



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 13, 2026 – 06:58 PM UTC

PDB ID : 4Z3Y / pdb_00004z3y
Title : Active site complex BamBC of Benzoyl Coenzyme A reductase in complex with Benzoyl-CoA
Authors : Weinert, T.; Kung, J.W.; Weidenweber, S.; Huwiler, S.G.; Boll, M.; Ermler, U.
Deposited on : 2015-04-01
Resolution : 2.36 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

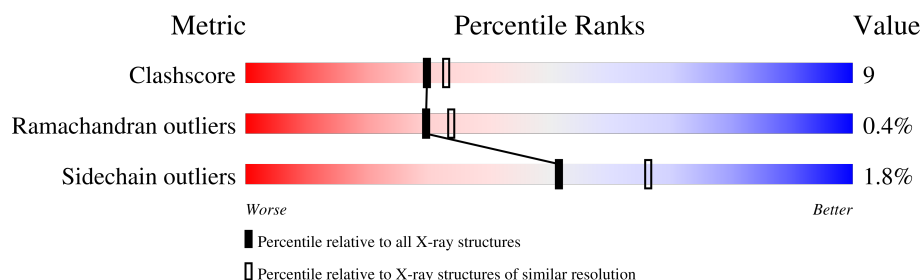
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.36 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	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)

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	79% 20% .
1	B	653	80% 19% .
1	C	653	75% 24% .
1	D	653	77% 22% .
2	E	179	77% 13% 9%
2	F	179	73% 21% . 5%
2	G	179	78% 15% . 6%
2	H	179	78% 12% 10%

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
7	UNL	B	705	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 26541 atoms, of which 160 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.

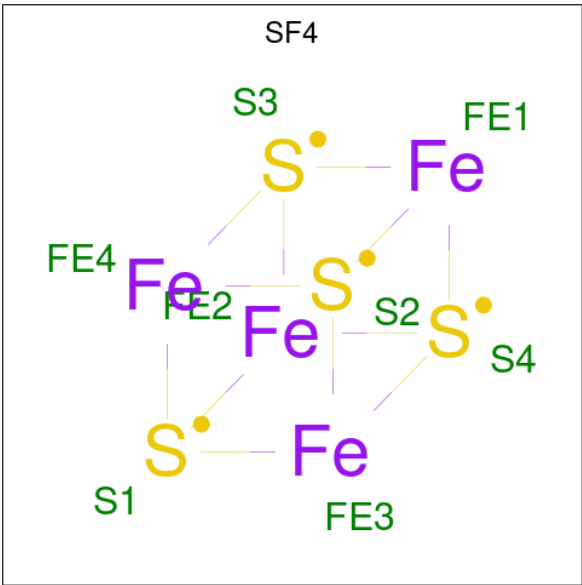
- Molecule 1 is a protein called Benzoyl-CoA reductase, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	653	Total	C	N	O	S	0	0	0
			5186	3311	876	966	33			
1	B	653	Total	C	N	O	S	0	0	0
			5189	3313	876	966	34			
1	C	653	Total	C	N	O	S	0	0	0
			5189	3313	876	966	34			
1	D	652	Total	C	N	O	S	0	0	0
			5178	3306	874	965	33			

- 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	162	Total	C	N	O	S	0	0	0
			1230	764	217	235	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 IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



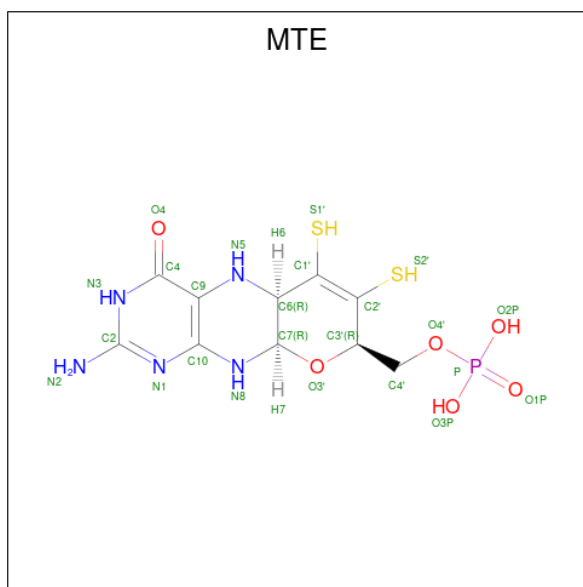
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Fe	S	0	0
			8	4	4		
3	B	1	Total	Fe	S	0	0
			8	4	4		
3	C	1	Total	Fe	S	0	0
			8	4	4		
3	D	1	Total	Fe	S	0	0
			8	4	4		
3	E	1	Total	Fe	S	0	0
			8	4	4		
3	E	1	Total	Fe	S	0	0
			8	4	4		
3	E	1	Total	Fe	S	0	0
			8	4	4		
3	F	1	Total	Fe	S	0	0
			8	4	4		
3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

Continued on next page...

Continued from previous page...

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

- Molecule 4 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
4	A	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		
4	A	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		
4	B	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		
4	B	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		
4	C	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		
4	C	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		
4	D	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		
4	D	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		

- Molecule 5 is TUNGSTEN ION (CCD ID: W) (formula: W).

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

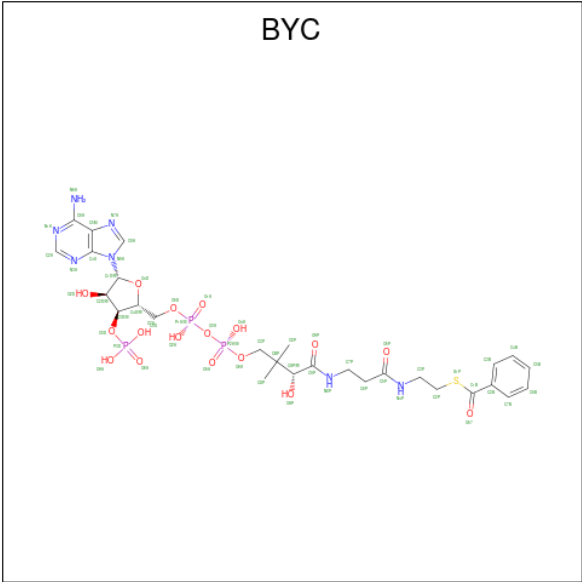
- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 7 is UNKNOWN LIGAND (CCD ID: UNL) (formula:).

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

- Molecule 8 is benzoyl coenzyme A (CCD ID: BYC) (formula: C₂₈H₄₀N₇O₁₇P₃S).



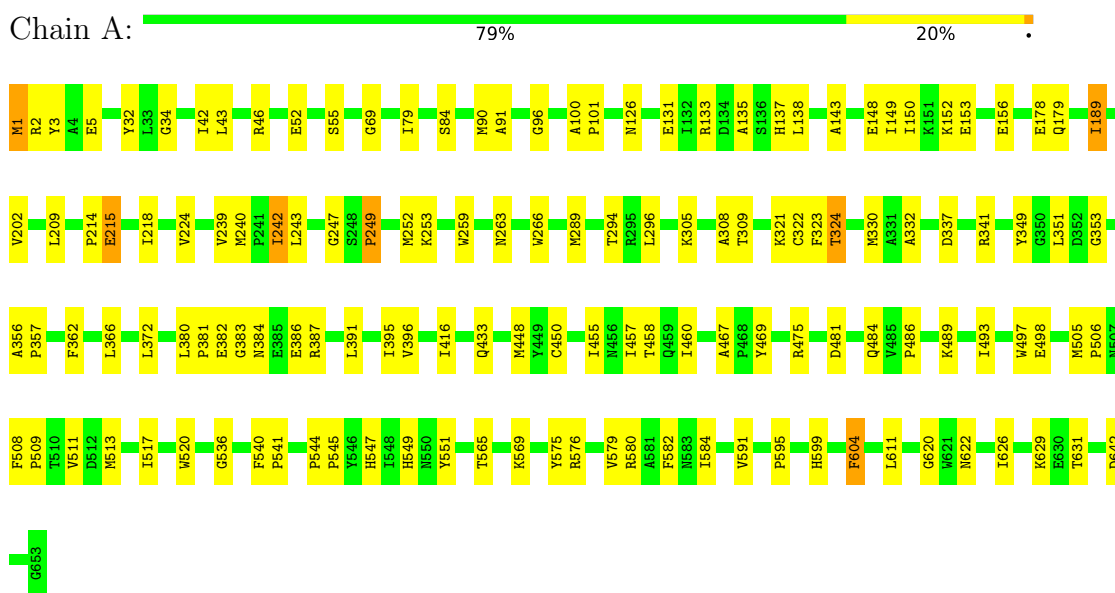
Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
8	A	1	Total	C	H	N	O	P	S	0	0
			96	28	40	7	17	3	1		
8	B	1	Total	C	H	N	O	P	S	0	0
			96	28	40	7	17	3	1		
8	C	1	Total	C	H	N	O	P	S	0	0
			96	28	40	7	17	3	1		
8	D	1	Total	C	H	N	O	P	S	0	0
			96	28	40	7	17	3	1		

3 Residue-property plots

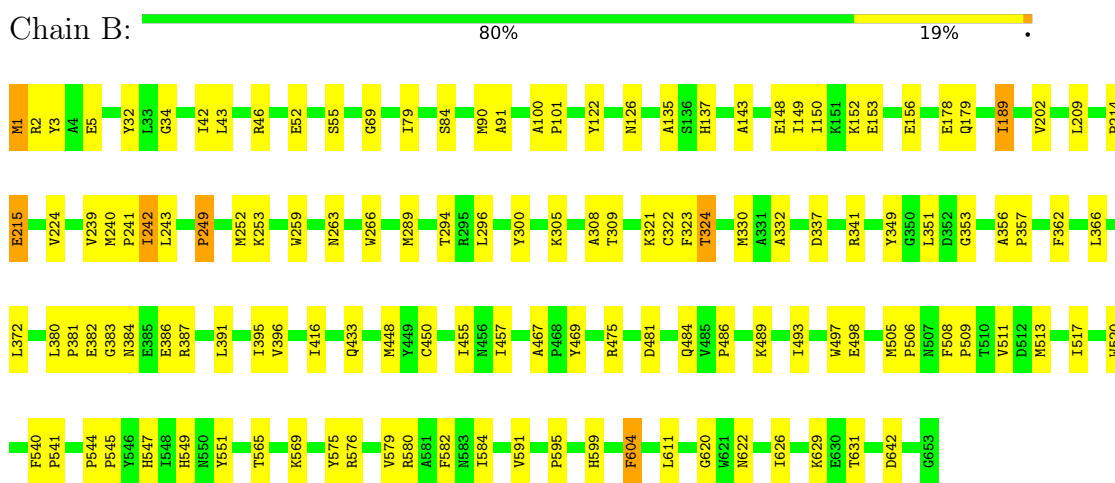
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

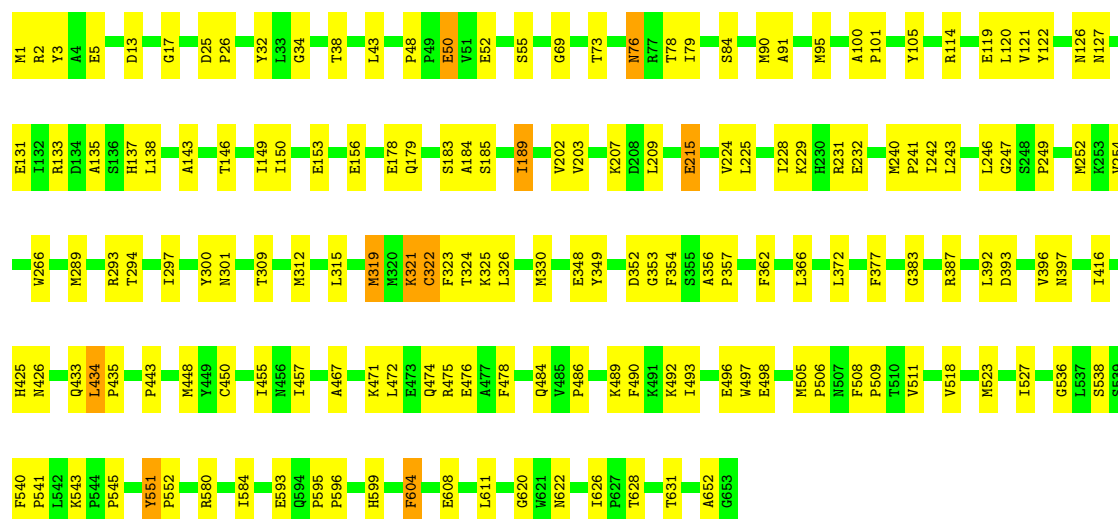


- Molecule 1: Benzoyl-CoA reductase, putative



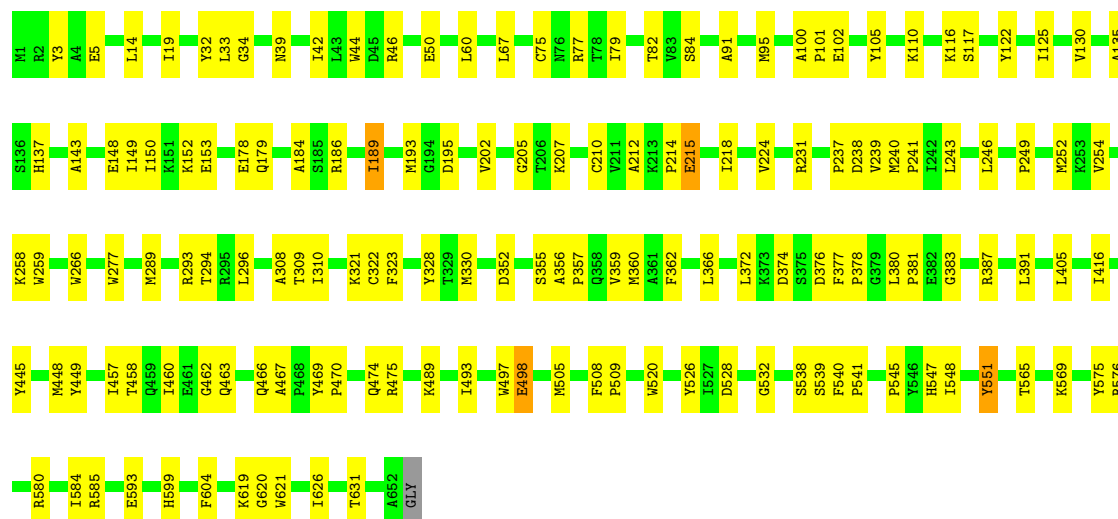
- Molecule 1: Benzoyl-CoA reductase, putative

Chain C:  75% 24% .



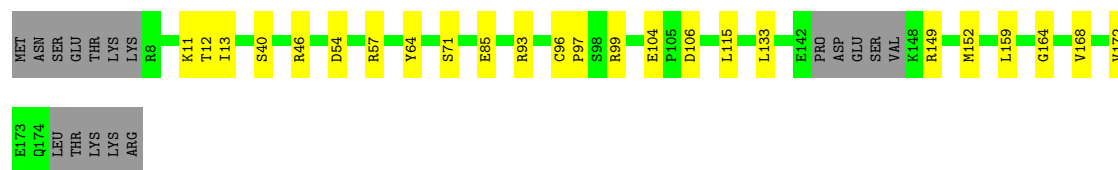
• Molecule 1: Benzoyl-CoA reductase, putative

Chain D:  77% 22% .



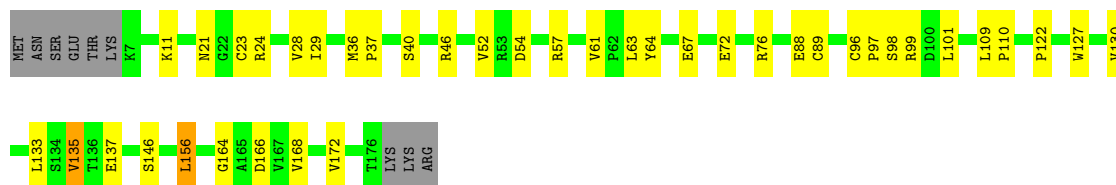
• Molecule 2: Iron-sulfur cluster-binding oxidoreductase, putative benzoyl-CoA reductase electron transfer protein

Chain E:  77% 13% 9%



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

Chain F:  73% 21% 5%



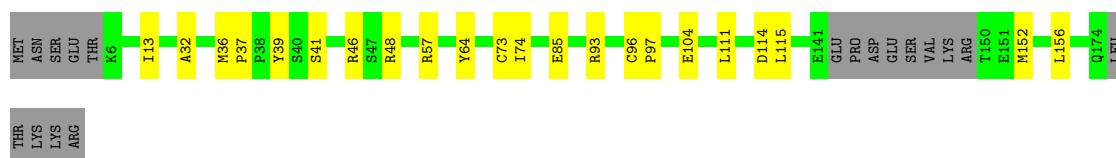
- Molecule 2: Iron-sulfur cluster-binding oxidoreductase, putative benzoyl-CoA reductase electron transfer protein

Chain G:  78% 15% 6%



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

Chain H:  78% 12% 10%



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	125.77Å 116.26Å 143.97Å 90.00° 110.43° 90.00°	Depositor
Resolution (Å)	79.80 – 2.36	Depositor
% Data completeness (in resolution range)	94.3 (79.80-2.36)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.17	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 2.37Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.241 , 0.275	Depositor
Wilson B-factor (Å ²)	46.8	Xtriage
Anisotropy	0.301	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	26541	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.33% 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: MTE, UNL, W, MG, SF4, BYC

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	0.26	0/5312	0.69	2/7181 (0.0%)
1	B	0.26	0/5315	0.69	2/7184 (0.0%)
1	C	0.26	0/5315	0.72	6/7184 (0.1%)
1	D	0.26	0/5304	0.71	4/7172 (0.1%)
2	E	0.26	0/1251	0.73	0/1693
2	F	0.26	0/1343	0.75	0/1819
2	G	0.26	0/1344	0.76	3/1819 (0.2%)
2	H	0.26	0/1242	0.75	0/1681
All	All	0.26	0/26426	0.71	17/35733 (0.0%)

There are no bond length outliers.

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	604	PHE	CA-C-N	6.30	126.51	119.32
1	C	604	PHE	C-N-CA	6.30	126.51	119.32
1	C	240	MET	CA-C-N	6.08	126.26	119.32
1	C	240	MET	C-N-CA	6.08	126.26	119.32
1	C	322	CYS	CB-CA-C	-6.01	109.66	116.63

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5186	0	5115	85	0
1	B	5189	0	5122	85	0
1	C	5189	0	5122	105	0
1	D	5178	0	5101	96	0
2	E	1230	0	1174	16	0
2	F	1317	0	1266	25	0
2	G	1315	0	1263	22	0
2	H	1221	0	1158	16	0
3	A	8	0	0	0	0
3	B	8	0	0	0	0
3	C	8	0	0	1	0
3	D	8	0	0	0	0
3	E	24	0	0	0	0
3	F	24	0	0	0	0
3	G	24	0	0	1	0
3	H	24	0	0	0	0
4	A	48	0	20	4	0
4	B	48	0	20	7	0
4	C	48	0	20	1	0
4	D	48	0	20	2	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	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	1	0
7	B	1	0	0	2	0
7	C	1	0	0	0	0
7	D	1	0	0	1	0
8	A	56	40	36	5	0
8	B	56	40	36	4	0
8	C	56	40	36	7	0
8	D	56	40	36	3	0
All	All	26381	160	25545	443	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 9.

The worst 5 of 443 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:380:LEU:HD12	1:B:381:PRO:HD2	1.37	1.06
1:A:380:LEU:HD12	1:A:381:PRO:HD2	1.37	1.00
1:D:84:SER:HB2	1:D:91:ALA:HB2	1.54	0.89
1:C:356:ALA:HB3	1:C:357:PRO:HD3	1.65	0.79
1:C:242:ILE:HG13	1:C:243:LEU:HG	1.66	0.78

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	651/653 (100%)	624 (96%)	24 (4%)	3 (0%)	24	27
1	B	651/653 (100%)	624 (96%)	24 (4%)	3 (0%)	24	27
1	C	651/653 (100%)	623 (96%)	24 (4%)	4 (1%)	21	24
1	D	650/653 (100%)	626 (96%)	22 (3%)	2 (0%)	36	43
2	E	158/179 (88%)	154 (98%)	4 (2%)	0	100	100
2	F	169/179 (94%)	168 (99%)	1 (1%)	0	100	100
2	G	169/179 (94%)	165 (98%)	4 (2%)	0	100	100
2	H	157/179 (88%)	156 (99%)	1 (1%)	0	100	100
All	All	3256/3328 (98%)	3140 (96%)	104 (3%)	12 (0%)	30	34

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	652	ALA
1	D	33	LEU
1	C	622	ASN
1	A	249	PRO
1	A	305	LYS

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	547/548 (100%)	537 (98%)	10 (2%)	51	66
1	B	548/548 (100%)	538 (98%)	10 (2%)	51	66
1	C	548/548 (100%)	535 (98%)	13 (2%)	43	57
1	D	546/548 (100%)	537 (98%)	9 (2%)	55	70
2	E	133/159 (84%)	132 (99%)	1 (1%)	73	84
2	F	148/159 (93%)	144 (97%)	4 (3%)	39	52
2	G	147/159 (92%)	144 (98%)	3 (2%)	48	63
2	H	132/159 (83%)	132 (100%)	0	100	100
All	All	2749/2828 (97%)	2699 (98%)	50 (2%)	51	66

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	319	MET
1	D	189	ILE
2	G	99	ARG
1	C	321	LYS
1	C	599	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	433	GLN
1	C	230	HIS
2	G	42	ASN
1	C	301	ASN
1	A	433	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 40 ligands modelled in this entry, 8 are monoatomic and 4 are unknown - leaving 28 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	MTE	C	702	5,6	21,26,26	2.86	8 (38%)	19,40,40	2.12	5 (26%)
8	BYC	D	707	-	57,59,59	0.28	0	81,87,87	0.50	1 (1%)
4	MTE	B	703	5,6	21,26,26	2.87	8 (38%)	19,40,40	2.02	5 (26%)
4	MTE	B	702	5,6	21,26,26	2.91	8 (38%)	19,40,40	1.96	5 (26%)
8	BYC	B	707	-	57,59,59	0.31	0	81,87,87	0.49	1 (1%)
3	SF4	H	1001	2	0,12,12	-	-	-		
3	SF4	B	701	1	0,12,12	-	-	-		
3	SF4	F	1001	2	0,12,12	-	-	-		
4	MTE	D	703	5,6	21,26,26	2.96	8 (38%)	19,40,40	2.28	5 (26%)
3	SF4	F	1002	2	0,12,12	-	-	-		
8	BYC	C	707	-	57,59,59	0.32	0	81,87,87	0.45	0
4	MTE	A	702	5,6	21,26,26	2.91	8 (38%)	19,40,40	2.05	5 (26%)
3	SF4	G	1003	2	0,12,12	-	-	-		
3	SF4	C	701	1	0,12,12	-	-	-		
3	SF4	E	1002	2	0,12,12	-	-	-		
3	SF4	G	1002	2	0,12,12	-	-	-		
3	SF4	H	1003	2	0,12,12	-	-	-		
4	MTE	D	704	5,6	21,26,26	2.97	8 (38%)	19,40,40	2.33	7 (36%)
8	BYC	A	707	-	57,59,59	0.31	0	81,87,87	0.50	1 (1%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SF4	A	701	1	0,12,12	-	-	-		
3	SF4	H	1002	2	0,12,12	-	-	-		
3	SF4	G	1001	2	0,12,12	-	-	-		
3	SF4	E	1001	2	0,12,12	-	-	-		
3	SF4	D	702	1	0,12,12	-	-	-		
3	SF4	F	1003	2	0,12,12	-	-	-		
4	MTE	C	703	5,6	21,26,26	2.87	8 (38%)	19,40,40	2.08	5 (26%)
4	MTE	A	703	5,6	21,26,26	3.01	9 (42%)	19,40,40	2.10	6 (31%)
3	SF4	E	1003	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	MTE	C	702	5,6	-	0/6/34/34	0/3/3/3
8	BYC	D	707	-	-	11/55/71/71	0/4/4/4
4	MTE	B	703	5,6	-	3/6/34/34	0/3/3/3
4	MTE	B	702	5,6	-	0/6/34/34	0/3/3/3
8	BYC	B	707	-	-	15/55/71/71	0/4/4/4
3	SF4	H	1001	2	-	-	0/6/5/5
3	SF4	B	701	1	-	-	0/6/5/5
3	SF4	F	1001	2	-	-	0/6/5/5
4	MTE	D	703	5,6	-	0/6/34/34	0/3/3/3
8	BYC	C	707	-	-	14/55/71/71	0/4/4/4
3	SF4	F	1002	2	-	-	0/6/5/5
4	MTE	A	702	5,6	-	0/6/34/34	0/3/3/3
3	SF4	G	1003	2	-	-	0/6/5/5
8	BYC	A	707	-	-	14/55/71/71	0/4/4/4
3	SF4	C	701	1	-	-	0/6/5/5
3	SF4	E	1002	2	-	-	0/6/5/5
4	MTE	D	704	5,6	-	5/6/34/34	0/3/3/3
3	SF4	G	1002	2	-	-	0/6/5/5
3	SF4	H	1003	2	-	-	0/6/5/5
3	SF4	A	701	1	-	-	0/6/5/5
3	SF4	H	1002	2	-	-	0/6/5/5
3	SF4	G	1001	2	-	-	0/6/5/5
3	SF4	E	1001	2	-	-	0/6/5/5
3	SF4	D	702	1	-	-	0/6/5/5
4	MTE	C	703	5,6	-	3/6/34/34	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SF4	F	1003	2	-	-	0/6/5/5
4	MTE	A	703	5,6	-	5/6/34/34	0/3/3/3
3	SF4	E	1003	2	-	-	0/6/5/5

The worst 5 of 65 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	703	MTE	C10-N8	8.32	1.44	1.35
4	D	704	MTE	C10-N8	8.08	1.43	1.35
4	D	703	MTE	C10-N8	8.08	1.43	1.35
4	B	702	MTE	C10-N8	7.99	1.43	1.35
4	B	703	MTE	C10-N8	7.88	1.43	1.35

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	703	MTE	O3'-C7-C6	-5.34	105.40	108.96
4	D	704	MTE	C2-N3-C4	-5.02	116.00	125.11
4	B	703	MTE	C2-N3-C4	-4.95	116.14	125.11
4	A	703	MTE	C2-N3-C4	-4.87	116.27	125.11
4	B	702	MTE	C2-N3-C4	-4.82	116.38	125.11

There are no chirality outliers.

5 of 70 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	703	MTE	C2'-C3'-C4'-O4'
4	A	703	MTE	C4'-O4'-P-O1P
4	A	703	MTE	C4'-O4'-P-O2P
4	A	703	MTE	C4'-O4'-P-O3P
4	B	703	MTE	C4'-O4'-P-O1P

There are no ring outliers.

12 monomers are involved in 35 short contacts:

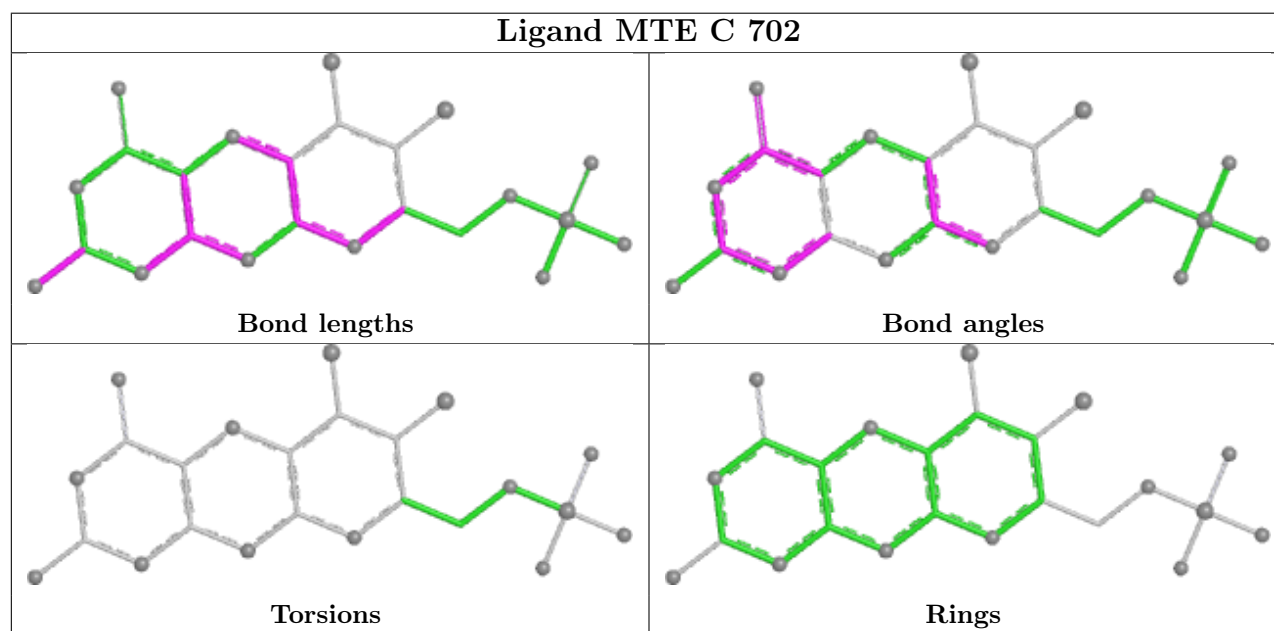
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	D	707	BYC	3	0
4	B	703	MTE	5	0
4	B	702	MTE	4	0
8	B	707	BYC	4	0
4	D	703	MTE	2	0

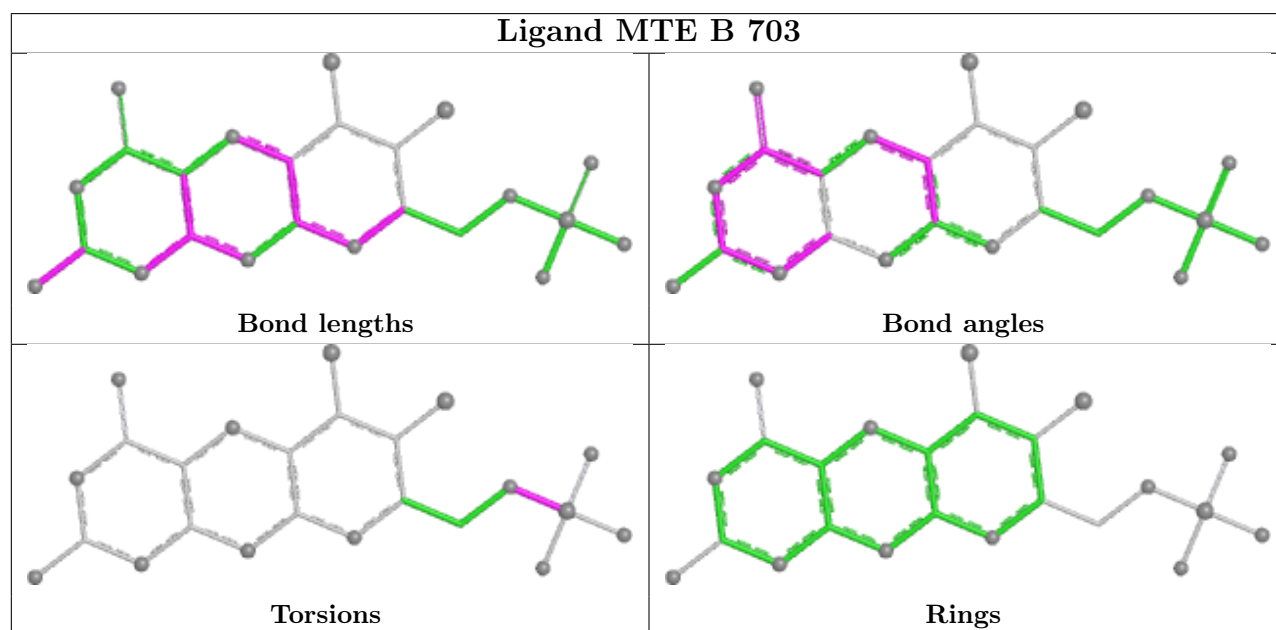
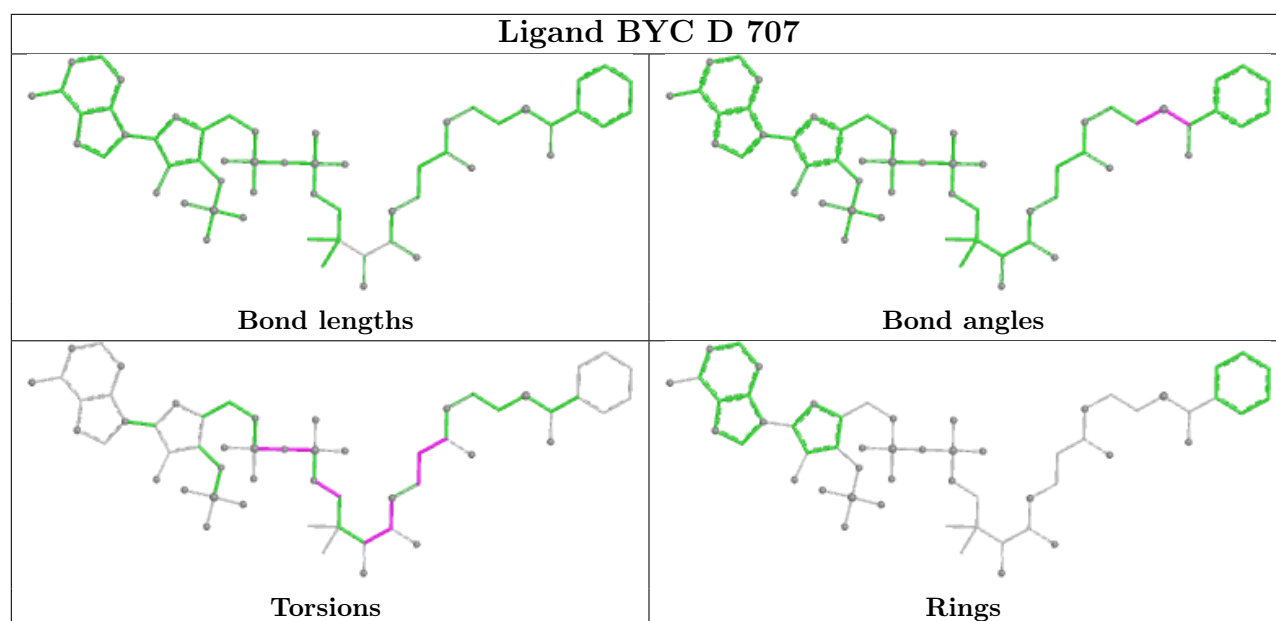
Continued on next page...

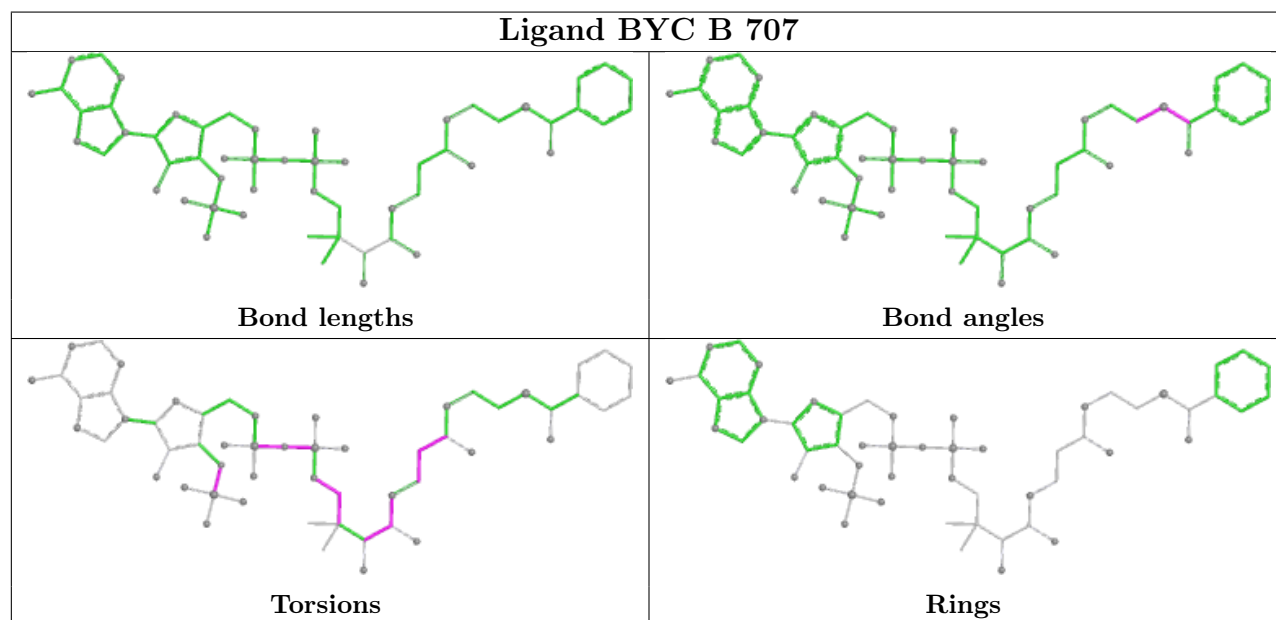
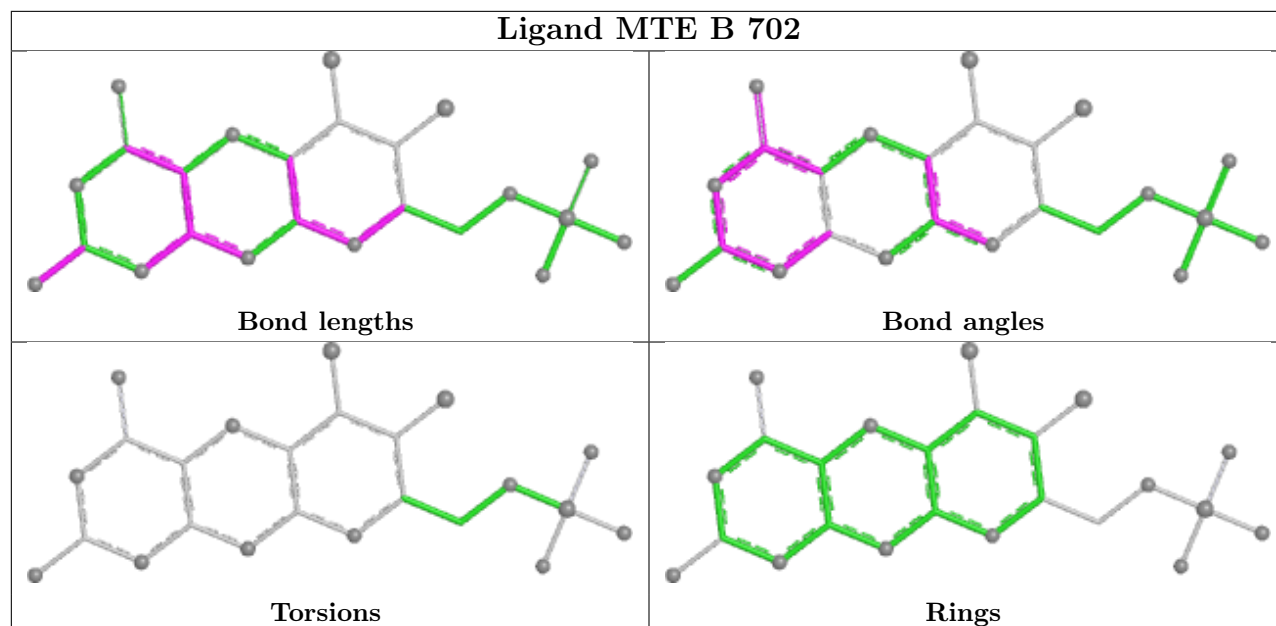
Continued from previous page...

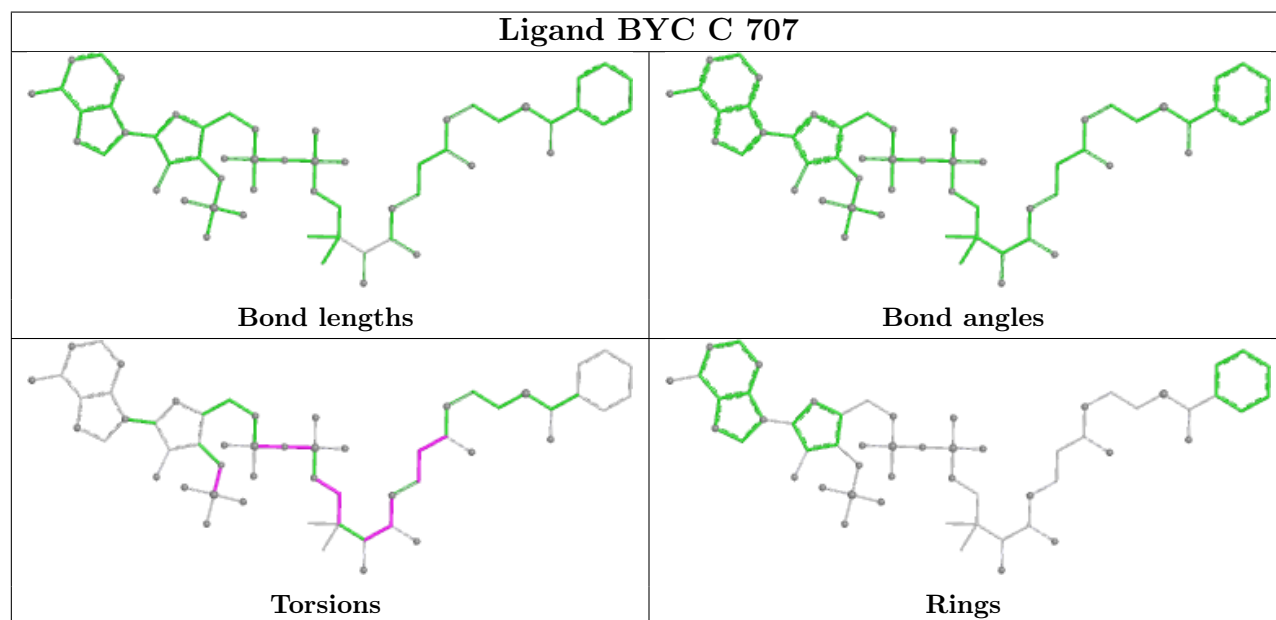
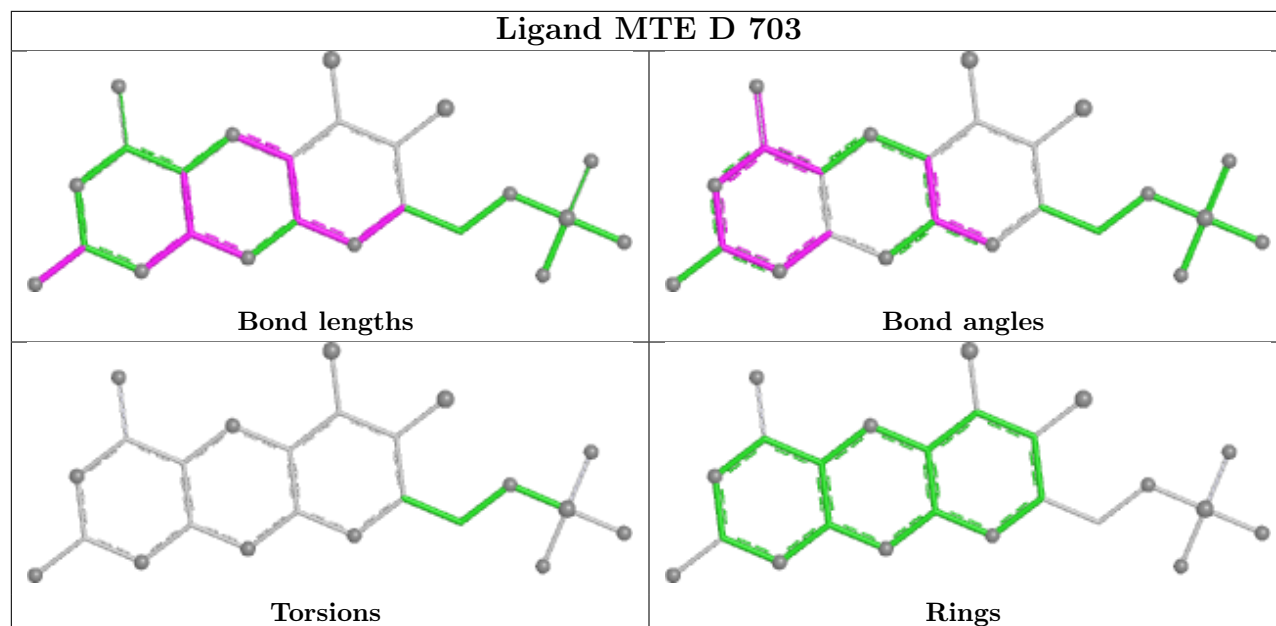
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	C	707	BYC	7	0
4	A	702	MTE	3	0
3	C	701	SF4	1	0
3	G	1002	SF4	1	0
8	A	707	BYC	5	0
4	C	703	MTE	1	0
4	A	703	MTE	1	0

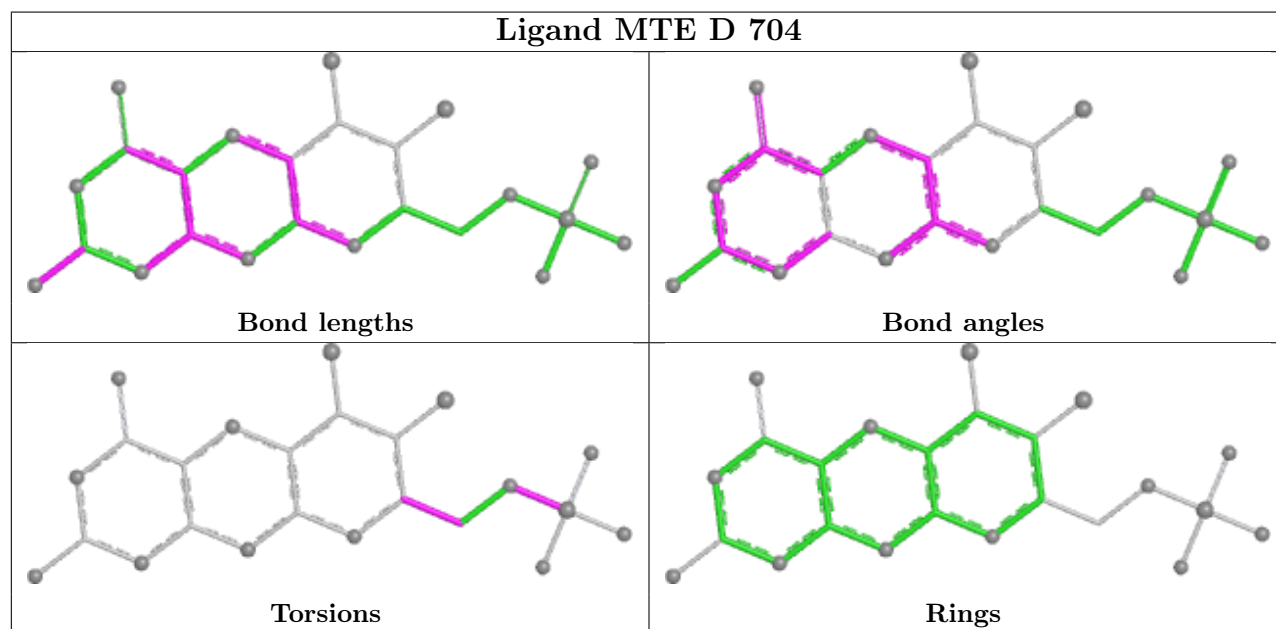
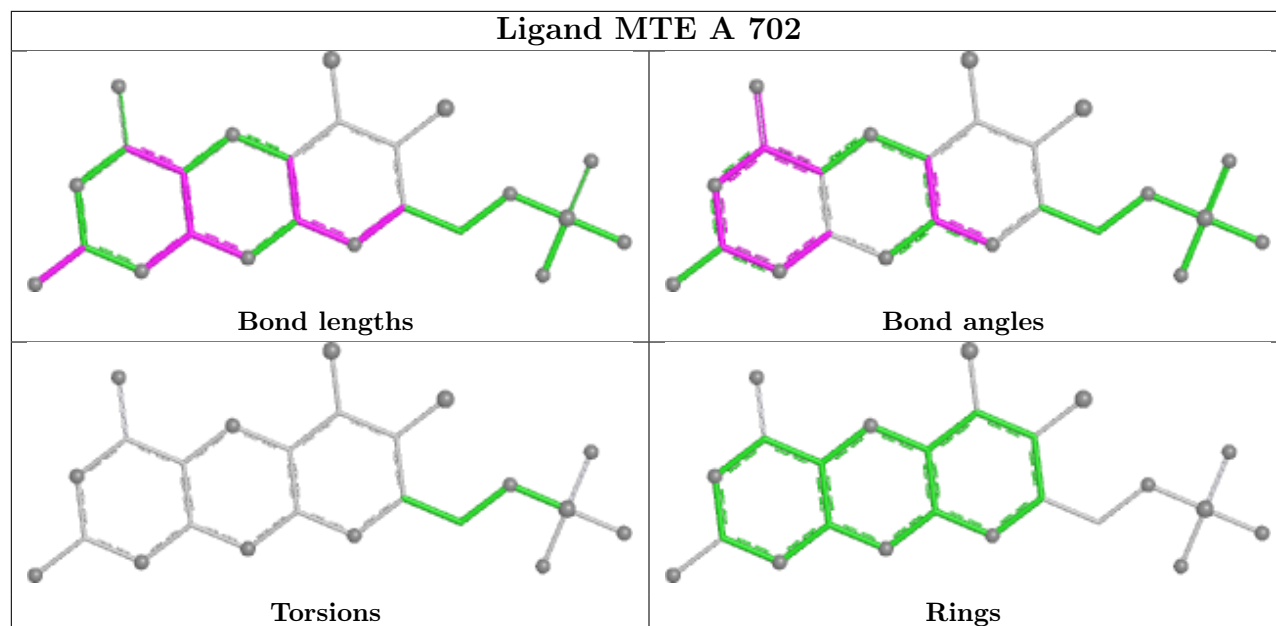
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

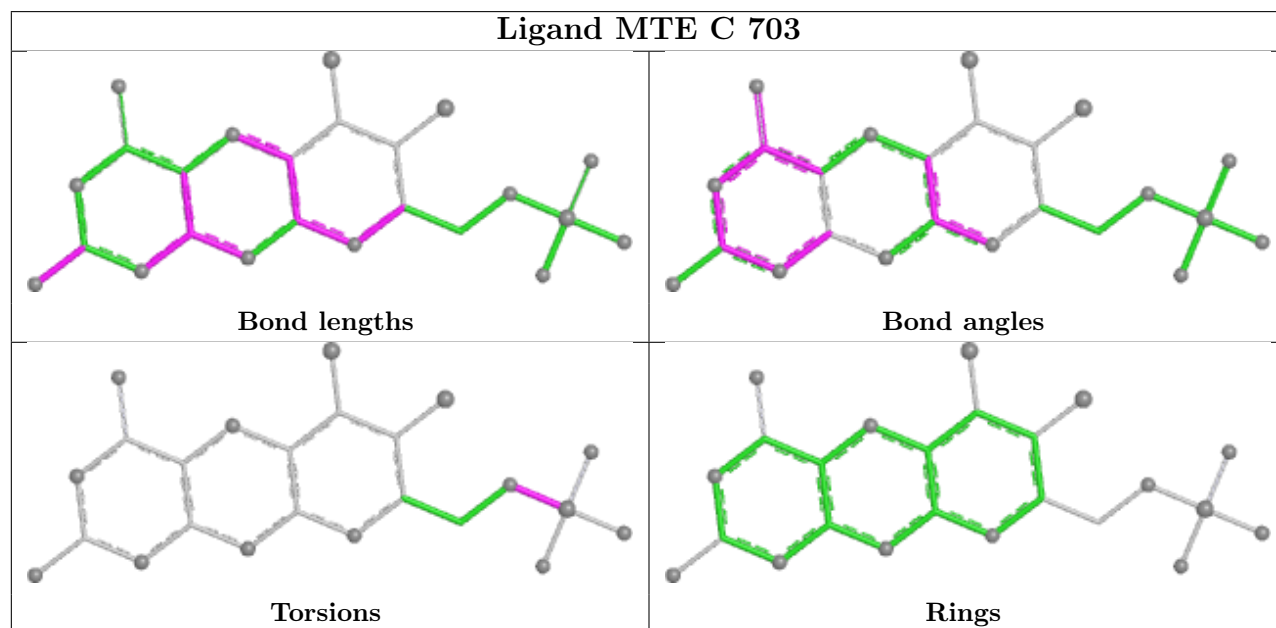
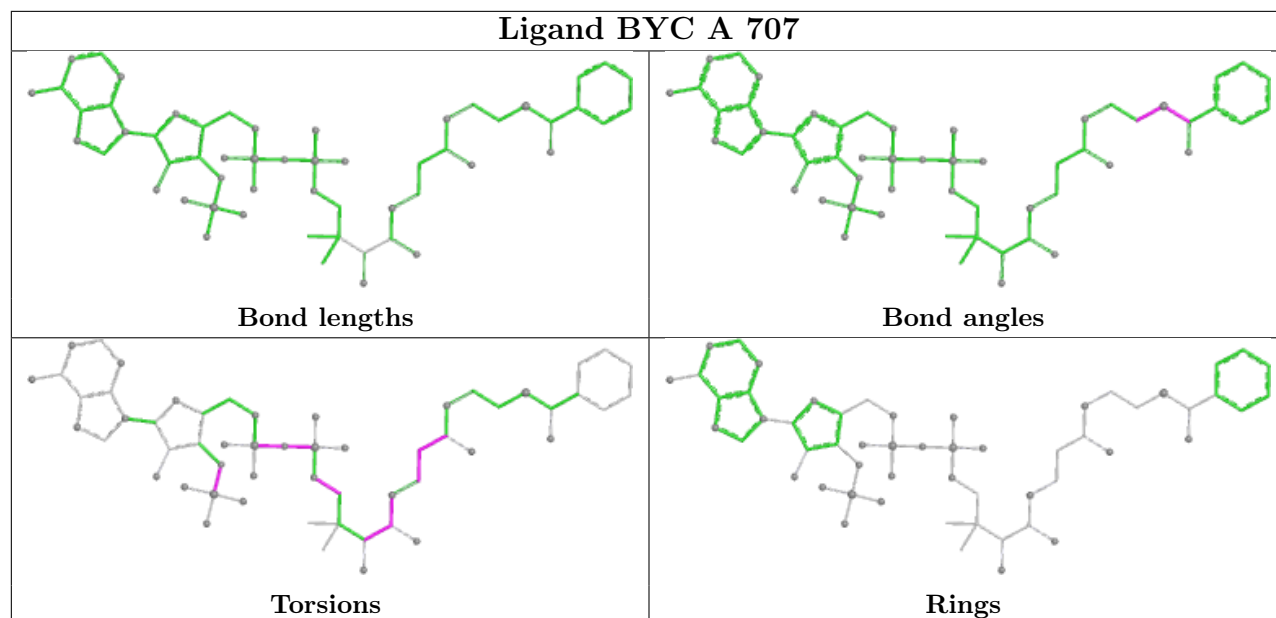


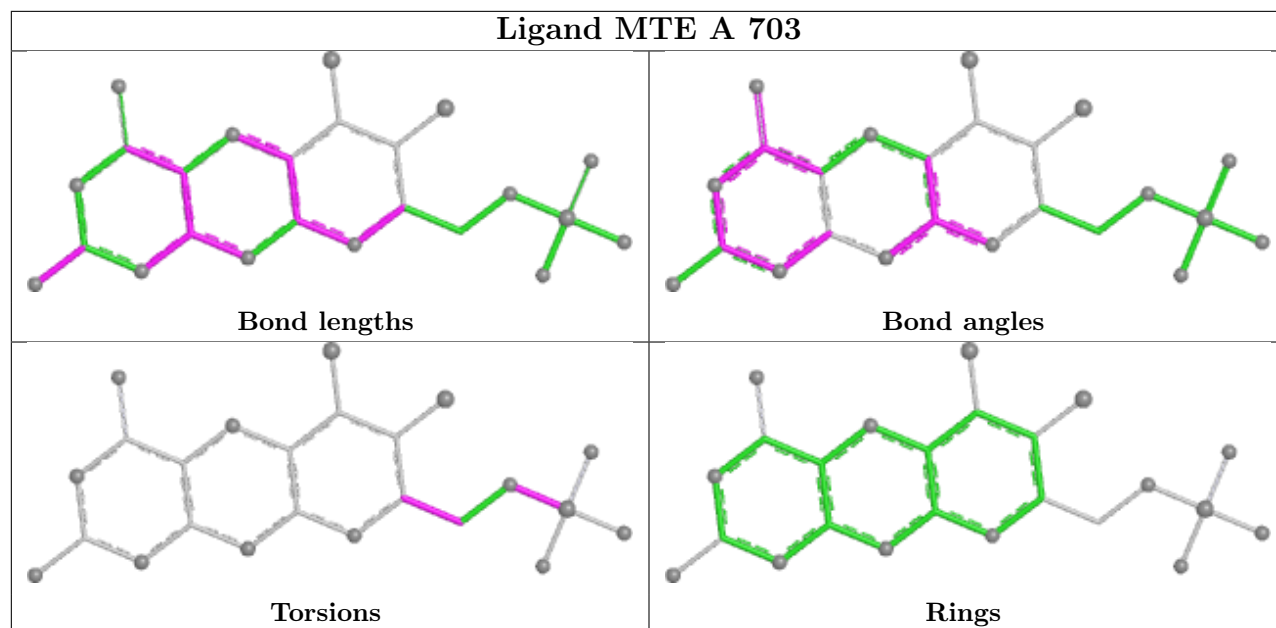












5.7 Other polymers [i](#)

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.

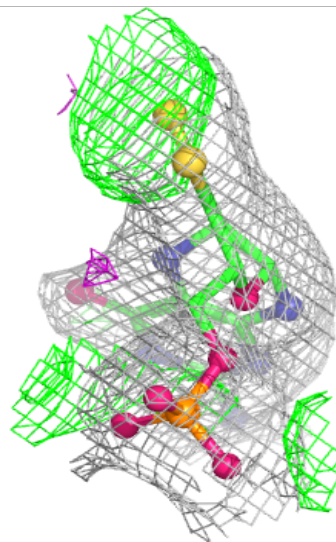
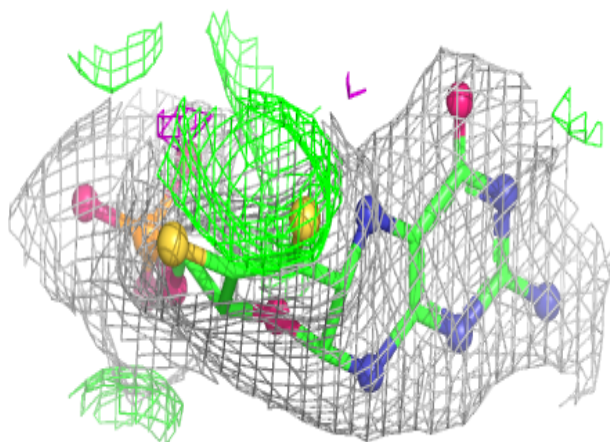
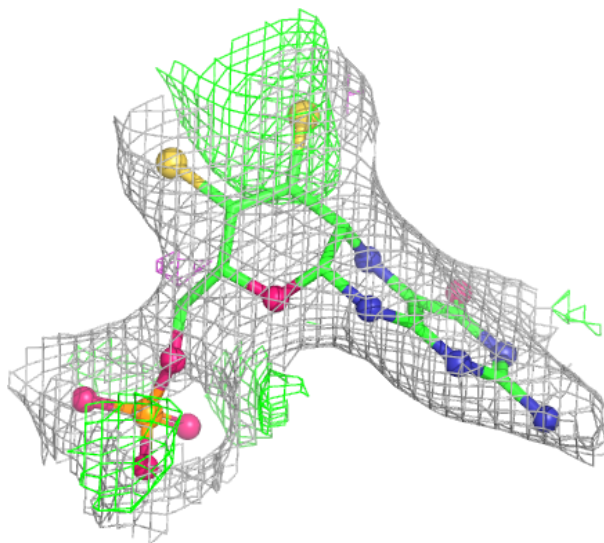
6.4 Ligands

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.

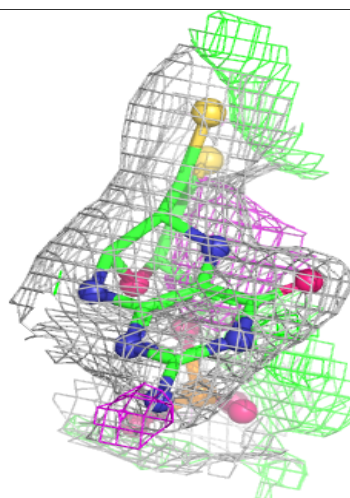
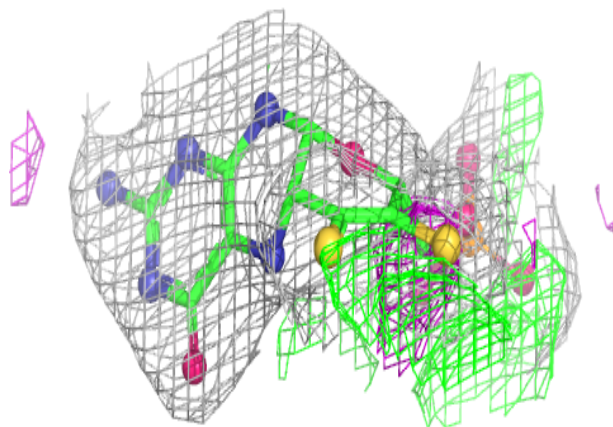
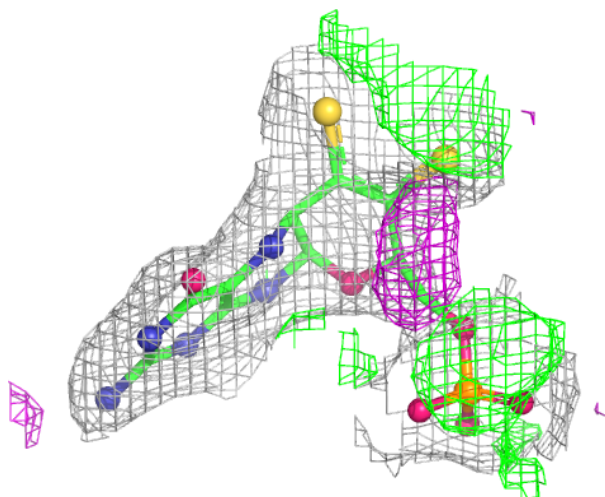
Electron density around MTE A 702:

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



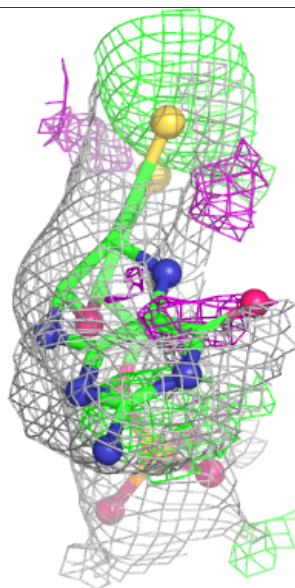
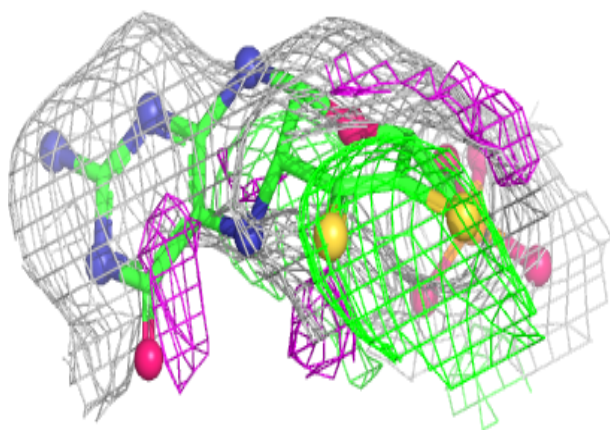
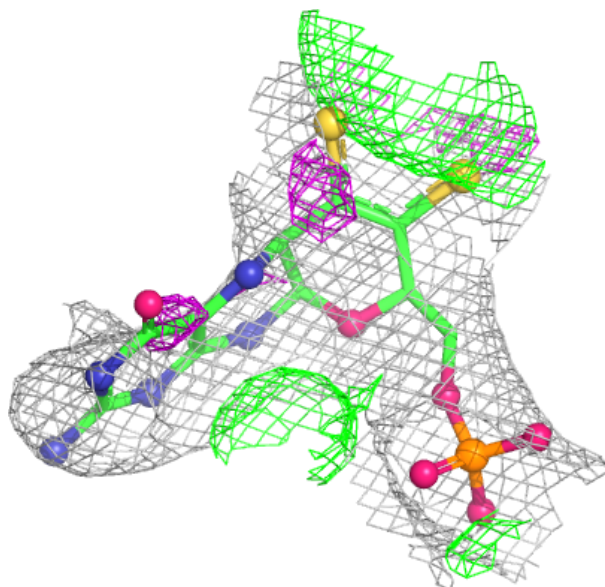
Electron density around MTE A 703:

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



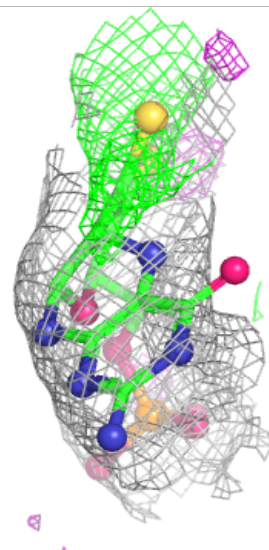
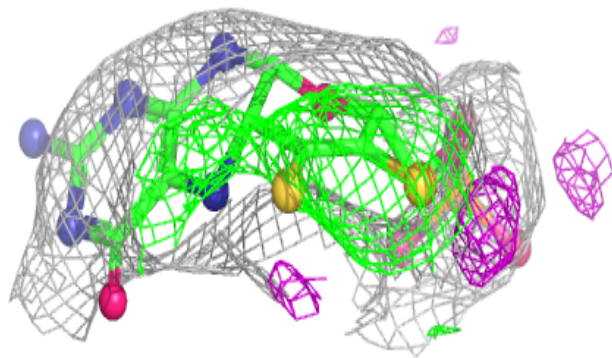
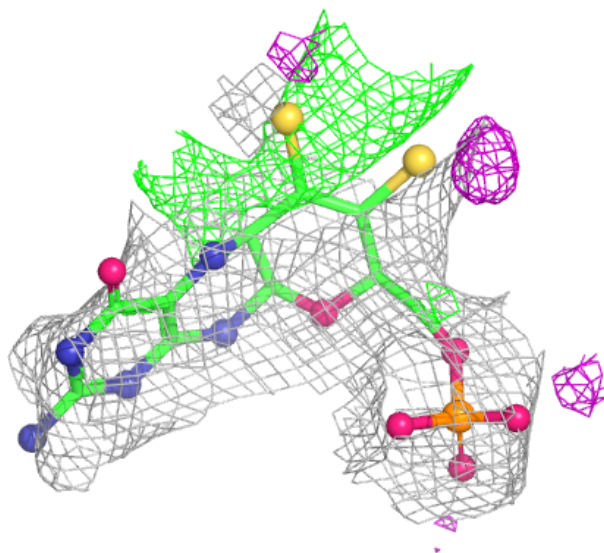
Electron density around MTE B 702:

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



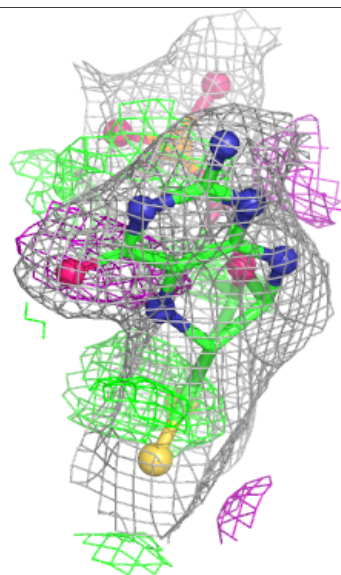
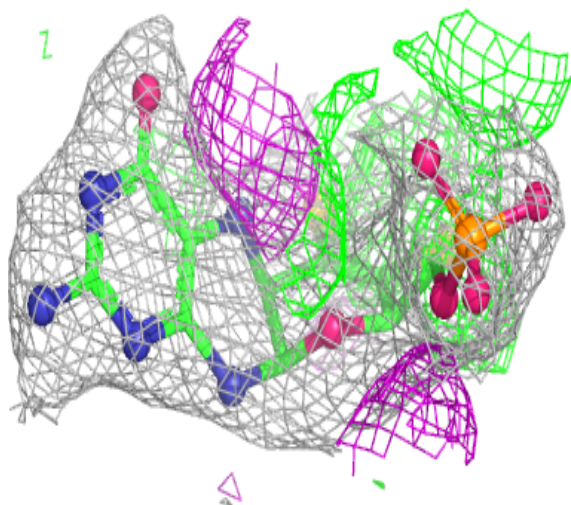
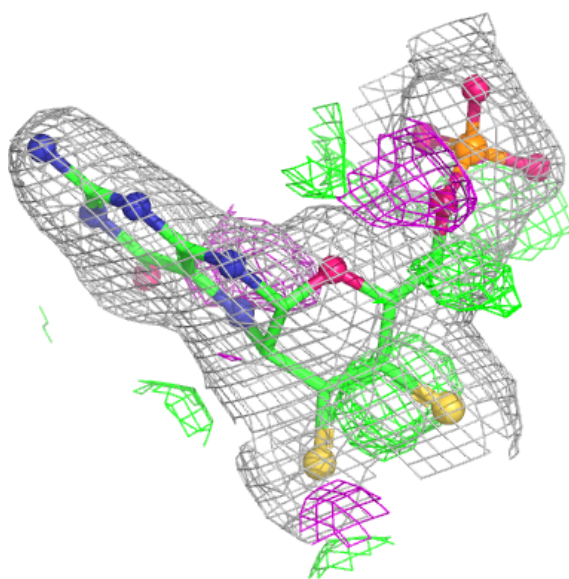
Electron density around MTE B 703:

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



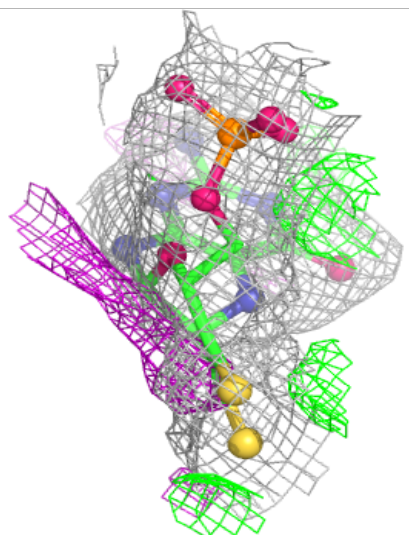
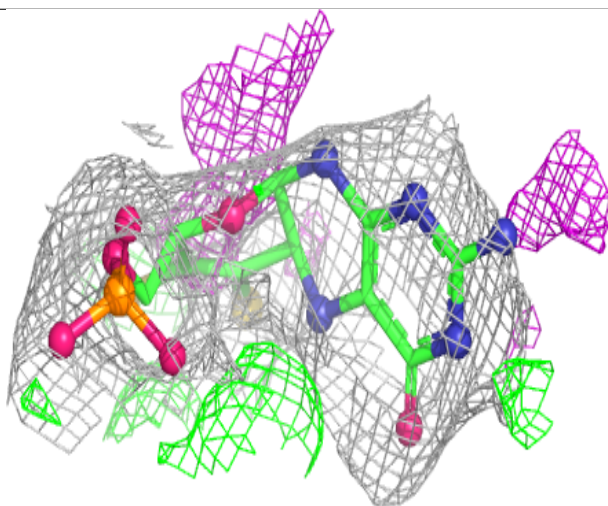
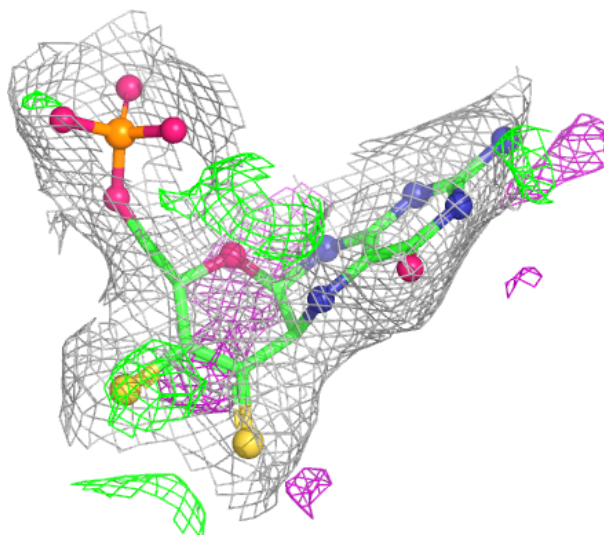
Electron density around MTE C 702:

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



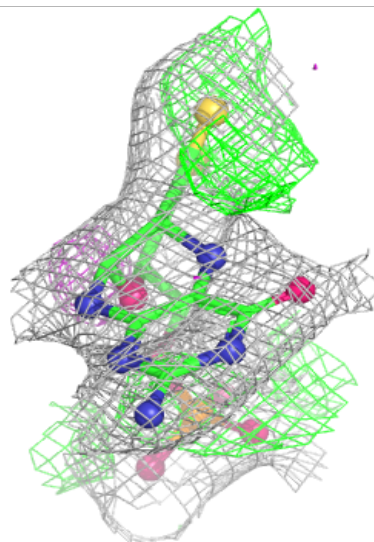
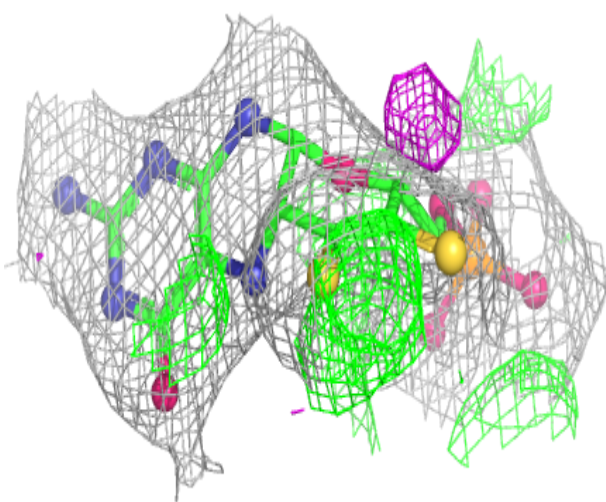
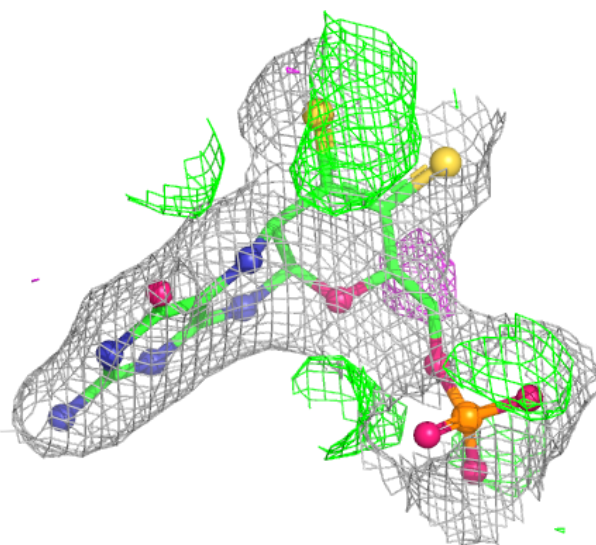
Electron density around MTE C 703:

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



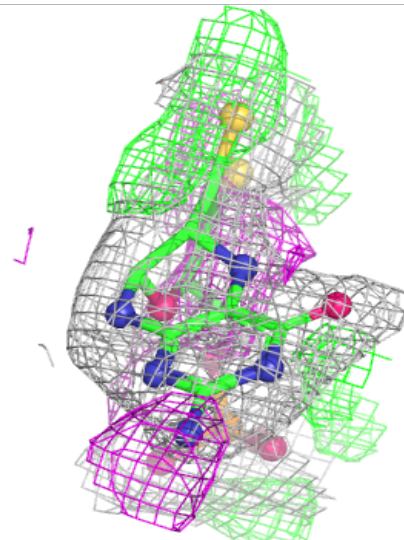
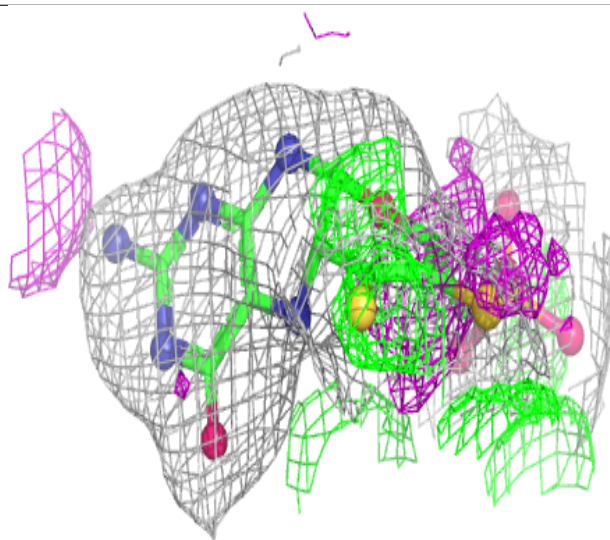
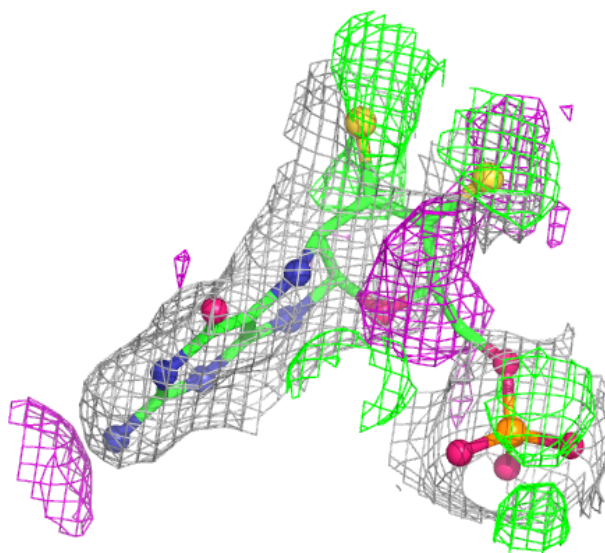
Electron density around MTE D 703:

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



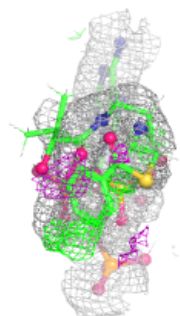
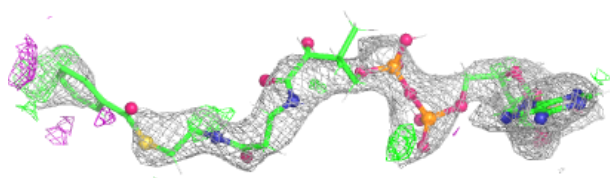
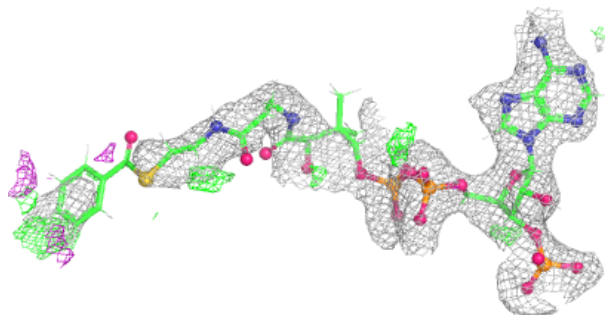
Electron density around MTE D 704:

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

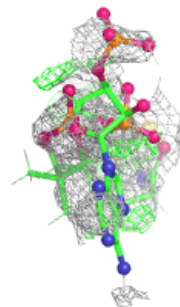
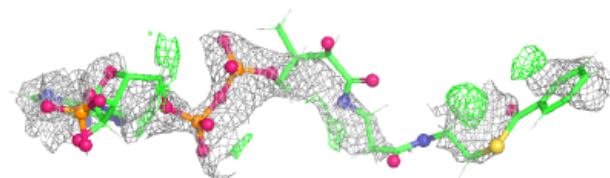
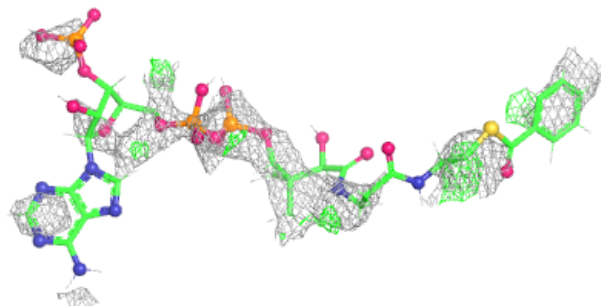


Electron density around BYC A 707:

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

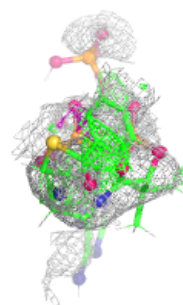
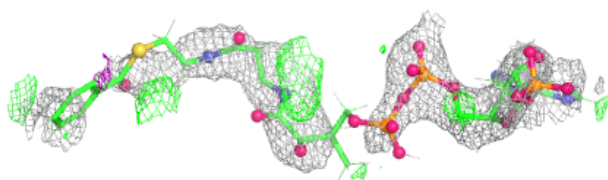
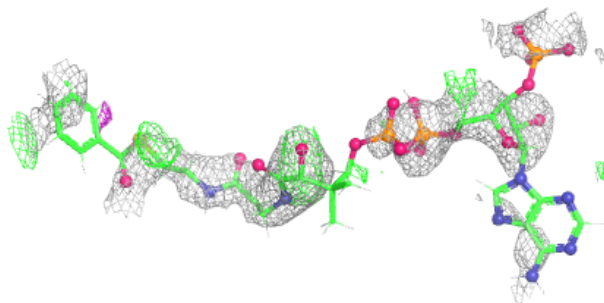
**Electron density around BYC B 707:**

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

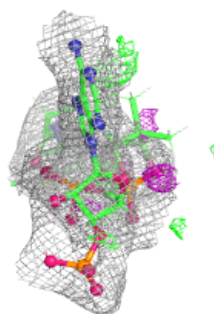
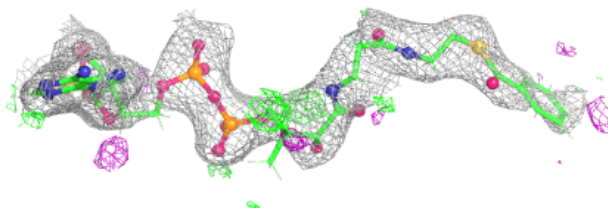
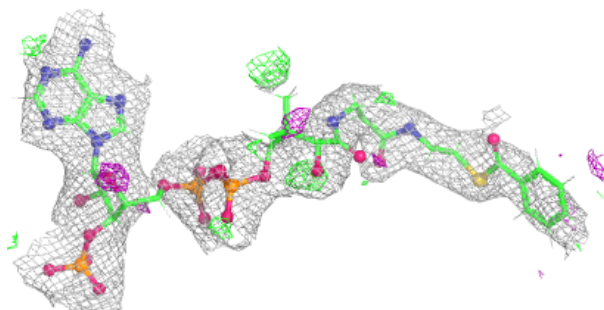


Electron density around BYC C 707:

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

**Electron density around BYC D 707:**

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



6.5 Other polymers

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