



# wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 10, 2023 – 05:06 am GMT

PDB ID : 2V98  
Title : Structure of the complex of TcAChE with 1-(2-nitrophenyl)-2,2,2- trifluoro ethyl-arsenocholine after a 9 seconds annealing to room temperature, during the first 5 seconds of which laser irradiation at 266nm took place  
Authors : Colletier, J.-P.; Sanson, B.; Royant, A.; Specht, A.; Nachon, F.; Masson, P.; Zaccai, G.; Sussman, J.L.; Goeldner, M.; Silman, I.; Bourgeois, D.; Weik, M.  
Deposited on : 2007-08-22  
Resolution : 3.00 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](mailto: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>.

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The following versions of software and data (see [references](#) ①) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.36  
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) : 2.36

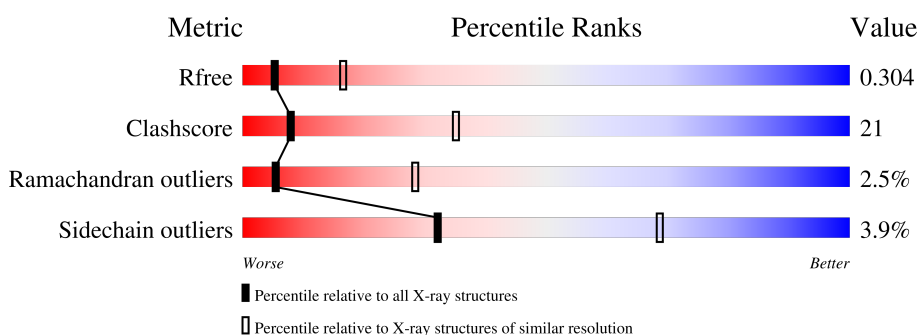
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)

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  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	537	
1	B	537	

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	CL	A	1536[A]	-	-	X	-
2	CL	A	1536[B]	-	-	X	-
3	CFQ	A	1538[A]	-	-	X	-

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<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
3	CFQ	B	1537[A]	-	-	X	-

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 18984 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.

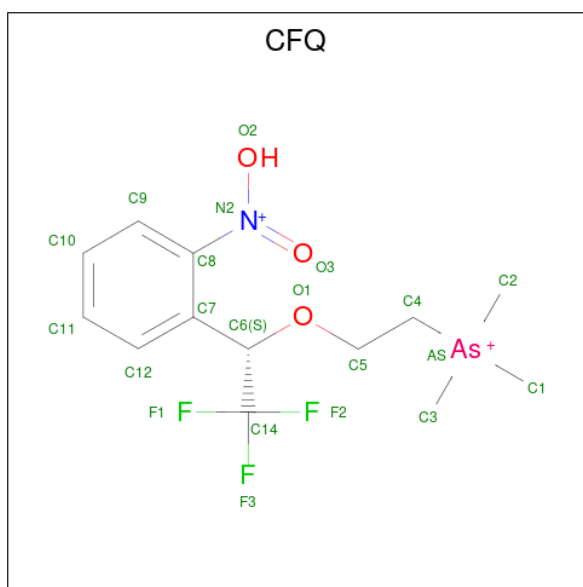
- Molecule 1 is a protein called ACETYLCHOLINESTERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	528	Total 8362	C 5382	N 1406	O 1530	S 44	0	528	0
1	B	532	Total 8398	C 5406	N 1410	O 1538	S 44	0	532	0

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total 2 Cl 2	0	1

- Molecule 3 is 1-(2-nitrophenyl)-2,2,2-trifluoroethyl]-arsenocholine (three-letter code: CFQ) (formula: C<sub>13</sub>H<sub>19</sub>AsF<sub>3</sub>NO<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	As	C	F	N			O
3	A	1	Total 42	As 2	C 26	F 6	N 2	O 6	0	1

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	As	C	F	N	O		
3	A	1	Total	As	C	F	N	O	0	1
			42	2	26	6	2	6		
3	B	1	Total	As	C	F	N	O	0	1
			42	2	26	6	2	6		
3	B	1	Total	As	C	F	N	O	0	1
			42	2	26	6	2	6		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	Total	C	N	O	0	1
			28	16	2	10		
4	A	1	Total	C	N	O	0	1
			28	16	2	10		
4	B	1	Total	C	N	O	0	1
			28	16	2	10		
4	B	1	Total	C	N	O	0	1
			28	16	2	10		

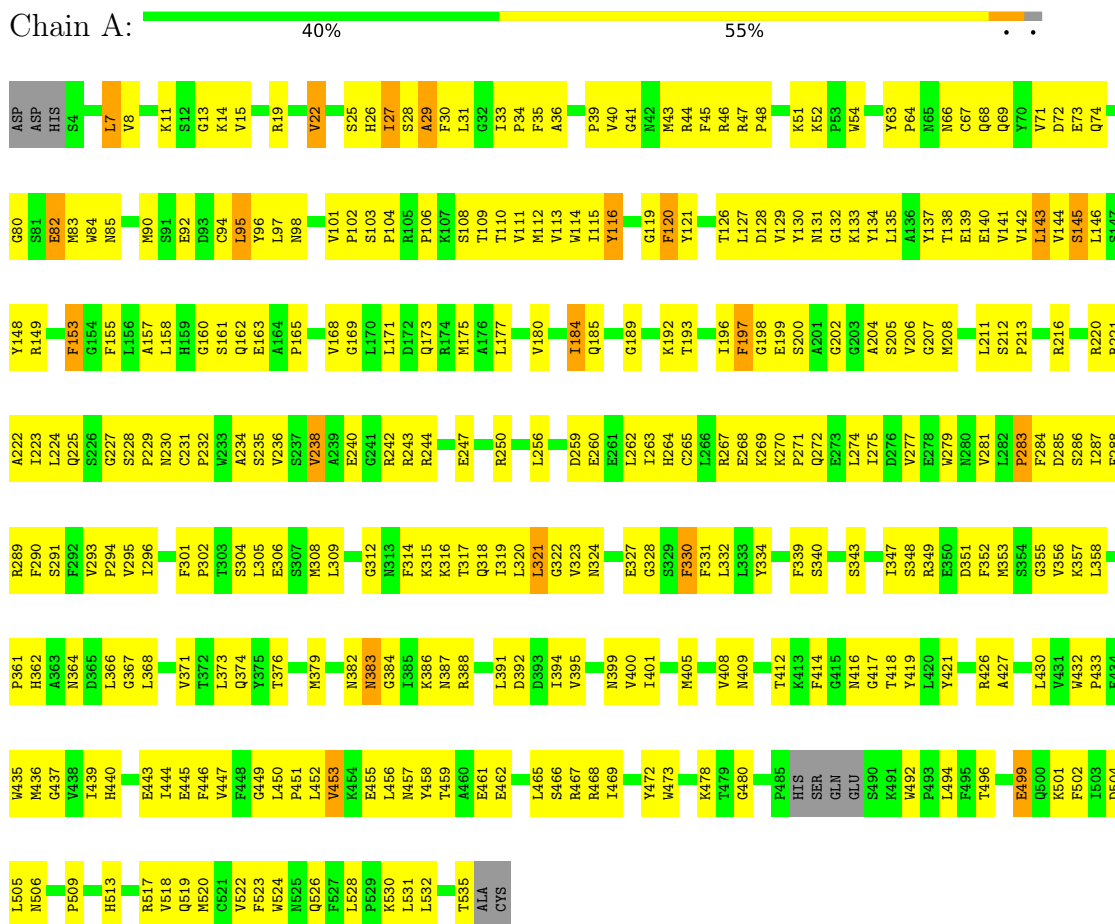
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	925	Total	O	0	814
			925	925		
5	B	1017	Total	O	0	919
			1017	1017		

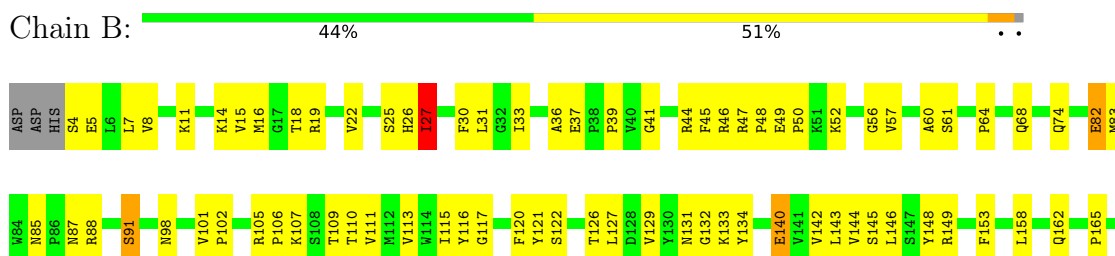
### 3 Residue-property plots

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.

- Molecule 1: ACETYLCHOLINESTERASE



- Molecule 1: ACETYLCHOLINESTERASE







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	91.62Å 104.47Å 148.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 3.00 19.85 – 3.00	Depositor EDS
% Data completeness (in resolution range)	96.4 (8.00-3.00) 99.3 (19.85-3.00)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.71 (at 2.98Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.202 , 0.249 0.284 , 0.304	Depositor DCC
$R_{free}$ test set	2672 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	52.7	Xtrriage
Anisotropy	0.624	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 66.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.41$ , $\langle L^2 \rangle = 0.24$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	18984	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 42.68 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.9698e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: CFQ, NAG, CL

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	0.54	0/8604	0.71	2/11686 (0.0%)
1	B	0.54	0/8642	0.73	2/11738 (0.0%)
All	All	0.54	0/17246	0.72	4/23424 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	27[A]	ILE	CB-CA-C	-5.59	100.43	111.60
1	B	27[B]	ILE	CB-CA-C	-5.59	100.43	111.60
1	A	494[A]	LEU	CA-CB-CG	5.29	127.47	115.30
1	A	494[B]	LEU	CA-CB-CG	5.29	127.47	115.30

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	8362	0	8036	354	0
1	B	8398	0	8068	324	0
2	A	2	0	0	6	0
3	A	84	0	32	31	0
3	B	84	0	32	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	56	0	52	1	0
4	B	56	0	52	0	0
5	A	925	0	0	69	0
5	B	1017	0	0	67	0
All	All	18984	0	16272	715	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 21.

The worst 5 of 715 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)
3:B:1537[A]:CFQ:C4	3:B:1537[A]:CFQ:AS	2.21	1.49
3:A:1538[A]:CFQ:C4	3:A:1538[A]:CFQ:AS	2.23	1.47
3:B:1537[A]:CFQ:AS	3:B:1537[A]:CFQ:C1	2.23	1.47
3:B:1537[A]:CFQ:AS	3:B:1537[A]:CFQ:C2	2.23	1.46
3:A:1537[A]:CFQ:AS	3:A:1537[A]:CFQ:C4	2.24	1.46

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	1048/537 (195%)	892 (85%)	128 (12%)	28 (3%)	5	26
1	B	1060/537 (197%)	910 (86%)	126 (12%)	24 (2%)	6	30
All	All	2108/1074 (196%)	1802 (86%)	254 (12%)	52 (2%)	5	28

5 of 52 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	27[A]	ILE
1	A	27[B]	ILE
1	A	95[A]	LEU
1	A	95[B]	LEU
1	B	27[A]	ILE

### 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	900/469 (192%)	868 (96%)	32 (4%)	35	70
1	B	902/469 (192%)	864 (96%)	38 (4%)	30	66
All	All	1802/938 (192%)	1732 (96%)	70 (4%)	32	69

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	473[B]	TRP
1	B	494[B]	LEU
1	B	505[B]	LEU
1	A	358[A]	LEU
1	A	330[B]	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 2 are monoatomic - leaving 16 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	CFQ	B	1536[A]	-	16,21,21	3.24	5 (31%)	20,31,31	1.65	5 (25%)
3	CFQ	A	1537[A]	-	16,21,21	3.11	6 (37%)	20,31,31	1.53	5 (25%)
3	CFQ	B	1537[B]	-	16,21,21	3.17	5 (31%)	20,31,31	1.77	7 (35%)
4	NAG	B	1538[B]	-	14,14,15	0.54	0	17,19,21	0.71	0
3	CFQ	B	1536[B]	-	16,21,21	3.03	5 (31%)	20,31,31	1.70	5 (25%)
3	CFQ	A	1537[B]	-	16,21,21	2.92	6 (37%)	20,31,31	1.58	4 (20%)
4	NAG	B	1539[A]	-	14,14,15	0.77	0	17,19,21	0.62	0
3	CFQ	A	1538[A]	-	16,21,21	2.89	5 (31%)	20,31,31	1.93	6 (30%)
4	NAG	B	1539[B]	-	14,14,15	0.53	0	17,19,21	0.65	0
3	CFQ	A	1538[B]	-	16,21,21	3.20	6 (37%)	20,31,31	1.78	6 (30%)
4	NAG	A	1539[A]	-	14,14,15	0.68	0	17,19,21	1.07	2 (11%)
4	NAG	A	1540[A]	-	14,14,15	0.57	0	17,19,21	0.53	0
4	NAG	A	1539[B]	-	14,14,15	0.55	0	17,19,21	0.76	0
4	NAG	A	1540[B]	-	14,14,15	0.61	0	17,19,21	0.65	0
3	CFQ	B	1537[A]	-	16,21,21	3.02	6 (37%)	20,31,31	1.85	6 (30%)
4	NAG	B	1538[A]	-	14,14,15	0.70	0	17,19,21	0.85	1 (5%)

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	CFQ	B	1536[A]	-	-	1/18/21/21	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CFQ	A	1537[A]	-	-	4/18/21/21	0/1/1/1
3	CFQ	B	1537[B]	-	-	1/18/21/21	0/1/1/1
4	NAG	B	1538[B]	-	-	2/6/23/26	0/1/1/1
3	CFQ	B	1536[B]	-	-	2/18/21/21	0/1/1/1
3	CFQ	A	1537[B]	-	-	7/18/21/21	0/1/1/1
4	NAG	B	1539[A]	-	-	0/6/23/26	0/1/1/1
3	CFQ	A	1538[A]	-	-	8/18/21/21	0/1/1/1
4	NAG	B	1539[B]	-	-	2/6/23/26	0/1/1/1
3	CFQ	A	1538[B]	-	-	4/18/21/21	0/1/1/1
4	NAG	A	1539[A]	-	-	2/6/23/26	0/1/1/1
4	NAG	A	1540[A]	-	-	0/6/23/26	0/1/1/1
4	NAG	A	1539[B]	-	-	4/6/23/26	0/1/1/1
4	NAG	A	1540[B]	-	-	2/6/23/26	0/1/1/1
3	CFQ	B	1537[A]	-	-	9/18/21/21	0/1/1/1
4	NAG	B	1538[A]	-	-	4/6/23/26	0/1/1/1

The worst 5 of 44 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1536[A]	CFQ	C7-C6	7.58	1.60	1.51
3	A	1538[B]	CFQ	C7-C6	7.42	1.60	1.51
3	A	1537[A]	CFQ	C7-C6	7.32	1.60	1.51
3	B	1537[A]	CFQ	C8-C7	7.06	1.49	1.39
3	B	1537[B]	CFQ	C8-C7	7.04	1.49	1.39

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1538[A]	CFQ	C9-C8-C7	-4.63	116.80	121.35
3	B	1537[A]	CFQ	C9-C8-C7	-4.52	116.92	121.35
3	B	1537[B]	CFQ	C9-C8-C7	-3.99	117.43	121.35
3	A	1537[A]	CFQ	C5-O1-C6	3.79	119.17	114.01
3	B	1536[A]	CFQ	C9-C8-C7	-3.68	117.74	121.35

There are no chirality outliers.

5 of 52 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1537[A]	CFQ	O1-C6-C7-C8

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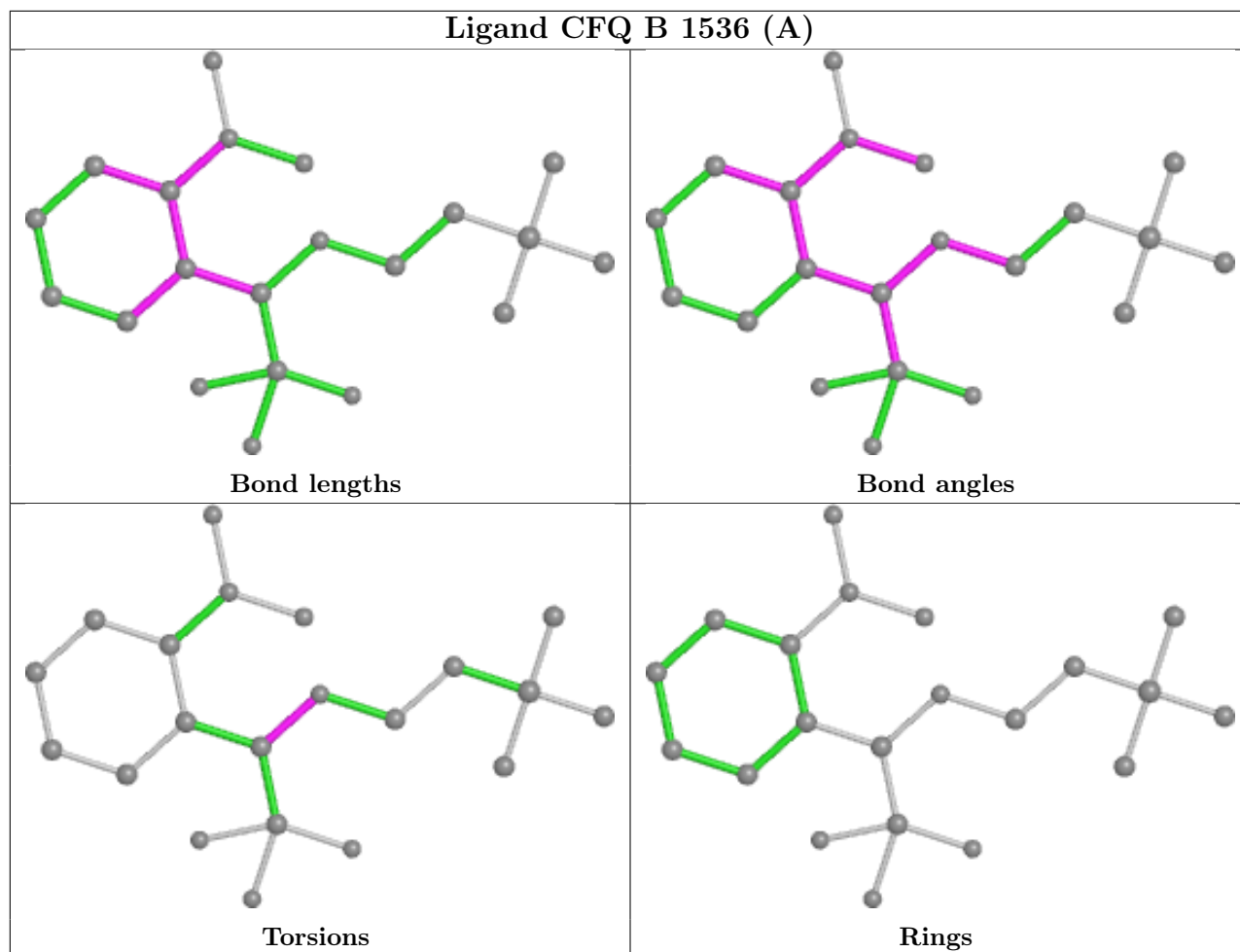
Mol	Chain	Res	Type	Atoms
3	A	1537[A]	CFQ	C14-C6-C7-C12
3	A	1537[B]	CFQ	F1-C14-C6-O1
3	A	1537[B]	CFQ	F2-C14-C6-O1
3	A	1538[A]	CFQ	F2-C14-C6-O1

There are no ring outliers.

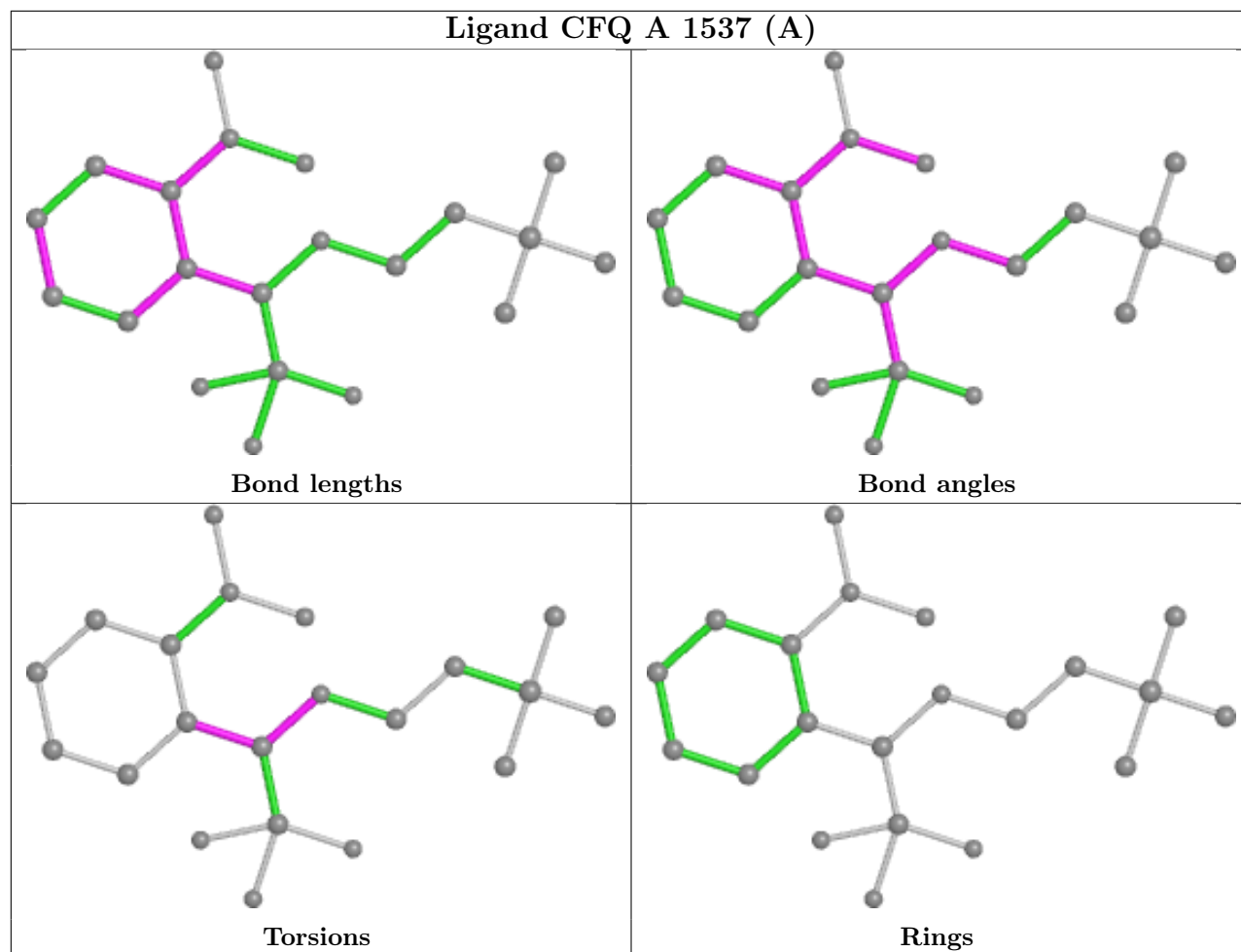
9 monomers are involved in 58 short contacts:

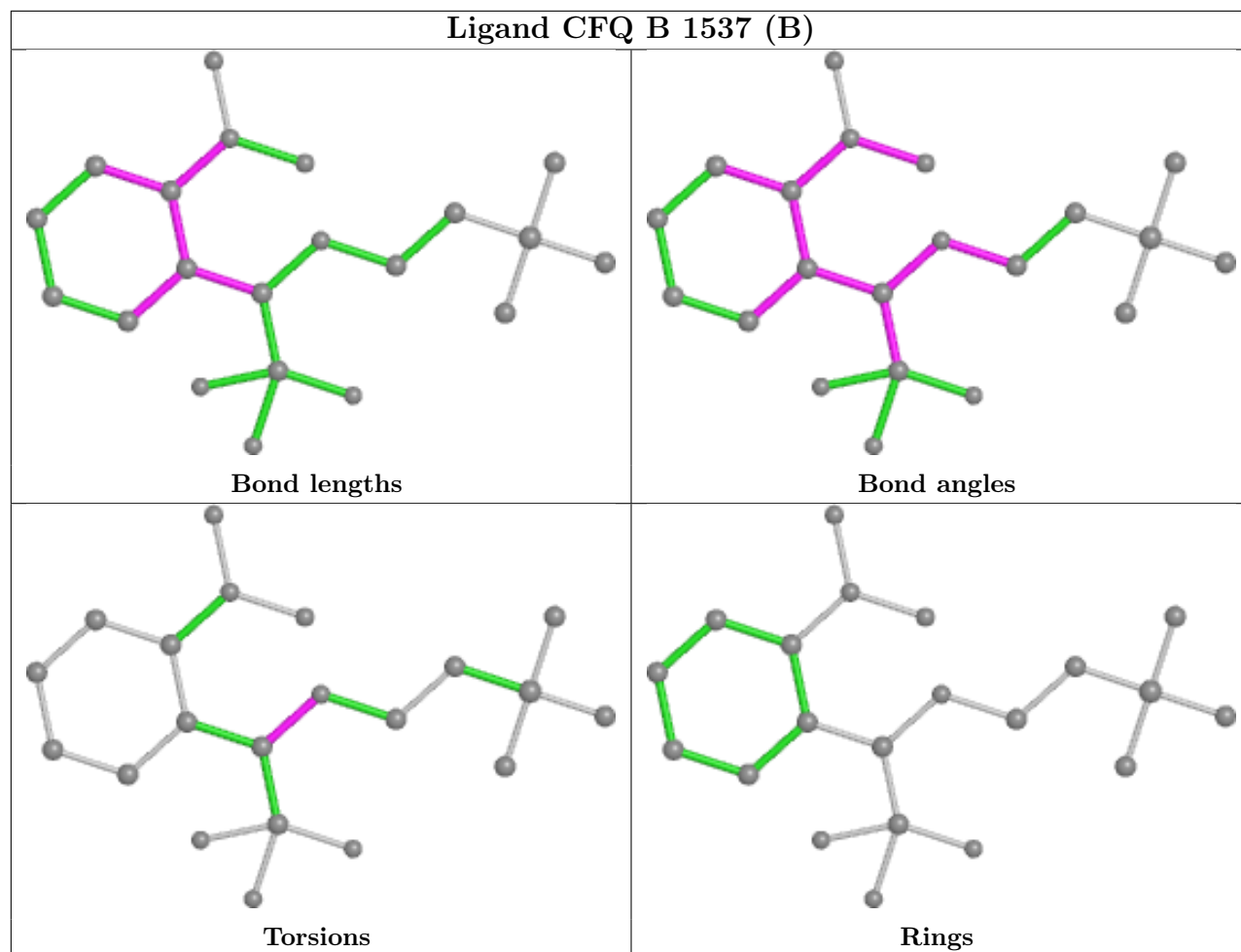
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1536[A]	CFQ	6	0
3	A	1537[A]	CFQ	8	0
3	B	1537[B]	CFQ	5	0
3	B	1536[B]	CFQ	5	0
3	A	1537[B]	CFQ	5	0
3	A	1538[A]	CFQ	12	0
3	A	1538[B]	CFQ	6	0
4	A	1540[B]	NAG	1	0
3	B	1537[A]	CFQ	10	0

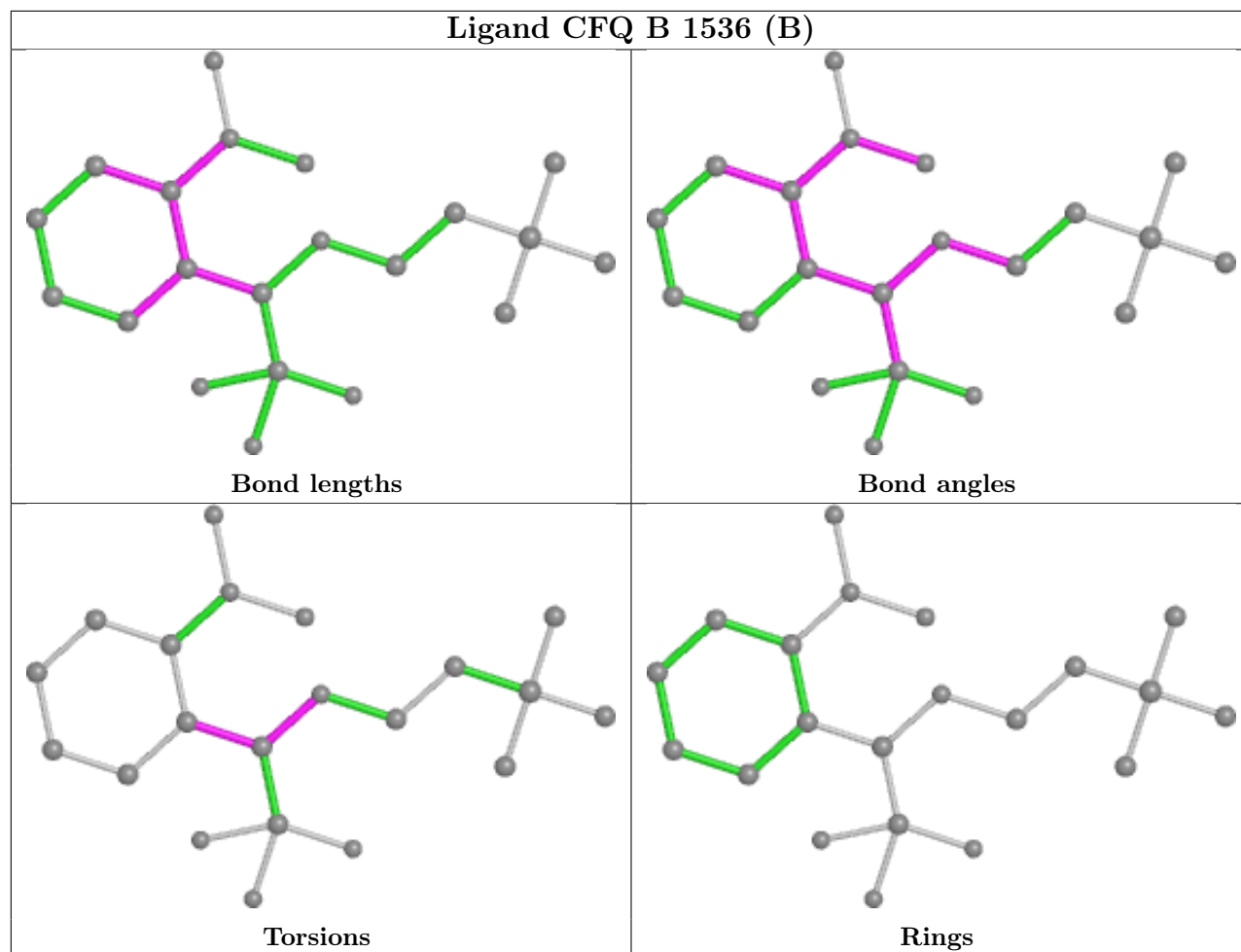
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

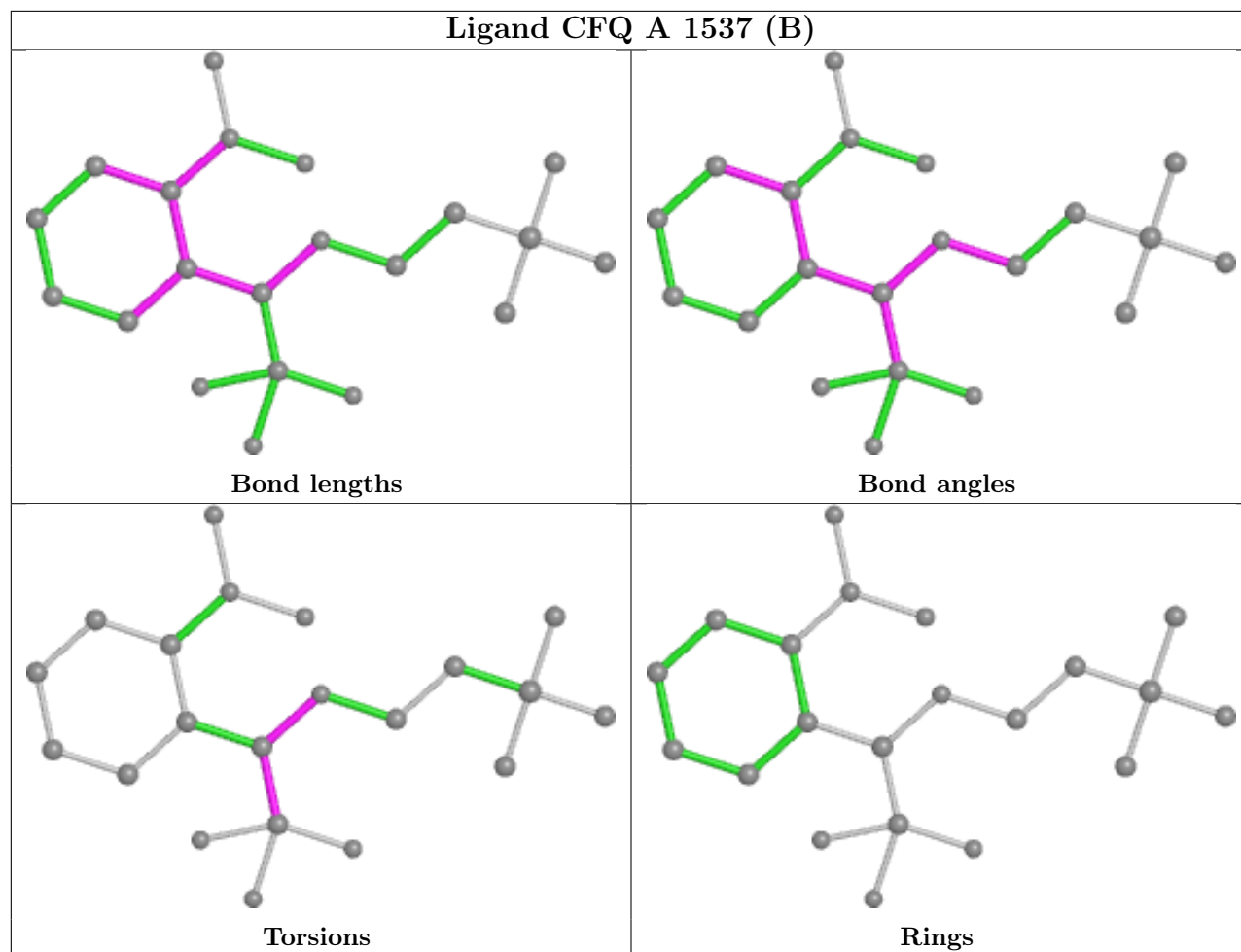


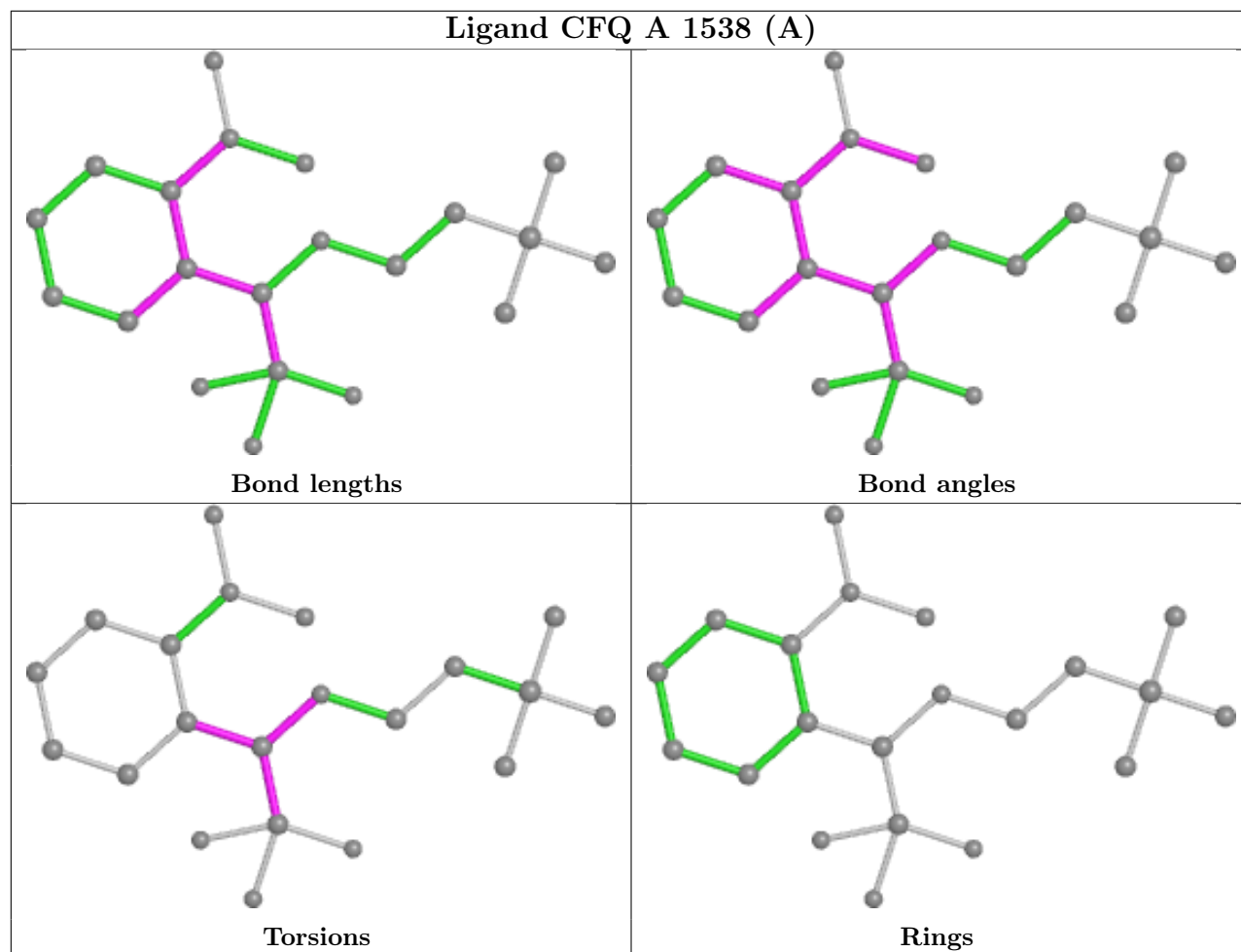


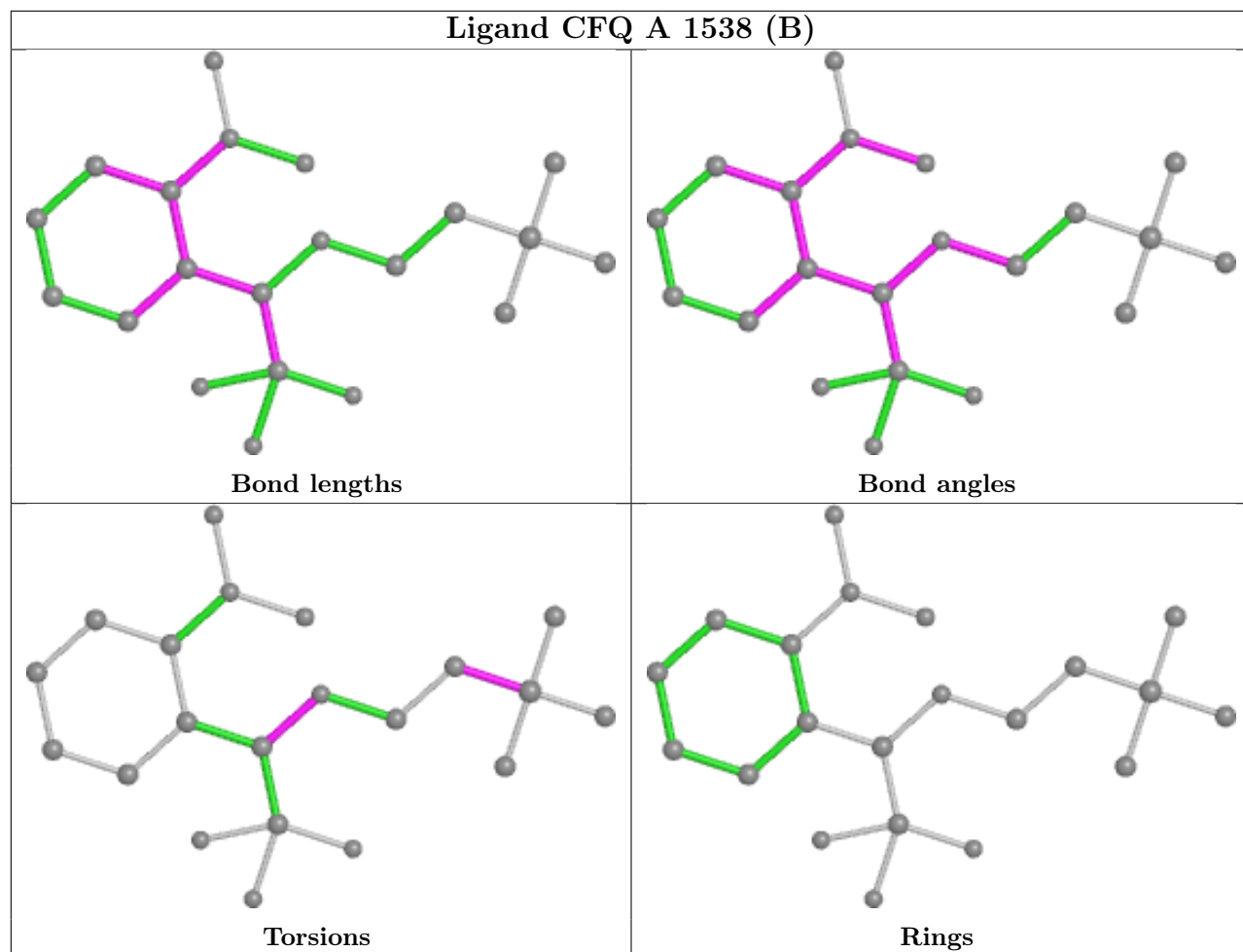


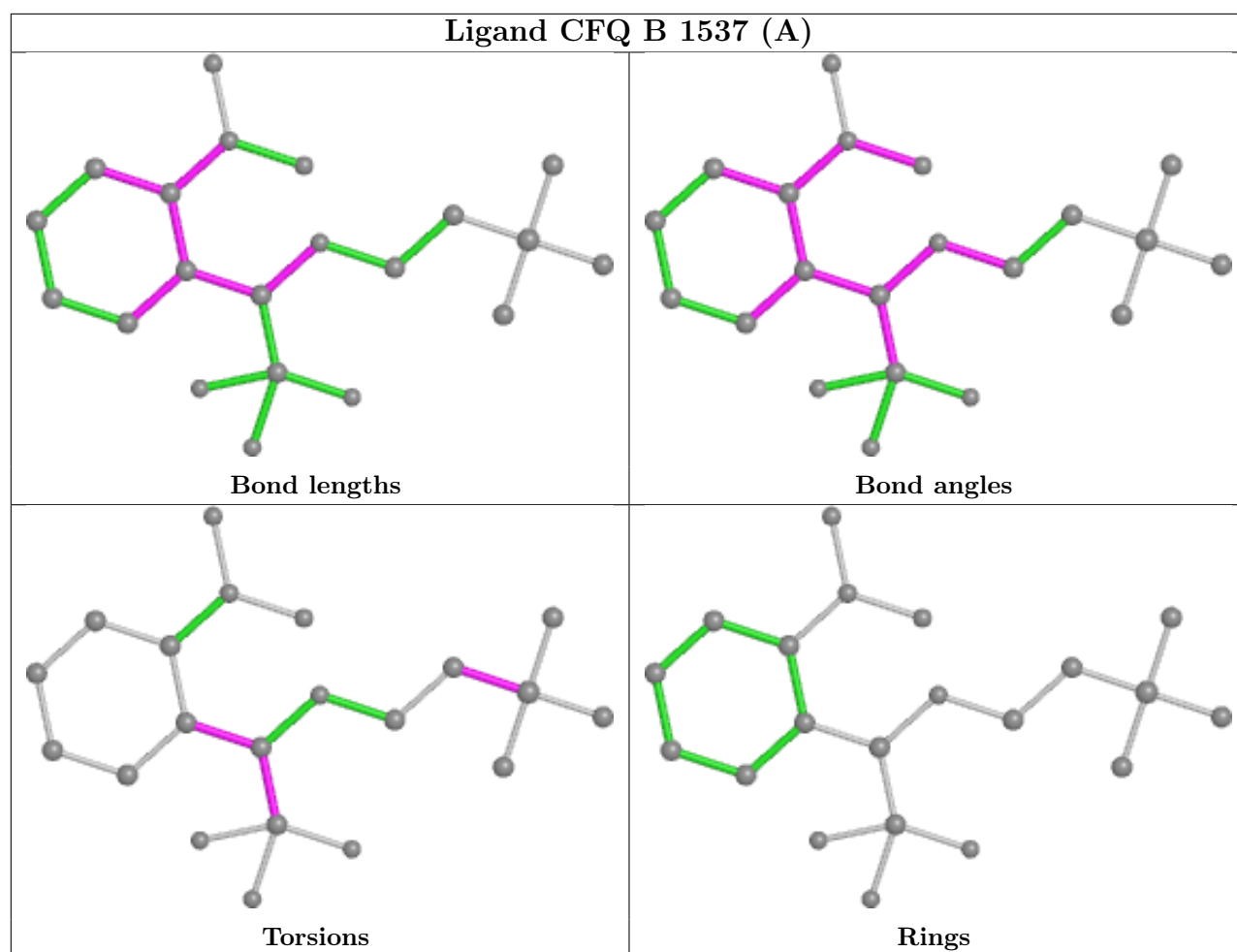












## 5.7 Other polymers [i](#)

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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands

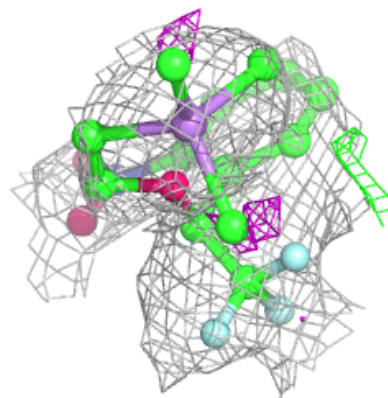
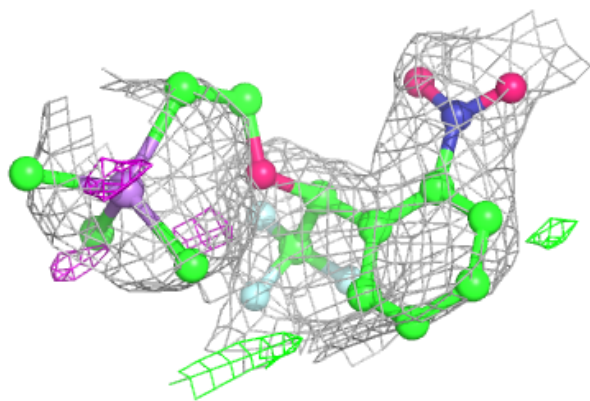
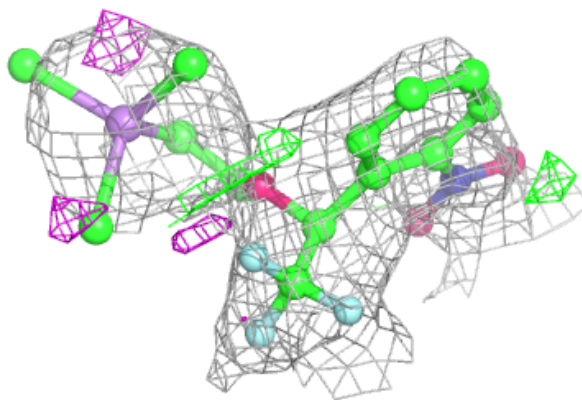
Unable to reproduce the depositors R factor - this section is therefore empty.

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.



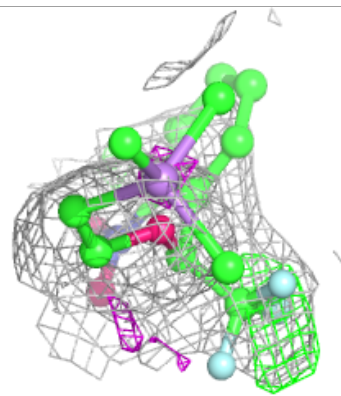
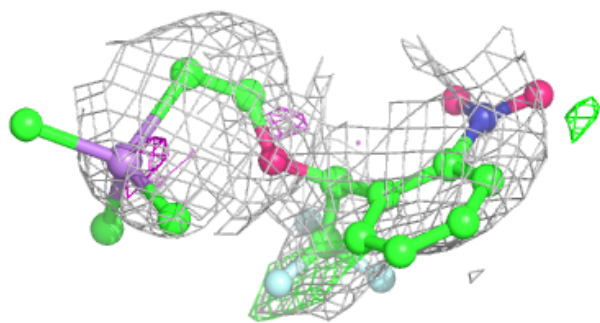
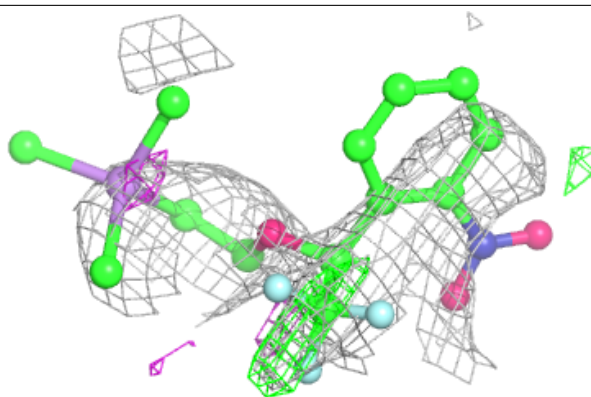
**Electron density around CFQ A 1537 (A):**

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

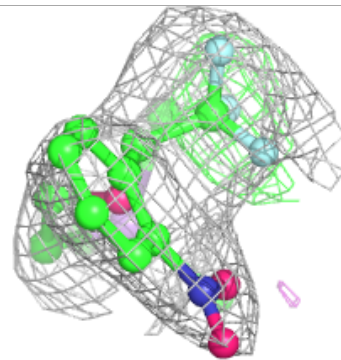
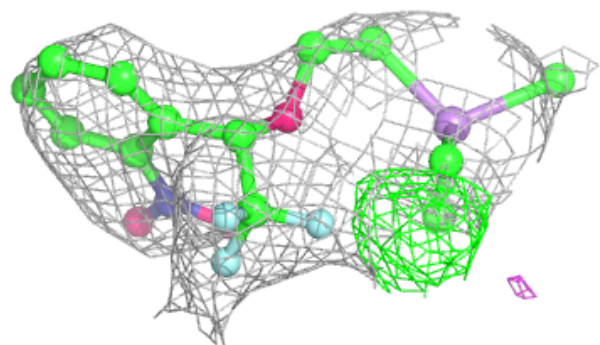
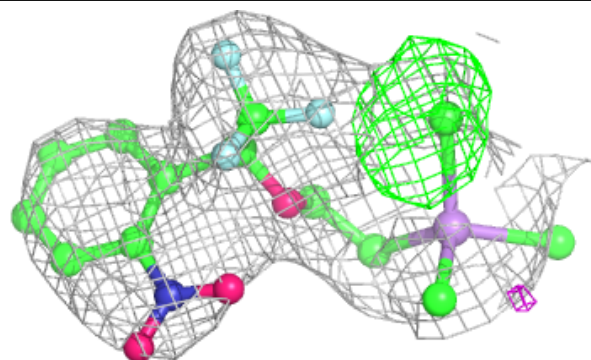


**Electron density around CFQ A 1537 (B):**

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

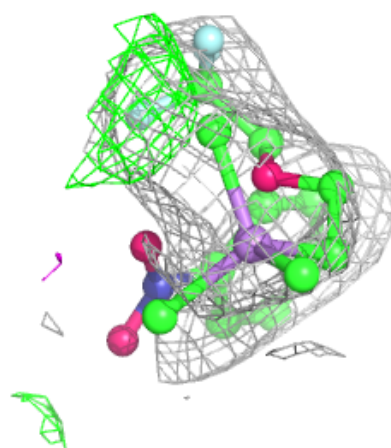
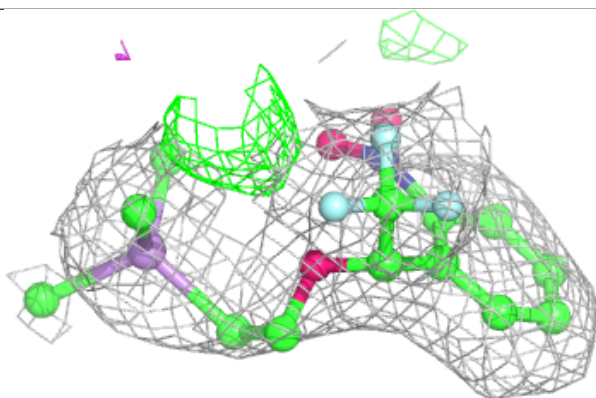
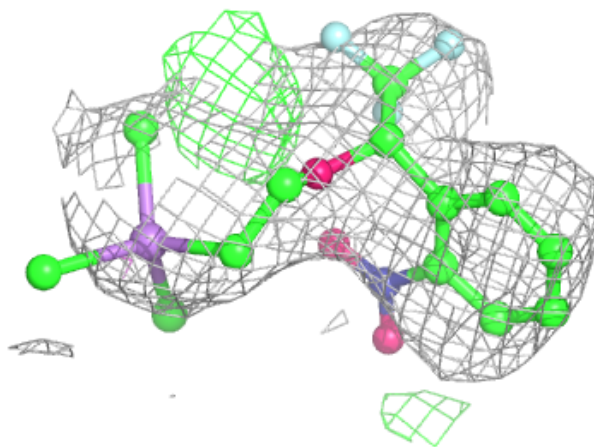
**Electron density around CFQ A 1538 (A):**

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



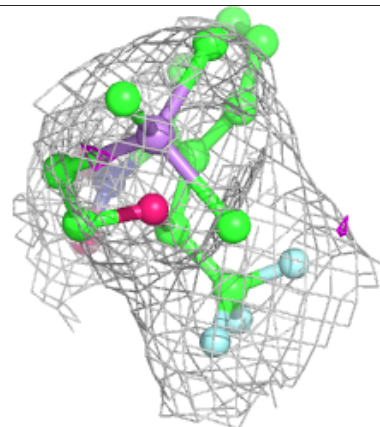
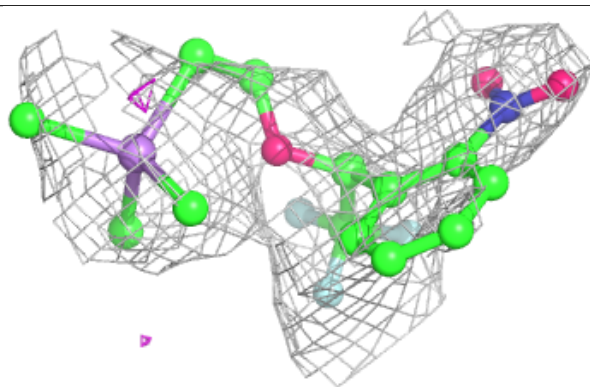
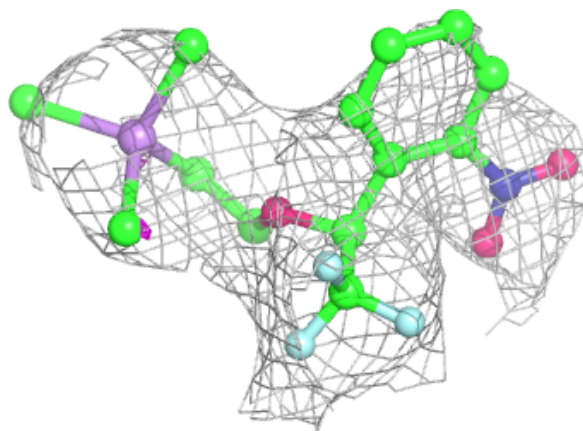
**Electron density around CFQ A 1538 (B):**

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



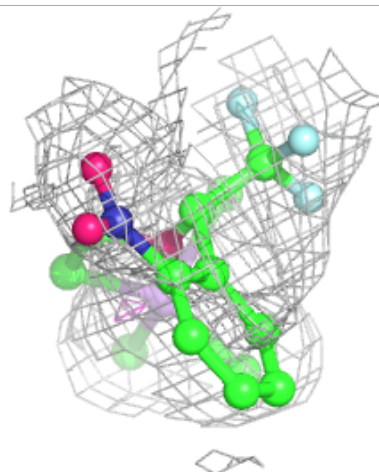
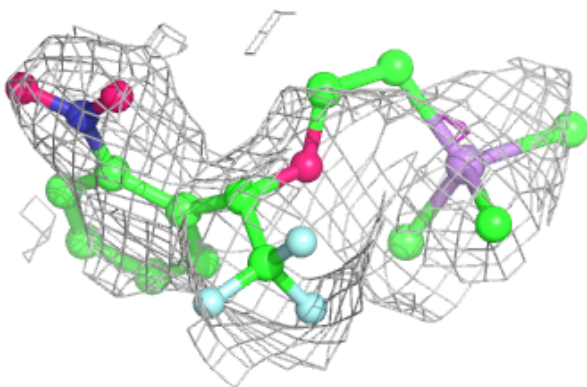
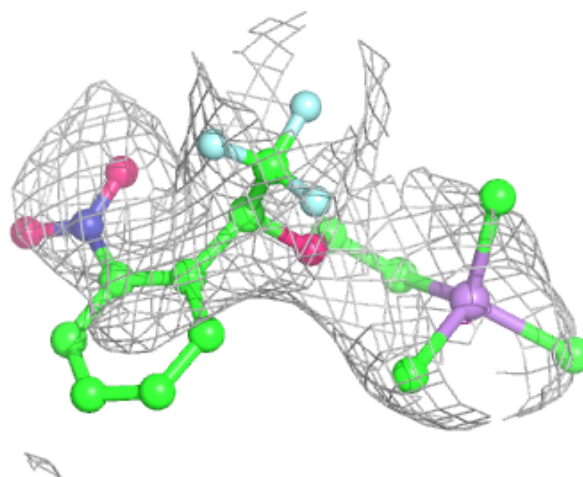
**Electron density around CFQ B 1536 (A):**

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



**Electron density around CFQ B 1536 (B):**

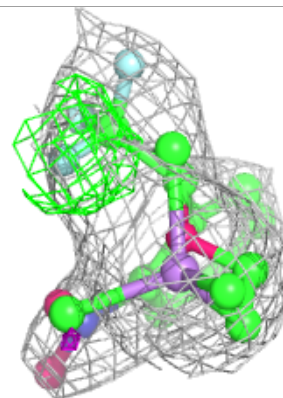
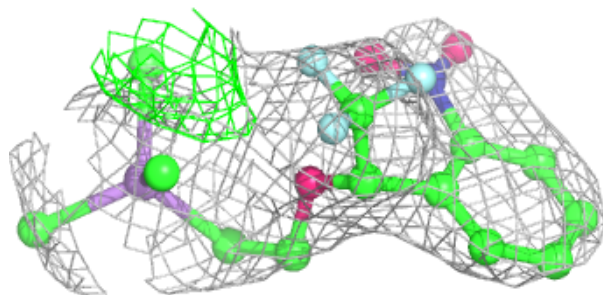
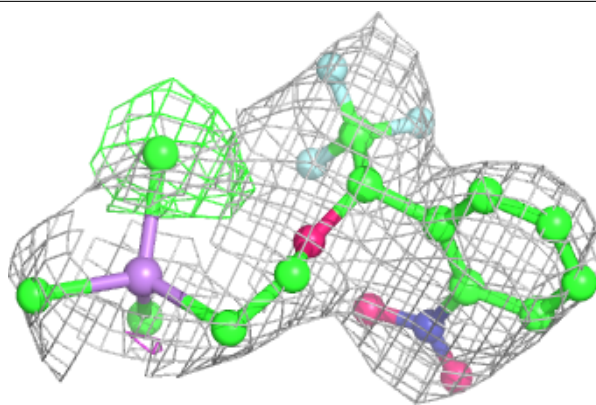
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



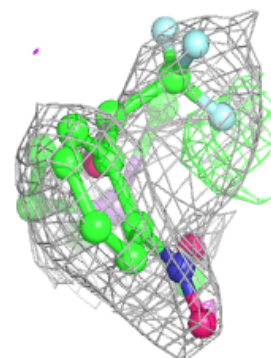
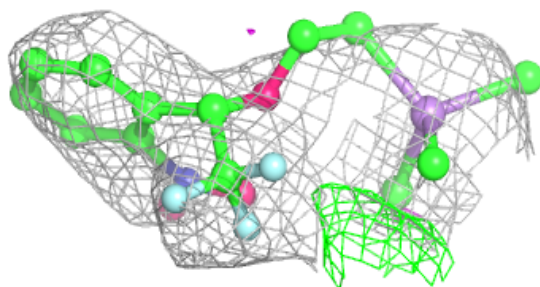
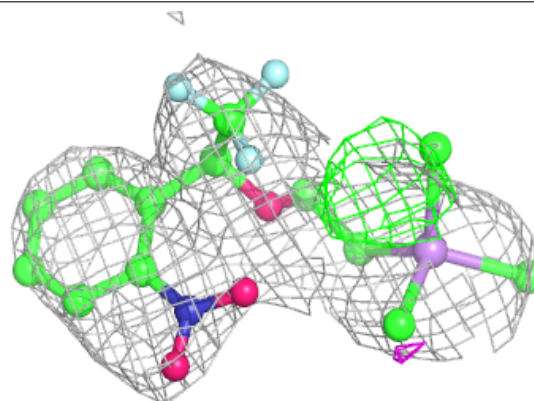


**Electron density around CFQ B 1537 (A):**

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

**Electron density around CFQ B 1537 (B):**

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



## 6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.