



wwPDB X-ray Structure Validation Summary Report ⓘ

May 17, 2020 – 01:52 am BST

PDB ID : 4Z87
Title : Structure of the IMP dehydrogenase from *Ashbya gossypii* bound to GDP
Authors : Buey, R.M.; de Pereda, J.M.; Revuelta, J.L.
Deposited on : 2015-04-08
Resolution : 2.25 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

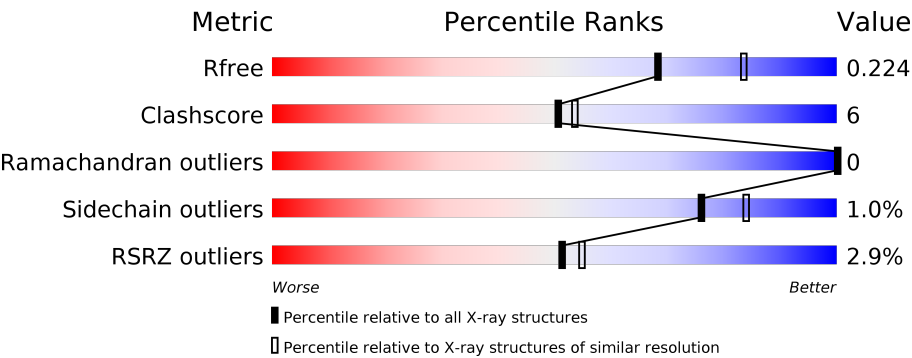
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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 on 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	525	<div><div>2%</div><div>89%6%5%</div></div>
1	B	525	<div><div>2%</div><div>86%9%5%</div></div>
1	C	525	<div><div>4%</div><div>84%9%6%</div></div>
1	D	525	<div><div>3%</div><div>85%7%8%</div></div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	5GP	A	601	-	-	X	-
2	5GP	B	601	-	-	X	-
2	5GP	D	600	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 30096 atoms, of which 14571 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.

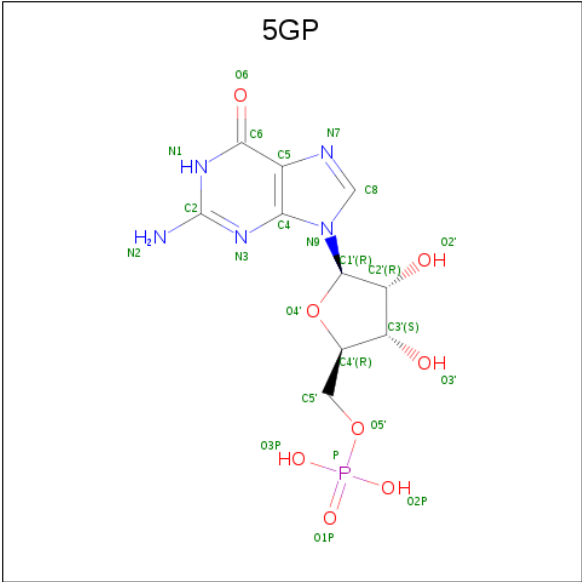
- Molecule 1 is a protein called Inosine-5'-monophosphate dehydrogenase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	498	Total	C	H	N	O	S	0	0	0
			7418	2333	3700	637	722	26			
1	B	498	Total	C	H	N	O	S	0	0	0
			7331	2310	3647	639	710	25			
1	C	495	Total	C	H	N	O	S	0	0	0
			7102	2257	3511	624	685	25			
1	D	484	Total	C	H	N	O	S	0	1	0
			7080	2239	3503	621	692	25			

There are 12 discrepancies between the modelled and reference sequences:

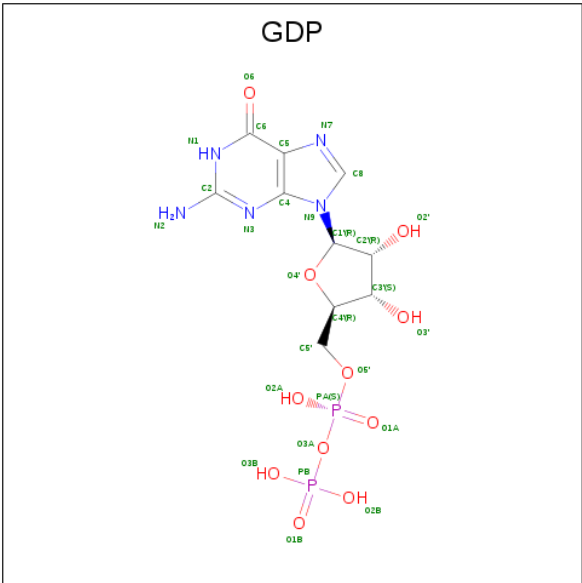
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q756Z6
A	-1	SER	-	expression tag	UNP Q756Z6
A	0	HIS	-	expression tag	UNP Q756Z6
B	-2	GLY	-	expression tag	UNP Q756Z6
B	-1	SER	-	expression tag	UNP Q756Z6
B	0	HIS	-	expression tag	UNP Q756Z6
C	-2	GLY	-	expression tag	UNP Q756Z6
C	-1	SER	-	expression tag	UNP Q756Z6
C	0	HIS	-	expression tag	UNP Q756Z6
D	-2	GLY	-	expression tag	UNP Q756Z6
D	-1	SER	-	expression tag	UNP Q756Z6
D	0	HIS	-	expression tag	UNP Q756Z6

- Molecule 2 is GUANOSINE-5'-MONOPHOSPHATE (three-letter code: 5GP) (formula: C₁₀H₁₄N₅O₈P).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	P	0	0
			35	10	11	5	8	1		
2	B	1	Total	C	H	N	O	P	0	0
			35	10	11	5	8	1		
2	C	1	Total	C	H	N	O	P	0	0
			35	10	11	5	8	1		
2	D	1	Total	C	H	N	O	P	0	0
			35	10	11	5	8	1		

- Molecule 3 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	P	0	0
			39	10	11	5	11	2		
3	A	1	Total	C	H	N	O	P	0	0
			39	10	11	5	11	2		
3	A	1	Total	C	H	N	O	P	0	1
			78	20	22	10	22	4		
3	B	1	Total	C	H	N	O	P	0	0
			39	10	11	5	11	2		
3	B	1	Total	C	H	N	O	P	0	0
			39	10	11	5	11	2		
3	B	1	Total	C	H	N	O	P	0	0
			39	10	11	5	11	2		
3	C	1	Total	C	H	N	O	P	0	0
			39	10	11	5	11	2		
3	C	1	Total	C	H	N	O	P	0	0
			39	10	11	5	11	2		
3	C	1	Total	C	H	N	O	P	0	0
			39	10	11	5	11	2		
3	D	1	Total	C	H	N	O	P	0	0
			39	10	11	5	11	2		
3	D	1	Total	C	H	N	O	P	0	0
			39	10	11	5	11	2		
3	D	1	Total	C	H	N	O	P	0	1
			78	20	22	10	22	4		

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	K	0	0
			1	1		
4	A	1	Total	K	0	0
			1	1		
4	D	1	Total	K	0	0
			1	1		
4	C	1	Total	K	0	0
			1	1		

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			7	2	3	2		
5	B	1	Total	C	H	O	0	0
			7	2	3	2		
5	C	1	Total	C	H	O	0	0
			7	2	3	2		
5	C	1	Total	C	H	O	0	0
			7	2	3	2		

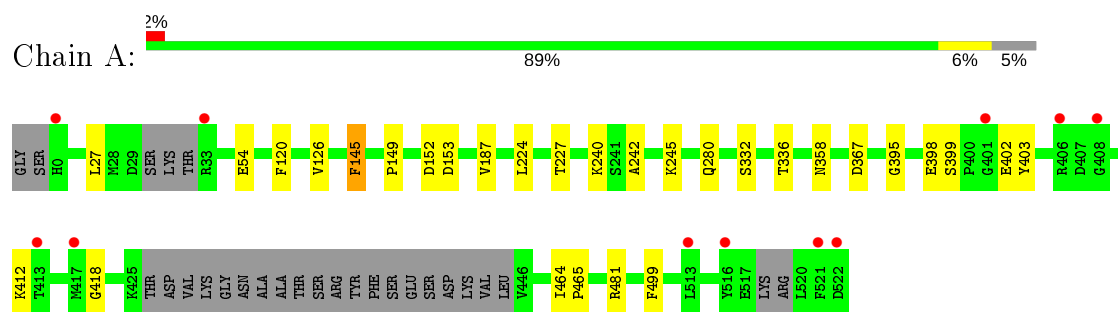
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	150	Total	O	0	0
			150	150		
6	B	140	Total	O	0	0
			140	140		
6	C	79	Total	O	0	0
			79	79		
6	D	78	Total	O	0	0
			78	78		

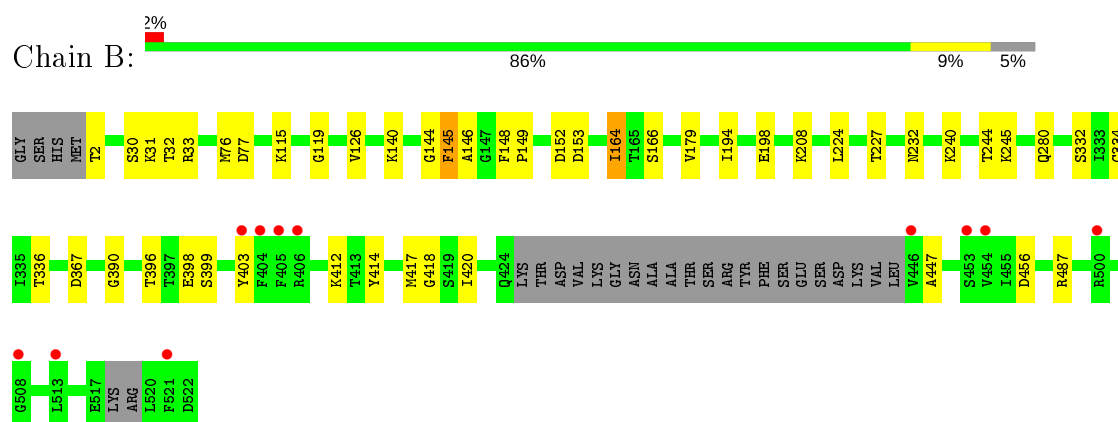
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

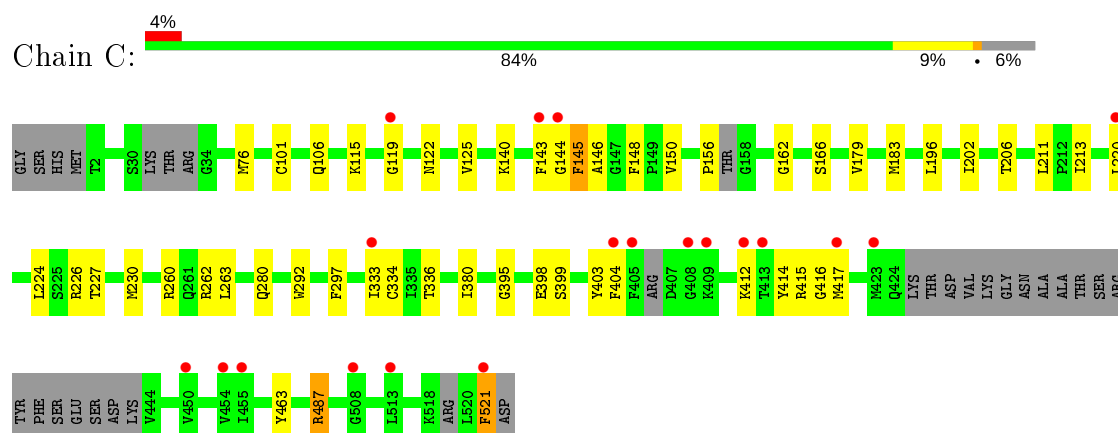
- Molecule 1: Inosine-5'-monophosphate dehydrogenase



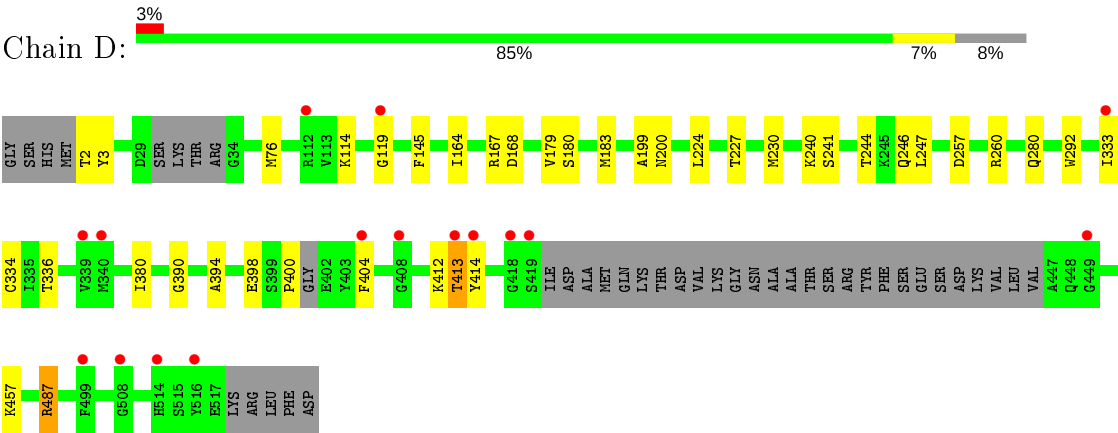
- Molecule 1: Inosine-5'-monophosphate dehydrogenase



- Molecule 1: Inosine-5'-monophosphate dehydrogenase



● Molecule 1: Inosine-5'-monophosphate dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 4	Depositor
Cell constants a, b, c, α , β , γ	122.04Å 122.04Å 147.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.03 – 2.25 47.03 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.03-2.25) 100.0 (47.03-2.10)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.51 (at 2.10Å)	Xtriage
Refinement program	PHENIX dev_1839	Depositor
R, R_{free}	0.195 , 0.225 0.203 , 0.224	Depositor DCC
R_{free} test set	6148 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	43.2	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 37.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.094 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	30096	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.51% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, K, 5GP, ACT

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	0.27	0/3771	0.44	0/5094
1	B	0.31	0/3736	0.49	0/5053
1	C	0.31	0/3640	0.48	0/4925
1	D	0.35	0/3631	0.52	0/4910
All	All	0.31	0/14778	0.48	0/19982

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	3718	3700	3698	29	0
1	B	3684	3647	3650	43	0
1	C	3591	3511	3508	52	0
1	D	3577	3503	3512	43	2
2	A	24	11	12	7	0
2	B	24	11	12	7	0
2	C	24	11	12	3	0
2	D	24	11	12	8	0
3	A	112	44	48	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	84	33	36	2	0
3	C	84	33	36	2	2
3	D	112	44	48	7	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	4	3	3	0	0
5	B	4	3	3	0	0
5	C	8	6	6	0	0
6	A	150	0	0	2	0
6	B	140	0	0	2	0
6	C	79	0	0	0	0
6	D	78	0	0	1	0
All	All	15525	14571	14596	169	2

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 6.

The worst 5 of 169 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:400:PRO:C	1:D:412:LYS:HZ1	1.49	1.15
1:D:227:THR:HG21	3:D:602:GDP:O2A	1.46	1.13
1:D:400:PRO:C	1:D:412:LYS:NZ	2.06	1.09
1:C:150:VAL:HB	1:C:183:MET:HE1	1.36	1.04
1:B:418:GLY:N	2:B:601:5GP:O6	2.01	0.94

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:167:ARG:HH12	3:C:602:GDP:O1A[1_556]	1.11	0.49
1:D:167:ARG:NH1	3:C:602:GDP:O1A[1_556]	1.89	0.31

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	490/525 (93%)	477 (97%)	13 (3%)	0	100	100
1	B	492/525 (94%)	478 (97%)	14 (3%)	0	100	100
1	C	483/525 (92%)	470 (97%)	13 (3%)	0	100	100
1	D	477/525 (91%)	469 (98%)	8 (2%)	0	100	100
All	All	1942/2100 (92%)	1894 (98%)	48 (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	396/431 (92%)	394 (100%)	2 (0%)	88	92
1	B	387/431 (90%)	382 (99%)	5 (1%)	69	79
1	C	365/431 (85%)	361 (99%)	4 (1%)	73	82
1	D	373/431 (86%)	369 (99%)	4 (1%)	73	82
All	All	1521/1724 (88%)	1506 (99%)	15 (1%)	76	84

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	487	ARG
1	C	145	PHE
1	D	280	GLN

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Mol	Chain	Res	Type
1	B	280	GLN
1	D	145	PHE

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

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 26 ligands modelled in this entry, 4 are monoatomic - leaving 22 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
3	GDP	B	604	-	24,30,30	1.12	1 (4%)	31,47,47	2.04	9 (29%)
3	GDP	C	604	-	24,30,30	1.17	2 (8%)	31,47,47	2.06	7 (22%)
2	5GP	A	601	-	22,26,26	1.26	2 (9%)	27,40,40	1.96	7 (25%)
2	5GP	B	601	-	22,26,26	1.22	2 (9%)	27,40,40	2.05	9 (33%)
3	GDP	B	602	-	24,30,30	1.20	2 (8%)	31,47,47	2.00	7 (22%)
5	ACT	B	606	-	1,3,3	4.35	1 (100%)	0,3,3	0.00	-
3	GDP	A	602	-	24,30,30	1.08	1 (4%)	31,47,47	2.02	8 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GDP	D	601	-	24,30,30	1.17	1 (4%)	31,47,47	2.08	7 (22%)
2	5GP	C	601	-	22,26,26	1.20	1 (4%)	27,40,40	1.94	6 (22%)
3	GDP	B	603	-	24,30,30	1.06	2 (8%)	31,47,47	2.01	8 (25%)
3	GDP	D	602	-	24,30,30	1.10	2 (8%)	31,47,47	2.03	8 (25%)
3	GDP	A	603	-	24,30,30	1.10	2 (8%)	31,47,47	1.85	7 (22%)
2	5GP	D	600	-	22,26,26	1.15	2 (9%)	27,40,40	1.98	7 (25%)
5	ACT	C	607	-	1,3,3	1.12	0	0,3,3	0.00	-
5	ACT	C	606	-	1,3,3	0.40	0	0,3,3	0.00	-
3	GDP	A	604[A]	-	24,30,30	1.11	2 (8%)	31,47,47	1.87	8 (25%)
3	GDP	A	604[B]	-	24,30,30	1.07	2 (8%)	31,47,47	1.89	6 (19%)
3	GDP	C	602	-	24,30,30	1.13	2 (8%)	31,47,47	1.91	7 (22%)
3	GDP	D	603[B]	-	24,30,30	1.25	2 (8%)	31,47,47	2.07	7 (22%)
5	ACT	A	606	-	1,3,3	4.00	1 (100%)	0,3,3	0.00	-
3	GDP	C	603	-	24,30,30	1.15	2 (8%)	31,47,47	1.96	8 (25%)
3	GDP	D	603[A]	-	24,30,30	1.18	2 (8%)	31,47,47	1.96	9 (29%)

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	GDP	B	604	-	-	1/12/32/32	0/3/3/3
3	GDP	C	604	-	-	5/12/32/32	0/3/3/3
3	GDP	A	602	-	-	3/12/32/32	0/3/3/3
2	5GP	B	601	-	-	0/6/26/26	0/3/3/3
3	GDP	A	604[B]	-	-	4/12/32/32	0/3/3/3
2	5GP	C	601	-	-	0/6/26/26	0/3/3/3
3	GDP	B	603	-	-	2/12/32/32	0/3/3/3
3	GDP	A	603	-	-	1/12/32/32	0/3/3/3
2	5GP	D	600	-	-	0/6/26/26	0/3/3/3
3	GDP	D	602	-	-	2/12/32/32	0/3/3/3
3	GDP	B	602	-	-	0/12/32/32	0/3/3/3
3	GDP	C	602	-	-	5/12/32/32	0/3/3/3
3	GDP	D	603[B]	-	-	4/12/32/32	0/3/3/3
3	GDP	A	604[A]	-	-	5/12/32/32	0/3/3/3
3	GDP	D	601	-	-	4/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GDP	C	603	-	-	2/12/32/32	0/3/3/3
2	5GP	A	601	-	-	3/6/26/26	0/3/3/3
3	GDP	D	603[A]	-	-	2/12/32/32	0/3/3/3

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	5GP	C6-C5	4.57	1.49	1.41
3	D	601	GDP	C6-C5	4.40	1.48	1.41
3	D	603[B]	GDP	C6-C5	4.35	1.48	1.41
5	B	606	ACT	CH3-C	4.35	1.54	1.48
3	C	604	GDP	C6-C5	4.26	1.48	1.41

The worst 5 of 135 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	601	GDP	C2-N3-C4	5.28	121.38	115.36
2	A	601	5GP	C2-N3-C4	5.04	121.12	115.36
3	A	602	GDP	C2-N3-C4	5.04	121.12	115.36
2	B	601	5GP	C2-N3-C4	5.01	121.08	115.36
3	A	602	GDP	C6-C5-C4	-4.96	116.07	120.80

There are no chirality outliers.

5 of 43 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	604	GDP	C5'-O5'-PA-O1A
3	C	604	GDP	PA-O3A-PB-O2B
3	C	604	GDP	PA-O3A-PB-O3B
2	A	601	5GP	C5'-O5'-P-O3P
2	A	601	5GP	C3'-C4'-C5'-O5'

There are no ring outliers.

16 monomers are involved in 47 short contacts:

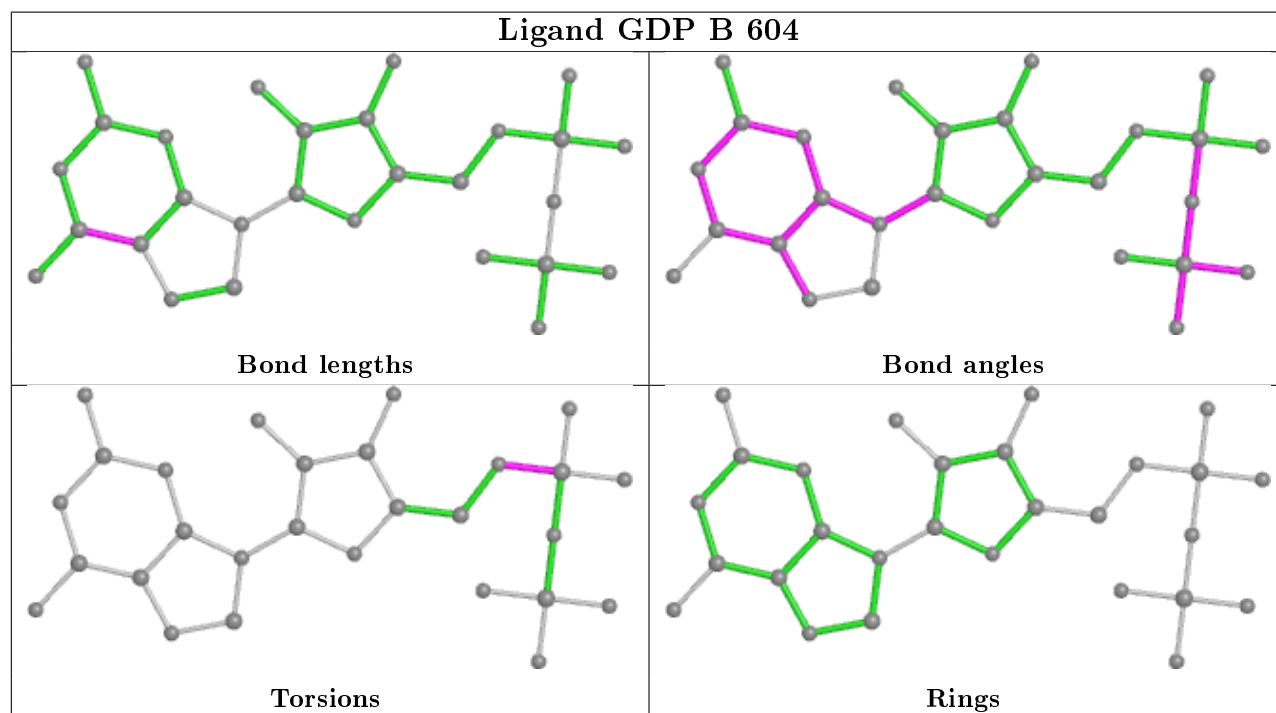
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	604	GDP	1	0
3	C	604	GDP	1	0
2	A	601	5GP	7	0
2	B	601	5GP	7	0

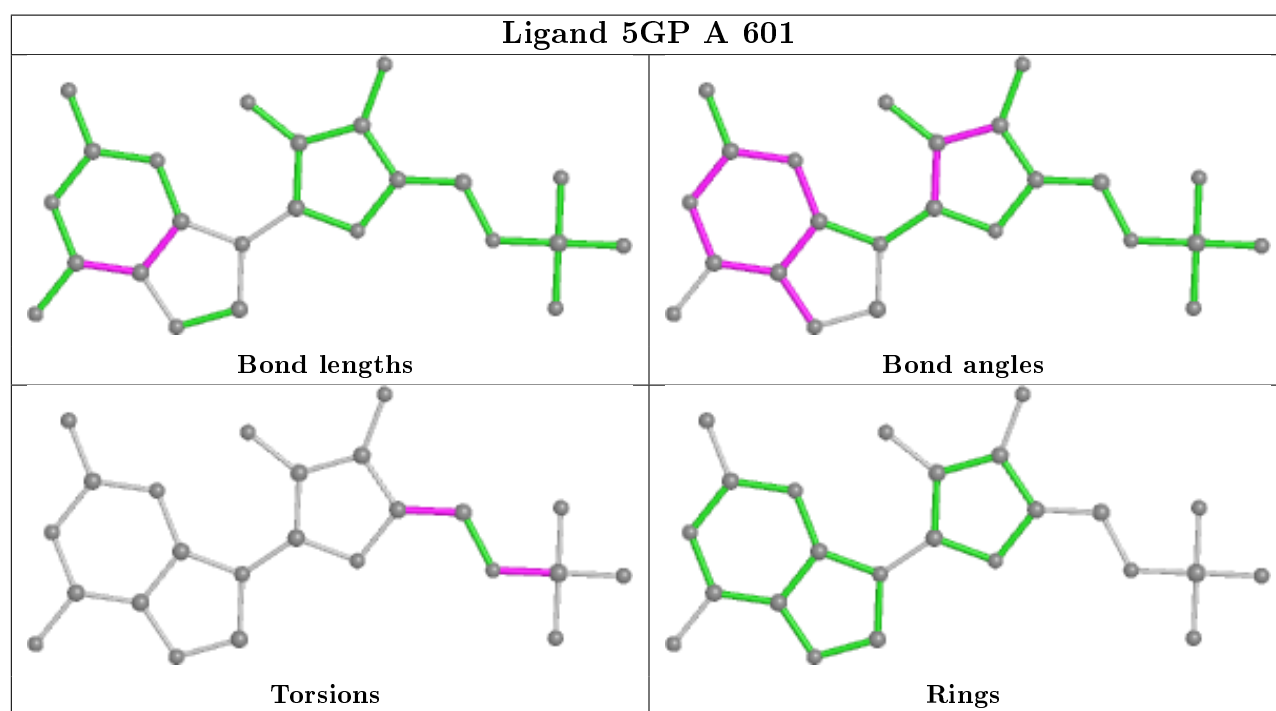
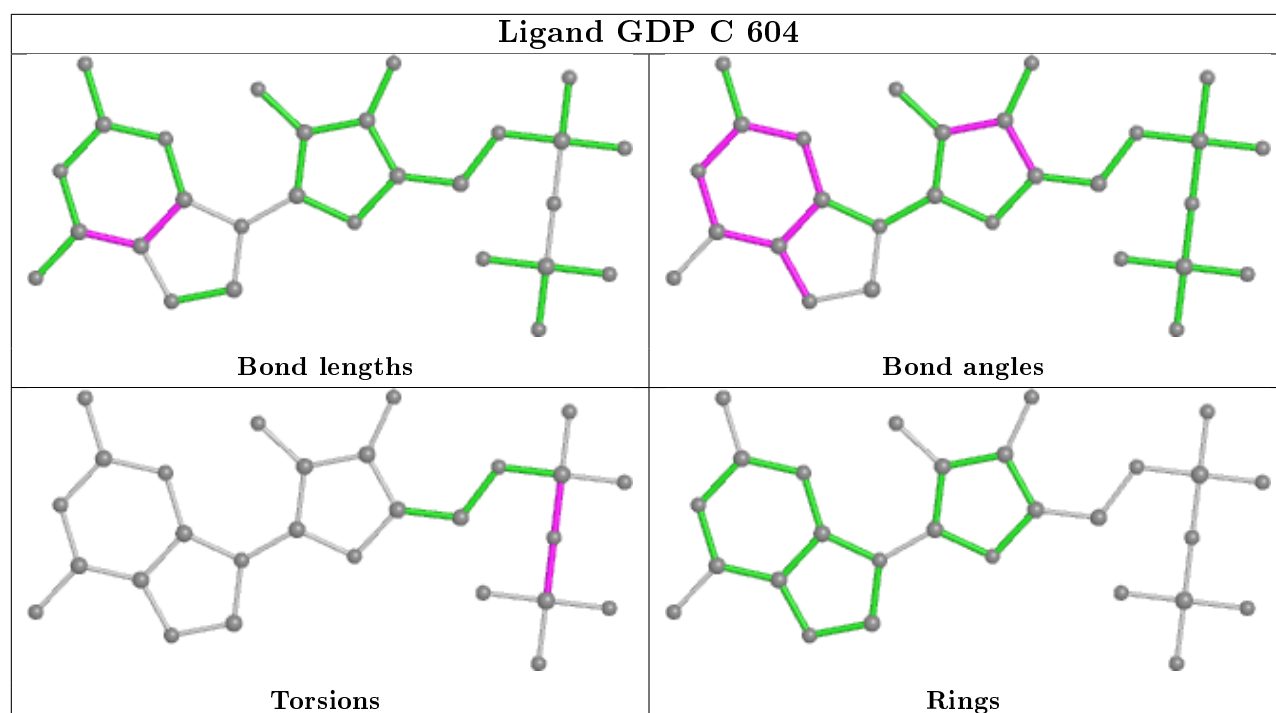
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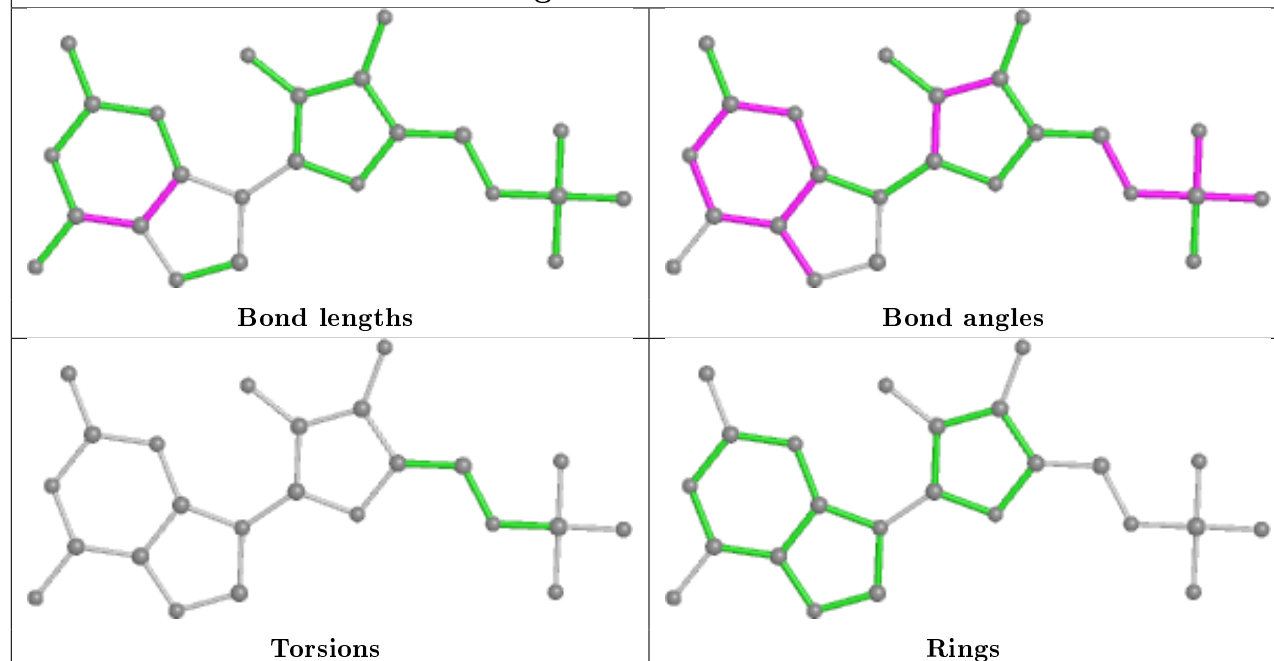
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	601	GDP	2	0
2	C	601	5GP	3	0
3	B	603	GDP	1	0
3	D	602	GDP	3	0
3	A	603	GDP	4	0
2	D	600	5GP	8	0
3	A	604[A]	GDP	3	0
3	A	604[B]	GDP	2	0
3	C	602	GDP	0	2
3	D	603[B]	GDP	1	0
3	C	603	GDP	1	0
3	D	603[A]	GDP	1	0

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.

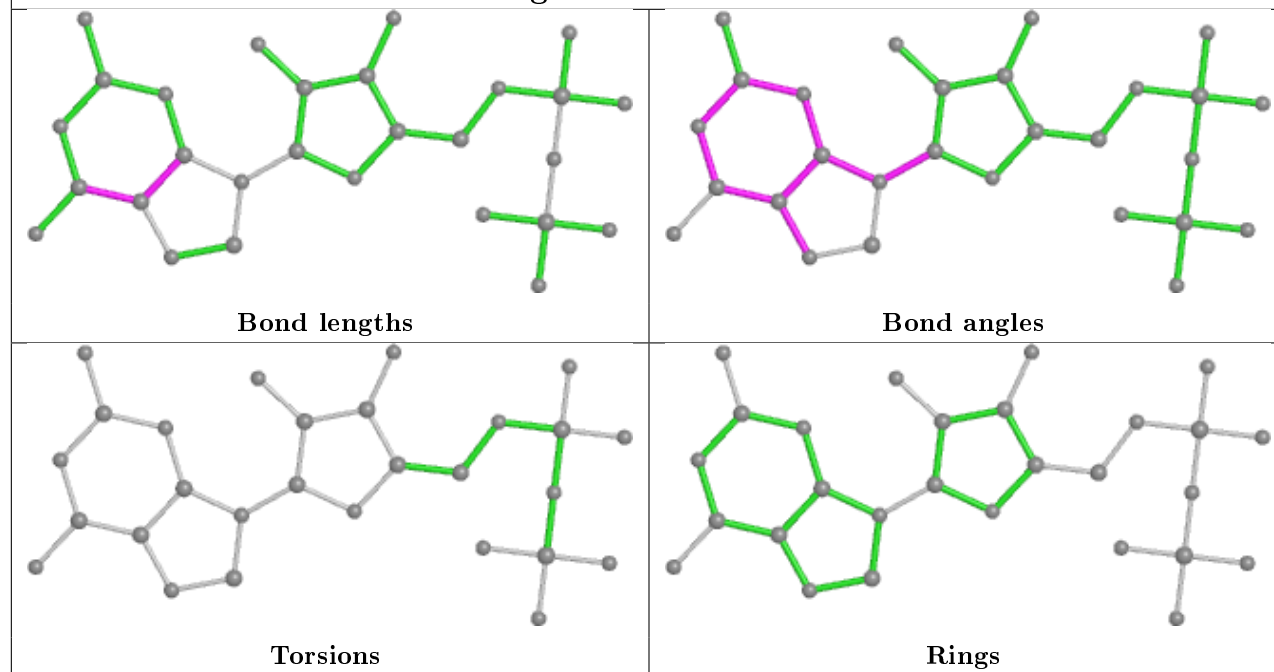


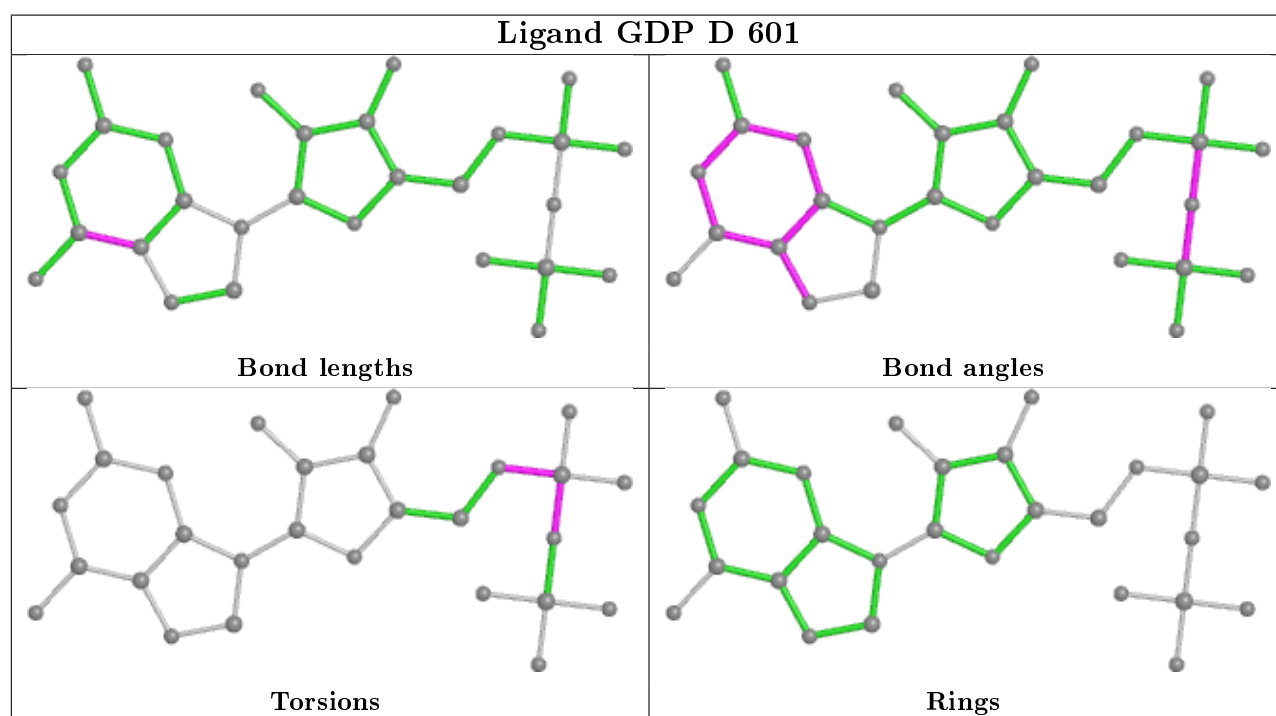
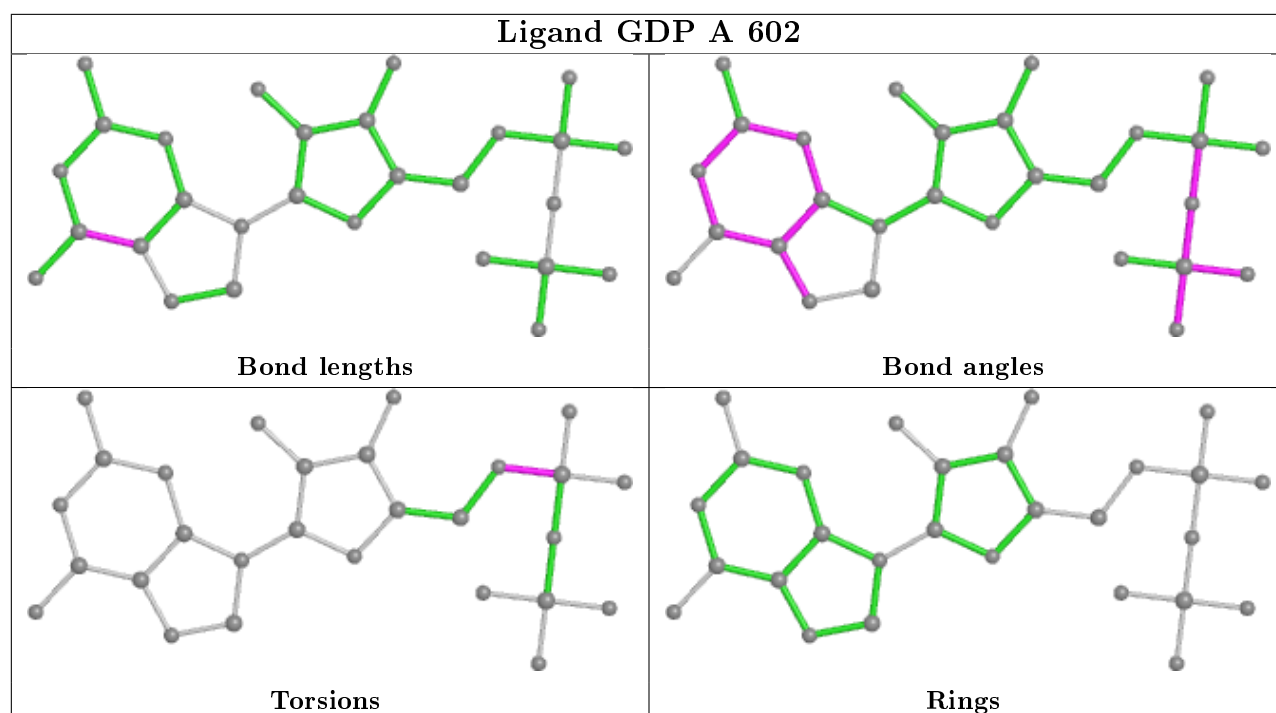


Ligand 5GP B 601

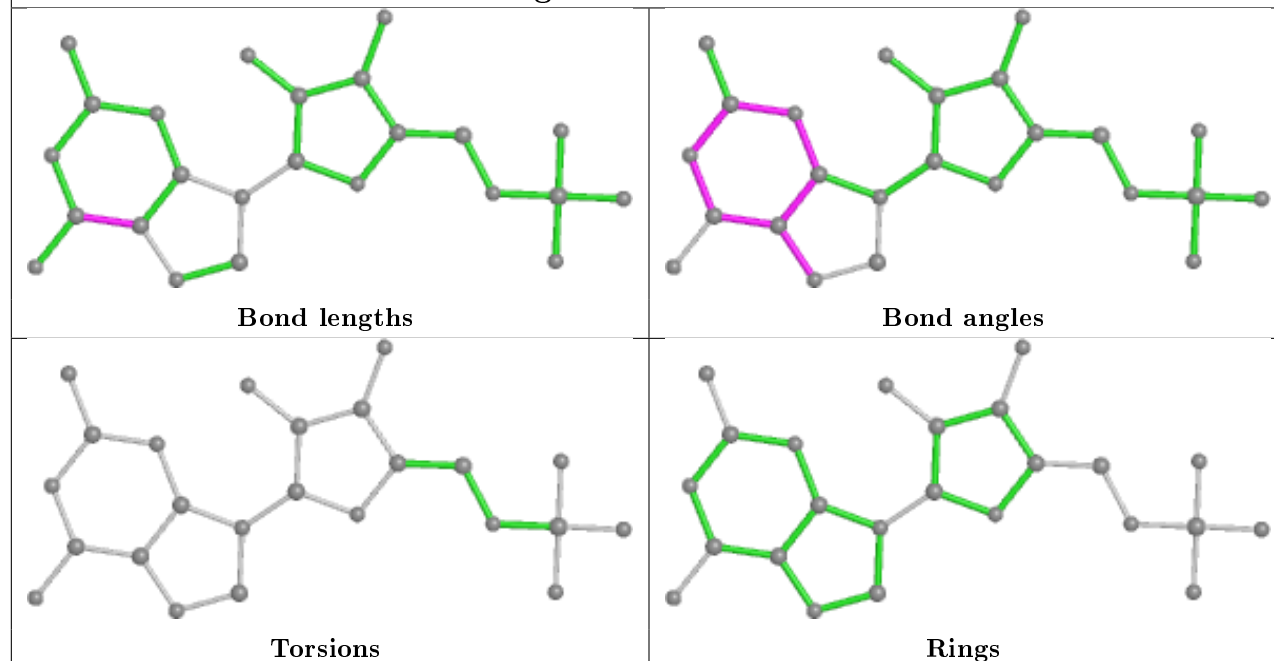


Ligand GDP B 602

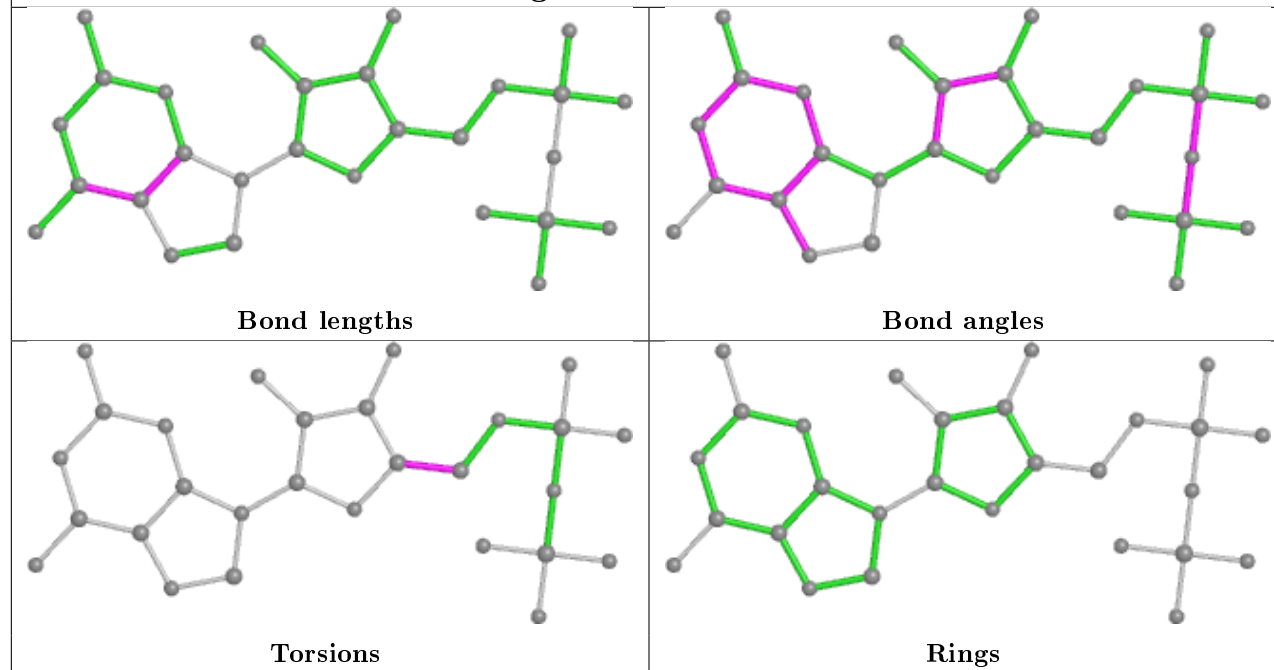


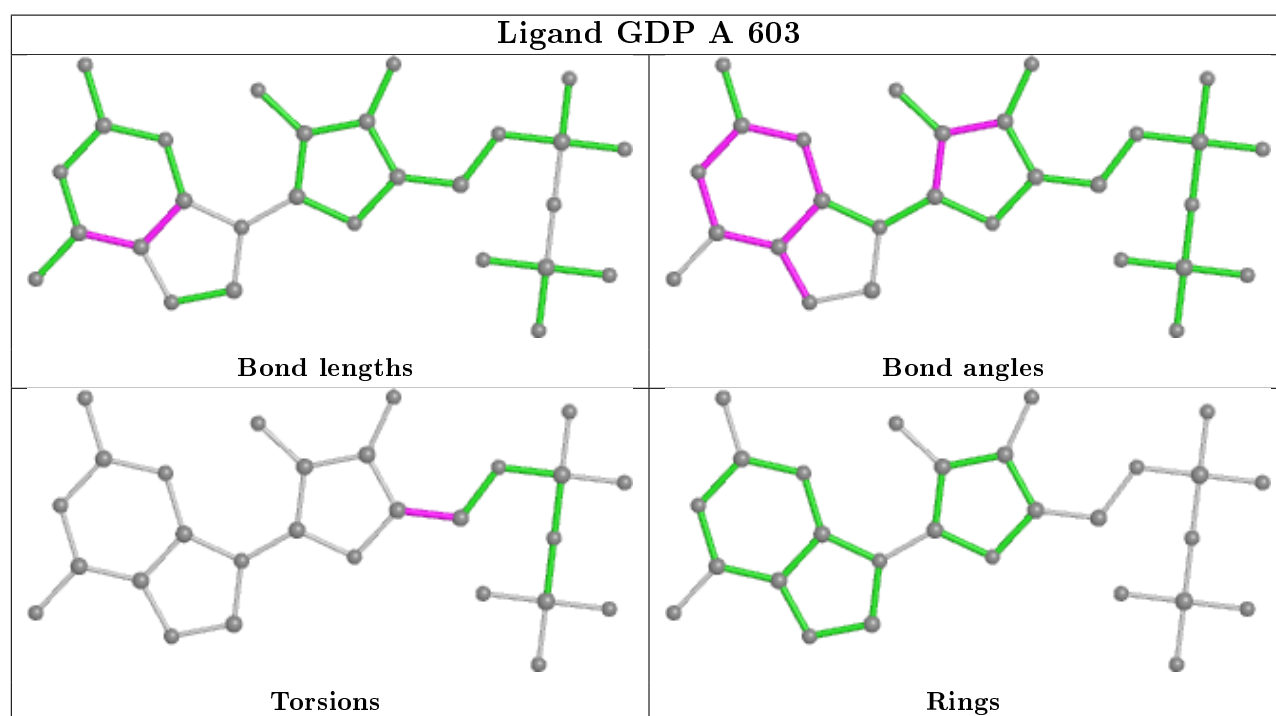
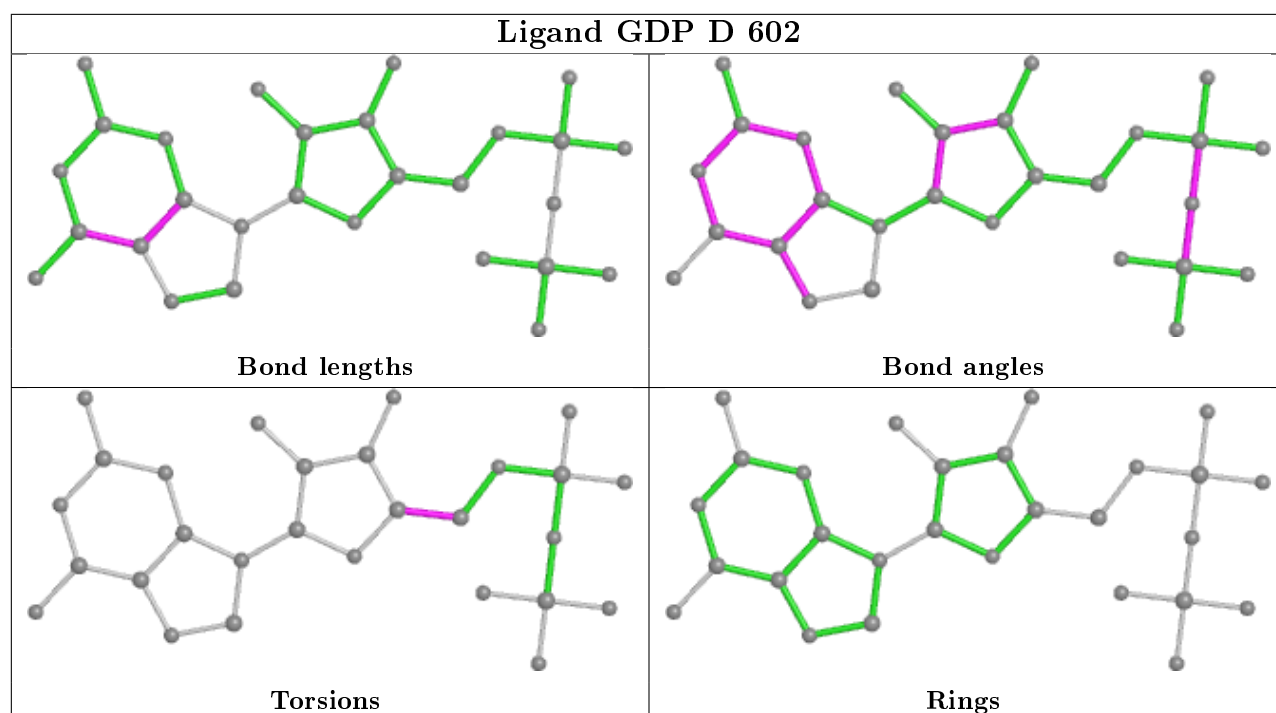


Ligand 5GP C 601

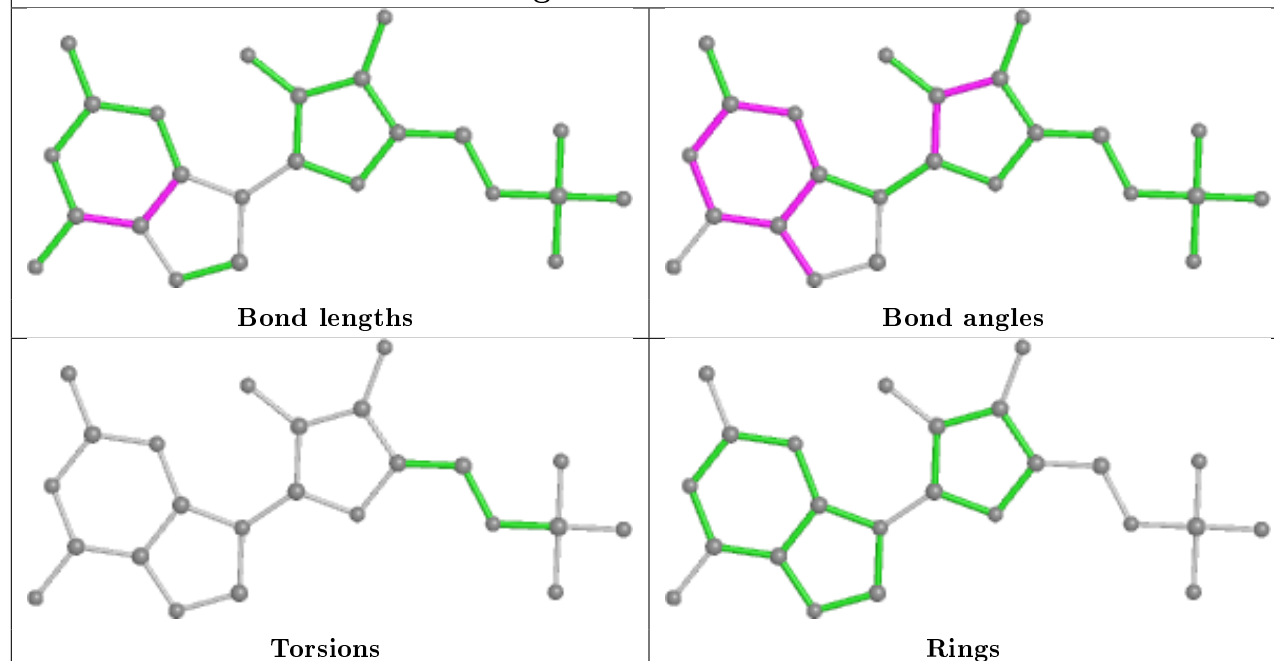


Ligand GDP B 603

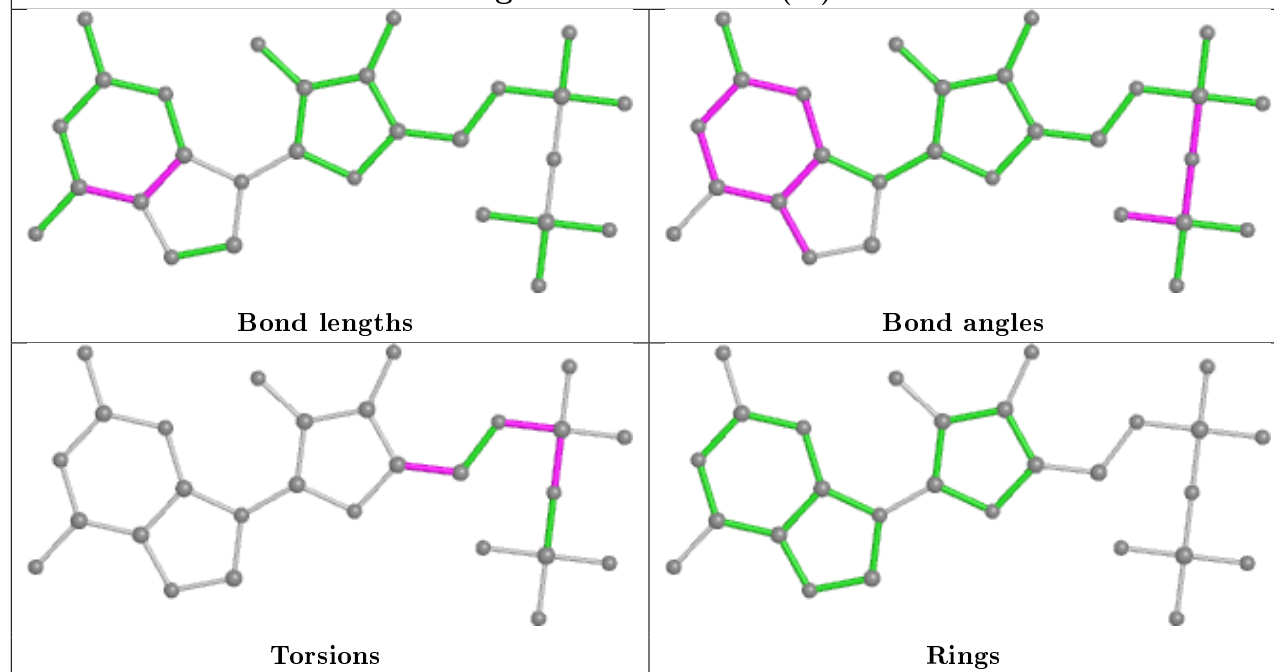




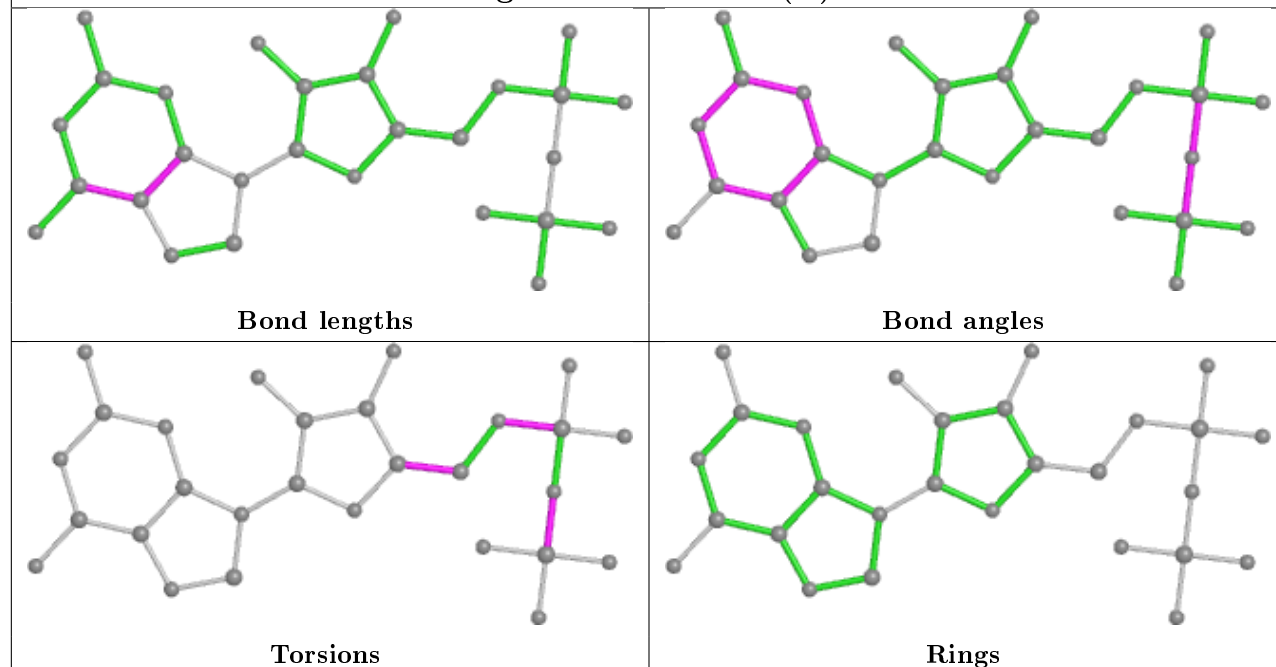
Ligand 5GP D 600



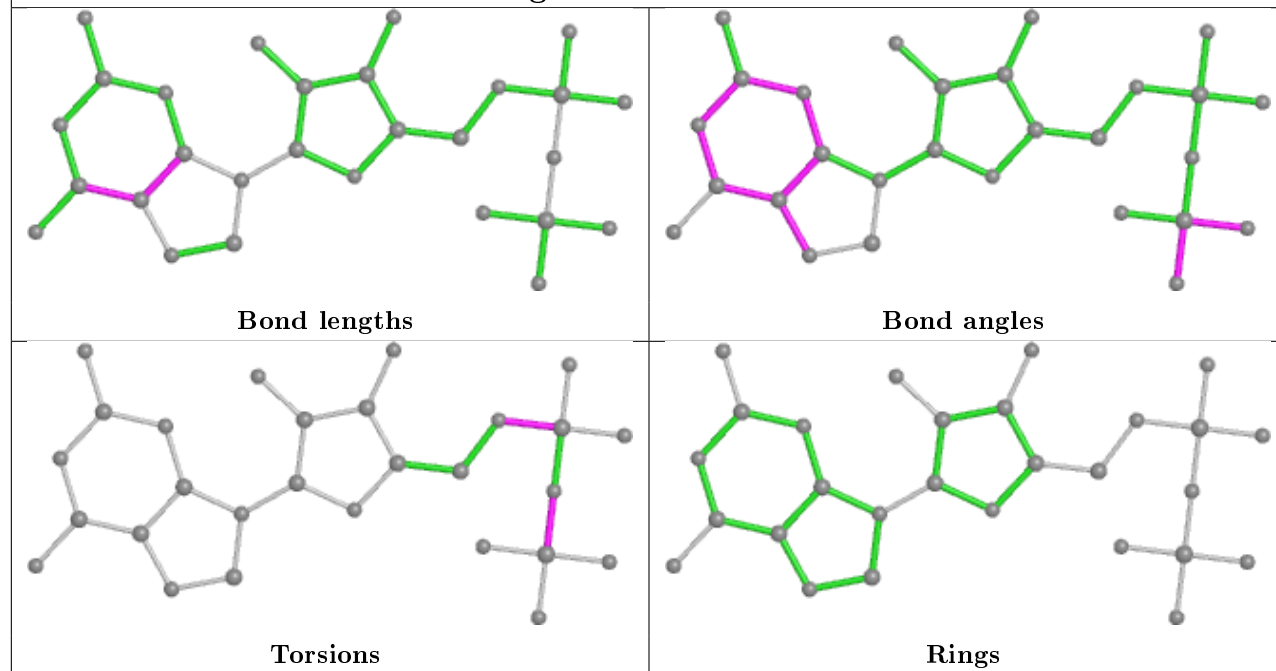
Ligand GDP A 604 (A)



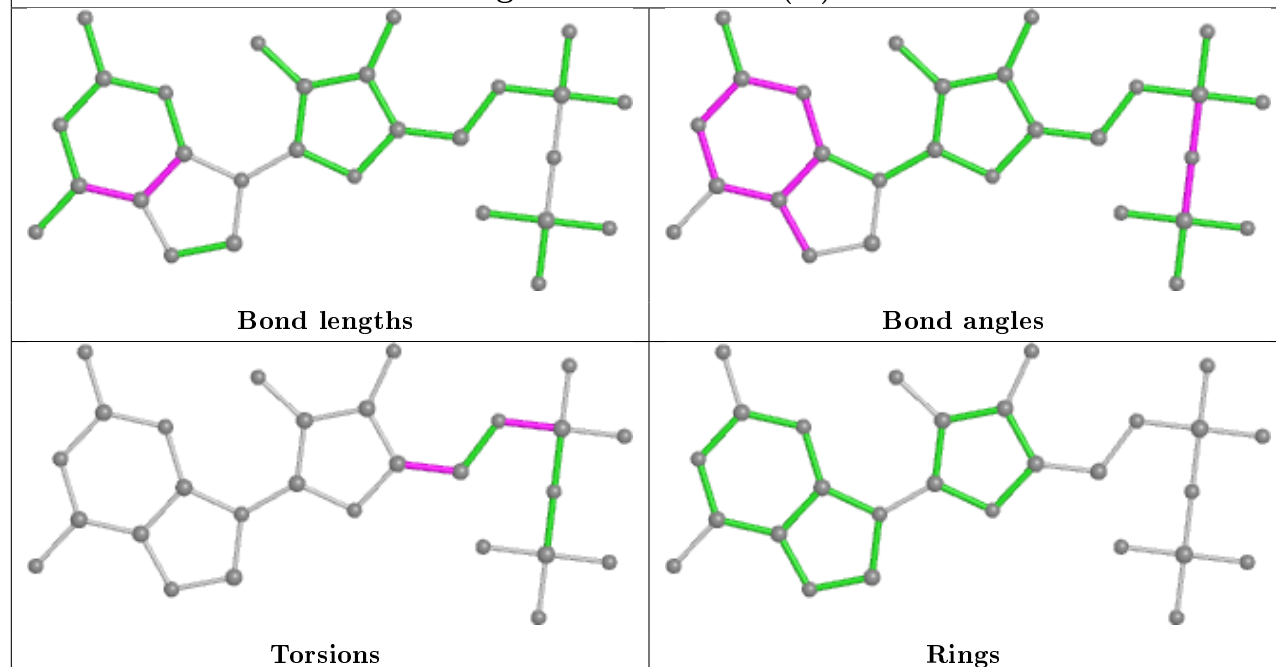
Ligand GDP A 604 (B)



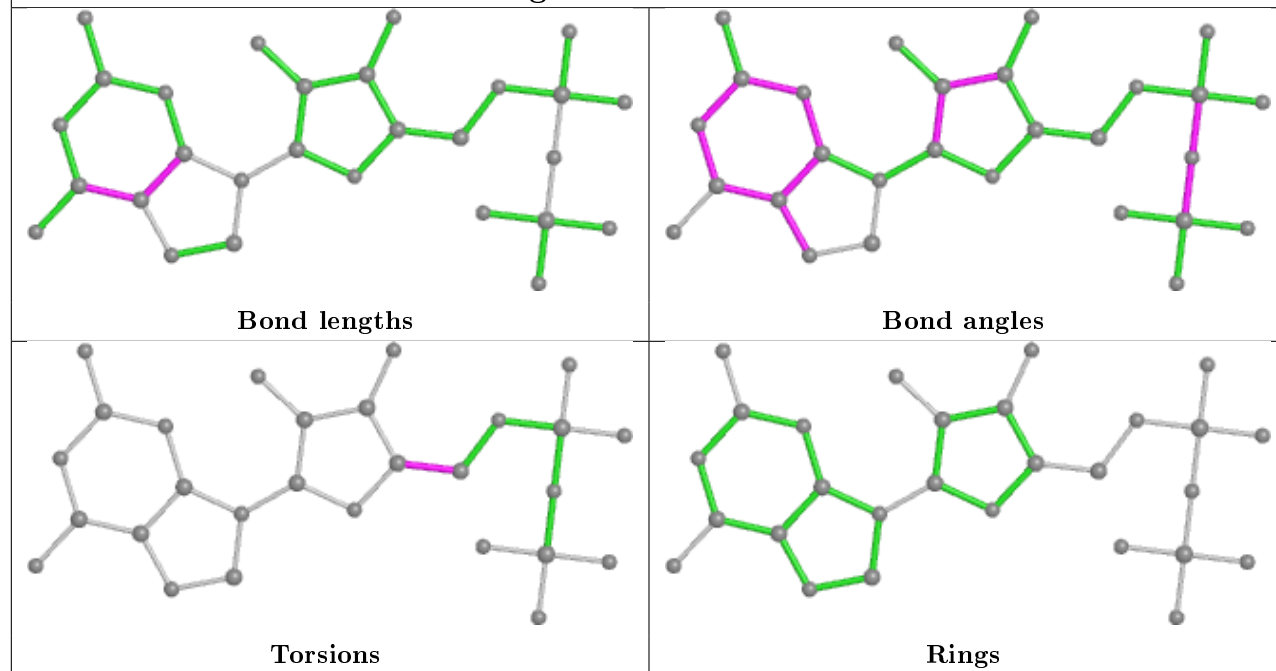
Ligand GDP C 602

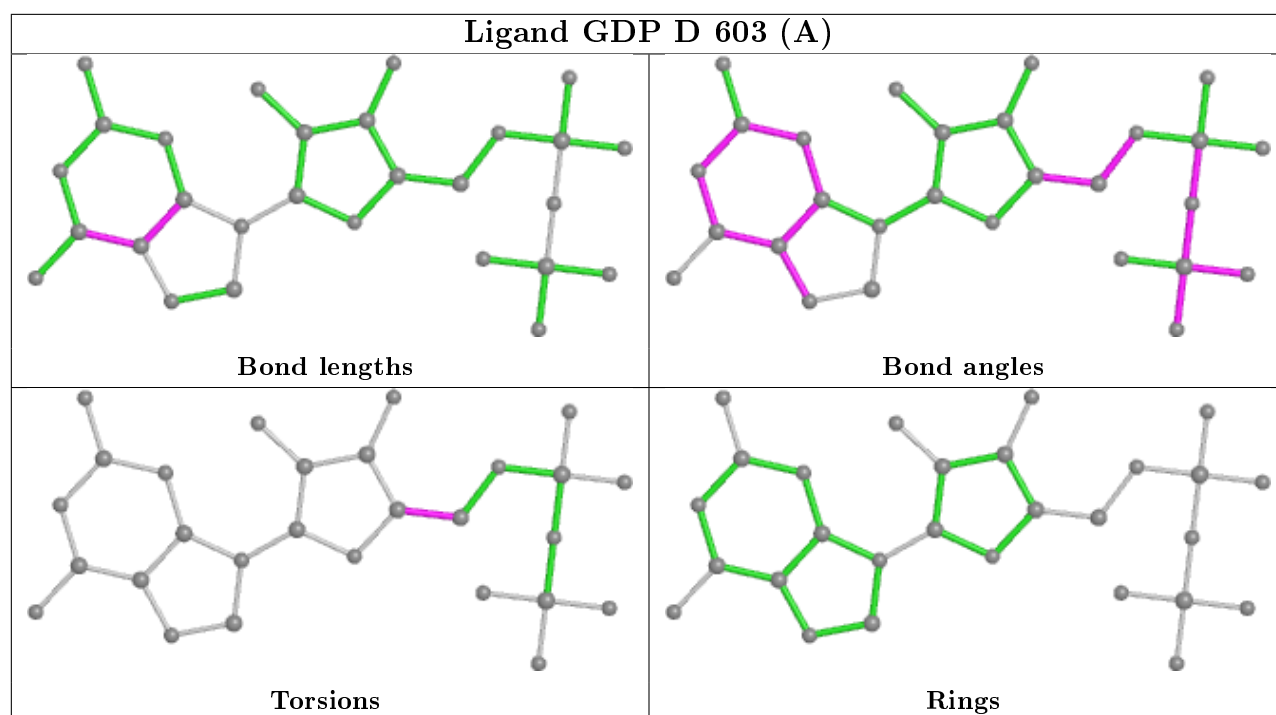


Ligand GDP D 603 (B)



Ligand GDP C 603





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	498/525 (94%)	-0.10	11 (2%) 62 65	26, 42, 78, 118	0
1	B	498/525 (94%)	-0.16	11 (2%) 62 65	30, 47, 85, 136	0
1	C	495/525 (94%)	0.01	19 (3%) 40 43	33, 59, 98, 135	0
1	D	484/525 (92%)	-0.09	16 (3%) 46 48	37, 56, 90, 286	0
All	All	1975/2100 (94%)	-0.08	57 (2%) 51 55	26, 50, 90, 286	0

The worst 5 of 57 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	419	SER	8.7
1	D	418	GLY	5.6
1	C	513	LEU	5.1
1	C	404	PHE	4.6
1	B	446	VAL	4.5

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

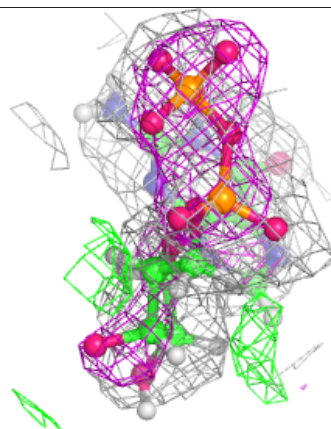
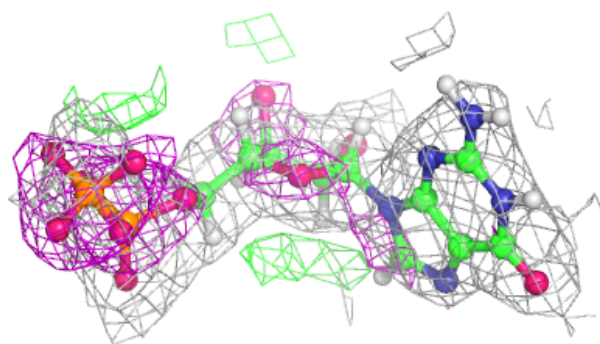
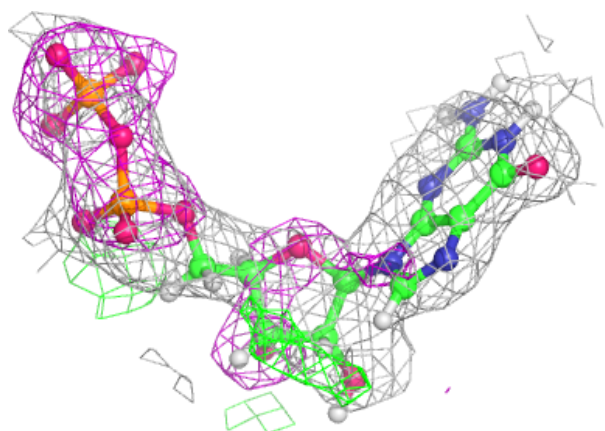
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	GDP	C	604	28/28	0.73	0.28	47,58,71,72	0
4	K	C	605	1/1	0.77	0.16	90,90,90,90	0
3	GDP	B	604	28/28	0.81	0.15	54,78,105,107	0
5	ACT	C	607	4/4	0.83	0.16	66,68,79,79	0
3	GDP	D	603[B]	28/28	0.83	0.14	53,63,76,76	39
3	GDP	D	603[A]	28/28	0.83	0.14	56,65,75,78	39
4	K	D	604	1/1	0.85	0.07	62,62,62,62	0
3	GDP	A	604[A]	28/28	0.88	0.15	47,58,71,72	39
3	GDP	A	604[B]	28/28	0.88	0.15	47,58,71,72	39
2	5GP	B	601	24/24	0.91	0.15	40,58,77,80	0
5	ACT	B	606	4/4	0.92	0.14	62,65,76,76	0
2	5GP	D	600	24/24	0.92	0.16	47,84,200,240	0
3	GDP	D	601	28/28	0.92	0.11	56,65,82,84	0
5	ACT	A	606	4/4	0.92	0.08	67,71,84,84	0
5	ACT	C	606	4/4	0.92	0.10	62,67,75,75	0
2	5GP	C	601	24/24	0.93	0.14	49,73,88,91	0
4	K	B	605	1/1	0.93	0.07	51,51,51,51	0
3	GDP	C	602	28/28	0.93	0.11	56,69,96,96	0
2	5GP	A	601	24/24	0.94	0.12	43,56,72,76	0
3	GDP	C	603	28/28	0.95	0.10	46,60,71,74	0
3	GDP	A	602	28/28	0.95	0.13	38,50,60,66	0
3	GDP	A	603	28/28	0.96	0.13	29,40,53,56	0
3	GDP	B	602	28/28	0.96	0.12	39,45,60,63	0
3	GDP	B	603	28/28	0.96	0.13	30,38,50,54	0
3	GDP	D	602	28/28	0.97	0.09	45,54,65,66	0
4	K	A	605	1/1	0.98	0.05	47,47,47,47	0

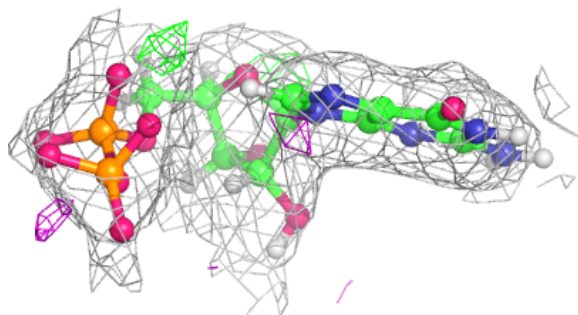
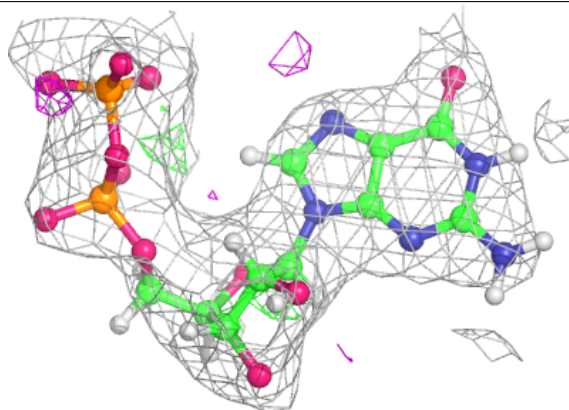
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around GDP C 604:

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

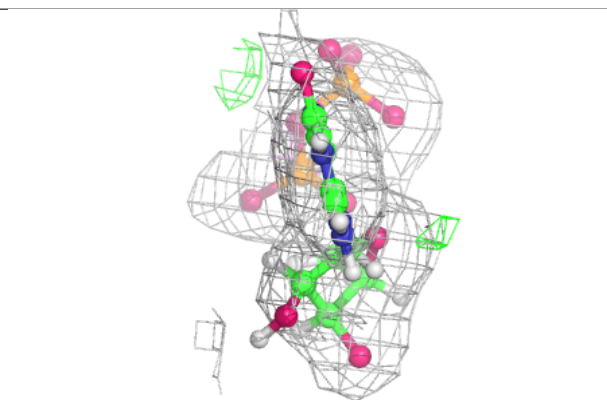
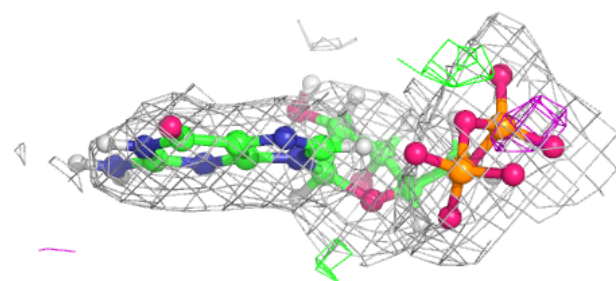
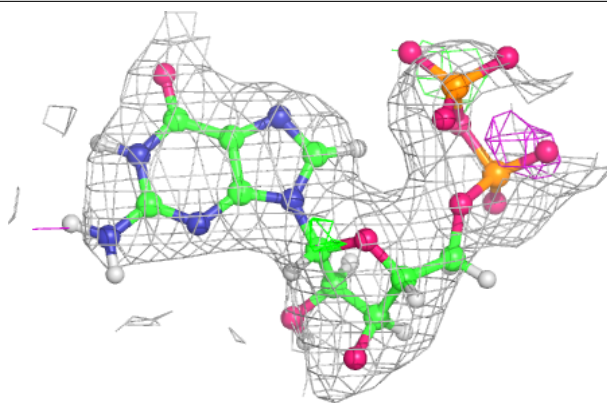
**Electron density around GDP B 604:**

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

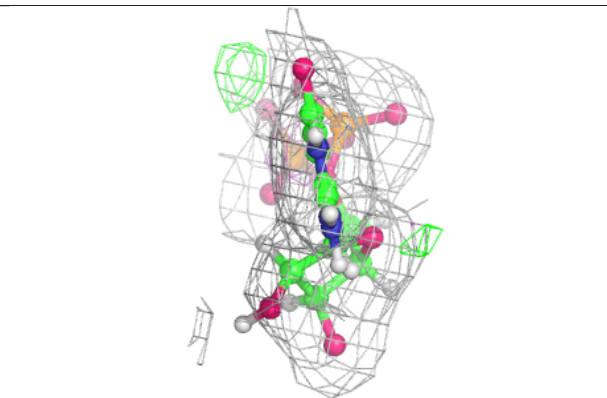
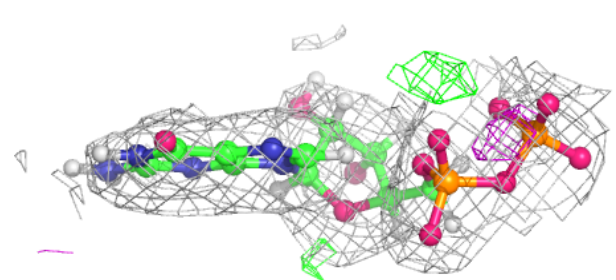
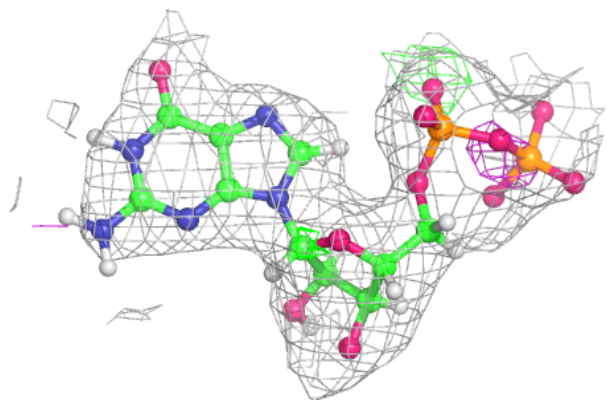


Electron density around GDP D 603 (B):

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

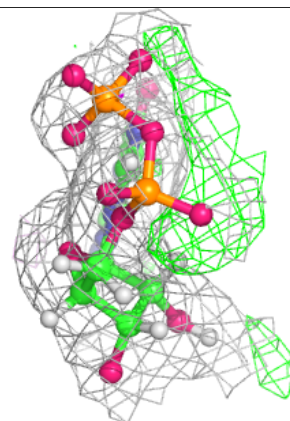
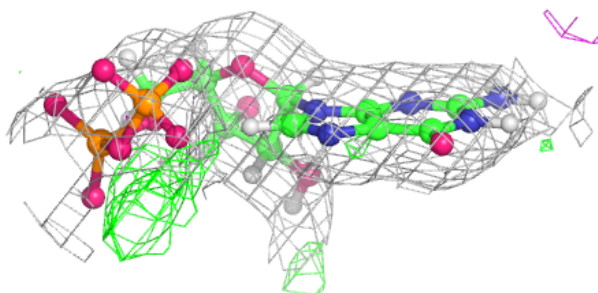
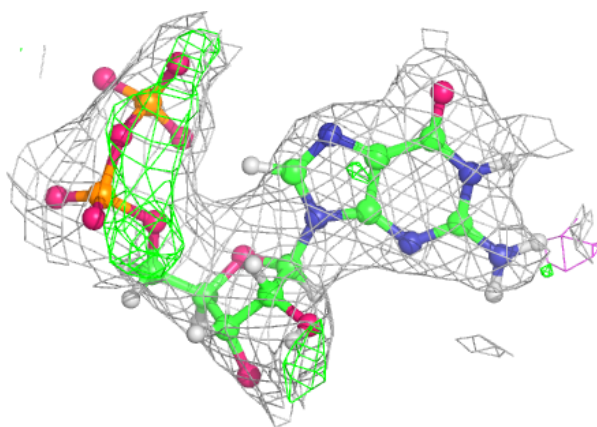
**Electron density around GDP D 603 (A):**

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

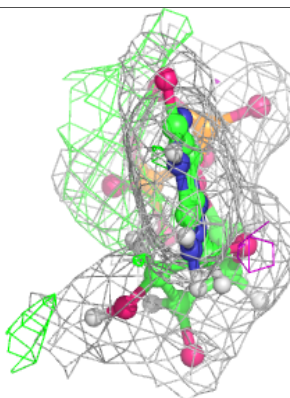
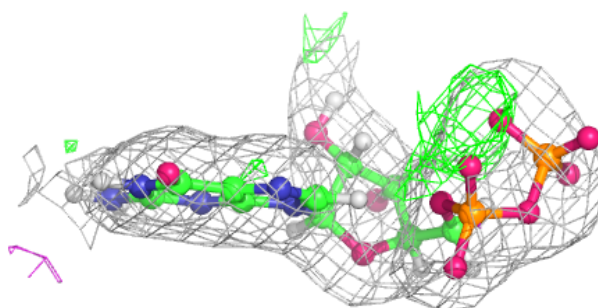
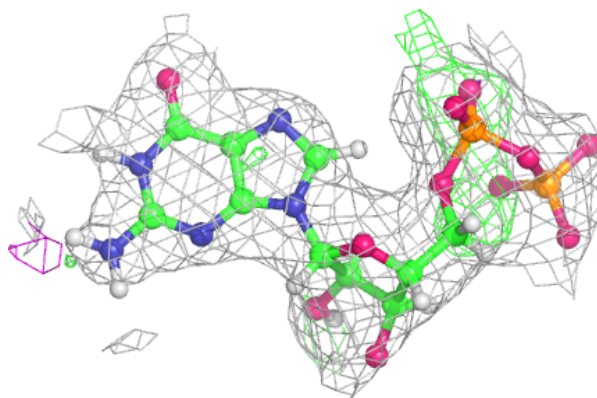


Electron density around GDP A 604 (A):

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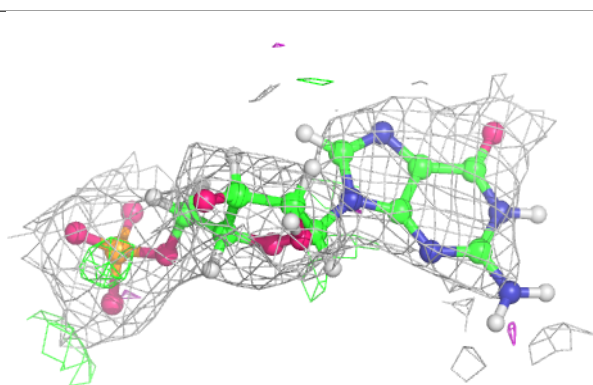
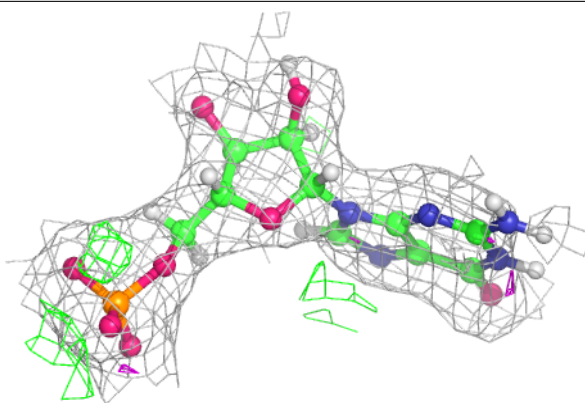
**Electron density around GDP A 604 (B):**

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and green (positive)

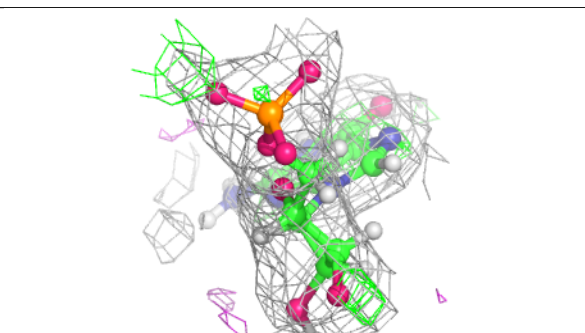
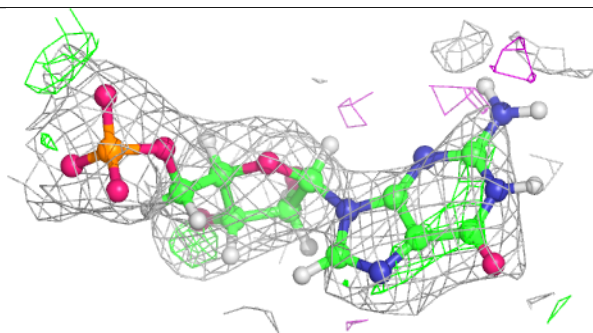
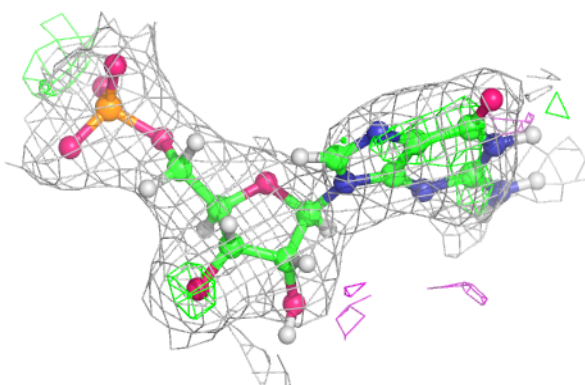


Electron density around 5GP B 601:

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and green (positive)

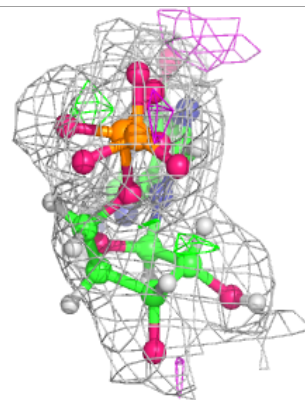
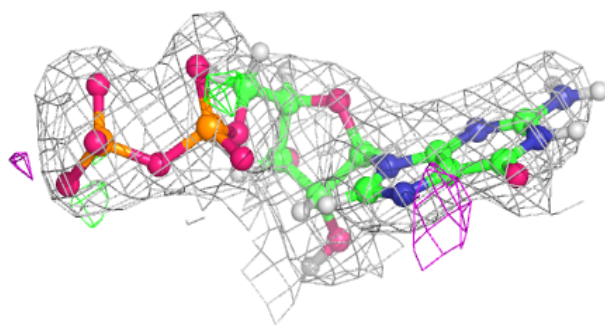
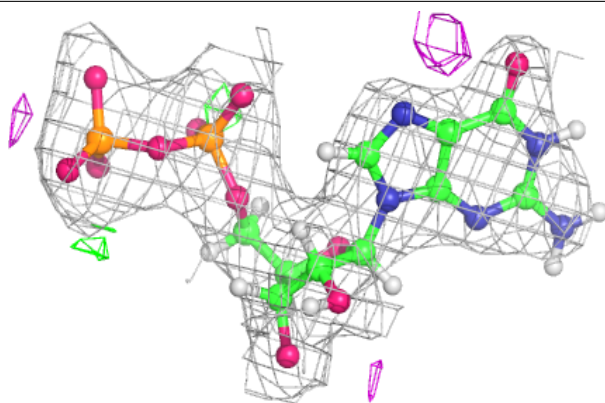
**Electron density around 5GP D 600:**

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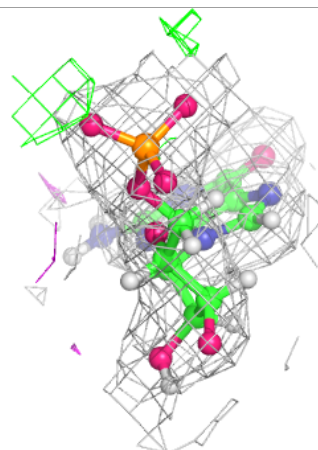
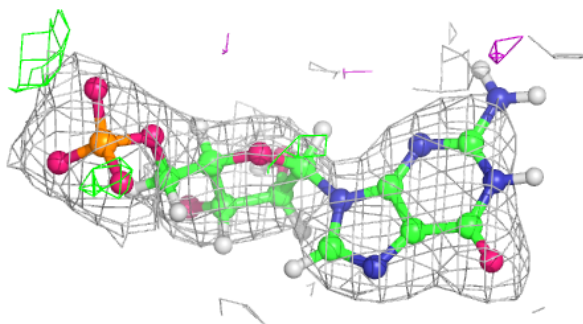
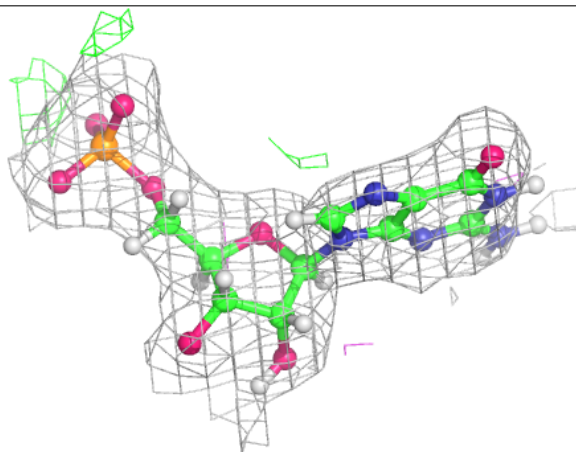


Electron density around GDP D 601:

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and green (positive)

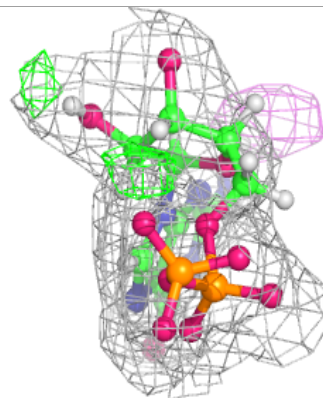
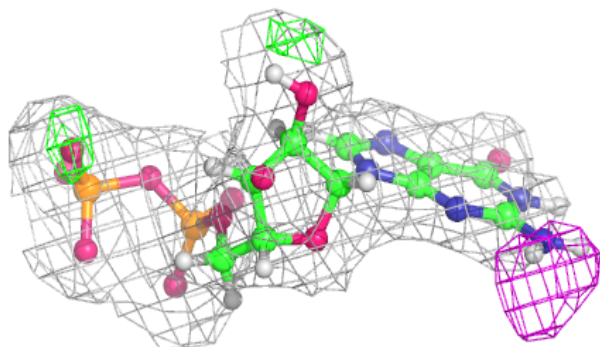
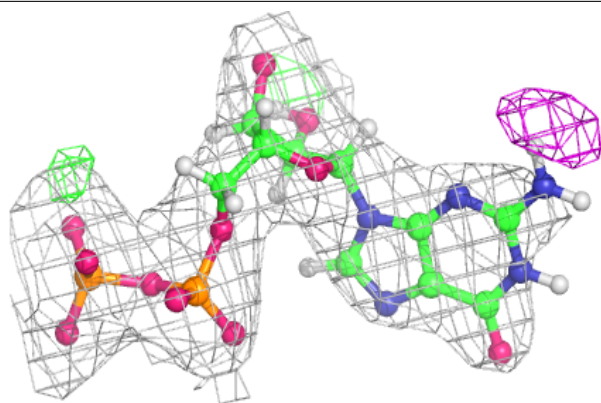
**Electron density around 5GP C 601:**

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and green (positive)

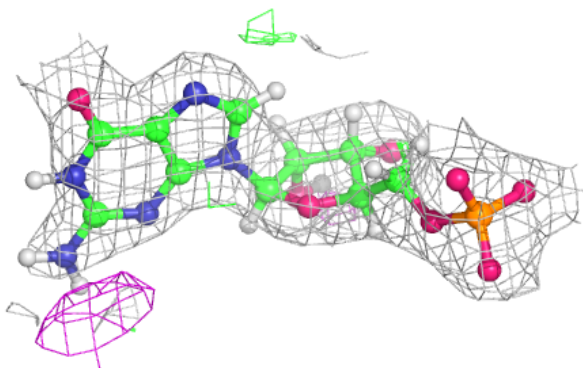
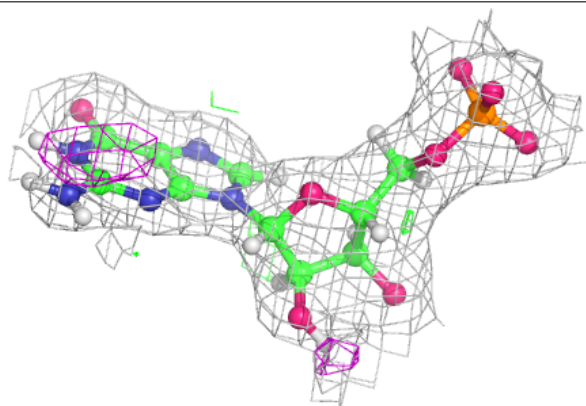


Electron density around GDP C 602:

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

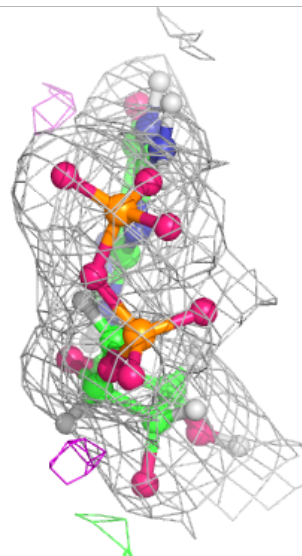
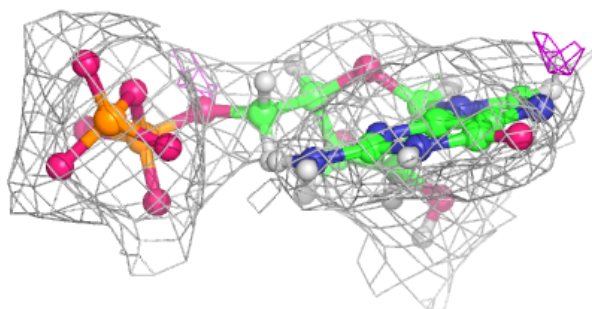
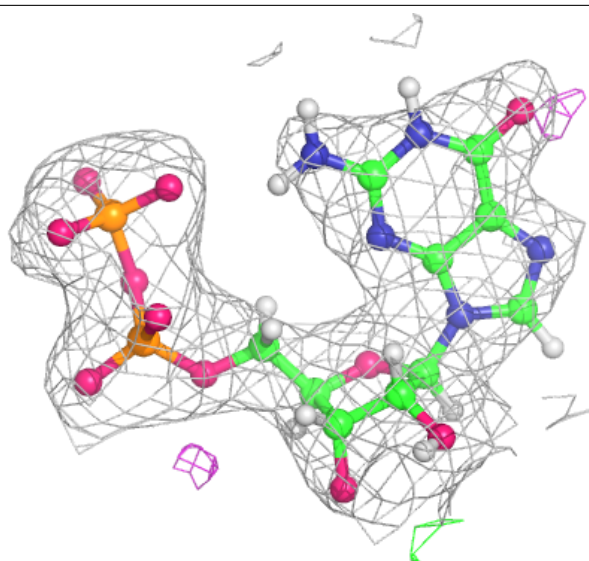
**Electron density around 5GP A 601:**

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and green (positive)



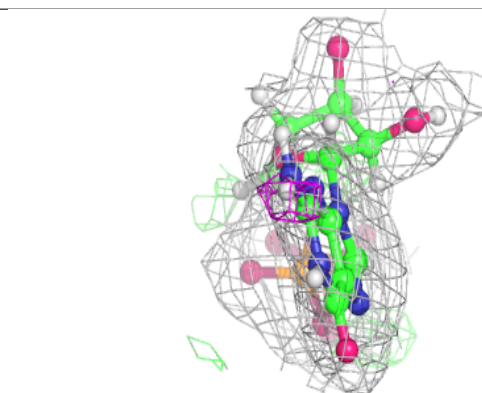
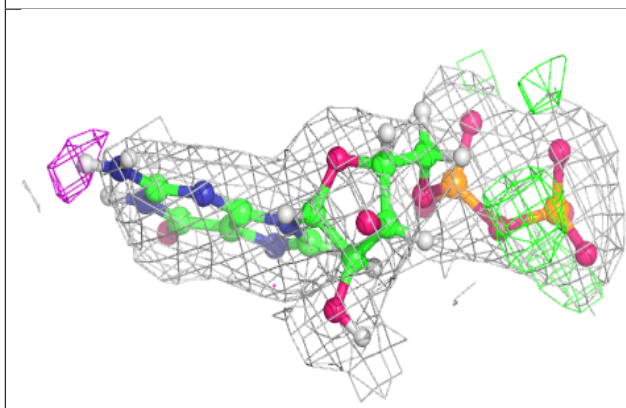
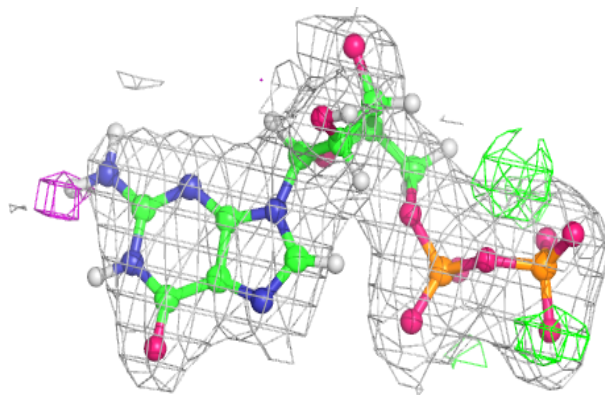
Electron density around GDP C 603:

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and green (positive)



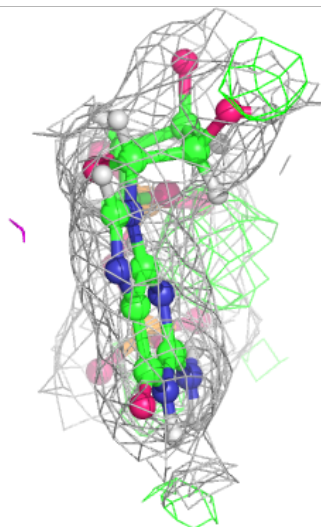
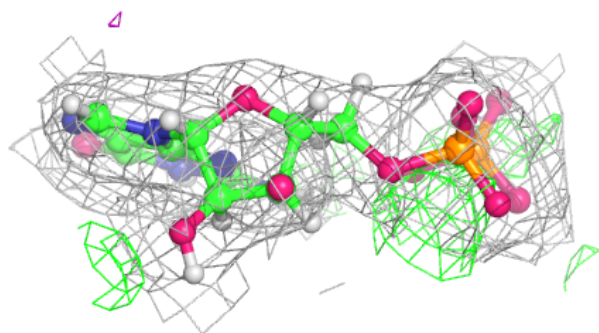
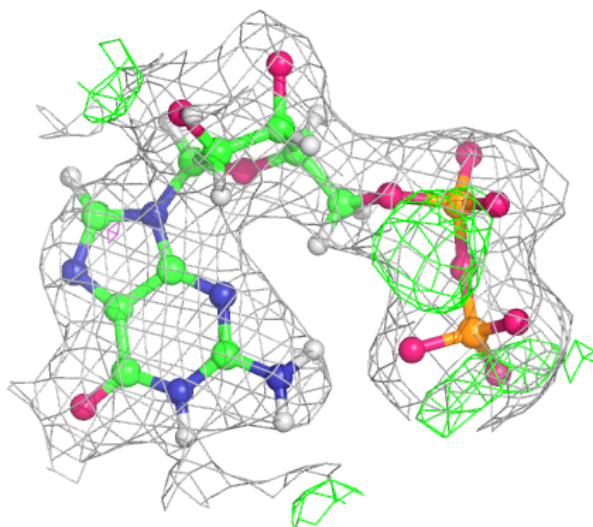
Electron density around GDP A 602:

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



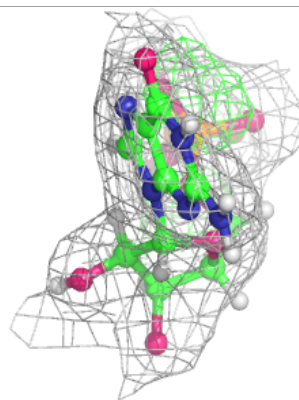
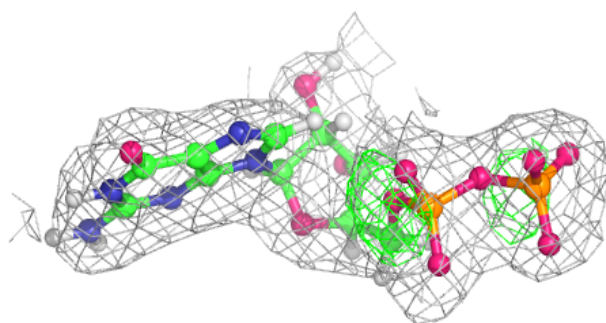
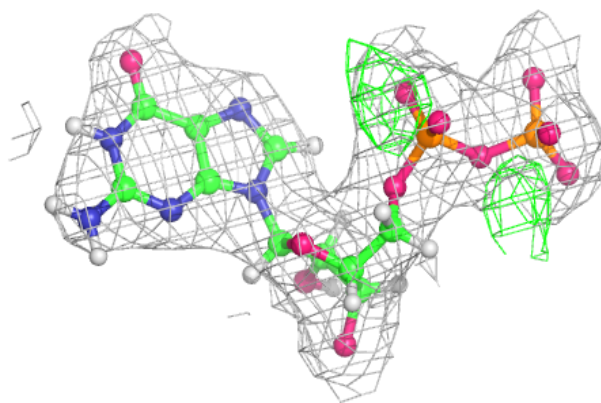
Electron density around GDP A 603:

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



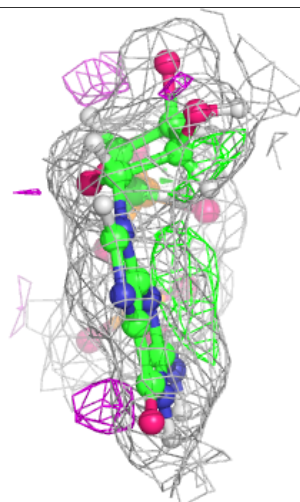
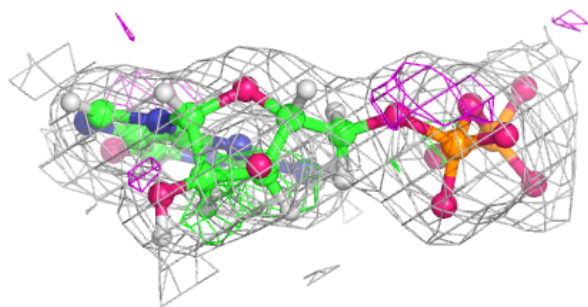
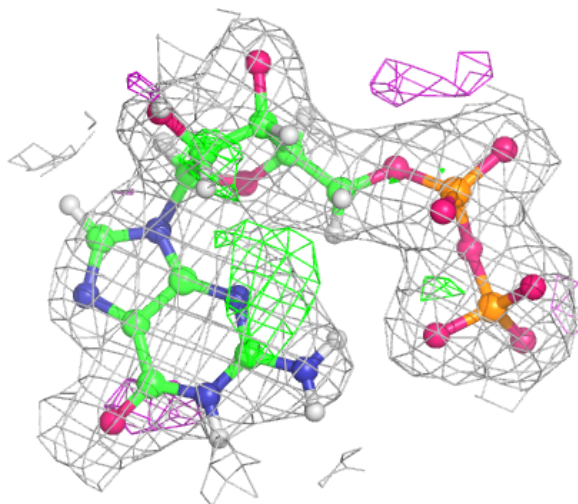
Electron density around GDP B 602:

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



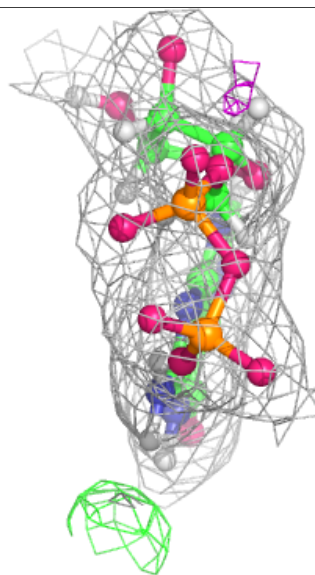
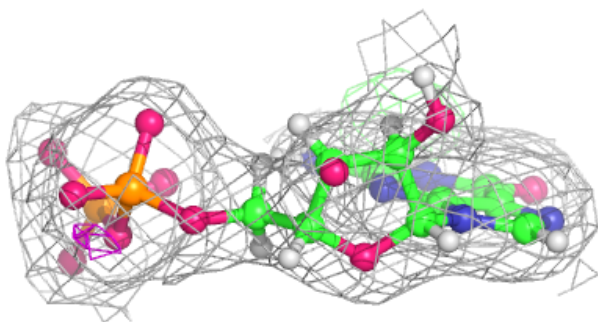
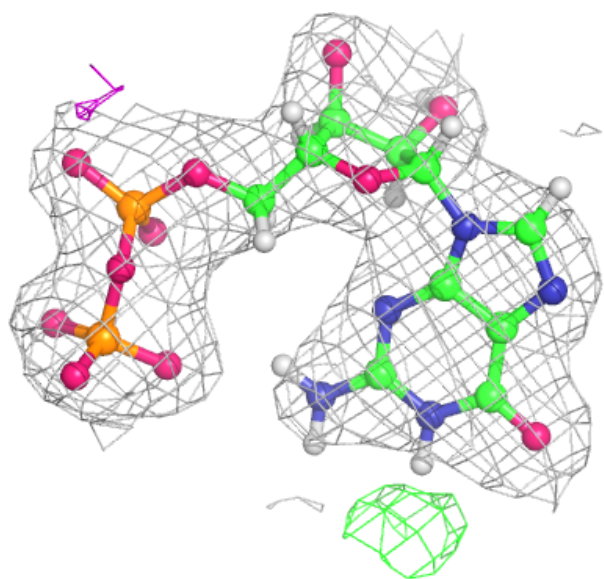
Electron density around GDP B 603:

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



Electron density around GDP D 602:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.