



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 5, 2026 – 07:14 AM EDT

PDB ID : 4ERM / pdb_00004erm
Title : Crystal structure of the dATP inhibited E. coli class Ia ribonucleotide reductase complex at 4 Angstroms resolution
Authors : Zimanyi, C.M.; Drennan, C.L.
Deposited on : 2012-04-20
Resolution : 3.95 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 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

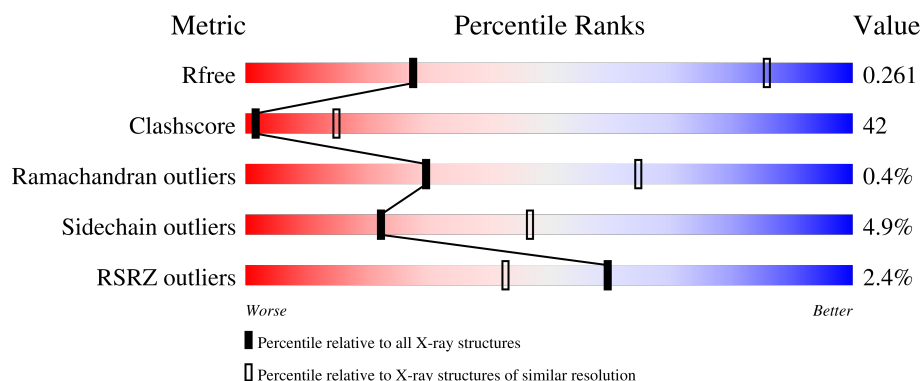
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

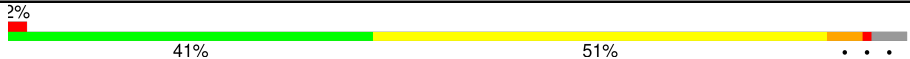
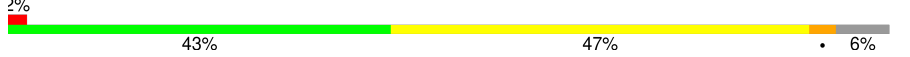
The reported resolution of this entry is 3.95 Å.

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	1046 (4.16-3.76)
Clashscore	190562	1019 (4.14-3.78)
Ramachandran outliers	187476	1031 (4.16-3.76)
Sidechain outliers	187428	1024 (4.16-3.76)
RSRZ outliers	180081	1046 (4.16-3.76)

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	
1	B	761	
1	C	761	
1	D	761	
2	E	375	

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Mol	Chain	Length	Quality of chain
2	F	375	
2	G	375	
2	H	375	

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	DAT	D	802	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 35345 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.

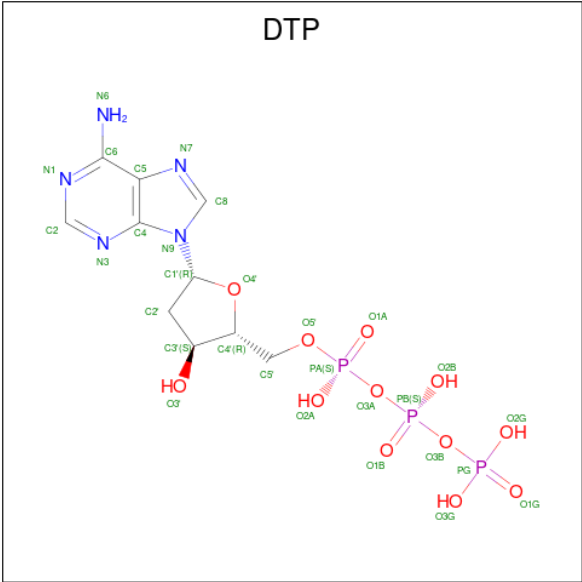
- Molecule 1 is a protein called Ribonucleoside-diphosphate reductase 1 subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	733	Total	C	N	O	S	0	0	0
			5841	3710	1003	1104	24			
1	B	734	Total	C	N	O	S	0	0	0
			5845	3712	1004	1105	24			
1	C	731	Total	C	N	O	S	0	0	0
			5821	3696	1000	1101	24			
1	D	733	Total	C	N	O	S	0	0	0
			5837	3708	1002	1103	24			

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

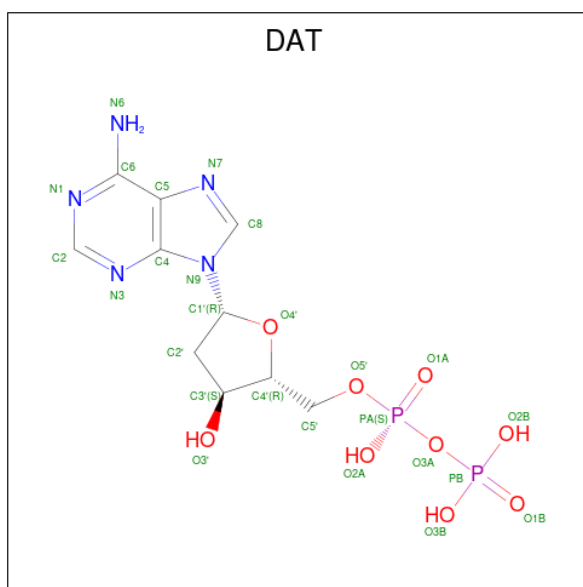
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	352	Total	C	N	O	S	0	0	0
			2885	1841	478	553	13			
2	F	356	Total	C	N	O	S	0	0	0
			2917	1861	483	560	13			
2	G	356	Total	C	N	O	S	0	0	0
			2917	1861	483	560	13			
2	H	356	Total	C	N	O	S	0	0	0
			2914	1859	482	560	13			

- Molecule 3 is 2'-DEOXYADENOSINE 5'-TRIPHOSPHATE (CCD ID: DTP) (formula: $C_{10}H_{16}N_5O_{12}P_3$)



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			30	10	5	12	3		
3	A	1	Total	C	N	O	P	0	0
			30	10	5	12	3		
3	B	1	Total	C	N	O	P	0	0
			30	10	5	12	3		
3	B	1	Total	C	N	O	P	0	0
			30	10	5	12	3		
3	C	1	Total	C	N	O	P	0	0
			30	10	5	12	3		
3	C	1	Total	C	N	O	P	0	0
			30	10	5	12	3		
3	D	1	Total	C	N	O	P	0	0
			30	10	5	12	3		
3	D	1	Total	C	N	O	P	0	0
			30	10	5	12	3		

- Molecule 4 is 2'-DEOXYADENOSINE-5'-DIPHOSPHATE (CCD ID: DAT) (formula: C₁₀H₁₅N₅O₉P₂).

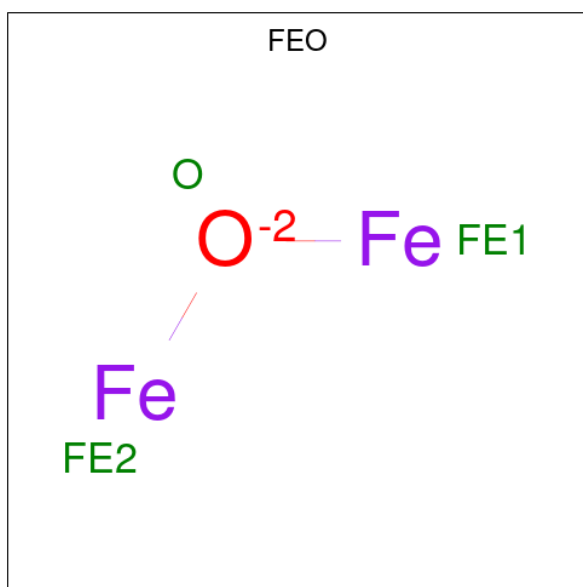


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			26	10	5	9	2		
4	B	1	Total	C	N	O	P	0	0
			26	10	5	9	2		
4	C	1	Total	C	N	O	P	0	0
			26	10	5	9	2		
4	D	1	Total	C	N	O	P	0	0
			26	10	5	9	2		

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

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

- Molecule 6 is MU-OXO-DIIRON (CCD ID: FEO) (formula: Fe₂O).



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

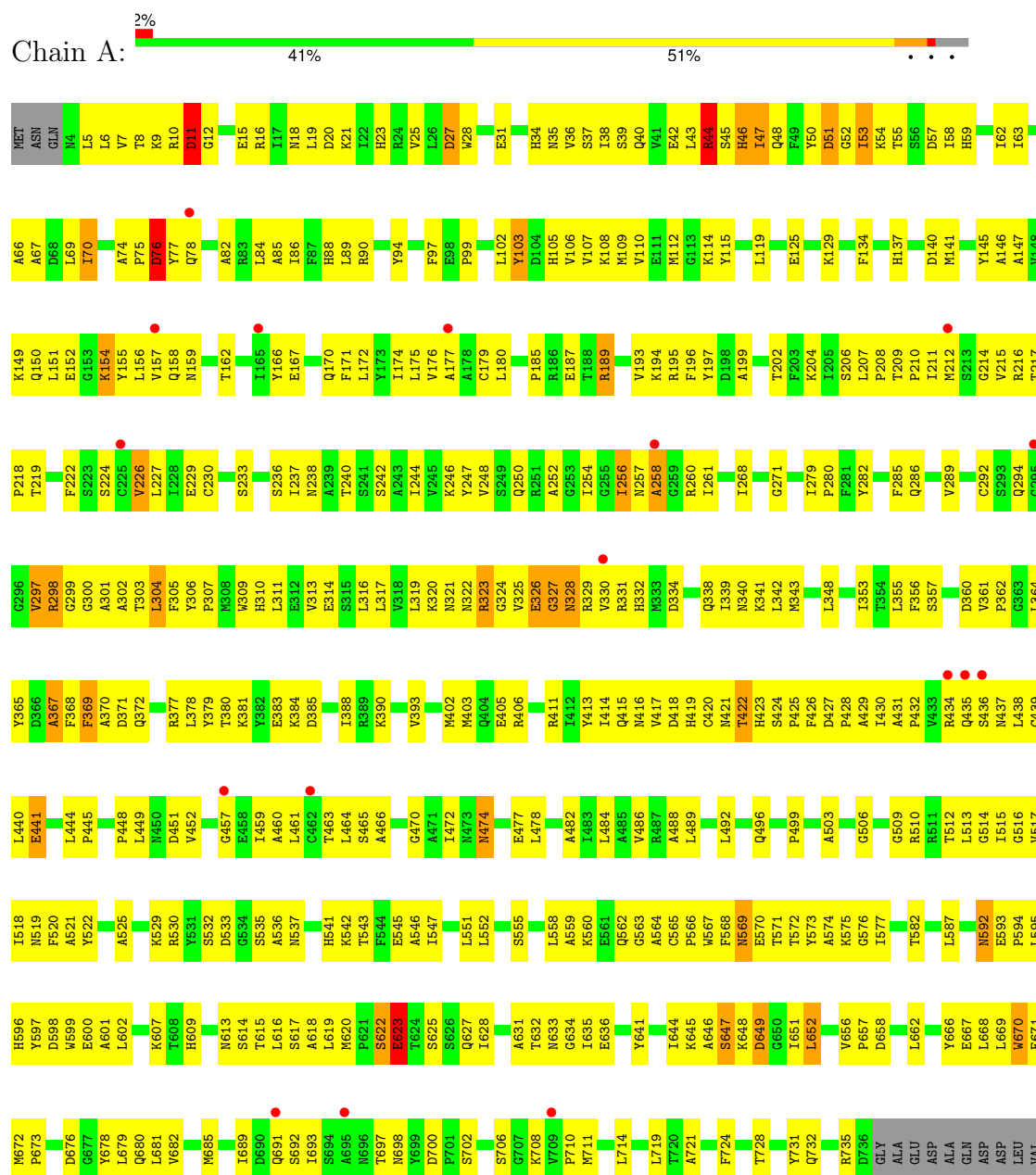
- Molecule 7 is water.

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

3 Residue-property plots

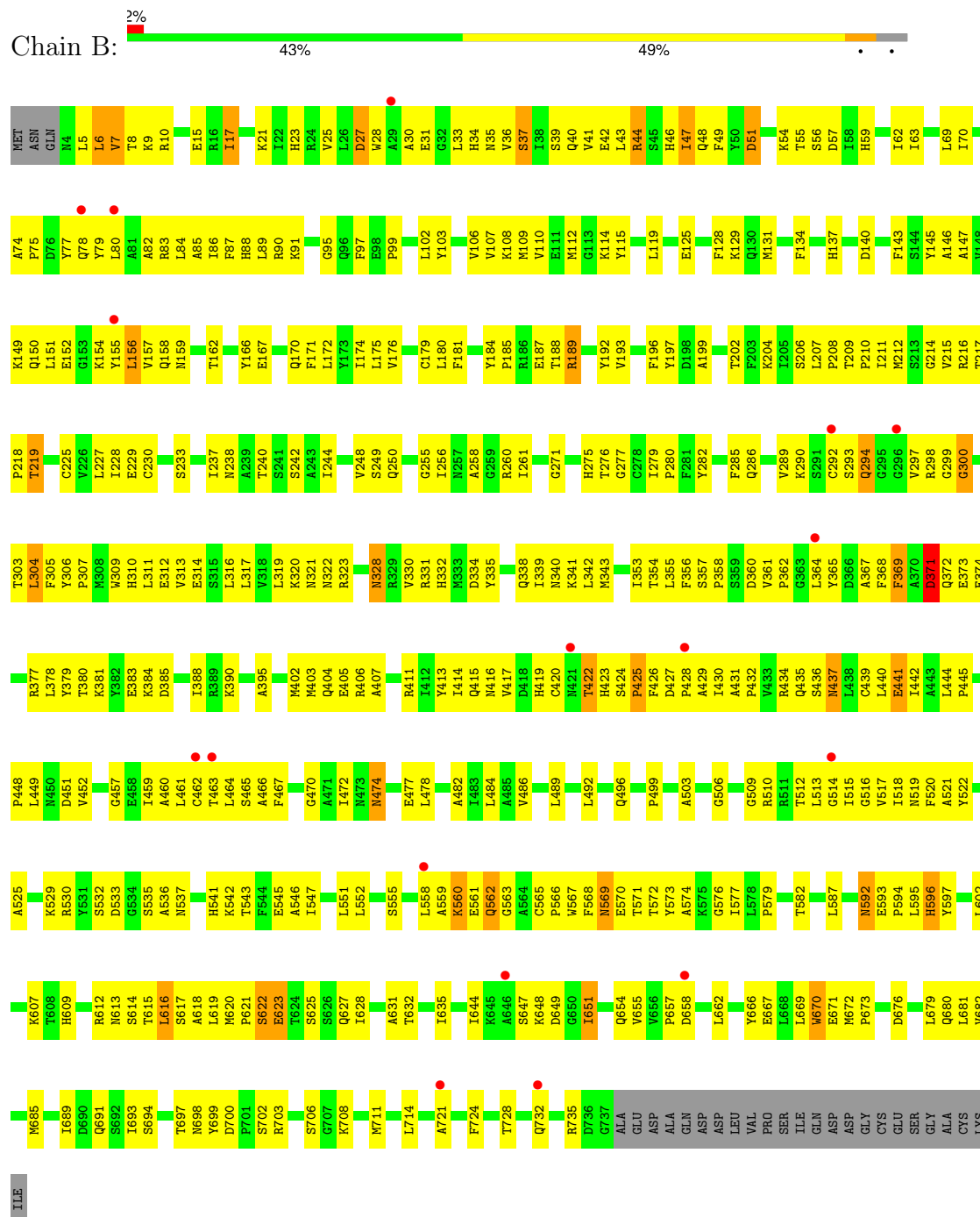
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

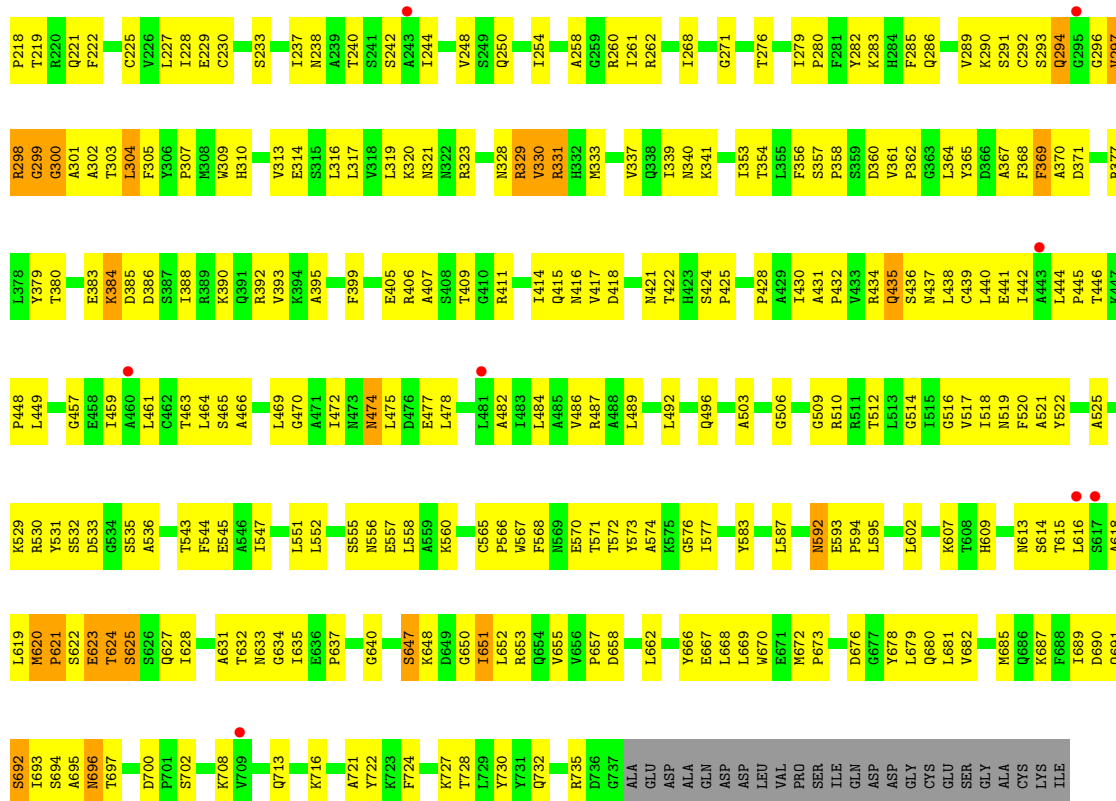
- Molecule 1: Ribonucleoside-diphosphate reductase 1 subunit alpha



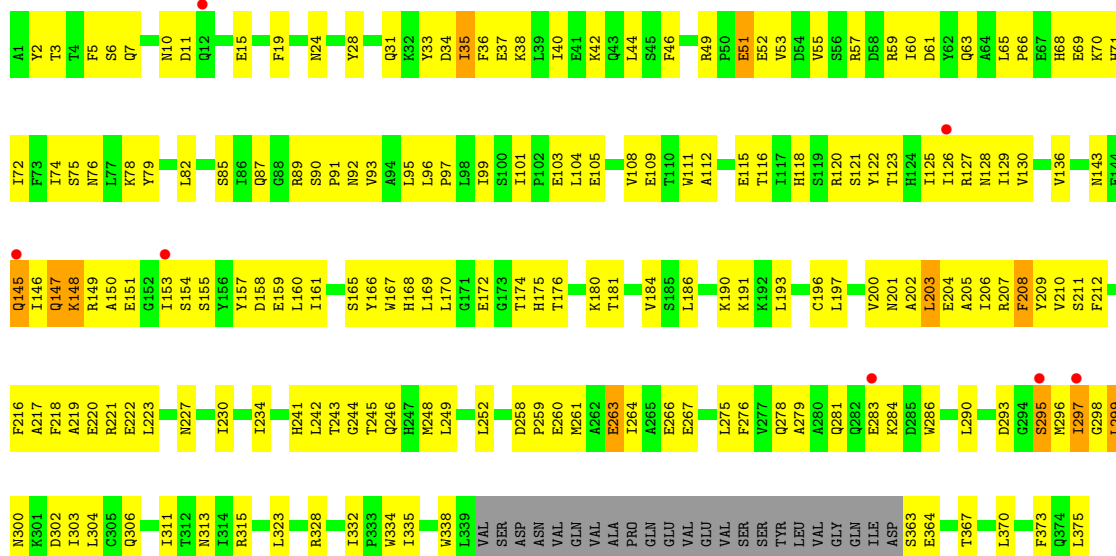
PRO
SER
ILE
GLN
ASP
ASP
GLY
CYS
GLU
SER
GLY
ALA
CYS
LYS
ILE

● Molecule 1: Ribonucleoside-diphosphate reductase 1 subunit alpha

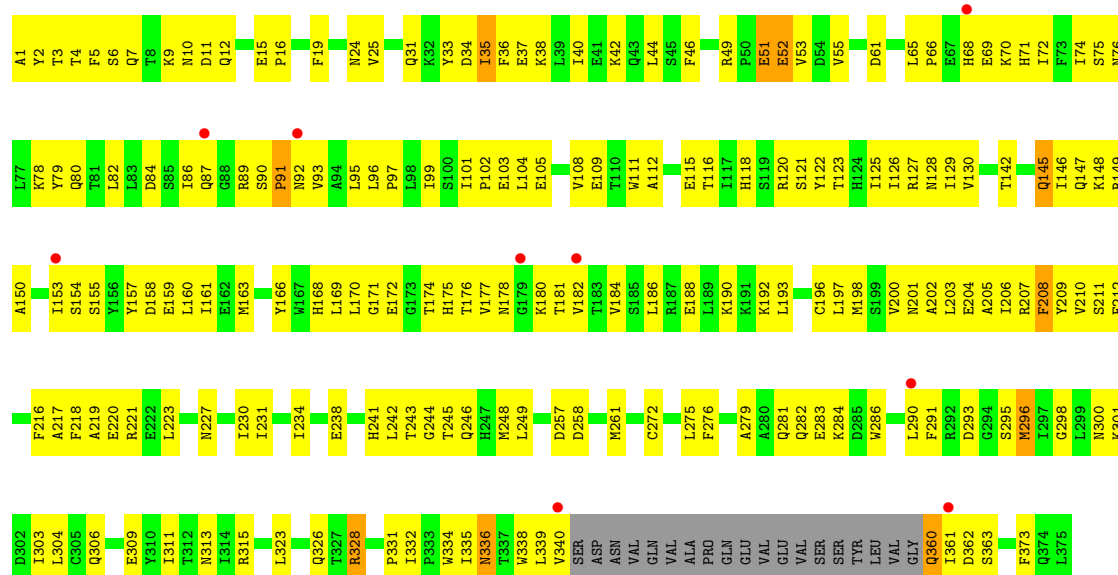




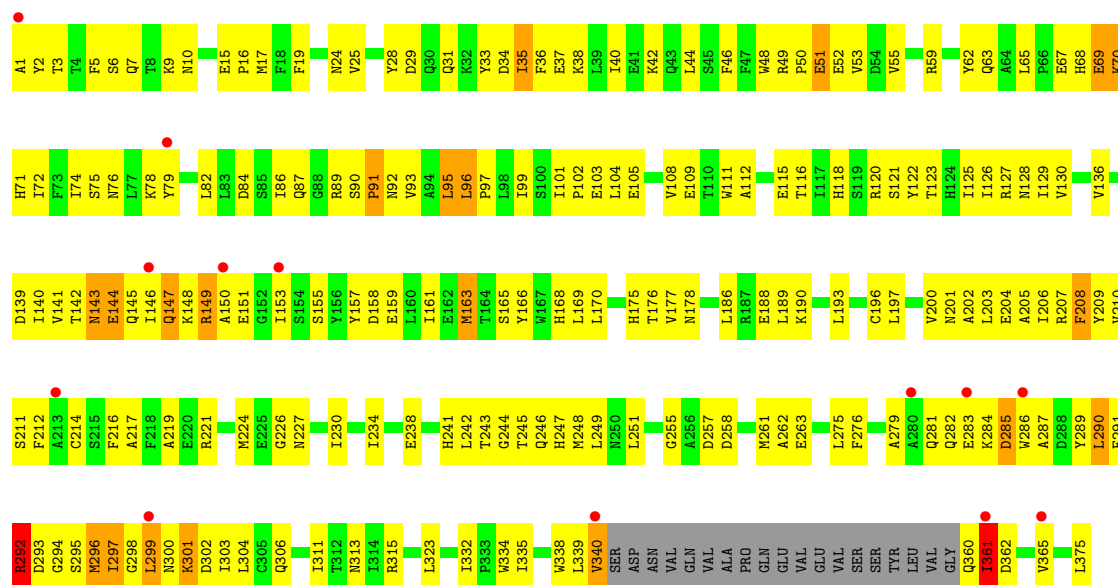
Chain E: 2% 43% 47% 6%



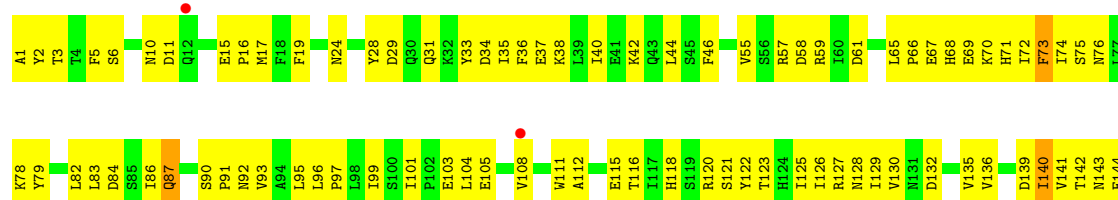
Chain F: 2% 43% 50% 5%



• Molecule 2: Ribonucleoside-diphosphate reductase 1 subunit beta



• Molecule 2: Ribonucleoside-diphosphate reductase 1 subunit beta



Q145	R221	C304	Q305	E222	L223	Q306	T307	V308	I146	K148	R149	A150	E151	G152	I153	S154	S155	Y156	Y157	D158	E159	L160	I161	E162	M163	H168	L169	L170	H175	T176	V177	V182	L186	K190	K191	K192	L193	C196	L197	V200	N201	A202	L203	E204	A205	I206	R207	F208	Y209	S211	F212	A213	G214	S215	F216	A219	E220
I147	M224	E225	Q226	N227	A228	K229	L230	I234	Q235	R236	H241	L242	T243	G244	T245	Q246	H247	M248	L249	N250	L251	D257	D258	M261	L275	Q278	A279	A280	Q281	Q282	E283	K284	D285	W286	A287	D288	Y289	L290	F291	R292	D293	G294	S295	W296	L297	G298	L299	N300	K301	D302	I303						
I311	T312	N313	I314	R315	L323	Q326	T327	R328	P331	I332	F333	W334	I335	W338	L339	V340	S341	ASP	ASN	VAL	GLN	VAL	ALA	PRO	GLN	GLU	VAL	GLU	VAL	SER	SER	TYR	LEU	VAL	GLY	GLN	I361	D362	S363	E364	V365	L375															

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	280.47Å 155.74Å 166.92Å 90.00° 119.07° 90.00°	Depositor
Resolution (Å)	30.00 – 3.95 30.00 – 3.95	Depositor EDS
% Data completeness (in resolution range)	96.1 (30.00-3.95) 95.9 (30.00-3.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.62 (at 3.98Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.259 , 0.284 0.240 , 0.261	Depositor DCC
R_{free} test set	2527 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å ²)	95.3	Xtriage
Anisotropy	0.470	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 64.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	35345	wwPDB-VP
Average B, all atoms (Å ²)	111.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.55% 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: DAT, FEO, MG, DTP

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	0.32	1/5969 (0.0%)	0.81	20/8085 (0.2%)
1	B	0.31	1/5973 (0.0%)	0.79	11/8090 (0.1%)
1	C	0.31	0/5949	0.78	13/8057 (0.2%)
1	D	0.30	1/5965 (0.0%)	0.76	8/8079 (0.1%)
2	E	0.36	2/2949 (0.1%)	0.76	3/3998 (0.1%)
2	F	0.28	0/2981	0.72	2/4042 (0.0%)
2	G	0.30	0/2981	0.73	0/4042
2	H	0.30	0/2978	0.80	6/4038 (0.1%)
All	All	0.31	5/35745 (0.0%)	0.78	63/48431 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	203	LEU	C-N	9.06	1.47	1.33
2	E	207	ARG	C-N	-6.29	1.25	1.33
1	B	48	GLN	C-N	5.92	1.41	1.33
1	A	48	GLN	C-N	5.91	1.41	1.33
1	D	48	GLN	C-N	5.87	1.41	1.33

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	303	ILE	N-CA-C	14.37	124.21	110.42
2	H	141	VAL	N-CA-C	9.76	120.28	110.82
1	A	372	GLN	N-CA-C	8.28	120.38	111.36
2	E	203	LEU	CA-C-N	-7.39	108.12	120.68
2	E	203	LEU	C-N-CA	-7.39	108.12	120.68

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5841	0	5767	518	0
1	B	5845	0	5770	521	0
1	C	5821	0	5742	503	0
1	D	5837	0	5764	479	0
2	E	2885	0	2813	215	0
2	F	2917	0	2845	247	0
2	G	2917	0	2845	293	0
2	H	2914	0	2842	240	0
3	A	60	0	22	1	0
3	B	60	0	22	8	0
3	C	60	0	22	10	0
3	D	60	0	22	9	0
4	A	26	0	12	3	0
4	B	26	0	12	1	0
4	C	26	0	12	5	0
4	D	26	0	12	9	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	E	3	0	0	0	0
6	F	3	0	0	0	0
6	G	3	0	0	0	0
6	H	3	0	0	0	0
7	E	2	0	0	1	0
7	F	2	0	0	1	0
7	G	2	0	0	0	0
7	H	2	0	0	1	0
All	All	35345	0	34524	2901	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 42.

The worst 5 of 2901 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:B:354:THR:HG21	1:B:356:PHE:CZ	1.44	1.52
1:A:646:ALA:HB2	1:A:651:ILE:CG2	1.40	1.52
1:A:646:ALA:CB	1:A:651:ILE:HG22	1.41	1.46
1:A:297:VAL:CG1	1:A:298:ARG:HG2	1.50	1.41
1:A:53:ILE:HD11	1:A:58:ILE:CD1	1.50	1.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	731/761 (96%)	687 (94%)	40 (6%)	4 (0%)	24	60
1	B	732/761 (96%)	693 (95%)	37 (5%)	2 (0%)	36	69
1	C	729/761 (96%)	690 (95%)	36 (5%)	3 (0%)	30	65
1	D	731/761 (96%)	694 (95%)	33 (4%)	4 (0%)	24	60
2	E	348/375 (93%)	336 (97%)	12 (3%)	0	100	100
2	F	352/375 (94%)	338 (96%)	13 (4%)	1 (0%)	36	69
2	G	352/375 (94%)	336 (96%)	13 (4%)	3 (1%)	14	48
2	H	352/375 (94%)	339 (96%)	13 (4%)	0	100	100
All	All	4327/4544 (95%)	4113 (95%)	197 (5%)	17 (0%)	30	65

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	GLY
1	A	300	GLY
1	B	300	GLY
1	C	299	GLY
1	C	300	GLY

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	629/651 (97%)	601 (96%)	28 (4%)	24	48
1	B	629/651 (97%)	597 (95%)	32 (5%)	21	46
1	C	626/651 (96%)	594 (95%)	32 (5%)	21	46
1	D	628/651 (96%)	596 (95%)	32 (5%)	21	46
2	E	319/340 (94%)	305 (96%)	14 (4%)	25	49
2	F	323/340 (95%)	312 (97%)	11 (3%)	32	55
2	G	323/340 (95%)	297 (92%)	26 (8%)	11	35
2	H	323/340 (95%)	312 (97%)	11 (3%)	32	55
All	All	3800/3964 (96%)	3614 (95%)	186 (5%)	22	47

5 of 186 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	592	ASN
2	F	296	MET
1	D	647	SER
2	E	208	PHE
2	G	51	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 159 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	31	GLN
2	G	336	ASN
2	F	124	HIS
2	G	21	GLN
2	H	145	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 20 ligands modelled in this entry, 4 are monoatomic - leaving 16 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$
6	FEO	E	501	2,7	0,2,2	-	-	-		
4	DAT	C	802	-	27,28,28	2.05	11 (40%)	41,43,43	1.98	10 (24%)
6	FEO	F	501	2,7	0,2,2	-	-	-		
4	DAT	B	802	-	27,28,28	1.99	10 (37%)	41,43,43	2.03	10 (24%)
4	DAT	A	802	-	27,28,28	1.99	11 (40%)	41,43,43	2.22	12 (29%)
3	DTP	D	801	-	31,32,32	1.75	6 (19%)	46,50,50	1.73	10 (21%)
6	FEO	G	501	2,7	0,2,2	-	-	-		
3	DTP	B	803	5	31,32,32	1.73	6 (19%)	46,50,50	1.72	10 (21%)
3	DTP	C	803	5	31,32,32	1.72	6 (19%)	46,50,50	1.72	10 (21%)
3	DTP	C	801	-	31,32,32	1.75	6 (19%)	46,50,50	1.73	10 (21%)
4	DAT	D	802	-	27,28,28	1.99	10 (37%)	41,43,43	1.97	12 (29%)
3	DTP	A	803	5	31,32,32	1.72	6 (19%)	46,50,50	1.68	10 (21%)
6	FEO	H	501	2,7	0,2,2	-	-	-		
3	DTP	D	803	5	31,32,32	1.73	7 (22%)	46,50,50	1.73	10 (21%)
3	DTP	B	801	-	31,32,32	1.78	8 (25%)	46,50,50	1.73	10 (21%)
3	DTP	A	801	-	31,32,32	1.75	6 (19%)	46,50,50	1.73	10 (21%)

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
4	DAT	C	802	-	-	3/16/28/28	0/3/3/3
4	DAT	B	802	-	-	9/16/28/28	0/3/3/3
4	DAT	A	802	-	-	1/16/28/28	0/3/3/3
3	DTP	D	801	-	-	4/22/34/34	0/3/3/3
3	DTP	B	803	5	-	1/22/34/34	0/3/3/3
3	DTP	C	803	5	-	4/22/34/34	0/3/3/3
3	DTP	C	801	-	-	4/22/34/34	0/3/3/3
4	DAT	D	802	-	-	5/16/28/28	0/3/3/3
3	DTP	A	803	5	-	1/22/34/34	0/3/3/3
3	DTP	D	803	5	-	4/22/34/34	0/3/3/3
3	DTP	B	801	-	-	6/22/34/34	0/3/3/3
3	DTP	A	801	-	-	4/22/34/34	0/3/3/3

The worst 5 of 93 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	802	DAT	PA-O3A	-5.75	1.53	1.59
4	C	802	DAT	PA-O3A	-5.67	1.53	1.59
4	B	802	DAT	PA-O3A	-5.62	1.53	1.59
4	D	802	DAT	PA-O3A	-5.62	1.53	1.59
3	A	803	DTP	C6-N6	5.06	1.47	1.34

The worst 5 of 124 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	802	DAT	O4'-C1'-N9	7.04	120.60	107.96
4	D	802	DAT	C5-C4-N3	-5.49	119.16	126.72
4	C	802	DAT	C5-C4-N3	-5.46	119.19	126.72
4	A	802	DAT	C5-C4-N3	-5.44	119.23	126.72
4	B	802	DAT	C5-C4-N3	-5.40	119.28	126.72

There are no chirality outliers.

5 of 46 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	801	DTP	C5'-O5'-PA-O1A
3	A	801	DTP	C5'-O5'-PA-O2A
3	A	801	DTP	C5'-O5'-PA-O3A

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Mol	Chain	Res	Type	Atoms
3	A	803	DTP	PB-O3B-PG-O3G
3	B	801	DTP	C5'-O5'-PA-O2A

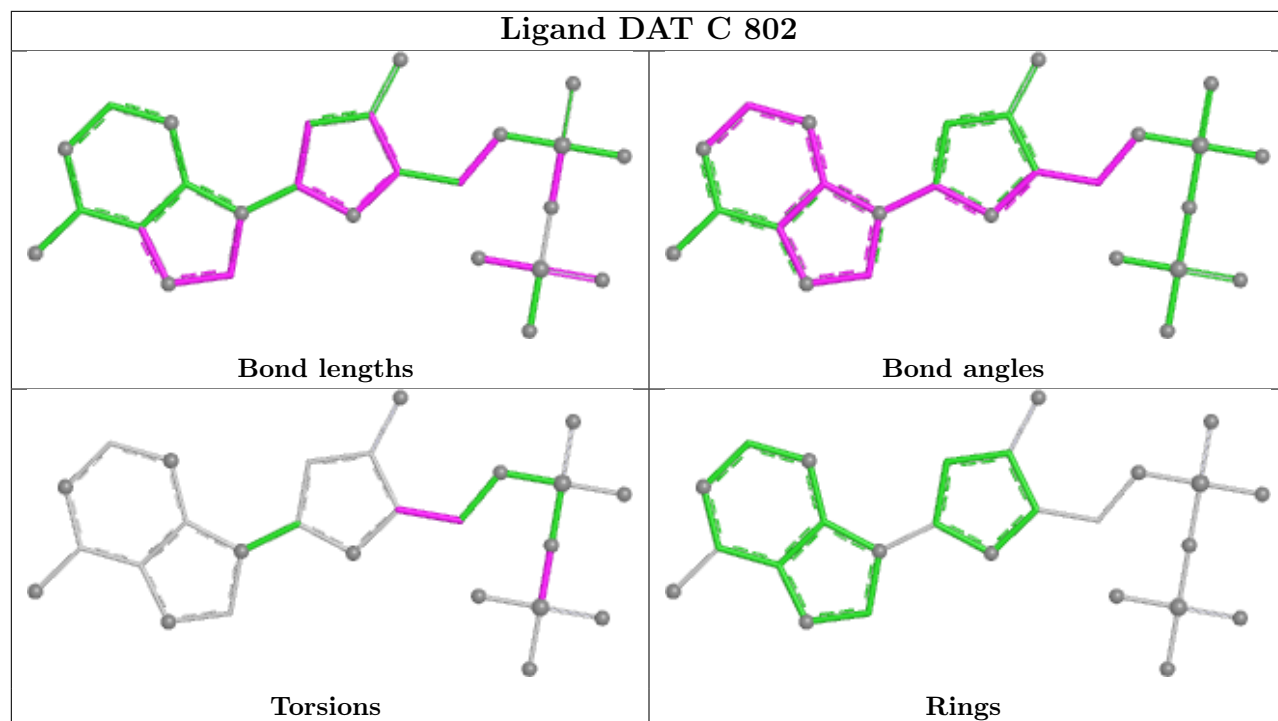
There are no ring outliers.

11 monomers are involved in 46 short contacts:

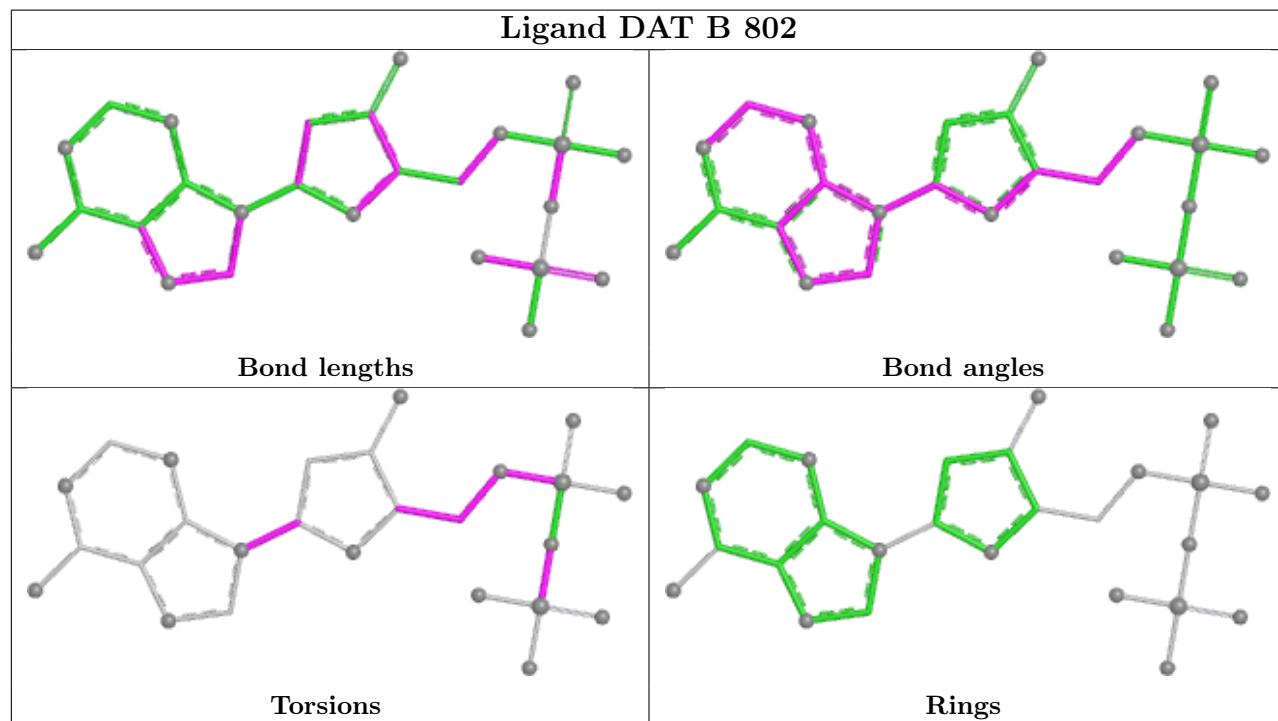
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	802	DAT	5	0
4	B	802	DAT	1	0
4	A	802	DAT	3	0
3	D	801	DTP	5	0
3	B	803	DTP	3	0
3	C	803	DTP	3	0
3	C	801	DTP	7	0
4	D	802	DAT	9	0
3	A	803	DTP	1	0
3	D	803	DTP	4	0
3	B	801	DTP	5	0

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.

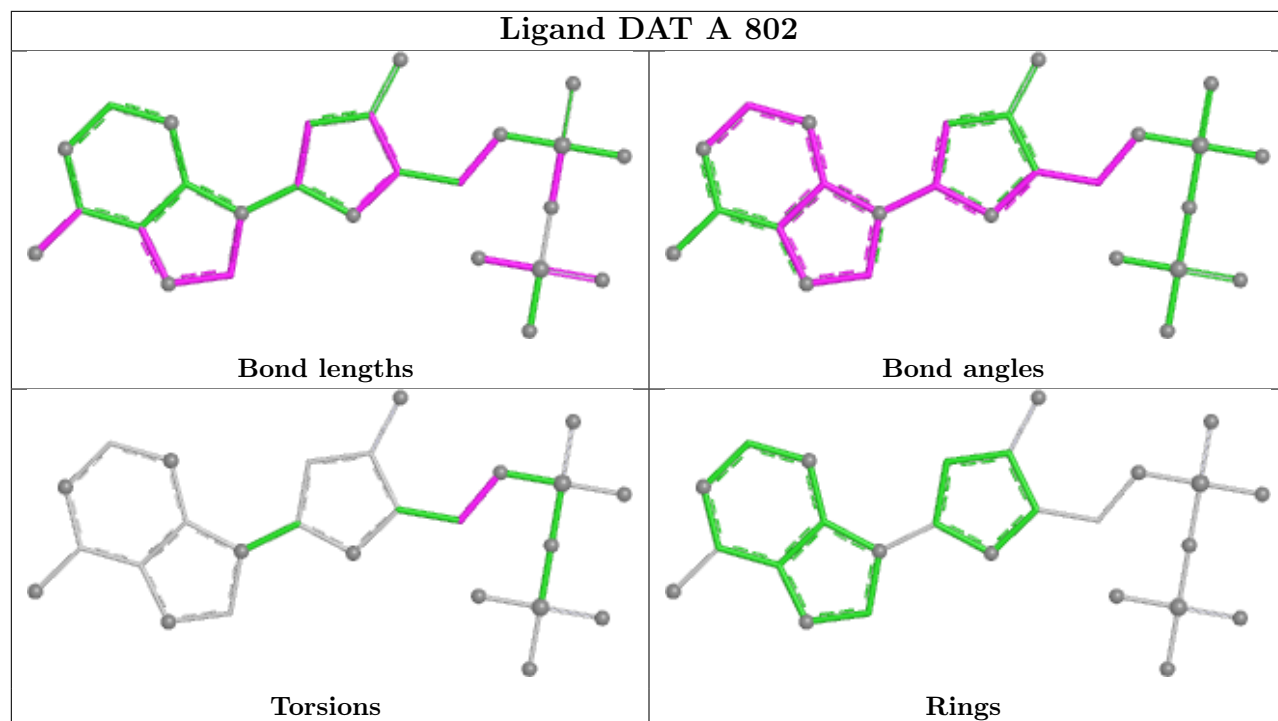
Ligand DAT C 802



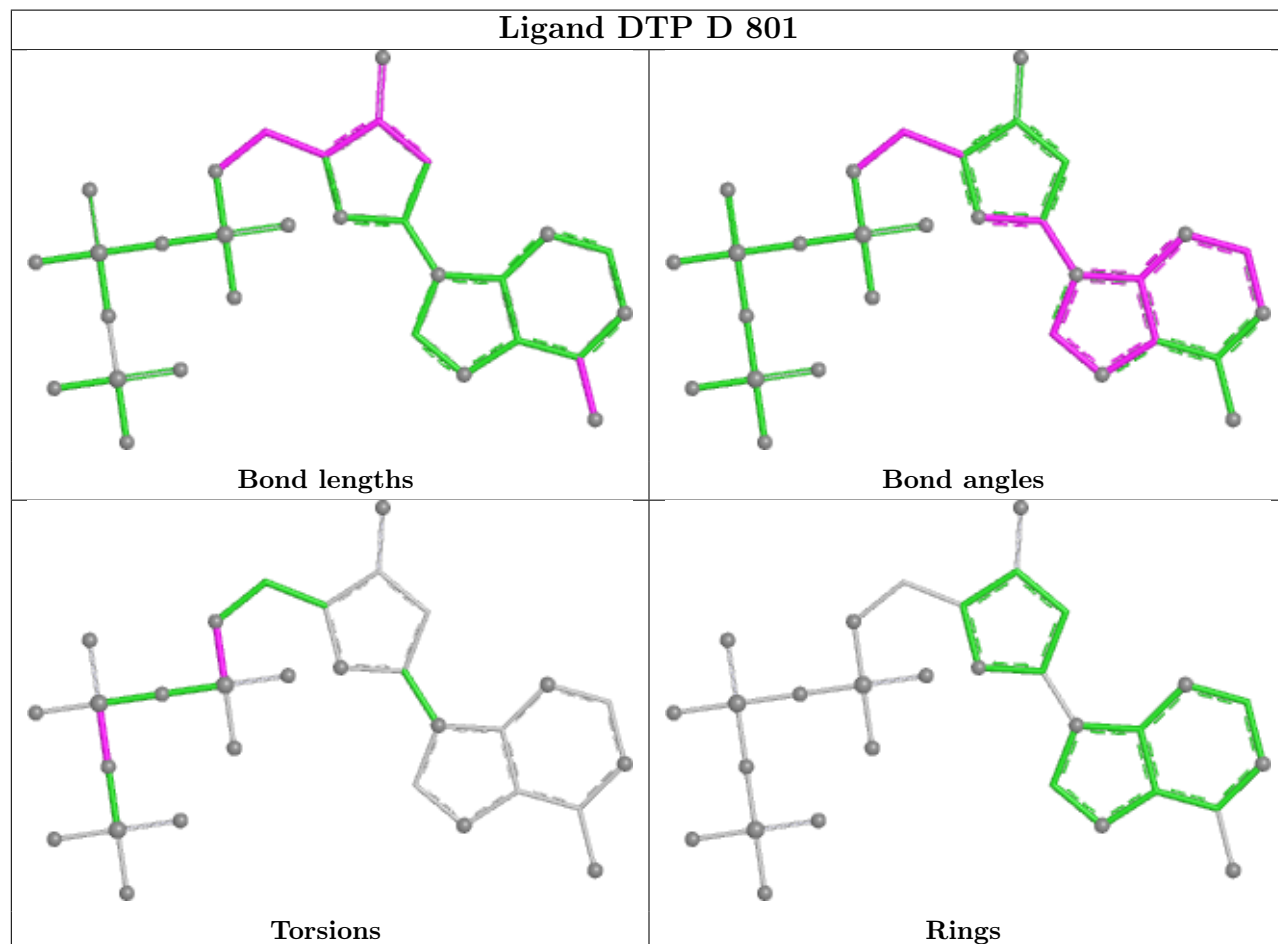
Ligand DAT B 802

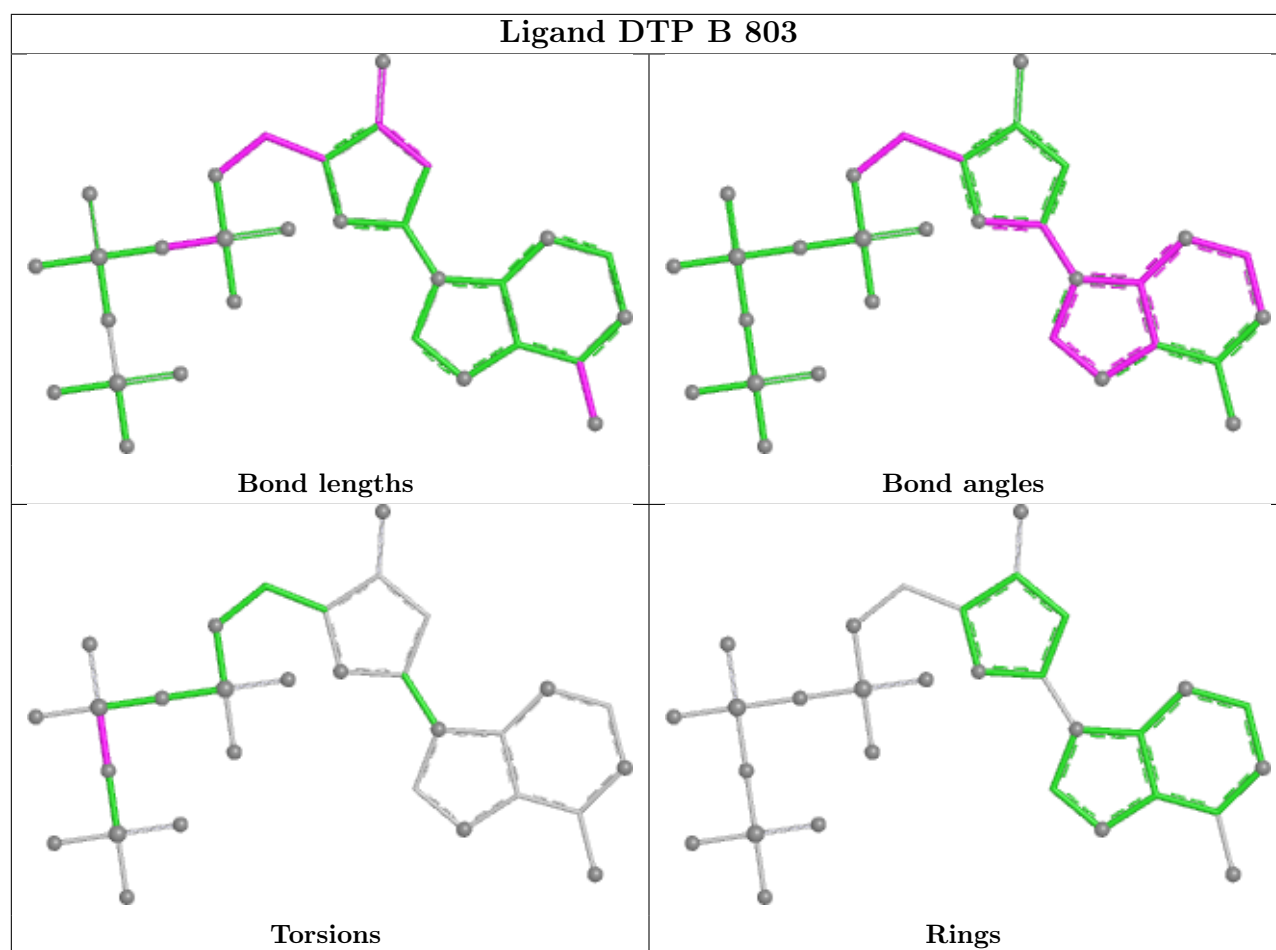


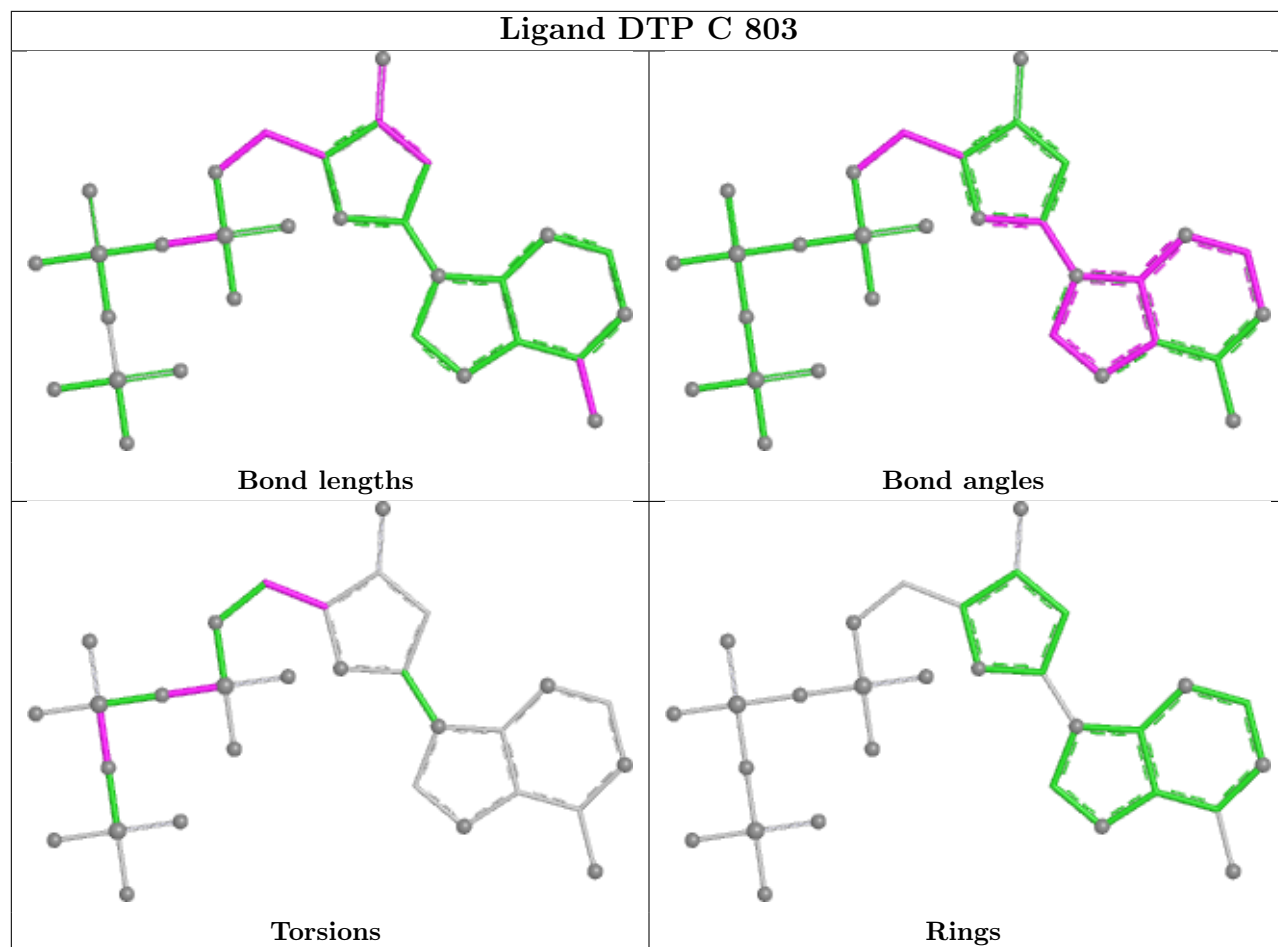
Ligand DAT A 802

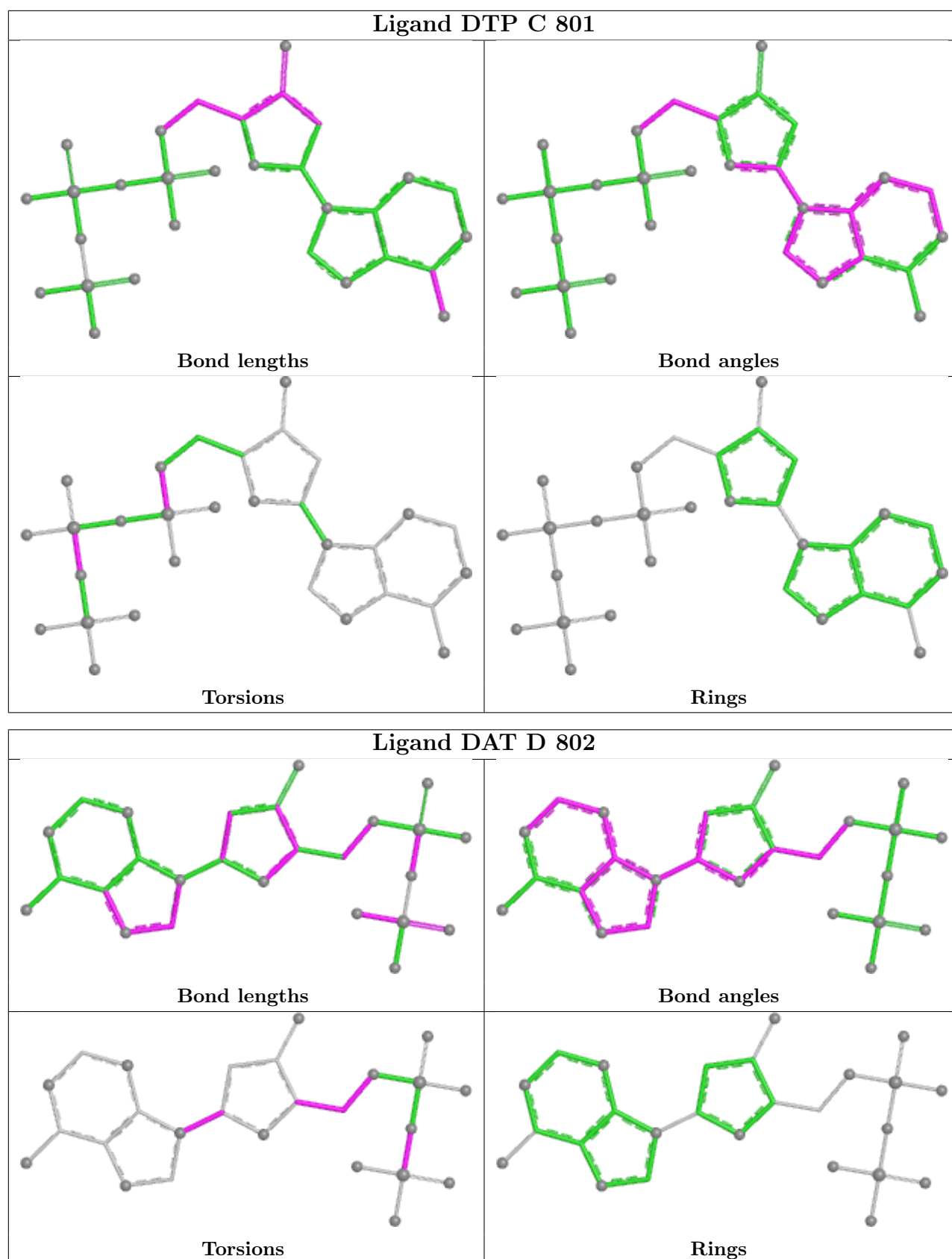


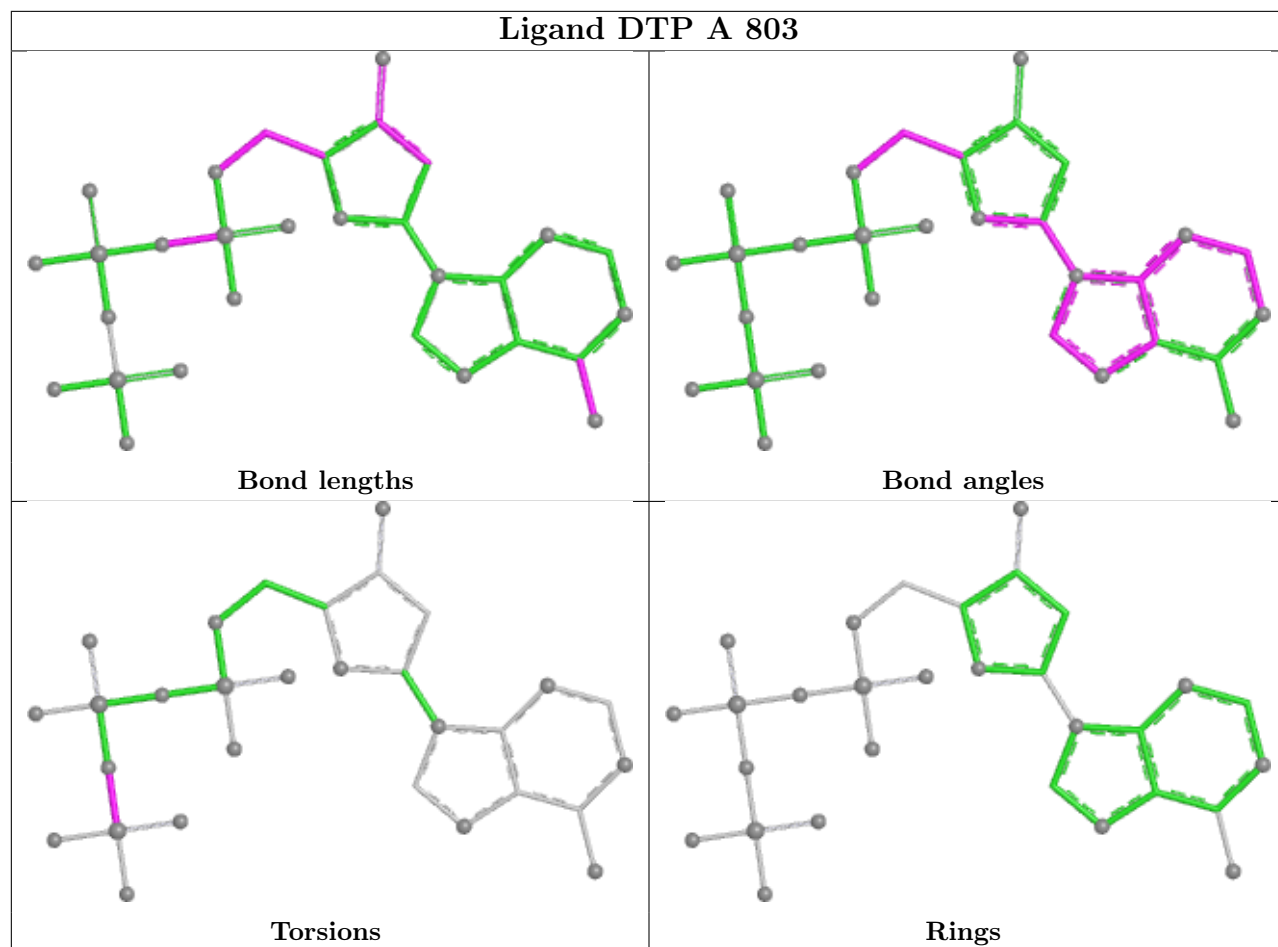
Ligand DTP D 801

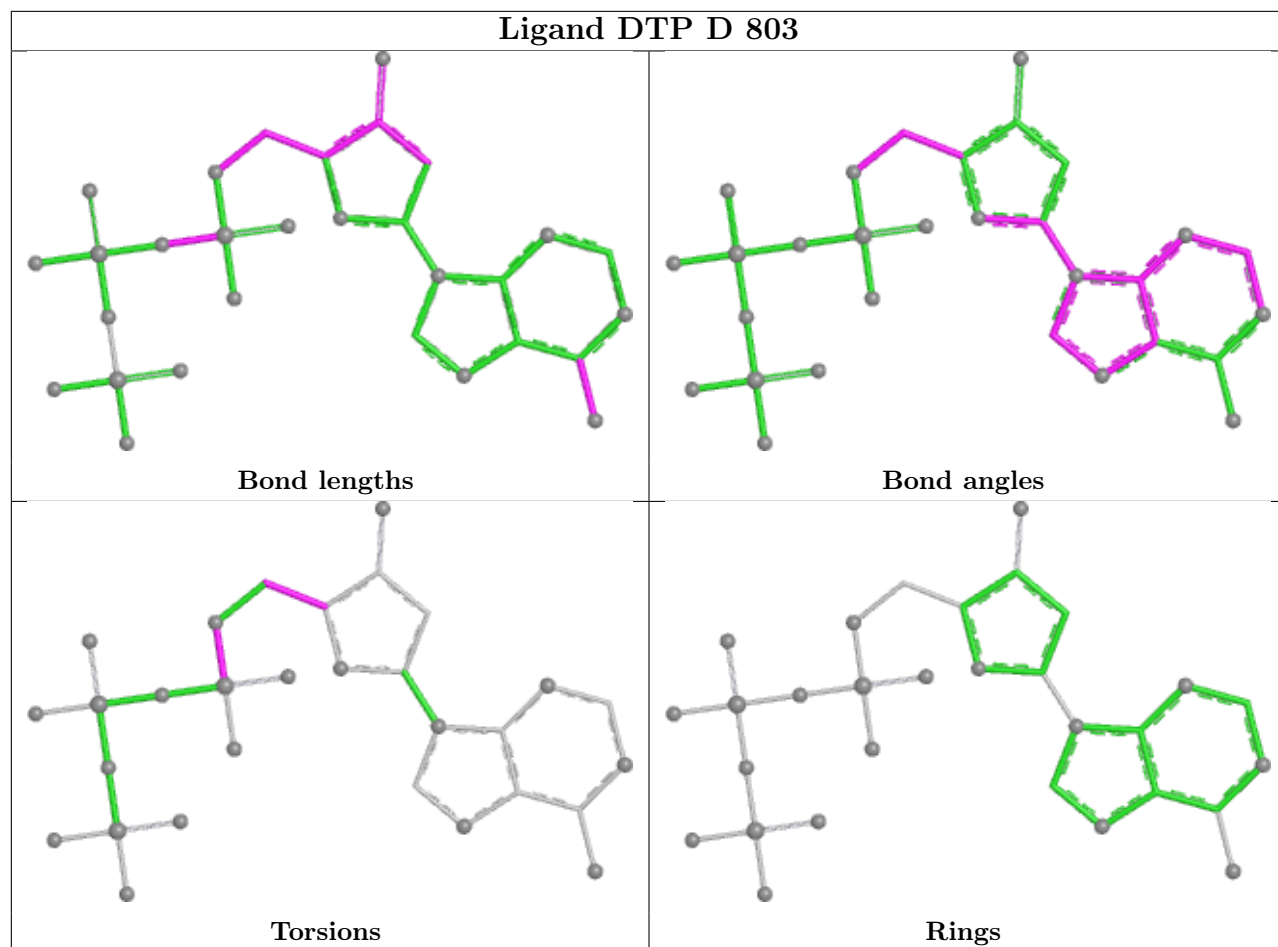


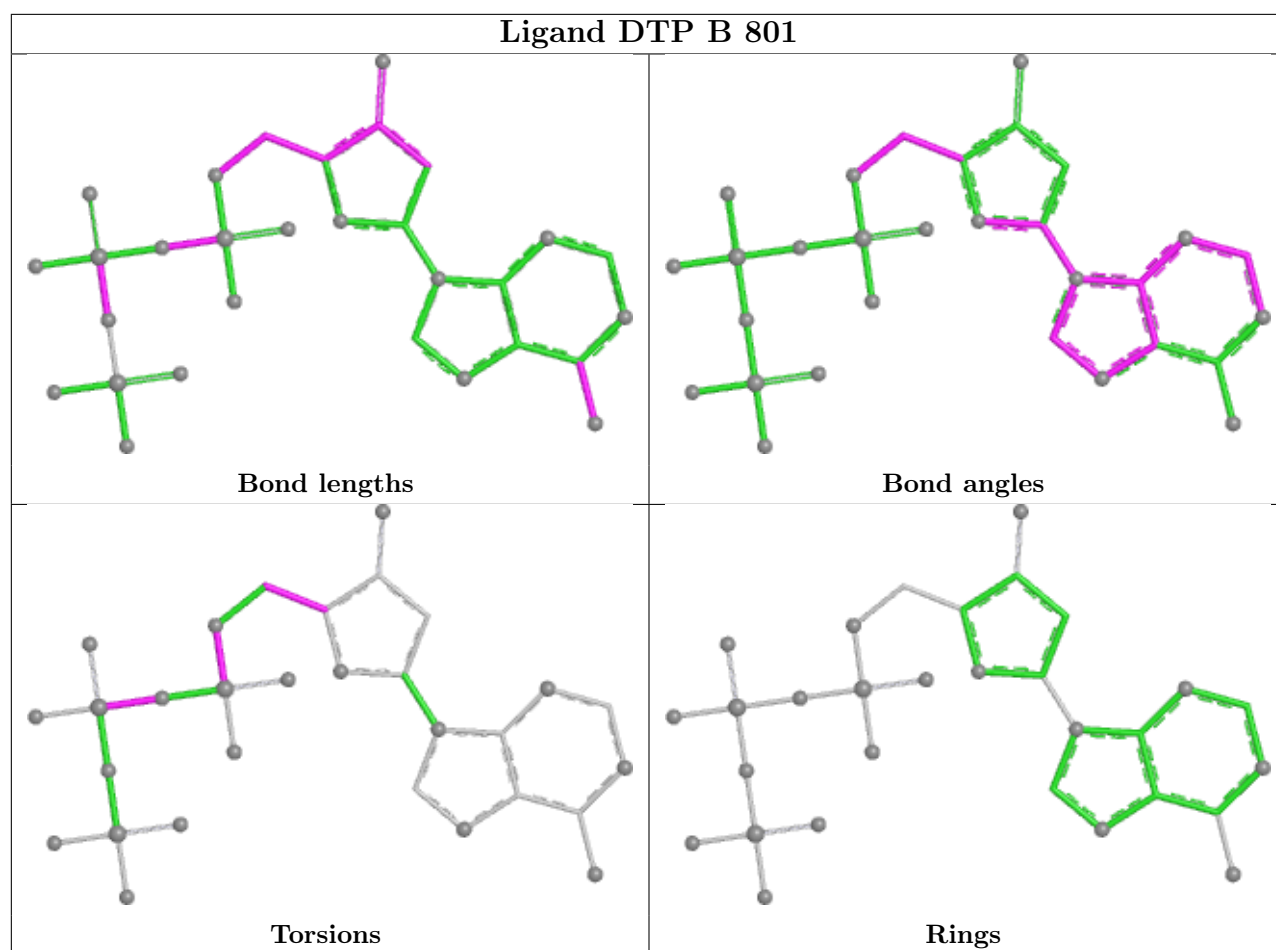


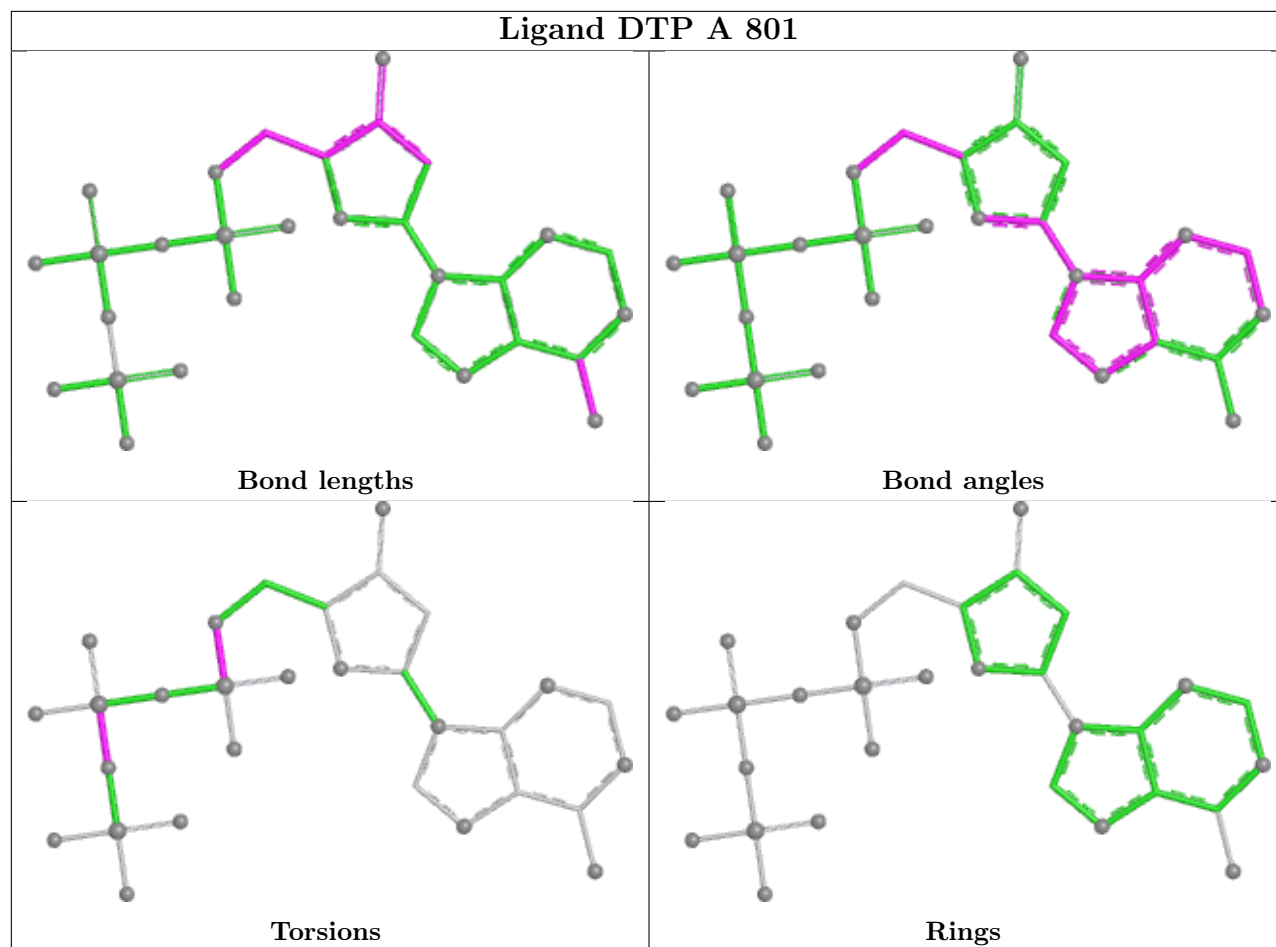












5.7 Other polymers [i](#)

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	733/761 (96%)	0.43	17 (2%) 61 43	56, 95, 121, 142	0
1	B	734/761 (96%)	0.46	17 (2%) 61 43	59, 101, 127, 151	0
1	C	731/761 (96%)	0.50	16 (2%) 62 44	101, 130, 150, 160	0
1	D	733/761 (96%)	0.48	13 (1%) 67 48	89, 128, 151, 163	0
2	E	352/375 (93%)	0.49	7 (1%) 65 46	72, 117, 154, 176	0
2	F	356/375 (94%)	0.47	9 (2%) 58 41	55, 91, 131, 158	0
2	G	356/375 (94%)	0.45	13 (3%) 45 33	59, 97, 145, 192	0
2	H	356/375 (94%)	0.41	11 (3%) 51 36	65, 98, 145, 174	0
All	All	4351/4544 (95%)	0.46	103 (2%) 59 43	55, 110, 146, 192	0

The worst 5 of 103 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	G	153	ILE	4.0
2	F	153	ILE	3.8
1	B	78	GLN	3.6
1	B	292	CYS	3.5
1	A	462	CYS	3.1

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 ⓘ

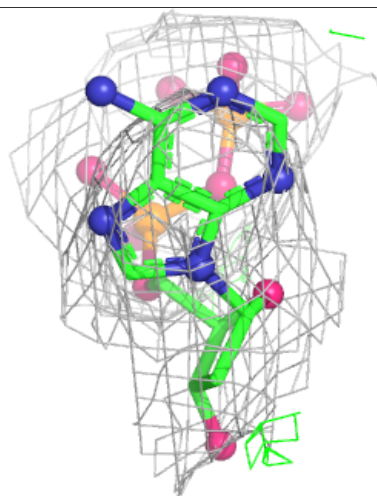
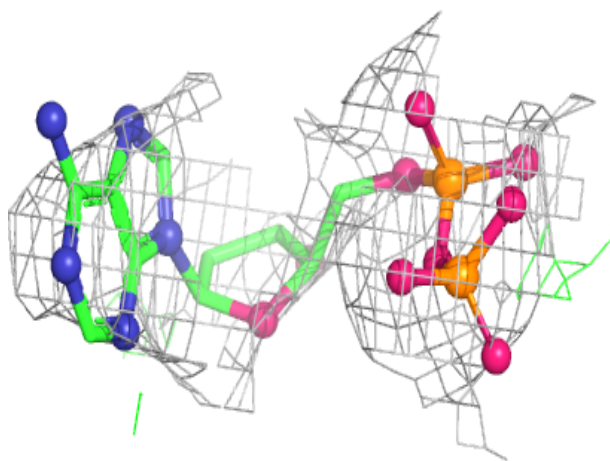
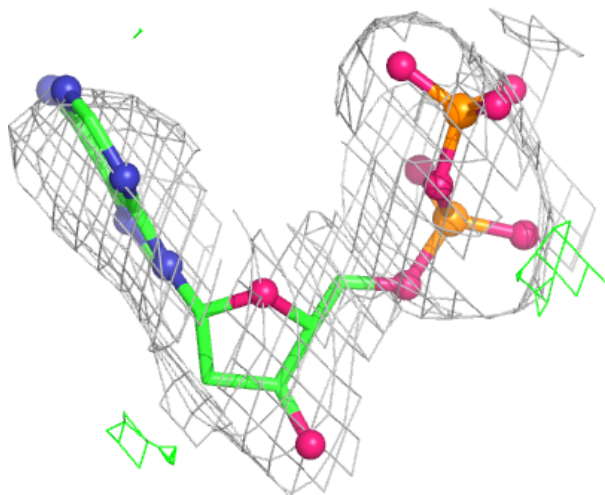
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	MG	A	804	1/1	0.43	0.24	94,94,94,94	0
5	MG	B	804	1/1	0.48	0.21	94,94,94,94	0
5	MG	C	804	1/1	0.51	0.20	123,123,123,123	0
5	MG	D	804	1/1	0.60	0.19	118,118,118,118	0
4	DAT	C	802	26/26	0.76	0.13	156,156,156,156	0
4	DAT	D	802	26/26	0.79	0.14	156,156,156,156	0
4	DAT	B	802	26/26	0.80	0.14	149,149,149,149	0
3	DTP	C	801	30/30	0.81	0.14	175,175,175,175	0
3	DTP	D	801	30/30	0.82	0.15	140,140,140,140	0
4	DAT	A	802	26/26	0.88	0.12	126,126,126,126	0
3	DTP	B	801	30/30	0.89	0.14	111,111,111,111	0
3	DTP	C	803	30/30	0.91	0.07	123,123,123,123	0
3	DTP	A	801	30/30	0.91	0.12	124,124,124,124	0
3	DTP	D	803	30/30	0.92	0.08	118,118,118,118	0
3	DTP	B	803	30/30	0.94	0.07	94,94,94,94	0
3	DTP	A	803	30/30	0.95	0.08	94,94,94,94	0
6	FEO	G	501	3/3	0.98	0.06	78,78,78,78	0
6	FEO	F	501	3/3	0.99	0.05	61,61,61,61	0
6	FEO	E	501	3/3	0.99	0.04	89,89,89,89	0
6	FEO	H	501	3/3	0.99	0.03	69,69,69,69	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.

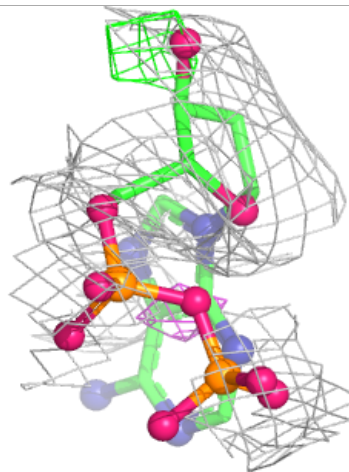
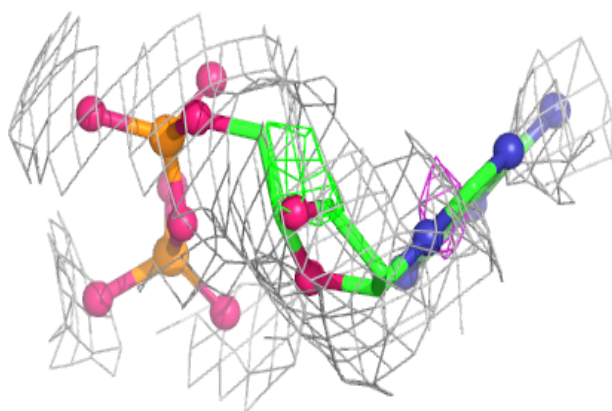
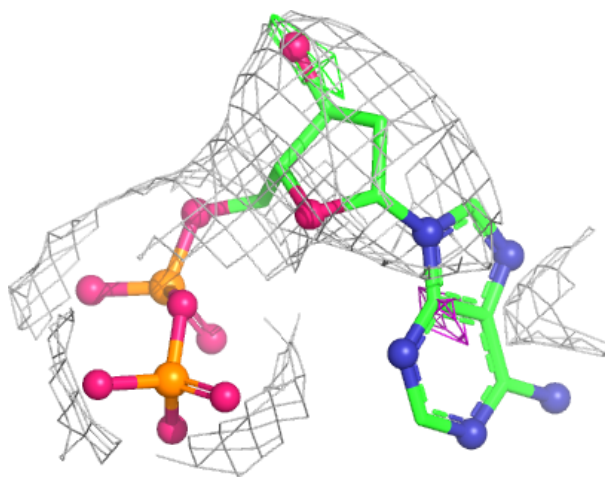
Electron density around DAT C 802:

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



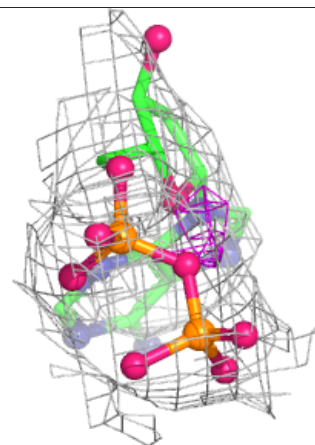
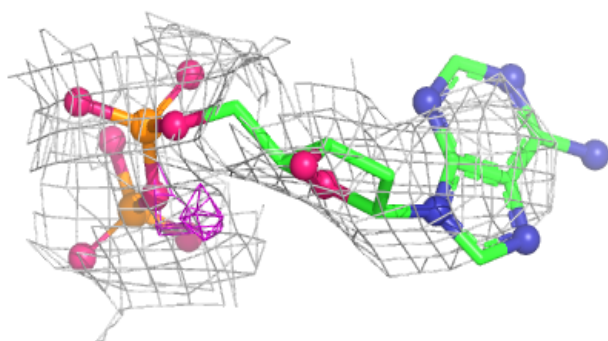
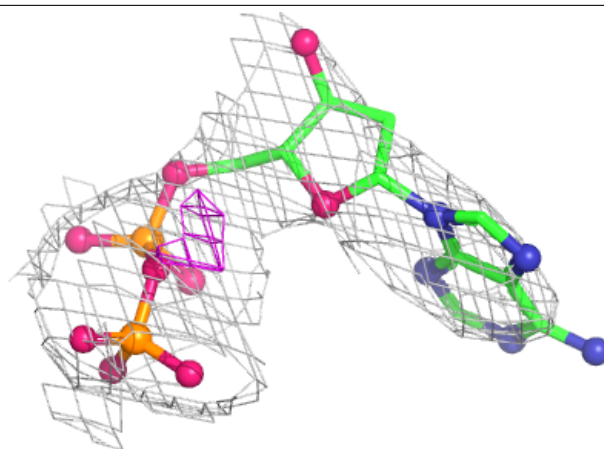
Electron density around DAT D 802:

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and green (positive)



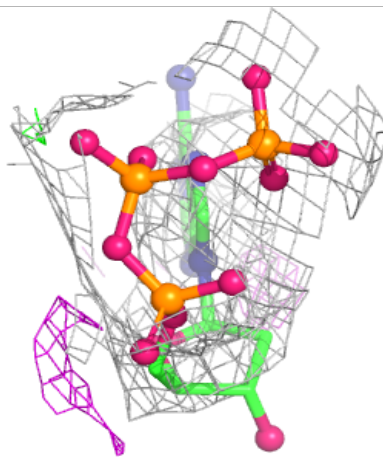
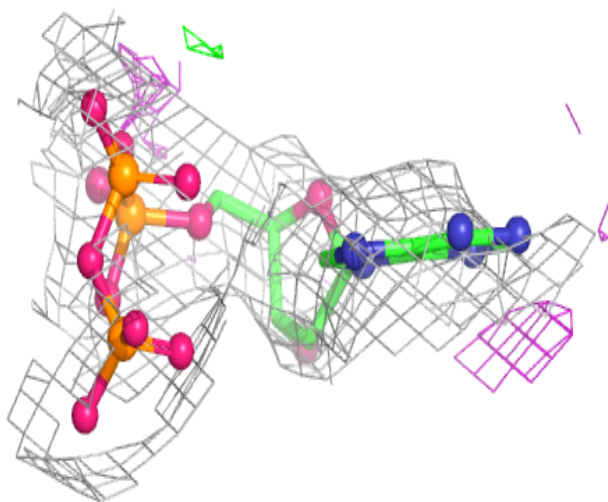
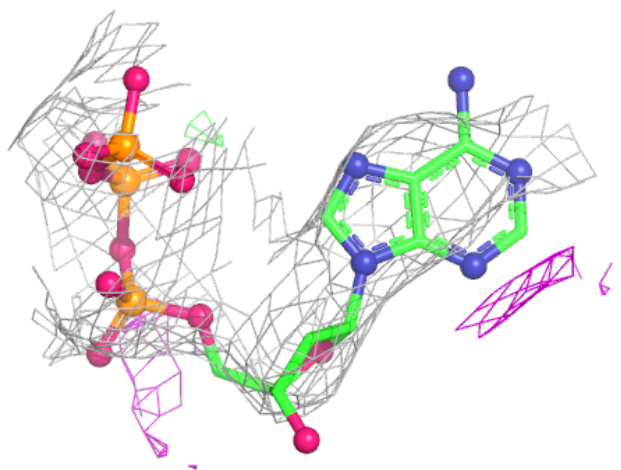
Electron density around DAT B 802:

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



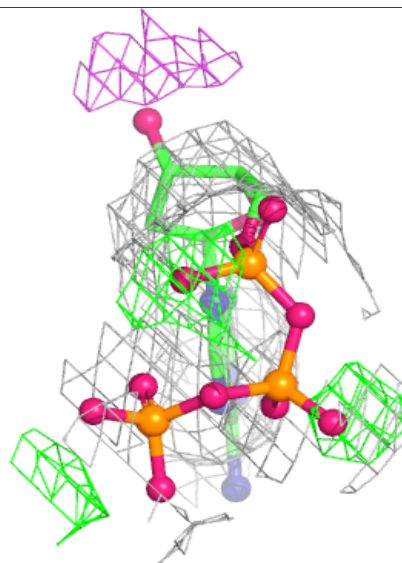
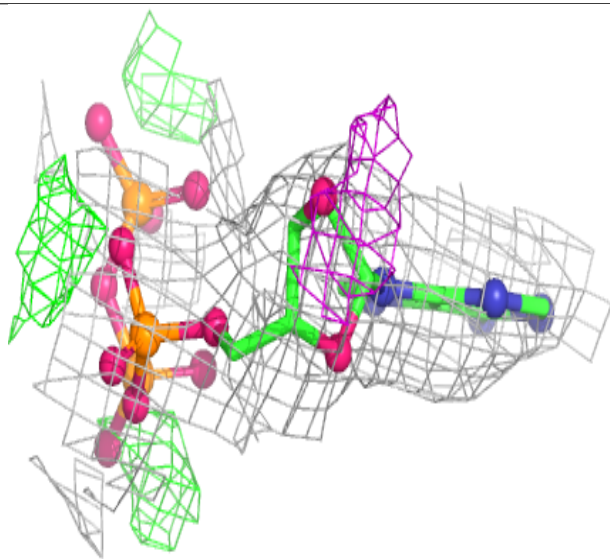
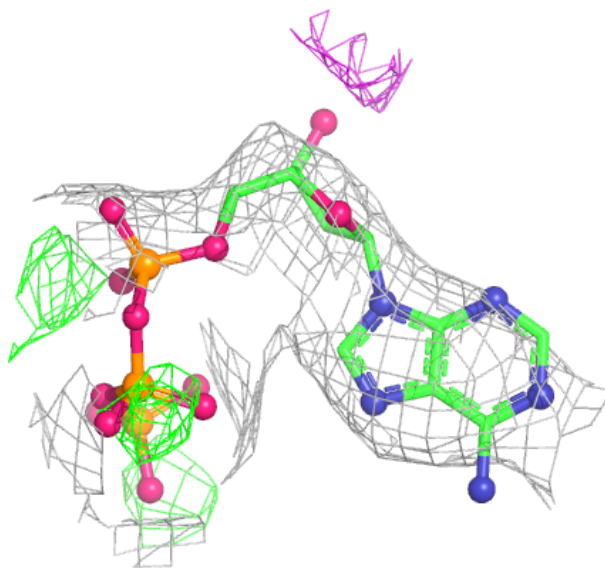
Electron density around DTP C 801:

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



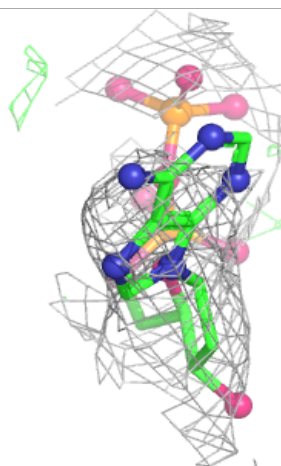
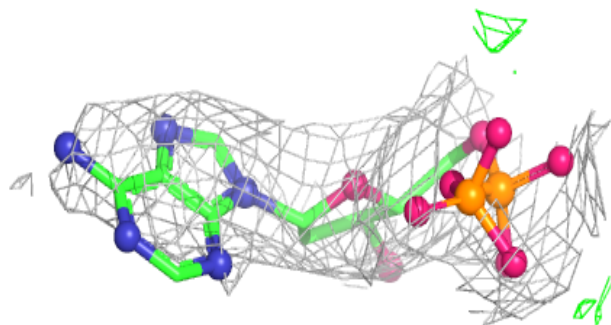
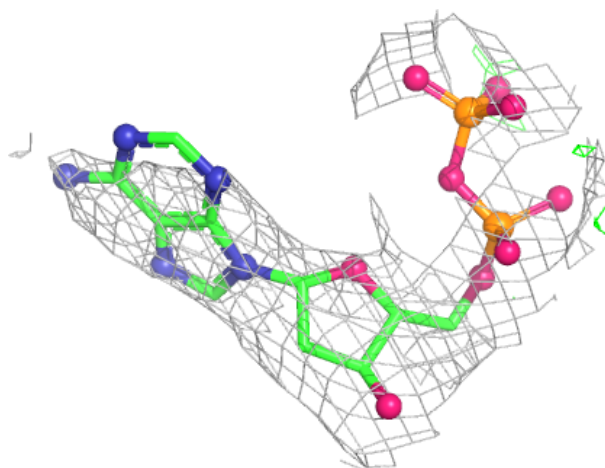
Electron density around DTP D 801:

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and green (positive)



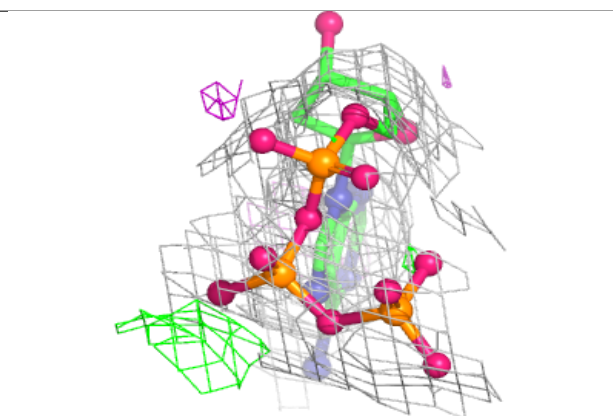
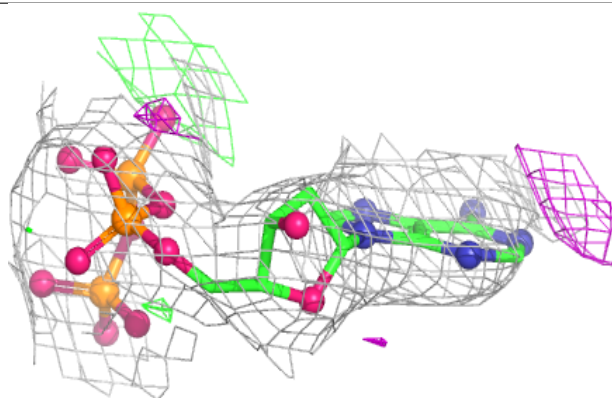
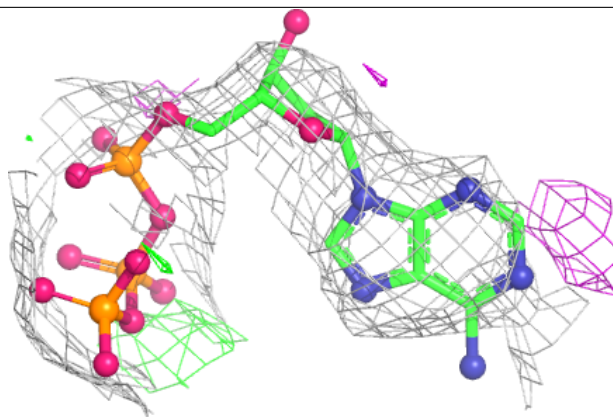
Electron density around DAT A 802:

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and green (positive)

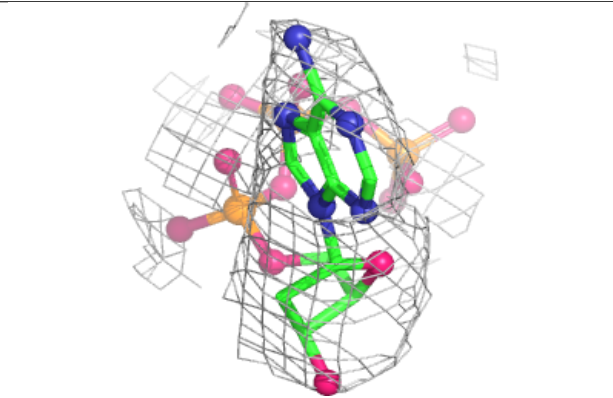
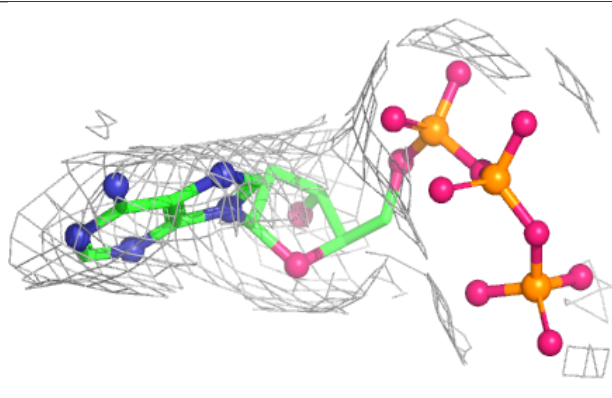
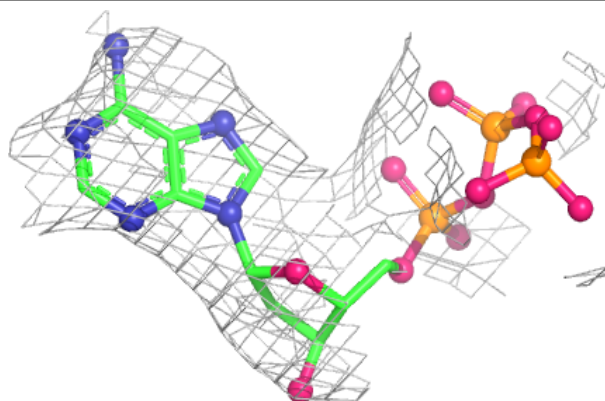


Electron density around DTP B 801:

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and green (positive)

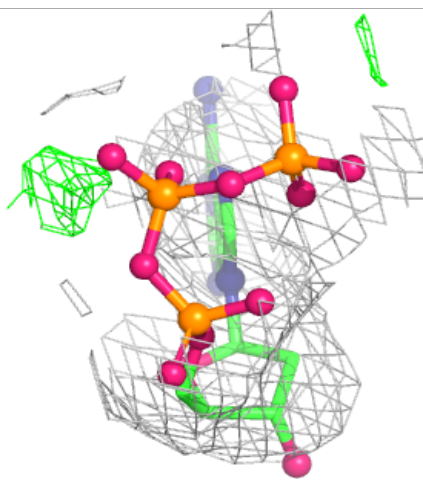
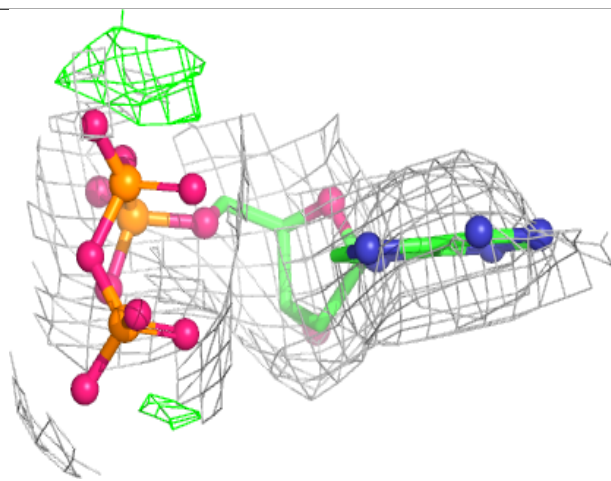
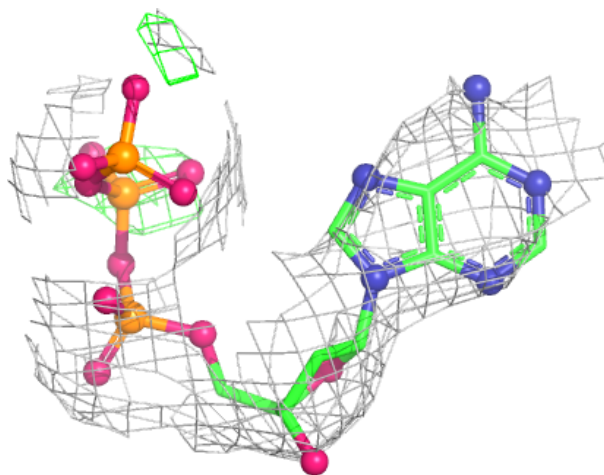
**Electron density around DTP C 803:**

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and green (positive)



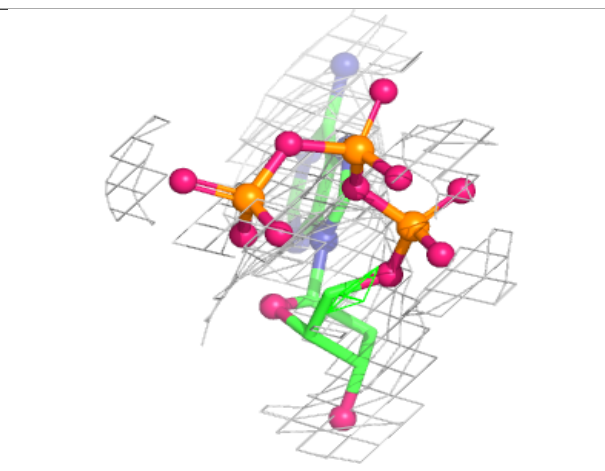
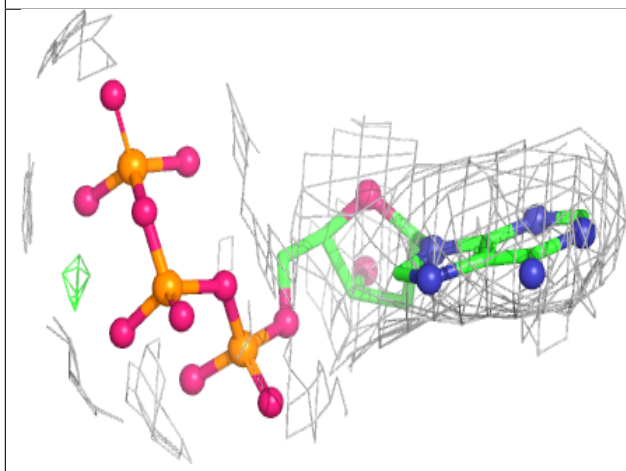
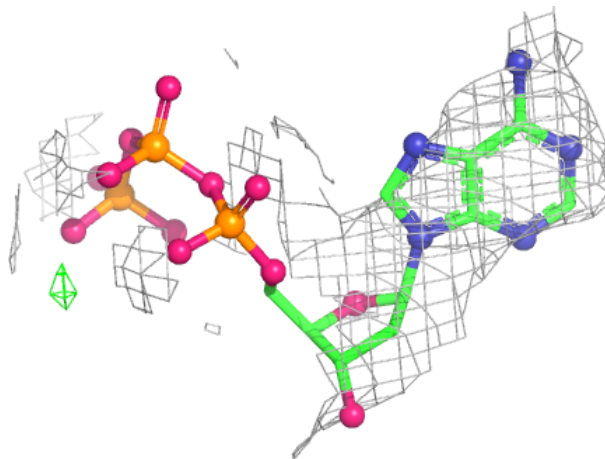
Electron density around DTP A 801:

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and green (positive)



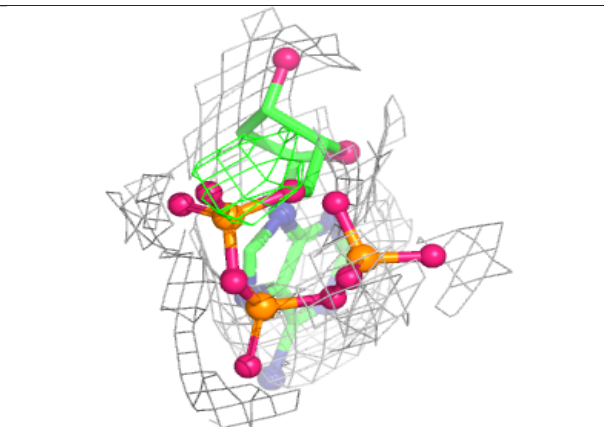
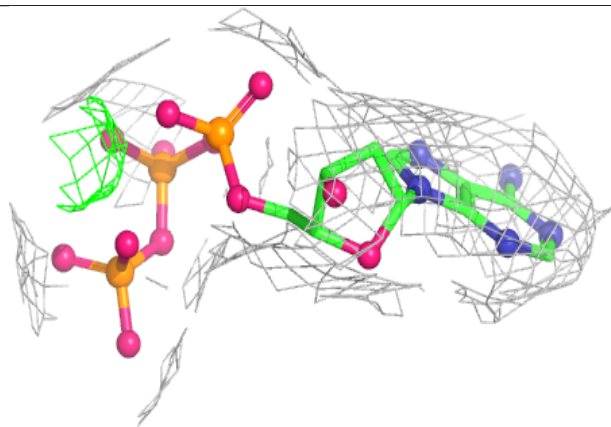
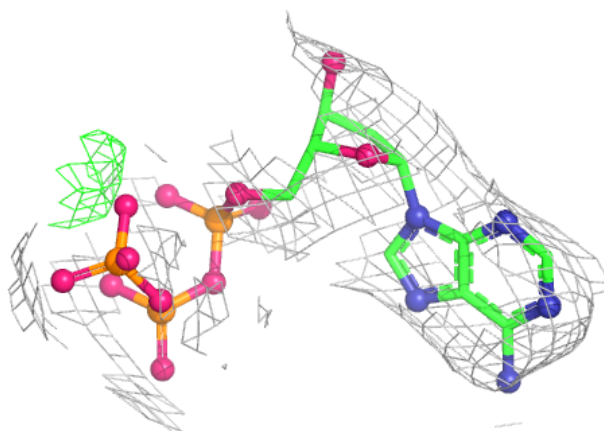
Electron density around DTP D 803:

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and green (positive)

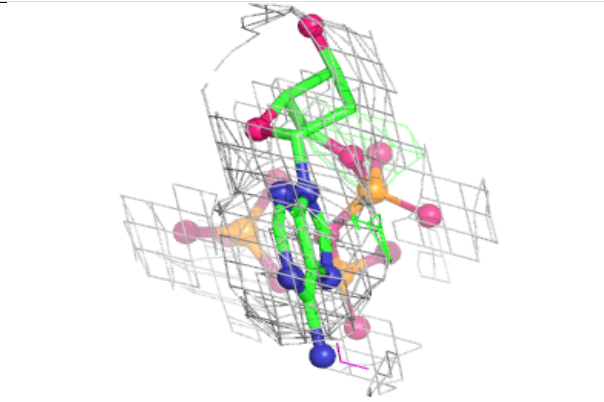
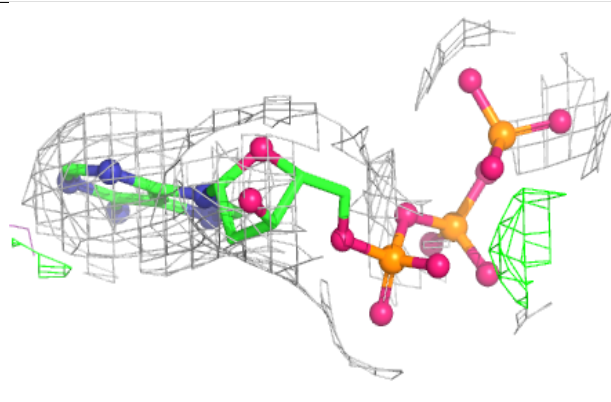
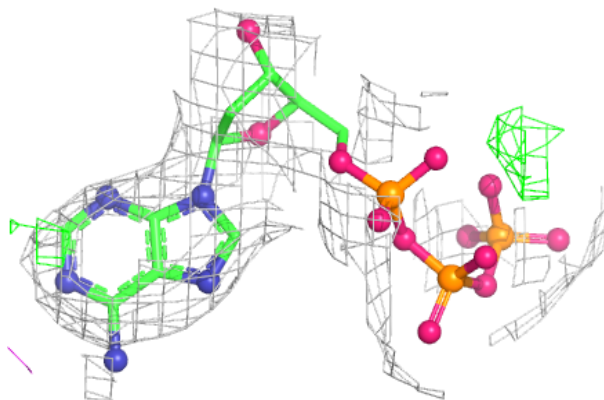


Electron density around DTP B 803:

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

**Electron density around DTP A 803:**

$2mF_o-DF_c$ (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.