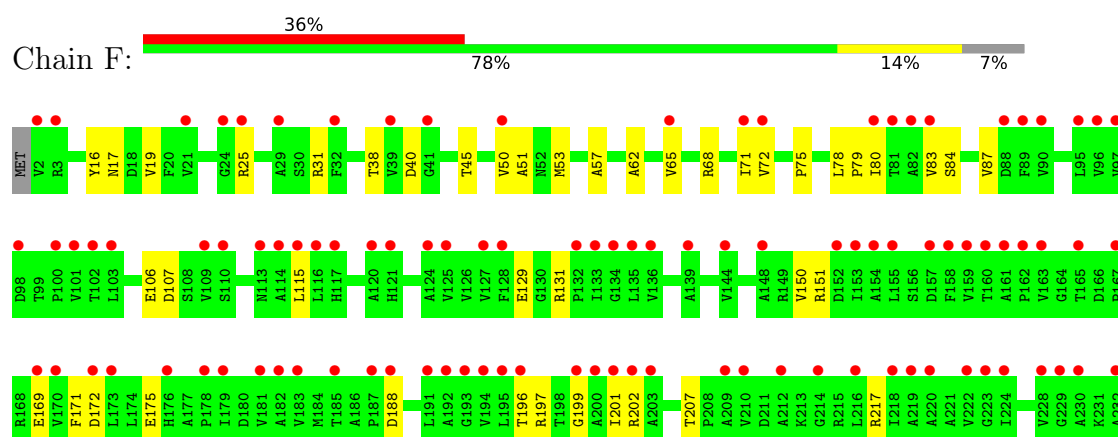
• Molecule 1: GMP reductase

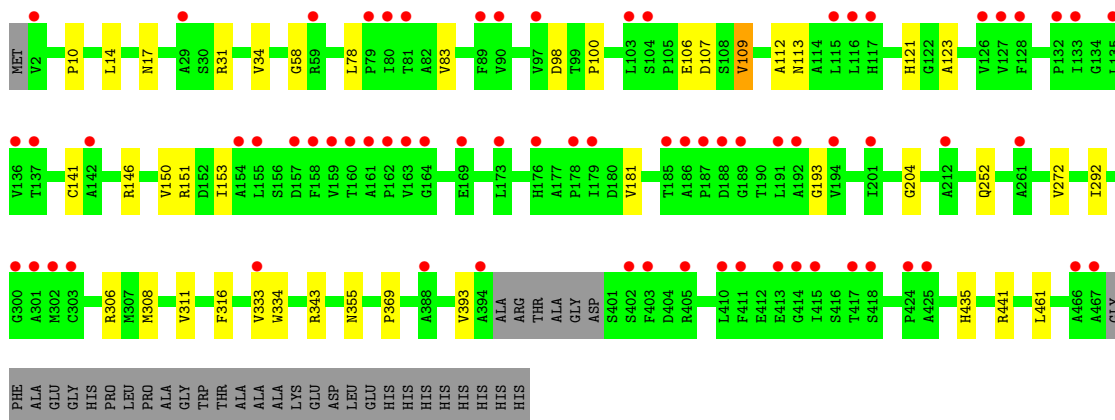


• Molecule 1: GMP reductase



• Molecule 1: GMP reductase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	113.08Å 145.93Å 146.32Å 90.00° 95.93° 90.00°	Depositor
Resolution (Å)	112.48 – 2.30 112.48 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.4 (112.48-2.30) 99.5 (112.48-2.30)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.02 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.21_5204	Depositor
R, R_{free}	0.250 , 0.274 0.251 , 0.275	Depositor DCC
R_{free} test set	10407 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	58.1	Xtriage
Anisotropy	0.153	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 42.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	27456	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 43.20 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.8267e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: 5GP, GTP

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	0.08	0/3397	0.22	0/4625
1	B	0.08	0/3397	0.23	0/4625
1	C	0.07	0/3397	0.21	0/4625
1	D	0.08	0/3397	0.22	0/4625
1	E	0.09	0/3397	0.23	0/4625
1	F	0.12	0/3397	0.26	0/4625
1	G	0.08	0/3397	0.22	0/4625
1	H	0.08	0/3397	0.22	0/4625
All	All	0.09	0/27176	0.23	0/37000

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	3344	0	3343	22	0
1	B	3344	0	3343	24	0
1	C	3344	0	3343	20	0
1	D	3344	0	3343	22	0
1	E	3344	0	3343	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	3344	0	3343	47	0
1	G	3344	0	3343	25	0
1	H	3344	0	3343	22	0
2	A	24	0	12	0	0
2	B	24	0	12	0	0
2	C	24	0	12	0	0
2	D	24	0	12	0	0
2	E	24	0	12	0	0
2	F	24	0	12	0	0
2	G	24	0	12	0	0
2	H	24	0	12	0	0
3	A	64	0	24	0	0
3	B	64	0	24	0	0
3	C	64	0	24	0	0
3	D	64	0	24	0	0
3	E	64	0	24	0	0
3	F	64	0	24	2	0
3	G	64	0	24	0	0
3	H	64	0	24	0	0
All	All	27456	0	27032	193	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.

All (193) 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:F:342:PRO:HB3	1:F:436:ILE:HA	1.73	0.70
1:F:17:ASN:OD1	1:F:343:ARG:NH2	2.27	0.67
1:H:17:ASN:OD1	1:H:343:ARG:NH2	2.28	0.66
1:F:45:THR:HG21	1:F:207:THR:HB	1.78	0.65
1:A:404:ASP:HA	1:A:407:ARG:HD3	1.79	0.64
1:F:106:GLU:OE2	1:F:151:ARG:NH2	2.22	0.64
1:H:106:GLU:OE2	1:H:151:ARG:NH1	2.28	0.64
1:F:275:ASN:ND2	1:F:296:GLY:O	2.30	0.63
1:H:141:CYS:O	1:H:146:ARG:NH2	2.31	0.63
1:B:146:ARG:HA	1:B:146:ARG:HE	1.64	0.63
1:C:17:ASN:OD1	1:C:343:ARG:NH2	2.32	0.62
1:F:78:LEU:HD12	1:F:79:PRO:HD2	1.82	0.61
1:C:272:VAL:HG22	1:C:292:ILE:HB	1.82	0.61
1:F:196:THR:HG23	1:F:199:GLY:H	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:272:VAL:HG22	1:E:292:ILE:HB	1.83	0.61
1:F:282:THR:HG23	1:F:293:VAL:HG21	1.83	0.60
1:H:272:VAL:HG22	1:H:292:ILE:HB	1.83	0.60
1:B:123:ALA:HB3	1:B:181:VAL:HG21	1.84	0.60
1:C:78:LEU:HD12	1:C:79:PRO:HD2	1.85	0.59
1:B:31:ARG:NH1	1:B:442:SER:OG	2.35	0.59
1:C:342:PRO:HB3	1:C:436:ILE:HA	1.84	0.59
1:F:454:GLU:HB3	1:F:458:LYS:HE3	1.84	0.58
1:G:272:VAL:HG22	1:G:292:ILE:HB	1.86	0.57
1:E:78:LEU:HD12	1:E:79:PRO:HD2	1.86	0.57
1:E:244:VAL:HG22	1:E:272:VAL:HB	1.87	0.57
1:D:272:VAL:HG22	1:D:292:ILE:HB	1.87	0.56
1:B:131:ARG:NH1	1:B:188:ASP:O	2.38	0.56
1:F:217:ARG:HH11	1:F:241:ASP:HB3	1.71	0.55
1:H:100:PRO:HD3	1:H:193:GLY:HA2	1.88	0.55
1:C:123:ALA:HB3	1:C:181:VAL:HG21	1.89	0.55
1:B:272:VAL:HG22	1:B:292:ILE:HB	1.89	0.55
1:G:464:GLN:OE1	1:H:306:ARG:NH1	2.36	0.55
1:A:17:ASN:OD1	1:A:343:ARG:NH2	2.38	0.55
1:H:316:PHE:HZ	1:H:461:LEU:HD13	1.72	0.55
1:G:334:TRP:CD1	1:G:355:ASN:HB2	2.42	0.54
1:E:407:ARG:NH2	1:H:204:GLY:O	2.40	0.54
1:F:171:PHE:CE2	1:F:201:ILE:HD11	2.43	0.54
1:A:435:HIS:NE2	1:B:308:MET:SD	2.81	0.54
1:B:339:VAL:O	1:B:340:ARG:NH1	2.39	0.54
1:F:171:PHE:HE2	1:F:201:ILE:HD11	1.74	0.53
1:F:25:ARG:HH21	1:G:253:ALA:HB2	1.74	0.53
1:H:252:GLN:HE22	1:H:393:VAL:HG11	1.73	0.53
1:F:19:VAL:HG23	1:F:347:LEU:HD13	1.90	0.53
1:G:225:ASN:O	1:G:231:LYS:NZ	2.42	0.53
1:F:71:ILE:HD12	1:F:217:ARG:HB3	1.92	0.52
1:C:100:PRO:HD3	1:C:193:GLY:HA2	1.92	0.52
1:C:343:ARG:NH1	1:C:344:ASP:OD1	2.43	0.52
1:E:123:ALA:HB3	1:E:181:VAL:HG21	1.92	0.52
1:A:272:VAL:HG22	1:A:292:ILE:HB	1.91	0.52
1:F:342:PRO:HG2	1:G:308:MET:HA	1.91	0.51
1:E:170:VAL:HG21	1:E:184:MET:HE1	1.92	0.51
1:A:184:MET:HE3	1:A:195:LEU:HB3	1.93	0.51
1:F:251:HIS:HB2	1:F:276:VAL:HG12	1.91	0.51
1:B:31:ARG:NH2	1:C:411:PHE:O	2.44	0.51
1:F:258:ALA:O	1:F:262:VAL:HG23	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:25:ARG:NH2	1:G:253:ALA:HB2	2.27	0.50
1:G:435:HIS:NE2	1:H:308:MET:SD	2.85	0.50
1:A:316:PHE:HZ	1:A:461:LEU:HD13	1.77	0.50
1:G:302:MET:HA	1:G:307:MET:HE3	1.93	0.50
1:D:106:GLU:O	1:D:149:ARG:HD3	2.12	0.50
1:F:31:ARG:HB3	1:F:441:ARG:HB3	1.93	0.49
1:D:302:MET:HA	1:D:307:MET:HE3	1.95	0.49
1:E:333:VAL:HG12	1:E:353:ALA:HA	1.94	0.49
1:F:435:HIS:NE2	1:G:308:MET:SD	2.85	0.49
1:D:100:PRO:HD3	1:D:193:GLY:HA2	1.95	0.49
1:E:282:THR:HG23	1:E:293:VAL:HG21	1.95	0.48
1:H:31:ARG:HB3	1:H:441:ARG:HB3	1.94	0.48
1:F:255:MET:HE1	1:F:273:ALA:HB1	1.94	0.48
1:A:106:GLU:OE2	1:A:151:ARG:NH2	2.46	0.48
1:B:316:PHE:HZ	1:B:461:LEU:HD13	1.78	0.48
1:C:147:PHE:HB3	3:F:502[B]:GTP:H4'	1.95	0.48
1:E:228:VAL:HG11	1:E:258:ALA:HB1	1.94	0.48
1:F:202:ARG:NH2	1:F:434:ASP:OD2	2.42	0.48
1:F:175:GLU:HA	1:F:197:ARG:NH1	2.28	0.48
1:H:123:ALA:HB3	1:H:181:VAL:HG21	1.96	0.48
1:A:308:MET:SD	1:D:435:HIS:NE2	2.86	0.48
1:D:107:ASP:O	1:D:150:VAL:HG13	2.13	0.48
1:F:83:VAL:O	1:F:87:VAL:HG23	2.14	0.47
1:E:454:GLU:HB3	1:E:458:LYS:HD2	1.96	0.47
1:A:100:PRO:HD3	1:A:193:GLY:HA2	1.97	0.47
1:E:308:MET:SD	1:H:435:HIS:NE2	2.88	0.47
1:E:334:TRP:CD1	1:E:355:ASN:HB2	2.50	0.47
1:F:78:LEU:HD23	1:F:83:VAL:HG22	1.97	0.47
1:G:100:PRO:HD3	1:G:193:GLY:HA2	1.97	0.46
1:F:80:ILE:O	1:F:84:SER:OG	2.28	0.46
1:B:91:LYS:HB3	1:B:215:ARG:HD2	1.98	0.46
1:B:100:PRO:HD3	1:B:193:GLY:HA2	1.98	0.46
1:E:292:ILE:HD12	1:E:332:HIS:HB2	1.98	0.46
1:F:129:GLU:O	1:F:131:ARG:NH1	2.44	0.46
1:E:171:PHE:CE1	1:E:201:ILE:HD11	2.50	0.46
1:D:404:ASP:HA	1:D:407:ARG:HD3	1.97	0.46
1:G:379:ARG:HE	1:G:380:PRO:HD2	1.80	0.46
1:E:89:PHE:O	1:E:93:ARG:HG2	2.16	0.46
1:A:403:PHE:HB2	1:D:168:ARG:CZ	2.46	0.46
1:C:404:ASP:N	1:C:404:ASP:OD1	2.46	0.46
1:B:78:LEU:HD23	1:B:83:VAL:HG22	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:78:LEU:HD23	1:C:83:VAL:HG22	1.98	0.45
1:D:78:LEU:HD23	1:D:83:VAL:HG22	1.98	0.45
1:E:34:VAL:O	1:E:441:ARG:NH1	2.47	0.45
1:F:40:ASP:HA	1:F:332:HIS:CD2	2.51	0.45
1:F:50:VAL:HB	1:F:72:VAL:HA	1.98	0.45
1:G:40:ASP:OD2	1:G:355:ASN:ND2	2.49	0.45
1:A:224:ILE:HD11	1:A:393:VAL:HG22	1.98	0.45
1:D:109:VAL:HA	1:D:112:ALA:HB3	1.97	0.45
1:H:98:ASP:OD2	1:H:121:HIS:HE1	1.99	0.45
1:A:78:LEU:HD23	1:A:83:VAL:HG22	1.99	0.45
1:F:68:ARG:HH21	1:F:202:ARG:HB2	1.82	0.45
1:G:74:LEU:HD21	1:G:218:ILE:HD11	1.99	0.45
1:H:58:GLY:HA3	1:H:369:PRO:HG3	1.98	0.45
1:B:31:ARG:HB3	1:B:441:ARG:HB3	1.98	0.45
1:F:434:ASP:OD2	1:G:410:LEU:HD11	2.17	0.45
1:G:109:VAL:HA	1:G:112:ALA:HB3	1.98	0.45
1:H:34:VAL:O	1:H:441:ARG:NH1	2.50	0.44
1:F:38:THR:HG21	1:F:355:ASN:HD21	1.83	0.44
1:F:171:PHE:C	1:F:171:PHE:CD1	2.96	0.44
1:G:123:ALA:HB3	1:G:181:VAL:HG21	1.99	0.44
1:E:279:ALA:O	1:E:283:ARG:HG2	2.17	0.44
1:A:197:ARG:O	1:A:201:ILE:HG12	2.18	0.44
1:A:403:PHE:CE1	1:D:201:ILE:HD13	2.52	0.44
1:D:91:LYS:HB3	1:D:215:ARG:HD2	1.99	0.44
1:D:184:MET:HE3	1:D:195:LEU:HB3	2.00	0.44
1:G:446:TYR:CG	1:H:311:VAL:HG11	2.53	0.44
1:F:349:LEU:HD13	1:F:452:LEU:HD22	1.99	0.44
1:G:31:ARG:HB3	1:G:441:ARG:HB3	2.00	0.44
1:C:91:LYS:NZ	1:C:241:ASP:OD2	2.41	0.43
1:F:51:ALA:HB3	1:F:53:MET:HE2	1.99	0.43
1:A:58:GLY:HA3	1:A:369:PRO:HG3	1.99	0.43
1:F:107:ASP:O	1:F:150:VAL:HG23	2.18	0.43
1:D:10:PRO:HG3	1:D:14:LEU:HD21	1.99	0.43
1:E:57:ALA:HB3	1:E:75:PRO:HD3	2.00	0.43
1:B:53:MET:HB2	1:B:56:VAL:HG12	1.99	0.43
1:C:10:PRO:HG3	1:C:14:LEU:HD21	2.01	0.43
1:C:147:PHE:HB3	3:F:502[A]:GTP:H4'	1.99	0.43
1:F:65:VAL:HG23	1:F:433:LEU:HD11	2.00	0.43
1:H:10:PRO:HG3	1:H:14:LEU:HD21	2.00	0.43
1:E:104:SER:N	1:E:107:ASP:OD2	2.46	0.43
1:B:401:SER:OG	1:B:402:SER:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:435:HIS:NE2	1:C:308:MET:SD	2.92	0.43
1:F:169:GLU:HA	1:F:172:ASP:OD2	2.18	0.43
1:F:62:ALA:HA	1:F:72:VAL:HG21	2.01	0.43
1:B:10:PRO:HG3	1:B:14:LEU:HD21	2.01	0.43
1:A:217:ARG:HA	1:A:241:ASP:OD2	2.19	0.42
1:A:403:PHE:CD2	1:A:407:ARG:HD2	2.53	0.42
1:C:197:ARG:O	1:C:201:ILE:HG12	2.19	0.42
1:D:123:ALA:HB3	1:D:181:VAL:HG21	2.02	0.42
1:E:78:LEU:HD23	1:E:83:VAL:HG22	1.99	0.42
1:E:334:TRP:NE1	1:E:355:ASN:HB2	2.34	0.42
1:D:168:ARG:HA	1:D:168:ARG:HD2	1.92	0.42
1:H:78:LEU:HD23	1:H:83:VAL:HG22	2.01	0.42
1:E:377:ASP:HB2	1:E:379:ARG:HG3	2.00	0.42
1:F:171:PHE:C	1:F:171:PHE:HD1	2.27	0.42
1:G:10:PRO:HG3	1:G:14:LEU:HD21	2.02	0.42
1:G:387:MET:HB3	1:G:390:LYS:HB2	2.02	0.42
1:H:334:TRP:CD1	1:H:355:ASN:HB2	2.54	0.42
1:B:224:ILE:HD11	1:B:393:VAL:HG22	2.01	0.42
1:D:334:TRP:CD1	1:D:355:ASN:HB2	2.55	0.42
1:E:60:ARG:HG2	1:E:119:ARG:HH11	1.84	0.42
1:E:62:ALA:HA	1:E:72:VAL:HG21	2.02	0.42
1:E:149:ARG:HB2	1:E:151:ARG:HG2	2.01	0.42
1:H:109:VAL:HA	1:H:112:ALA:HB3	2.01	0.42
1:D:57:ALA:HB3	1:D:75:PRO:HD3	2.02	0.42
1:E:174:LEU:HD11	1:E:182:ALA:HB2	2.02	0.42
1:G:62:ALA:HA	1:G:72:VAL:HG21	2.01	0.42
1:C:147:PHE:CZ	1:F:115:LEU:HG	2.55	0.41
1:E:339:VAL:O	1:E:340:ARG:NH1	2.49	0.41
1:D:244:VAL:HG22	1:D:272:VAL:HB	2.02	0.41
1:B:81:THR:O	1:B:85:GLU:HG3	2.21	0.41
1:D:169:GLU:O	1:D:173:LEU:HG	2.19	0.41
1:B:228:VAL:HG11	1:B:258:ALA:HB1	2.02	0.41
1:E:76:GLN:NE2	1:E:390:LYS:O	2.51	0.41
1:C:136:VAL:HG21	1:C:150:VAL:HG13	2.03	0.41
1:E:60:ARG:HG2	1:E:119:ARG:NH1	2.36	0.41
1:C:57:ALA:HB3	1:C:75:PRO:HD3	2.01	0.41
1:A:131:ARG:HG2	1:A:190:THR:HA	2.03	0.41
1:E:107:ASP:O	1:E:150:VAL:HG23	2.20	0.41
1:A:31:ARG:HB3	1:A:441:ARG:HB3	2.02	0.41
1:B:170:VAL:HG11	1:B:195:LEU:HD23	2.03	0.41
1:F:188:ASP:OD1	1:F:188:ASP:N	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:228:VAL:HG11	1:D:258:ALA:HB1	2.03	0.41
1:F:57:ALA:HB3	1:F:75:PRO:HD3	2.02	0.41
1:A:57:ALA:HB3	1:A:75:PRO:HD3	2.02	0.40
1:A:168:ARG:CZ	1:B:403:PHE:HB2	2.51	0.40
1:A:446:TYR:CG	1:B:311:VAL:HG11	2.56	0.40
1:C:180:ASP:OD2	1:C:197:ARG:HD3	2.21	0.40
1:B:78:LEU:HD12	1:B:79:PRO:HD2	2.04	0.40
1:D:197:ARG:O	1:D:201:ILE:HG12	2.21	0.40
1:E:195:LEU:HD13	1:E:196:THR:O	2.21	0.40
1:F:16:TYR:HB3	1:F:343:ARG:HH12	1.87	0.40
1:F:343:ARG:HD3	1:G:306:ARG:O	2.22	0.40
1:G:57:ALA:HB3	1:G:75:PRO:HD3	2.03	0.40
1:H:107:ASP:O	1:H:150:VAL:HG23	2.21	0.40
1:F:316:PHE:HZ	1:F:461:LEU:HD13	1.85	0.40
1:G:79:PRO:O	1:G:83:VAL:HG23	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	456/496 (92%)	442 (97%)	14 (3%)	0	100	100
1	B	456/496 (92%)	443 (97%)	13 (3%)	0	100	100
1	C	456/496 (92%)	442 (97%)	14 (3%)	0	100	100
1	D	456/496 (92%)	442 (97%)	14 (3%)	0	100	100
1	E	456/496 (92%)	439 (96%)	17 (4%)	0	100	100
1	F	456/496 (92%)	440 (96%)	16 (4%)	0	100	100
1	G	456/496 (92%)	439 (96%)	17 (4%)	0	100	100
1	H	456/496 (92%)	439 (96%)	17 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	3648/3968 (92%)	3526 (97%)	122 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	345/372 (93%)	344 (100%)	1 (0%)	86	93
1	B	345/372 (93%)	345 (100%)	0	100	100
1	C	345/372 (93%)	344 (100%)	1 (0%)	86	93
1	D	345/372 (93%)	344 (100%)	1 (0%)	86	93
1	E	345/372 (93%)	341 (99%)	4 (1%)	63	79
1	F	345/372 (93%)	344 (100%)	1 (0%)	86	93
1	G	345/372 (93%)	344 (100%)	1 (0%)	86	93
1	H	345/372 (93%)	341 (99%)	4 (1%)	63	79
All	All	2760/2976 (93%)	2747 (100%)	13 (0%)	81	90

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	333	VAL
1	C	404	ASP
1	D	333	VAL
1	E	81	THR
1	E	113	ASN
1	E	196	THR
1	E	333	VAL
1	F	235	LEU
1	G	333	VAL
1	H	109	VAL
1	H	113	ASN
1	H	153	ILE

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Mol	Chain	Res	Type
1	H	333	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	176	HIS
1	A	341	HIS
1	B	113	ASN
1	B	117	HIS
1	B	341	HIS
1	C	176	HIS
1	C	341	HIS
1	D	117	HIS
1	D	332	HIS
1	D	464	GLN
1	E	328	GLN
1	E	341	HIS
1	F	252	GLN
1	F	341	HIS
1	G	332	HIS
1	H	121	HIS
1	H	252	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 ⓘ

24 ligands are modelled in this entry.

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	$\# Z > 2$
3	GTP	E	502[A]	-	33,34,34	0.59	0	50,54,54	0.47	0
3	GTP	C	502[A]	-	33,34,34	0.58	0	50,54,54	0.46	0
3	GTP	G	502[A]	-	33,34,34	0.59	0	50,54,54	0.47	0
2	5GP	B	501	-	26,26,26	0.41	0	39,40,40	0.50	0
3	GTP	E	502[B]	-	33,34,34	0.58	0	50,54,54	0.46	0
3	GTP	C	502[B]	-	33,34,34	0.59	0	50,54,54	0.46	0
3	GTP	F	502[A]	-	33,34,34	0.58	0	50,54,54	0.47	0
3	GTP	G	502[B]	-	33,34,34	0.59	0	50,54,54	0.46	0
2	5GP	F	501	-	26,26,26	0.40	0	39,40,40	0.49	0
2	5GP	A	501	-	26,26,26	0.41	0	39,40,40	0.49	0
2	5GP	C	501	-	26,26,26	0.41	0	39,40,40	0.51	0
3	GTP	H	502[A]	-	33,34,34	0.58	0	50,54,54	0.47	0
3	GTP	B	502[A]	-	33,34,34	0.59	0	50,54,54	0.47	0
3	GTP	F	502[B]	-	33,34,34	0.59	0	50,54,54	0.47	0
3	GTP	A	502[A]	-	33,34,34	0.57	0	50,54,54	0.46	0
3	GTP	D	502[A]	-	33,34,34	0.59	0	50,54,54	0.46	0
3	GTP	H	502[B]	-	33,34,34	0.59	0	50,54,54	0.47	0
2	5GP	H	501	-	26,26,26	0.41	0	39,40,40	0.51	0
3	GTP	B	502[B]	-	33,34,34	0.59	0	50,54,54	0.46	0
3	GTP	A	502[B]	-	33,34,34	0.59	0	50,54,54	0.46	0
3	GTP	D	502[B]	-	33,34,34	0.58	0	50,54,54	0.46	0
2	5GP	E	501	-	26,26,26	0.41	0	39,40,40	0.50	0
2	5GP	G	501	-	26,26,26	0.41	0	39,40,40	0.50	0
2	5GP	D	501	-	26,26,26	0.41	0	39,40,40	0.50	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GTP	E	502[A]	-	-	2/22/38/38	0/3/3/3
3	GTP	C	502[A]	-	-	7/22/38/38	0/3/3/3
3	GTP	G	502[A]	-	-	4/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	5GP	B	501	-	-	0/10/26/26	0/3/3/3
3	GTP	E	502[B]	-	-	2/22/38/38	0/3/3/3
3	GTP	C	502[B]	-	-	5/22/38/38	0/3/3/3
3	GTP	F	502[A]	-	-	4/22/38/38	0/3/3/3
3	GTP	G	502[B]	-	-	1/22/38/38	0/3/3/3
2	5GP	F	501	-	-	0/10/26/26	0/3/3/3
2	5GP	A	501	-	-	0/10/26/26	0/3/3/3
2	5GP	C	501	-	-	0/10/26/26	0/3/3/3
3	GTP	H	502[A]	-	-	2/22/38/38	0/3/3/3
3	GTP	B	502[A]	-	-	2/22/38/38	0/3/3/3
3	GTP	F	502[B]	-	-	3/22/38/38	0/3/3/3
3	GTP	A	502[A]	-	-	4/22/38/38	0/3/3/3
3	GTP	D	502[A]	-	-	3/22/38/38	0/3/3/3
3	GTP	H	502[B]	-	-	1/22/38/38	0/3/3/3
2	5GP	H	501	-	-	0/10/26/26	0/3/3/3
3	GTP	B	502[B]	-	-	3/22/38/38	0/3/3/3
3	GTP	A	502[B]	-	-	3/22/38/38	0/3/3/3
3	GTP	D	502[B]	-	-	1/22/38/38	0/3/3/3
2	5GP	E	501	-	-	0/10/26/26	0/3/3/3
2	5GP	G	501	-	-	0/10/26/26	0/3/3/3
2	5GP	D	501	-	-	0/10/26/26	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (47) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502[B]	GTP	C5'-O5'-PA-O3A
3	B	502[B]	GTP	PB-O3B-PG-O3G
3	C	502[A]	GTP	C5'-O5'-PA-O3A
3	C	502[A]	GTP	C5'-O5'-PA-O1A
3	C	502[A]	GTP	O4'-C4'-C5'-O5'
3	C	502[A]	GTP	C3'-C4'-C5'-O5'
3	C	502[B]	GTP	O4'-C4'-C5'-O5'
3	F	502[B]	GTP	PB-O3B-PG-O3G
3	F	502[A]	GTP	O4'-C4'-C5'-O5'
3	C	502[B]	GTP	C3'-C4'-C5'-O5'
3	F	502[A]	GTP	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
3	E	502[B]	GTP	PB-O3B-PG-O1G
3	B	502[A]	GTP	PG-O3B-PB-O1B
3	D	502[A]	GTP	PA-O3A-PB-O1B
3	E	502[A]	GTP	PG-O3B-PB-O1B
3	F	502[A]	GTP	PG-O3B-PB-O1B
3	G	502[A]	GTP	PG-O3B-PB-O1B
3	H	502[A]	GTP	PG-O3B-PB-O1B
3	C	502[A]	GTP	PG-O3B-PB-O2B
3	C	502[B]	GTP	PB-O3A-PA-O2A
3	D	502[A]	GTP	PG-O3B-PB-O2B
3	A	502[B]	GTP	C5'-O5'-PA-O1A
3	C	502[A]	GTP	C5'-O5'-PA-O2A
3	B	502[A]	GTP	PG-O3B-PB-O2B
3	B	502[B]	GTP	PB-O3A-PA-O2A
3	C	502[A]	GTP	PG-O3B-PB-O1B
3	D	502[A]	GTP	PG-O3B-PB-O1B
3	E	502[B]	GTP	PB-O3A-PA-O2A
3	F	502[A]	GTP	PG-O3B-PB-O2B
3	G	502[A]	GTP	PG-O3B-PB-O2B
3	H	502[A]	GTP	PG-O3B-PB-O2B
3	B	502[B]	GTP	PB-O3B-PG-O1G
3	F	502[B]	GTP	PB-O3B-PG-O1G
3	H	502[B]	GTP	PB-O3B-PG-O1G
3	A	502[A]	GTP	PB-O3A-PA-O1A
3	E	502[A]	GTP	PG-O3B-PB-O2B
3	A	502[A]	GTP	PB-O3B-PG-O1G
3	C	502[B]	GTP	PB-O3B-PG-O1G
3	A	502[A]	GTP	PB-O3B-PG-O2G
3	A	502[A]	GTP	PB-O3A-PA-O2A
3	C	502[B]	GTP	PB-O3A-PA-O1A
3	D	502[B]	GTP	PB-O3A-PA-O2A
3	F	502[B]	GTP	PB-O3A-PA-O2A
3	G	502[A]	GTP	PA-O3A-PB-O1B
3	G	502[B]	GTP	PB-O3A-PA-O2A
3	A	502[B]	GTP	PG-O3B-PB-O2B
3	G	502[A]	GTP	PA-O3A-PB-O3B

There are no ring outliers.

2 monomers are involved in 2 short contacts:

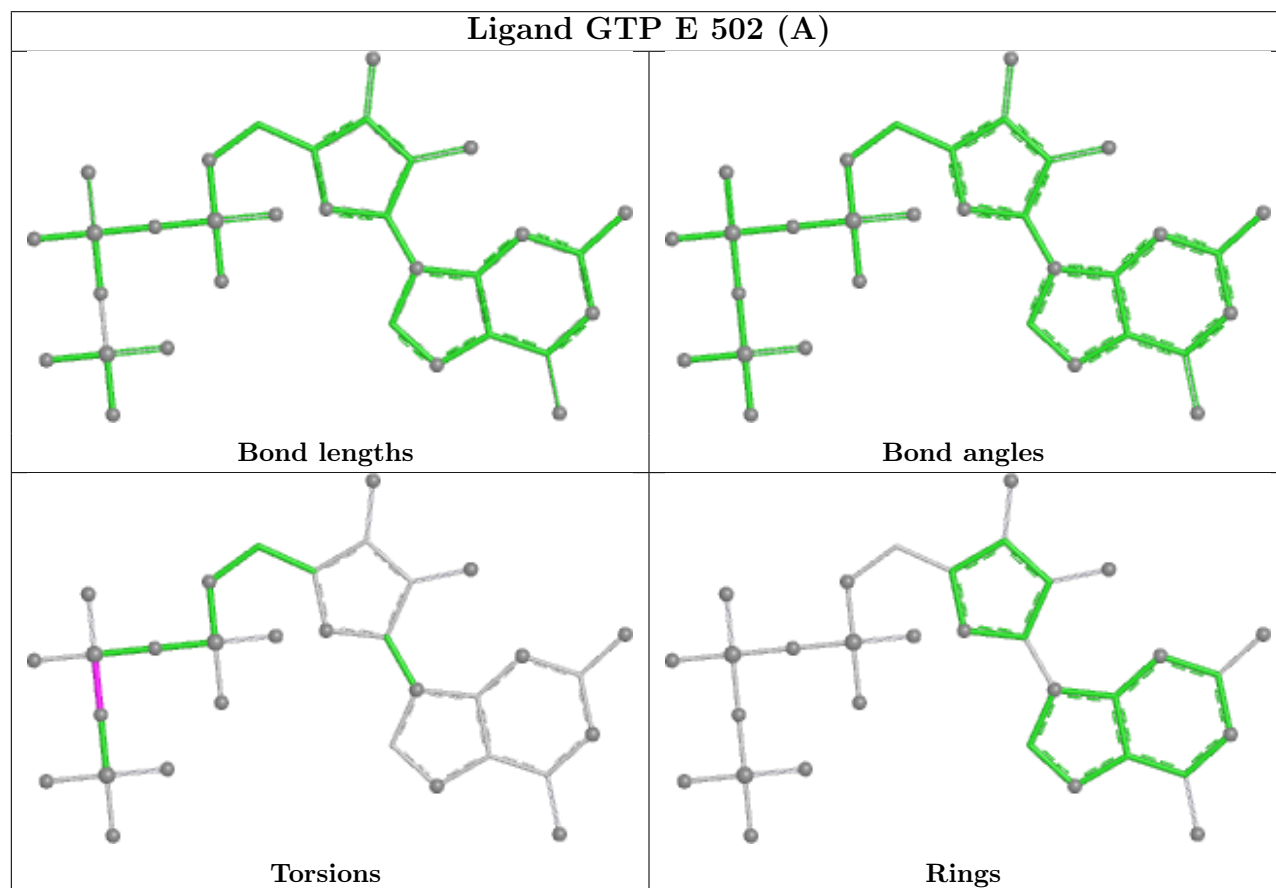
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	502[A]	GTP	1	0

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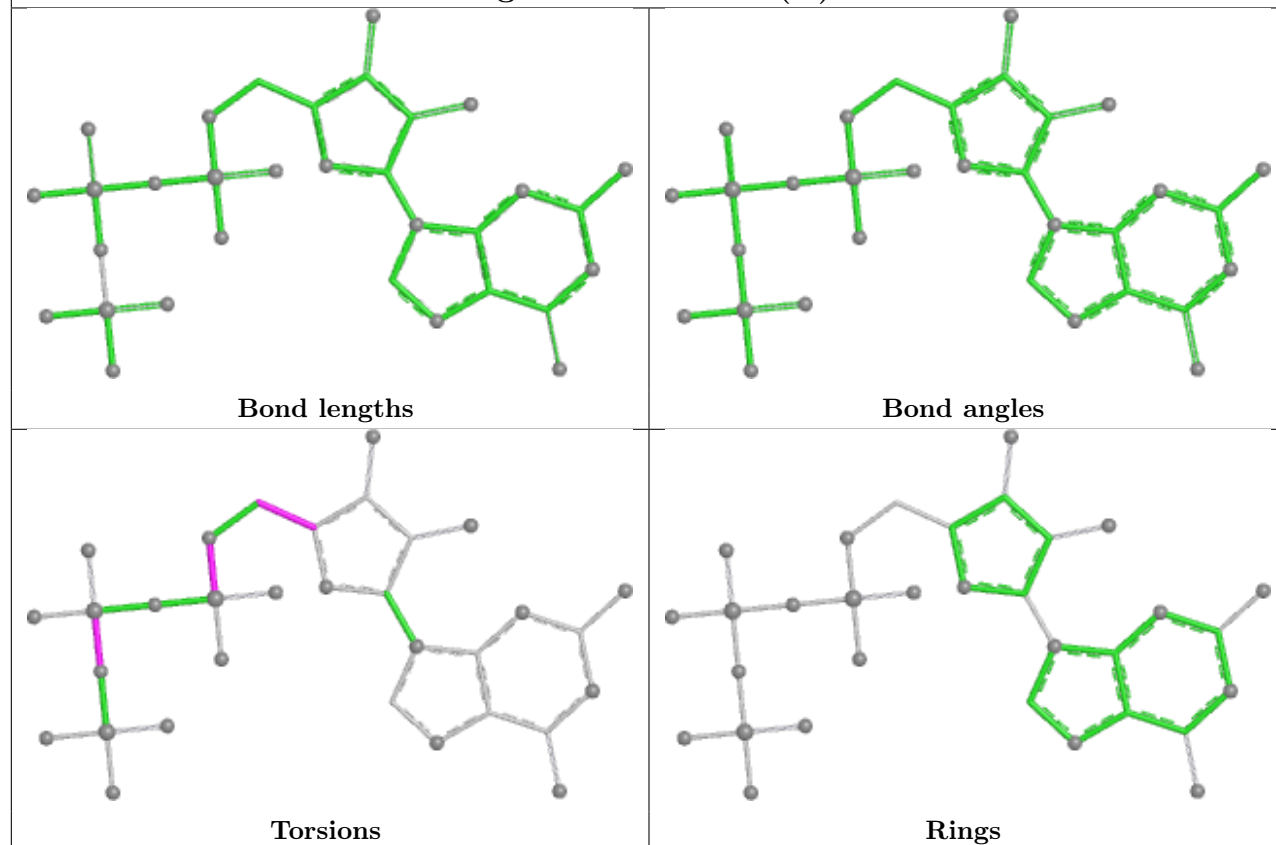
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	502[B]	GTP	1	0

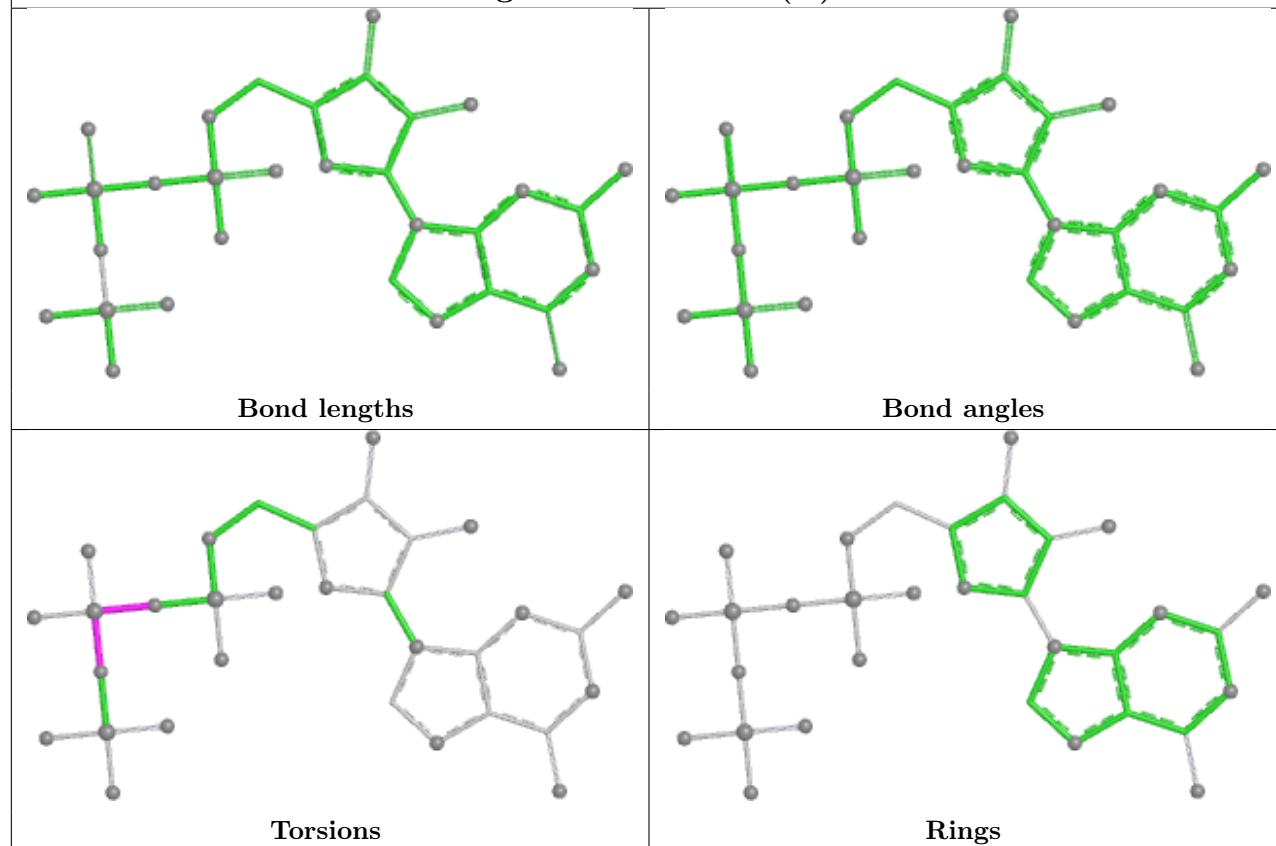
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



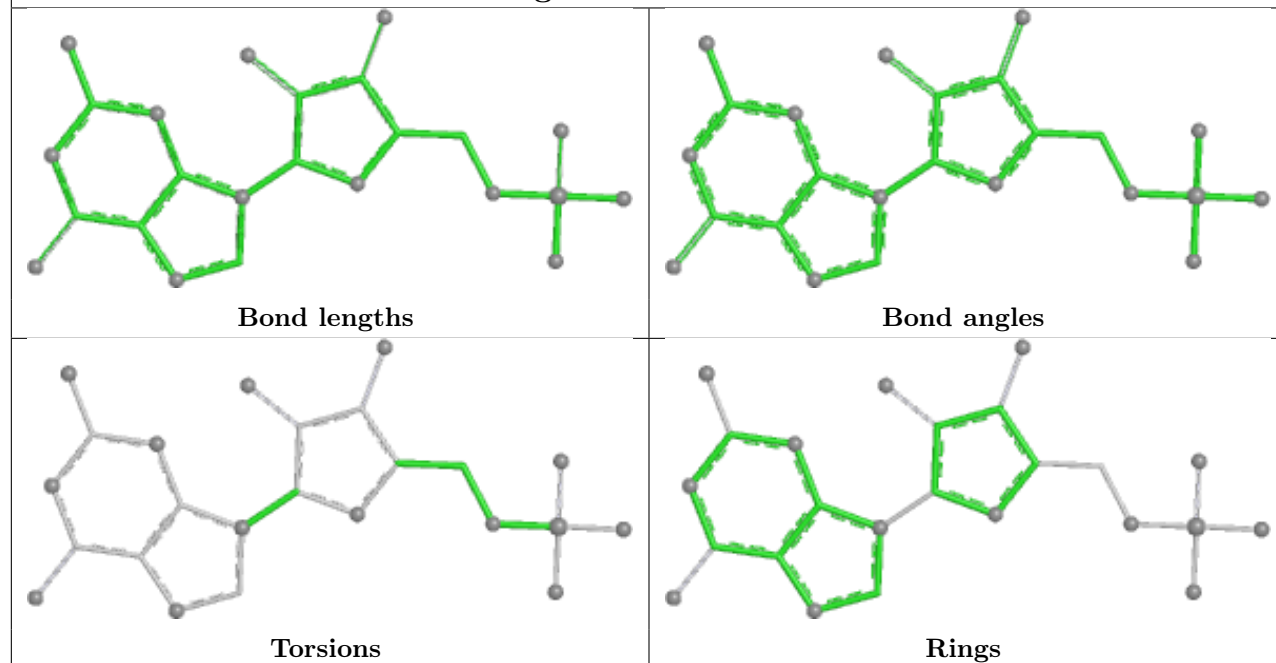
Ligand GTP C 502 (A)



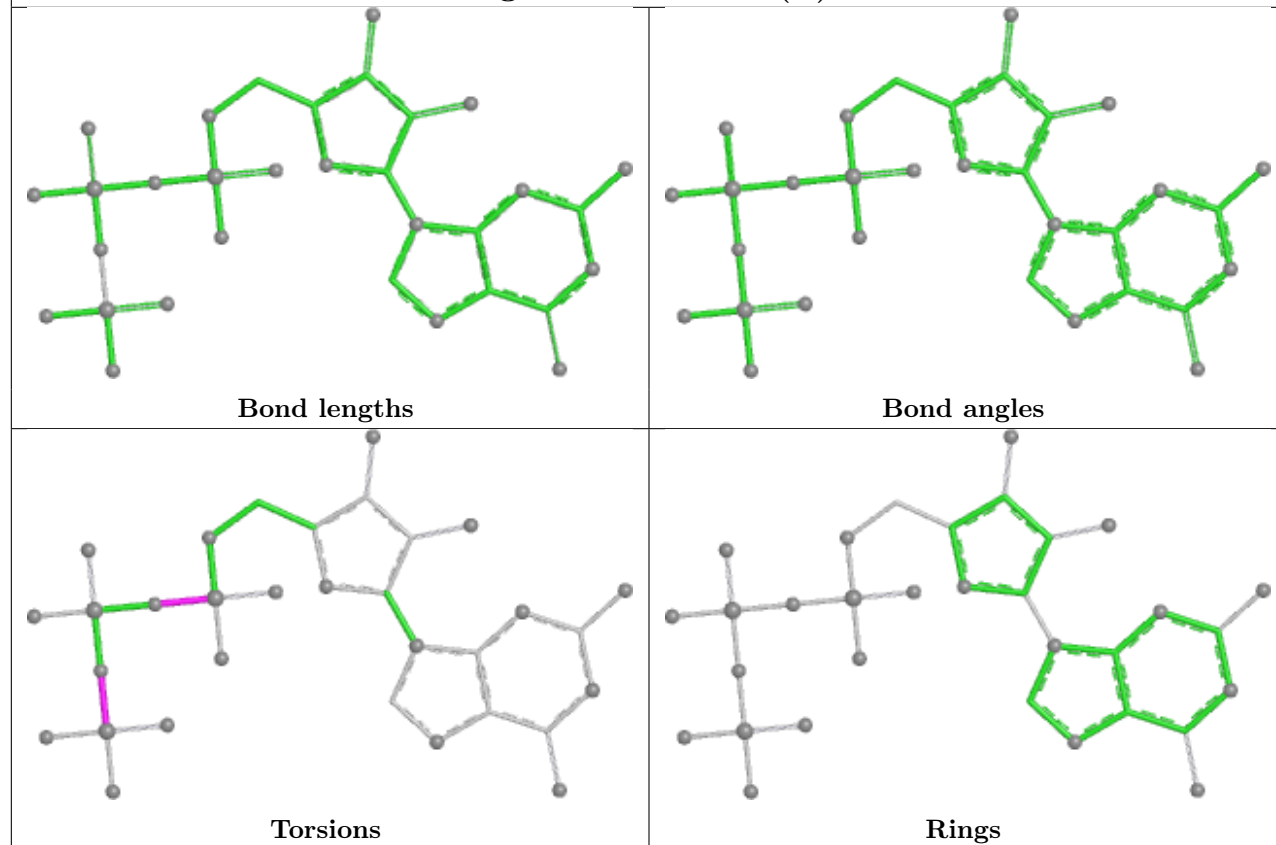
Ligand GTP G 502 (A)



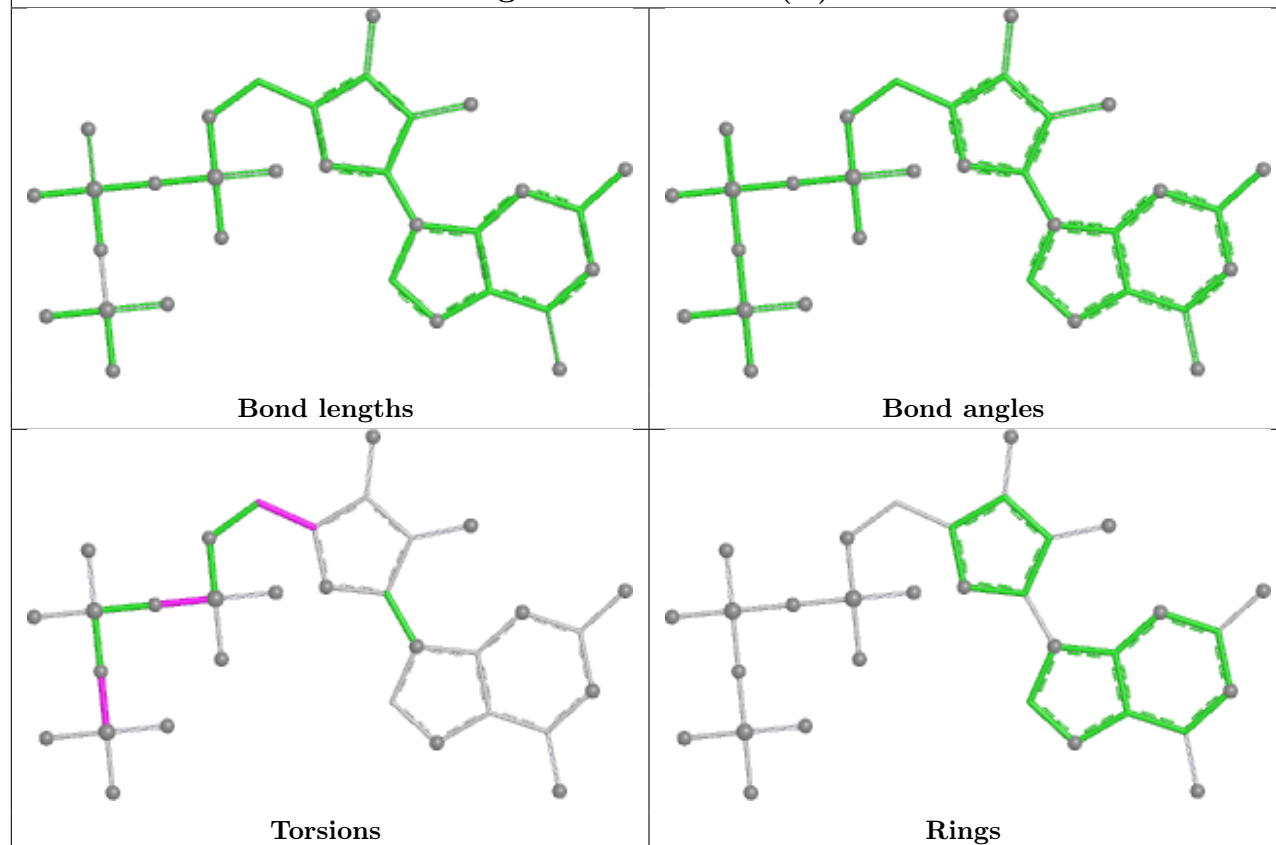
Ligand 5GP B 501



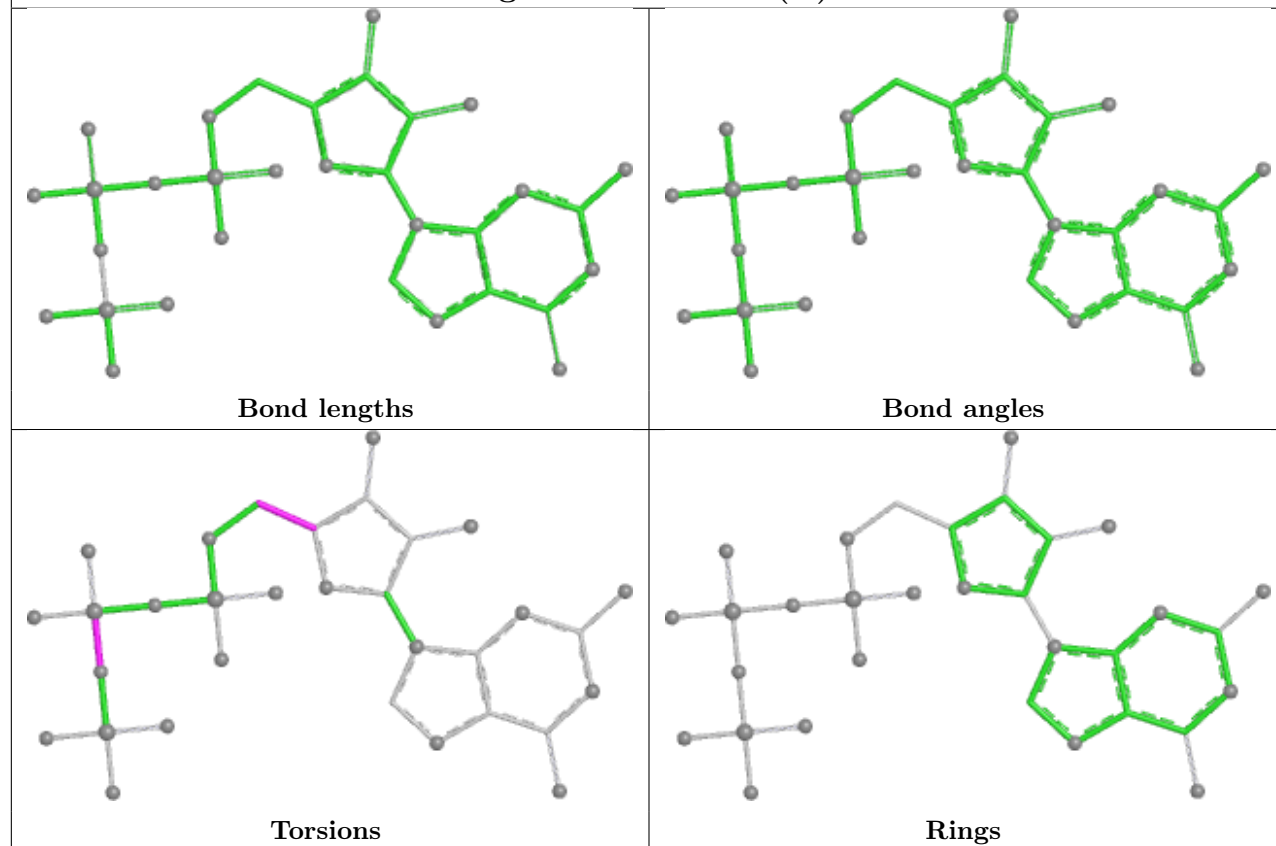
Ligand GTP E 502 (B)



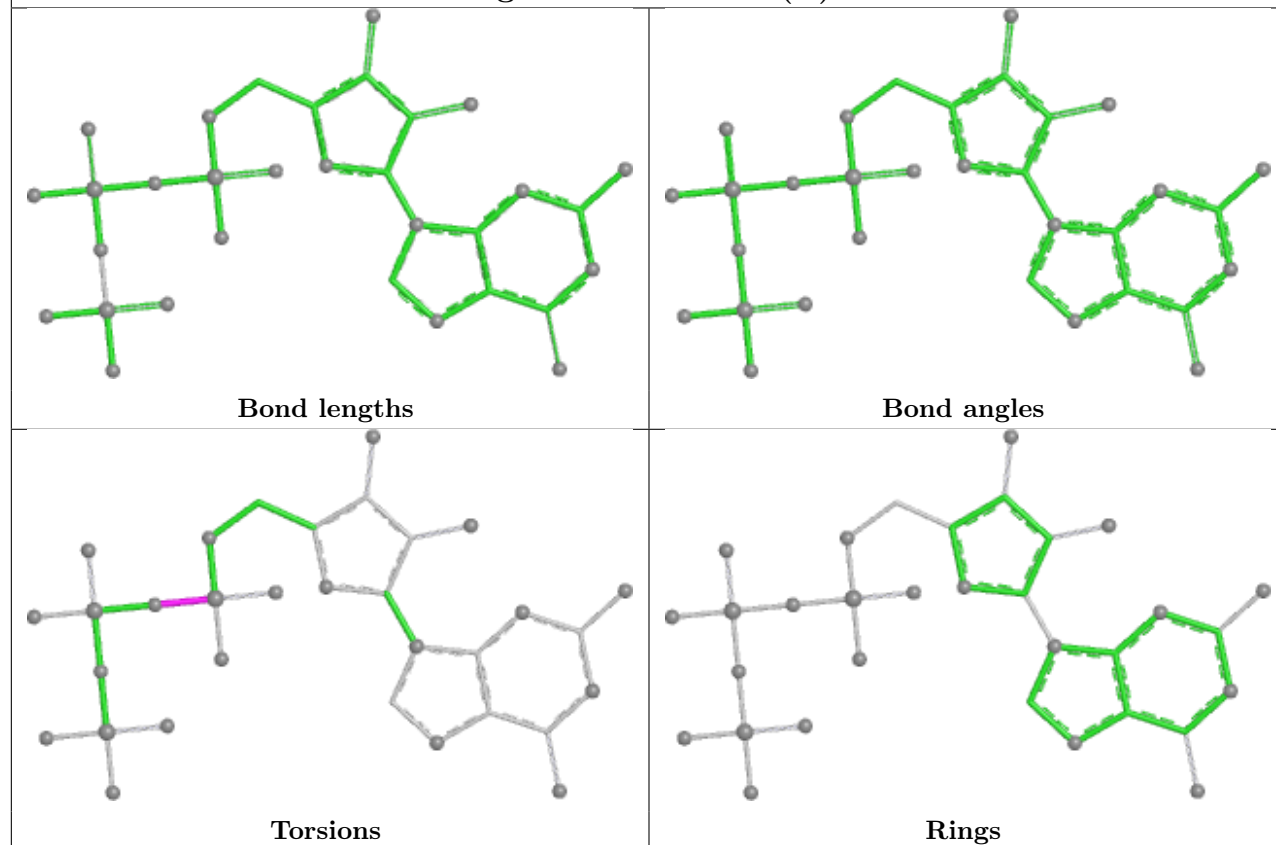
Ligand GTP C 502 (B)



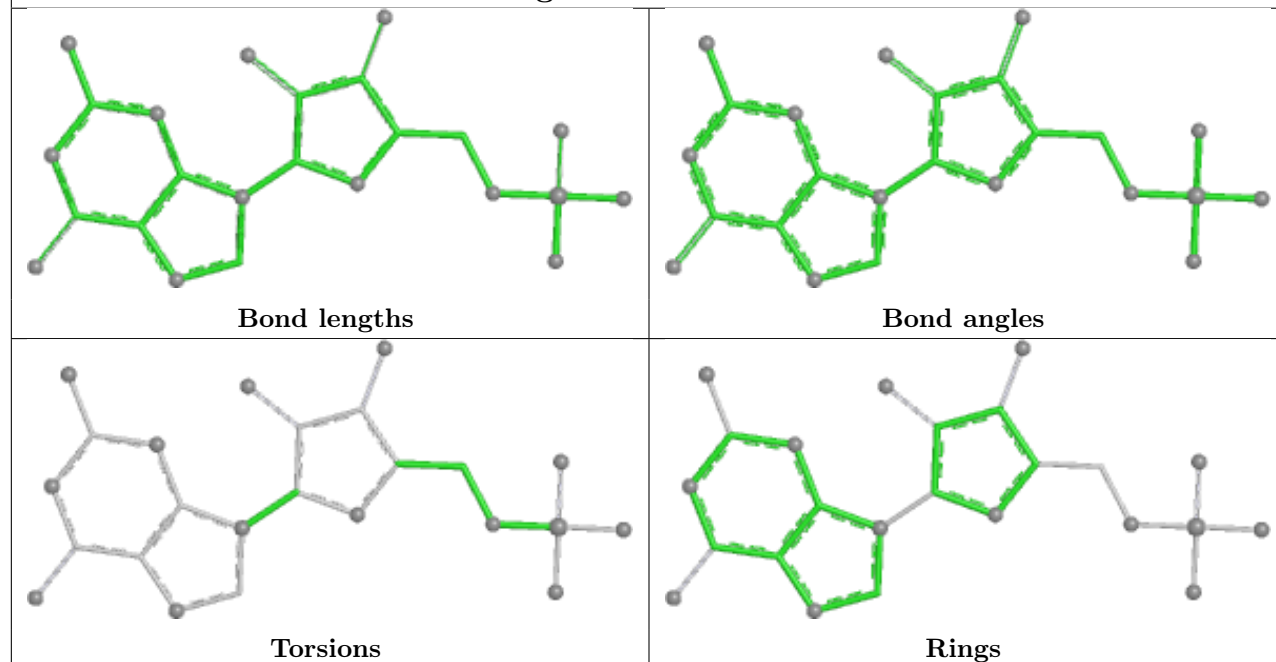
Ligand GTP F 502 (A)



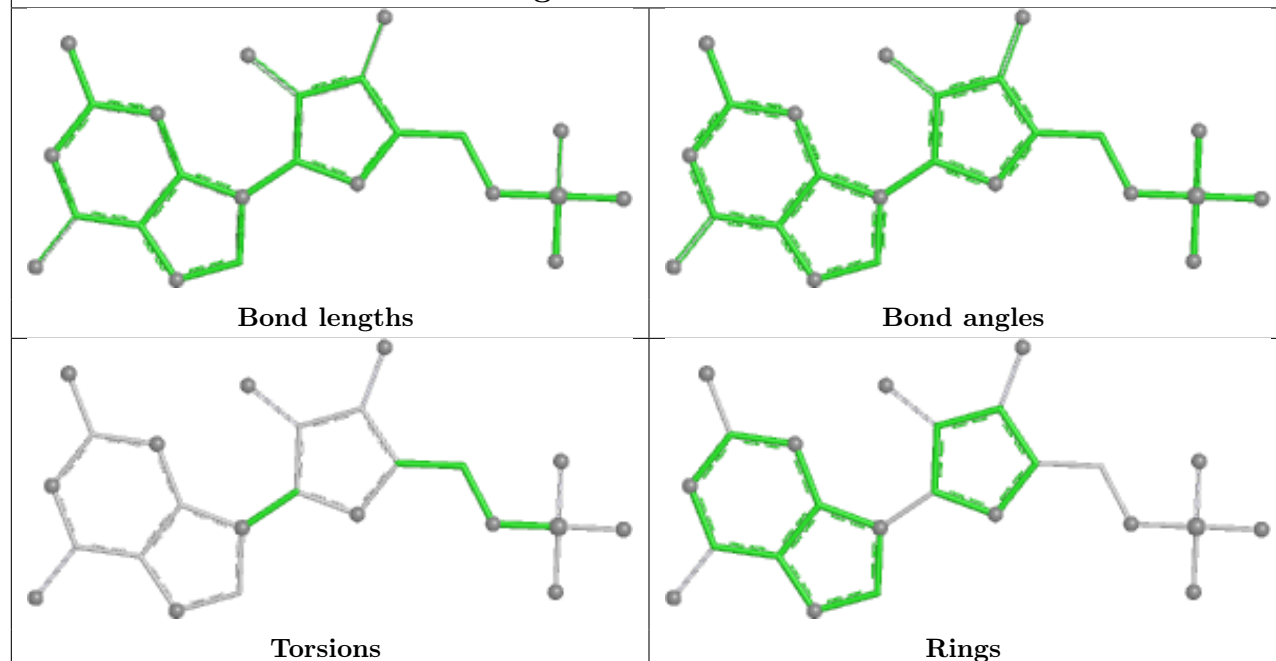
Ligand GTP G 502 (B)



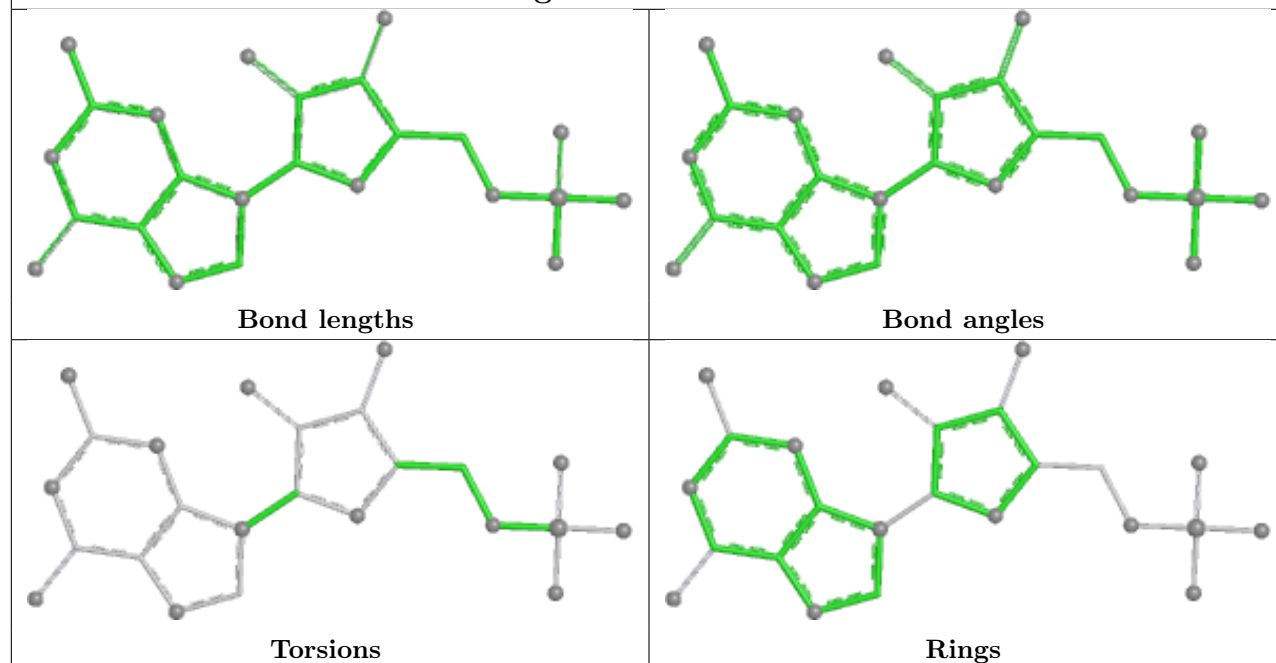
Ligand 5GP F 501



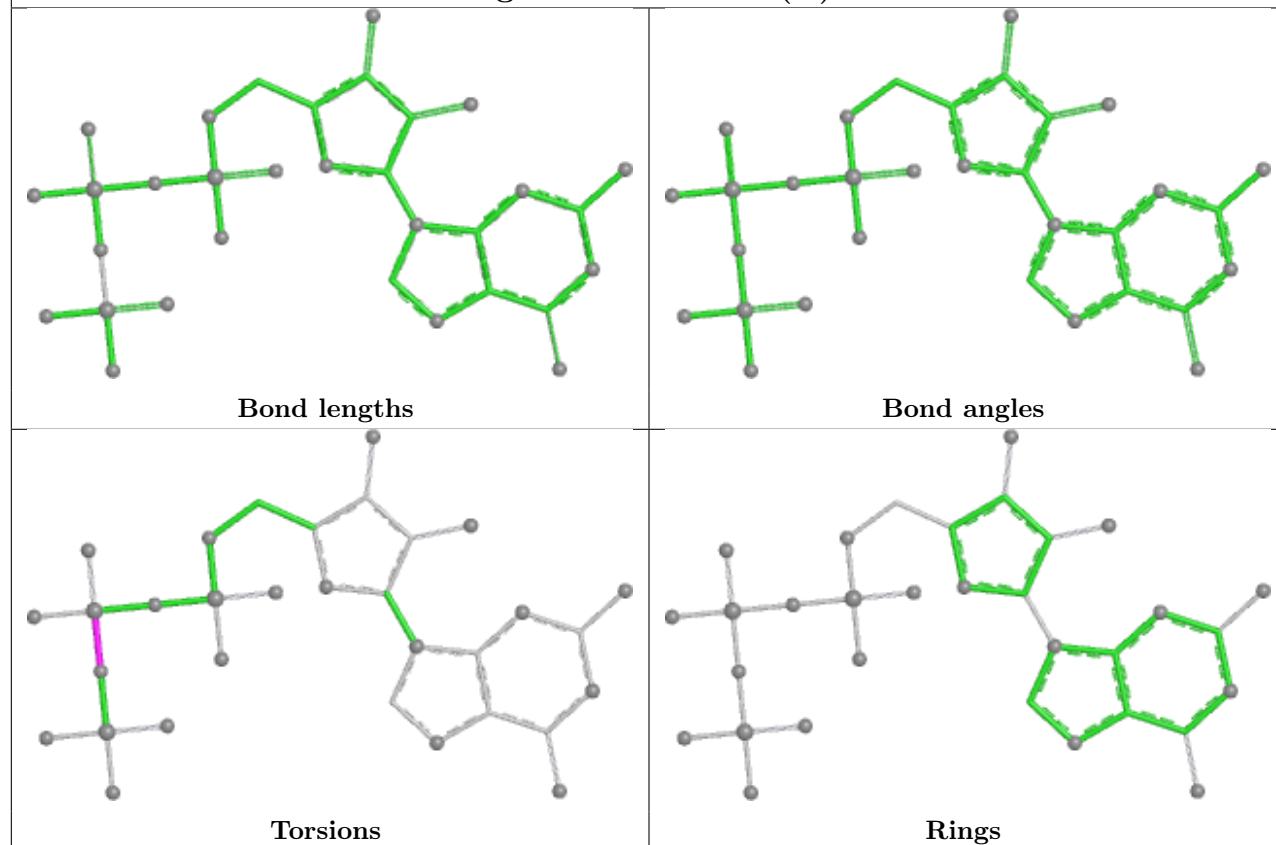
Ligand 5GP A 501



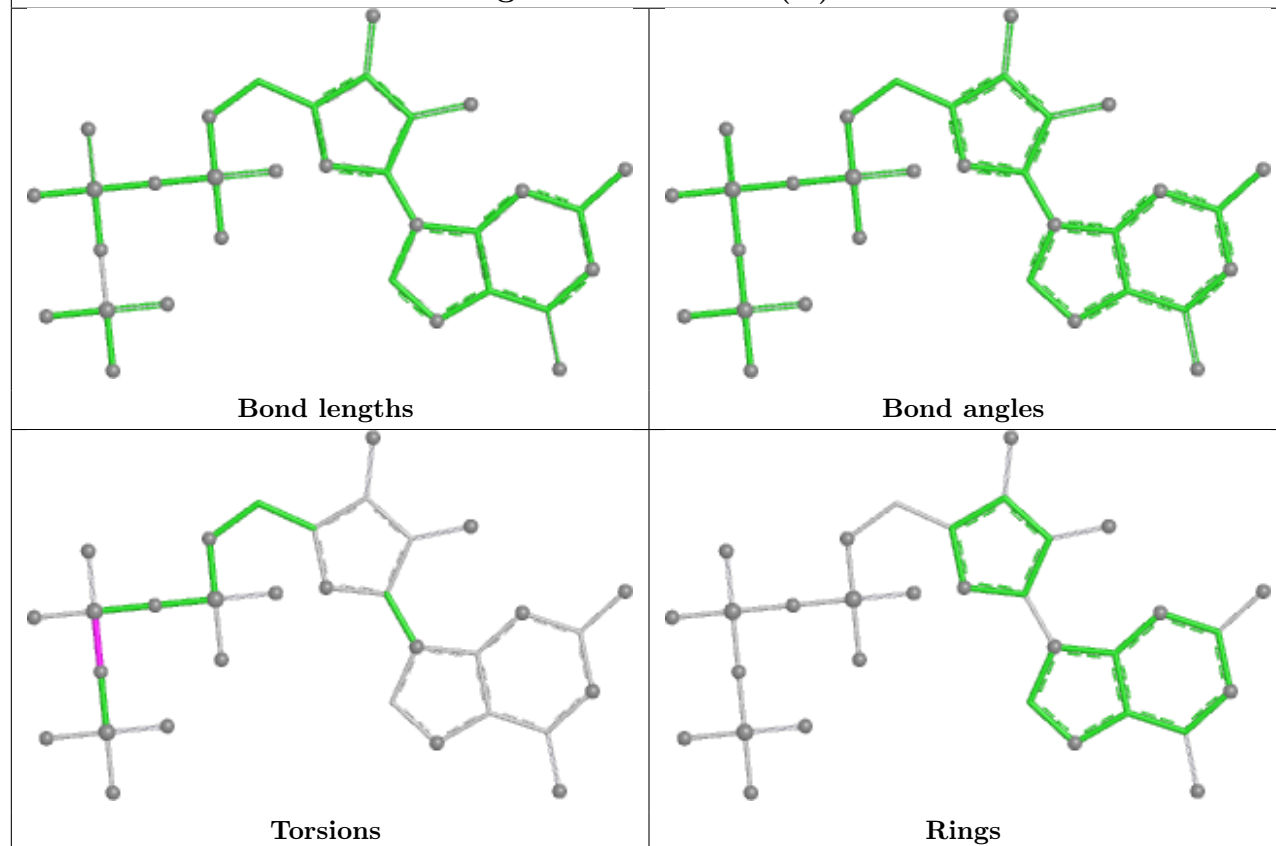
Ligand 5GP C 501



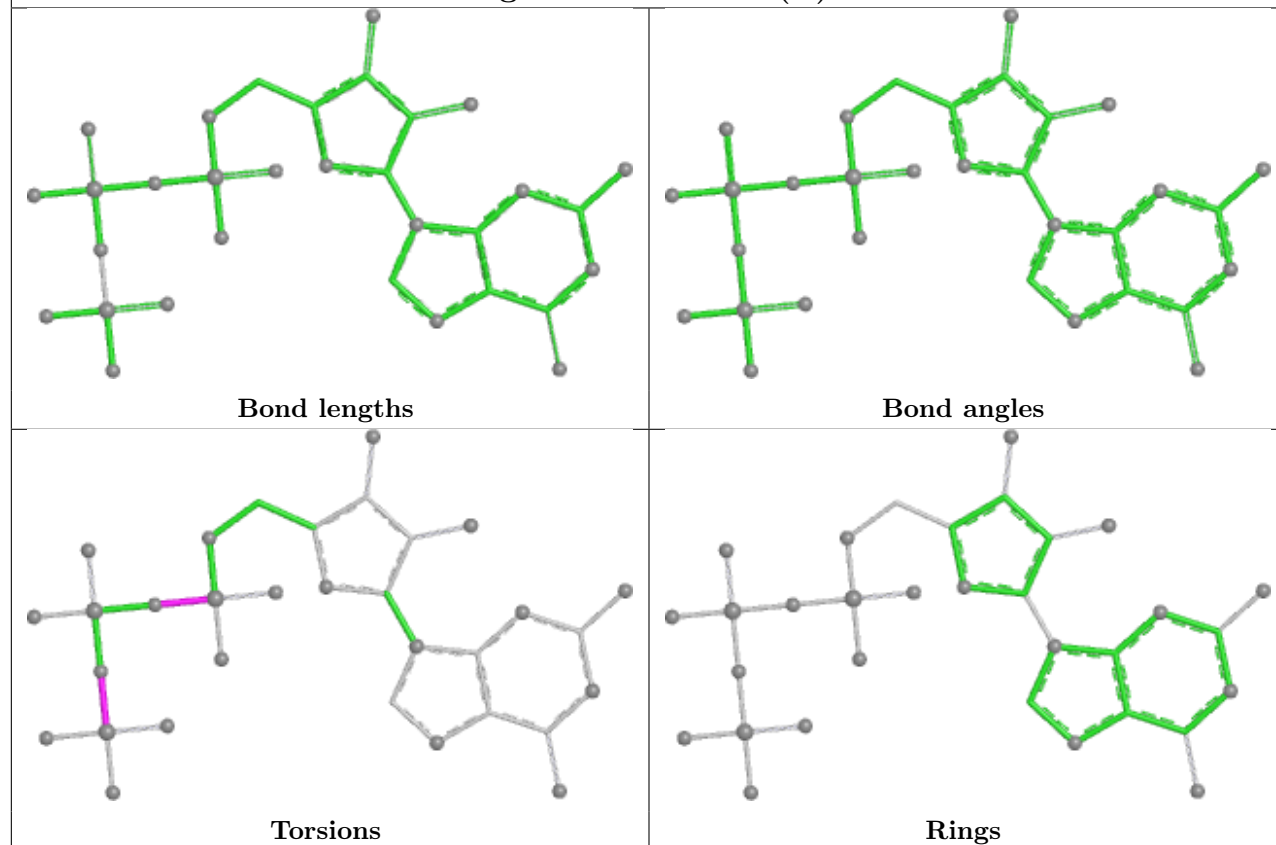
Ligand GTP H 502 (A)



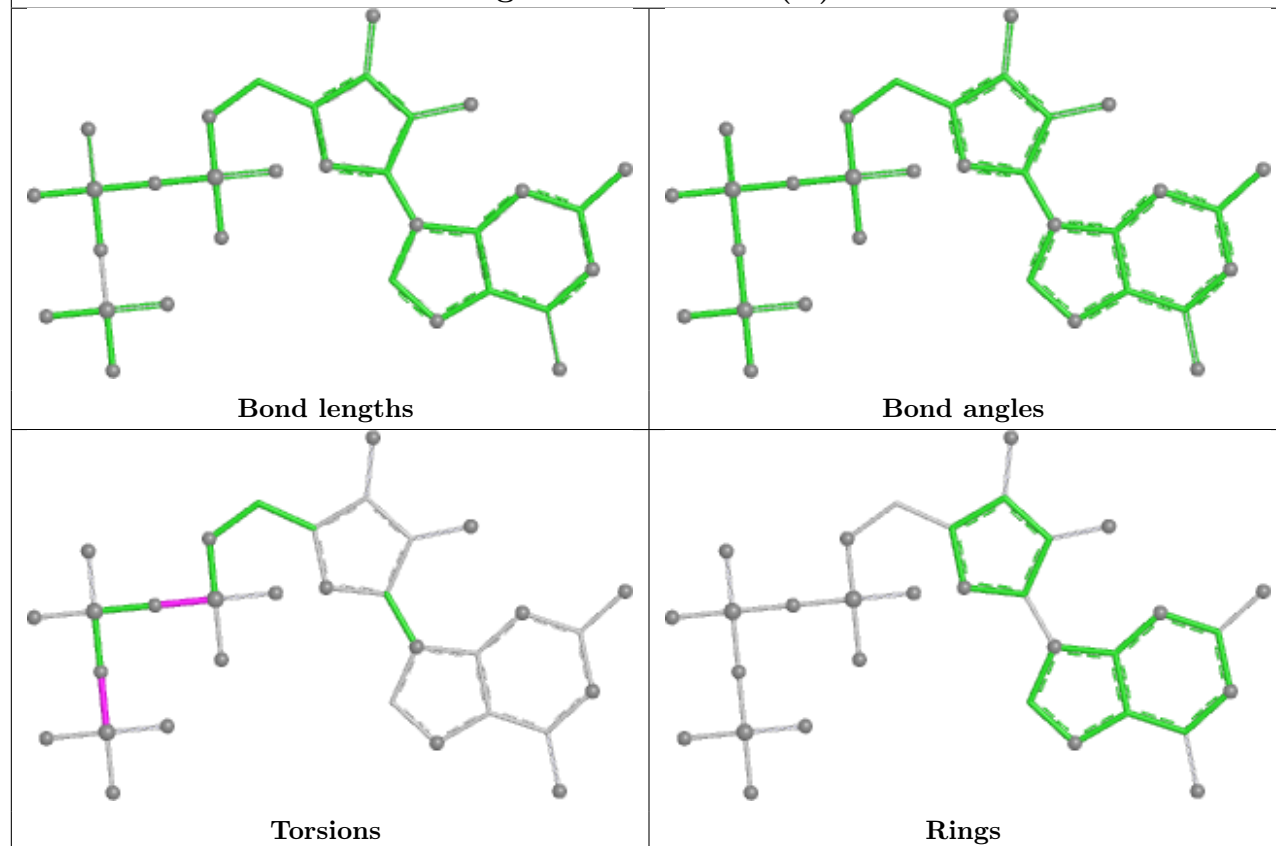
Ligand GTP B 502 (A)



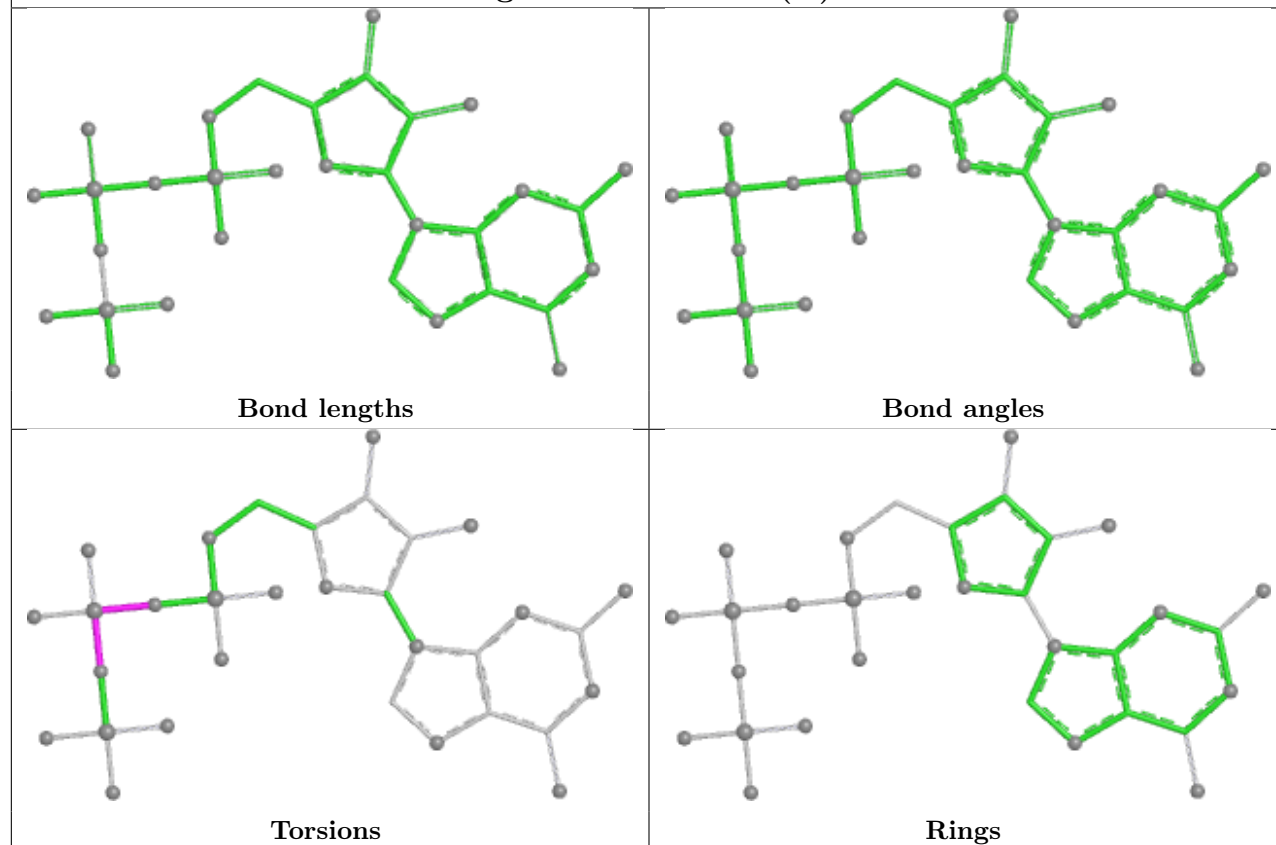
Ligand GTP F 502 (B)



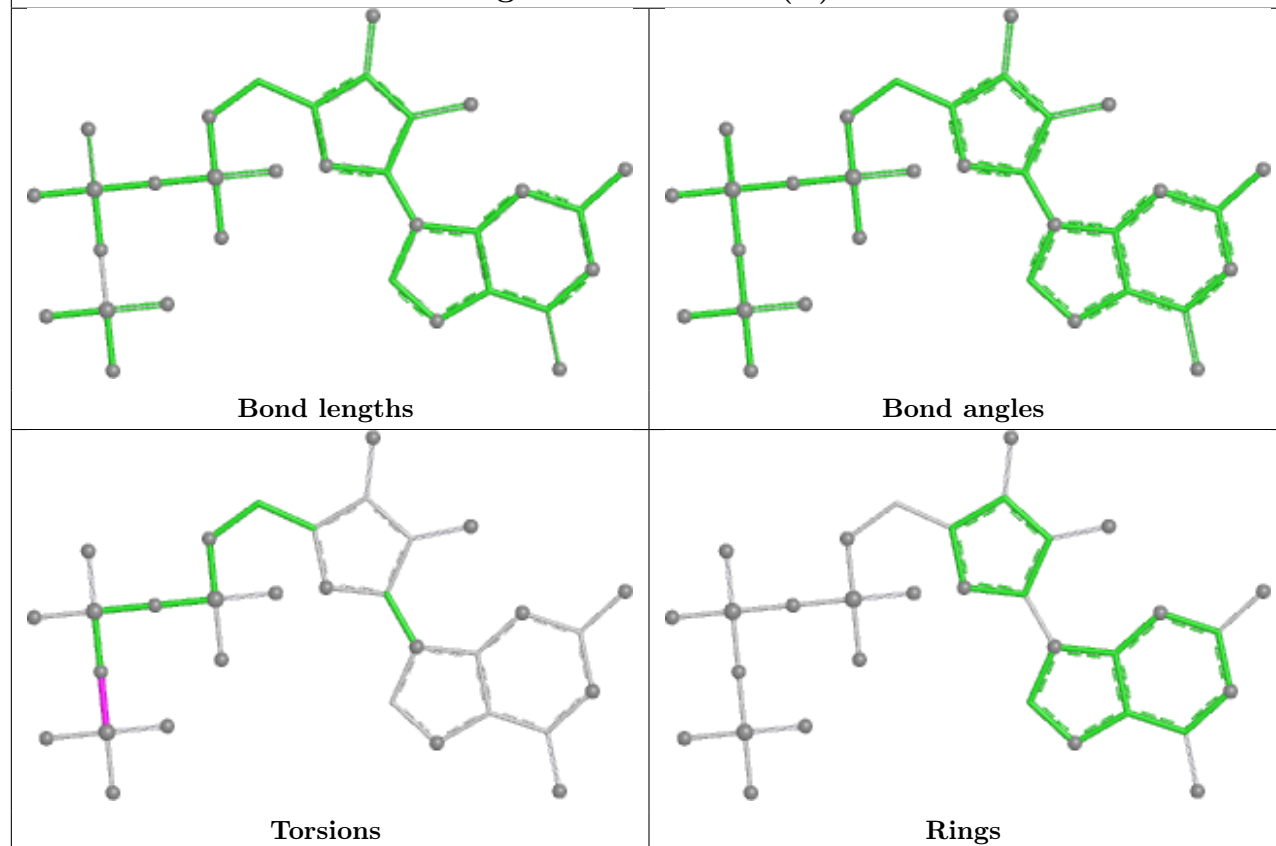
Ligand GTP A 502 (A)



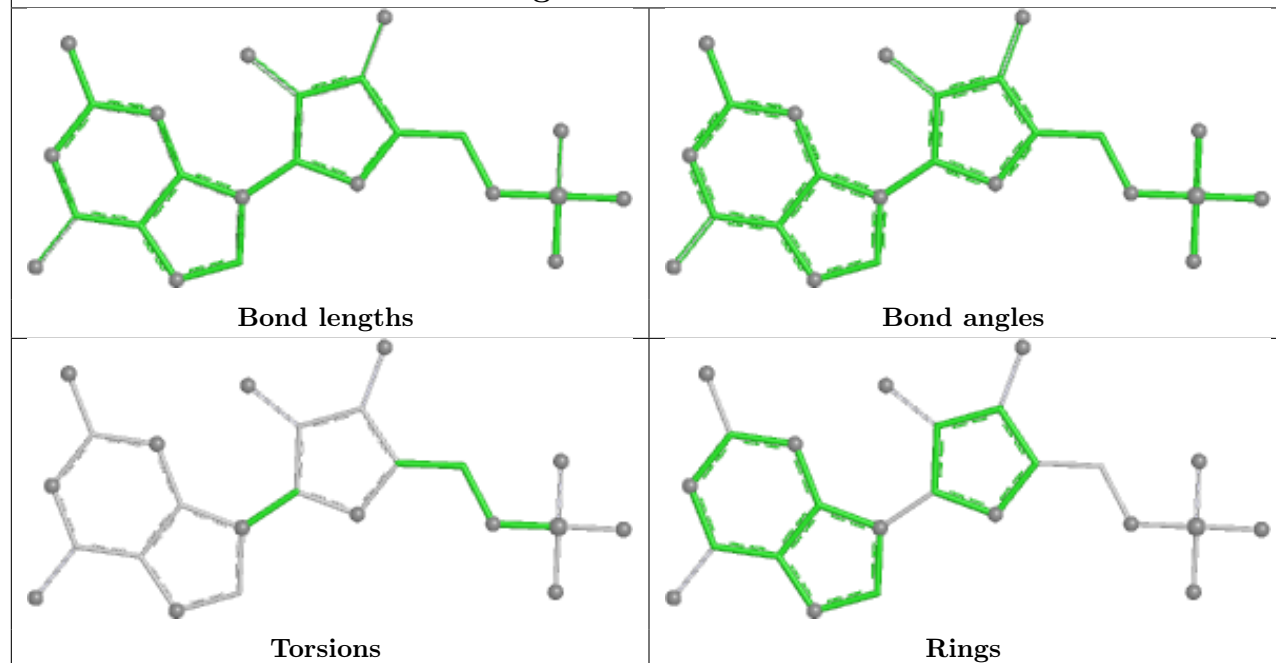
Ligand GTP D 502 (A)



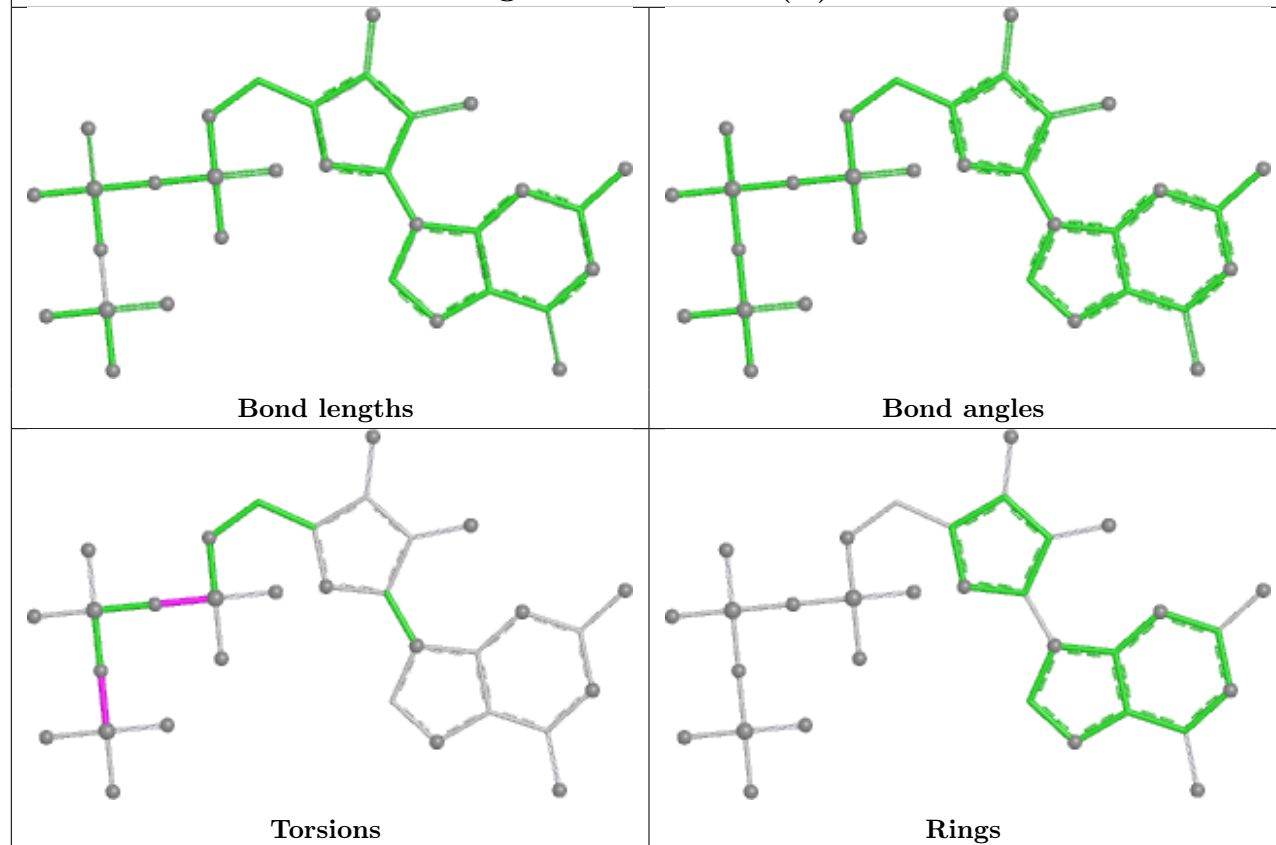
Ligand GTP H 502 (B)



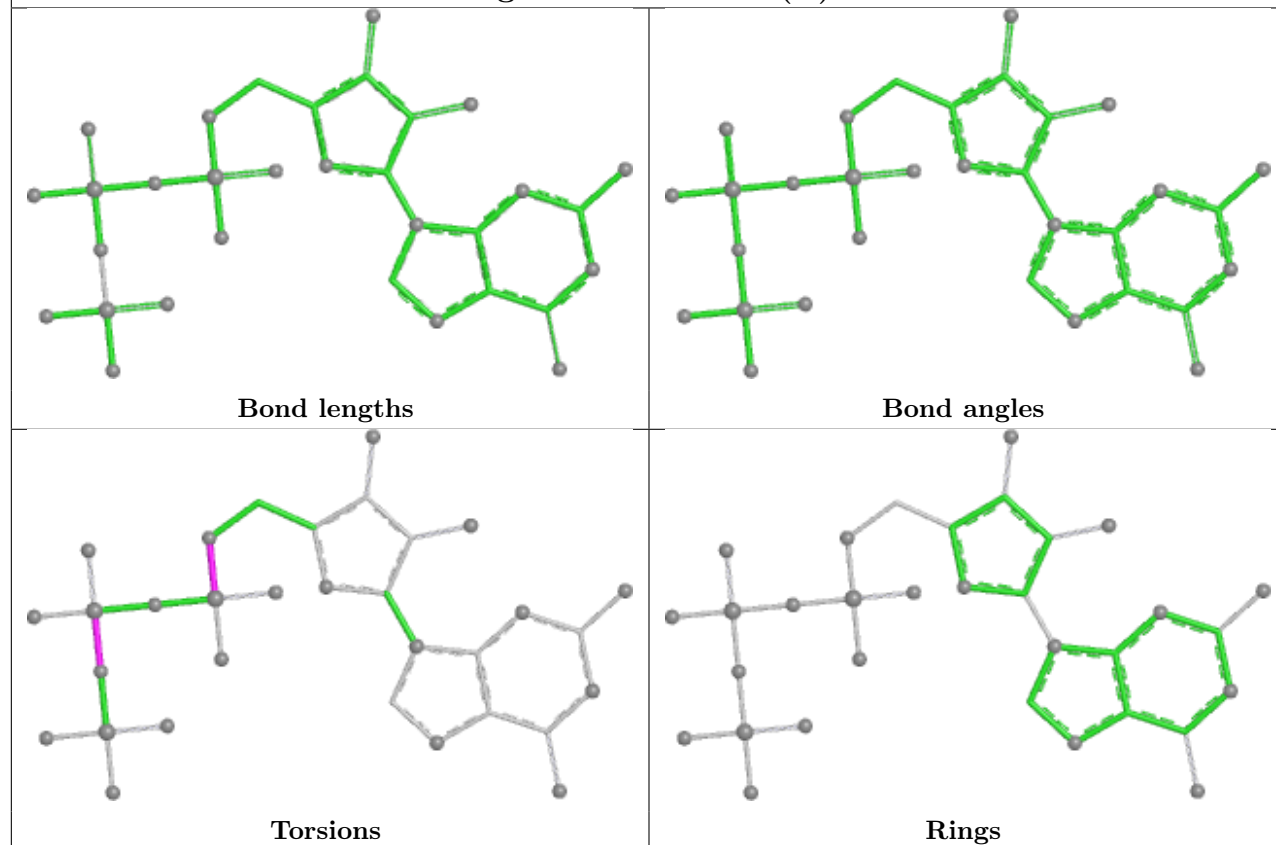
Ligand 5GP H 501



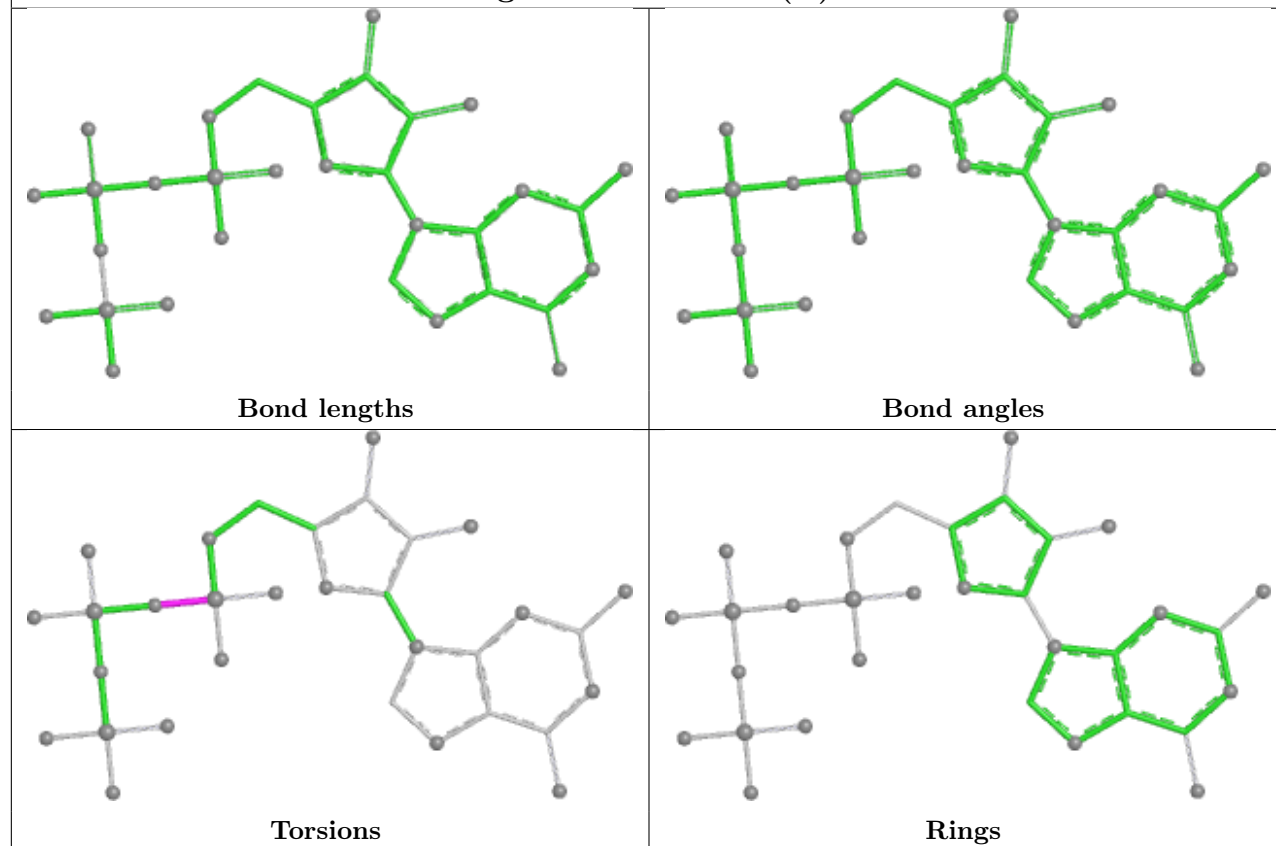
Ligand GTP B 502 (B)



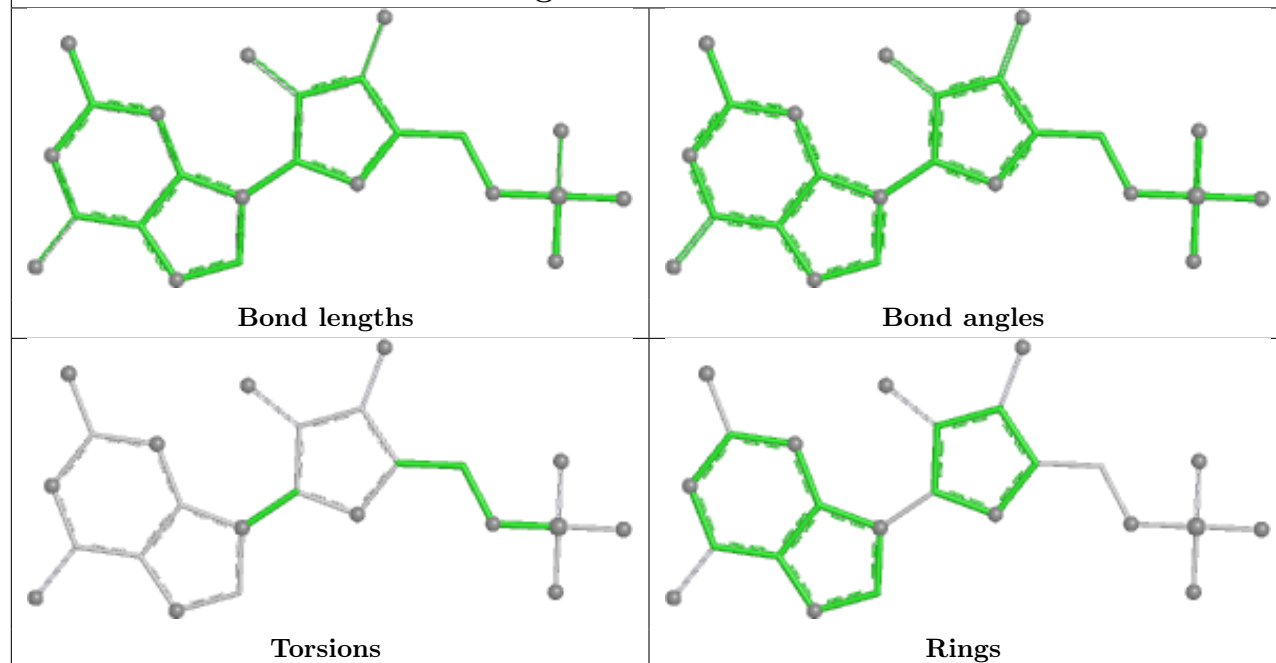
Ligand GTP A 502 (B)



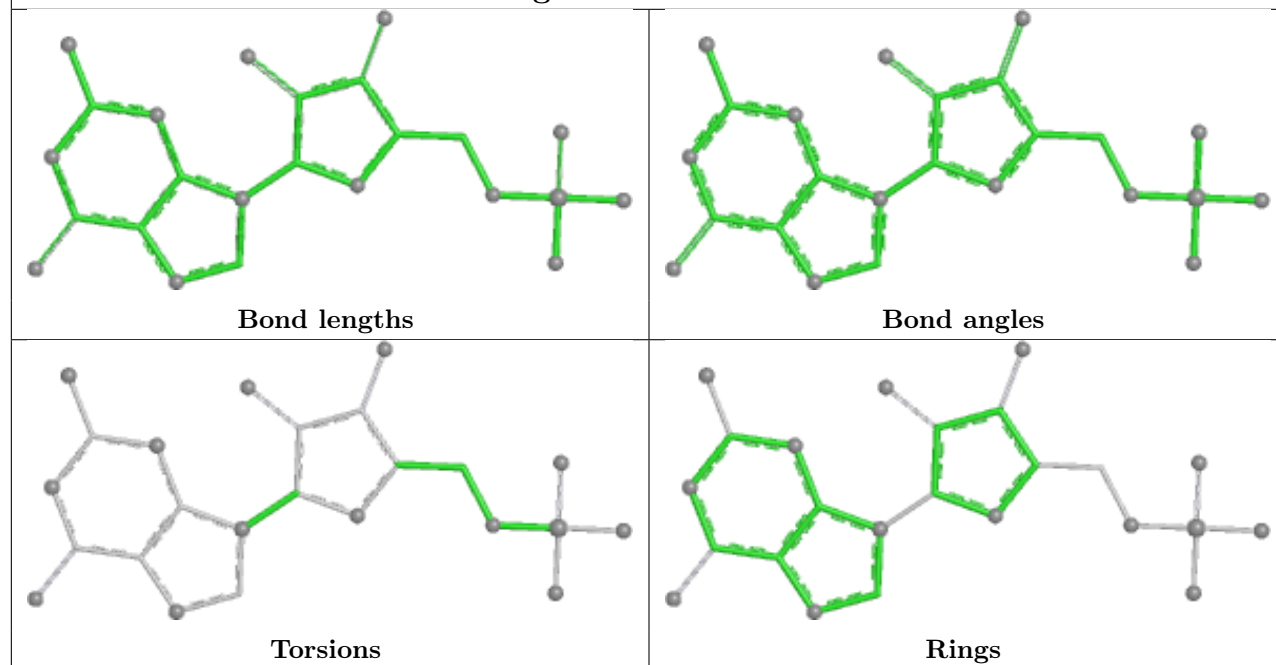
Ligand GTP D 502 (B)

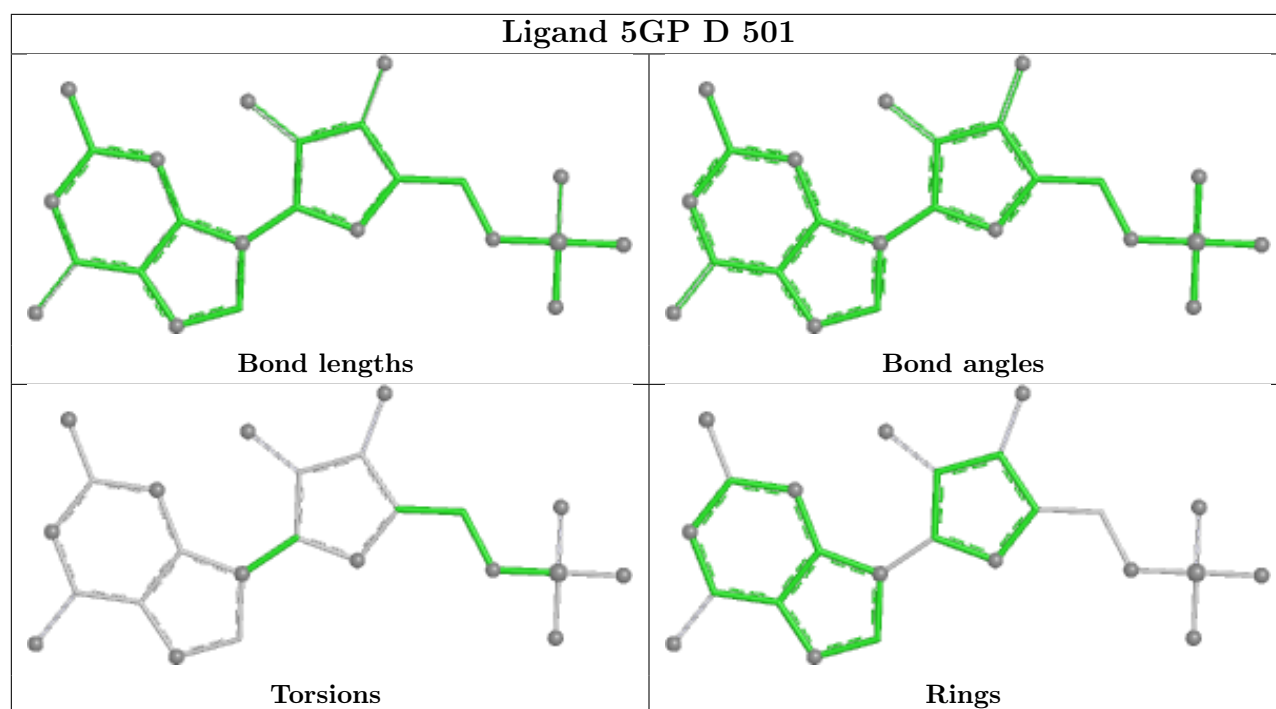


Ligand 5GP E 501



Ligand 5GP G 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	460/496 (92%)	0.47	28 (6%)	27 29	35, 49, 79, 102	0
1	B	460/496 (92%)	0.62	32 (6%)	22 24	38, 54, 81, 108	0
1	C	460/496 (92%)	0.77	32 (6%)	22 24	40, 59, 86, 108	0
1	D	460/496 (92%)	0.57	27 (5%)	28 30	36, 54, 81, 107	0
1	E	460/496 (92%)	1.62	135 (29%)	1 1	49, 75, 102, 126	0
1	F	460/496 (92%)	1.87	180 (39%)	1 0	60, 86, 110, 128	0
1	G	460/496 (92%)	1.50	117 (25%)	1 2	48, 72, 101, 128	0
1	H	460/496 (92%)	1.12	70 (15%)	5 6	44, 63, 94, 113	0
All	All	3680/3968 (92%)	1.07	621 (16%)	4 5	35, 63, 97, 128	0

All (621) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	403	PHE	5.7
1	F	163	VAL	5.7
1	A	403	PHE	5.6
1	E	128	PHE	5.1
1	E	193	GLY	5.0
1	H	414	GLY	4.9
1	C	124	ALA	4.8
1	E	163	VAL	4.8
1	F	80	ILE	4.7
1	C	403	PHE	4.7
1	E	155	LEU	4.6
1	E	191	LEU	4.6
1	H	155	LEU	4.6
1	F	194	VAL	4.6
1	G	194	VAL	4.5
1	E	187	PRO	4.4

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Mol	Chain	Res	Type	RSRZ
1	F	158	PHE	4.4
1	E	178	PRO	4.3
1	F	103	LEU	4.3
1	C	123	ALA	4.3
1	E	158	PHE	4.3
1	F	120	ALA	4.3
1	F	191	LEU	4.3
1	G	467	ALA	4.2
1	F	117	HIS	4.1
1	C	109	VAL	4.1
1	E	116	LEU	4.1
1	G	281	GLY	4.1
1	F	415	ILE	4.1
1	E	339	VAL	4.1
1	G	2	VAL	4.0
1	F	394	ALA	4.0
1	G	411	PHE	4.0
1	H	128	PHE	4.0
1	G	117	HIS	4.0
1	F	223	GLY	4.0
1	H	187	PRO	4.0
1	F	179	ILE	4.0
1	F	155	LEU	3.9
1	F	300	GLY	3.9
1	E	411	PHE	3.9
1	F	222	VAL	3.9
1	C	302	MET	3.9
1	E	161	ALA	3.9
1	F	374	PHE	3.8
1	D	300	GLY	3.8
1	D	394	ALA	3.8
1	H	467	ALA	3.8
1	D	401	SER	3.8
1	G	155	LEU	3.8
1	F	157	ASP	3.8
1	G	325	ALA	3.8
1	F	411	PHE	3.8
1	H	411	PHE	3.8
1	F	271	LEU	3.8
1	F	364	GLY	3.8
1	G	272	VAL	3.8
1	H	185	THR	3.7

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Mol	Chain	Res	Type	RSRZ
1	H	394	ALA	3.7
1	D	301	ALA	3.7
1	E	325	ALA	3.7
1	D	403	PHE	3.7
1	F	245	ILE	3.7
1	G	191	LEU	3.7
1	F	273	ALA	3.7
1	F	301	ALA	3.7
1	G	415	ILE	3.6
1	H	179	ILE	3.6
1	H	163	VAL	3.6
1	G	394	ALA	3.6
1	G	128	PHE	3.6
1	F	41	GLY	3.6
1	G	300	GLY	3.6
1	F	65	VAL	3.6
1	F	109	VAL	3.6
1	F	334	TRP	3.6
1	E	132	PRO	3.6
1	E	192	ALA	3.6
1	B	409	GLY	3.6
1	F	132	PRO	3.6
1	F	185	THR	3.5
1	E	194	VAL	3.5
1	F	187	PRO	3.5
1	F	128	PHE	3.5
1	H	117	HIS	3.5
1	E	273	ALA	3.5
1	F	127	VAL	3.5
1	H	303	CYS	3.5
1	G	116	LEU	3.5
1	E	394	ALA	3.4
1	H	466	ALA	3.4
1	F	148	ALA	3.4
1	G	187	PRO	3.4
1	E	447	VAL	3.4
1	A	467	ALA	3.4
1	C	394	ALA	3.4
1	F	116	LEU	3.4
1	H	415	ILE	3.4
1	G	158	PHE	3.4
1	H	158	PHE	3.4

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Mol	Chain	Res	Type	RSRZ
1	F	160	THR	3.4
1	F	72	VAL	3.4
1	F	272	VAL	3.4
1	G	159	VAL	3.4
1	B	326	ALA	3.4
1	C	148	ALA	3.3
1	G	278	SER	3.3
1	H	191	LEU	3.3
1	F	218	ILE	3.3
1	H	178	PRO	3.3
1	B	467	ALA	3.3
1	F	170	VAL	3.3
1	E	296	GLY	3.3
1	F	242	LEU	3.3
1	G	103	LEU	3.3
1	E	179	ILE	3.3
1	F	192	ALA	3.3
1	G	331	GLY	3.3
1	G	267	LEU	3.3
1	F	303	CYS	3.3
1	H	403	PHE	3.3
1	E	467	ALA	3.2
1	G	273	ALA	3.2
1	C	239	GLY	3.2
1	G	134	GLY	3.2
1	F	153	ILE	3.2
1	E	356	VAL	3.2
1	E	117	HIS	3.2
1	G	303	CYS	3.2
1	E	184	MET	3.2
1	E	97	VAL	3.2
1	F	232	ALA	3.2
1	F	134	GLY	3.2
1	E	169	GLU	3.2
1	F	100	PRO	3.2
1	E	154	ALA	3.2
1	F	183	VAL	3.2
1	C	405	ARG	3.1
1	C	401	SER	3.1
1	C	466	ALA	3.1
1	F	193	GLY	3.1
1	F	238	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
1	H	161	ALA	3.1
1	E	272	VAL	3.1
1	E	269	LEU	3.1
1	D	415	ILE	3.1
1	G	133	ILE	3.1
1	G	160	THR	3.1
1	G	239	GLY	3.1
1	A	29	ALA	3.1
1	A	466	ALA	3.1
1	B	29	ALA	3.1
1	E	120	ALA	3.1
1	F	295	VAL	3.1
1	H	159	VAL	3.1
1	F	173	LEU	3.1
1	F	243	LEU	3.1
1	G	179	ILE	3.1
1	E	160	THR	3.1
1	F	176	HIS	3.1
1	G	176	HIS	3.1
1	F	114	ALA	3.1
1	F	161	ALA	3.1
1	E	159	VAL	3.1
1	F	115	LEU	3.1
1	F	235	LEU	3.1
1	F	366	TYR	3.1
1	F	467	ALA	3.1
1	F	2	VAL	3.1
1	F	178	PRO	3.1
1	E	185	THR	3.0
1	H	157	ASP	3.0
1	D	57	ALA	3.0
1	H	2	VAL	3.0
1	F	121	HIS	3.0
1	E	389	SER	3.0
1	F	337	GLY	3.0
1	B	466	ALA	3.0
1	F	167	PRO	3.0
1	F	230	ALA	3.0
1	E	174	LEU	3.0
1	H	97	VAL	3.0
1	H	116	LEU	3.0
1	H	160	THR	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	147	PHE	3.0
1	F	162	PRO	3.0
1	G	178	PRO	3.0
1	D	467	ALA	3.0
1	F	326	ALA	3.0
1	G	154	ALA	3.0
1	G	466	ALA	3.0
1	E	2	VAL	3.0
1	F	135	LEU	3.0
1	F	276	VAL	3.0
1	G	163	VAL	3.0
1	G	410	LEU	3.0
1	E	130	GLY	3.0
1	G	223	GLY	3.0
1	F	89	PHE	2.9
1	H	132	PRO	3.0
1	C	410	LEU	2.9
1	E	109	VAL	2.9
1	E	189	GLY	2.9
1	F	113	ASN	2.9
1	B	147	PHE	2.9
1	C	29	ALA	2.9
1	F	95	LEU	2.9
1	F	203	ALA	2.9
1	F	449	ALA	2.9
1	F	452	LEU	2.9
1	G	252	GLN	2.9
1	E	43	GLY	2.9
1	E	148	ALA	2.9
1	F	29	ALA	2.9
1	F	269	LEU	2.9
1	G	80	ILE	2.9
1	F	268	GLY	2.9
1	G	274	GLY	2.9
1	F	299	PRO	2.9
1	F	425	ALA	2.9
1	G	192	ALA	2.9
1	E	170	VAL	2.9
1	E	181	VAL	2.9
1	G	97	VAL	2.9
1	G	127	VAL	2.9
1	F	246	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	E	162	PRO	2.8
1	C	301	ALA	2.8
1	D	411	PHE	2.8
1	F	124	ALA	2.8
1	G	170	VAL	2.8
1	G	153	ILE	2.8
1	F	329	LEU	2.8
1	G	212	ALA	2.8
1	B	3	ARG	2.8
1	C	402	SER	2.8
1	G	402	SER	2.8
1	E	236	ALA	2.8
1	F	182	ALA	2.8
1	A	411	PHE	2.8
1	E	28	VAL	2.8
1	F	90	VAL	2.8
1	F	196	THR	2.8
1	G	137	THR	2.8
1	E	157	ASP	2.8
1	E	219	ALA	2.8
1	F	220	ALA	2.8
1	G	120	ALA	2.8
1	E	32	PHE	2.8
1	B	2	VAL	2.8
1	F	159	VAL	2.8
1	C	467	ALA	2.7
1	D	2	VAL	2.7
1	E	222	VAL	2.7
1	E	333	VAL	2.7
1	E	459	VAL	2.7
1	F	50	VAL	2.7
1	F	165	THR	2.7
1	H	137	THR	2.7
1	G	250	GLY	2.7
1	G	330	GLY	2.7
1	B	110	SER	2.7
1	C	116	LEU	2.7
1	E	422	LEU	2.7
1	A	123	ALA	2.7
1	E	301	ALA	2.7
1	F	209	ALA	2.7
1	F	236	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	147	PHE	2.7
1	B	333	VAL	2.7
1	F	262	VAL	2.7
1	F	333	VAL	2.7
1	E	371	ASP	2.7
1	F	133	ILE	2.7
1	F	330	GLY	2.7
1	E	412	GLU	2.7
1	B	394	ALA	2.7
1	E	200	ALA	2.7
1	E	203	ALA	2.7
1	H	176	HIS	2.7
1	F	403	PHE	2.7
1	G	183	VAL	2.7
1	H	333	VAL	2.7
1	H	300	GLY	2.7
1	E	271	LEU	2.7
1	G	265	LEU	2.7
1	B	301	ALA	2.6
1	F	212	ALA	2.6
1	G	234	ALA	2.6
1	G	147	PHE	2.6
1	A	2	VAL	2.6
1	B	401	SER	2.6
1	D	466	ALA	2.6
1	B	411	PHE	2.6
1	E	355	ASN	2.6
1	G	374	PHE	2.6
1	D	405	ARG	2.6
1	C	2	VAL	2.6
1	E	127	VAL	2.6
1	E	190	THR	2.6
1	F	244	VAL	2.6
1	G	218	ILE	2.6
1	B	408	LYS	2.6
1	E	52	ASN	2.6
1	G	157	ASP	2.6
1	E	100	PRO	2.6
1	E	409	GLY	2.6
1	G	181	VAL	2.6
1	B	402	SER	2.6
1	H	418	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	252	GLN	2.6
1	F	216	LEU	2.6
1	E	149	ARG	2.6
1	B	139	ALA	2.6
1	G	161	ALA	2.6
1	F	98	ASP	2.6
1	A	143	GLY	2.6
1	E	4	PHE	2.6
1	E	23	PRO	2.6
1	E	274	GLY	2.6
1	G	125	VAL	2.6
1	F	201	ILE	2.6
1	G	405	ARG	2.5
1	F	81	THR	2.5
1	G	299	PRO	2.5
1	G	417	THR	2.5
1	F	181	VAL	2.5
1	G	71	ILE	2.5
1	C	146	ARG	2.5
1	A	124	ALA	2.5
1	F	154	ALA	2.5
1	H	261	ALA	2.5
1	A	401	SER	2.5
1	C	181	VAL	2.5
1	E	228	VAL	2.5
1	F	265	LEU	2.5
1	A	425	ALA	2.5
1	B	148	ALA	2.5
1	E	212	ALA	2.5
1	G	193	GLY	2.5
1	D	417	THR	2.5
1	E	374	PHE	2.5
1	E	153	ILE	2.5
1	E	295	VAL	2.5
1	G	393	VAL	2.5
1	G	447	VAL	2.5
1	E	135	LEU	2.5
1	E	195	LEU	2.5
1	E	176	HIS	2.5
1	E	238	ALA	2.5
1	G	301	ALA	2.5
1	H	301	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
1	G	364	GLY	2.5
1	H	164	GLY	2.5
1	G	81	THR	2.4
1	A	30	SER	2.4
1	E	402	SER	2.4
1	D	408	LYS	2.4
1	G	182	ALA	2.4
1	A	193	GLY	2.4
1	A	331	GLY	2.4
1	H	169	GLU	2.4
1	G	185	THR	2.4
1	B	28	VAL	2.4
1	F	259	ILE	2.4
1	G	277	VAL	2.4
1	H	127	VAL	2.4
1	H	410	LEU	2.4
1	A	404	ASP	2.4
1	G	146	ARG	2.4
1	C	412	GLU	2.4
1	D	123	ALA	2.4
1	F	229	GLY	2.4
1	H	142	ALA	2.4
1	E	465	SER	2.4
1	E	90	VAL	2.4
1	F	144	VAL	2.4
1	G	262	VAL	2.4
1	F	267	LEU	2.4
1	G	235	LEU	2.4
1	G	285	LEU	2.4
1	A	426	ARG	2.4
1	H	424	PRO	2.4
1	E	24	GLY	2.4
1	E	230	ALA	2.4
1	E	427	GLY	2.4
1	F	234	ALA	2.4
1	F	466	ALA	2.4
1	H	192	ALA	2.4
1	F	39	VAL	2.4
1	F	228	VAL	2.4
1	E	216	LEU	2.4
1	F	373	LEU	2.4
1	G	169	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	27	ASP	2.3
1	F	188	ASP	2.3
1	E	448	GLY	2.3
1	F	214	GLY	2.3
1	G	427	GLY	2.3
1	C	192	ALA	2.3
1	H	81	THR	2.3
1	A	402	SER	2.3
1	E	56	VAL	2.3
1	F	286	ILE	2.3
1	F	3	ARG	2.3
1	E	366	TYR	2.3
1	E	408	LYS	2.3
1	H	79	PRO	2.3
1	H	162	PRO	2.3
1	A	301	ALA	2.3
1	C	406	ALA	2.3
1	F	200	ALA	2.3
1	F	288	ALA	2.3
1	G	261	ALA	2.3
1	H	425	ALA	2.3
1	E	84	SER	2.3
1	G	401	SER	2.3
1	F	202	ARG	2.3
1	E	201	ILE	2.3
1	E	218	ILE	2.3
1	G	90	VAL	2.3
1	H	136	VAL	2.3
1	F	410	LEU	2.3
1	F	152	ASP	2.3
1	E	105	PRO	2.3
1	E	270	PRO	2.3
1	E	439	GLY	2.3
1	G	214	GLY	2.3
1	E	253	ALA	2.3
1	H	29	ALA	2.3
1	E	81	THR	2.3
1	H	417	THR	2.3
1	D	402	SER	2.3
1	E	328	GLN	2.3
1	H	133	ILE	2.3
1	C	32	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
1	F	210	VAL	2.3
1	C	103	LEU	2.3
1	G	173	LEU	2.3
1	H	135	LEU	2.3
1	H	173	LEU	2.3
1	E	303	CYS	2.3
1	E	152	ASP	2.3
1	E	167	PRO	2.3
1	F	327	ARG	2.3
1	G	350	ALA	2.3
1	H	154	ALA	2.3
1	B	176	HIS	2.3
1	E	46	ILE	2.3
1	A	410	LEU	2.2
1	G	144	VAL	2.3
1	E	246	ASP	2.2
1	B	146	ARG	2.2
1	E	134	GLY	2.2
1	F	281	GLY	2.2
1	H	189	GLY	2.2
1	H	405	ARG	2.2
1	A	169	GLU	2.2
1	E	139	ALA	2.2
1	E	177	ALA	2.2
1	E	261	ALA	2.2
1	F	139	ALA	2.2
1	F	348	ALA	2.2
1	F	417	THR	2.2
1	G	106	GLU	2.2
1	H	212	ALA	2.2
1	E	401	SER	2.2
1	H	201	ILE	2.2
1	B	410	LEU	2.2
1	A	147	PHE	2.2
1	F	97	VAL	2.2
1	F	125	VAL	2.2
1	G	297	VAL	2.2
1	H	90	VAL	2.2
1	E	27	ASP	2.2
1	E	164	GLY	2.2
1	G	328	GLN	2.2
1	E	417	THR	2.2

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Mol	Chain	Res	Type	RSRZ
1	F	102	THR	2.2
1	G	240	ALA	2.2
1	H	388	ALA	2.2
1	F	402	SER	2.2
1	G	156	SER	2.2
1	G	416	SER	2.2
1	A	415	ILE	2.2
1	E	80	ILE	2.2
1	F	71	ILE	2.2
1	B	271	LEU	2.2
1	F	21	VAL	2.2
1	F	101	VAL	2.2
1	F	293	VAL	2.2
1	D	32	PHE	2.2
1	E	98	ASP	2.2
1	E	337	GLY	2.2
1	F	82	ALA	2.2
1	H	402	SER	2.2
1	E	415	ILE	2.2
1	G	329	LEU	2.2
1	E	73	VAL	2.2
1	F	136	VAL	2.2
1	F	32	PHE	2.2
1	F	172	ASP	2.2
1	F	169	GLU	2.2
1	F	414	GLY	2.2
1	B	123	ALA	2.2
1	D	124	ALA	2.2
1	E	449	ALA	2.2
1	F	219	ALA	2.2
1	F	406	ALA	2.2
1	G	263	ALA	2.2
1	C	327	ARG	2.1
1	C	426	ARG	2.1
1	H	80	ILE	2.1
1	E	334	TRP	2.1
1	B	77	ASP	2.1
1	B	144	VAL	2.1
1	E	188	ASP	2.1
1	F	255	MET	2.1
1	F	355	ASN	2.1
1	G	371	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	E	390	LYS	2.1
1	D	105	PRO	2.1
1	F	252	GLN	2.1
1	B	268	GLY	2.1
1	E	226	GLY	2.1
1	E	300	GLY	2.1
1	F	352	GLY	2.1
1	G	414	GLY	2.1
1	F	240	ALA	2.1
1	F	389	SER	2.1
1	H	104	SER	2.1
1	E	131	ARG	2.1
1	A	116	LEU	2.1
1	E	115	LEU	2.1
1	F	224	ILE	2.1
1	F	256	LEU	2.1
1	H	115	LEU	2.1
1	H	302	MET	2.1
1	F	275	ASN	2.1
1	F	339	VAL	2.1
1	F	369	PRO	2.1
1	F	447	VAL	2.1
1	F	460	VAL	2.1
1	G	295	VAL	2.1
1	G	332	HIS	2.1
1	C	411	PHE	2.1
1	E	147	PHE	2.1
1	G	403	PHE	2.1
1	H	89	PHE	2.1
1	F	199	GLY	2.1
1	H	59	ARG	2.1
1	A	148	ALA	2.1
1	F	110	SER	2.1
1	G	51	ALA	2.1
1	H	186	ALA	2.1
1	F	254	LYS	2.1
1	G	413	GLU	2.1
1	G	461	LEU	2.1
1	B	299	PRO	2.1
1	D	181	VAL	2.1
1	F	83	VAL	2.1
1	G	87	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	G	333	VAL	2.1
1	H	126	VAL	2.1
1	H	194	VAL	2.1
1	G	143	GLY	2.1
1	A	146	ARG	2.1
1	G	168	ARG	2.1
1	F	444	CYS	2.1
1	E	425	ALA	2.1
1	F	261	ALA	2.1
1	B	412	GLU	2.1
1	F	413	GLU	2.1
1	H	413	GLU	2.1
1	E	235	LEU	2.1
1	E	133	ILE	2.1
1	E	259	ILE	2.1
1	C	299	PRO	2.1
1	D	299	PRO	2.1
1	E	87	VAL	2.1
1	F	96	VAL	2.1
1	F	24	GLY	2.1
1	F	239	GLY	2.1
1	F	289	GLY	2.1
1	G	41	GLY	2.1
1	G	89	PHE	2.1
1	D	379	ARG	2.1
1	F	25	ARG	2.1
1	F	376	ARG	2.1
1	C	139	ALA	2.0
1	D	425	ALA	2.0
1	E	138	GLU	2.0
1	G	186	ALA	2.0
1	G	203	ALA	2.0
1	F	233	GLN	2.0
1	C	113	ASN	2.0
1	E	173	LEU	2.0
1	F	195	LEU	2.0
1	F	423	ASP	2.0
1	H	103	LEU	2.0
1	H	188	ASP	2.0
1	G	201	ILE	2.0
1	F	342	PRO	2.0
1	B	181	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
1	G	3	ARG	2.0
1	A	414	GLY	2.0
1	G	294	LYS	2.0
1	G	184	MET	2.0
1	E	165	THR	2.0
1	F	401	SER	2.0
1	G	99	THR	2.0
1	A	57	ALA	2.0
1	D	29	ALA	2.0
1	E	240	ALA	2.0
1	F	325	ALA	2.0
1	G	29	ALA	2.0
1	B	456	HIS	2.0
1	F	328	GLN	2.0
1	D	404	ASP	2.0
1	F	88	ASP	2.0
1	G	245	ILE	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(Å ²)	Q<0.9
3	GTP	E	502[A]	32/32	0.83	0.12	63,72,81,84	32
3	GTP	E	502[B]	32/32	0.83	0.12	64,73,80,84	32
3	GTP	G	502[A]	32/32	0.84	0.13	63,71,76,78	32
3	GTP	G	502[B]	32/32	0.84	0.13	63,71,75,78	32
3	GTP	F	502[A]	32/32	0.87	0.12	76,81,90,92	32
3	GTP	F	502[B]	32/32	0.87	0.12	76,82,89,91	32

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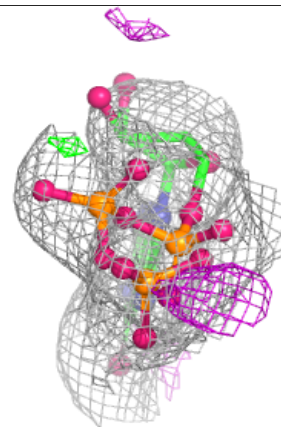
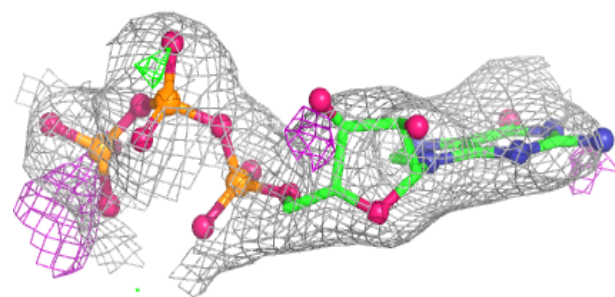
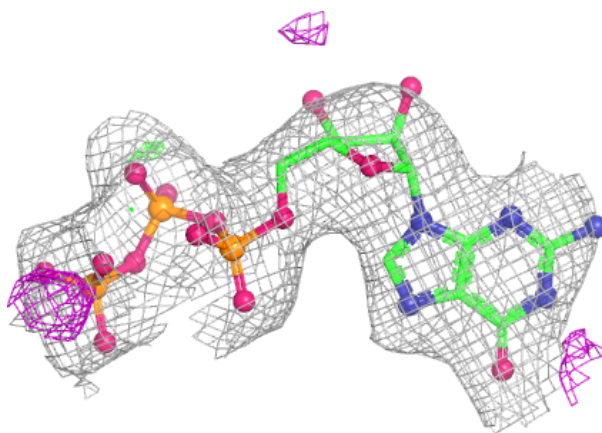
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	GTP	H	502[A]	32/32	0.87	0.12	57,66,72,73	32
3	GTP	H	502[B]	32/32	0.87	0.12	59,66,72,75	32
3	GTP	C	502[A]	32/32	0.89	0.12	55,67,75,85	32
3	GTP	C	502[B]	32/32	0.89	0.12	53,66,75,85	32
3	GTP	D	502[A]	32/32	0.90	0.11	47,60,64,66	32
3	GTP	D	502[B]	32/32	0.90	0.11	53,61,64,65	32
2	5GP	F	501	24/24	0.91	0.09	58,69,83,89	0
2	5GP	G	501	24/24	0.91	0.10	46,59,70,73	0
3	GTP	A	502[A]	32/32	0.92	0.10	40,58,63,66	32
3	GTP	A	502[B]	32/32	0.92	0.10	42,58,65,66	32
3	GTP	B	502[A]	32/32	0.92	0.10	53,63,69,71	32
3	GTP	B	502[B]	32/32	0.92	0.10	55,63,69,75	32
2	5GP	C	501	24/24	0.93	0.09	38,50,57,62	0
2	5GP	E	501	24/24	0.94	0.08	50,59,69,72	0
2	5GP	A	501	24/24	0.95	0.07	33,39,47,50	0
2	5GP	H	501	24/24	0.95	0.07	38,48,55,64	0
2	5GP	B	501	24/24	0.96	0.06	30,44,51,56	0
2	5GP	D	501	24/24	0.96	0.07	36,46,57,61	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.

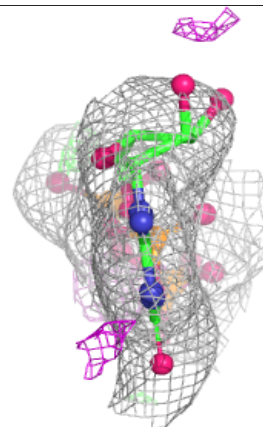
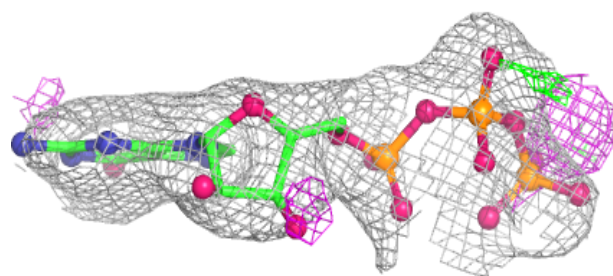
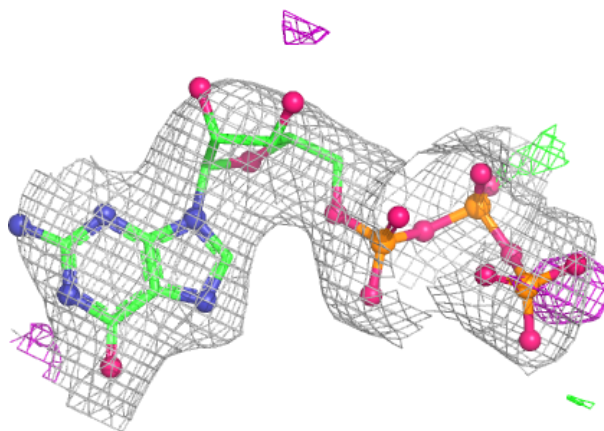
Electron density around GTP E 502 (A):

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

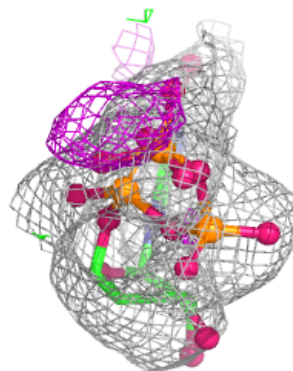
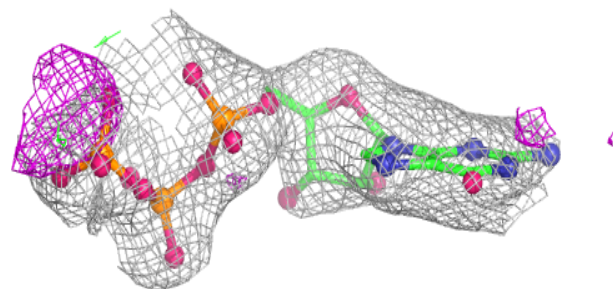
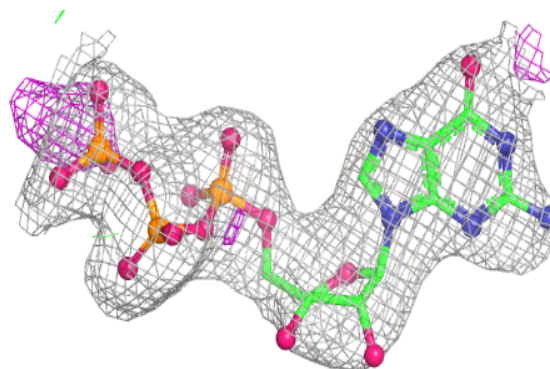


Electron density around GTP E 502 (B):

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

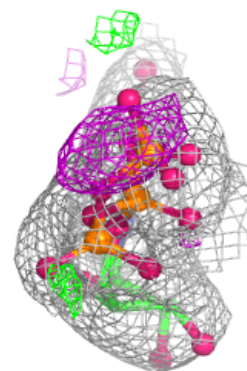
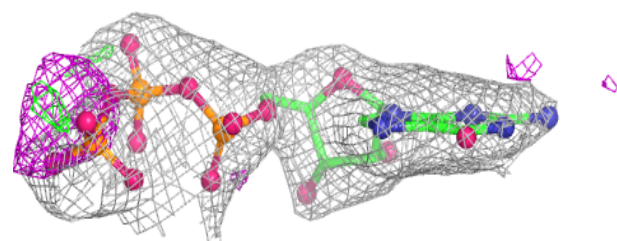
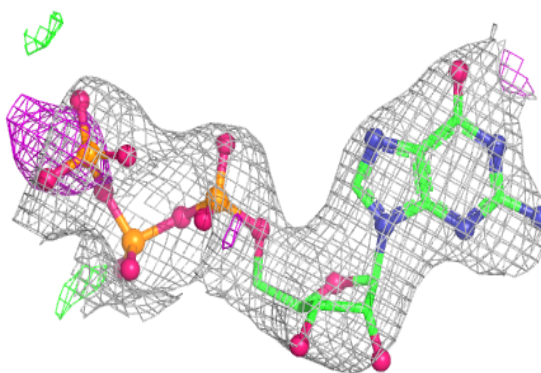
**Electron density around GTP G 502 (A):**

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

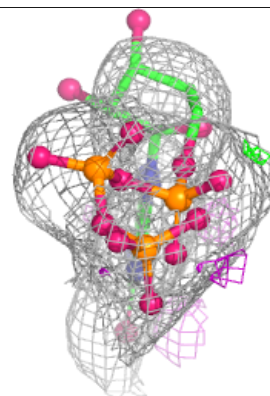
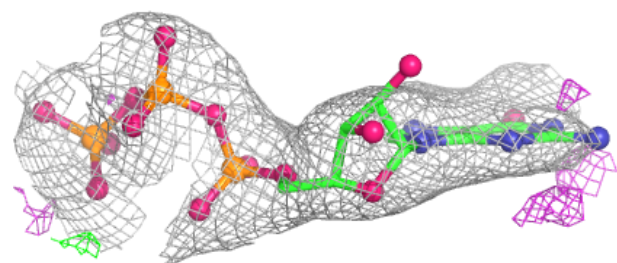
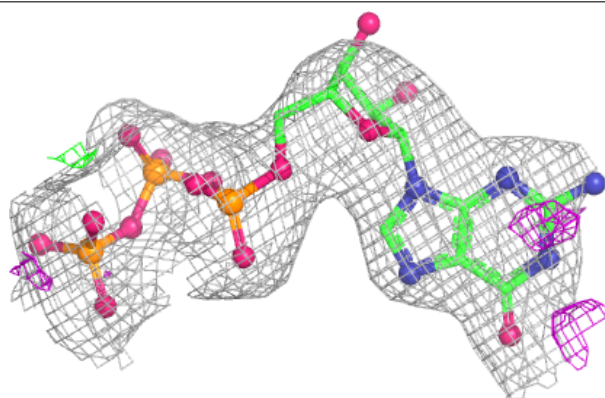


Electron density around GTP G 502 (B):

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

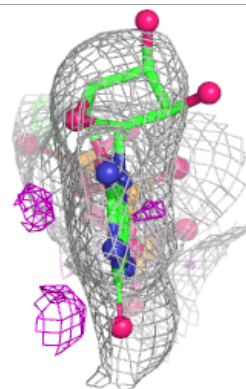
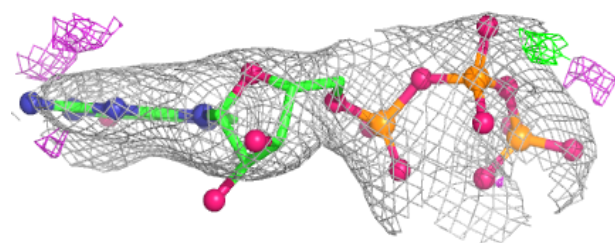
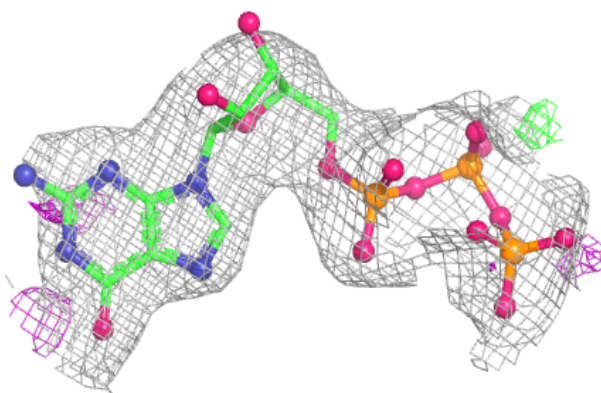
**Electron density around GTP F 502 (A):**

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

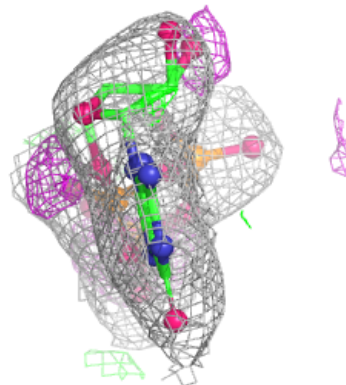
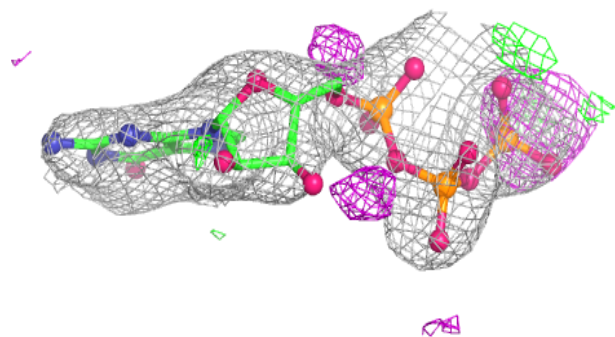
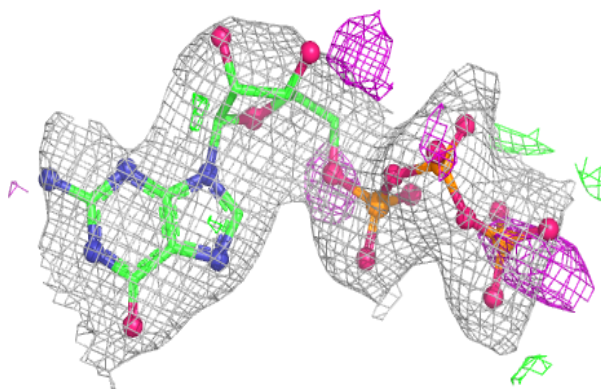


Electron density around GTP F 502 (B):

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

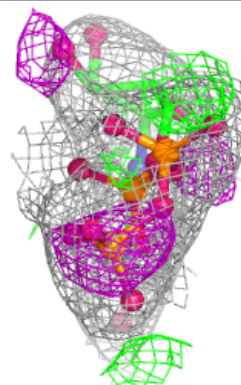
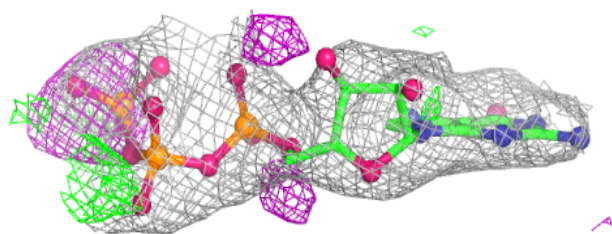
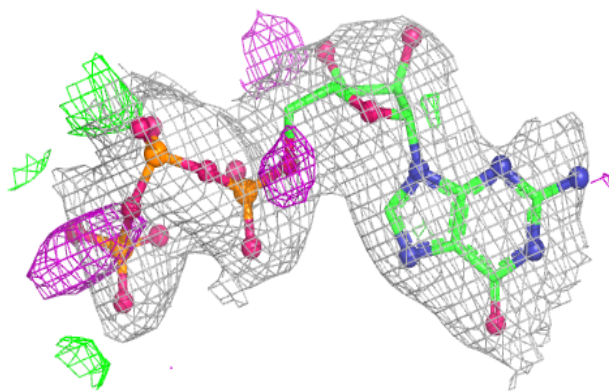
**Electron density around GTP H 502 (A):**

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

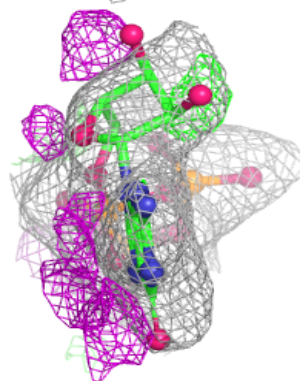
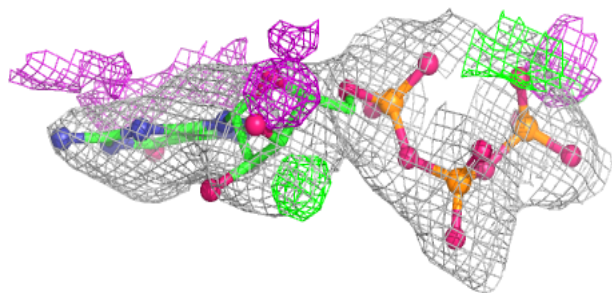
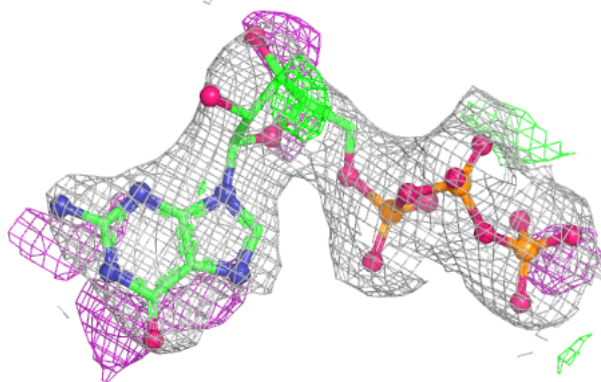


Electron density around GTP H 502 (B):

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

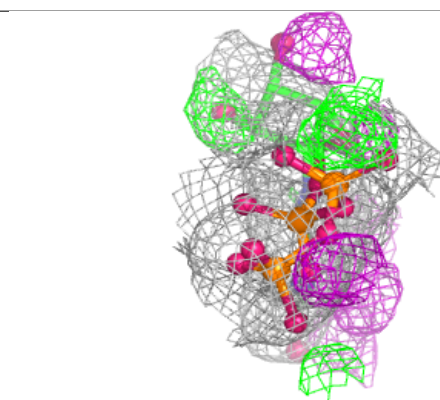
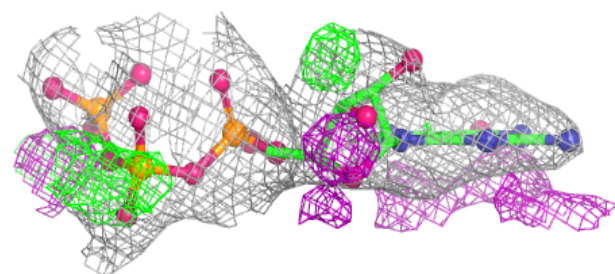
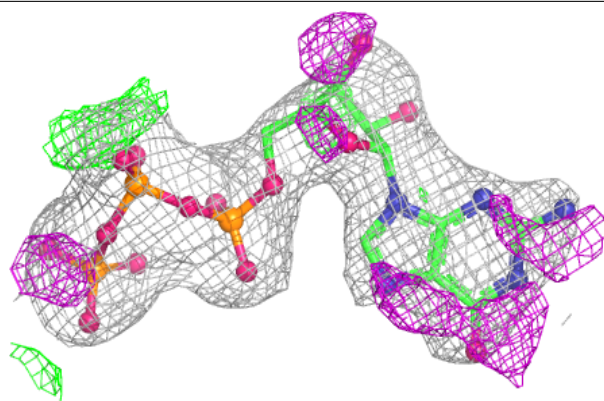
**Electron density around GTP C 502 (A):**

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

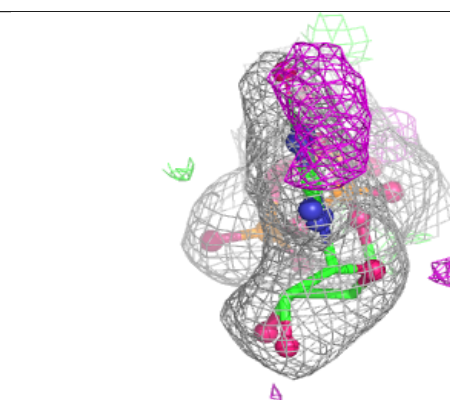
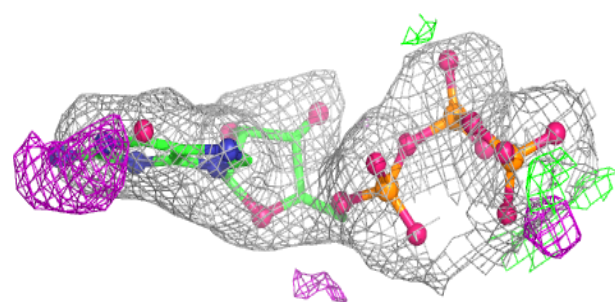
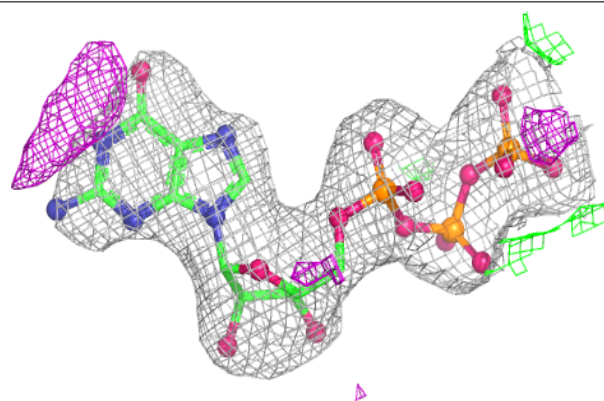


Electron density around GTP C 502 (B):

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

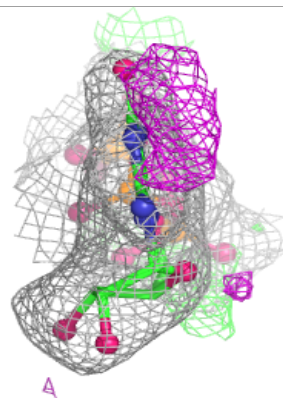
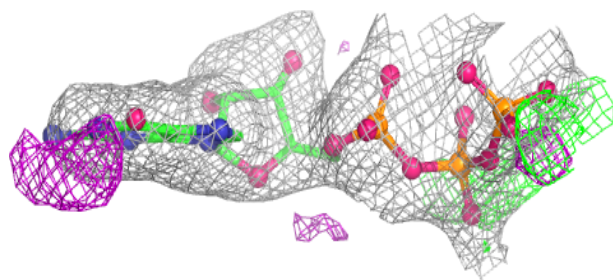
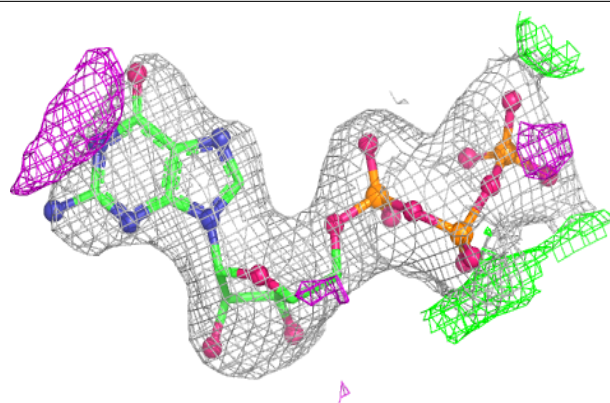
**Electron density around GTP D 502 (A):**

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

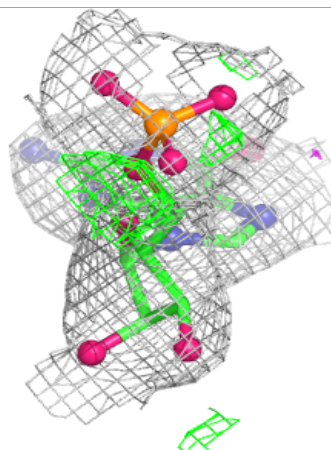
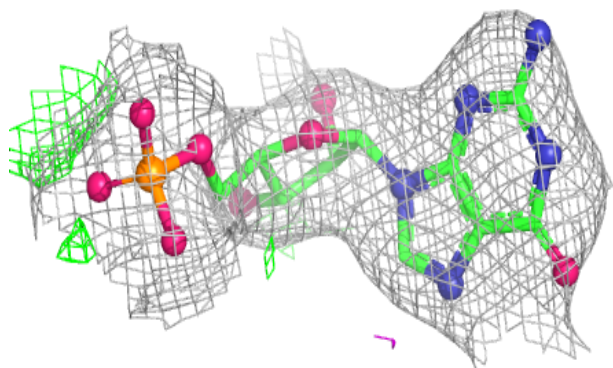
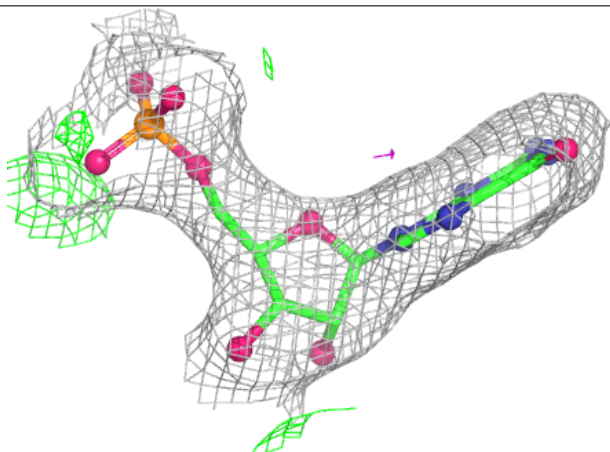


Electron density around GTP D 502 (B):

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

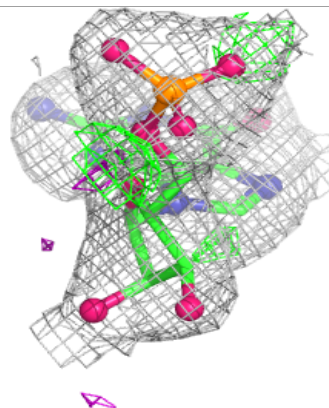
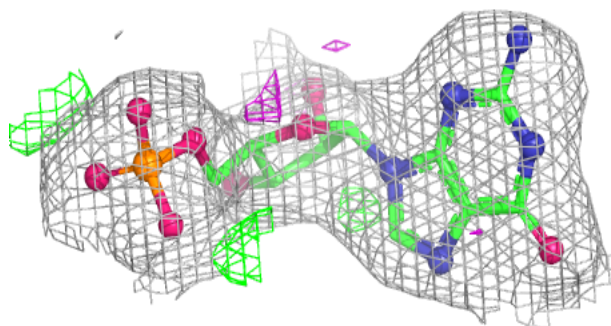
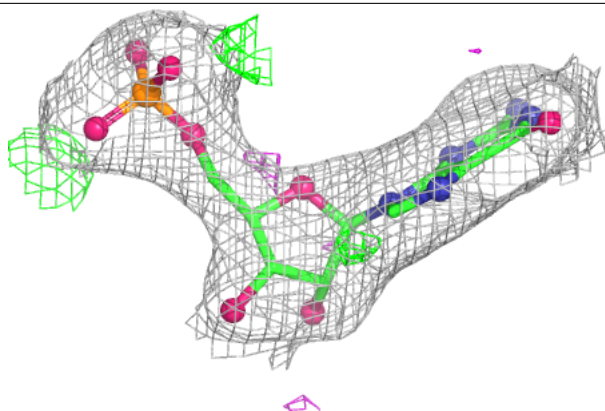
**Electron density around 5GP F 501:**

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

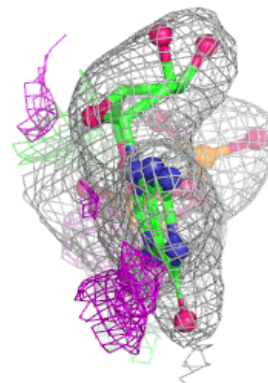
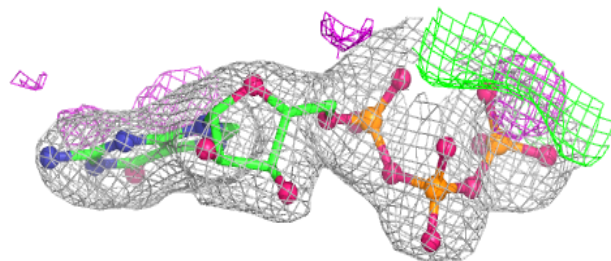
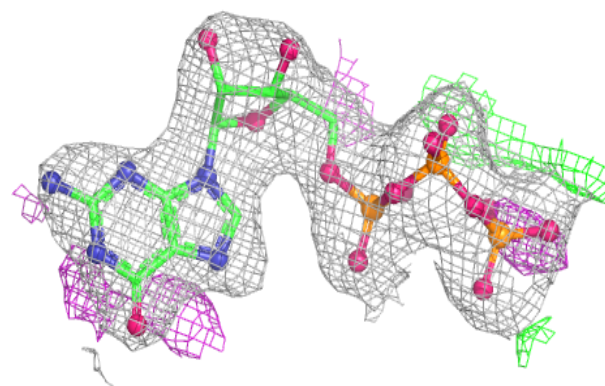


Electron density around 5GP G 501:

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

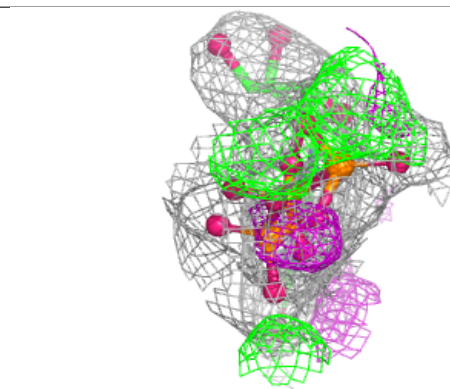
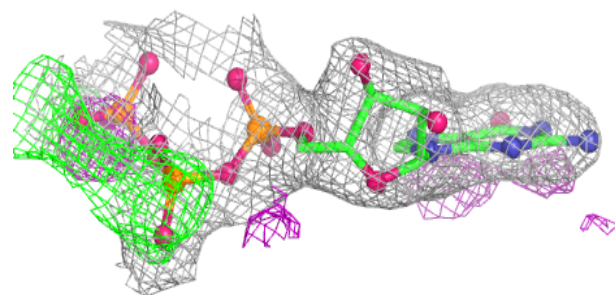
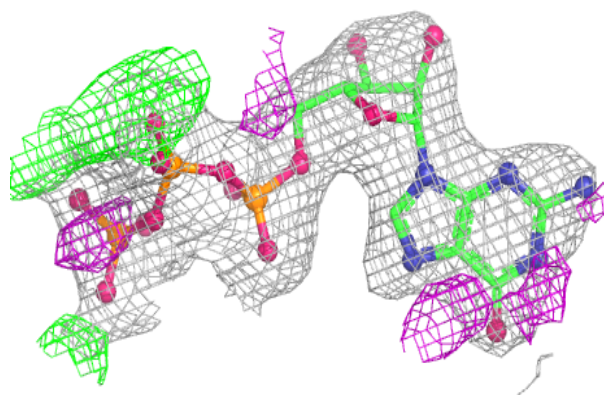
**Electron density around GTP A 502 (A):**

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

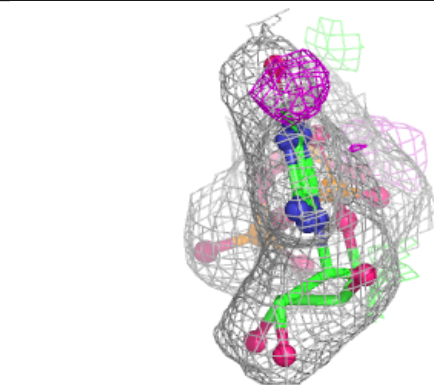
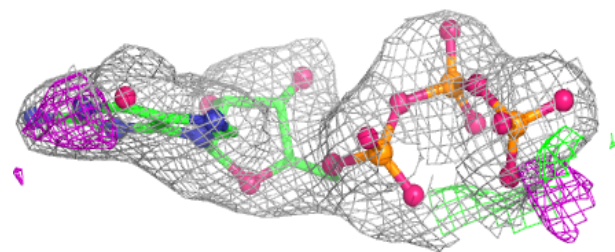
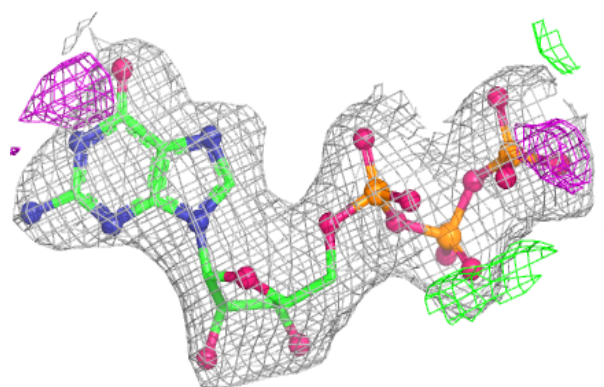


Electron density around GTP A 502 (B):

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

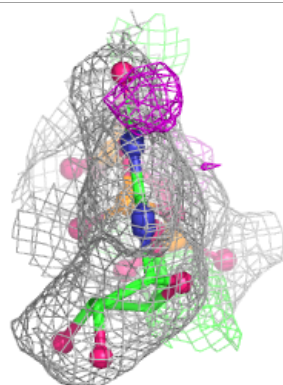
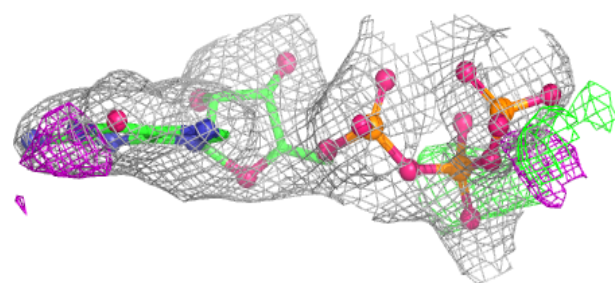
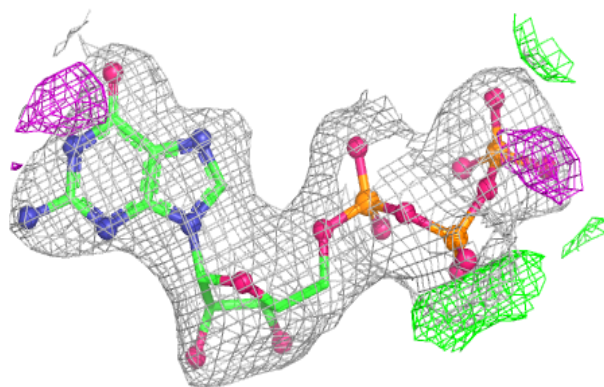
**Electron density around GTP B 502 (A):**

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

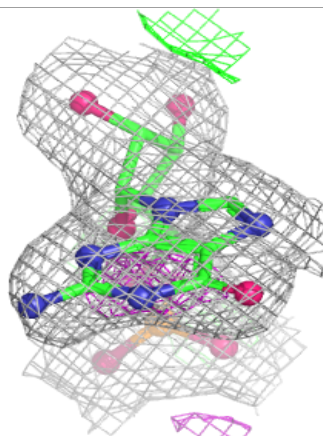
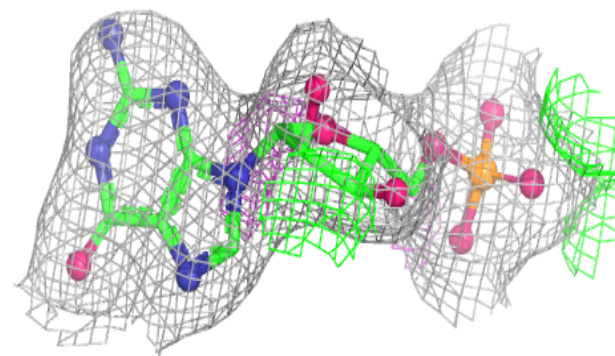
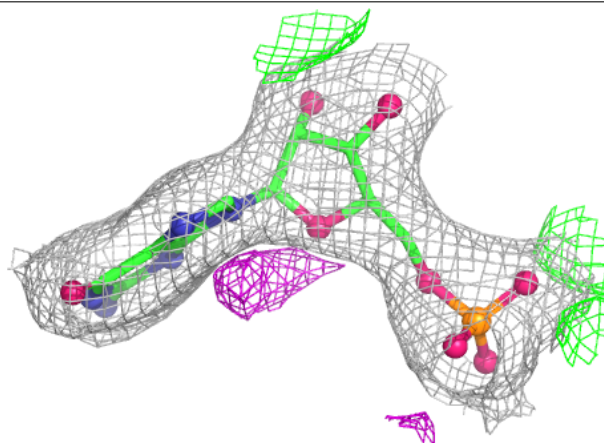


Electron density around GTP B 502 (B):

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

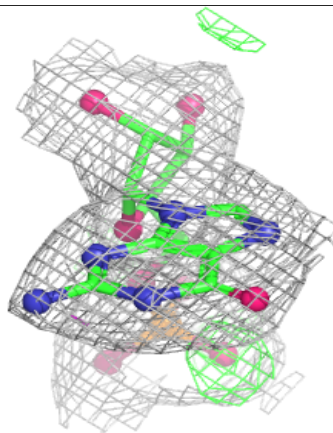
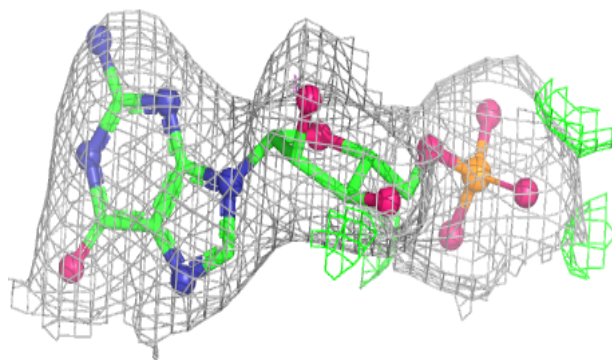
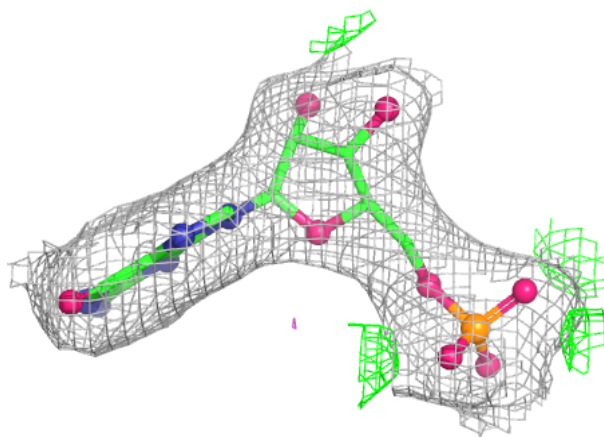
**Electron density around 5GP C 501:**

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



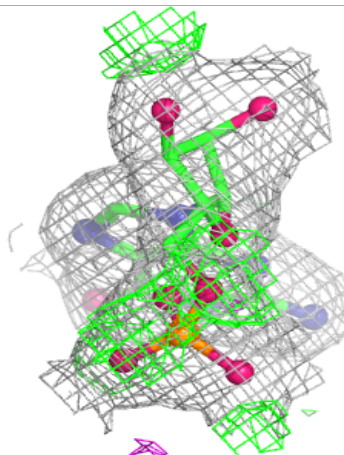
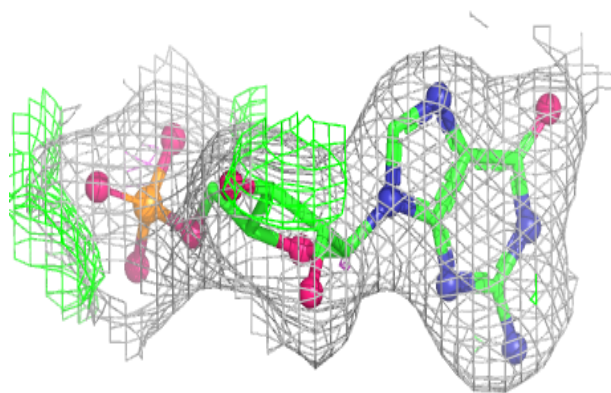
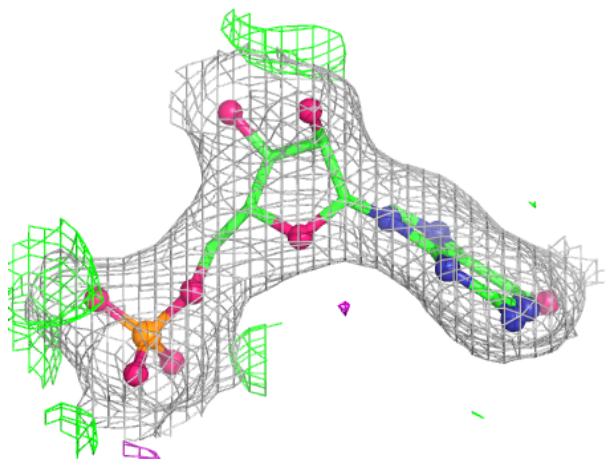
Electron density around 5GP E 501:

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



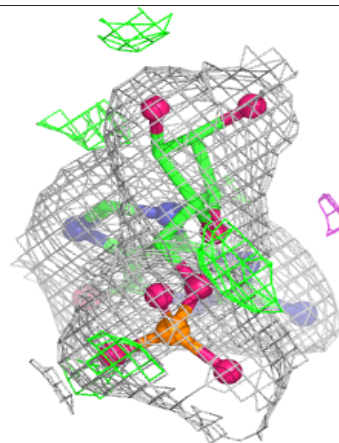
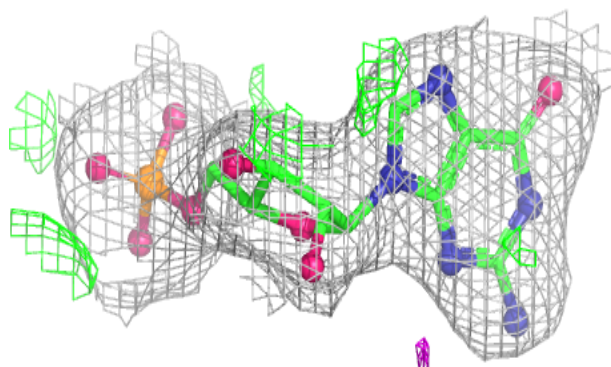
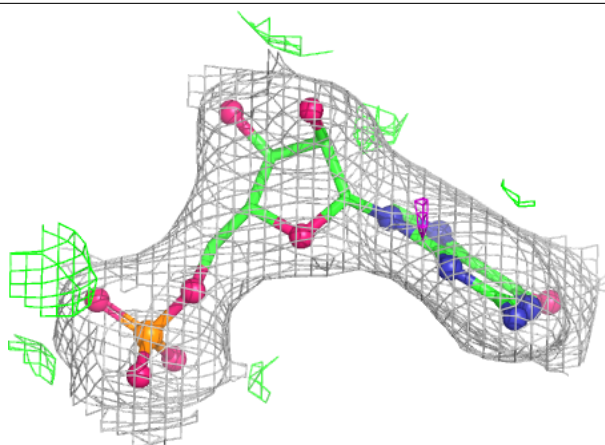
Electron density around 5GP A 501:

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



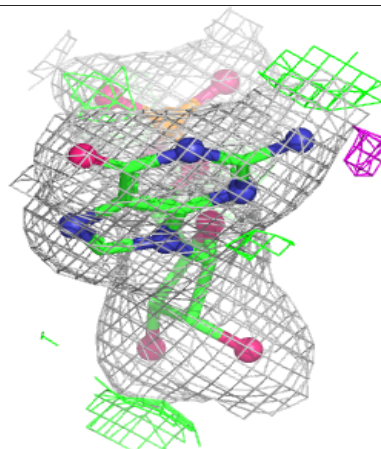
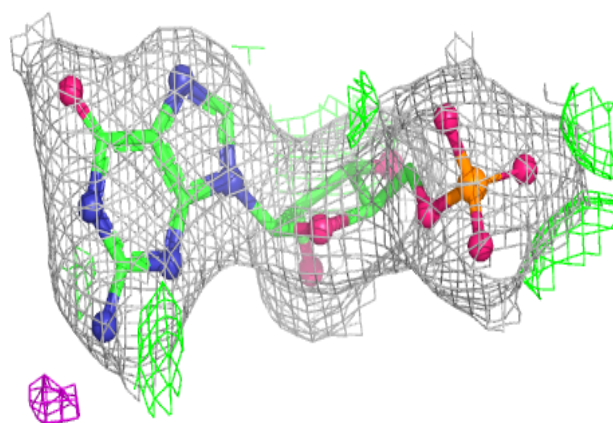
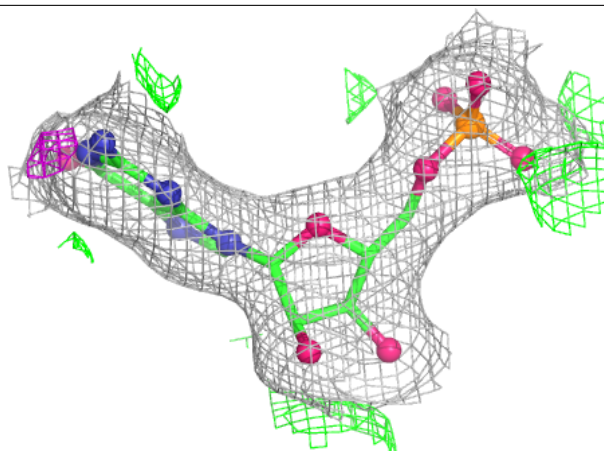
Electron density around 5GP H 501:

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



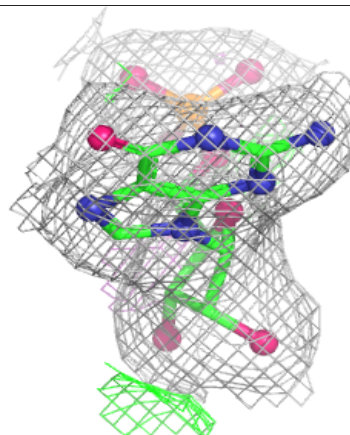
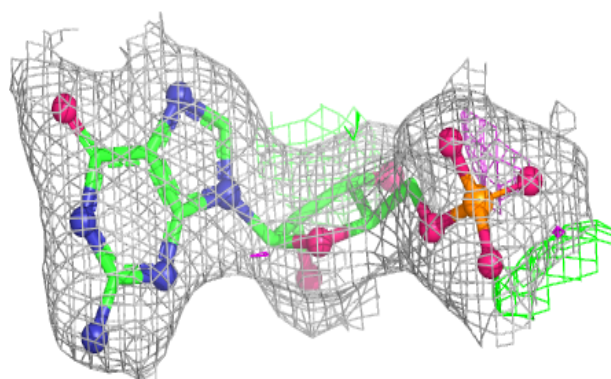
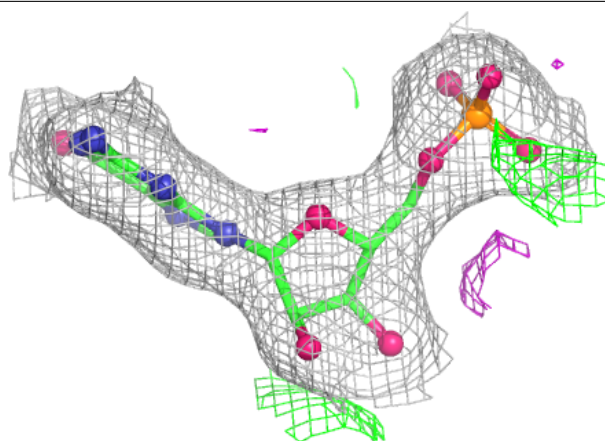
Electron density around 5GP B 501:

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



Electron density around 5GP 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.