



wwPDB X-ray Structure Validation Summary Report ⓘ

May 15, 2020 – 02:53 am BST

PDB ID : 1FXO
Title : THE STRUCTURAL BASIS OF THE CATALYTIC MECHANISM AND
REGULATION OF GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE (RMLA). TMP COMPLEX.
Authors : Blankenfeldt, W.; Lam, J.S.; Naismith, J.H.
Deposited on : 2000-09-26
Resolution : 1.66 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

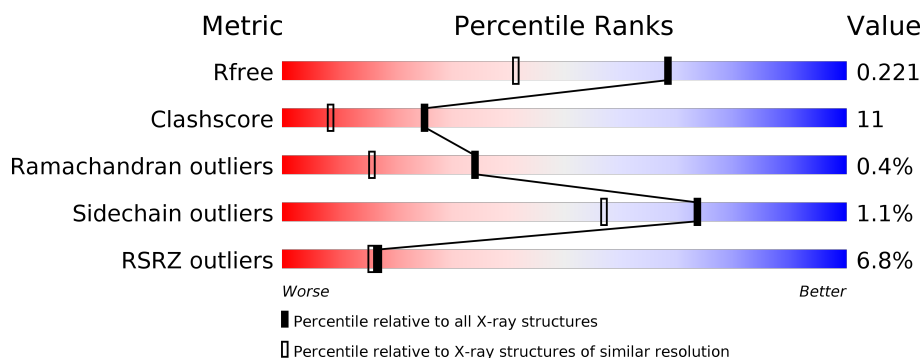
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.66 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.



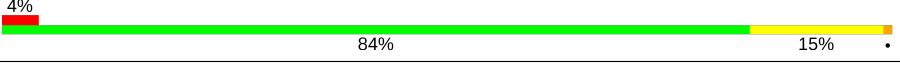

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1827 (1.66-1.66)
Clashscore	141614	1931 (1.66-1.66)
Ramachandran outliers	138981	1891 (1.66-1.66)
Sidechain outliers	138945	1891 (1.66-1.66)
RSRZ outliers	127900	1791 (1.66-1.66)

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	293	<div> <div>5%</div> <div> <div></div> <div>83%</div> <div>15%</div> </div> <div>•</div> </div>
1	B	293	<div> <div>5%</div> <div> <div></div> <div>84%</div> <div>15%</div> </div> <div>•</div> </div>
1	C	293	<div> <div>9%</div> <div> <div></div> <div>77%</div> <div>22%</div> </div> <div>•</div> </div>
1	D	293	<div> <div>8%</div> <div> <div></div> <div>85%</div> <div>13%</div> </div> <div>•</div> </div>
1	E	293	<div> <div>10%</div> <div> <div></div> <div>81%</div> <div>18%</div> </div> <div>•</div> </div>
1	F	293	<div> <div>7%</div> <div> <div></div> <div>78%</div> <div>20%</div> </div> <div>•</div> </div>

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Mol	Chain	Length	Quality of chain
1	G	293	
1	H	293	

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
2	SO4	D	3900	-	-	X	-
2	SO4	E	5700	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 22771 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 GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE.

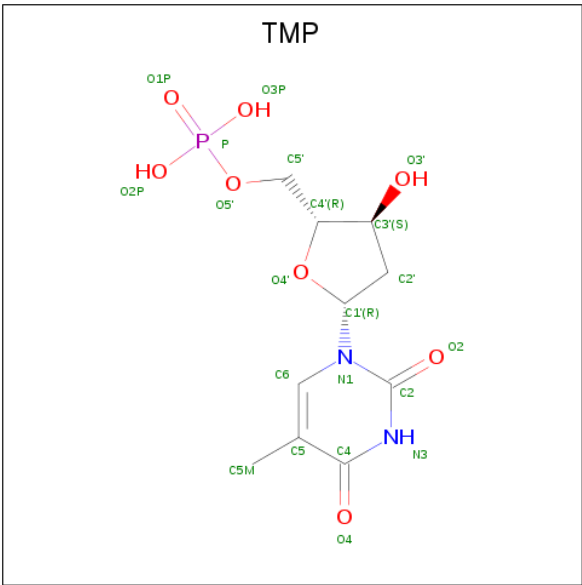
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	292	Total	C	N	O	S	0	11	0
			2376	1512	407	451	6			
1	B	293	Total	C	N	O	S	0	7	0
			2345	1495	397	446	7			
1	C	292	Total	C	N	O	S	0	14	0
			2397	1526	409	456	6			
1	D	292	Total	C	N	O	S	0	12	0
			2377	1516	400	455	6			
1	E	293	Total	C	N	O	S	0	6	0
			2337	1491	393	446	7			
1	F	293	Total	C	N	O	S	0	12	0
			2388	1523	402	456	7			
1	G	293	Total	C	N	O	S	0	6	0
			2333	1490	392	444	7			
1	H	292	Total	C	N	O	S	0	3	0
			2305	1473	388	438	6			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		
2	G	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is THYMIDINE-5'-PHOSPHATE (three-letter code: TMP) (formula: C₁₀H₁₅N₂O₈P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	1
			42	20	4	16	2		
3	A	1	Total	C	N	O	P	0	0
			21	10	2	8	1		
3	B	1	Total	C	N	O	P	0	1
			42	20	4	16	2		
3	B	1	Total	C	N	O	P	0	0
			21	10	2	8	1		
3	C	1	Total	C	N	O	P	0	1
			42	20	4	16	2		
3	C	1	Total	C	N	O	P	0	0
			21	10	2	8	1		
3	D	1	Total	C	N	O	P	0	1
			42	20	4	16	2		
3	D	1	Total	C	N	O	P	0	0
			21	10	2	8	1		
3	E	1	Total	C	N	O	P	0	0
			21	10	2	8	1		
3	E	1	Total	C	N	O	P	0	0
			21	10	2	8	1		
3	F	1	Total	C	N	O	P	0	1
			42	20	4	16	2		
3	F	1	Total	C	N	O	P	0	0
			21	10	2	8	1		
3	G	1	Total	C	N	O	P	0	1
			42	20	4	16	2		
3	G	1	Total	C	N	O	P	0	0
			21	10	2	8	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	H	1	Total	C	N	O	P	0	1
			42	20	4	16	2		
3	H	1	Total	C	N	O	P	0	0
			21	10	2	8	1		

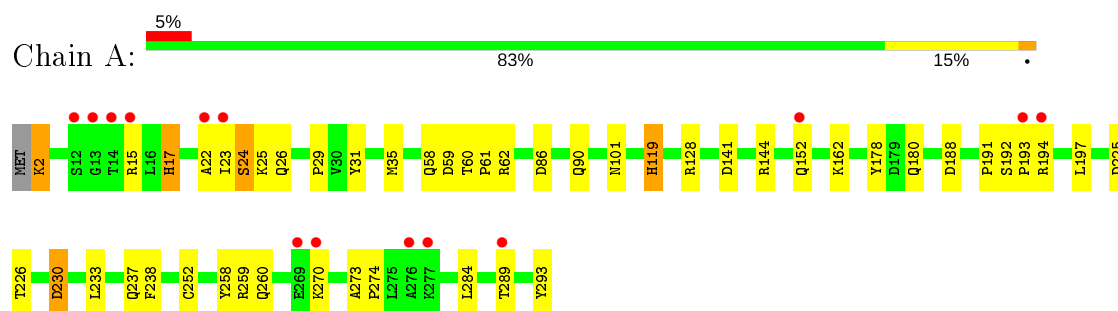
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	450	Total	O	0	0
			450	450		
4	B	486	Total	O	0	0
			486	486		
4	C	391	Total	O	0	0
			391	391		
4	D	381	Total	O	0	0
			381	381		
4	E	375	Total	O	0	0
			375	375		
4	F	399	Total	O	0	0
			399	399		
4	G	457	Total	O	0	0
			457	457		
4	H	426	Total	O	0	0
			426	426		

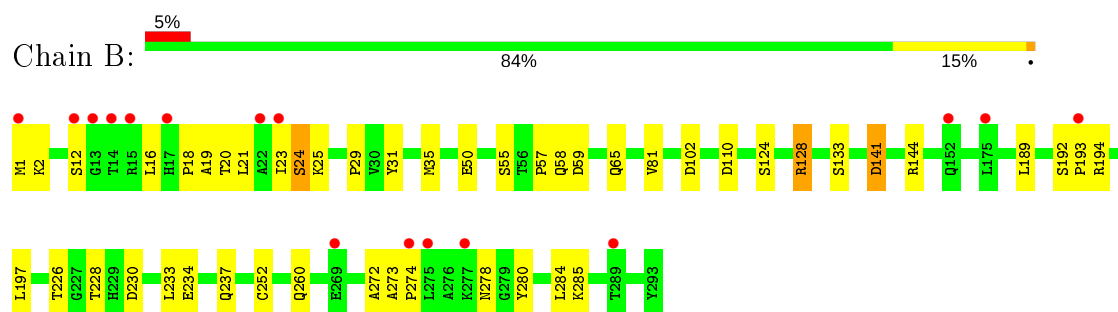
3 Residue-property plots [i](#)

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.

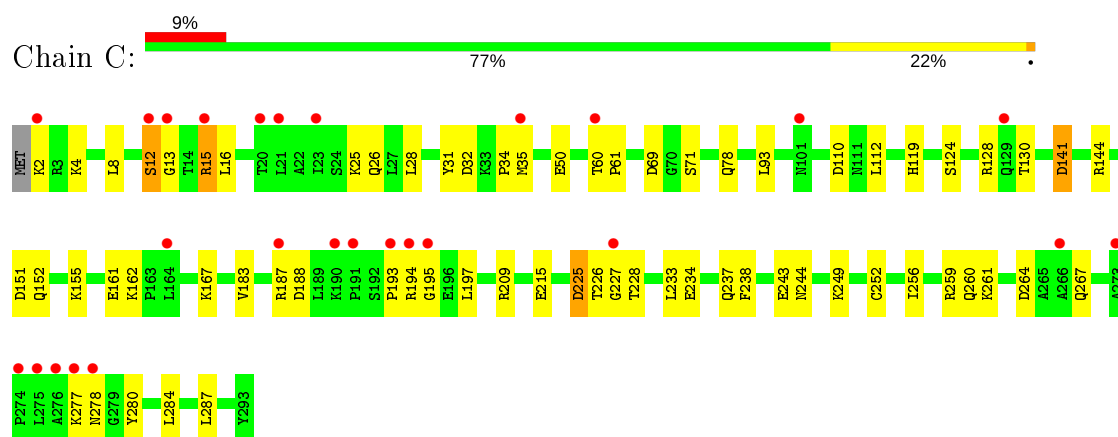
• Molecule 1: GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE



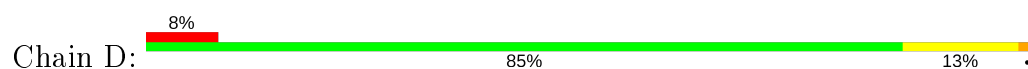
• Molecule 1: GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE

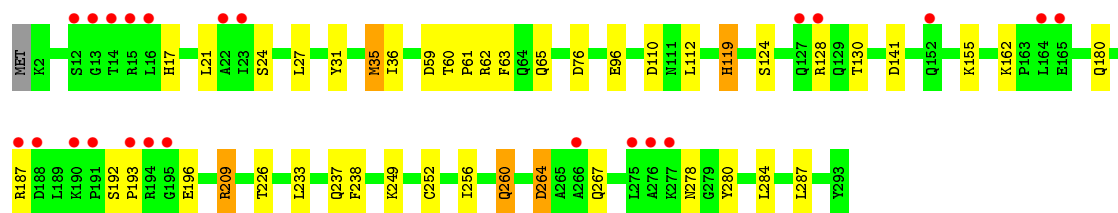


• Molecule 1: GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE

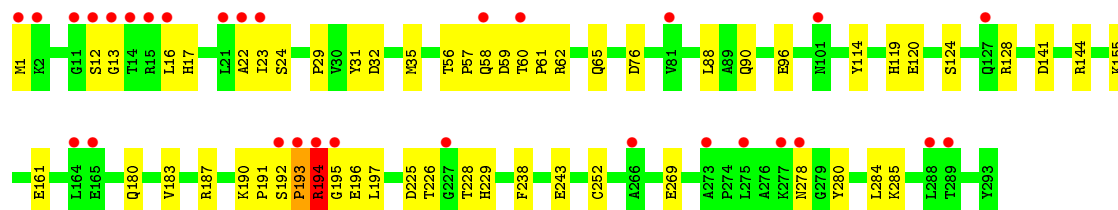
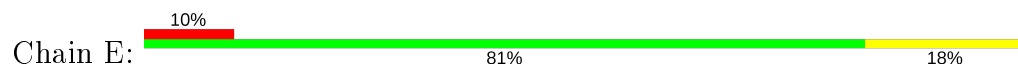


• Molecule 1: GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE

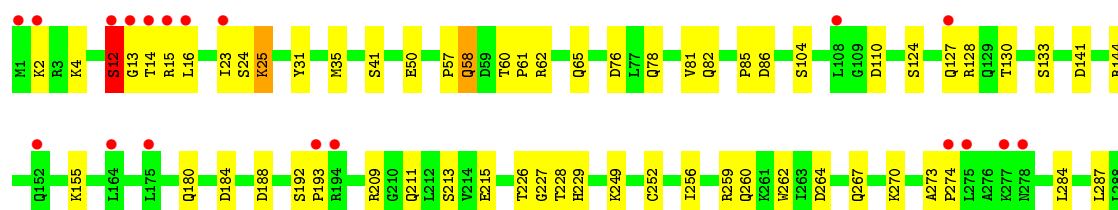
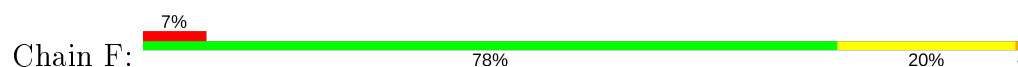




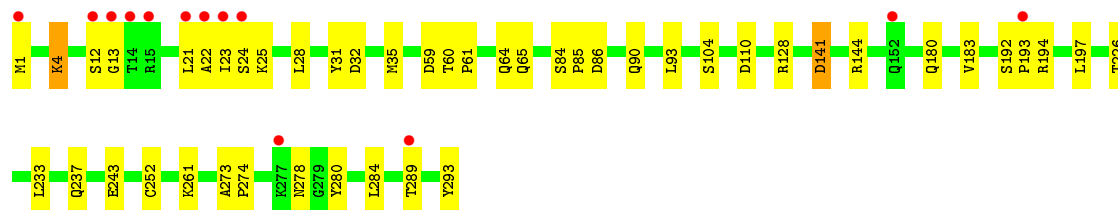
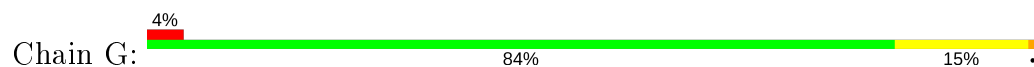
● Molecule 1: GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE



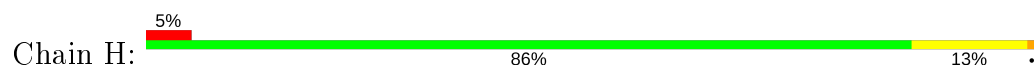
● Molecule 1: GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE

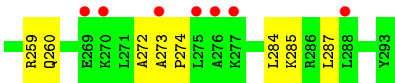


● Molecule 1: GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE



● Molecule 1: GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	71.49 Å 73.06 Å 134.74 Å 89.93° 80.92° 81.11°	Depositor
Resolution (Å)	73.00 – 1.66 32.04 – 1.66	Depositor EDS
% Data completeness (in resolution range)	94.3 (73.00-1.66) 94.0 (32.04-1.66)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 1.66 Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.142 , 0.196 0.174 , 0.221	Depositor DCC
R_{free} test set	14910 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	17.5	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 60.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	22771	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.24% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: TMP, SO4

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	1.02	4/2427 (0.2%)	0.97	5/3290 (0.2%)
1	B	1.03	1/2395 (0.0%)	1.01	6/3247 (0.2%)
1	C	0.97	0/2448	0.97	4/3318 (0.1%)
1	D	0.96	1/2427 (0.0%)	0.97	7/3291 (0.2%)
1	E	0.95	2/2387 (0.1%)	0.95	2/3237 (0.1%)
1	F	1.03	1/2438 (0.0%)	0.99	7/3305 (0.2%)
1	G	1.07	5/2383 (0.2%)	1.02	5/3233 (0.2%)
1	H	1.00	1/2355 (0.0%)	0.96	4/3195 (0.1%)
All	All	1.00	15/19260 (0.1%)	0.98	40/26116 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	D	0	2
1	E	0	2
All	All	0	6

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	128	ARG	CZ-NH2	-7.54	1.23	1.33
1	B	31	TYR	CD2-CE2	-6.79	1.29	1.39
1	E	114	TYR	CD2-CE2	6.63	1.49	1.39
1	A	128	ARG	CZ-NH2	-6.58	1.24	1.33
1	D	238	PHE	CE2-CZ	-6.44	1.25	1.37

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	194	ARG	NE-CZ-NH2	-8.21	116.20	120.30
1	F	12	SER	N-CA-C	-6.98	92.14	111.00
1	G	194	ARG	NE-CZ-NH1	6.64	123.62	120.30
1	G	128	ARG	NE-CZ-NH2	-6.64	116.98	120.30
1	B	141	ASP	CB-CG-OD2	6.60	124.24	118.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	119[A]	HIS	Sidechain
1	A	17	HIS	Sidechain
1	D	119	HIS	Sidechain
1	D	17	HIS	Sidechain
1	E	17	HIS	Sidechain

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	2376	0	2348	60	0
1	B	2345	0	2328	58	0
1	C	2397	0	2369	70	0
1	D	2377	0	2353	40	0
1	E	2337	0	2317	54	0
1	F	2388	0	2368	71	0
1	G	2333	0	2320	57	0
1	H	2305	0	2289	44	0
2	A	5	0	0	0	0
2	C	10	0	0	2	0
2	D	25	0	0	2	1
2	E	15	0	0	3	0
2	F	5	0	0	1	0
2	G	5	0	0	0	0
3	A	63	0	38	1	0
3	B	63	0	39	2	0
3	C	63	0	39	6	0
3	D	63	0	39	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	42	0	26	2	0
3	F	63	0	39	8	0
3	G	63	0	39	3	0
3	H	63	0	39	3	0
4	A	450	0	0	15	1
4	B	486	0	0	13	2
4	C	391	0	0	29	0
4	D	381	0	0	15	5
4	E	375	0	0	21	1
4	F	399	0	0	23	2
4	G	457	0	0	13	1
4	H	426	0	0	5	3
All	All	22771	0	18990	411	8

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 11.

The worst 5 of 411 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:24:SER:CB	1:D:27:LEU:HD12	1.51	1.39
1:D:24:SER:HB3	1:D:27:LEU:CD1	1.53	1.36
1:C:287:LEU:HD12	4:C:9821:HOH:O	1.37	1.22
1:G:141:ASP:OD2	1:G:144:ARG:HD3	1.48	1.14
1:F:78:GLN:NE2	4:F:9901:HOH:O	1.78	1.13

The worst 5 of 8 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)
4:D:9860:HOH:O	4:E:9857:HOH:O[1_655]	1.93	0.27
4:D:9569:HOH:O	4:H:9651:HOH:O[1_565]	2.01	0.19
4:D:9563:HOH:O	4:H:9651:HOH:O[1_565]	2.15	0.05
4:A:9763:HOH:O	4:F:9762:HOH:O[1_566]	2.15	0.05
2:D:3900:SO4:O2	4:B:9956:HOH:O[1_655]	2.16	0.04

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	301/293 (103%)	296 (98%)	4 (1%)	1 (0%)	41	22
1	B	298/293 (102%)	292 (98%)	6 (2%)	0	100	100
1	C	304/293 (104%)	296 (97%)	7 (2%)	1 (0%)	41	22
1	D	302/293 (103%)	297 (98%)	4 (1%)	1 (0%)	41	22
1	E	297/293 (101%)	291 (98%)	3 (1%)	3 (1%)	15	3
1	F	303/293 (103%)	298 (98%)	3 (1%)	2 (1%)	22	6
1	G	297/293 (101%)	293 (99%)	3 (1%)	1 (0%)	41	22
1	H	293/293 (100%)	287 (98%)	5 (2%)	1 (0%)	41	22
All	All	2395/2344 (102%)	2350 (98%)	35 (2%)	10 (0%)	34	16

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	12	SER
1	E	194	ARG
1	F	31	TYR
1	H	31	TYR
1	A	31	TYR

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	250/240 (104%)	246 (98%)	4 (2%)	62	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	247/240 (103%)	244 (99%)	3 (1%)	71	53
1	C	253/240 (105%)	250 (99%)	3 (1%)	71	53
1	D	251/240 (105%)	248 (99%)	3 (1%)	71	53
1	E	246/240 (102%)	244 (99%)	2 (1%)	81	70
1	F	252/240 (105%)	250 (99%)	2 (1%)	81	70
1	G	246/240 (102%)	245 (100%)	1 (0%)	91	85
1	H	242/240 (101%)	237 (98%)	5 (2%)	53	29
All	All	1987/1920 (104%)	1964 (99%)	23 (1%)	73	53

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	124[A]	SER
1	D	260	GLN
1	H	24	SER
1	D	124[B]	SER
1	E	29	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	282	GLN
1	G	17	HIS
1	G	237	GLN
1	E	119	HIS
1	F	58	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

36 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	A	3700	-	4,4,4	0.32	0	6,6,6	1.19	0
2	SO4	F	6700	-	4,4,4	0.21	0	6,6,6	0.27	0
3	TMP	G	9505[B]	-	19,22,22	1.83	6 (31%)	23,33,33	3.07	10 (43%)
3	TMP	E	9503	-	19,22,22	1.99	4 (21%)	23,33,33	3.66	10 (43%)
3	TMP	G	9505[A]	-	19,22,22	1.98	7 (36%)	23,33,33	4.18	11 (47%)
3	TMP	B	9500[B]	-	19,22,22	2.09	7 (36%)	23,33,33	2.52	6 (26%)
2	SO4	E	5800	-	4,4,4	0.15	0	6,6,6	0.36	0
3	TMP	B	9500[A]	-	19,22,22	2.12	7 (36%)	23,33,33	4.27	10 (43%)
2	SO4	G	7700	-	4,4,4	0.29	0	6,6,6	0.33	0
3	TMP	E	9511	-	19,22,22	1.76	4 (21%)	23,33,33	2.78	8 (34%)
2	SO4	E	5700	-	4,4,4	0.22	0	6,6,6	0.41	0
2	SO4	E	4700	-	4,4,4	0.14	0	6,6,6	0.90	0
3	TMP	A	9507	-	19,22,22	1.38	2 (10%)	23,33,33	1.73	4 (17%)
2	SO4	D	5100	-	4,4,4	0.40	0	6,6,6	1.14	0
3	TMP	B	9508	-	19,22,22	1.46	3 (15%)	23,33,33	2.47	5 (21%)
3	TMP	F	9504[B]	-	19,22,22	1.92	6 (31%)	23,33,33	3.10	7 (30%)
3	TMP	F	9504[A]	-	19,22,22	2.02	4 (21%)	23,33,33	2.95	6 (26%)
2	SO4	D	5200	-	4,4,4	0.15	0	6,6,6	0.50	0
2	SO4	D	5000	-	4,4,4	0.13	0	6,6,6	0.45	0
3	TMP	H	9514	-	19,22,22	1.60	3 (15%)	23,33,33	1.72	1 (4%)
3	TMP	H	9506[B]	-	19,22,22	1.99	7 (36%)	23,33,33	3.79	12 (52%)
2	SO4	D	3900	-	4,4,4	0.29	0	6,6,6	0.63	0
3	TMP	D	9502[B]	-	19,22,22	1.96	5 (26%)	23,33,33	2.64	5 (21%)
3	TMP	D	9502[A]	-	19,22,22	2.02	5 (26%)	23,33,33	4.09	11 (47%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	TMP	H	9506[A]	-	19,22,22	2.11	8 (42%)	23,33,33	3.90	10 (43%)
3	TMP	G	9513	-	19,22,22	1.24	2 (10%)	23,33,33	2.53	6 (26%)
3	TMP	A	8500[B]	-	19,22,22	2.00	6 (31%)	23,33,33	2.71	10 (43%)
2	SO4	C	3800	-	4,4,4	0.21	0	6,6,6	0.48	0
3	TMP	A	8500[A]	-	19,22,22	2.05	6 (31%)	23,33,33	2.79	14 (60%)
3	TMP	F	9512	-	19,22,22	1.42	3 (15%)	23,33,33	2.01	4 (17%)
2	SO4	C	4000	-	4,4,4	0.49	0	6,6,6	1.08	0
2	SO4	D	4800	-	4,4,4	0.19	0	6,6,6	0.12	0
3	TMP	C	9509	-	19,22,22	1.54	5 (26%)	23,33,33	2.70	4 (17%)
3	TMP	D	9510	-	19,22,22	1.45	4 (21%)	23,33,33	2.37	4 (17%)
3	TMP	C	9501[B]	-	19,22,22	1.89	6 (31%)	23,33,33	3.11	10 (43%)
3	TMP	C	9501[A]	-	19,22,22	2.05	7 (36%)	23,33,33	4.05	11 (47%)

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	TMP	G	9505[B]	-	-	0/7/22/22	0/2/2/2
3	TMP	E	9503	-	-	1/7/22/22	0/2/2/2
3	TMP	G	9505[A]	-	-	0/7/22/22	0/2/2/2
3	TMP	B	9500[B]	-	-	0/7/22/22	0/2/2/2
3	TMP	B	9500[A]	-	-	0/7/22/22	0/2/2/2
3	TMP	E	9511	-	-	2/7/22/22	0/2/2/2
3	TMP	A	9507	-	-	3/7/22/22	0/2/2/2
3	TMP	B	9508	-	-	3/7/22/22	0/2/2/2
3	TMP	F	9504[B]	-	-	1/7/22/22	0/2/2/2
3	TMP	F	9504[A]	-	-	0/7/22/22	0/2/2/2
3	TMP	H	9506[B]	-	-	4/7/22/22	0/2/2/2
3	TMP	H	9514	-	-	3/7/22/22	0/2/2/2
3	TMP	H	9506[A]	-	-	1/7/22/22	0/2/2/2
3	TMP	D	9502[B]	-	-	5/7/22/22	0/2/2/2
3	TMP	D	9502[A]	-	-	1/7/22/22	0/2/2/2
3	TMP	G	9513	-	-	3/7/22/22	0/2/2/2
3	TMP	A	8500[B]	-	-	2/7/22/22	0/2/2/2
3	TMP	A	8500[A]	-	-	5/7/22/22	0/2/2/2
3	TMP	F	9512	-	-	3/7/22/22	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	TMP	C	9509	-	-	3/7/22/22	0/2/2/2
3	TMP	D	9510	-	-	3/7/22/22	0/2/2/2
3	TMP	C	9501[B]	-	-	0/7/22/22	0/2/2/2
3	TMP	C	9501[A]	-	-	4/7/22/22	0/2/2/2

The worst 5 of 117 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	8500[B]	TMP	P-O2P	4.63	1.72	1.54
3	B	9500[A]	TMP	P-O3P	4.34	1.71	1.54
3	C	9501[B]	TMP	P-O2P	4.28	1.71	1.54
3	E	9503	TMP	P-O2P	4.26	1.71	1.54
3	B	9500[B]	TMP	P-O1P	4.25	1.64	1.50

The worst 5 of 179 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	9500[A]	TMP	C2'-C3'-C4'	-11.41	78.98	102.76
3	D	9502[A]	TMP	C2'-C3'-C4'	-11.38	79.05	102.76
3	G	9505[A]	TMP	C2'-C3'-C4'	-10.90	80.05	102.76
3	H	9506[A]	TMP	C2'-C3'-C4'	-10.74	80.38	102.76
3	C	9501[A]	TMP	C2'-C3'-C4'	-10.36	81.16	102.76

There are no chirality outliers.

5 of 47 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	9503	TMP	O4'-C1'-N1-C6
3	E	9511	TMP	C3'-C4'-C5'-O5'
3	E	9511	TMP	O4'-C1'-N1-C6
3	A	9507	TMP	C3'-C4'-C5'-O5'
3	A	9507	TMP	O4'-C1'-N1-C6

There are no ring outliers.

18 monomers are involved in 36 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	6700	SO4	1	0
3	E	9503	TMP	2	0
3	G	9505[A]	TMP	3	0

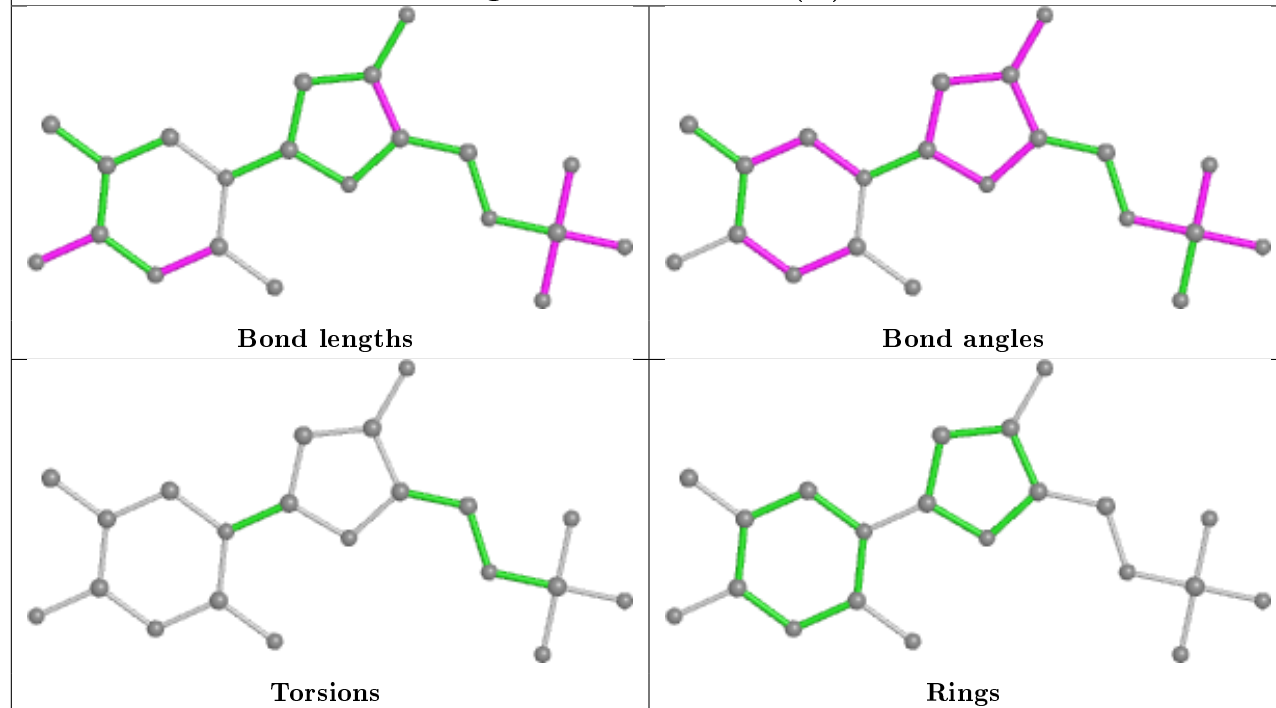
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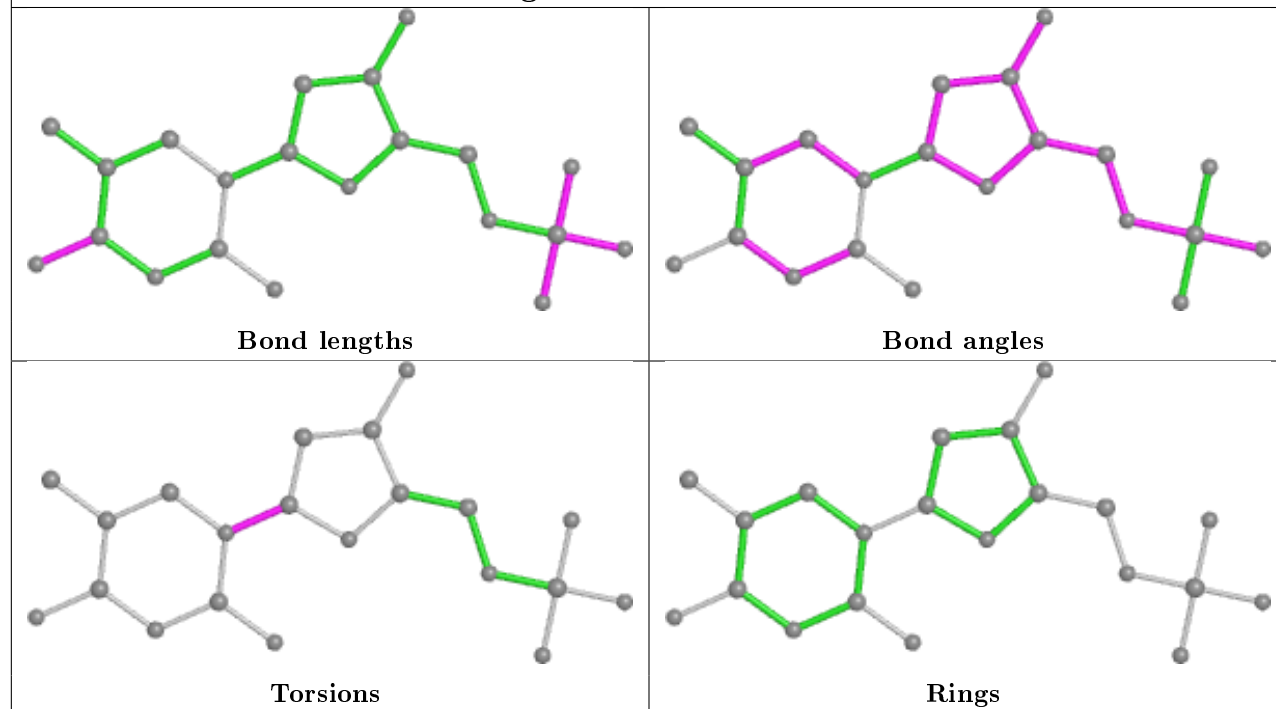
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	9500[A]	TMP	2	0
2	E	5700	SO4	2	0
2	E	4700	SO4	1	0
3	F	9504[B]	TMP	5	0
3	F	9504[A]	TMP	3	0
2	D	3900	SO4	1	1
3	D	9502[B]	TMP	1	0
3	D	9502[A]	TMP	1	0
3	H	9506[A]	TMP	3	0
2	C	3800	SO4	1	0
3	A	8500[A]	TMP	1	0
2	C	4000	SO4	1	0
2	D	4800	SO4	1	0
3	C	9501[B]	TMP	3	0
3	C	9501[A]	TMP	3	0

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

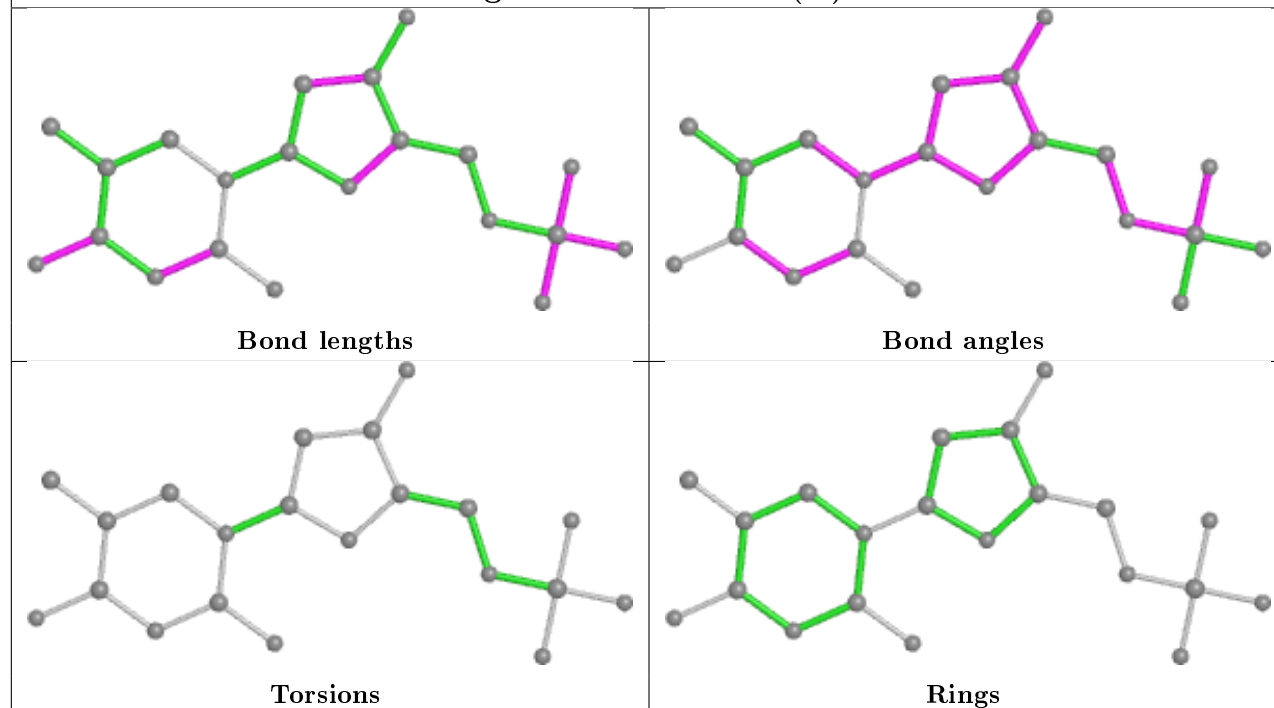
Ligand TMP G 9505 (B)



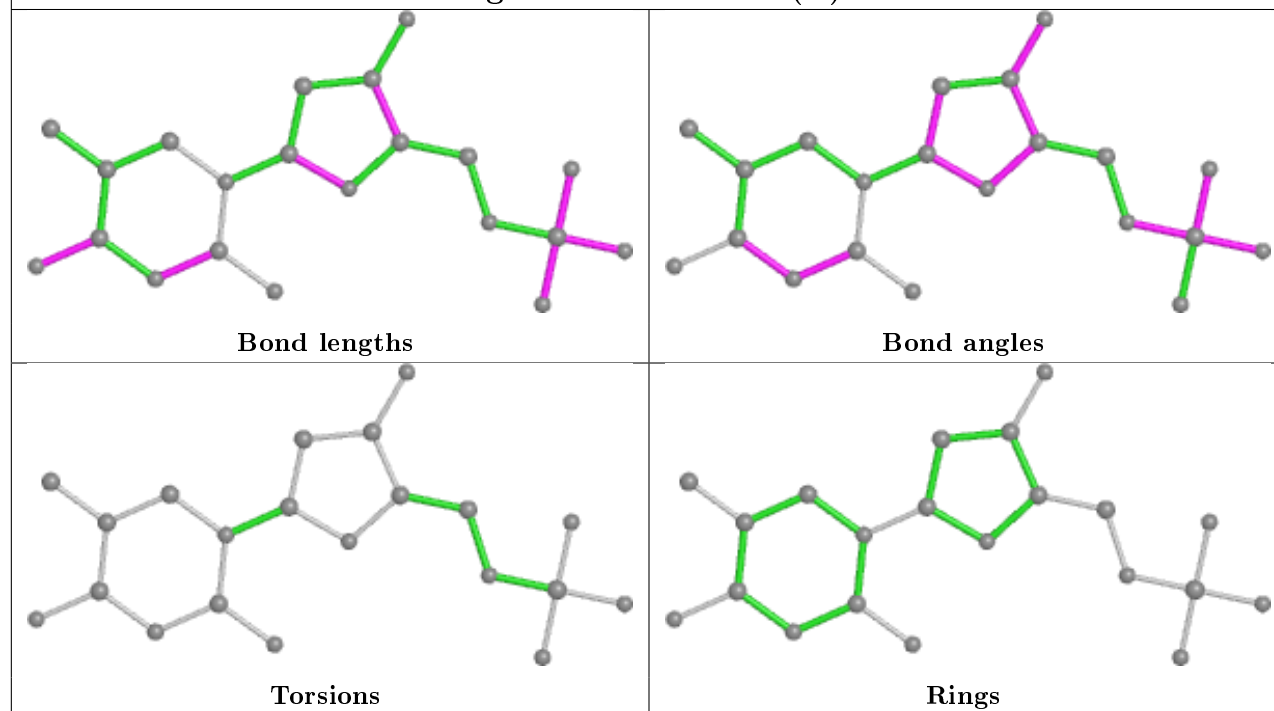
Ligand TMP E 9503



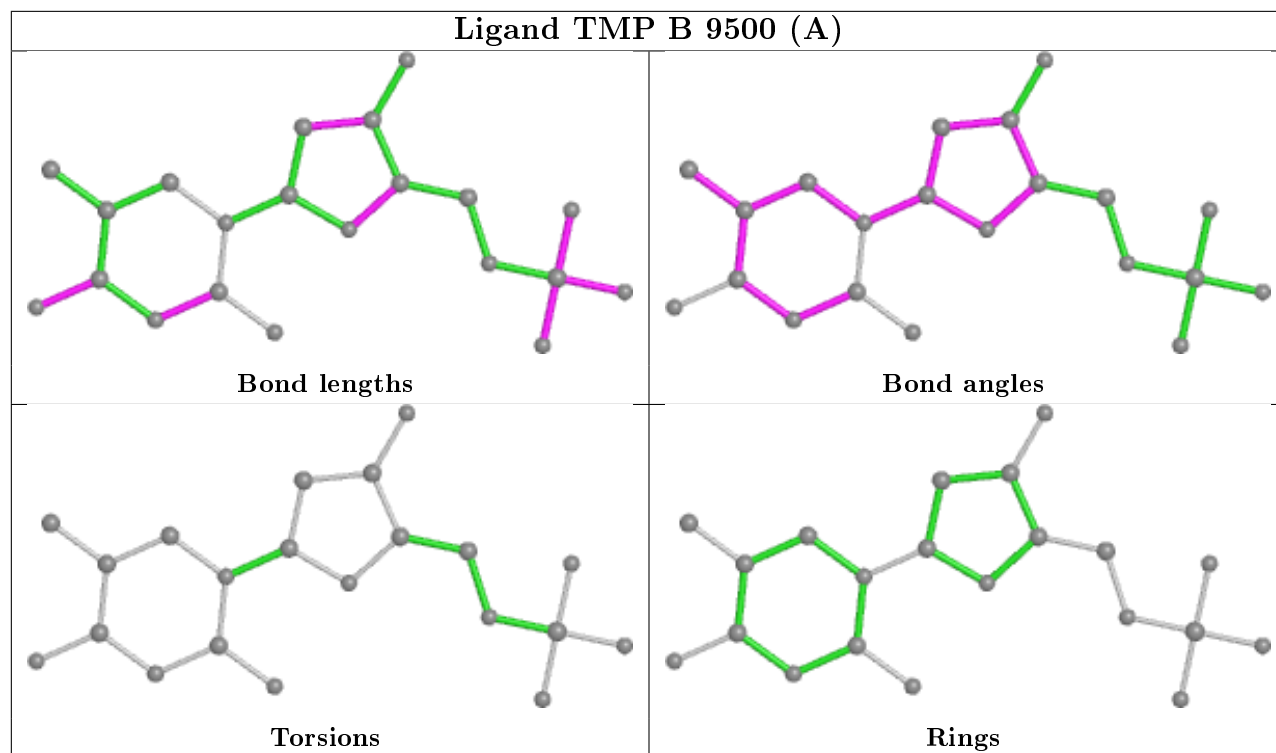
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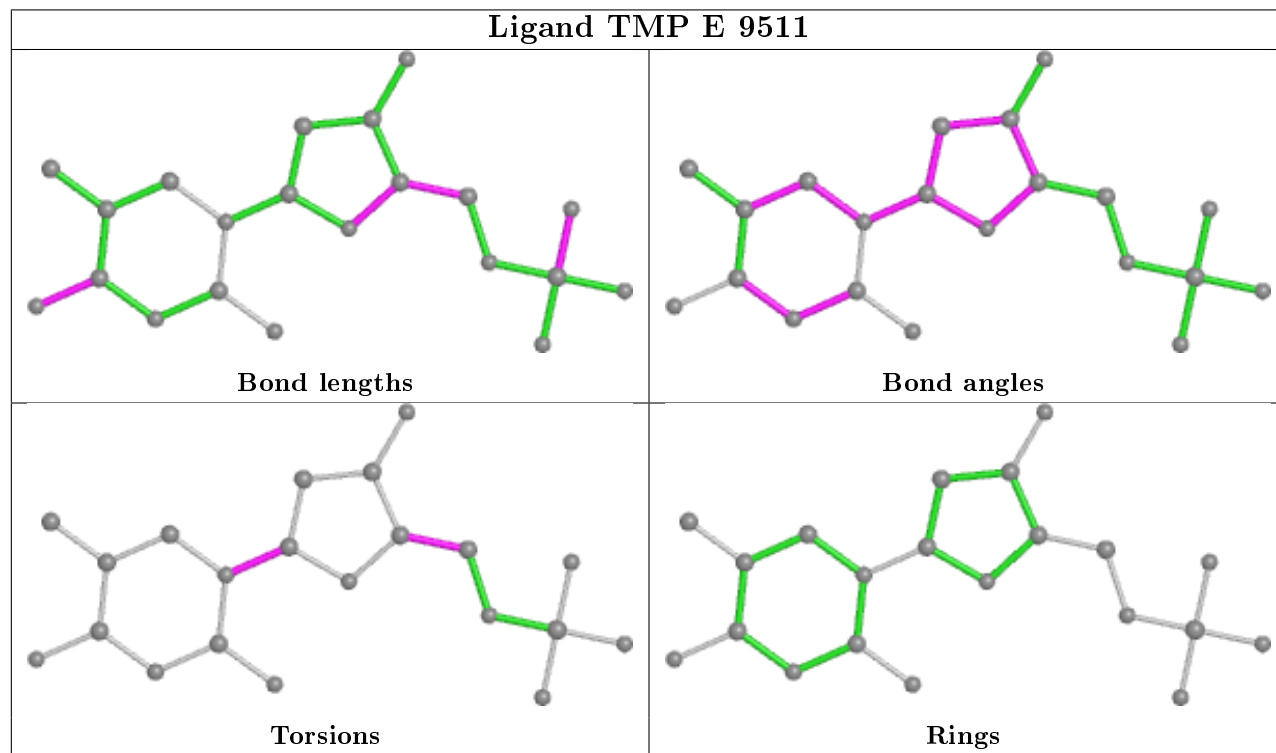
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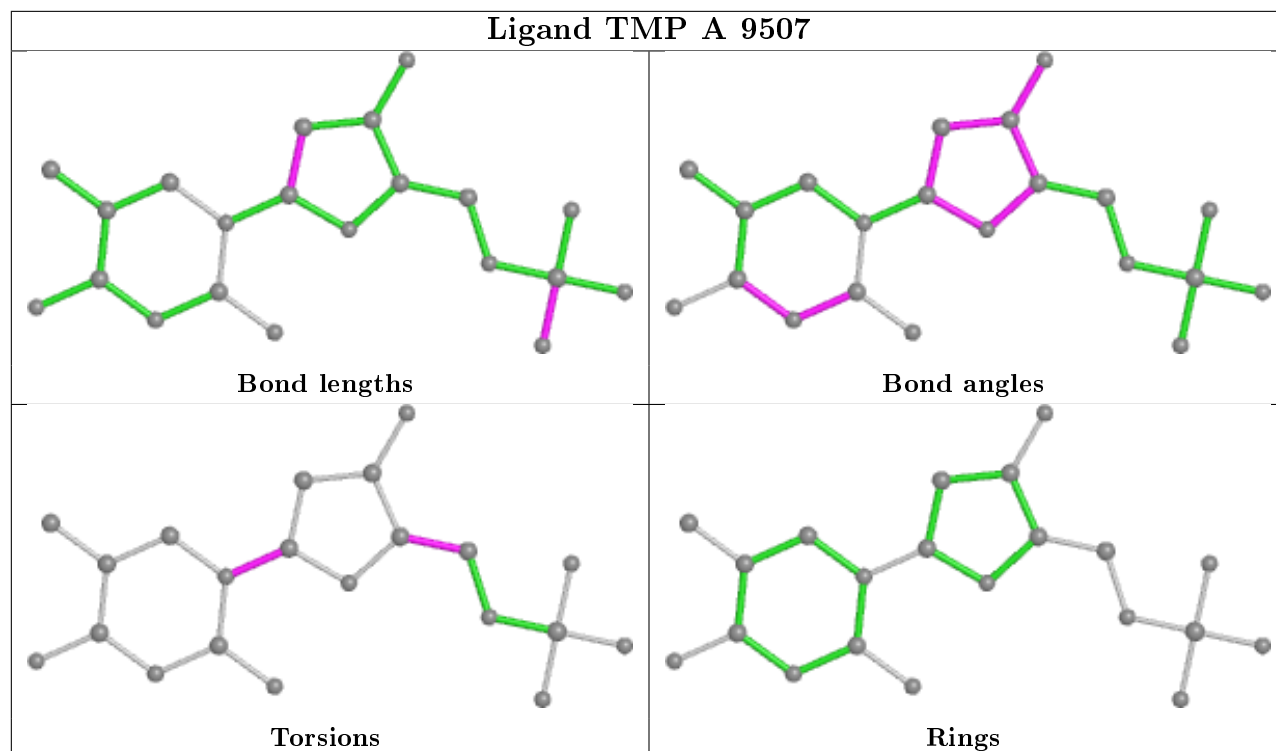
Ligand TMP B 9500 (A)



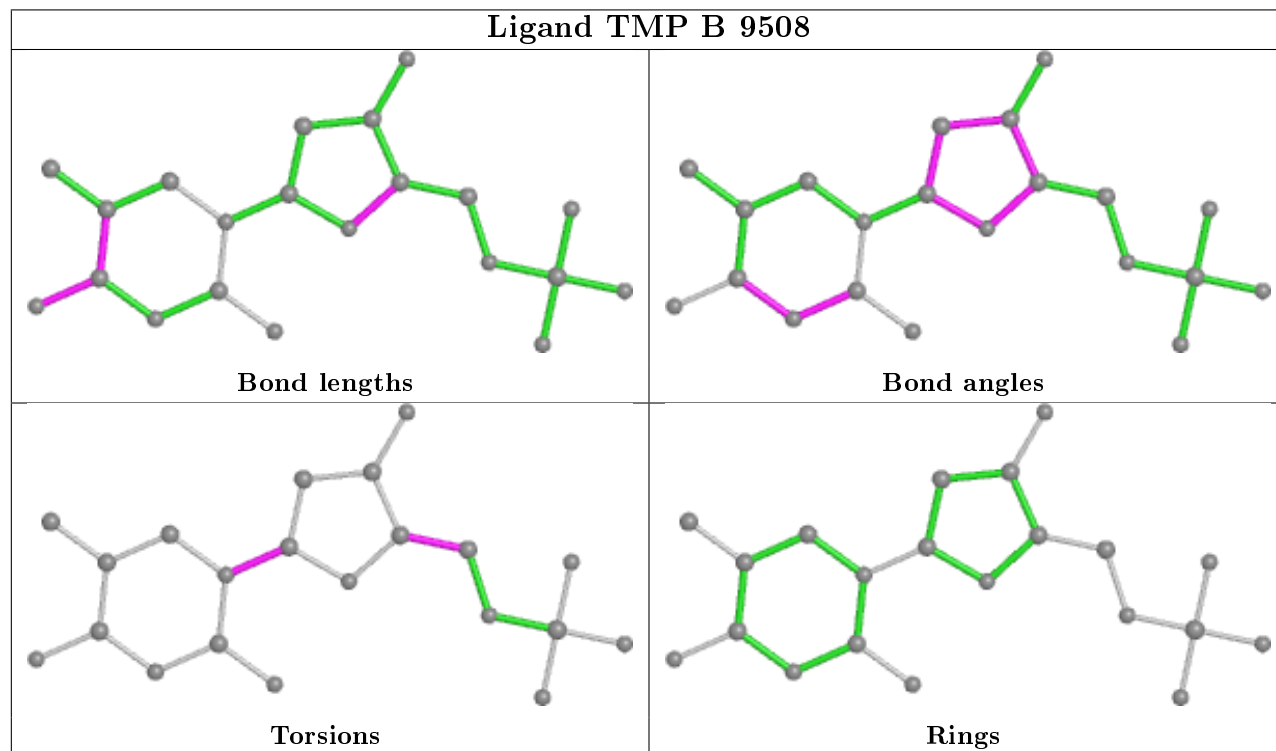
Ligand TMP E 9511



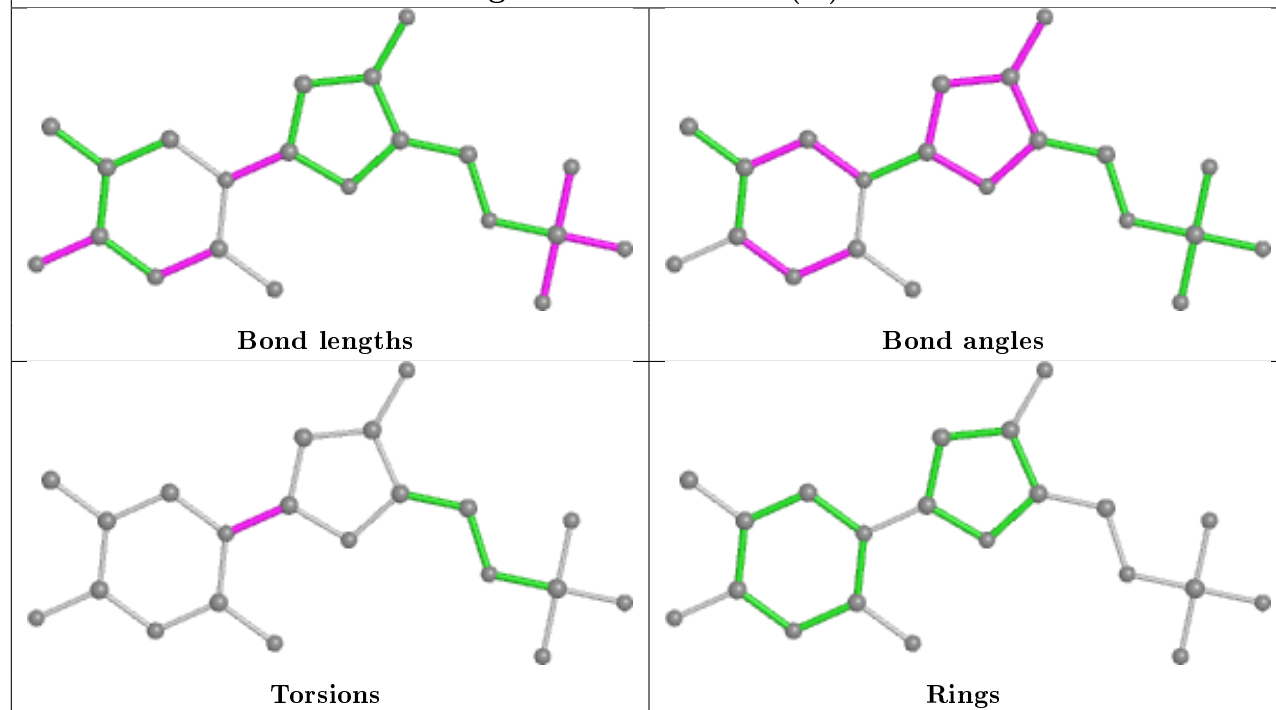
Ligand TMP A 9507



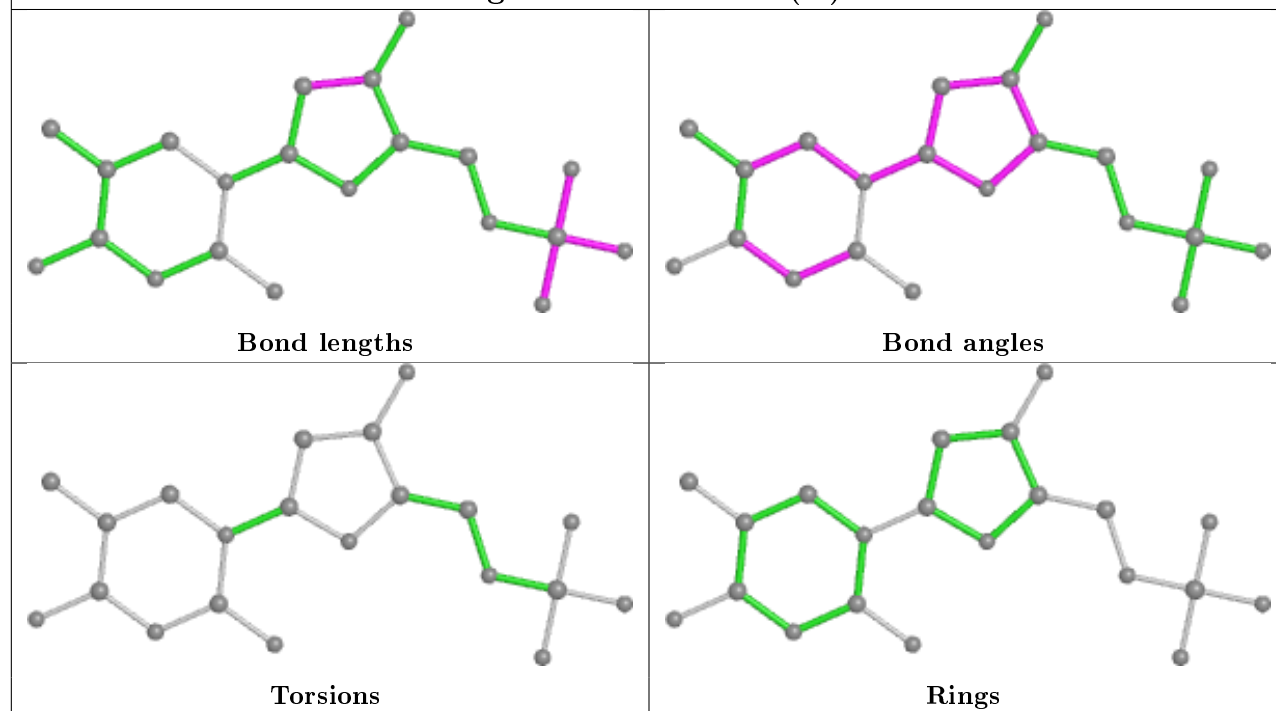
Ligand TMP B 9508



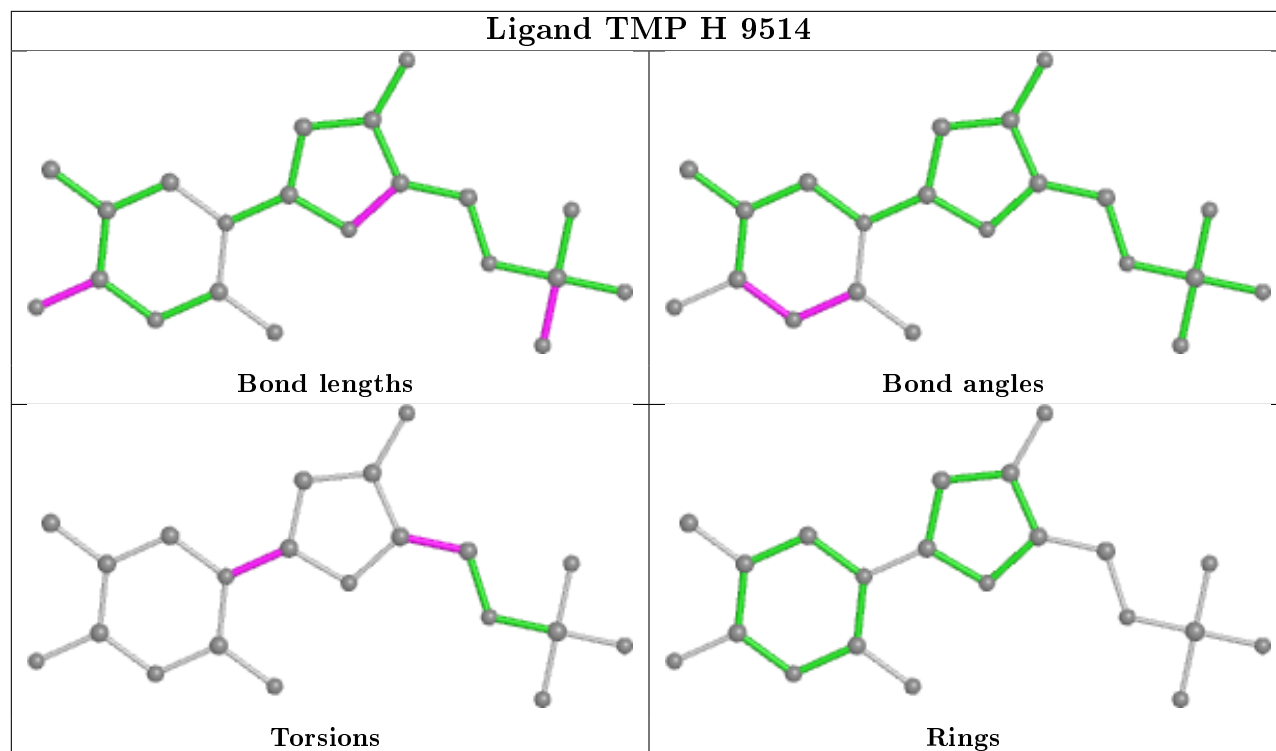
Ligand TMP F 9504 (B)



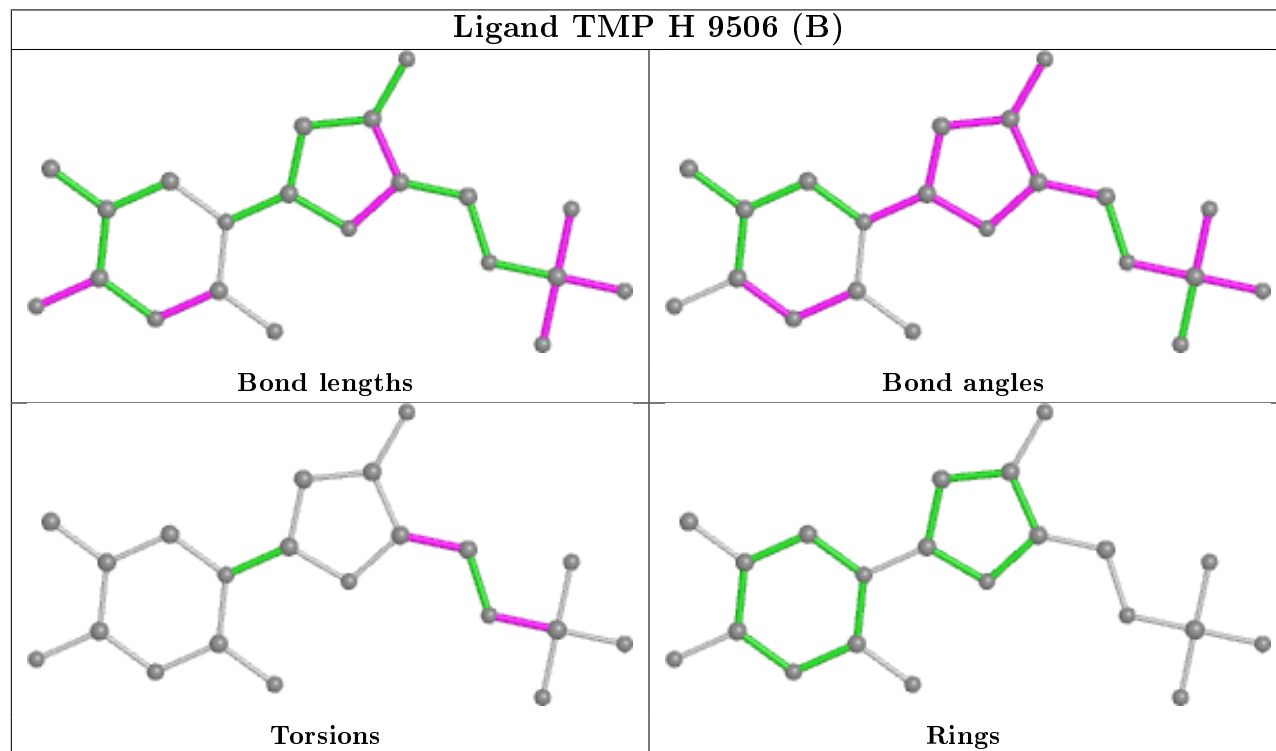
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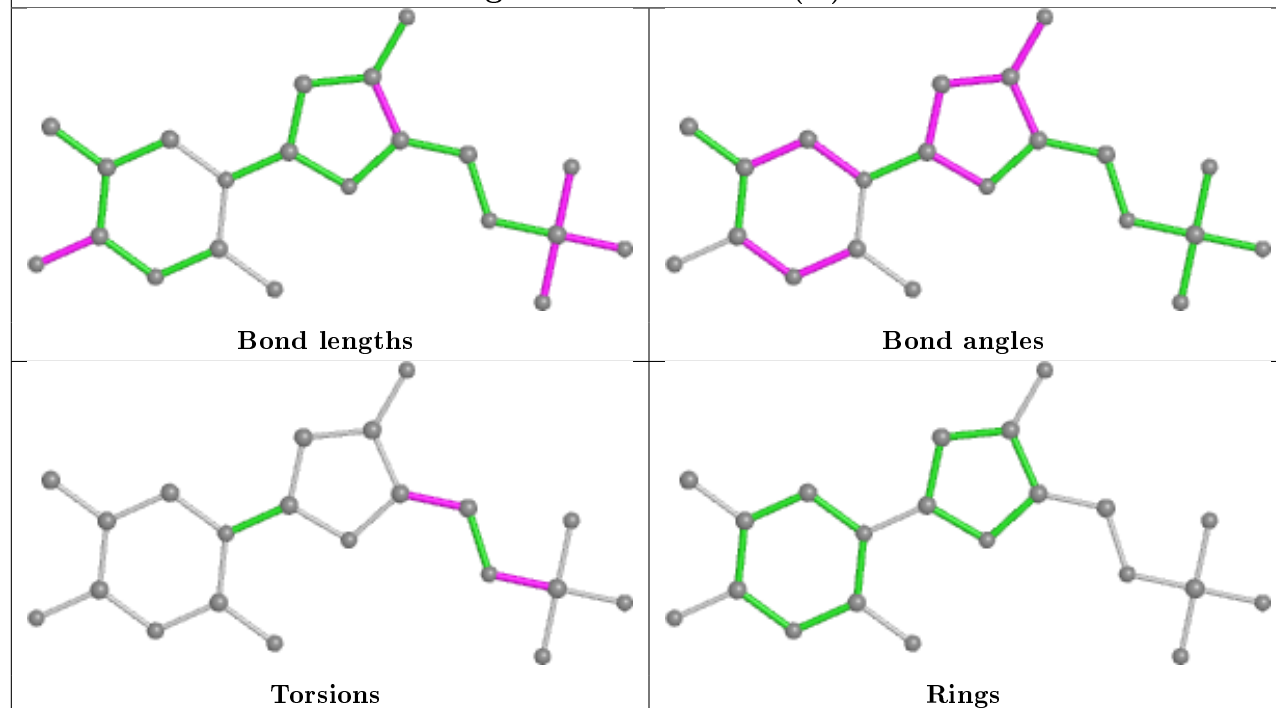
Ligand TMP H 9514



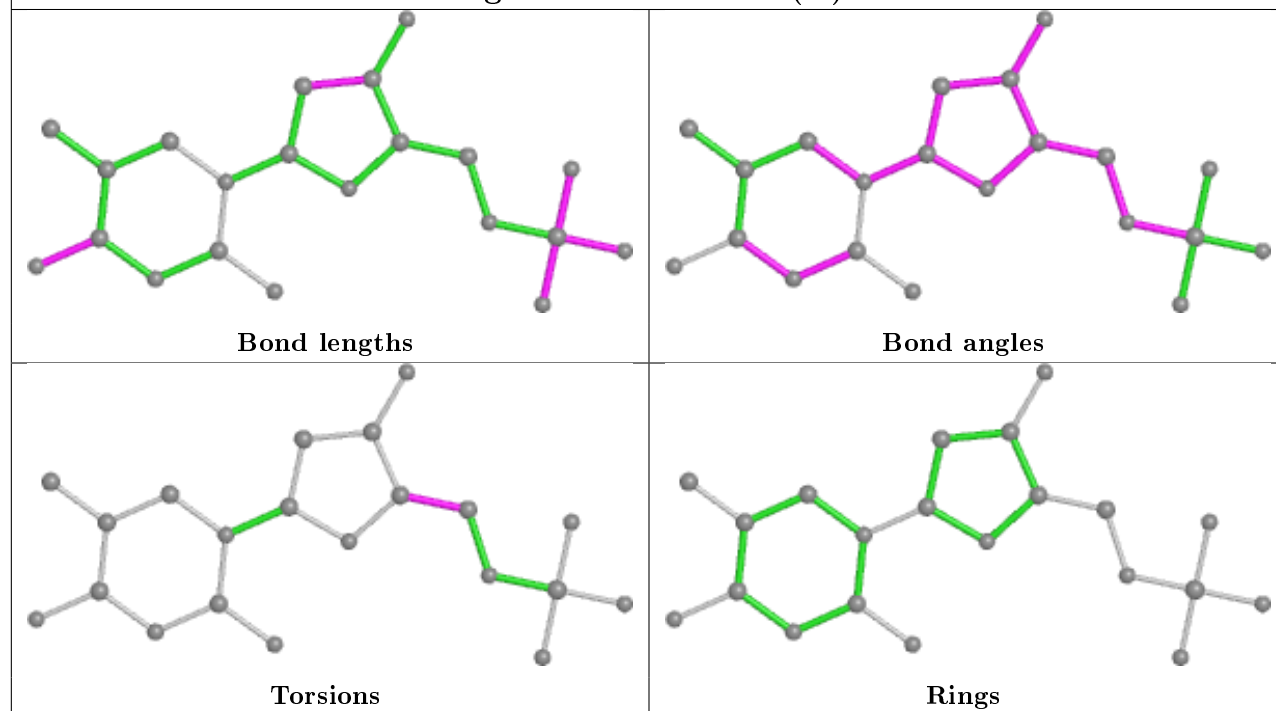
Ligand TMP H 9506 (B)



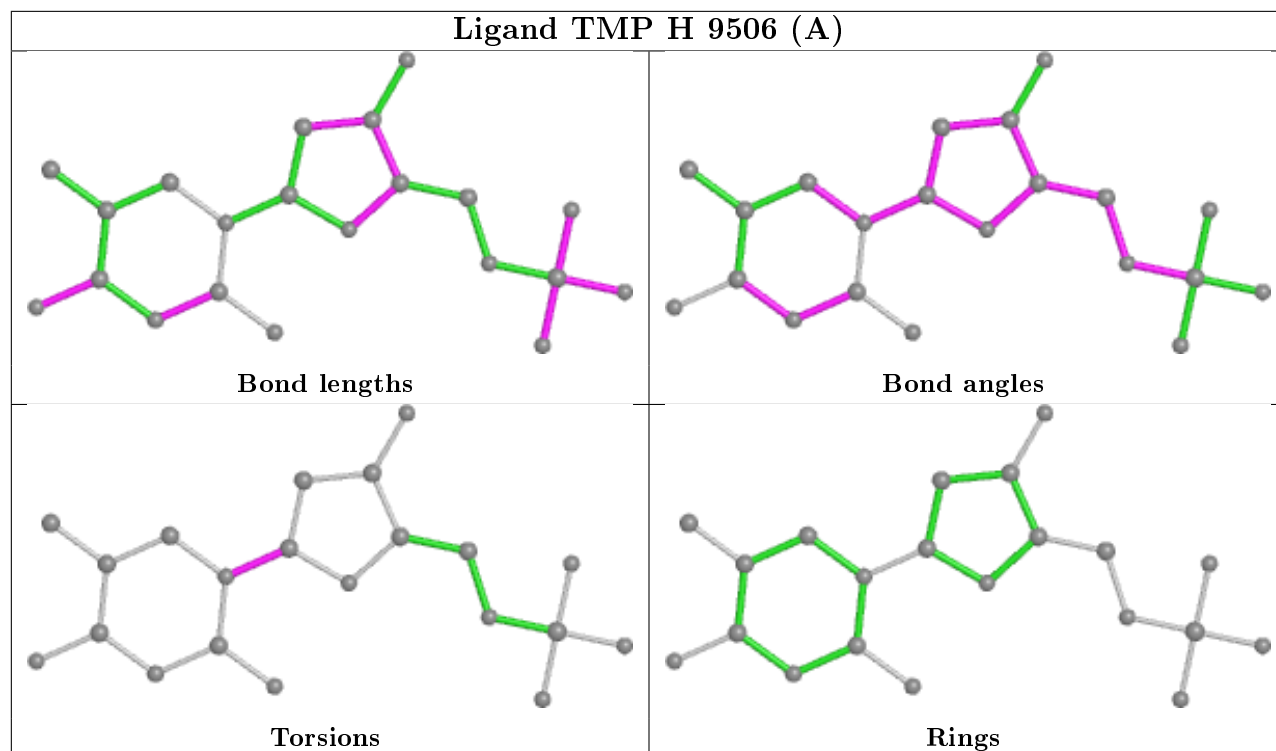
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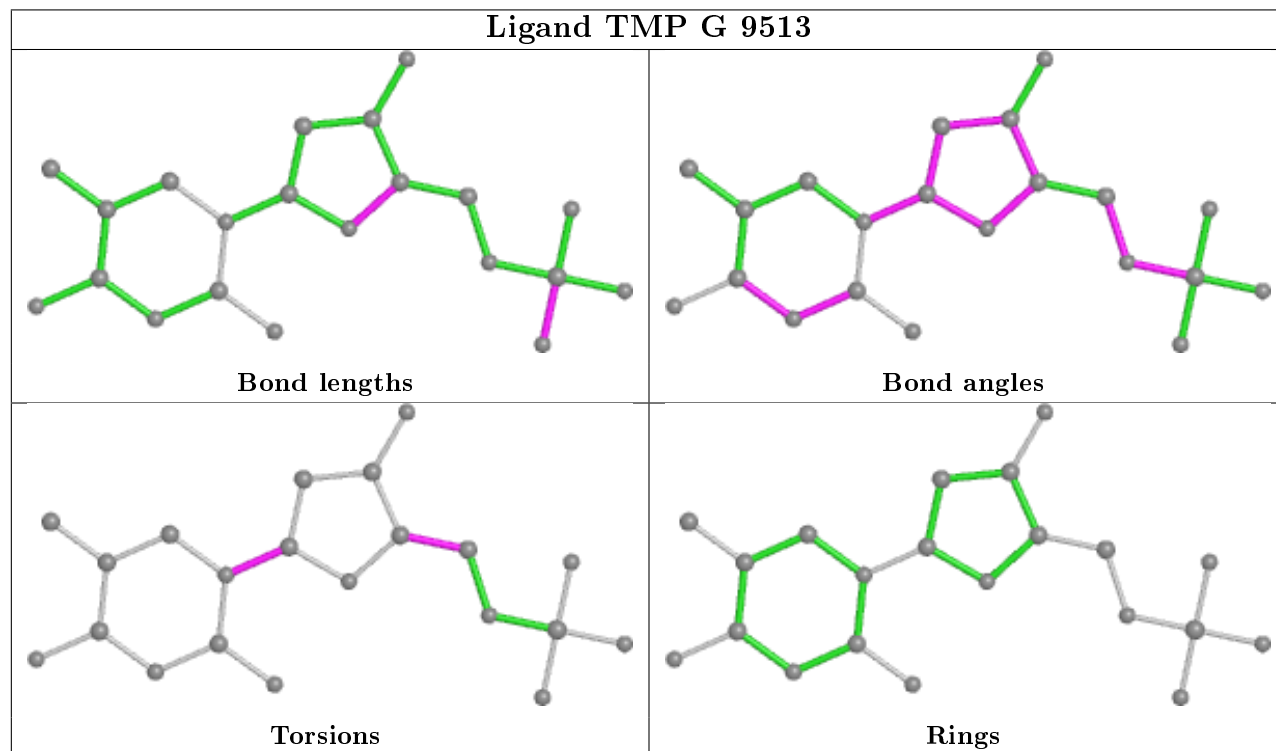
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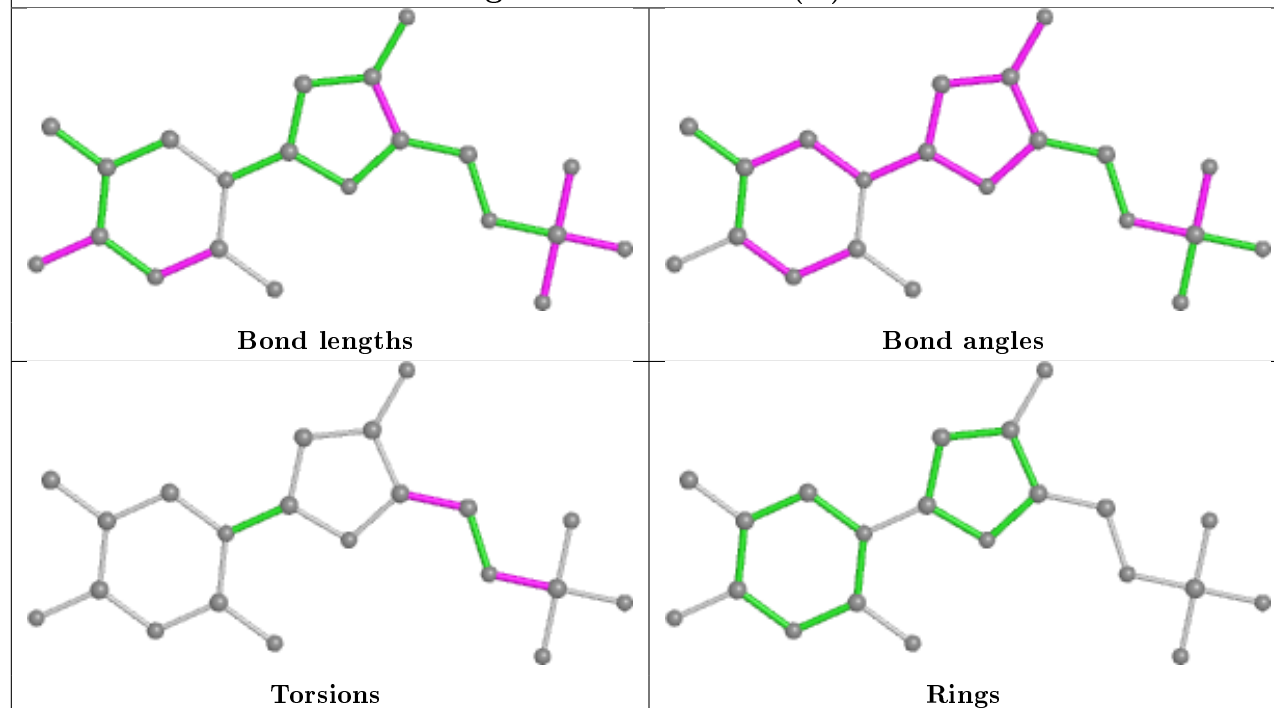
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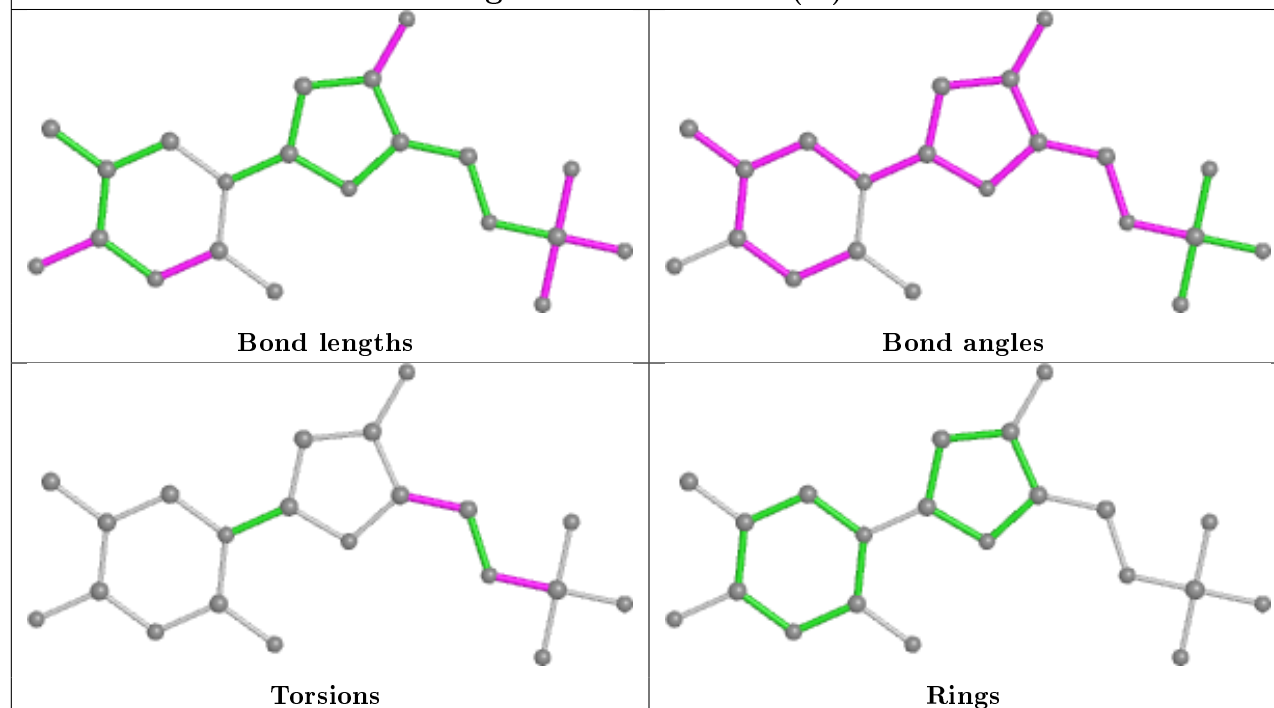
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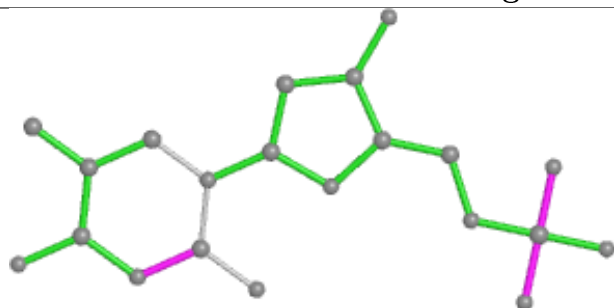
Ligand TMP A 8500 (B)



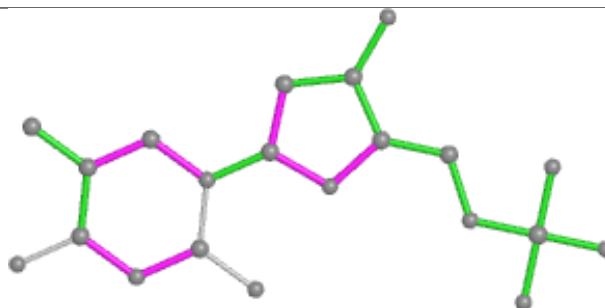
Ligand TMP A 8500 (A)



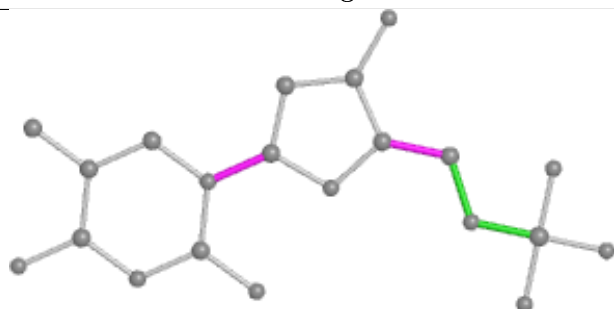
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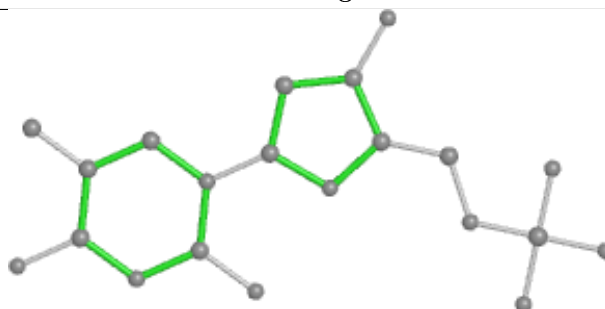
Bond lengths



Bond angles

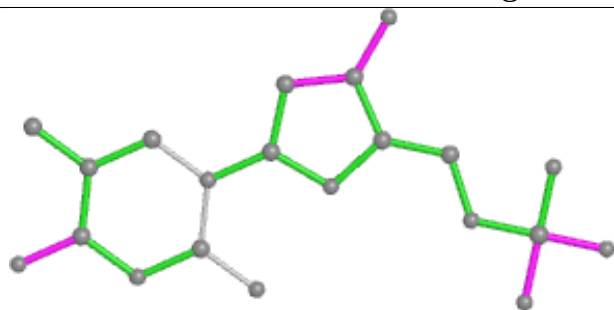


Torsions

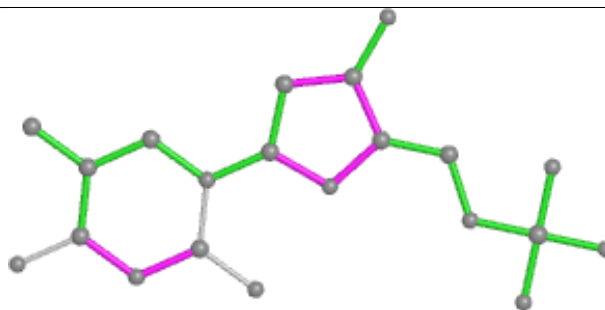


Rings

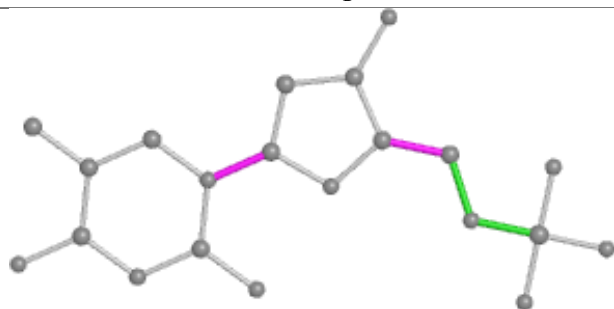
Ligand TMP C 9509



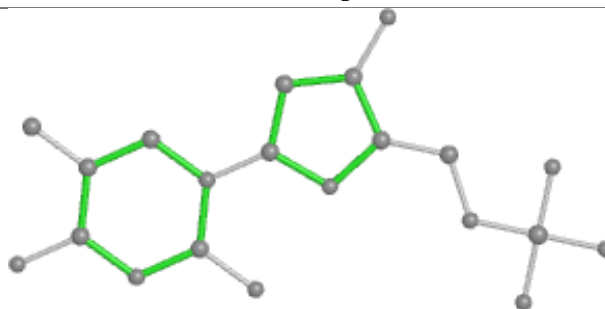
Bond lengths



Bond angles

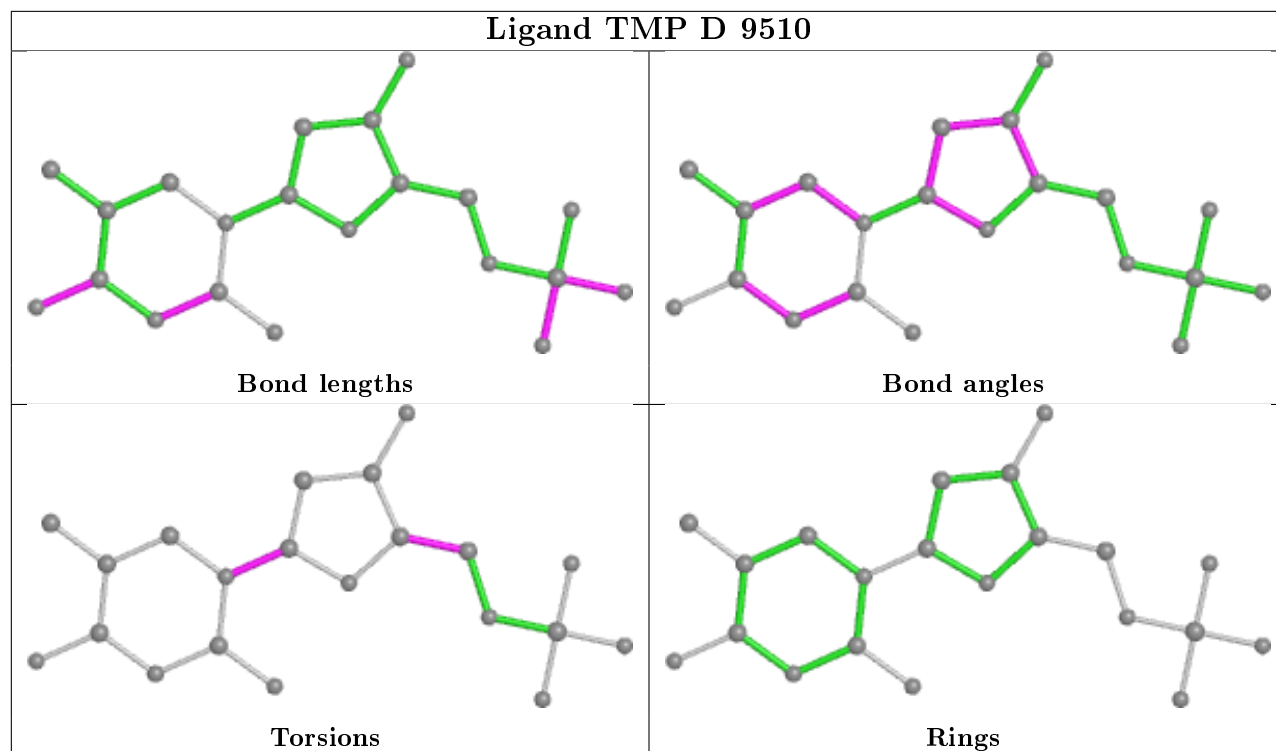


Torsions

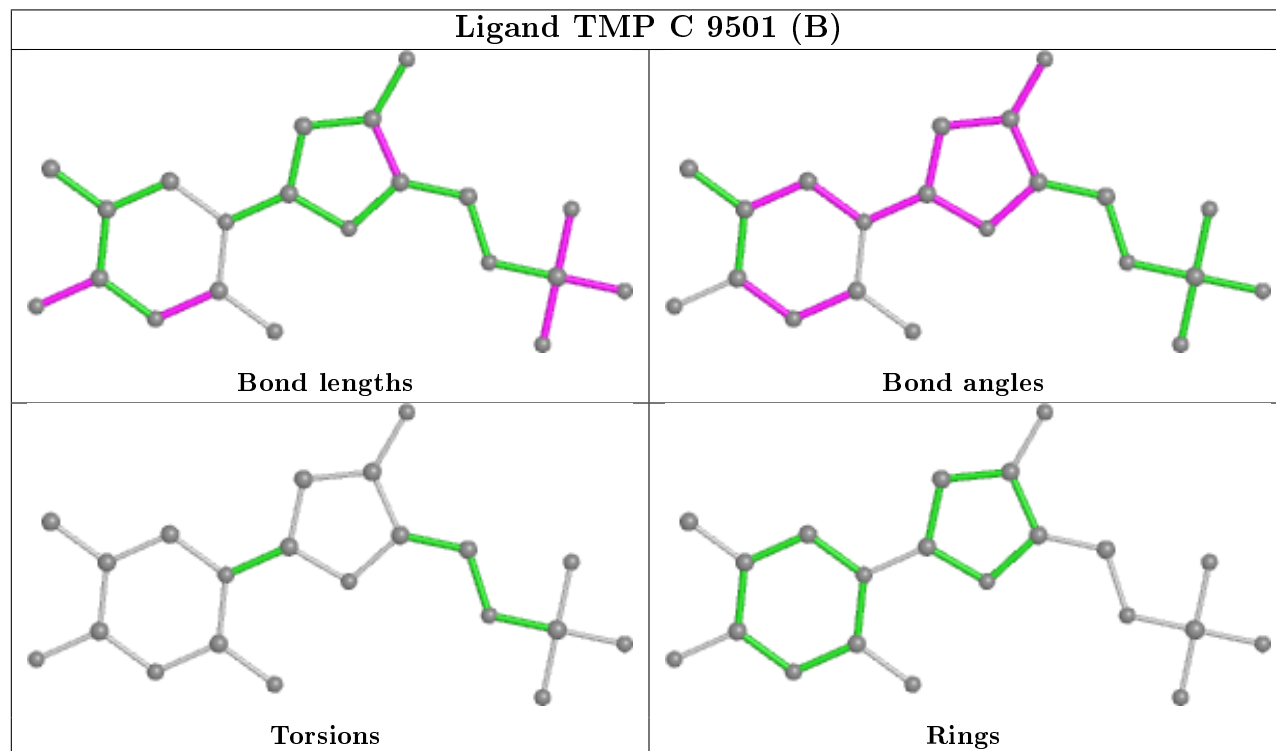


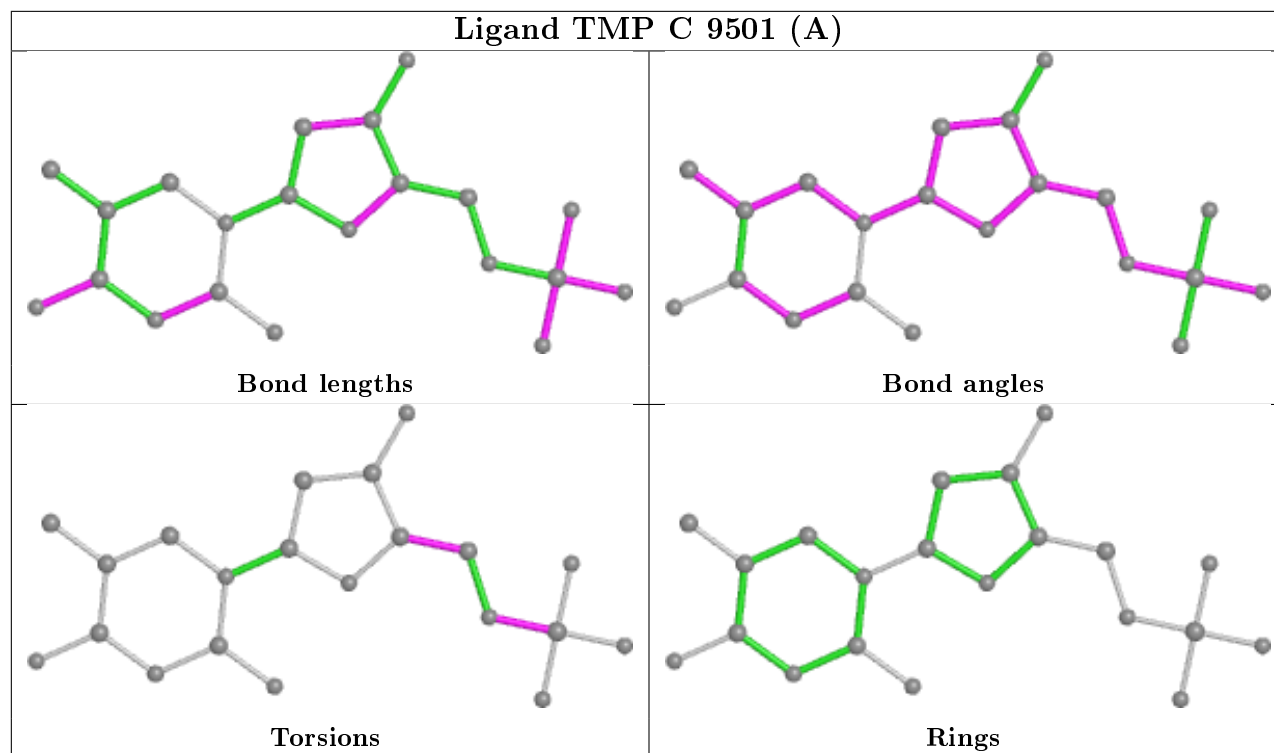
Rings

Ligand TMP D 9510



Ligand TMP C 9501 (B)





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	A	292/293 (99%)	0.13	14 (4%)	30	29	7, 12, 25, 43	0
1	B	293/293 (100%)	0.12	16 (5%)	25	24	6, 11, 26, 39	0
1	C	292/293 (99%)	0.24	26 (8%)	9	8	6, 13, 28, 42	0
1	D	292/293 (99%)	0.34	23 (7%)	12	12	7, 13, 30, 45	0
1	E	293/293 (100%)	0.52	30 (10%)	6	5	8, 15, 32, 52	0
1	F	293/293 (100%)	0.25	20 (6%)	17	16	6, 11, 29, 47	0
1	G	293/293 (100%)	0.12	13 (4%)	34	34	5, 10, 26, 40	0
1	H	292/293 (99%)	0.13	16 (5%)	25	24	8, 13, 26, 43	0
All	All	2340/2344 (99%)	0.23	158 (6%)	17	16	5, 12, 28, 52	0

The worst 5 of 158 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	193	PRO	9.0
1	F	13	GLY	8.9
1	E	195	GLY	8.6
1	E	12	SER	8.0
1	A	23	ILE	7.8

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

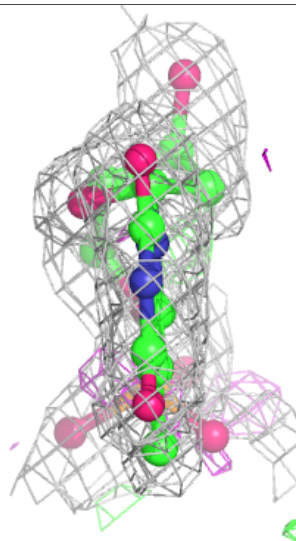
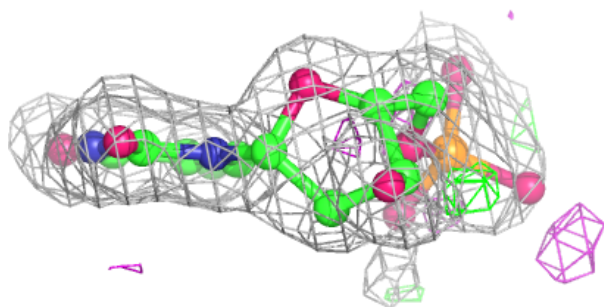
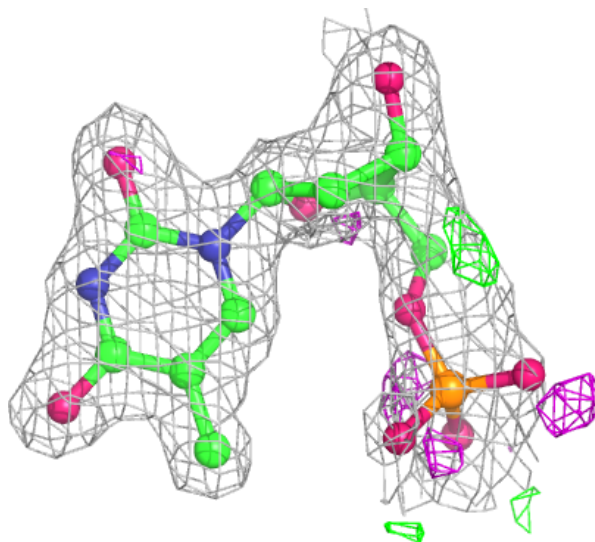
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	TMP	E	9503	21/21	0.83	0.13	27,34,50,51	0
3	TMP	G	9505[B]	21/21	0.84	0.16	18,27,30,34	21
3	TMP	G	9505[A]	21/21	0.84	0.16	15,16,27,28	21
3	TMP	F	9504[B]	21/21	0.86	0.16	10,13,22,23	21
3	TMP	F	9504[A]	21/21	0.86	0.16	14,26,43,46	21
2	SO4	D	5000	5/5	0.87	0.28	46,53,54,54	0
3	TMP	D	9502[B]	21/21	0.87	0.14	23,32,38,40	21
3	TMP	D	9502[A]	21/21	0.87	0.14	15,21,30,31	21
3	TMP	H	9506[B]	21/21	0.88	0.14	22,30,39,39	21
3	TMP	H	9506[A]	21/21	0.88	0.14	17,20,33,35	21
3	TMP	A	8500[B]	21/21	0.88	0.14	20,24,37,37	21
3	TMP	A	8500[A]	21/21	0.88	0.14	16,20,36,39	21
3	TMP	C	9501[B]	21/21	0.88	0.15	18,26,40,41	21
3	TMP	C	9501[A]	21/21	0.88	0.15	16,23,41,42	21
3	TMP	B	9500[A]	21/21	0.91	0.13	11,16,27,28	21
3	TMP	B	9500[B]	21/21	0.91	0.13	17,20,25,28	21
2	SO4	C	4000	5/5	0.92	0.17	40,42,45,48	0
2	SO4	D	5100	5/5	0.94	0.13	39,39,43,44	0
2	SO4	D	5200	5/5	0.94	0.22	41,47,49,50	0
2	SO4	E	5700	5/5	0.94	0.22	72,73,75,75	0
2	SO4	A	3700	5/5	0.95	0.19	35,36,40,46	0
2	SO4	D	4800	5/5	0.95	0.20	38,42,44,45	0
2	SO4	E	4700	5/5	0.96	0.13	34,36,37,42	0
2	SO4	F	6700	5/5	0.96	0.27	36,42,44,45	0
3	TMP	H	9514	21/21	0.96	0.12	12,14,17,20	0
3	TMP	F	9512	21/21	0.96	0.11	12,13,15,17	0
2	SO4	E	5800	5/5	0.97	0.23	39,44,45,47	0
2	SO4	D	3900	5/5	0.97	0.13	42,45,48,49	0
2	SO4	G	7700	5/5	0.97	0.20	45,47,49,50	0
3	TMP	A	9507	21/21	0.97	0.12	11,13,16,19	0
3	TMP	C	9509	21/21	0.97	0.11	13,14,16,19	0
3	TMP	D	9510	21/21	0.97	0.10	11,14,16,18	0
3	TMP	E	9511	21/21	0.97	0.10	14,14,18,19	0
3	TMP	B	9508	21/21	0.97	0.15	11,13,17,32	0
3	TMP	G	9513	21/21	0.98	0.13	10,12,15,19	0
2	SO4	C	3800	5/5	0.98	0.22	38,40,43,44	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.

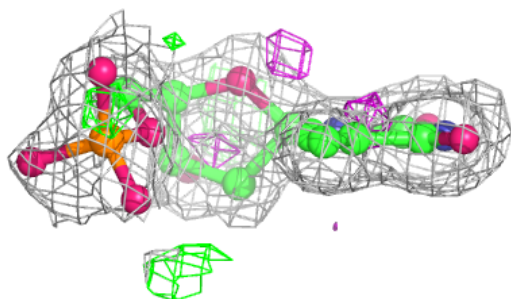
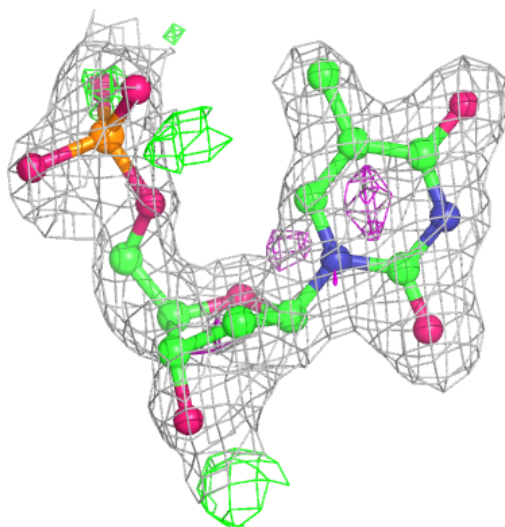
Electron density around TMP E 9503:

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



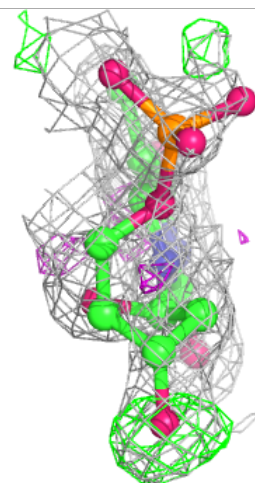
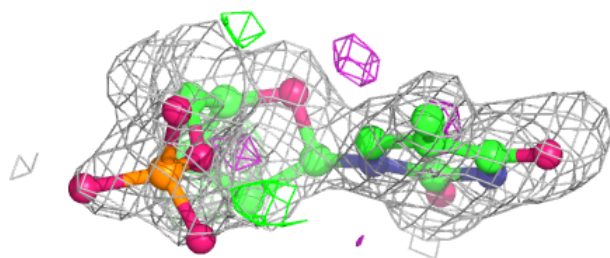
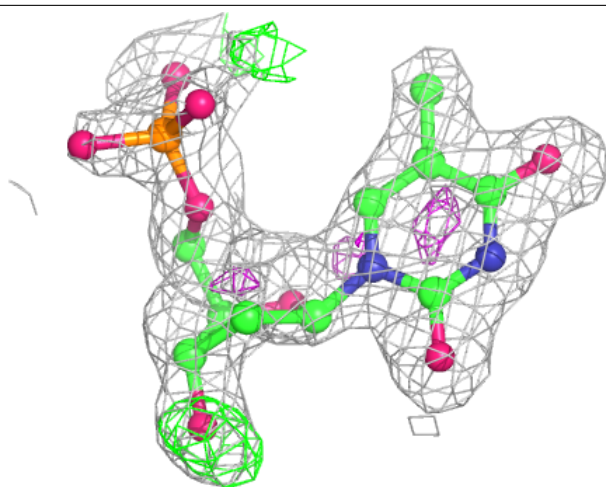
Electron density around TMP G 9505 (B):

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



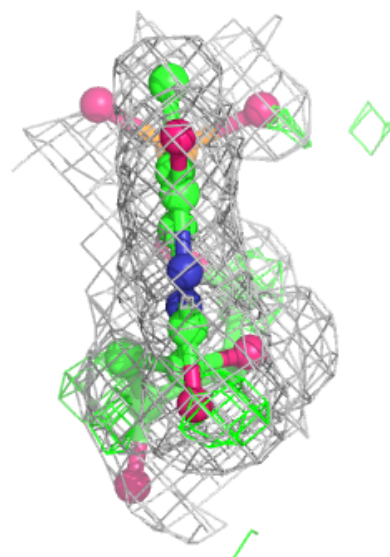
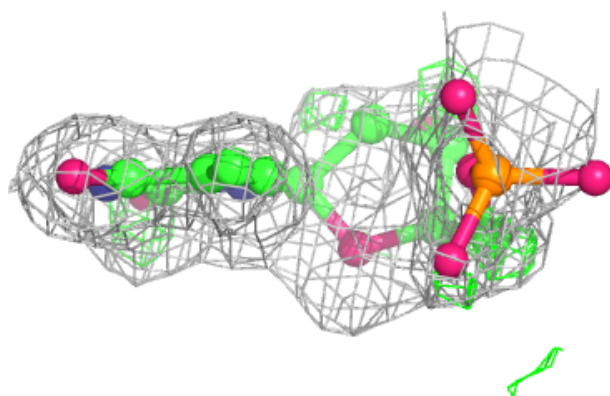
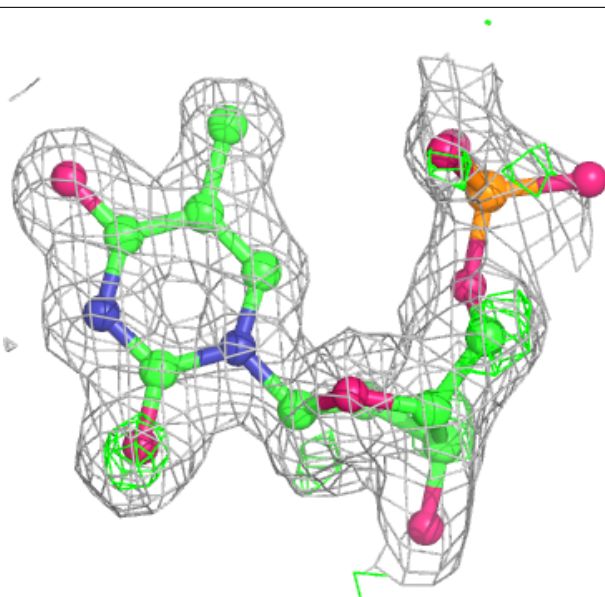
Electron density around TMP G 9505 (A):

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



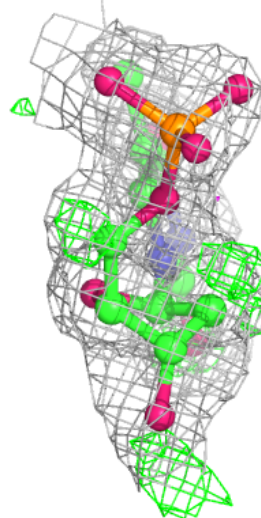
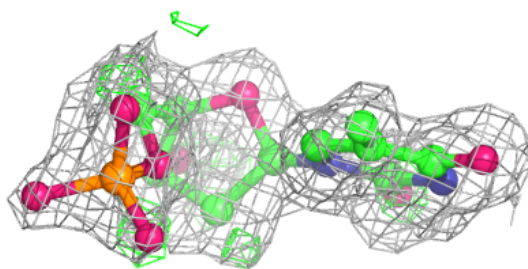
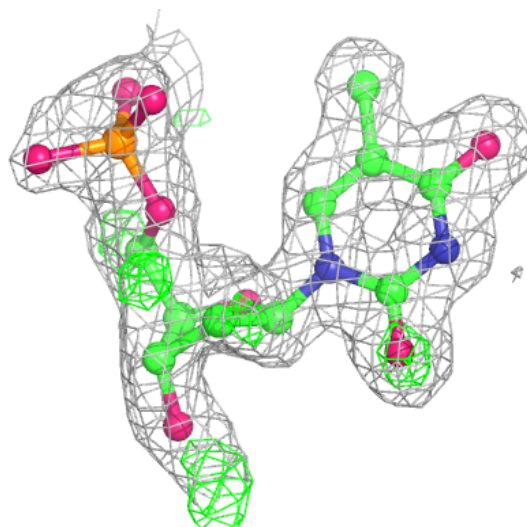
Electron density around TMP F 9504 (B):

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



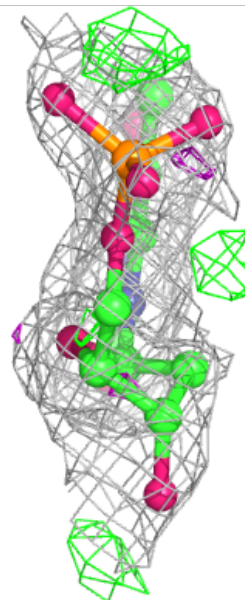
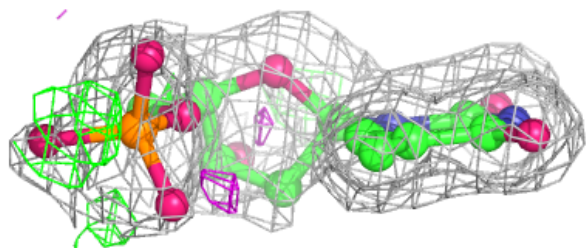
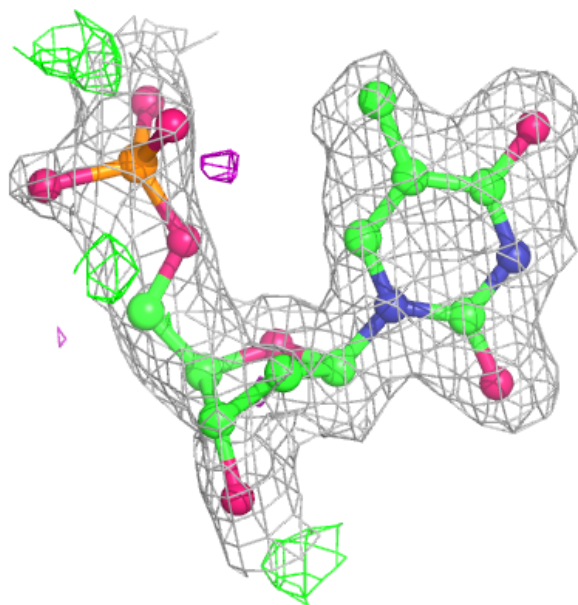
Electron density around TMP F 9504 (A):

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



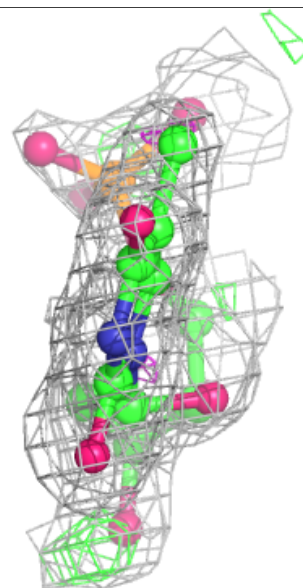
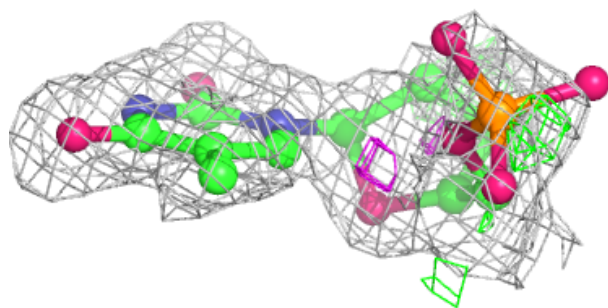
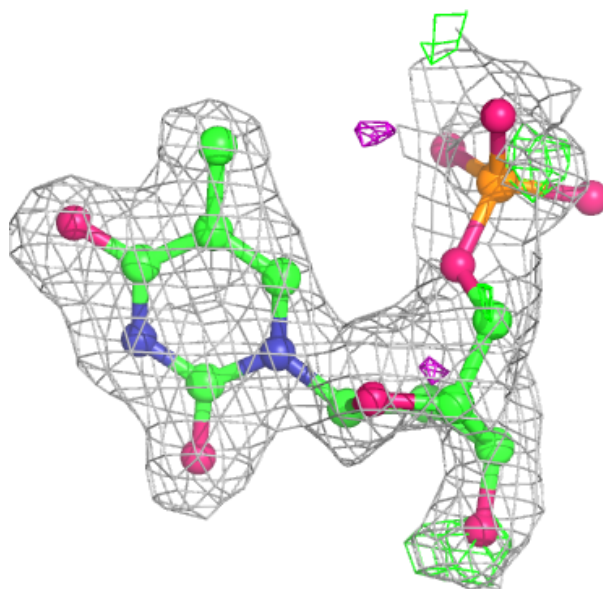
Electron density around TMP D 9502 (B):

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



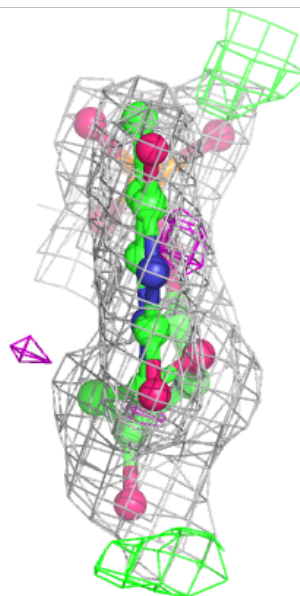
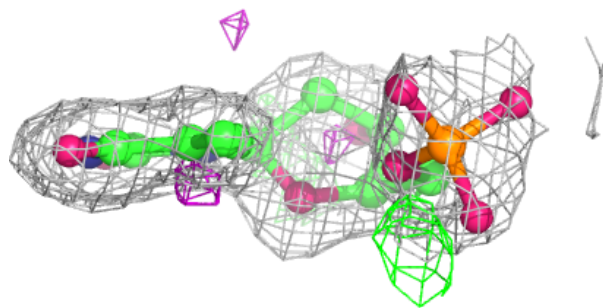
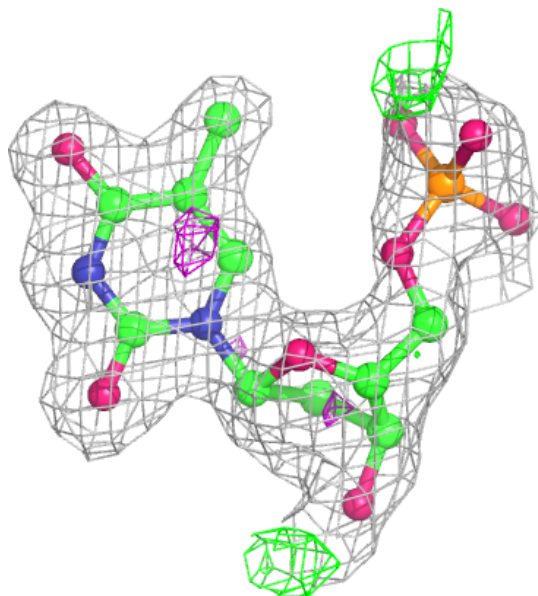
Electron density around TMP D 9502 (A):

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



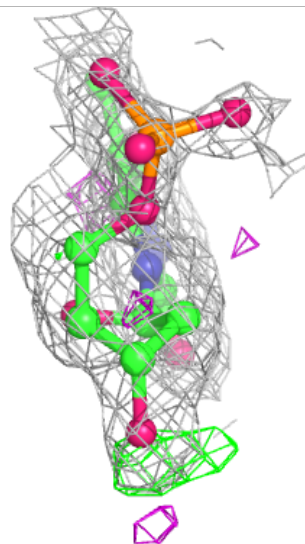
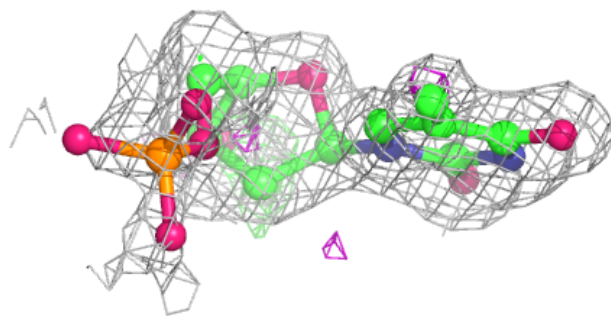
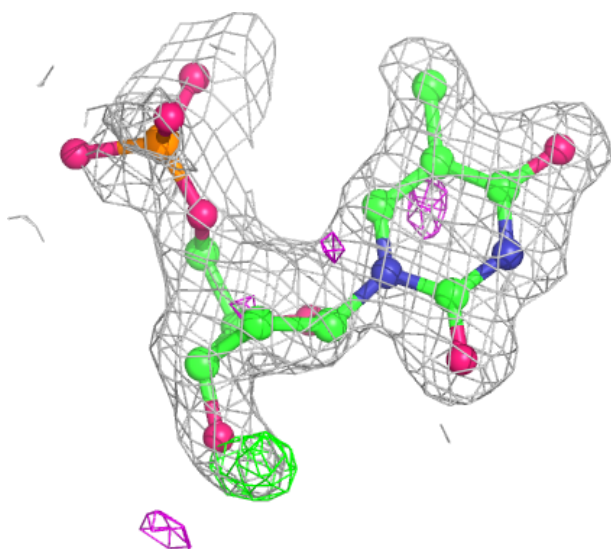
Electron density around TMP H 9506 (B):

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



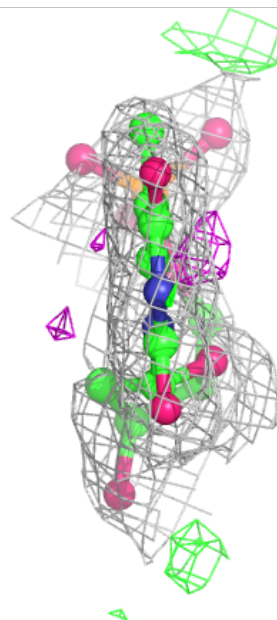
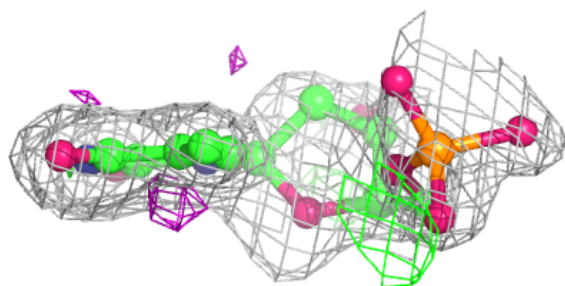
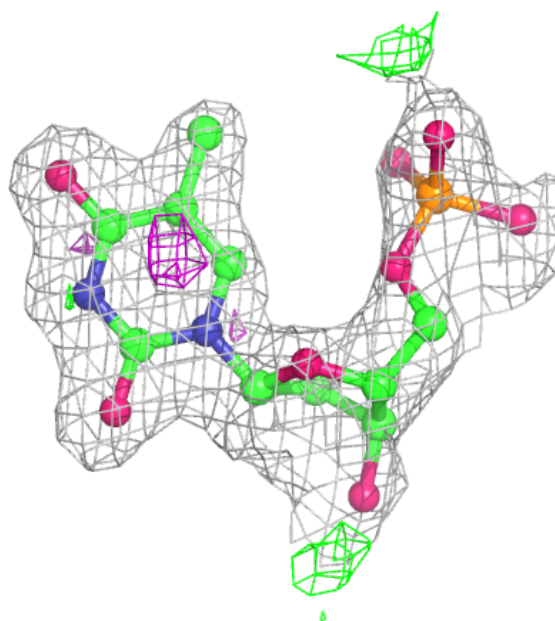
Electron density around TMP H 9506 (A):

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



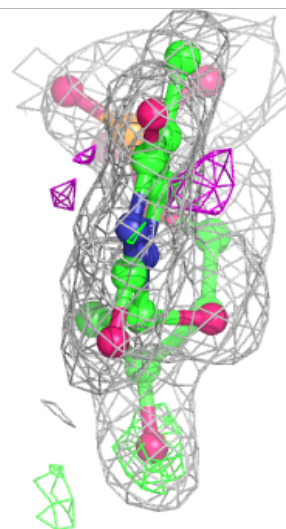
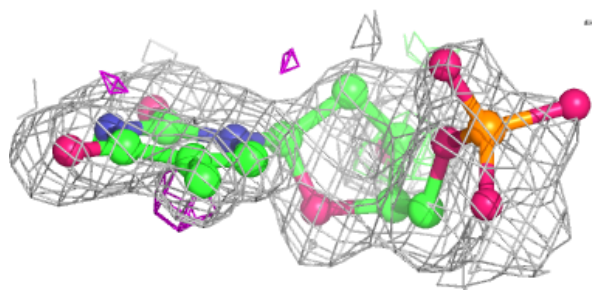
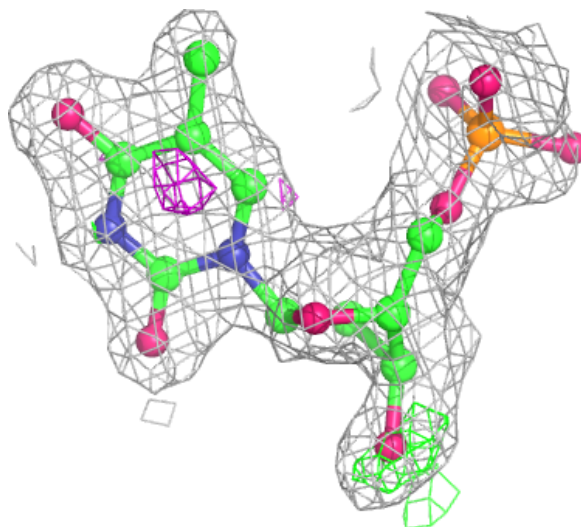
Electron density around TMP A 8500 (B):

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



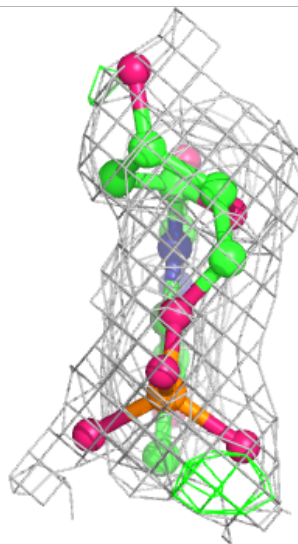
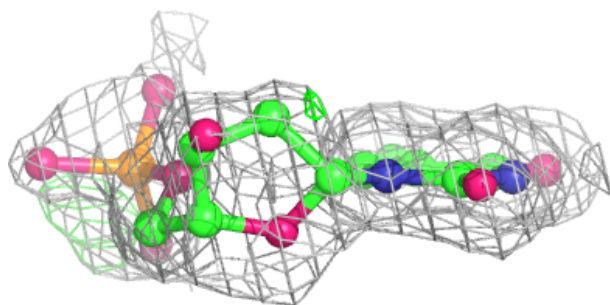
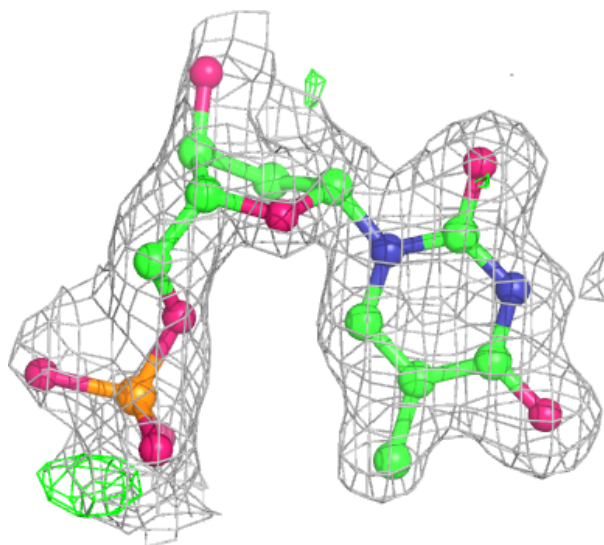
Electron density around TMP A 8500 (A):

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



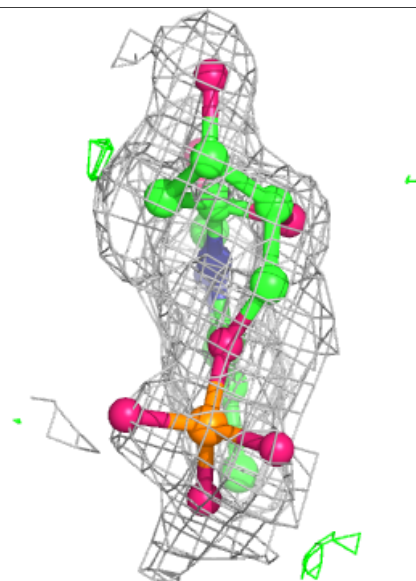
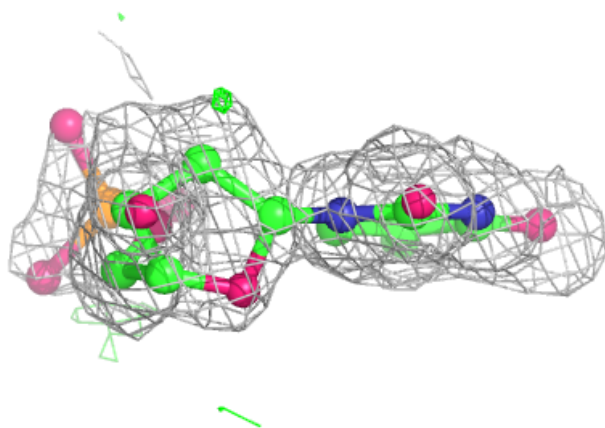
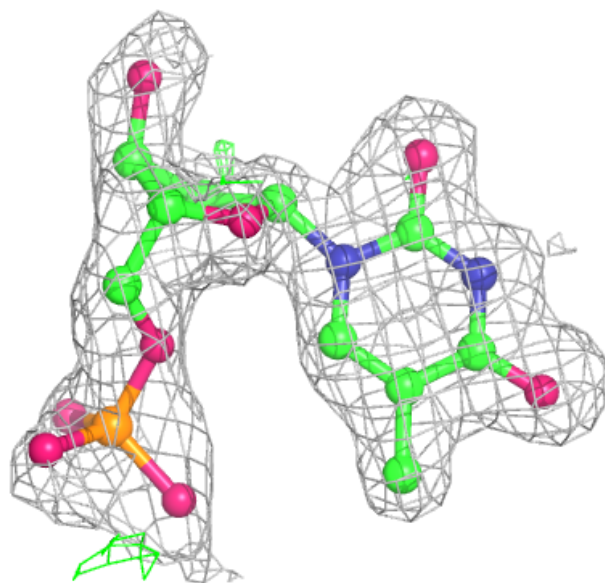
Electron density around TMP C 9501 (B):

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



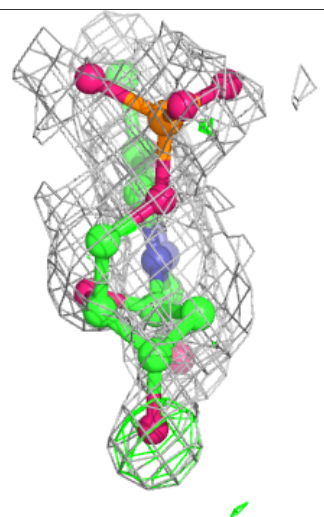
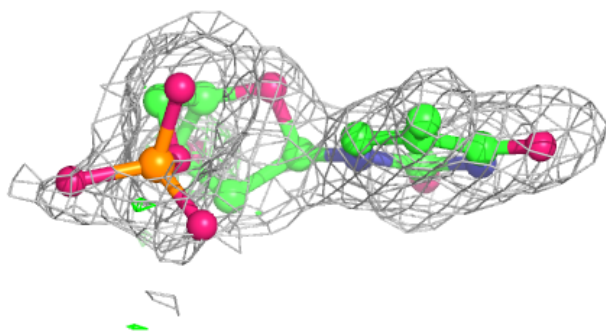
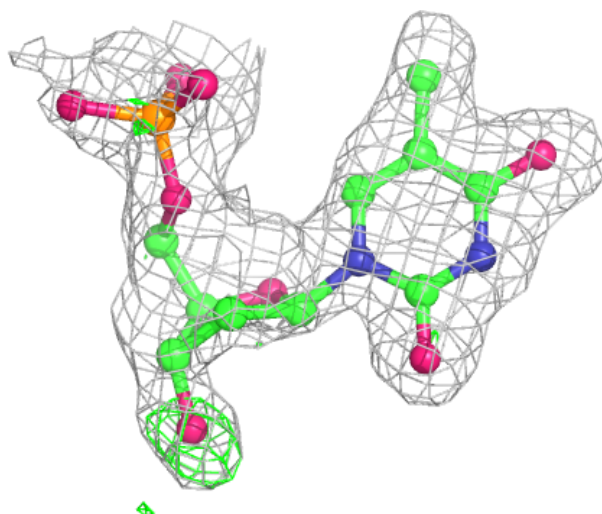
Electron density around TMP C 9501 (A):

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



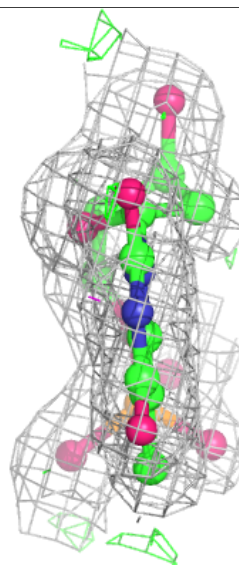
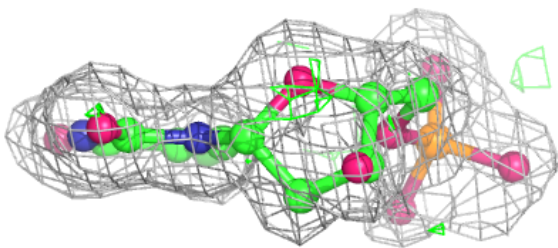
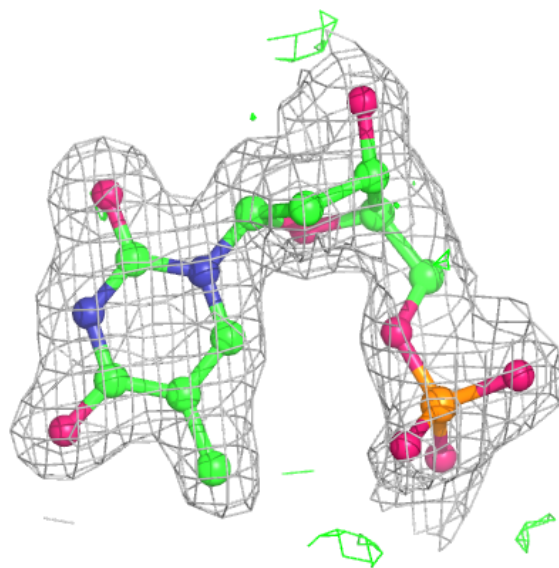
Electron density around TMP B 9500 (A):

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



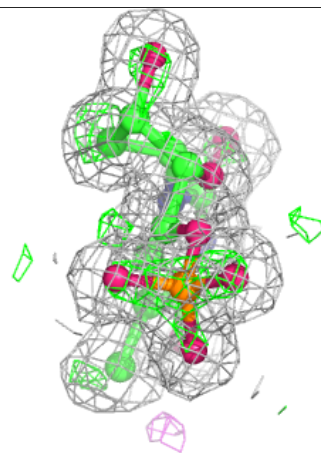
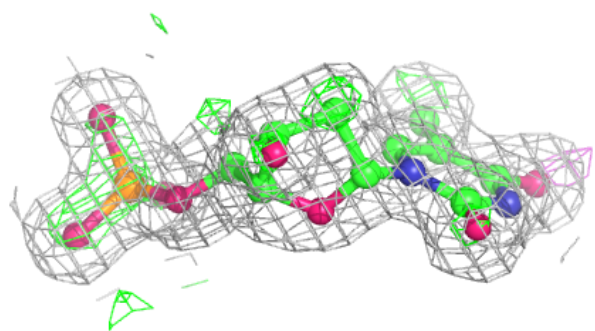
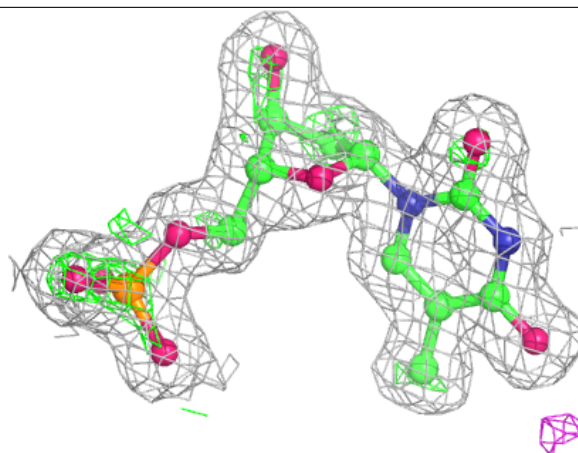
Electron density around TMP B 9500 (B):

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



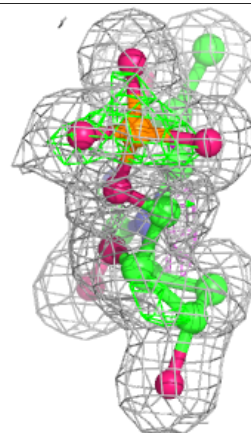
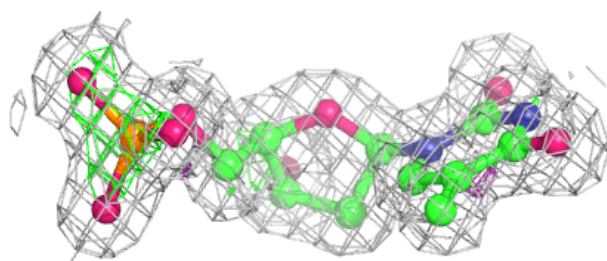
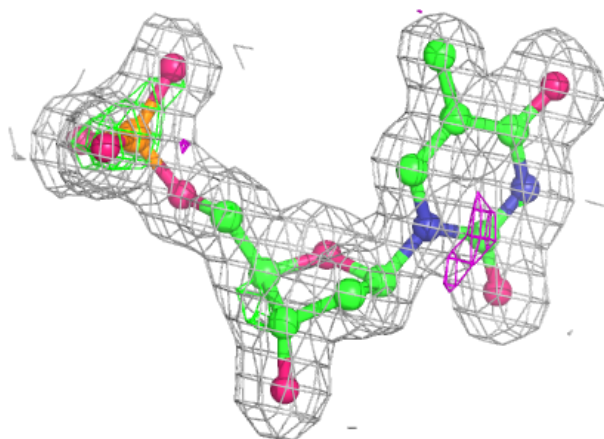
Electron density around TMP H 9514:

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



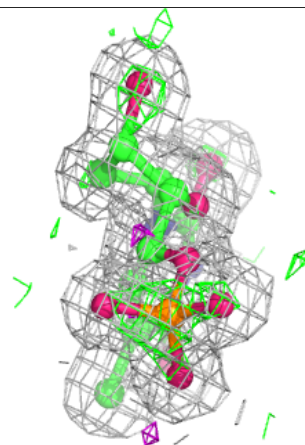
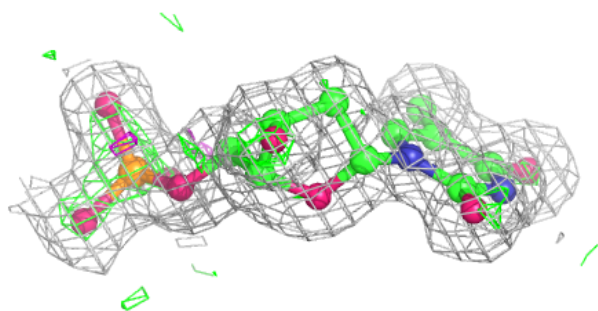
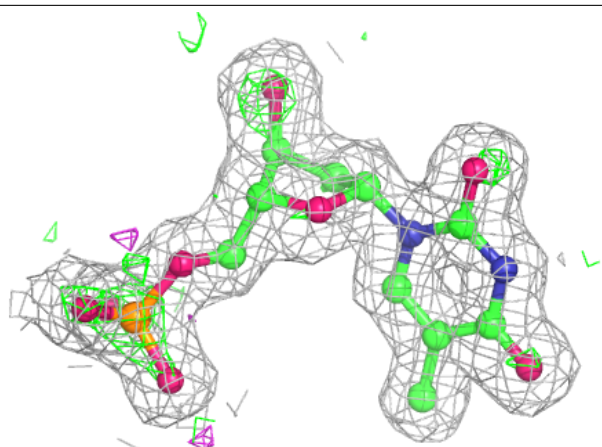
Electron density around TMP F 9512:

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



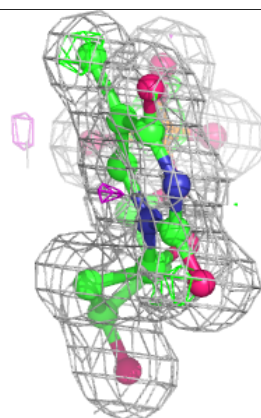
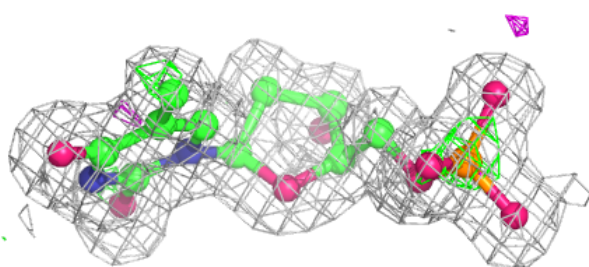
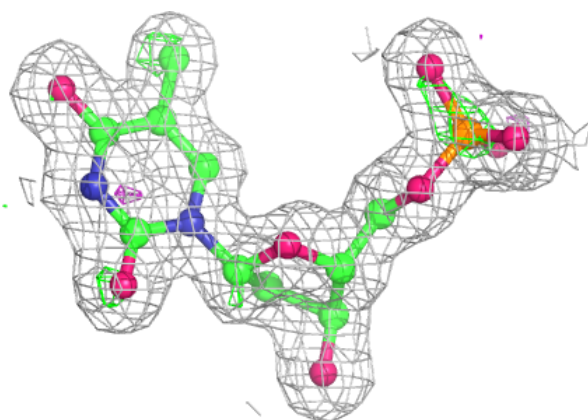
Electron density around TMP A 9507:

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



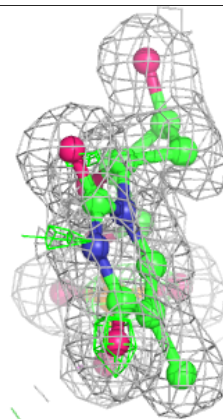
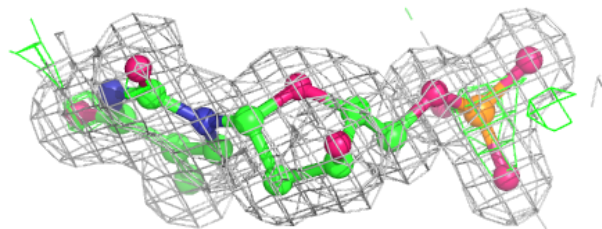
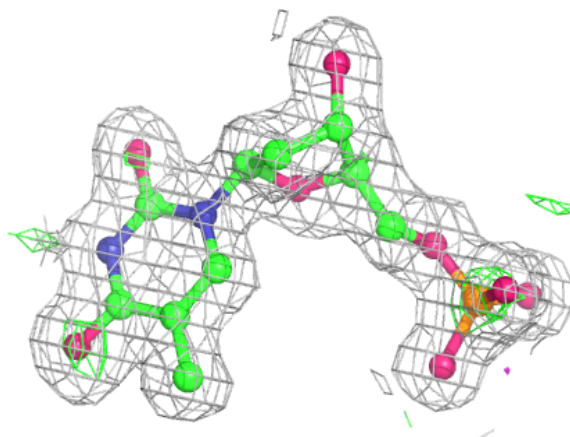
Electron density around TMP C 9509:

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



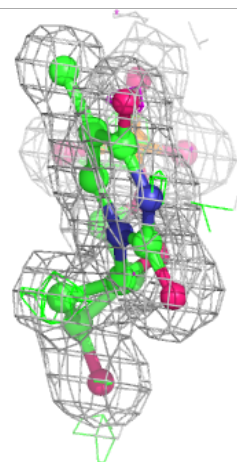
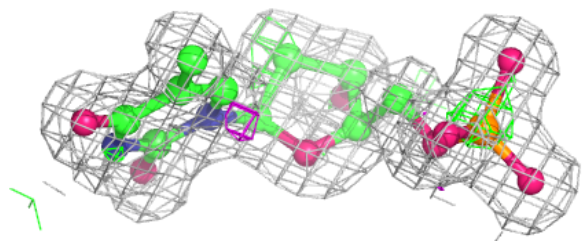
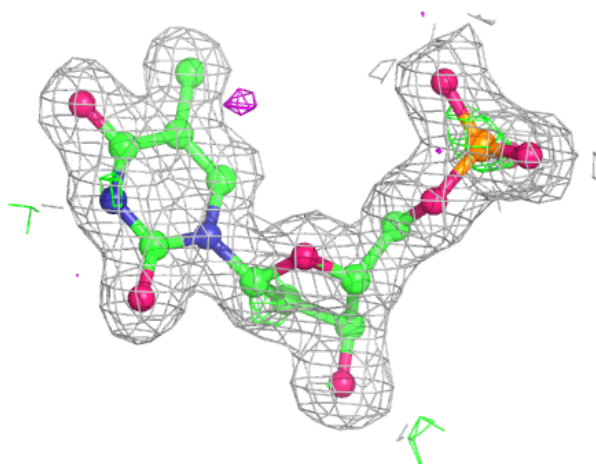
Electron density around TMP D 9510:

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



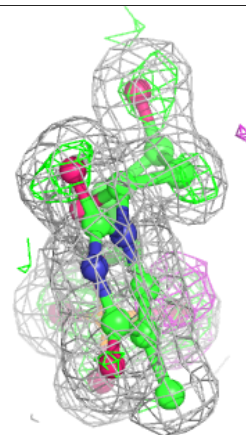
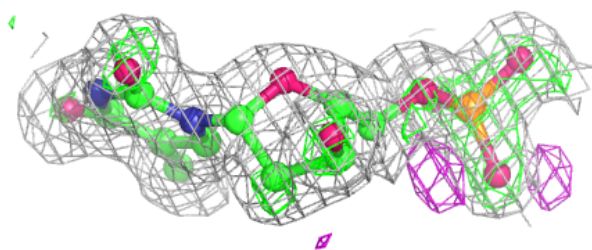
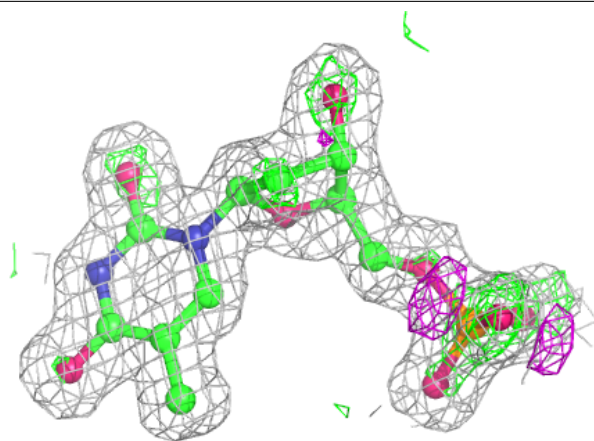
Electron density around TMP E 9511:

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



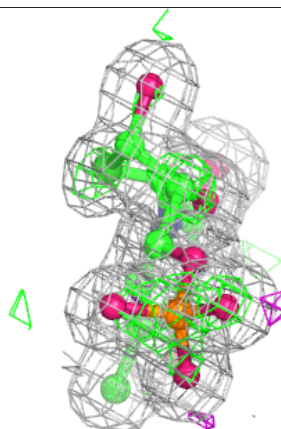
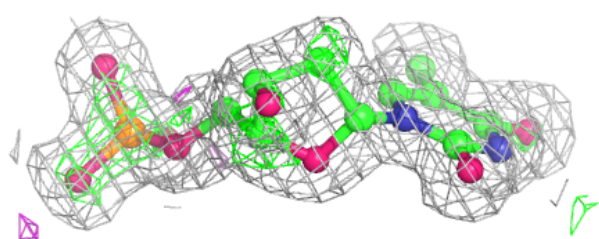
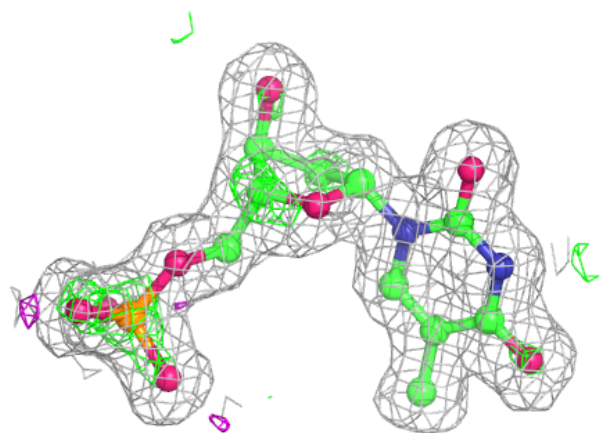
Electron density around TMP B 9508:

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



Electron density around TMP G 9513:

$2mF_o-DF_c$ (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.