



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 13, 2026 – 06:49 PM UTC

PDB ID : 4Z3Z / pdb_00004z3z
Title : Active site complex BamBC of Benzoyl Coenzyme A reductase in complex with Zinc
Authors : Weinert, T.; Kung, J.W.; Weidenweber, S.; Huwiler, S.G.; Boll, M.; Ermler, U.
Deposited on : 2015-04-01
Resolution : 2.67 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	:	FAILED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

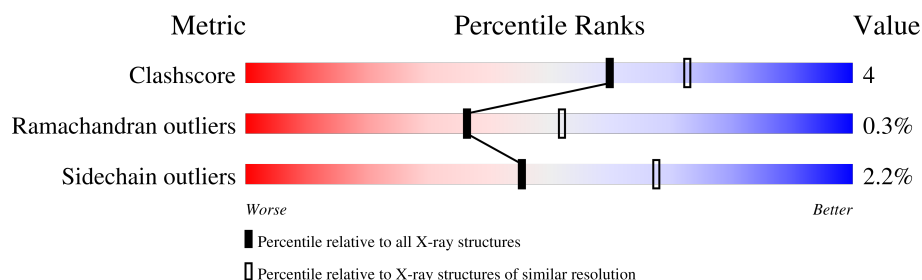
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.67 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))
Clashscore	190562	1141 (2.66-2.66)
Ramachandran outliers	187476	1126 (2.66-2.66)
Sidechain outliers	187428	1126 (2.66-2.66)

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 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 $\leq 5\%$.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	653	
1	B	653	
1	C	653	
1	D	653	
2	E	179	
2	F	179	
2	G	179	
2	H	179	

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	SF4	D	702	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 26146 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 Benzoyl-CoA reductase, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	652	Total	C	N	O	S	0	0	0
			5180	3308	875	963	34			
1	B	652	Total	C	N	O	S	0	0	0
			5180	3308	875	963	34			
1	C	652	Total	C	N	O	S	0	0	0
			5180	3308	875	963	34			
1	D	652	Total	C	N	O	S	0	0	0
			5180	3308	875	963	34			

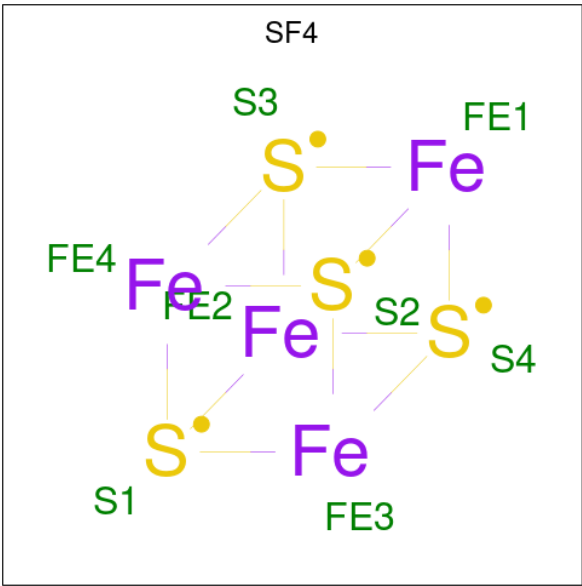
- Molecule 2 is a protein called Iron-sulfur cluster-binding oxidoreductase, putative benzoyl-CoA reductase electron transfer protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	163	Total	C	N	O	S	0	0	0
			1237	769	218	236	14			
2	F	170	Total	C	N	O	S	0	1	0
			1317	816	226	261	14			
2	G	169	Total	C	N	O	S	0	2	0
			1315	814	228	259	14			
2	H	161	Total	C	N	O	S	0	0	0
			1221	758	213	236	14			

- Molecule 3 is UNKNOWN LIGAND (CCD ID: UNL) (formula:).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	X	0	0
			1	1		
3	B	1	Total	X	0	0
			1	1		
3	C	1	Total	X	0	0
			1	1		
3	D	1	Total	X	0	0
			1	1		

- Molecule 4 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



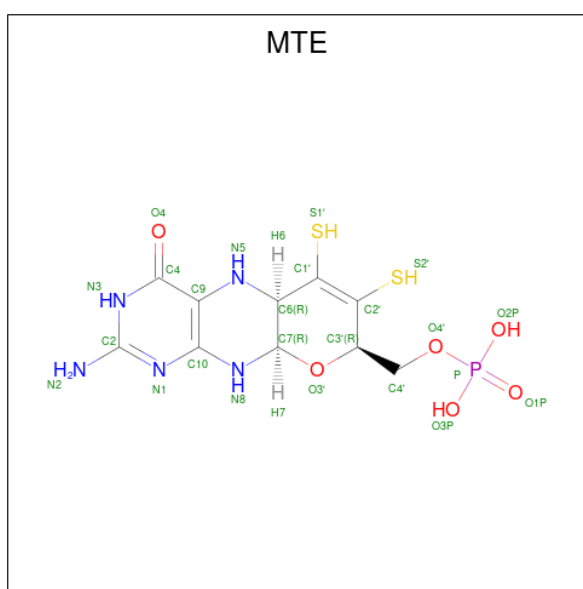
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	Fe	S	0	0
			8	4	4		
4	B	1	Total	Fe	S	0	0
			8	4	4		
4	C	1	Total	Fe	S	0	0
			8	4	4		
4	D	1	Total	Fe	S	0	0
			8	4	4		
4	E	1	Total	Fe	S	0	0
			8	4	4		
4	E	1	Total	Fe	S	0	0
			8	4	4		
4	E	1	Total	Fe	S	0	0
			8	4	4		
4	F	1	Total	Fe	S	0	0
			8	4	4		
4	F	1	Total	Fe	S	0	0
			8	4	4		
4	F	1	Total	Fe	S	0	0
			8	4	4		
4	G	1	Total	Fe	S	0	0
			8	4	4		
4	G	1	Total	Fe	S	0	0
			8	4	4		
4	G	1	Total	Fe	S	0	0
			8	4	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	H	1	Total	Fe	S	0	0
			8	4	4		
4	H	1	Total	Fe	S	0	0
			8	4	4		
4	H	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 5 is PHOSPHONIC ACIDMONO-(2-AMINO-5,6-DIMERCAPTO-4-OXO-3,7,8A, 9,10,10A-HEXAHYDRO-4H-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-7-YLMETHYL) ESTER (CCD ID: MTE) (formula: $C_{10}H_{14}N_5O_6PS_2$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		
5	A	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		
5	B	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		
5	B	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		
5	C	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		
5	C	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		
5	D	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	D	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		

- Molecule 6 is TUNGSTEN ION (CCD ID: W) (formula: W).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	W	0	0
			1	1		
6	B	1	Total	W	0	0
			1	1		
6	C	1	Total	W	0	0
			1	1		
6	D	1	Total	W	0	0
			1	1		

- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 8 is ZINC ION (CCD ID: ZN) (formula: Zn).

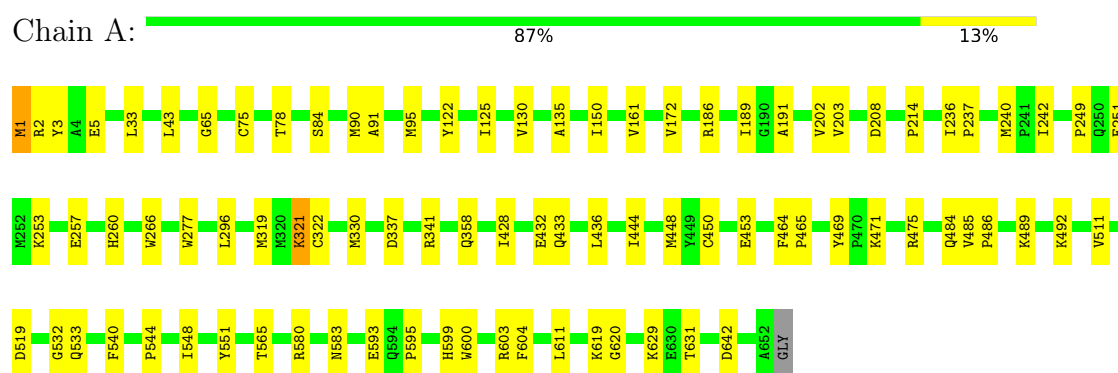
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	Zn	0	0
			1	1		
8	B	1	Total	Zn	0	0
			1	1		
8	C	1	Total	Zn	0	0
			1	1		
8	D	1	Total	Zn	0	0
			1	1		

3 Residue-property plots [i](#)

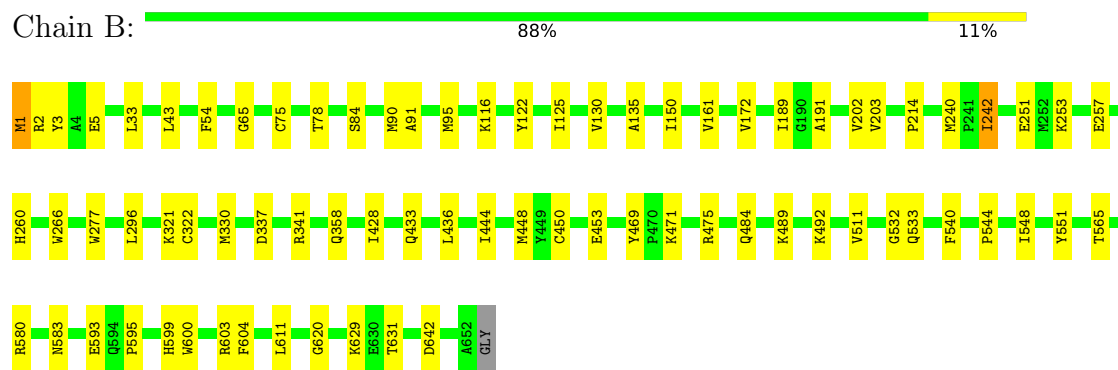
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS failed to run properly.

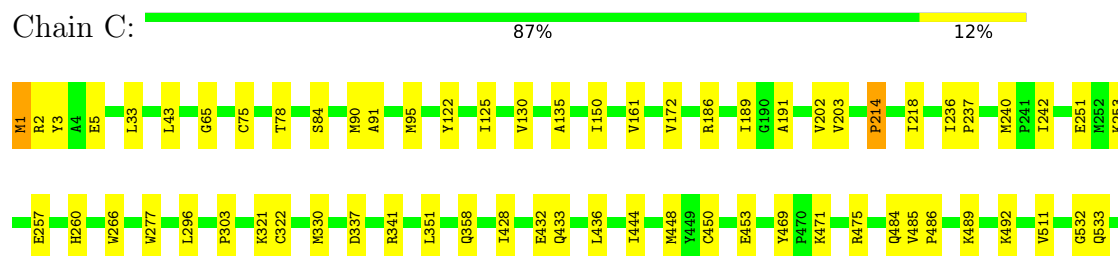
- Molecule 1: Benzoyl-CoA reductase, putative



- Molecule 1: Benzoyl-CoA reductase, putative



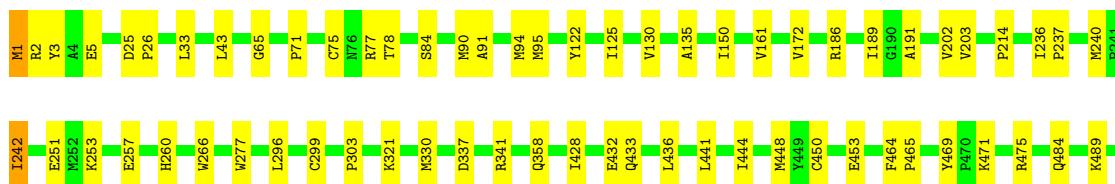
- Molecule 1: Benzoyl-CoA reductase, putative





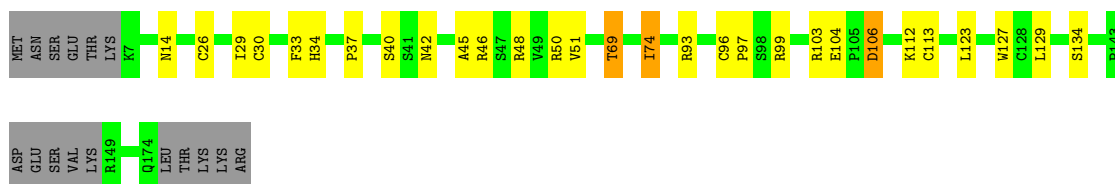
- Molecule 1: Benzoyl-CoA reductase, putative

Chain D: 86% 13%



- Molecule 2: Iron-sulfur cluster-binding oxidoreductase, putative benzoyl-CoA reductase electron transfer protein

Chain E: 75% 15% 9%



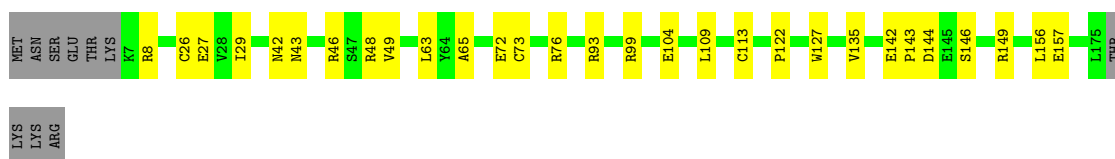
- Molecule 2: Iron-sulfur cluster-binding oxidoreductase, putative benzoyl-CoA reductase electron transfer protein

Chain F: 77% 16% 5%

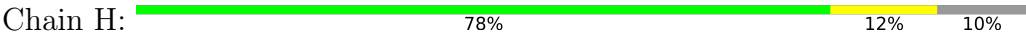


- Molecule 2: Iron-sulfur cluster-binding oxidoreductase, putative benzoyl-CoA reductase electron transfer protein

Chain G: 78% 16% 6%



● Molecule 2: Iron-sulfur cluster-binding oxidoreductase, putative benzoyl-CoA reductase electron transfer protein



4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	124.24Å 117.43Å 143.08Å 90.00° 111.04° 90.00°	Depositor
Resolution (Å)	82.51 – 2.67	Depositor
% Data completeness (in resolution range)	97.2 (82.51-2.67)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.14 (at 2.65Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.232 , 0.274	Depositor
Wilson B-factor (Å ²)	62.0	Xtriage
Anisotropy	0.258	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	26146	wwPDB-VP
Average B, all atoms (Å ²)	114.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.21% 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: UNL, MTE, SF4, MG, ZN, W

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	0.29	0/5306	0.71	6/7172 (0.1%)
1	B	0.29	0/5306	0.71	6/7172 (0.1%)
1	C	0.29	0/5306	0.71	6/7172 (0.1%)
1	D	0.29	0/5306	0.71	6/7172 (0.1%)
2	E	0.33	0/1259	0.77	0/1705
2	F	0.33	0/1343	0.75	0/1819
2	G	0.32	0/1344	0.78	0/1819
2	H	0.30	0/1242	0.76	0/1681
All	All	0.29	0/26412	0.72	24/35712 (0.1%)

There are no bond length outliers.

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	240	MET	CA-C-N	6.92	128.49	119.84
1	B	240	MET	C-N-CA	6.92	128.49	119.84
1	C	240	MET	CA-C-N	6.88	128.44	119.84
1	C	240	MET	C-N-CA	6.88	128.44	119.84
1	D	240	MET	CA-C-N	6.84	128.39	119.84

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	5180	0	5110	45	0
1	B	5180	0	5110	36	0
1	C	5180	0	5110	42	0
1	D	5180	0	5110	45	0
2	E	1237	0	1181	20	0
2	F	1317	0	1266	17	0
2	G	1315	0	1263	18	0
2	H	1221	0	1158	14	0
3	A	1	0	0	1	0
3	B	1	0	0	0	0
3	C	1	0	0	1	0
3	D	1	0	0	0	0
4	A	8	0	0	0	0
4	B	8	0	0	0	0
4	C	8	0	0	0	0
4	D	8	0	0	2	0
4	E	24	0	0	2	0
4	F	24	0	0	1	0
4	G	24	0	0	2	0
4	H	24	0	0	1	0
5	A	48	0	20	4	0
5	B	48	0	20	1	0
5	C	48	0	20	3	0
5	D	48	0	20	1	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
8	A	1	0	0	0	0
8	B	1	0	0	0	0
8	C	1	0	0	0	0
8	D	1	0	0	0	0
All	All	26146	0	25388	222	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 222 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)
2:G:73:CYS:HB2	4:G:1003:SF4:S1	2.03	0.97
3:C:701:UNL:X	5:C:703:MTE:S1'	2.62	0.88
2:E:34:HIS:NE2	4:E:1002:SF4:S1	2.57	0.77
1:D:299:CYS:HB2	4:D:702:SF4:S3	2.29	0.73
1:A:322:CYS:HB3	5:A:704:MTE:S1'	2.30	0.70

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	650/653 (100%)	614 (94%)	34 (5%)	2 (0%)	36	52
1	B	650/653 (100%)	613 (94%)	35 (5%)	2 (0%)	36	52
1	C	650/653 (100%)	613 (94%)	35 (5%)	2 (0%)	36	52
1	D	650/653 (100%)	613 (94%)	35 (5%)	2 (0%)	36	52
2	E	159/179 (89%)	151 (95%)	8 (5%)	0	100	100
2	F	169/179 (94%)	157 (93%)	11 (6%)	1 (1%)	21	34
2	G	169/179 (94%)	154 (91%)	15 (9%)	0	100	100
2	H	157/179 (88%)	146 (93%)	9 (6%)	2 (1%)	9	16
All	All	3254/3328 (98%)	3061 (94%)	182 (6%)	11 (0%)	36	52

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	107	SER
1	A	33	LEU
1	B	33	LEU
1	C	33	LEU
1	D	33	LEU

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	546/548 (100%)	537 (98%)	9 (2%)	55	74
1	B	546/548 (100%)	537 (98%)	9 (2%)	55	74
1	C	546/548 (100%)	537 (98%)	9 (2%)	55	74
1	D	546/548 (100%)	537 (98%)	9 (2%)	55	74
2	E	134/159 (84%)	128 (96%)	6 (4%)	24	42
2	F	148/159 (93%)	139 (94%)	9 (6%)	17	30
2	G	147/159 (92%)	142 (97%)	5 (3%)	32	53
2	H	132/159 (83%)	128 (97%)	4 (3%)	36	57
All	All	2745/2828 (97%)	2685 (98%)	60 (2%)	45	67

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	189	ILE
2	G	135	VAL
1	D	599	HIS
2	G	99	ARG
2	H	136	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	427	ASN
2	G	43	ASN
1	B	463	GLN
1	C	179	GLN
1	C	234	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 40 ligands modelled in this entry, 4 are unknown and 12 are monoatomic - leaving 24 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
4	SF4	F	1003	2	0,12,12	-	-	-		
4	SF4	G	1001	2	0,12,12	-	-	-		
5	MTE	B	703	7,6	21,26,26	2.84	8 (38%)	19,40,40	1.88	6 (31%)
5	MTE	A	703	5,7,6	21,26,26	3.03	8 (38%)	19,40,40	2.24	6 (31%)
4	SF4	F	1001	2	0,12,12	-	-	-		
5	MTE	C	704	7,6	21,26,26	2.89	7 (33%)	19,40,40	2.09	6 (31%)
5	MTE	D	703	7,6	21,26,26	2.74	8 (38%)	19,40,40	2.02	5 (26%)
5	MTE	A	704	5,7,6	21,26,26	2.70	8 (38%)	19,40,40	2.86	7 (36%)
4	SF4	H	1003	2	0,12,12	-	-	-		
5	MTE	D	704	7,6	21,26,26	2.88	7 (33%)	19,40,40	2.20	5 (26%)
4	SF4	F	1002	2	0,12,12	-	-	-		
5	MTE	B	704	7,6	21,26,26	2.96	7 (33%)	19,40,40	2.60	6 (31%)
4	SF4	E	1002	2	0,12,12	-	-	-		
4	SF4	C	702	1	0,12,12	-	-	-		
5	MTE	C	703	7,6	21,26,26	2.88	7 (33%)	19,40,40	2.07	5 (26%)
4	SF4	B	702	1	0,12,12	-	-	-		
4	SF4	G	1002	2	0,12,12	-	-	-		
4	SF4	A	702	1	0,12,12	-	-	-		
4	SF4	H	1002	2	0,12,12	-	-	-		
4	SF4	G	1003	2	0,12,12	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SF4	E	1003	2	0,12,12	-	-	-		
4	SF4	E	1001	2	0,12,12	-	-	-		
4	SF4	D	702	1	0,12,12	-	-	-		
4	SF4	H	1001	2	0,12,12	-	-	-		

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	SF4	F	1003	2	-	-	0/6/5/5
4	SF4	G	1001	2	-	-	0/6/5/5
5	MTE	B	703	7,6	-	0/6/34/34	0/3/3/3
5	MTE	A	703	5,7,6	-	2/6/34/34	0/3/3/3
4	SF4	F	1001	2	-	-	0/6/5/5
5	MTE	C	704	7,6	-	4/6/34/34	0/3/3/3
5	MTE	D	703	7,6	-	2/6/34/34	0/3/3/3
5	MTE	A	704	5,7,6	-	3/6/34/34	0/3/3/3
5	MTE	D	704	7,6	-	4/6/34/34	0/3/3/3
4	SF4	H	1003	2	-	-	0/6/5/5
4	SF4	F	1002	2	-	-	0/6/5/5
5	MTE	B	704	7,6	-	4/6/34/34	0/3/3/3
4	SF4	E	1002	2	-	-	0/6/5/5
4	SF4	C	702	1	-	-	0/6/5/5
5	MTE	C	703	7,6	-	0/6/34/34	0/3/3/3
4	SF4	B	702	1	-	-	0/6/5/5
4	SF4	G	1002	2	-	-	0/6/5/5
4	SF4	A	702	1	-	-	0/6/5/5
4	SF4	H	1002	2	-	-	0/6/5/5
4	SF4	G	1003	2	-	-	0/6/5/5
4	SF4	E	1003	2	-	-	0/6/5/5
4	SF4	E	1001	2	-	-	0/6/5/5
4	SF4	D	702	1	-	-	0/6/5/5
4	SF4	H	1001	2	-	-	0/6/5/5

The worst 5 of 60 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	704	MTE	C10-N8	8.94	1.44	1.35
5	C	704	MTE	C10-N8	8.35	1.44	1.35

Continued on next page...

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	703	MTE	C10-N8	8.34	1.44	1.35
5	A	703	MTE	C10-N8	8.32	1.44	1.35
5	B	703	MTE	C10-N8	7.90	1.43	1.35

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	704	MTE	O3'-C7-C6	6.93	113.59	108.96
5	B	704	MTE	O3'-C7-N8	-5.37	103.73	108.61
5	B	704	MTE	C2-N3-C4	-5.25	115.59	125.11
5	A	704	MTE	O3'-C7-N8	-5.18	103.90	108.61
5	A	704	MTE	C2-N3-C4	-4.98	116.07	125.11

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

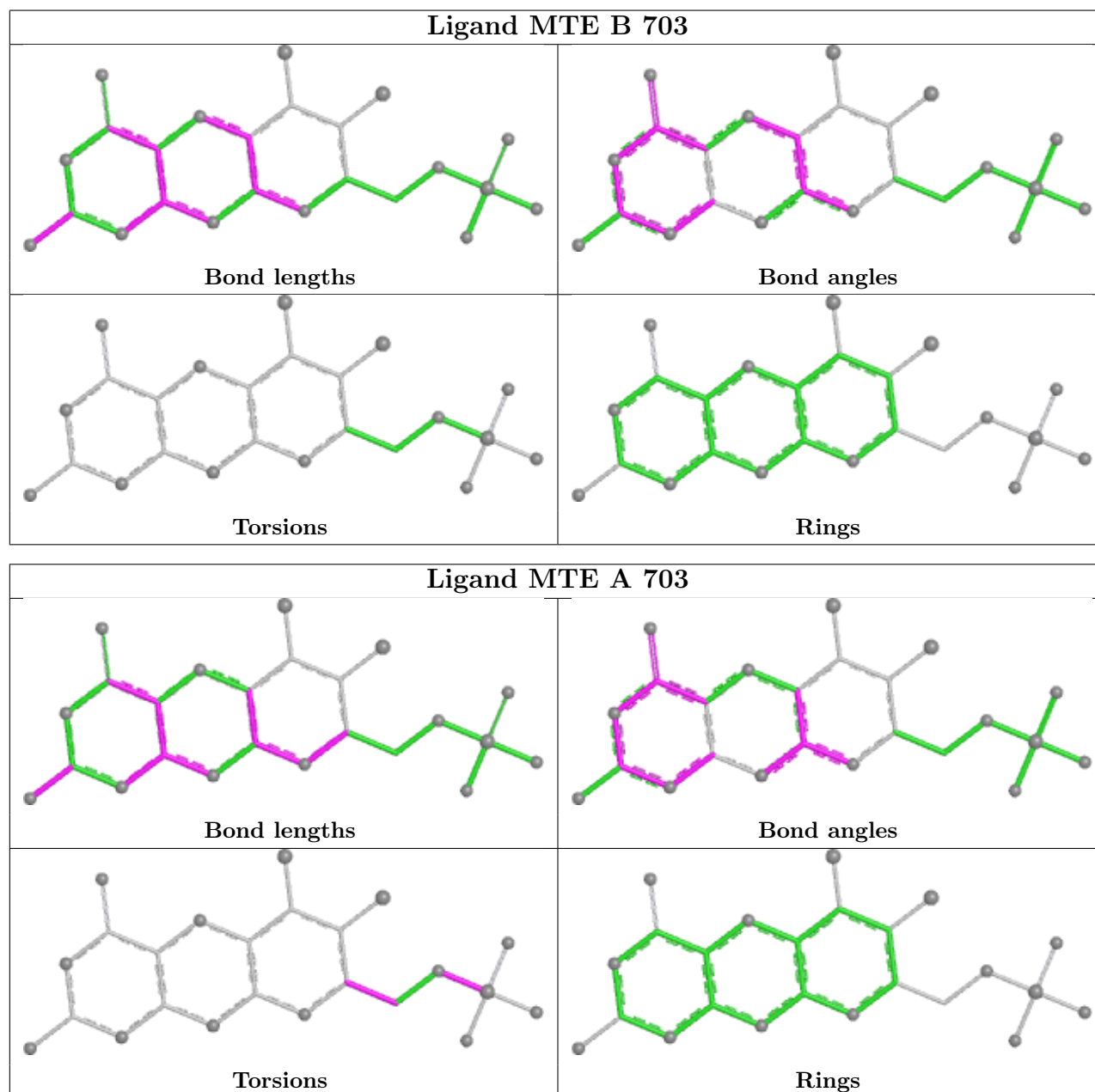
Mol	Chain	Res	Type	Atoms
5	A	703	MTE	O3'-C3'-C4'-O4'
5	A	703	MTE	C4'-O4'-P-O2P
5	A	704	MTE	C4'-O4'-P-O1P
5	A	704	MTE	C4'-O4'-P-O2P
5	A	704	MTE	C4'-O4'-P-O3P

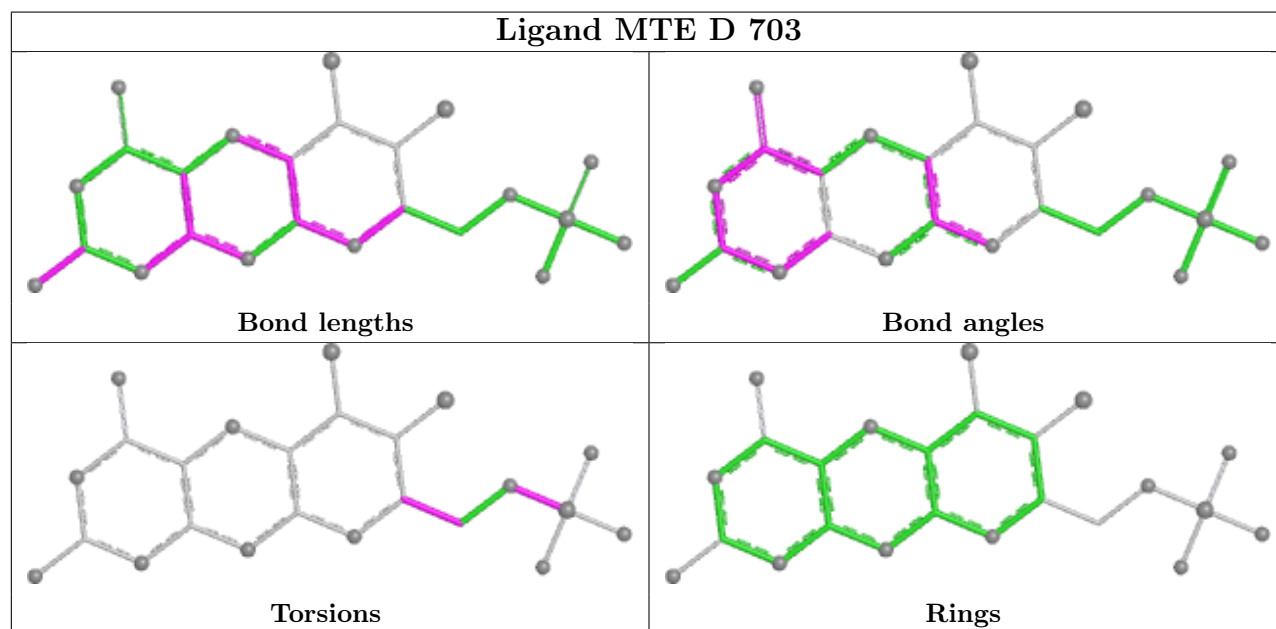
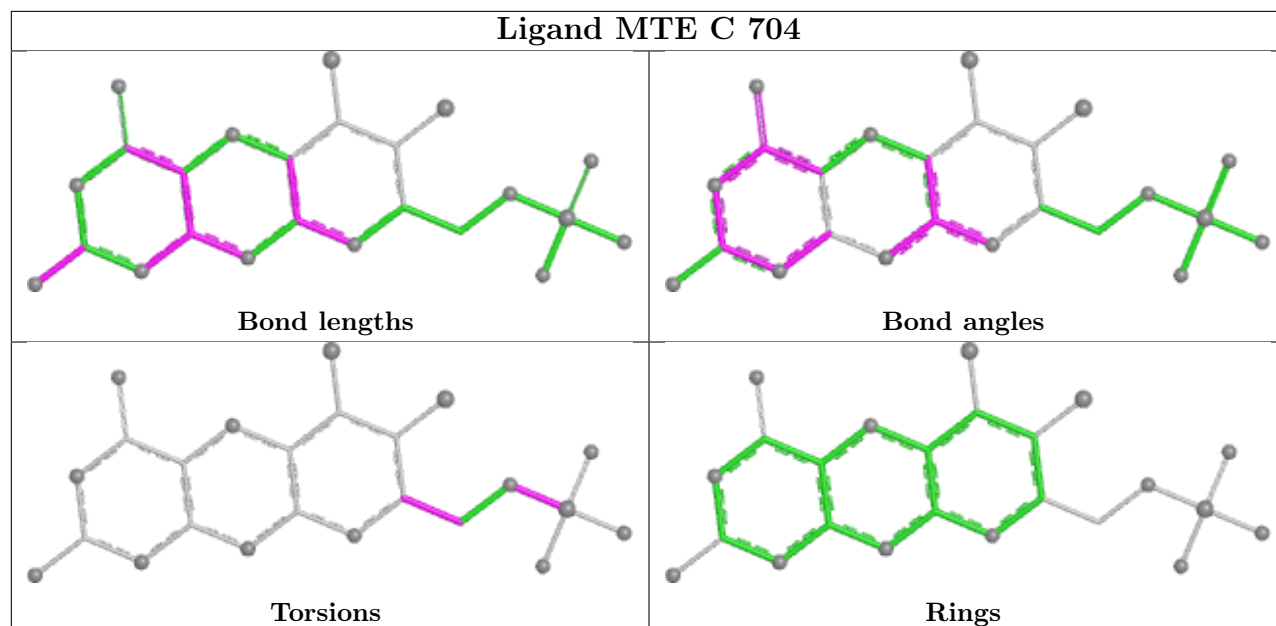
There are no ring outliers.

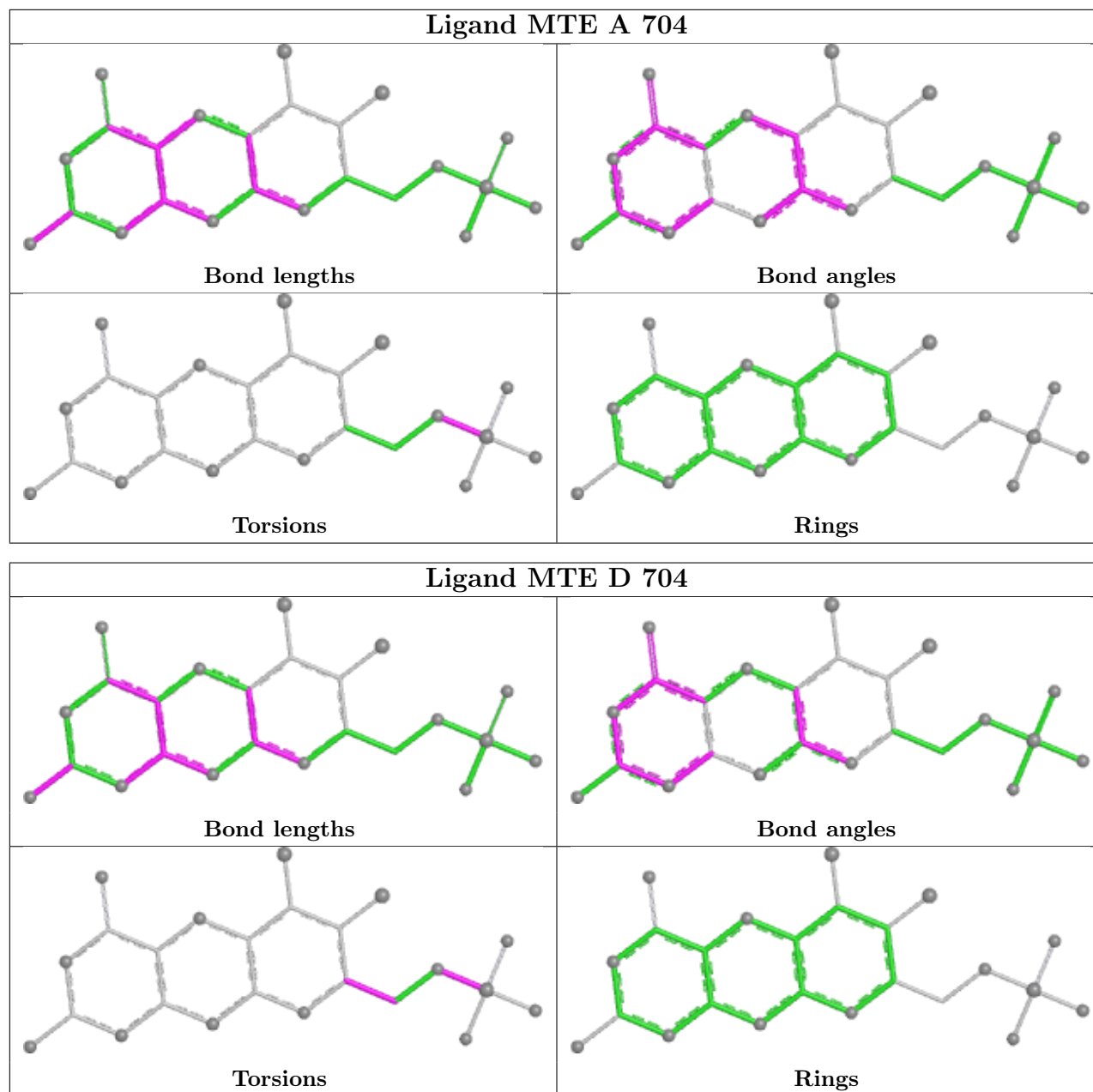
13 monomers are involved in 17 short contacts:

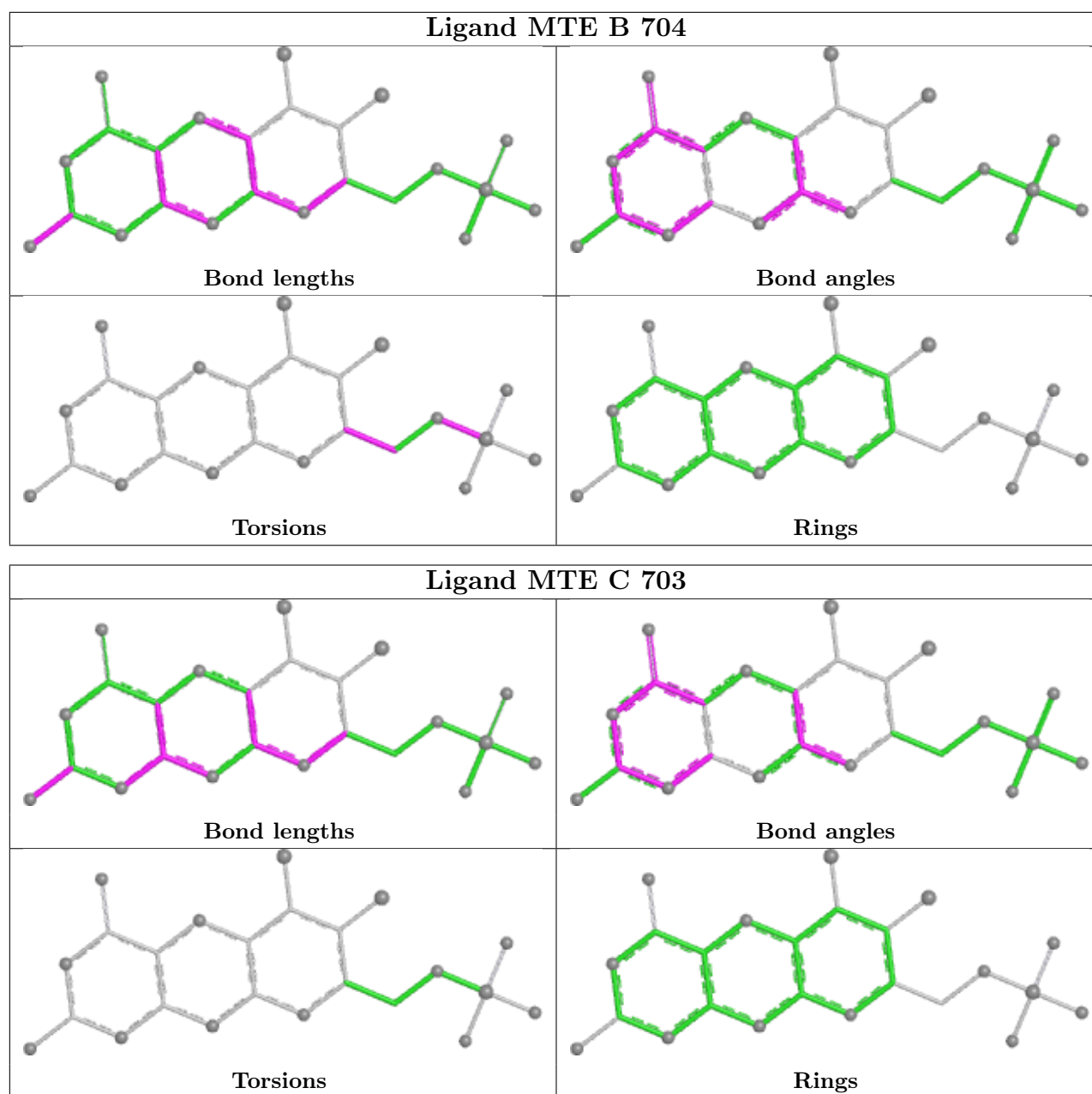
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	703	MTE	2	0
5	C	704	MTE	1	0
5	A	704	MTE	2	0
5	D	704	MTE	1	0
4	F	1002	SF4	1	0
5	B	704	MTE	1	0
4	E	1002	SF4	1	0
5	C	703	MTE	2	0
4	G	1002	SF4	1	0
4	H	1002	SF4	1	0
4	G	1003	SF4	1	0
4	E	1001	SF4	1	0
4	D	702	SF4	2	0

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.









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

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

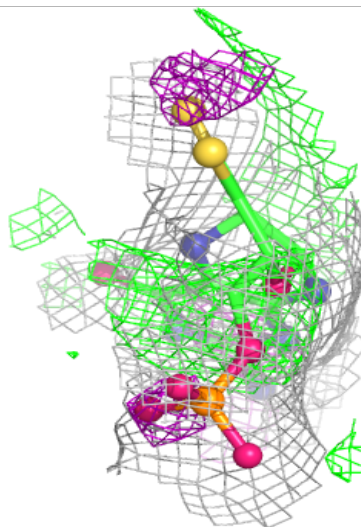
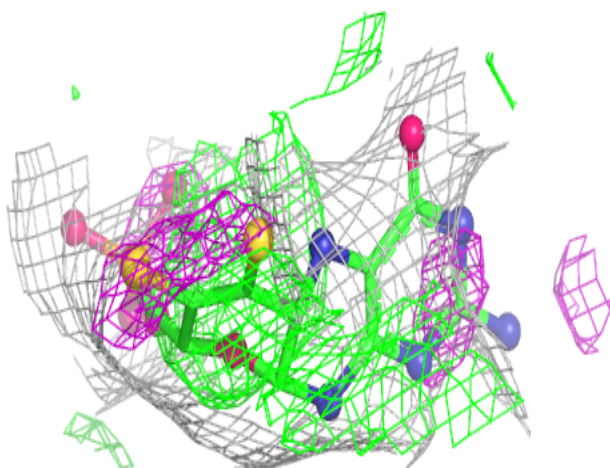
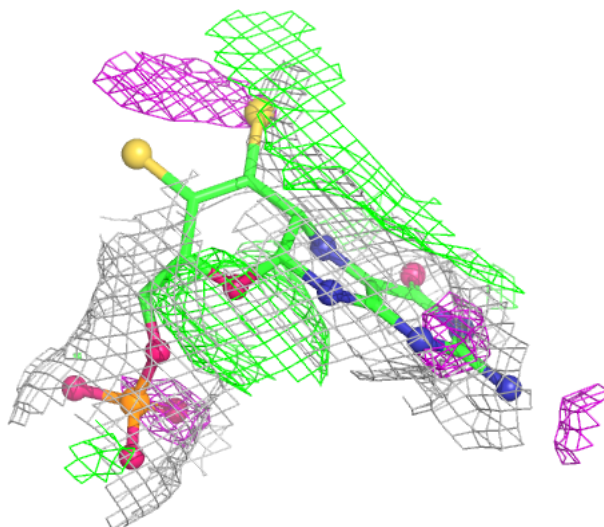
6.4 Ligands

EDS failed to run properly - this section is therefore empty.

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.

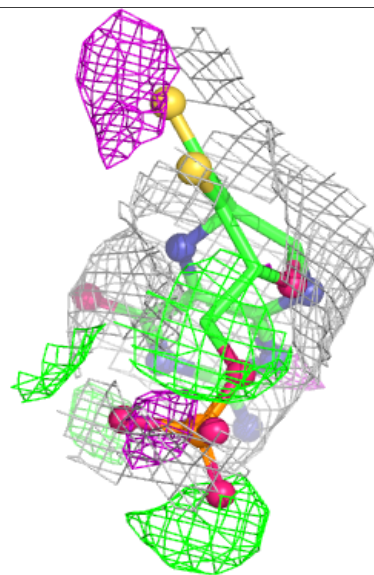
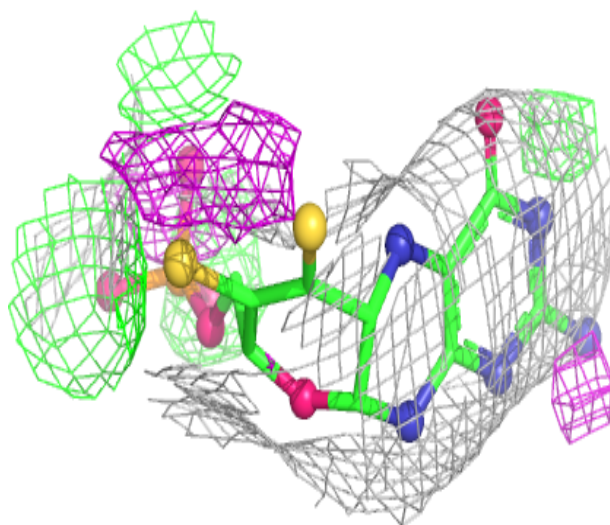
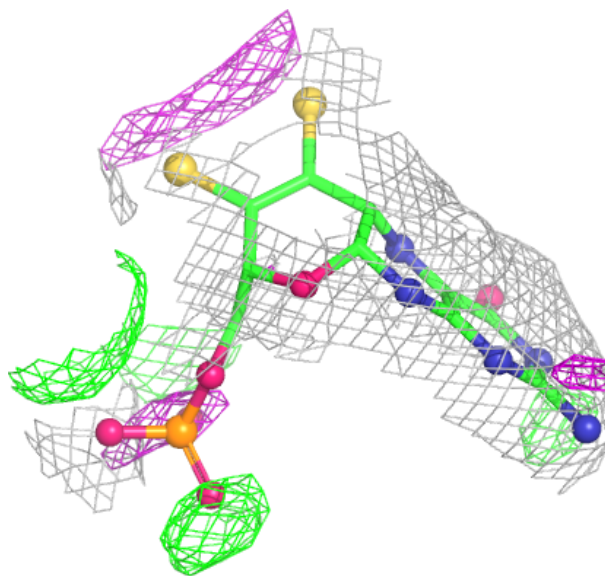
Electron density around MTE A 703:

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



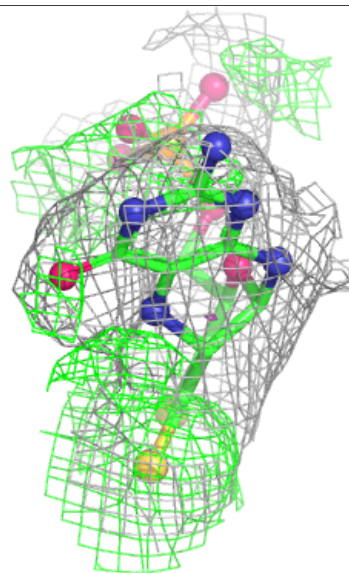
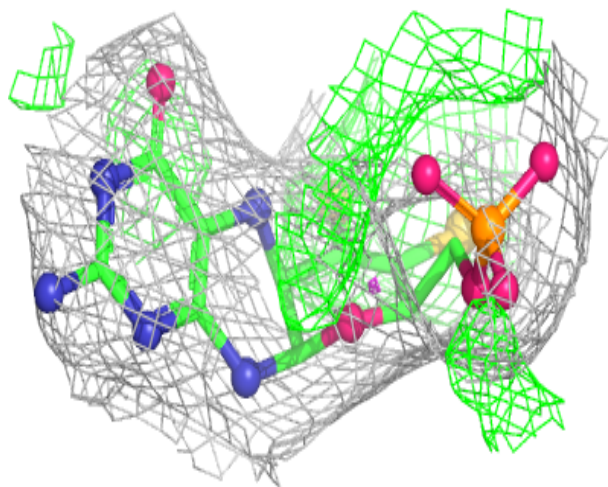
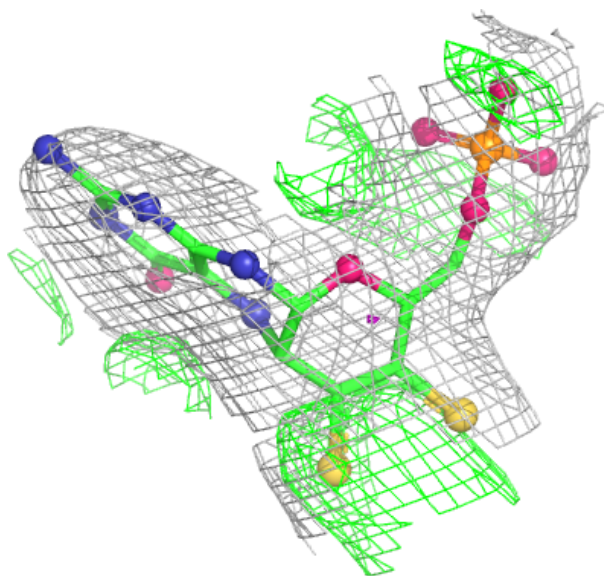
Electron density around MTE A 704:

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



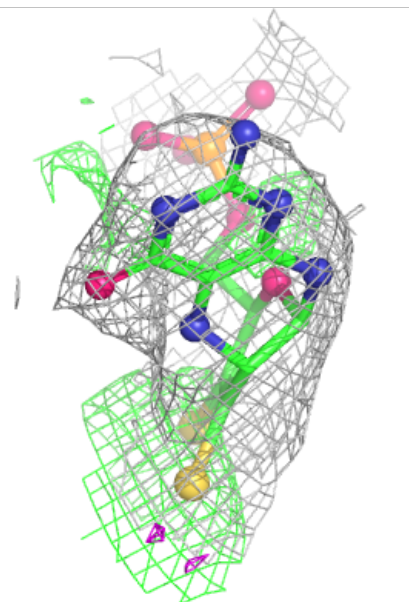
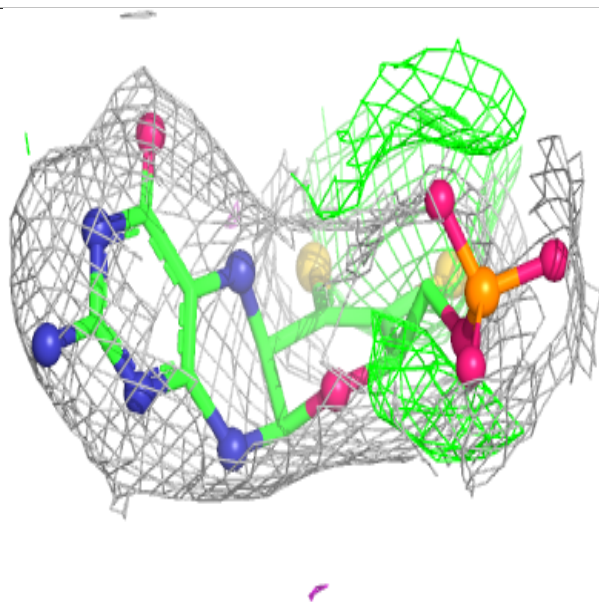
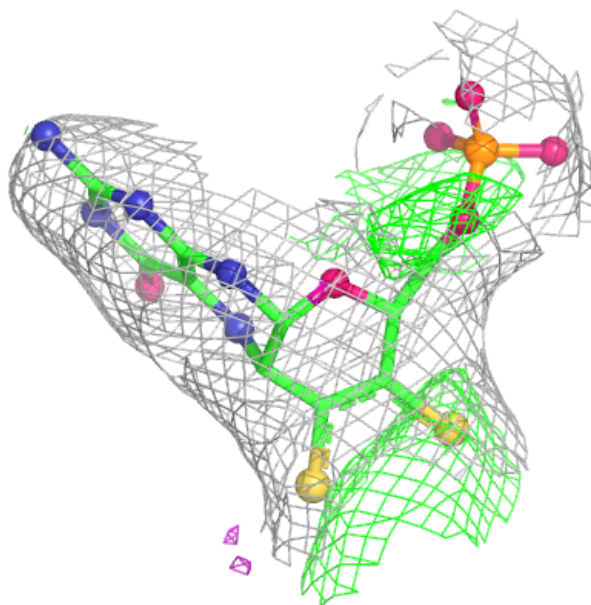
Electron density around MTE B 703:

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



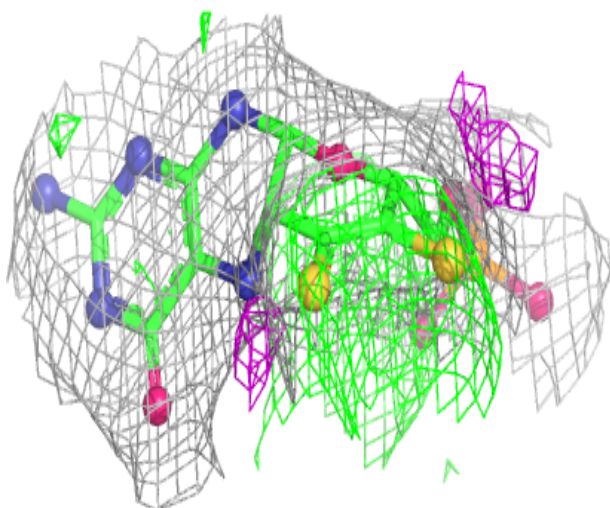
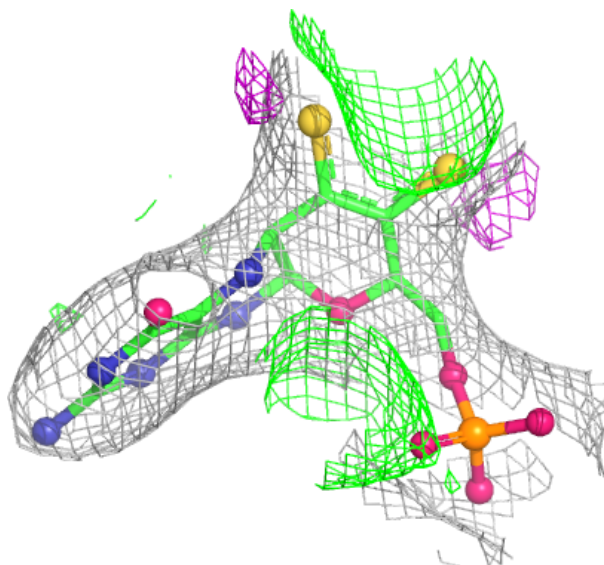
Electron density around MTE B 704:

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



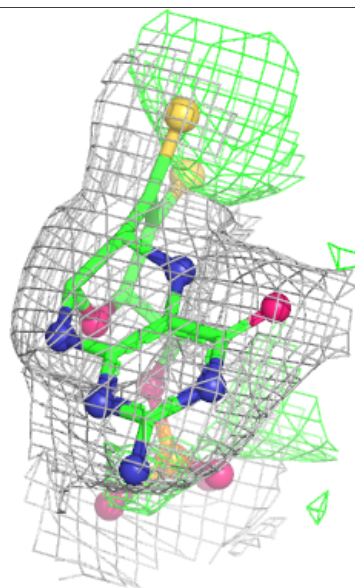
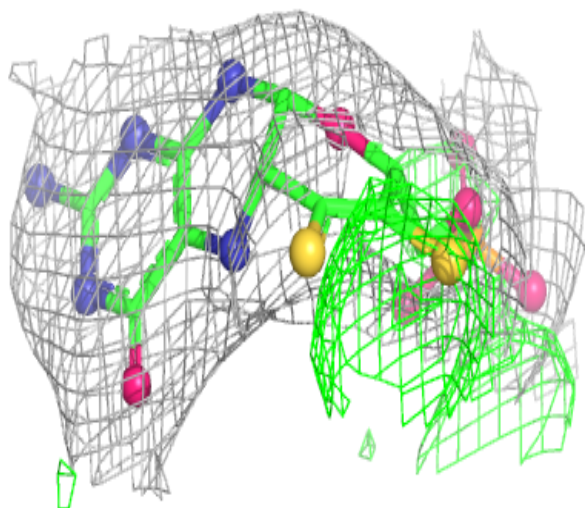
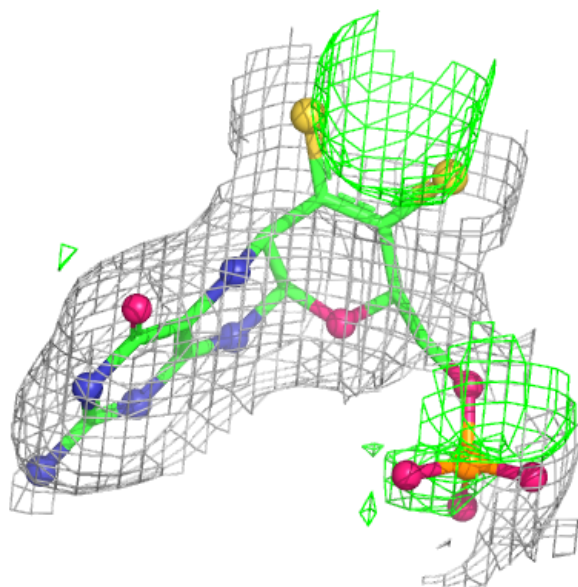
Electron density around MTE C 703:

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



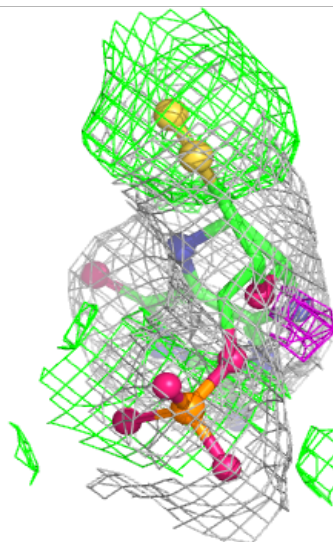
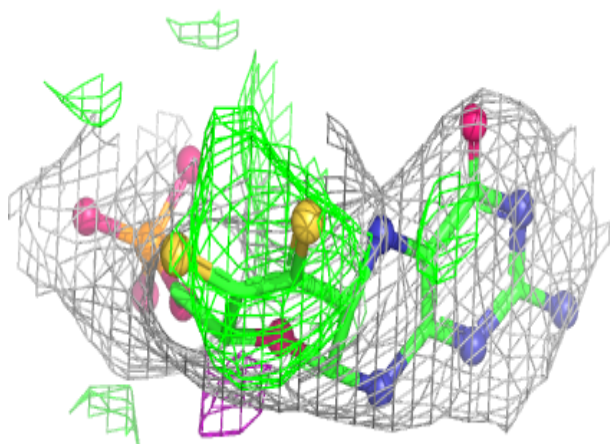
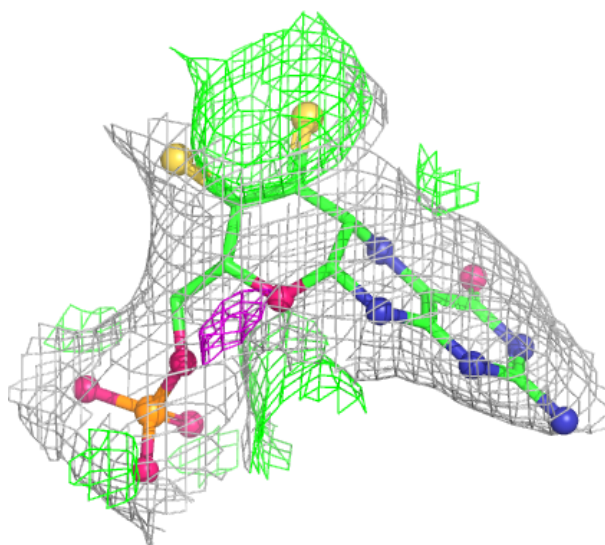
Electron density around MTE C 704:

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



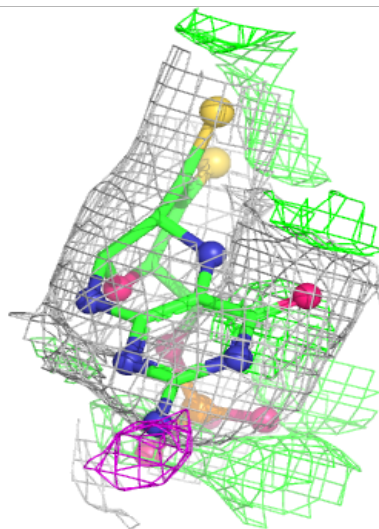
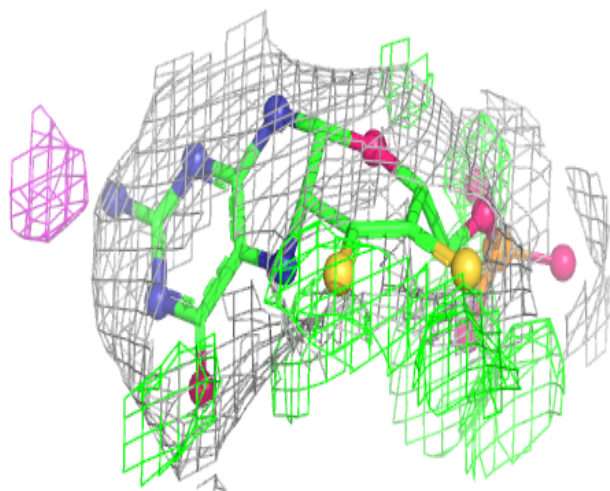
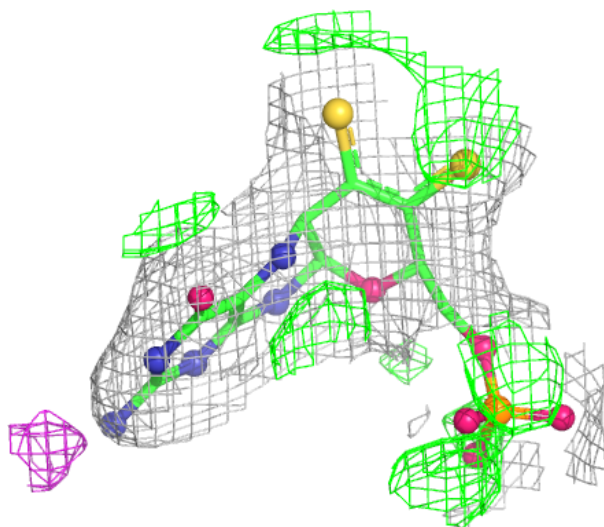
Electron density around MTE D 703:

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



Electron density around MTE D 704:

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



6.5 Other polymers [i](#)

EDS failed to run properly - this section is therefore empty.