



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 04:48 PM UTC

PDB ID : 5CNV / pdb_00005cnv
Title : Crystal structure of the dATP inhibited E. coli class Ia ribonucleotide reductase complex bound to GDP and TTP at 3.20 Angstroms resolution
Authors : Chen, P.Y.-T.; Zimanyi, C.M.; Funk, M.A.; Drennan, C.L.
Deposited on : 2015-07-18
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

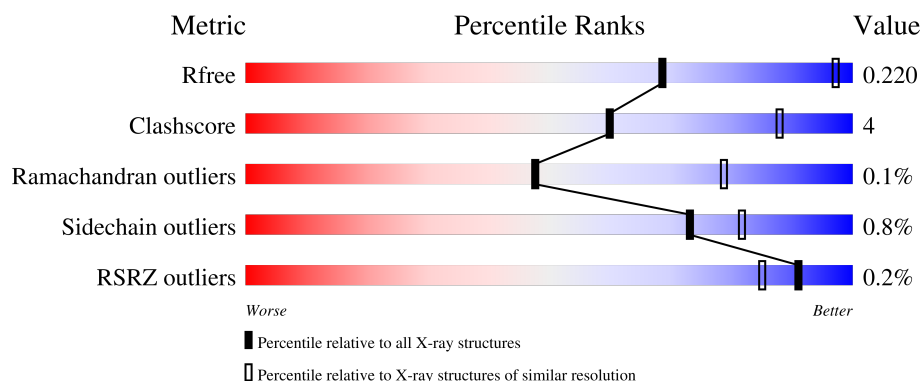
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

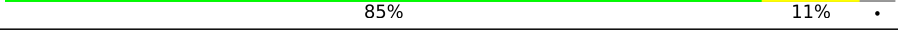
The reported resolution of this entry is 3.20 Å.

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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	761	 85% 12% .
1	B	761	 87% 9% .
1	C	761	 84% 13% .
1	D	761	 85% 11% .
2	E	375	 85% 8% 6%

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Mol	Chain	Length	Quality of chain
2	F	375	81% 14% 5%
2	G	375	84% 11% 5%
2	H	375	% 81% 15% .

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 35522 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.

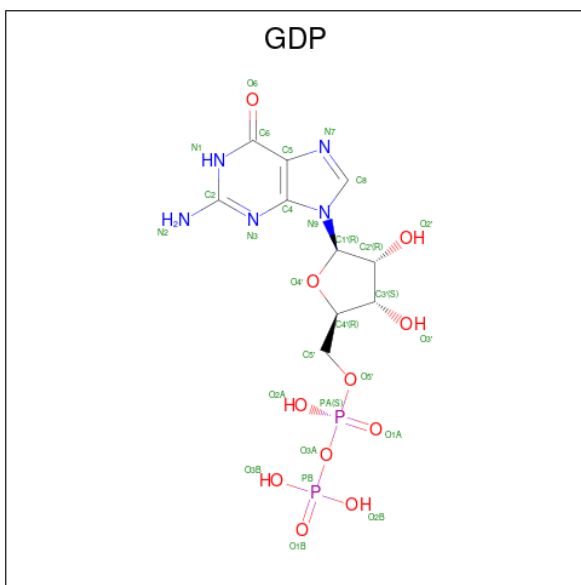
- Molecule 1 is a protein called Ribonucleoside-diphosphate reductase 1 subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	736	Total	C	N	O	S	0	0	0
			5854	3718	1005	1107	24			
1	B	732	Total	C	N	O	S	0	0	0
			5829	3703	1000	1102	24			
1	C	734	Total	C	N	O	S	0	0	0
			5841	3709	1003	1105	24			
1	D	734	Total	C	N	O	S	0	0	0
			5841	3709	1003	1105	24			

- Molecule 2 is a protein called Ribonucleoside-diphosphate reductase 1 subunit beta.

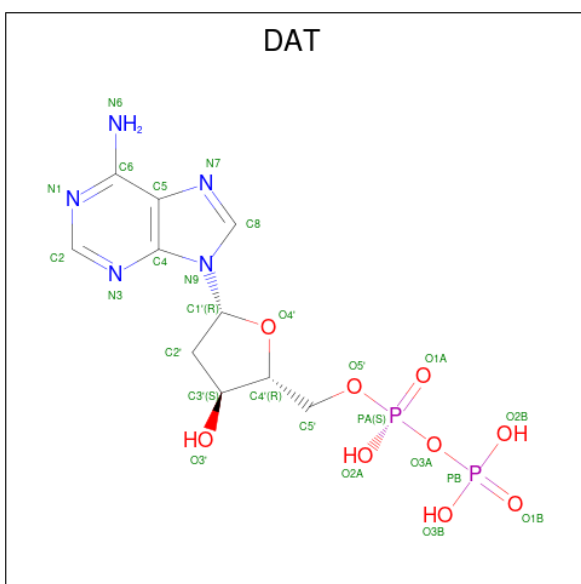
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	352	Total	C	N	O	S	0	0	0
			2867	1831	473	550	13			
2	F	357	Total	C	N	O	S	0	0	0
			2923	1864	484	562	13			
2	G	357	Total	C	N	O	S	0	0	0
			2907	1856	479	559	13			
2	H	359	Total	C	N	O	S	0	0	0
			2931	1869	485	564	13			

- Molecule 3 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



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

- Molecule 4 is 2'-DEOXYADENOSINE-5'-DIPHOSPHATE (CCD ID: DAT) (formula: $C_{10}H_{15}N_5O_9P_2$).

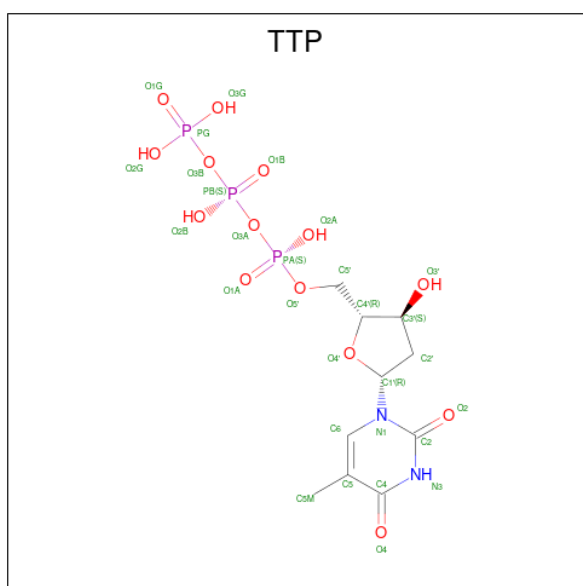


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			26	10	5	9	2		
4	B	1	Total	C	N	O	P	0	0
			26	10	5	9	2		
4	C	1	Total	C	N	O	P	0	0
			26	10	5	9	2		
4	D	1	Total	C	N	O	P	0	0
			26	10	5	9	2		

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Mg	0	0
			2	2		
5	B	2	Total	Mg	0	0
			2	2		
5	C	2	Total	Mg	0	0
			2	2		
5	D	2	Total	Mg	0	0
			2	2		

- Molecule 6 is THYMIDINE-5'-TRIPHOSPHATE (CCD ID: TTP) (formula: C₁₀H₁₇N₂O₁₄P₃).



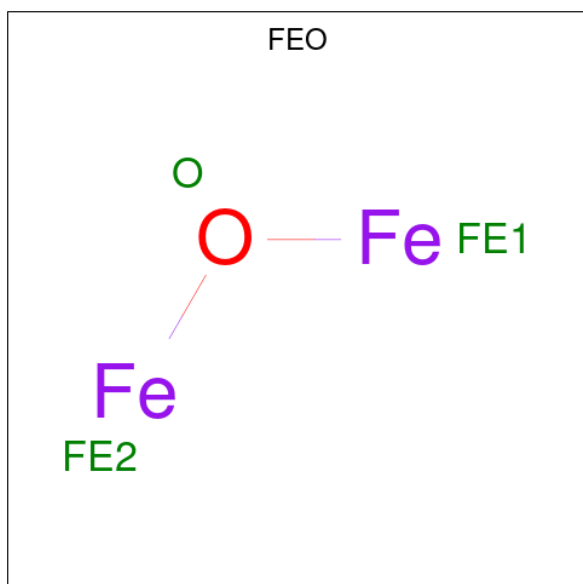
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	P	0	0
			29	10	2	14	3		
6	A	1	Total	C	N	O	P	0	0
			29	10	2	14	3		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	B	1	Total	C	N	O	P	0	0
			29	10	2	14	3		
6	B	1	Total	C	N	O	P	0	0
			29	10	2	14	3		
6	C	1	Total	C	N	O	P	0	0
			29	10	2	14	3		
6	C	1	Total	C	N	O	P	0	0
			29	10	2	14	3		
6	D	1	Total	C	N	O	P	0	0
			29	10	2	14	3		
6	D	1	Total	C	N	O	P	0	0
			29	10	2	14	3		

- Molecule 7 is MU-OXO-DIIRON (CCD ID: FEO) (formula: Fe_2O).

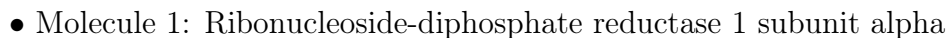
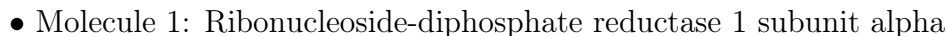


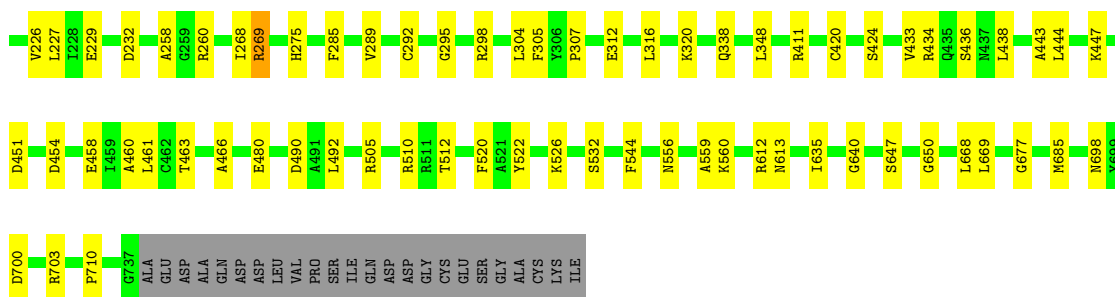
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	E	1	Total	Fe	O	0	0
			3	2	1		
7	F	1	Total	Fe	O	0	0
			3	2	1		
7	G	1	Total	Fe	O	0	0
			3	2	1		
7	H	1	Total	Fe	O	0	0
			3	2	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	9	Total 9	O 9	0	0
8	B	5	Total 5	O 5	0	0
8	C	13	Total 13	O 13	0	0
8	D	12	Total 12	O 12	0	0
8	E	4	Total 4	O 4	0	0
8	F	7	Total 7	O 7	0	0
8	G	5	Total 5	O 5	0	0
8	H	6	Total 6	O 6	0	0

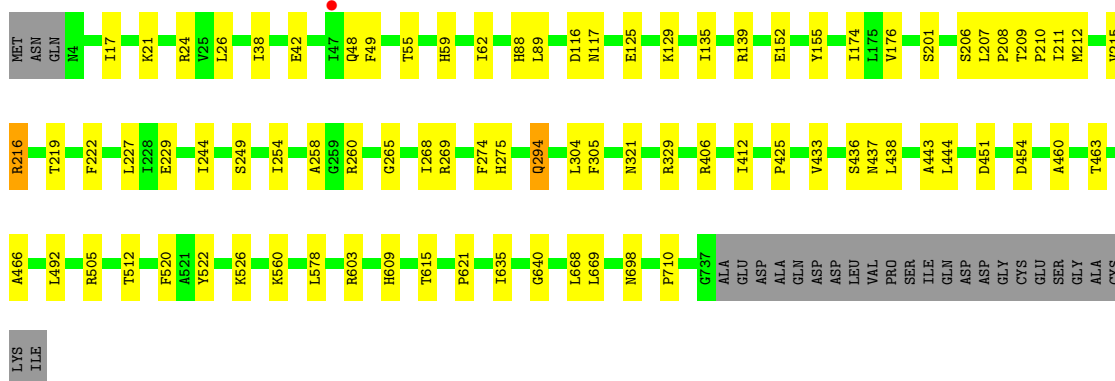
- Molecule 1: Ribonucleoside-diphosphate reductase 1 subunit alpha





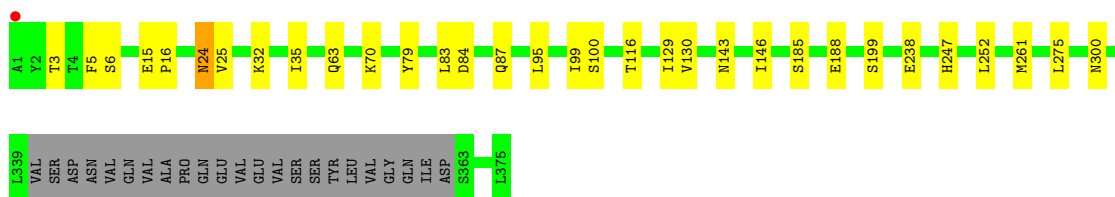
- Molecule 1: Ribonucleoside-diphosphate reductase 1 subunit alpha

Chain D: 85% 11% .



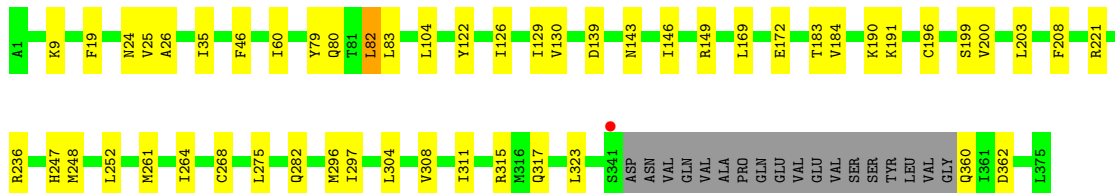
- Molecule 2: Ribonucleoside-diphosphate reductase 1 subunit beta

Chain E: 85% 8% 6%



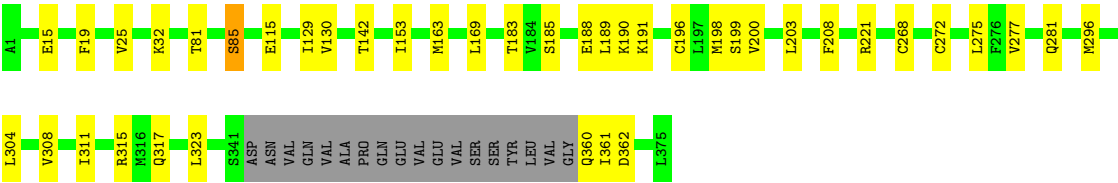
- Molecule 2: Ribonucleoside-diphosphate reductase 1 subunit beta

Chain F:  81% 14% 5%

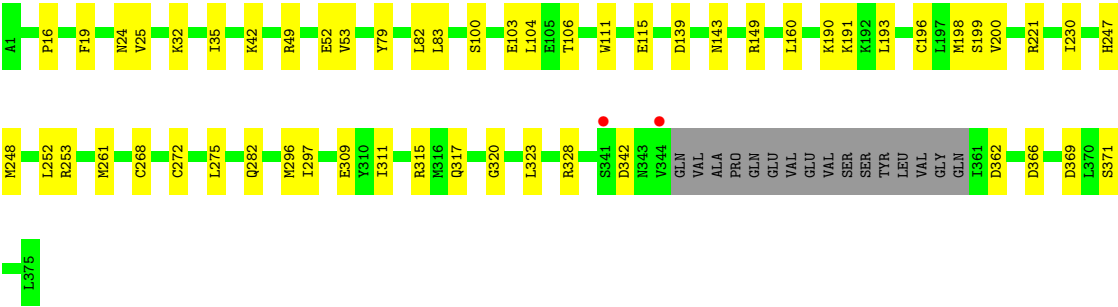
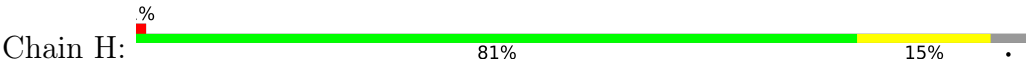


- Molecule 2: Ribonucleoside-diphosphate reductase 1 subunit beta

Chain G: 84% 11% 5%



• Molecule 2: Ribonucleoside-diphosphate reductase 1 subunit beta



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	274.78Å 157.75Å 165.77Å 90.00° 119.49° 90.00°	Depositor
Resolution (Å)	49.73 – 3.20 49.73 – 3.20	Depositor EDS
% Data completeness (in resolution range)	98.5 (49.73-3.20) 98.5 (49.73-3.20)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.02 (at 3.19Å)	Xtriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, R_{free}	0.190 , 0.219 0.194 , 0.220	Depositor DCC
R_{free} test set	5047 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	78.1	Xtriage
Anisotropy	0.096	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 21.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	35522	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.25% 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: TTP, GDP, DAT, FEO, MG

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	0.13	0/5982	0.34	0/8104
1	B	0.12	0/5957	0.33	0/8070
1	C	0.15	0/5969	0.36	0/8086
1	D	0.15	0/5969	0.35	0/8086
2	E	0.12	0/2931	0.30	0/3977
2	F	0.16	0/2987	0.35	0/4050
2	G	0.16	0/2971	0.34	0/4031
2	H	0.14	0/2995	0.33	0/4062
All	All	0.14	0/35761	0.34	0/48466

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	5854	0	5769	59	0
1	B	5829	0	5750	40	0
1	C	5841	0	5759	60	0
1	D	5841	0	5759	53	0
2	E	2867	0	2781	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	2923	0	2850	30	0
2	G	2907	0	2822	22	0
2	H	2931	0	2847	33	0
3	A	28	0	12	5	0
3	B	28	0	12	3	0
3	C	28	0	12	1	0
3	D	28	0	12	3	0
4	A	26	0	12	3	0
4	B	26	0	12	2	0
4	C	26	0	12	2	0
4	D	26	0	12	1	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
5	C	2	0	0	0	0
5	D	2	0	0	0	0
6	A	58	0	26	5	0
6	B	58	0	26	3	0
6	C	58	0	26	4	0
6	D	58	0	26	3	0
7	E	3	0	0	0	0
7	F	3	0	0	0	0
7	G	3	0	0	1	0
7	H	3	0	0	0	0
8	A	9	0	0	1	0
8	B	5	0	0	1	0
8	C	13	0	0	2	0
8	D	12	0	0	0	0
8	E	4	0	0	2	0
8	F	7	0	0	0	0
8	G	5	0	0	0	0
8	H	6	0	0	0	0
All	All	35522	0	34537	302	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 302 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:802:DAT:O1B	8:A:901:HOH:O	2.05	0.74
1:A:258:ALA:HB3	1:A:304:LEU:HD21	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:24:ARG:HH12	6:D:804:TTP:H4'	1.56	0.70
1:B:437:ASN:ND2	3:B:801:GDP:O3'	2.25	0.69
1:C:49:PHE:HE2	2:H:297:ILE:HD11	1.57	0.69

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	734/761 (96%)	713 (97%)	20 (3%)	1 (0%)	48	79
1	B	730/761 (96%)	710 (97%)	19 (3%)	1 (0%)	48	79
1	C	732/761 (96%)	710 (97%)	21 (3%)	1 (0%)	48	79
1	D	732/761 (96%)	712 (97%)	19 (3%)	1 (0%)	48	79
2	E	348/375 (93%)	343 (99%)	5 (1%)	0	100	100
2	F	353/375 (94%)	346 (98%)	7 (2%)	0	100	100
2	G	353/375 (94%)	348 (99%)	5 (1%)	0	100	100
2	H	355/375 (95%)	349 (98%)	6 (2%)	0	100	100
All	All	4337/4544 (95%)	4231 (98%)	102 (2%)	4 (0%)	48	79

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	216	ARG
1	B	216	ARG
1	C	216	ARG
1	D	216	ARG

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	628/651 (96%)	624 (99%)	4 (1%)	78	84
1	B	627/651 (96%)	625 (100%)	2 (0%)	86	88
1	C	628/651 (96%)	626 (100%)	2 (0%)	86	88
1	D	628/651 (96%)	622 (99%)	6 (1%)	68	80
2	E	315/340 (93%)	313 (99%)	2 (1%)	78	84
2	F	324/340 (95%)	317 (98%)	7 (2%)	45	71
2	G	320/340 (94%)	316 (99%)	4 (1%)	61	78
2	H	323/340 (95%)	321 (99%)	2 (1%)	78	84
All	All	3793/3964 (96%)	3764 (99%)	29 (1%)	73	82

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	24	ASN
2	H	25	VAL
2	F	25	VAL
2	G	85	SER
2	F	24	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	124	HIS
2	H	143	ASN
1	C	170	GLN
1	C	78	GLN
2	H	278	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 28 ligands modelled in this entry, 8 are monoatomic - leaving 20 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	A	801	-	29,30,30	1.19	4 (13%)	45,47,47	1.79	6 (13%)
6	TTP	D	804	5	29,30,30	1.36	7 (24%)	43,47,47	1.86	6 (13%)
3	GDP	D	801	-	29,30,30	1.19	4 (13%)	45,47,47	1.83	7 (15%)
4	DAT	C	802	5	27,28,28	1.54	5 (18%)	41,43,43	1.81	9 (21%)
7	FEO	E	501	2,8	0,2,2	-	-	-	-	-
6	TTP	B	804	5	29,30,30	1.44	8 (27%)	43,47,47	1.97	8 (18%)
6	TTP	A	805	5	29,30,30	1.44	9 (31%)	43,47,47	1.83	7 (16%)
6	TTP	C	804	5	29,30,30	1.41	8 (27%)	43,47,47	2.00	9 (20%)
6	TTP	C	805	5	29,30,30	1.38	8 (27%)	43,47,47	1.88	7 (16%)
6	TTP	D	805	5	29,30,30	1.62	8 (27%)	43,47,47	1.86	7 (16%)
6	TTP	A	804	5	29,30,30	1.46	8 (27%)	43,47,47	1.88	7 (16%)
4	DAT	B	802	5	27,28,28	1.53	5 (18%)	41,43,43	1.85	9 (21%)
3	GDP	C	801	-	29,30,30	1.20	3 (10%)	45,47,47	1.83	7 (15%)
7	FEO	G	501	2,8	0,2,2	-	-	-	-	-
4	DAT	A	802	5	27,28,28	1.48	6 (22%)	41,43,43	1.88	10 (24%)
7	FEO	H	501	2,8	0,2,2	-	-	-	-	-
4	DAT	D	802	5	27,28,28	1.56	5 (18%)	41,43,43	1.91	10 (24%)
7	FEO	F	501	2,8	0,2,2	-	-	-	-	-
3	GDP	B	801	-	29,30,30	1.17	2 (6%)	45,47,47	1.79	7 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	TTP	B	805	5	29,30,30	1.41	6 (20%)	43,47,47	1.76	6 (13%)

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
6	TTP	A	805	5	-	7/22/34/34	0/2/2/2
4	DAT	C	802	5	-	4/16/28/28	0/3/3/3
6	TTP	C	804	5	-	5/22/34/34	0/2/2/2
6	TTP	C	805	5	-	3/22/34/34	0/2/2/2
6	TTP	D	805	5	-	8/22/34/34	0/2/2/2
3	GDP	A	801	-	-	8/16/32/32	0/3/3/3
4	DAT	D	802	5	-	4/16/28/28	0/3/3/3
6	TTP	D	804	5	-	9/22/34/34	0/2/2/2
6	TTP	A	804	5	-	9/22/34/34	0/2/2/2
4	DAT	B	802	5	-	3/16/28/28	0/3/3/3
3	GDP	C	801	-	-	2/16/32/32	0/3/3/3
3	GDP	B	801	-	-	5/16/32/32	0/3/3/3
4	DAT	A	802	5	-	3/16/28/28	0/3/3/3
6	TTP	B	805	5	-	5/22/34/34	0/2/2/2
6	TTP	B	804	5	-	12/22/34/34	0/2/2/2
3	GDP	D	801	-	-	5/16/32/32	0/3/3/3

The worst 5 of 96 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	802	DAT	C5-C4	4.83	1.47	1.39
4	C	802	DAT	C5-C4	4.80	1.47	1.39
4	B	802	DAT	C5-C4	4.77	1.47	1.39
4	A	802	DAT	C5-C4	4.64	1.47	1.39
6	D	805	TTP	PB-O3A	3.63	1.63	1.59

The worst 5 of 122 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	801	GDP	C5-C4-N3	-6.30	118.37	128.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	801	GDP	C5-C4-N3	-6.24	118.45	128.39
3	B	801	GDP	C5-C4-N3	-6.18	118.55	128.39
3	C	801	GDP	C5-C4-N3	-6.16	118.59	128.39
4	B	802	DAT	C5-C4-N3	-5.92	118.56	126.72

There are no chirality outliers.

5 of 92 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	801	GDP	C5'-O5'-PA-O3A
3	A	801	GDP	C5'-O5'-PA-O1A
3	A	801	GDP	C5'-O5'-PA-O2A
3	B	801	GDP	PA-O3A-PB-O2B
3	B	801	GDP	PA-O3A-PB-O3B

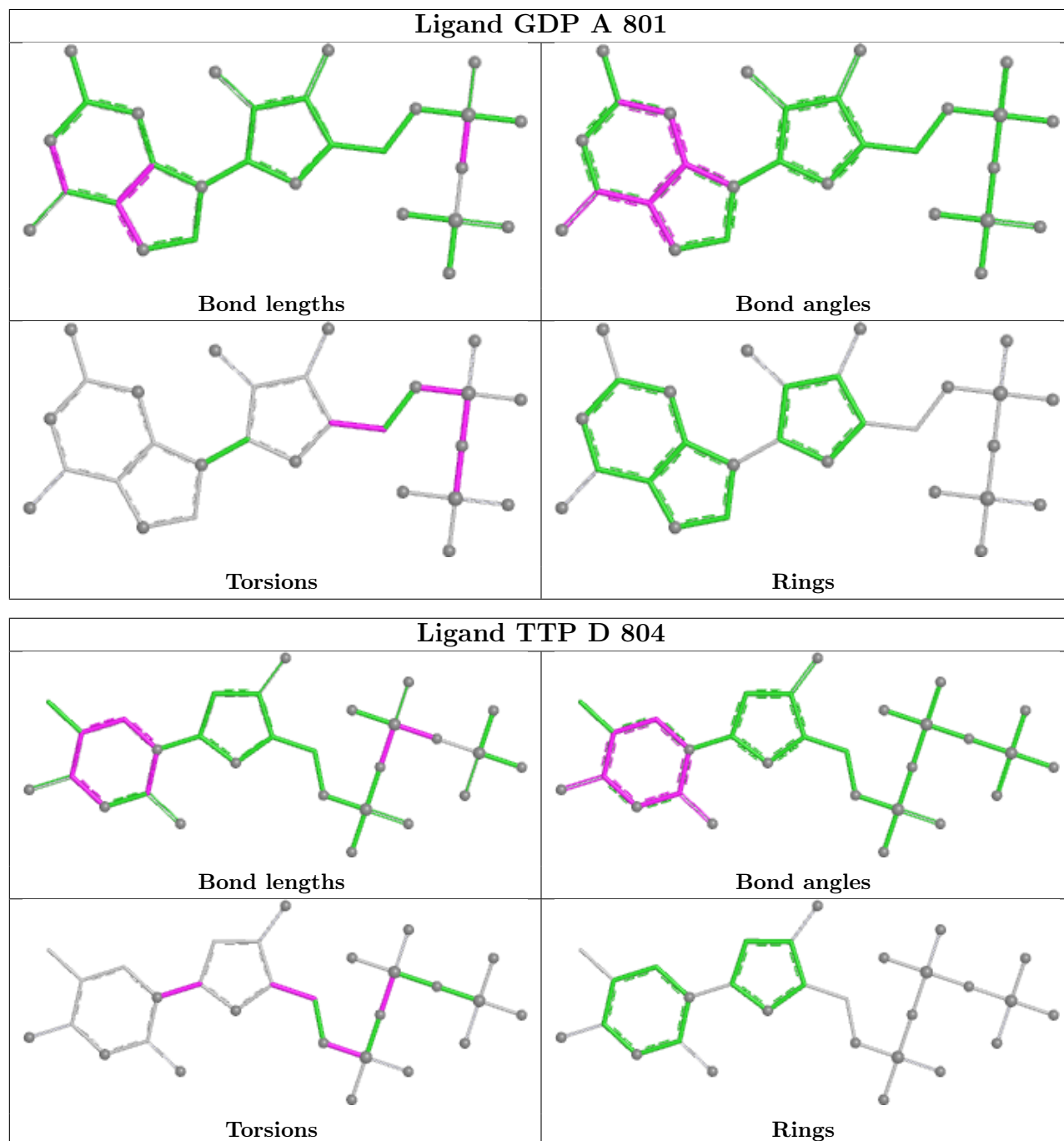
There are no ring outliers.

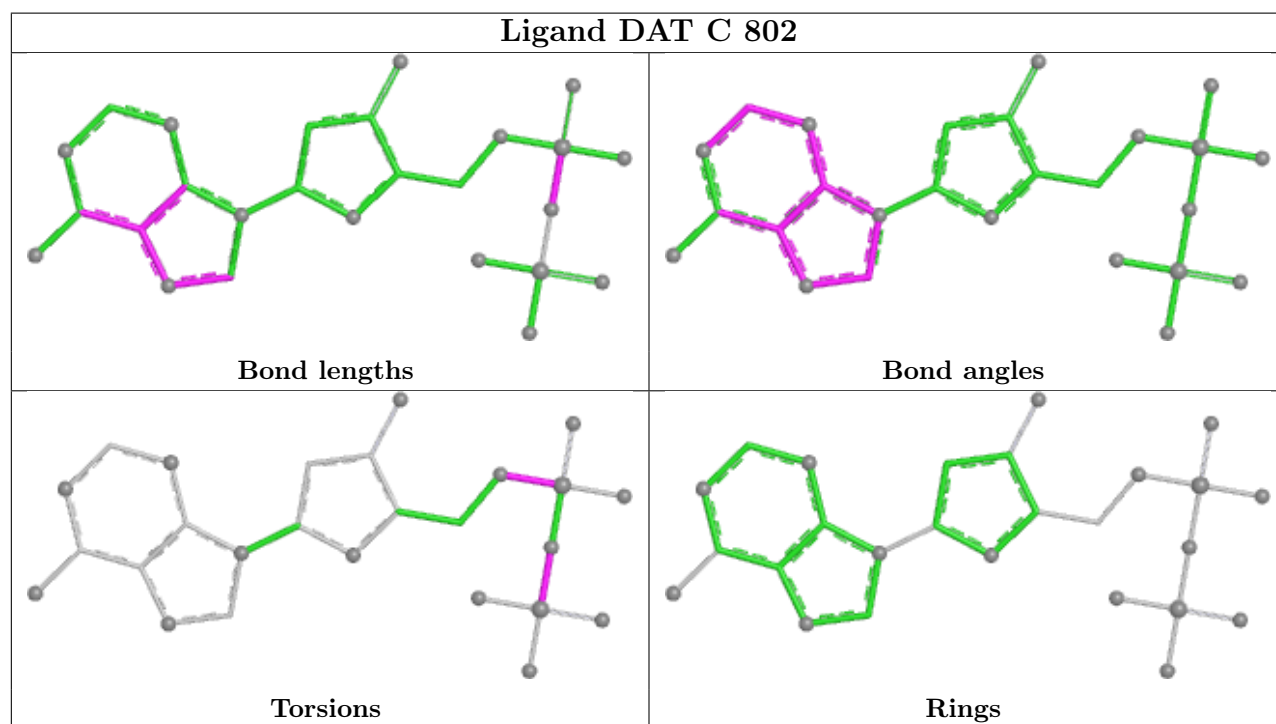
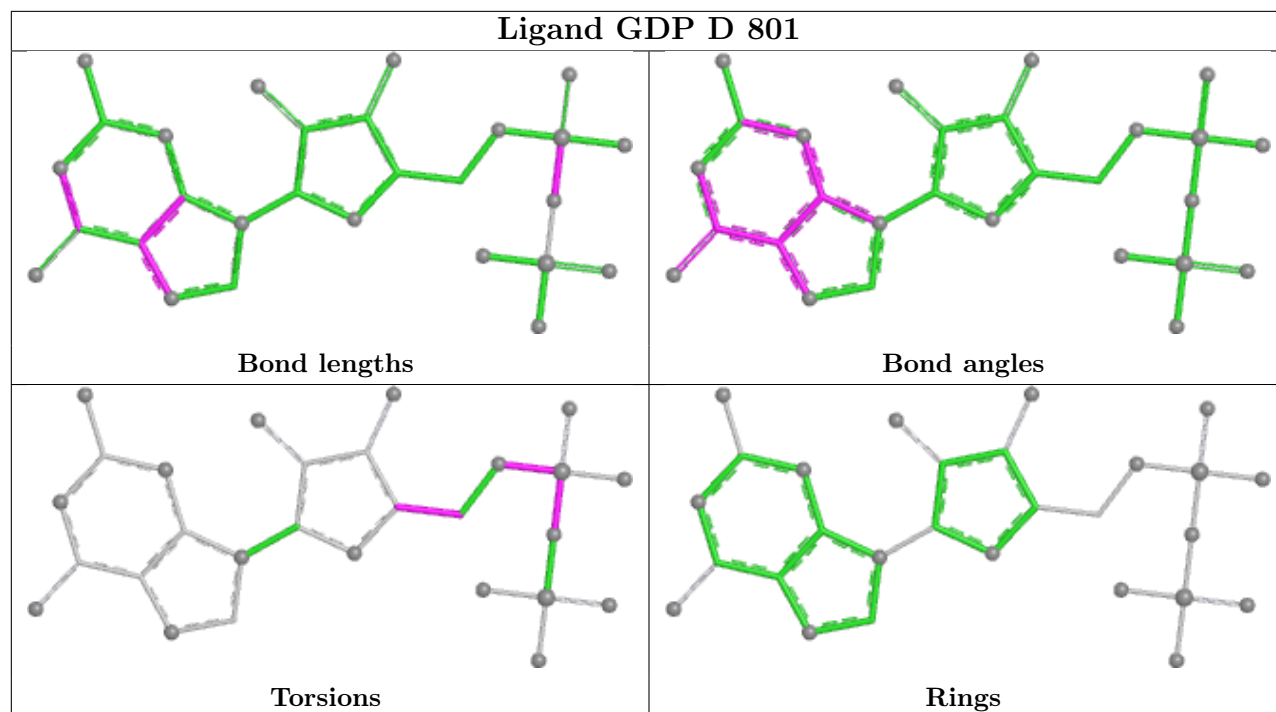
17 monomers are involved in 36 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	801	GDP	5	0
6	D	804	TTP	2	0
3	D	801	GDP	3	0
4	C	802	DAT	2	0
6	B	804	TTP	1	0
6	A	805	TTP	3	0
6	C	804	TTP	2	0
6	C	805	TTP	2	0
6	D	805	TTP	1	0
6	A	804	TTP	2	0
4	B	802	DAT	2	0
3	C	801	GDP	1	0
7	G	501	FEO	1	0
4	A	802	DAT	3	0
4	D	802	DAT	1	0
3	B	801	GDP	3	0
6	B	805	TTP	2	0

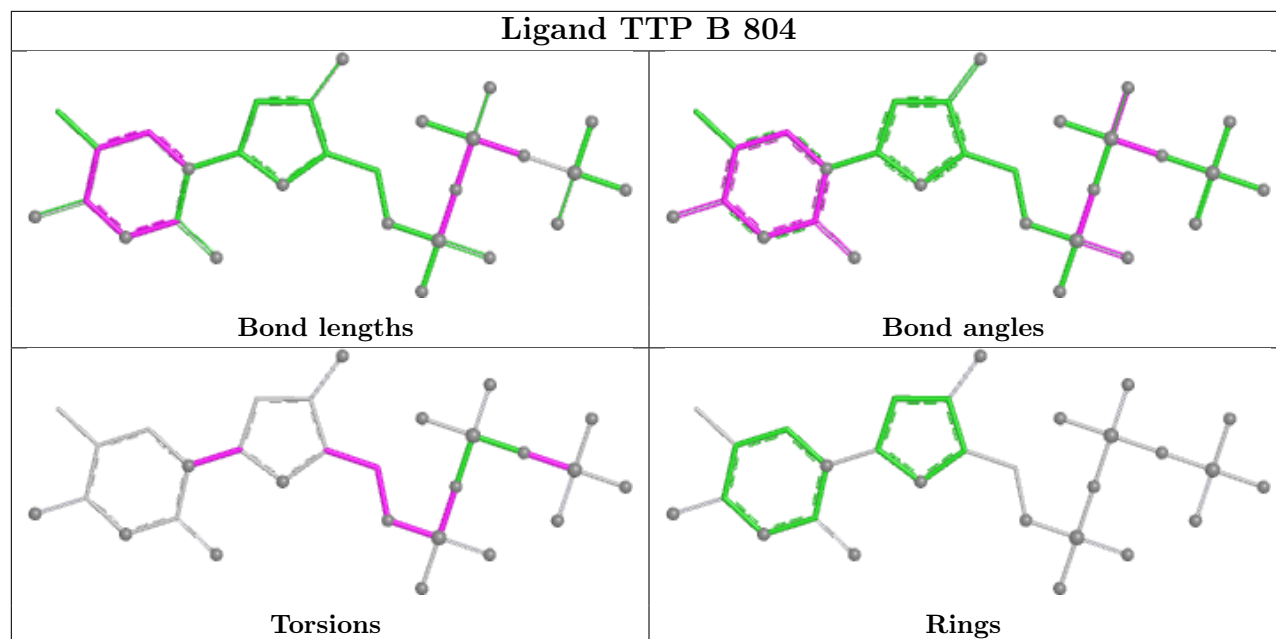
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

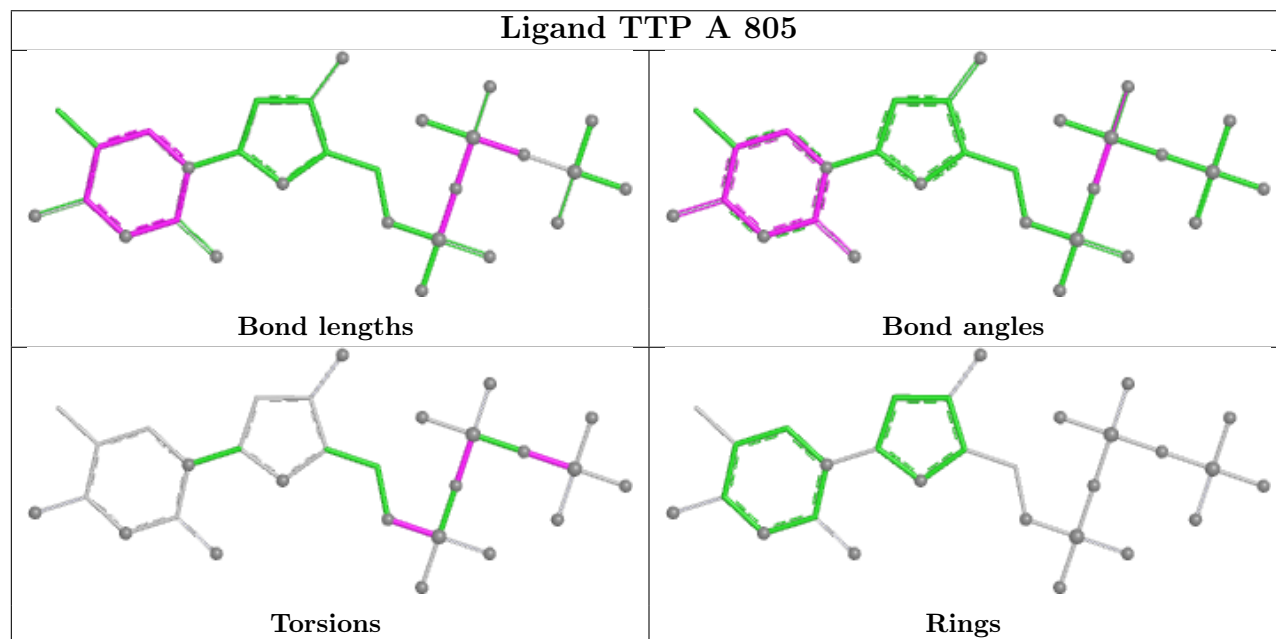




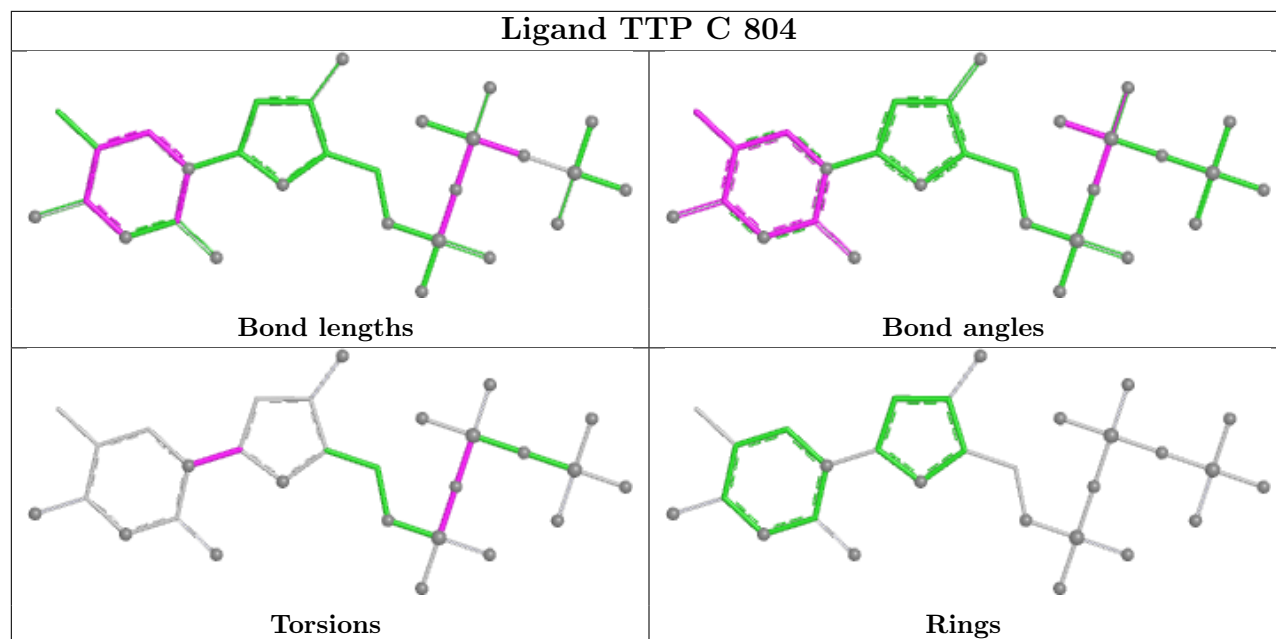
Ligand TTP B 804



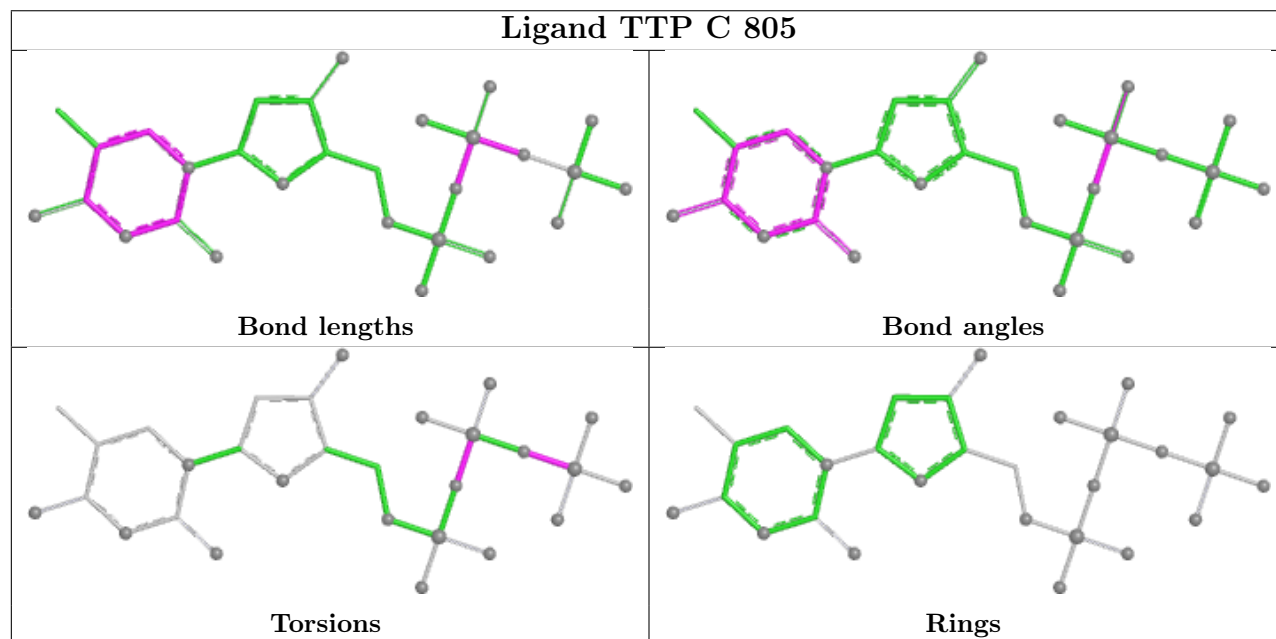
Ligand TTP A 805



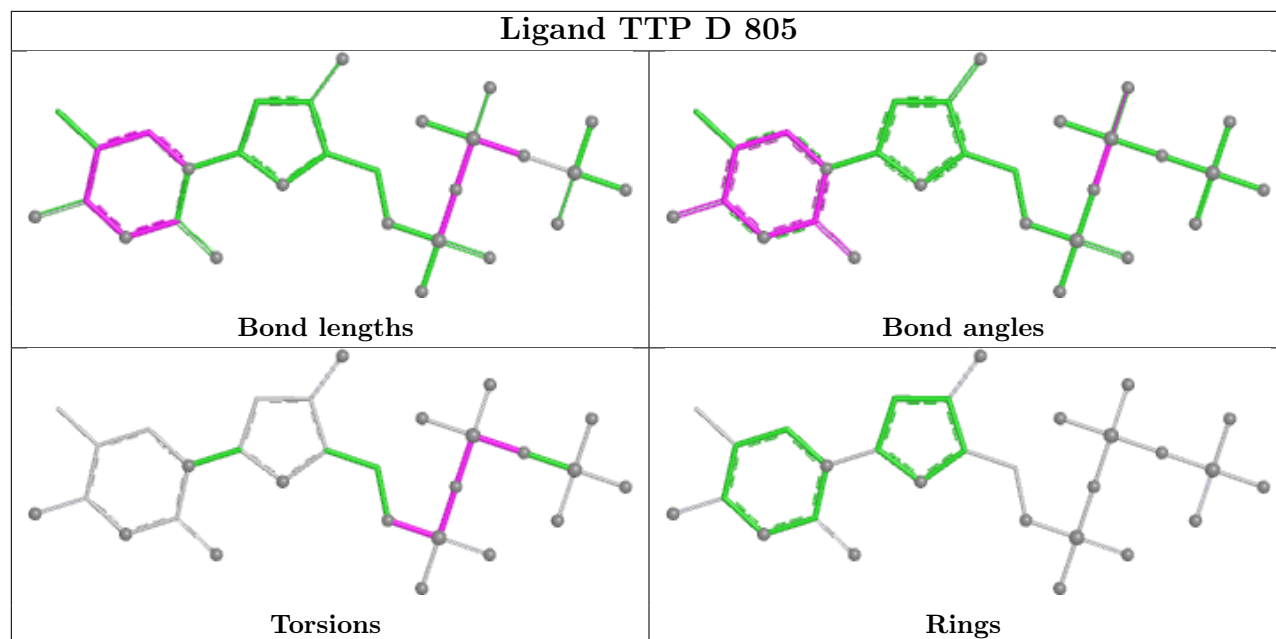
Ligand TTP C 804



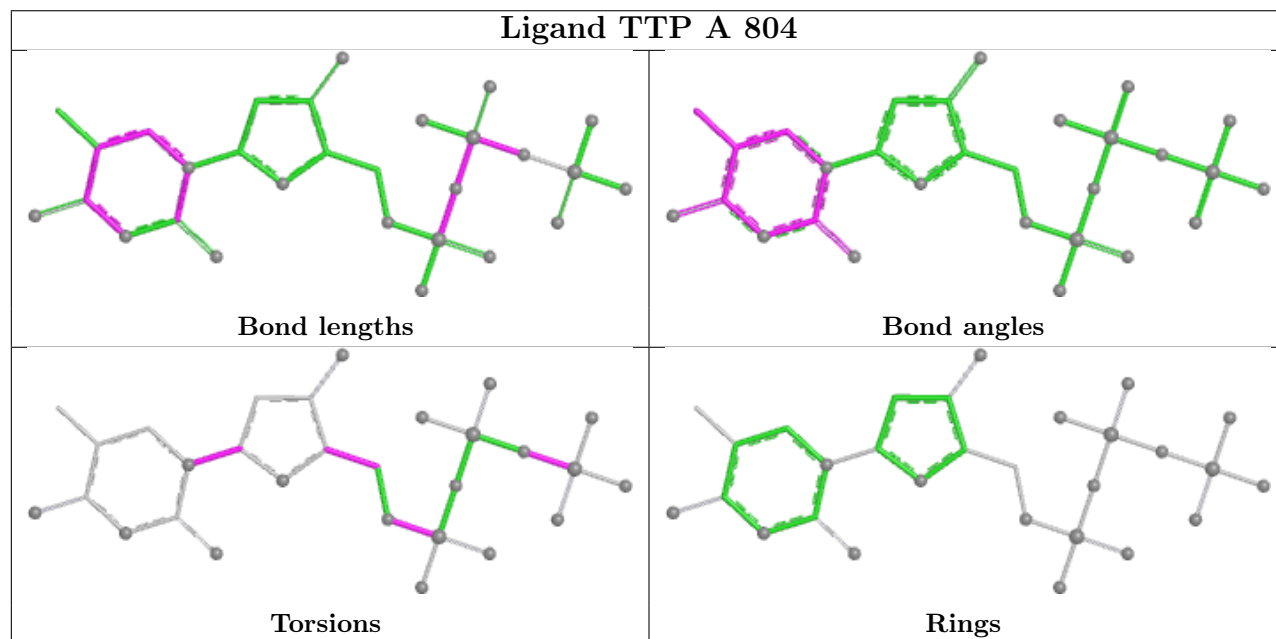
Ligand TTP C 805



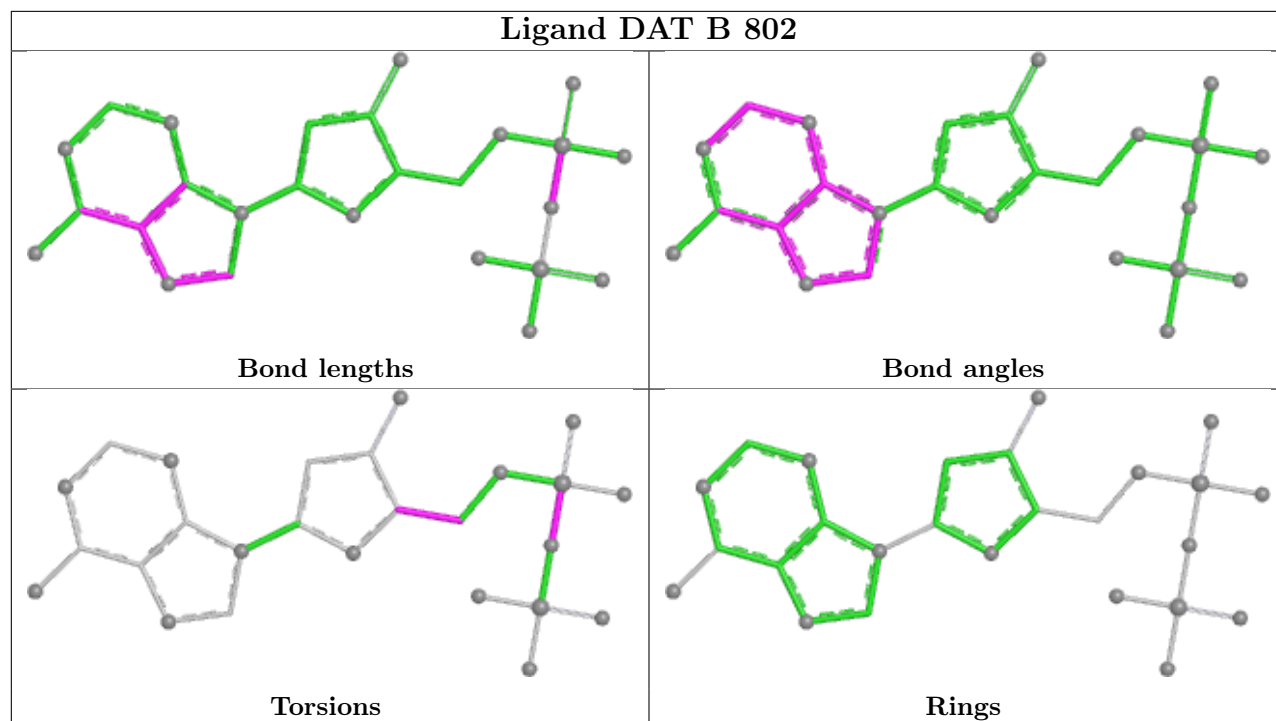
Ligand TTP D 805



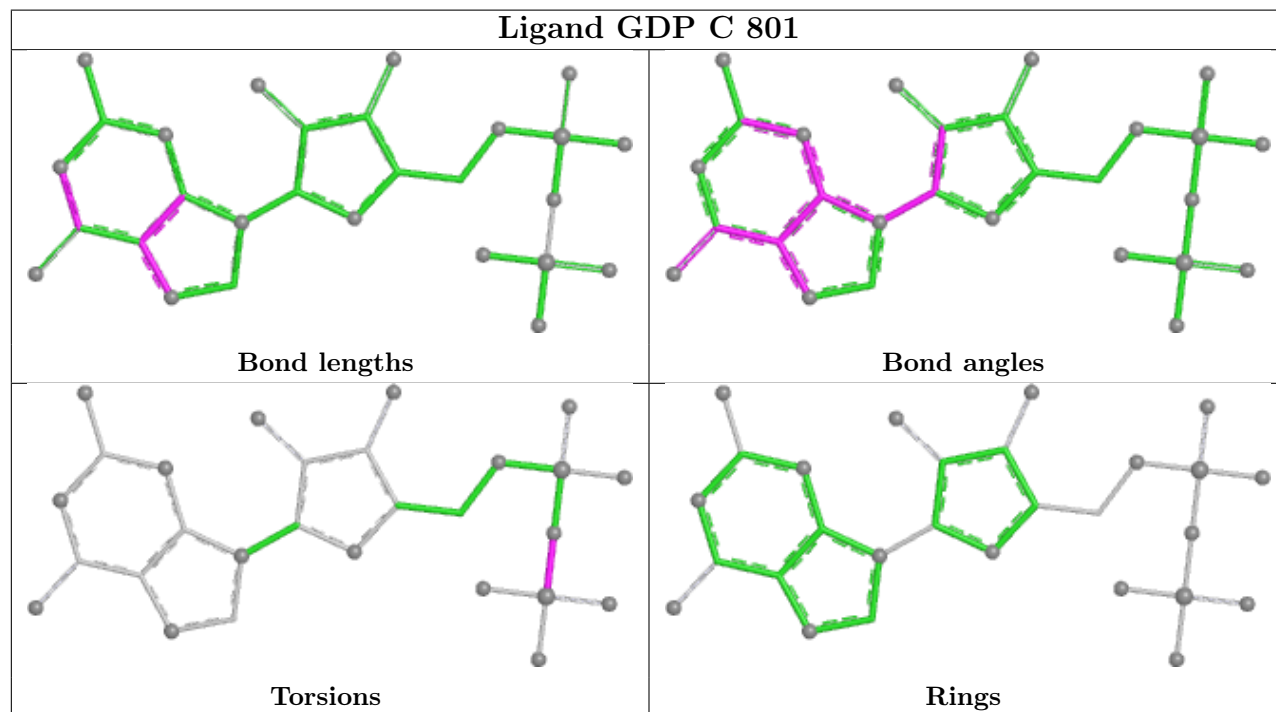
Ligand TTP A 804



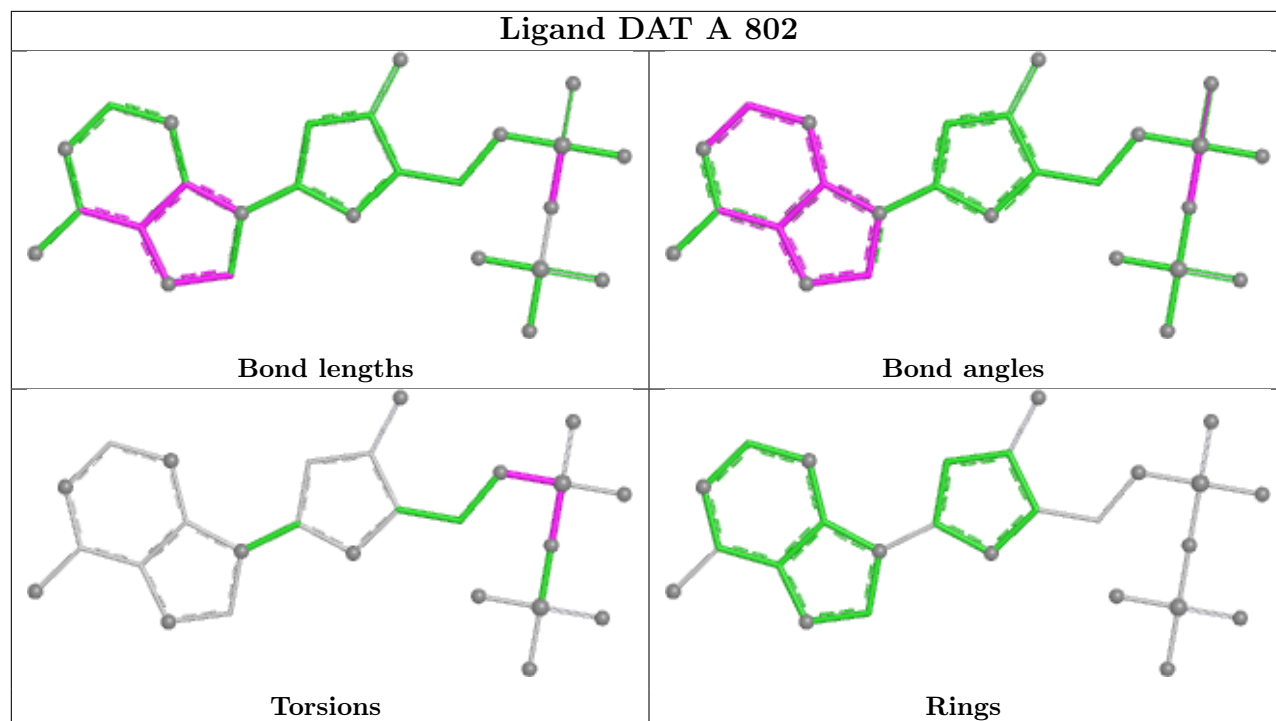
Ligand DAT B 802



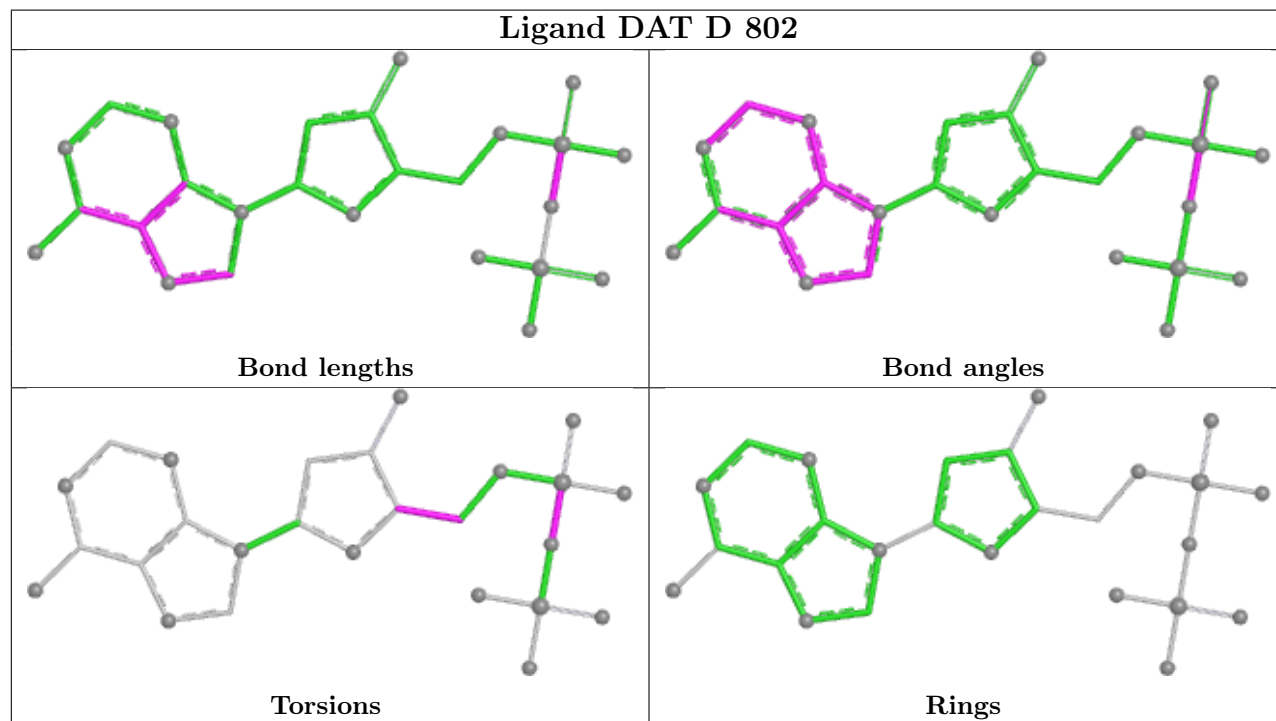
Ligand GDP C 801

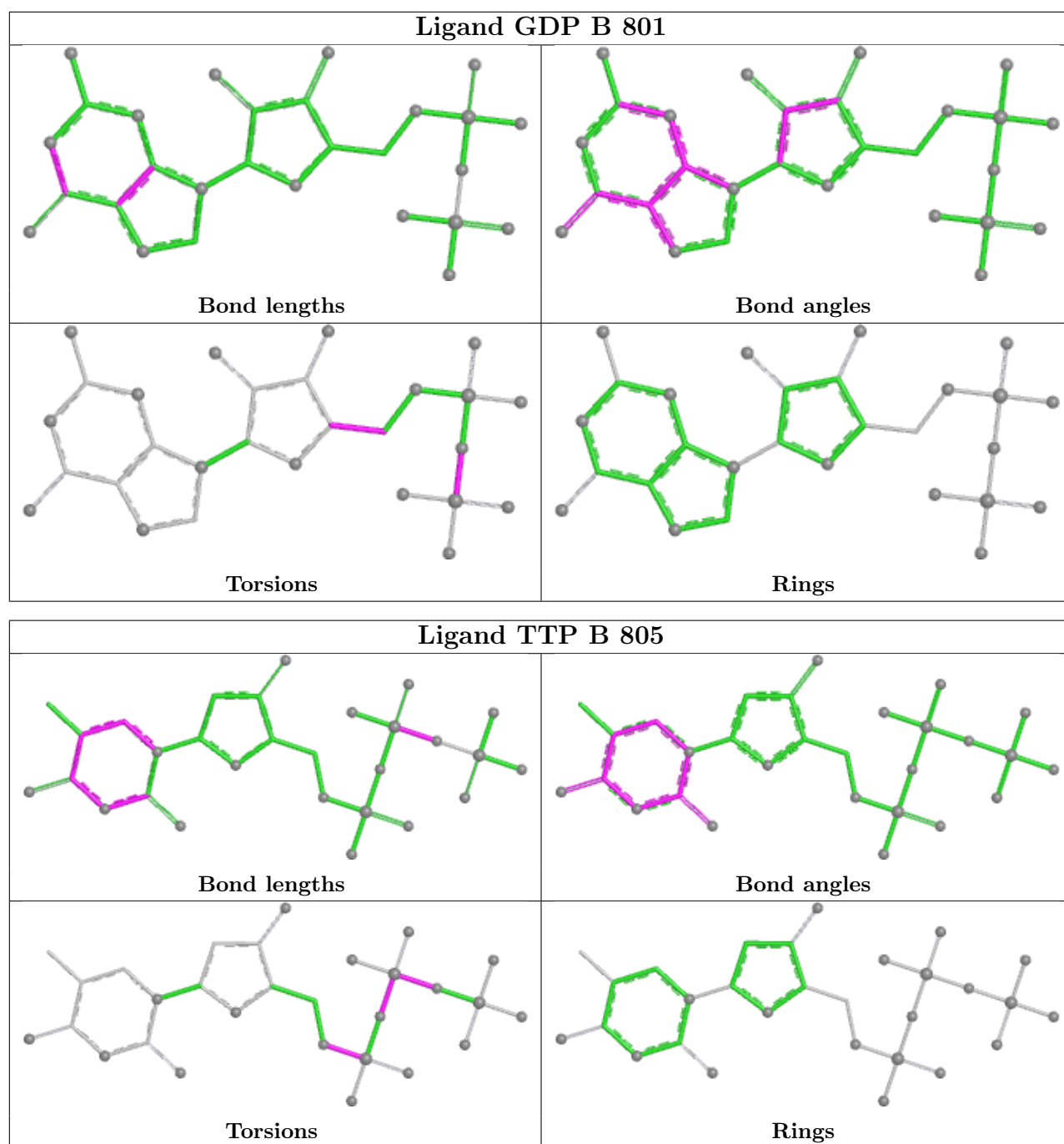


Ligand DAT A 802



Ligand DAT D 802





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	736/761 (96%)	-0.12	3 (0%) 88 79	59, 75, 88, 104	0
1	B	732/761 (96%)	0.09	2 (0%) 90 81	75, 91, 101, 108	0
1	C	734/761 (96%)	-0.40	0 100 100	47, 58, 74, 93	0
1	D	734/761 (96%)	-0.25	1 (0%) 92 89	47, 61, 85, 110	0
2	E	352/375 (93%)	0.07	1 (0%) 90 81	65, 86, 101, 117	0
2	F	357/375 (95%)	-0.42	1 (0%) 90 81	42, 54, 73, 95	0
2	G	357/375 (95%)	-0.46	0 100 100	39, 52, 77, 98	0
2	H	359/375 (95%)	-0.12	2 (0%) 85 73	58, 71, 92, 116	0
All	All	4361/4544 (95%)	-0.19	10 (0%) 91 85	39, 69, 97, 117	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	GLN	2.9
2	H	344	VAL	2.6
2	E	1	ALA	2.5
1	D	47	ILE	2.4
2	H	341	SER	2.4

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

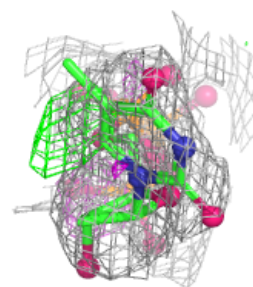
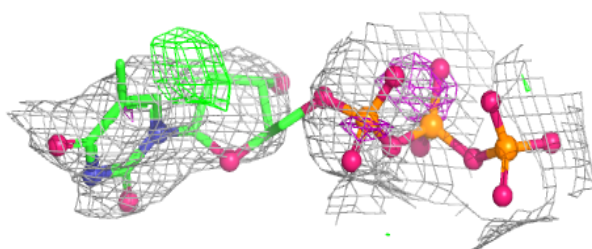
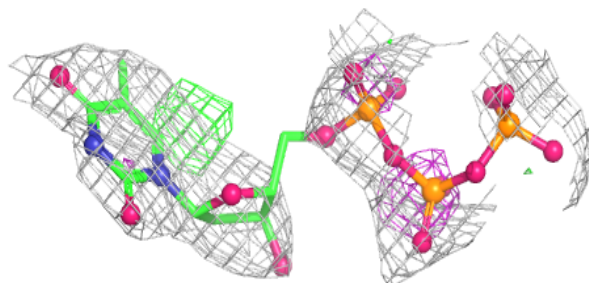
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	TTP	A	804	29/29	0.82	0.14	73,84,94,98	29
6	TTP	D	804	29/29	0.85	0.11	79,89,100,102	29
6	TTP	B	804	29/29	0.86	0.11	96,101,104,105	29
6	TTP	C	804	29/29	0.87	0.11	68,73,80,82	29
3	GDP	B	801	28/28	0.90	0.10	81,84,87,88	0
4	DAT	B	802	26/26	0.90	0.10	96,100,104,105	0
4	DAT	D	802	26/26	0.92	0.09	84,92,98,99	0
4	DAT	A	802	26/26	0.93	0.08	74,81,88,89	0
6	TTP	A	805	29/29	0.94	0.08	78,81,84,86	0
3	GDP	A	801	28/28	0.94	0.08	66,69,72,73	0
6	TTP	B	805	29/29	0.95	0.08	79,81,84,88	0
3	GDP	C	801	28/28	0.95	0.08	49,53,56,57	0
4	DAT	C	802	26/26	0.95	0.08	66,69,75,77	0
3	GDP	D	801	28/28	0.96	0.07	52,55,58,59	0
5	MG	C	803	1/1	0.97	0.04	73,73,73,73	0
5	MG	D	803	1/1	0.97	0.04	95,95,95,95	0
5	MG	A	803	1/1	0.97	0.07	93,93,93,93	0
6	TTP	C	805	29/29	0.97	0.07	53,56,61,65	0
5	MG	B	806	1/1	0.97	0.05	81,81,81,81	0
6	TTP	D	805	29/29	0.97	0.06	50,53,56,59	0
5	MG	A	806	1/1	0.98	0.04	81,81,81,81	0
5	MG	B	803	1/1	0.98	0.04	102,102,102,102	0
5	MG	C	806	1/1	0.98	0.04	59,59,59,59	0
5	MG	D	806	1/1	0.99	0.03	54,54,54,54	0
7	FEO	E	501	3/3	0.99	0.04	73,73,75,81	0
7	FEO	F	501	3/3	0.99	0.04	47,47,47,49	0
7	FEO	G	501	3/3	1.00	0.02	43,43,45,47	0
7	FEO	H	501	3/3	1.00	0.03	62,62,62,63	0

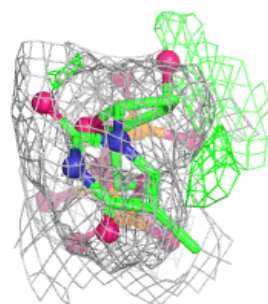
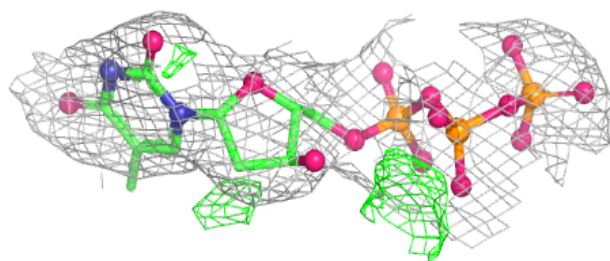
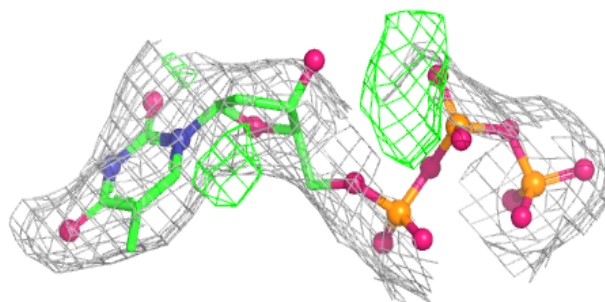
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around TTP A 804:

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

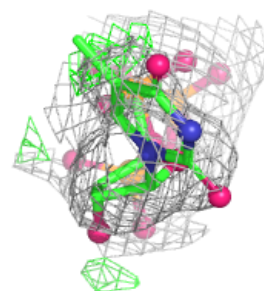
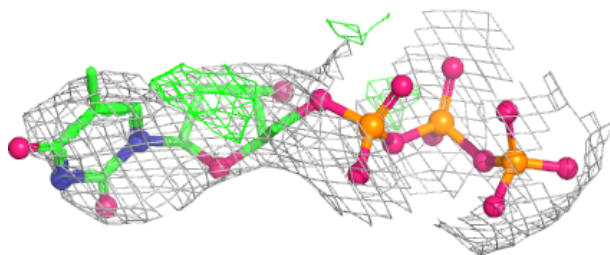
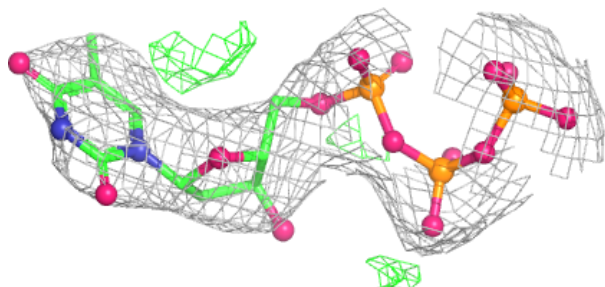
**Electron density around TTP D 804:**

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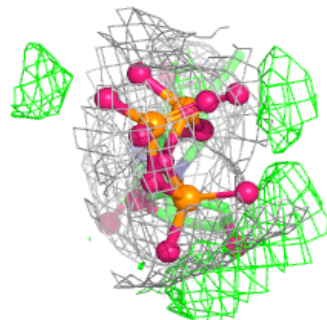
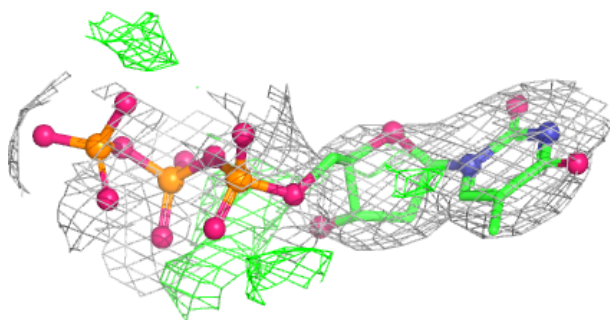
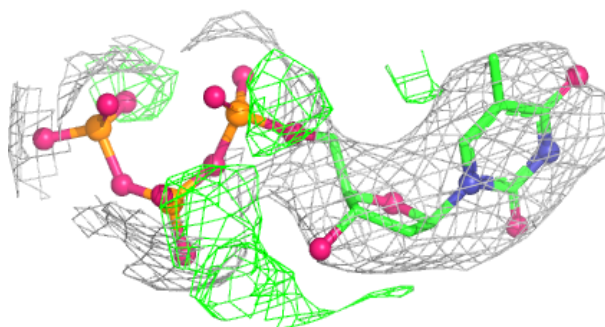


Electron density around TTP B 804:

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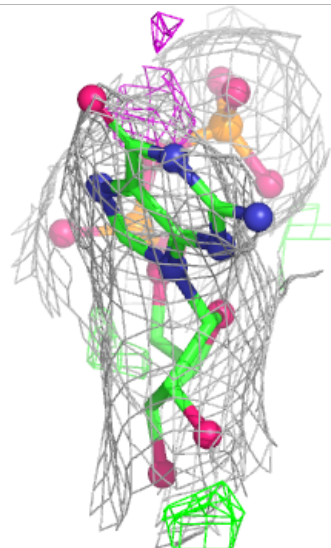
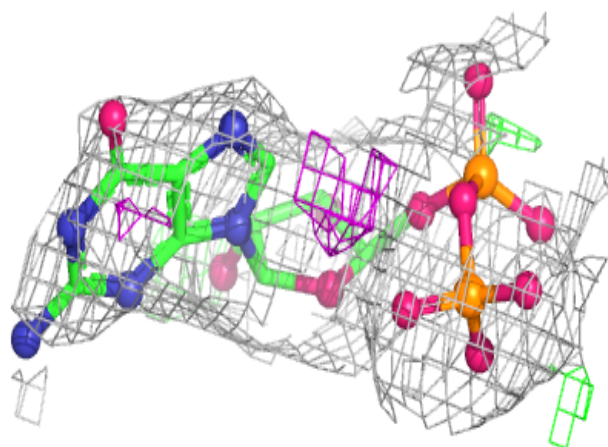
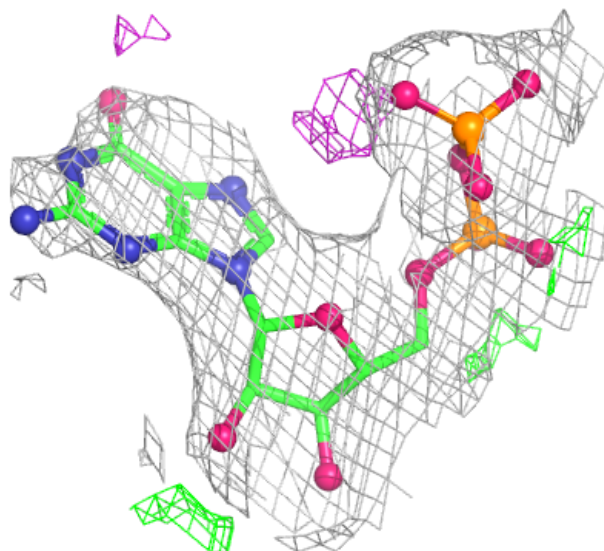
**Electron density around TTP C 804:**

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and green (positive)



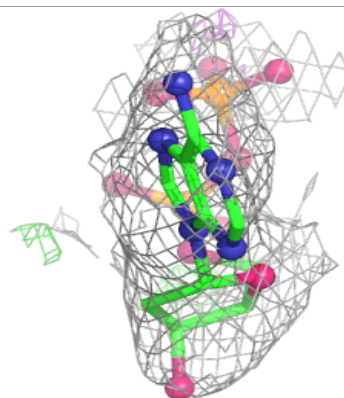
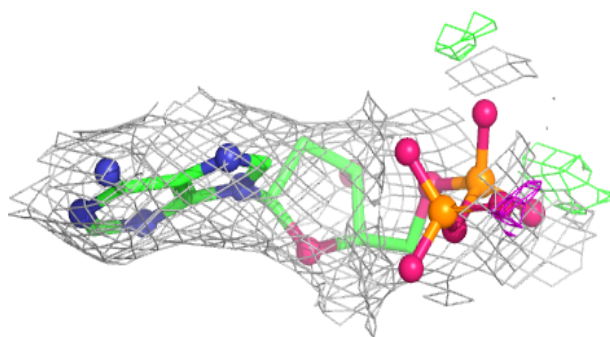
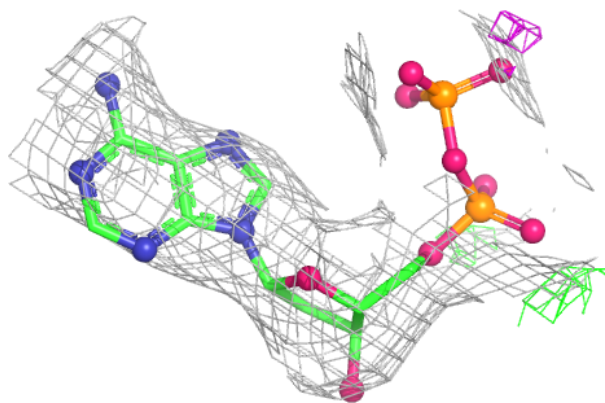
Electron density around GDP B 801:

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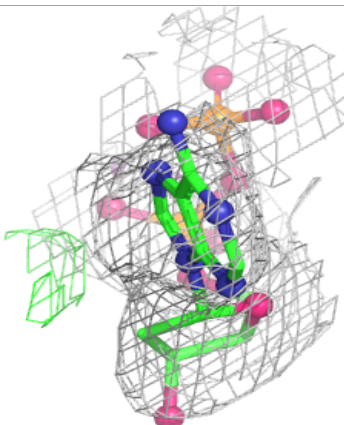
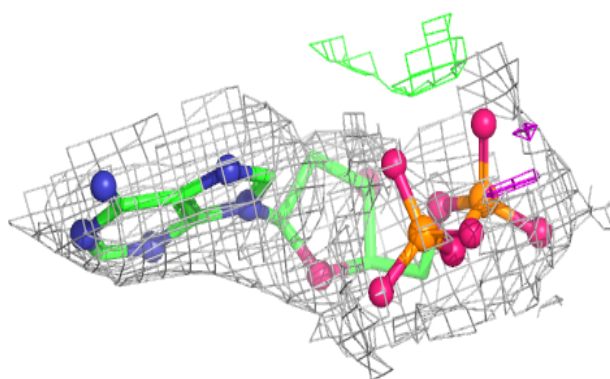
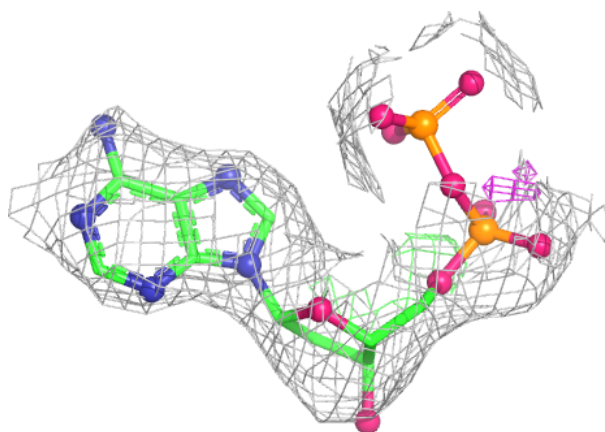


Electron density around DAT B 802:

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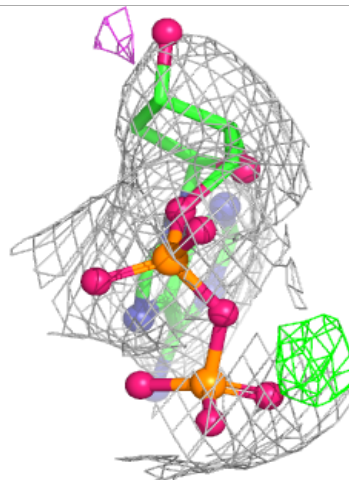
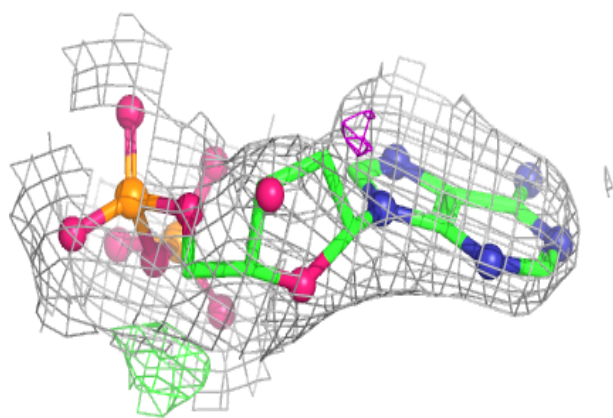
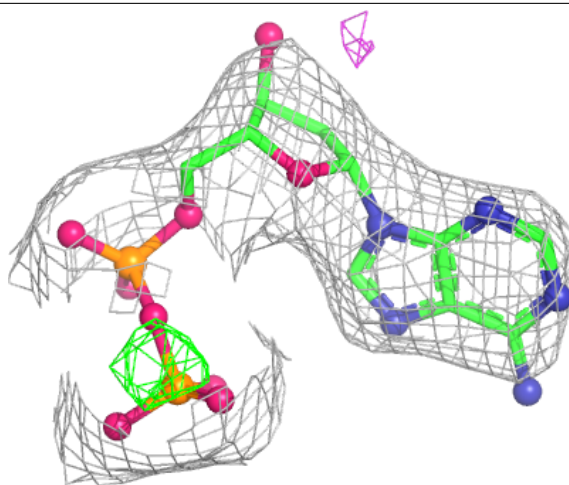
**Electron density around DAT D 802:**

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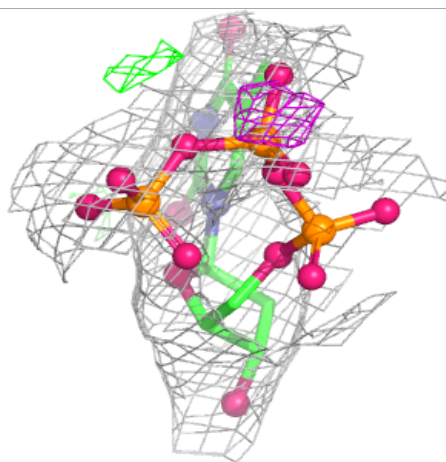
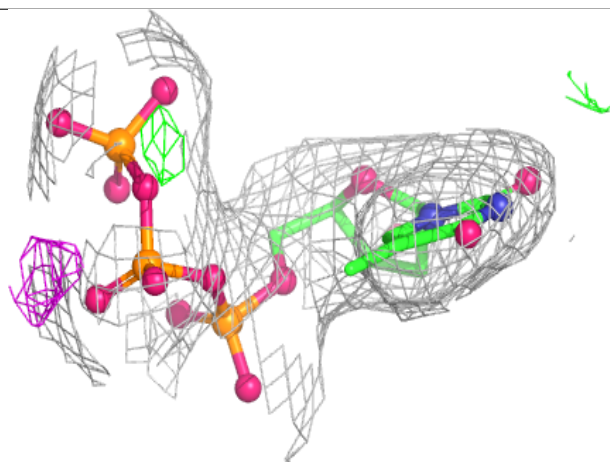
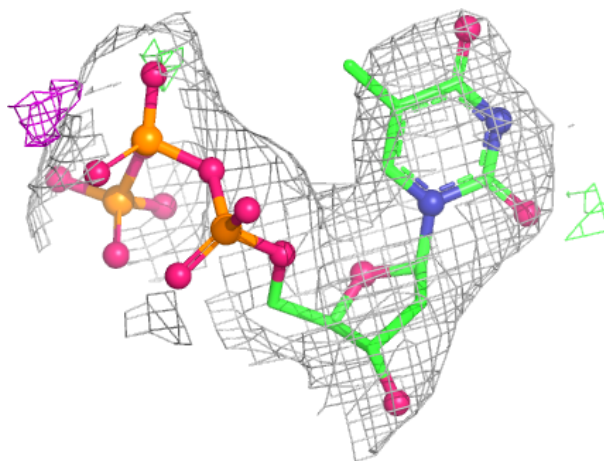
Electron density around DAT A 802:

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and green (positive)



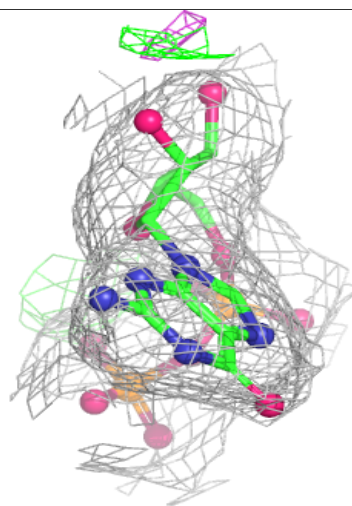
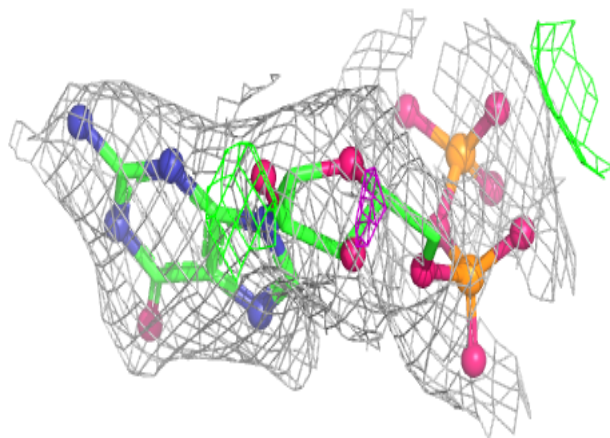
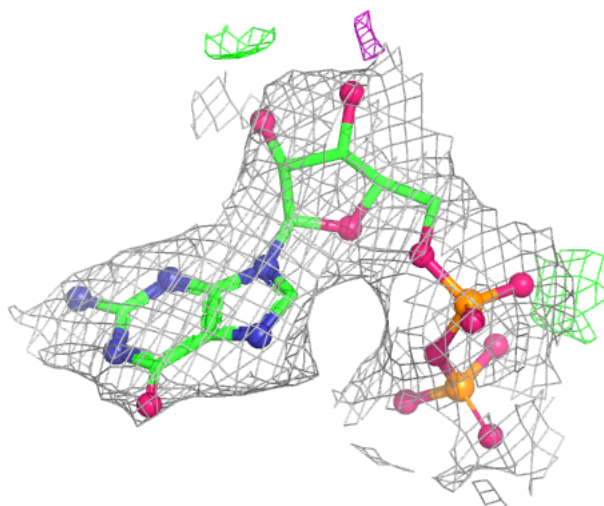
Electron density around TTP A 805:

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and green (positive)



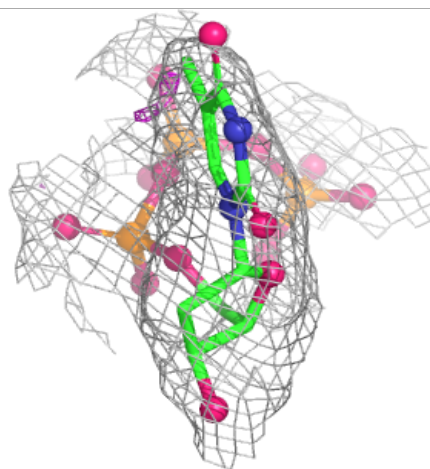
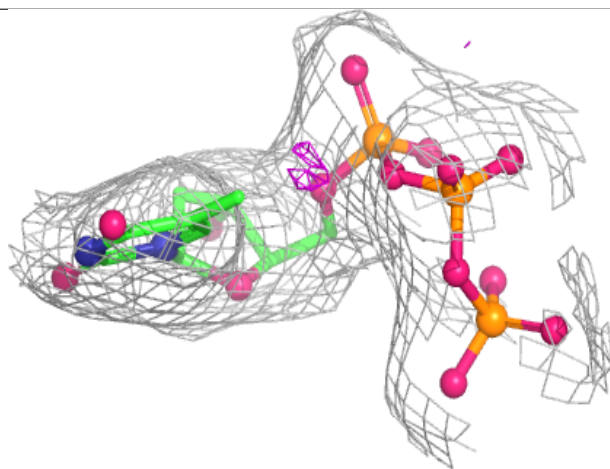
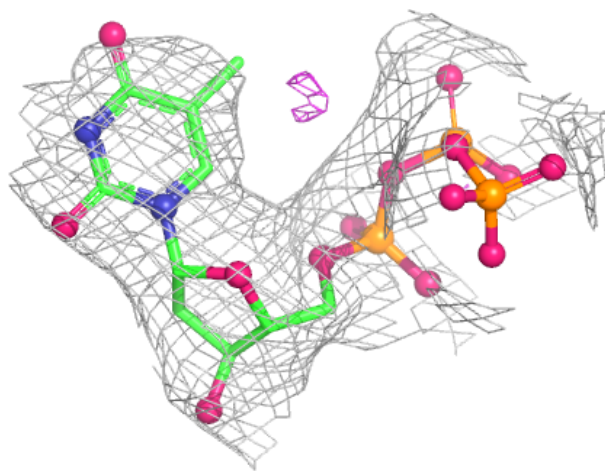
Electron density around GDP A 801:

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



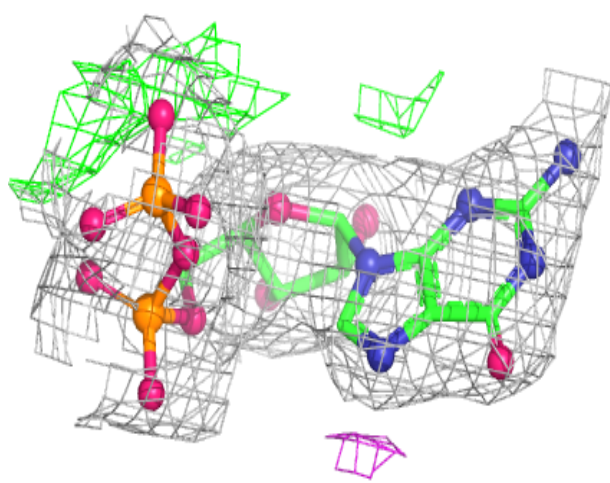
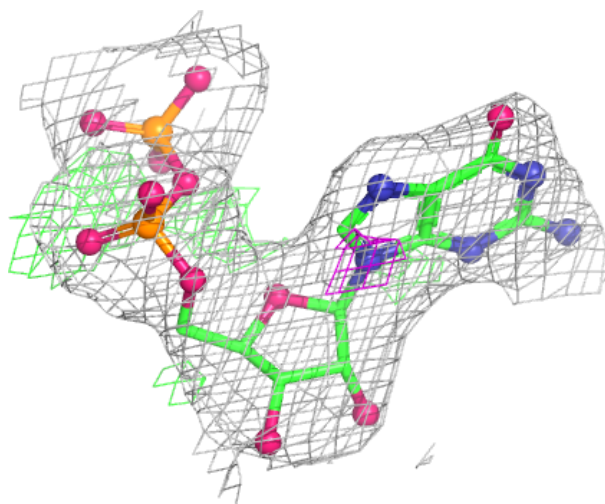
Electron density around TTP B 805:

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



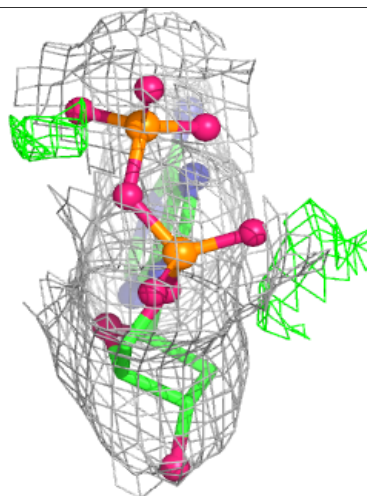
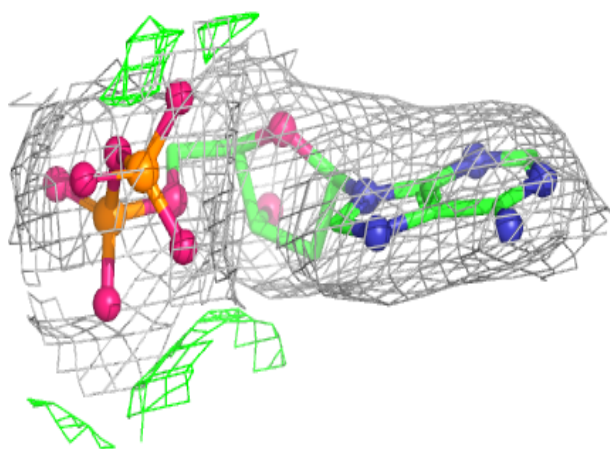
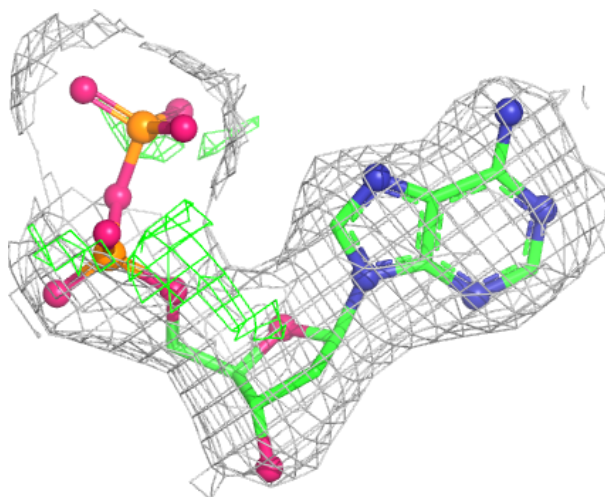
Electron density around GDP C 801:

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



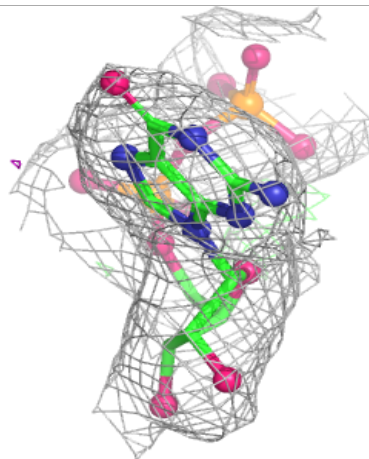
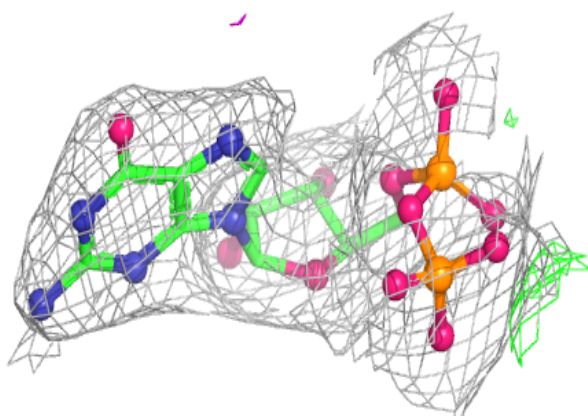
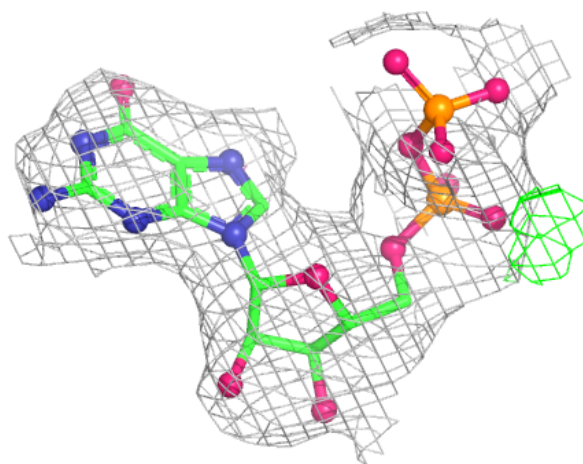
Electron density around DAT C 802:

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



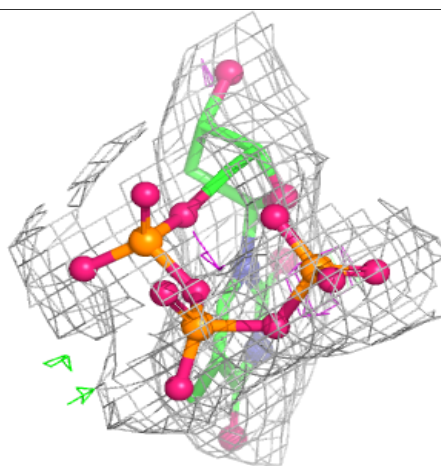
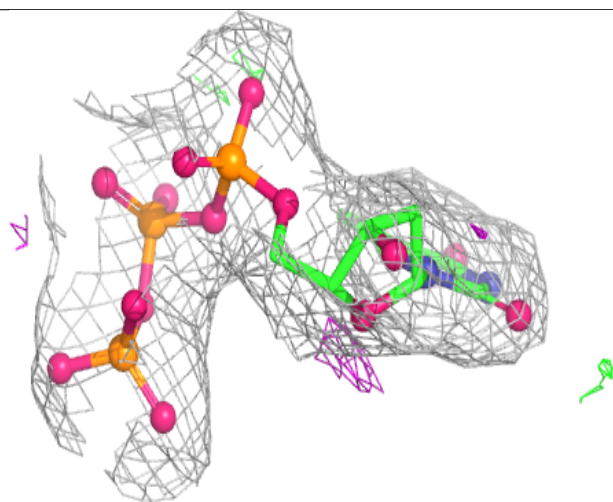
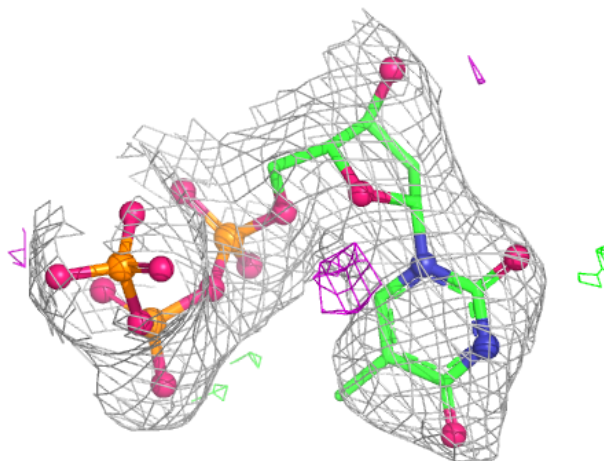
Electron density around GDP D 801:

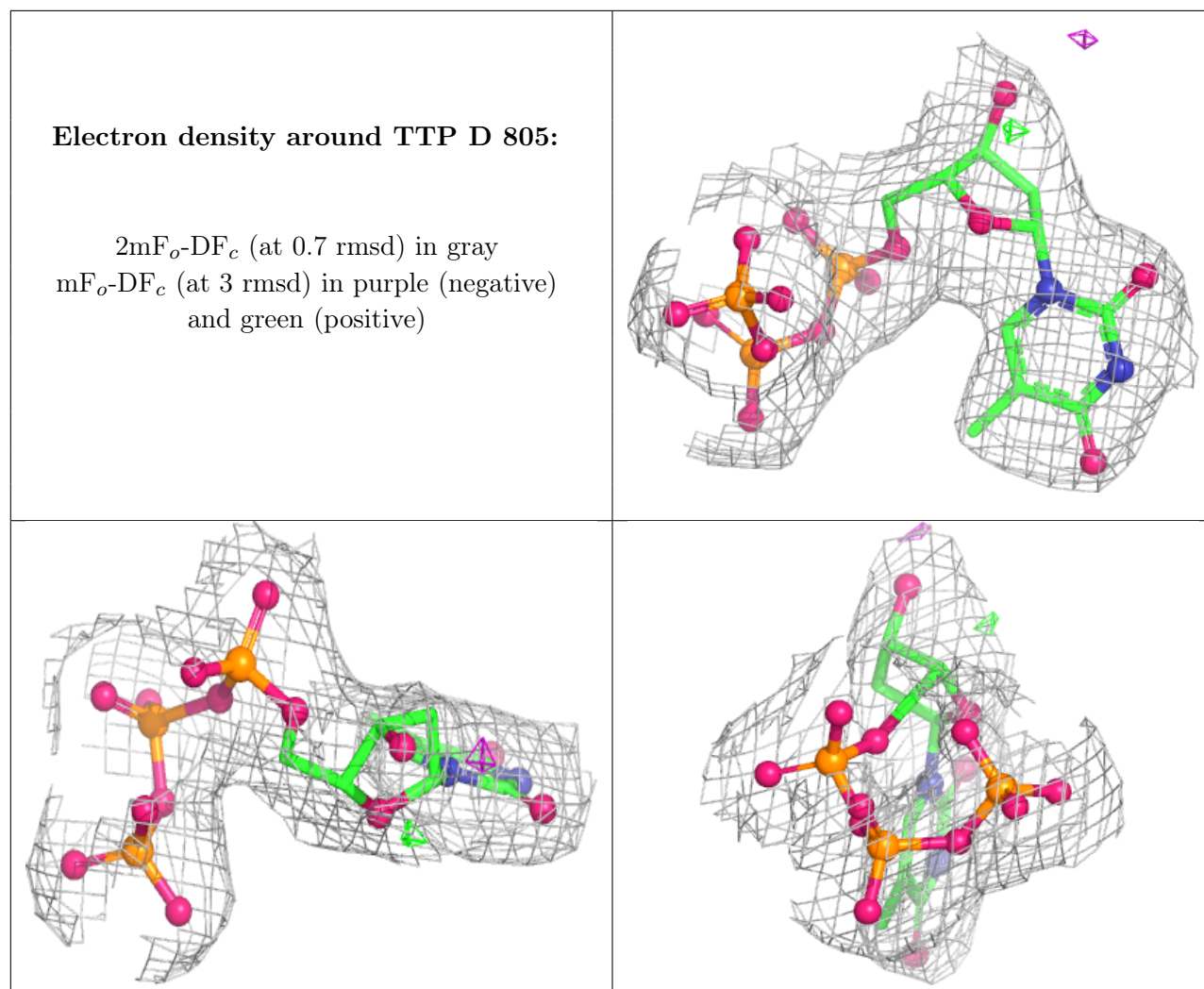
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around TTP C 805:

$2mF_o-DF_c$ (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.