



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 07:28 AM UTC

PDB ID : 2BS2 / pdb\_00002bs2  
Title : QUINOL:FUMARATE REDUCTASE FROM WOLINELLA SUCCINOGENES  
Authors : Lancaster, C.R.D.  
Deposited on : 2005-05-14  
Resolution : 1.78 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>.

---

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)  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

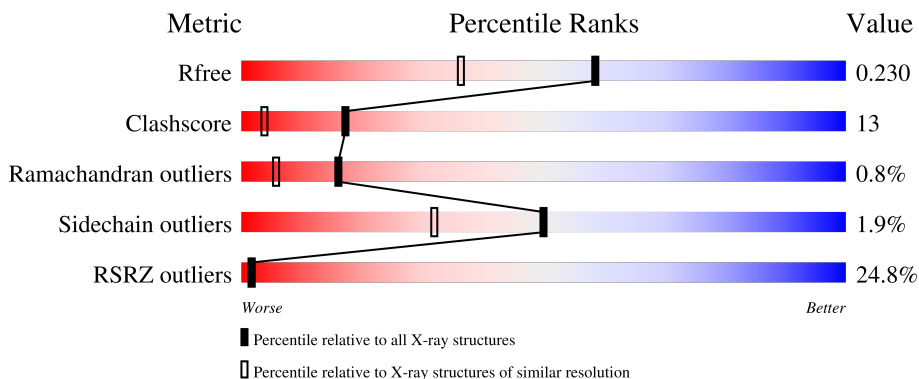
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.78 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



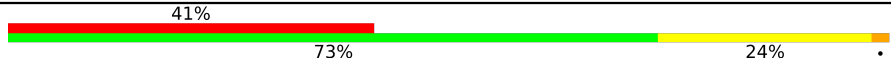
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	1365 (1.78-1.78)
Clashscore	190562	1395 (1.78-1.78)
Ramachandran outliers	187476	1382 (1.78-1.78)
Sidechain outliers	187428	1382 (1.78-1.78)
RSRZ outliers	180081	1365 (1.78-1.78)

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  $\leq 5\%$ . 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	660	 21% 75% 22% ..
1	D	660	 23% 74% 24% ..
2	B	241	 10% 78% 19% .
2	E	241	 15% 78% 20% .
3	C	256	 45% 73% 24% .

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
3	F	256	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a red segment on the left labeled '41%', a green segment in the middle labeled '73%', and a yellow segment on the right labeled '24%'. A small black dot is located at the far right end of the bar.</p>

## 2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 19666 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 QUINOL-FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	656	5145	3219	927	967	32	27	5	1
1	D	656	5125	3207	921	965	32	32	3	1

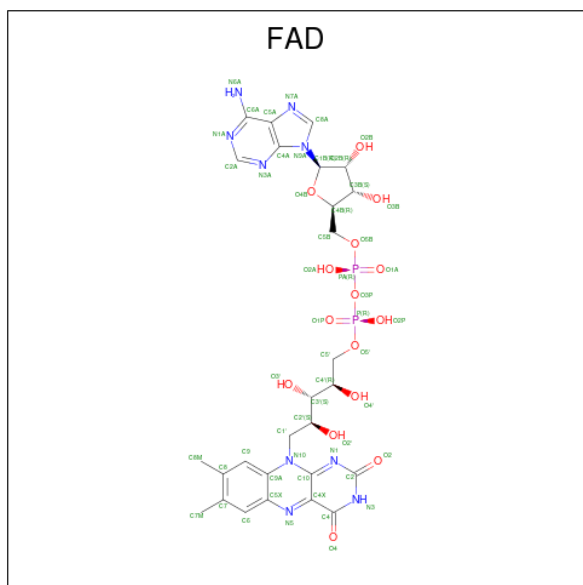
- Molecule 2 is a protein called QUINOL-FUMARATE REDUCTASE IRON-SULFUR SUBUNIT B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	240	1902	1199	324	355	24	6	1	1
2	E	240	1902	1199	324	355	24	6	1	1

- Molecule 3 is a protein called QUINOL-FUMARATE REDUCTASE DIHEME CYTOCHROME B SUBUNIT C.

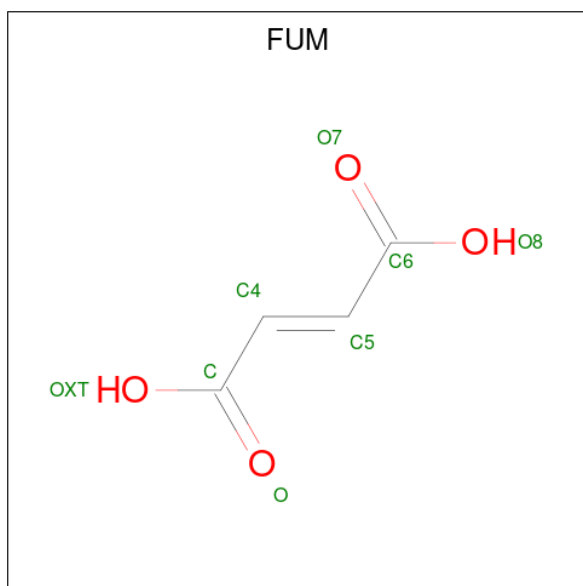
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	255	2099	1398	336	351	14	16	2	1
3	F	255	2099	1398	336	351	14	12	2	1

- Molecule 4 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: C<sub>27</sub>H<sub>33</sub>N<sub>9</sub>O<sub>15</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
4	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
4	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 5 is FUMARIC ACID (CCD ID: FUM) (formula:  $C_4H_4O_4$ ).

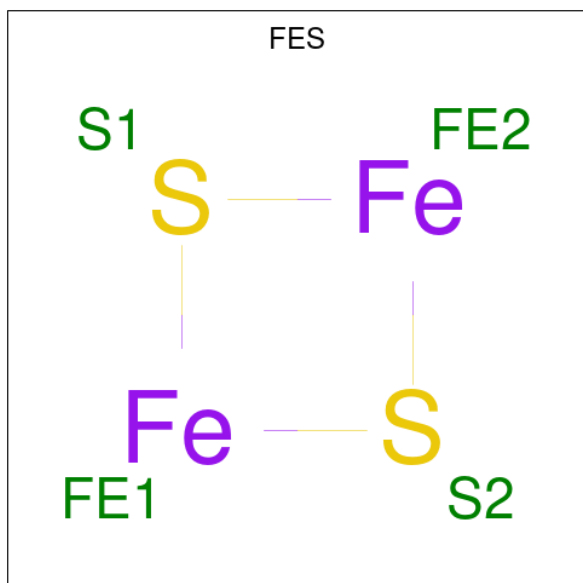


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
5	A	1	Total	C	O	0	0
			8	4	4		
5	D	1	Total	C	O	0	0
			8	4	4		

- Molecule 6 is SODIUM ION (CCD ID: NA) (formula: Na).

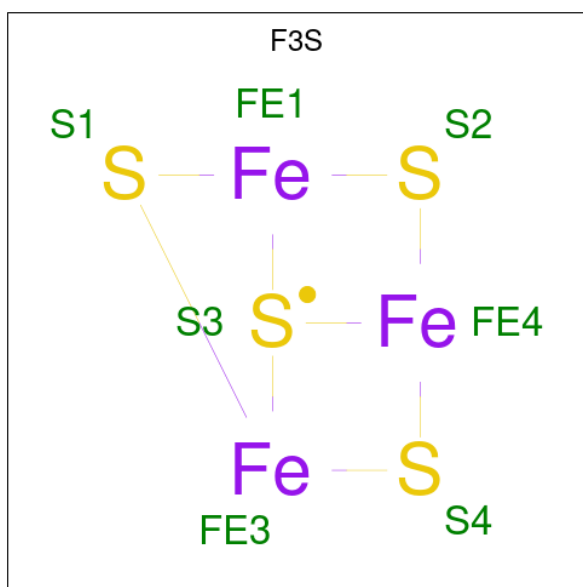
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Na 1 1	0	0
6	D	1	Total Na 1 1	0	0

- Molecule 7 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe<sub>2</sub>S<sub>2</sub>).



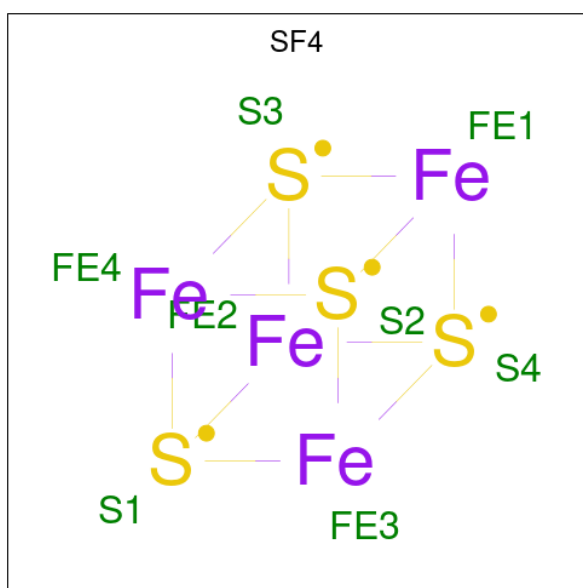
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total Fe S 4 2 2	0	0
7	E	1	Total Fe S 4 2 2	0	0

- Molecule 8 is FE3-S4 CLUSTER (CCD ID: F3S) (formula: Fe<sub>3</sub>S<sub>4</sub>).



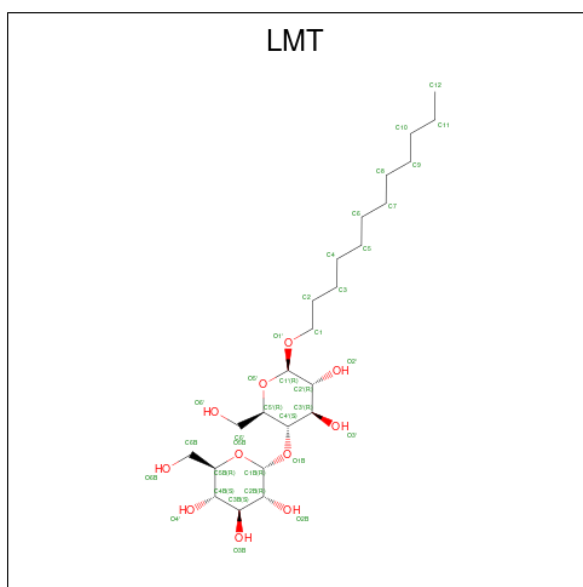
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	Fe	S	0	0
			7	3	4		
8	E	1	Total	Fe	S	0	0
			7	3	4		

- Molecule 9 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe<sub>4</sub>S<sub>4</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	Fe	S	0	0
			8	4	4		
9	E	1	Total	Fe	S	0	0
			8	4	4		





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	C	1	Total	C O	16	0
			35	24 11		
11	F	1	Total	C O	16	0
			35	24 11		

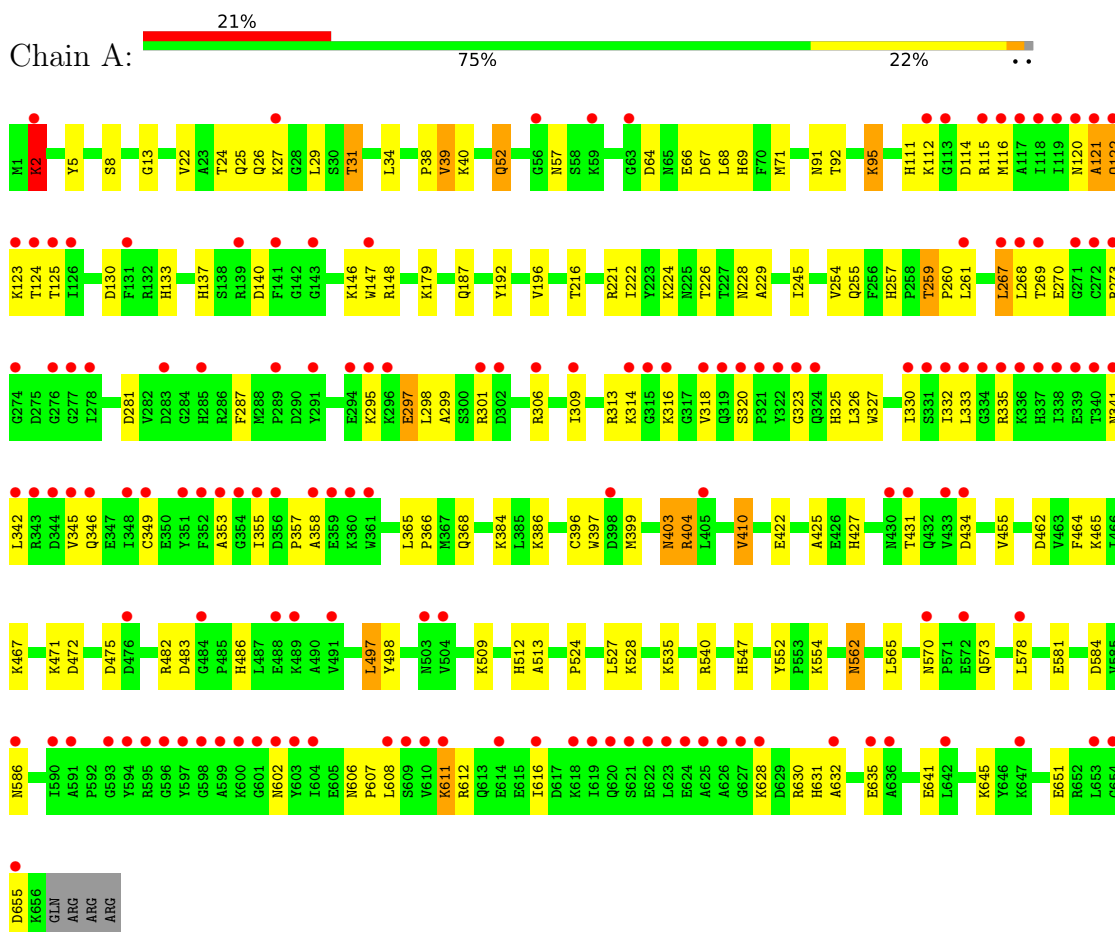
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	273	Total	O	1	0
			273	273		
12	B	155	Total	O	0	0
			155	155		
12	C	55	Total	O	0	0
			55	55		
12	D	287	Total	O	4	0
			287	287		
12	E	164	Total	O	0	0
			164	164		
12	F	56	Total	O	0	0
			56	56		

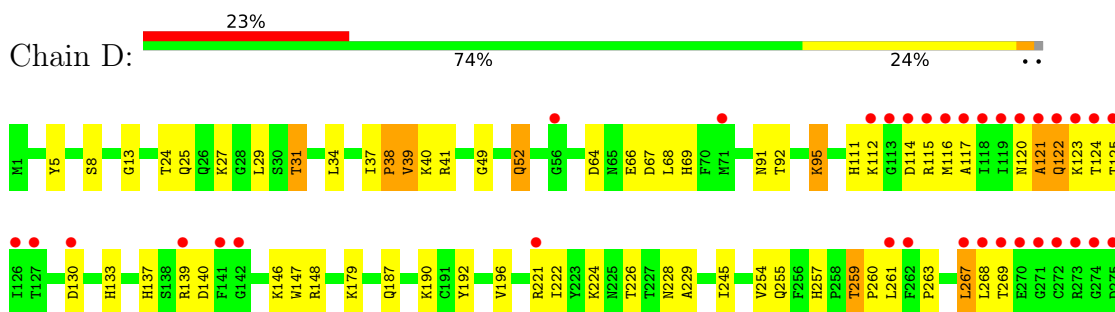
### 3 Residue-property plots

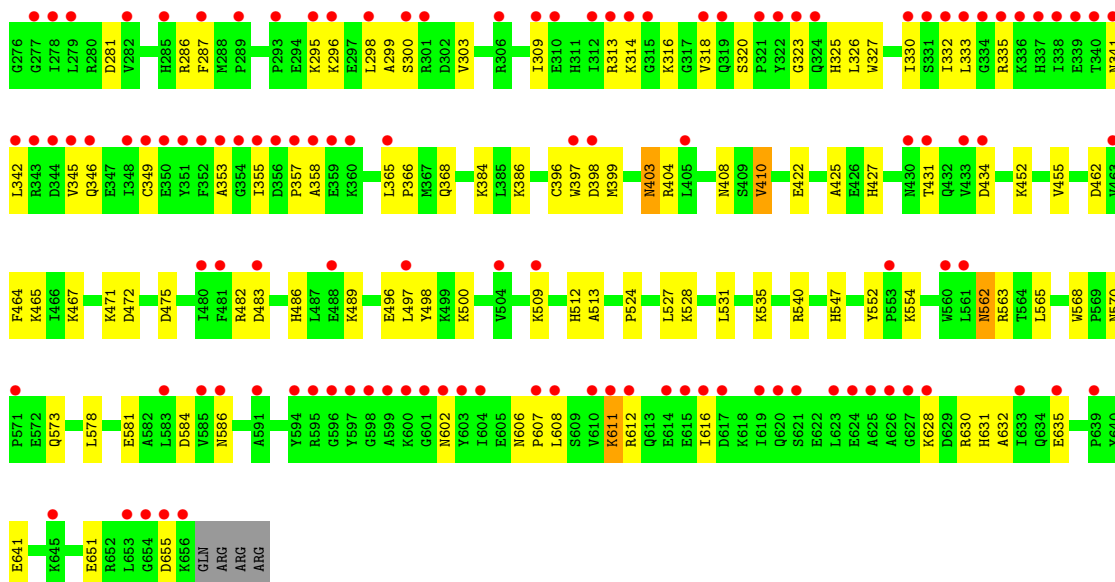
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: QUINOL-FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT A

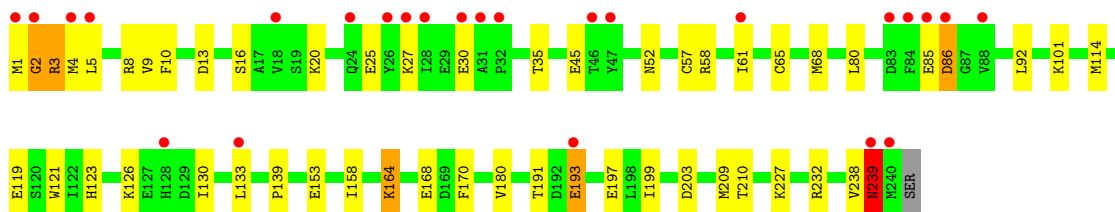
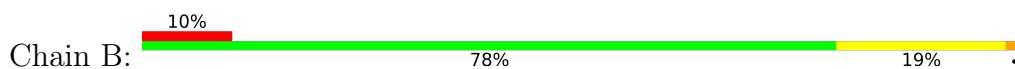


- Molecule 1: QUINOL-FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT A

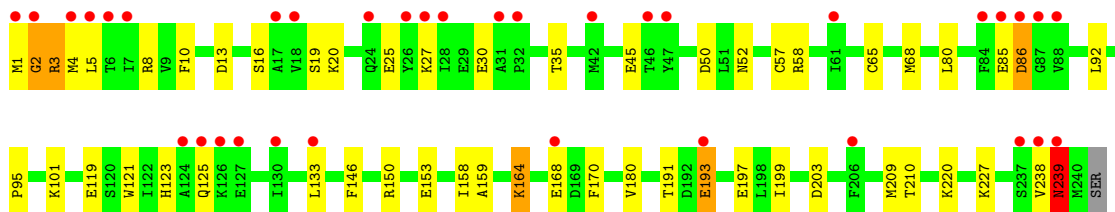
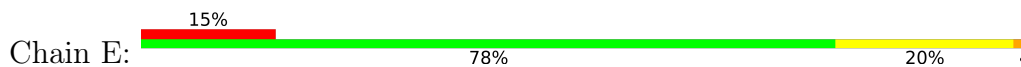




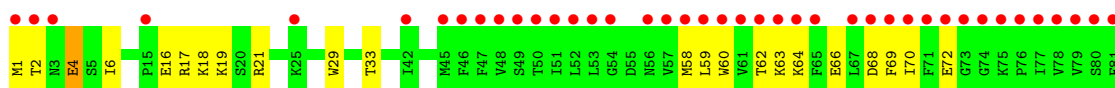
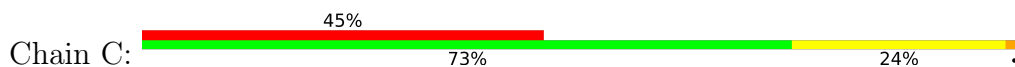
● Molecule 2: QUINOL-FUMARATE REDUCTASE IRON-SULFUR SUBUNIT B

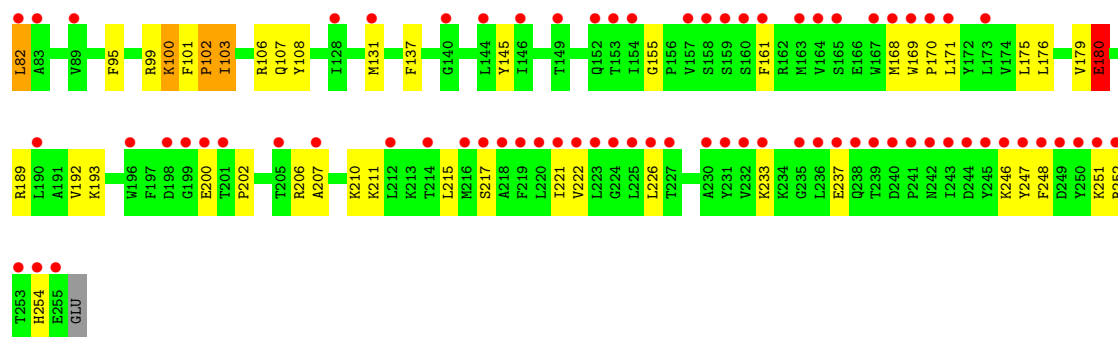


● Molecule 2: QUINOL-FUMARATE REDUCTASE IRON-SULFUR SUBUNIT B

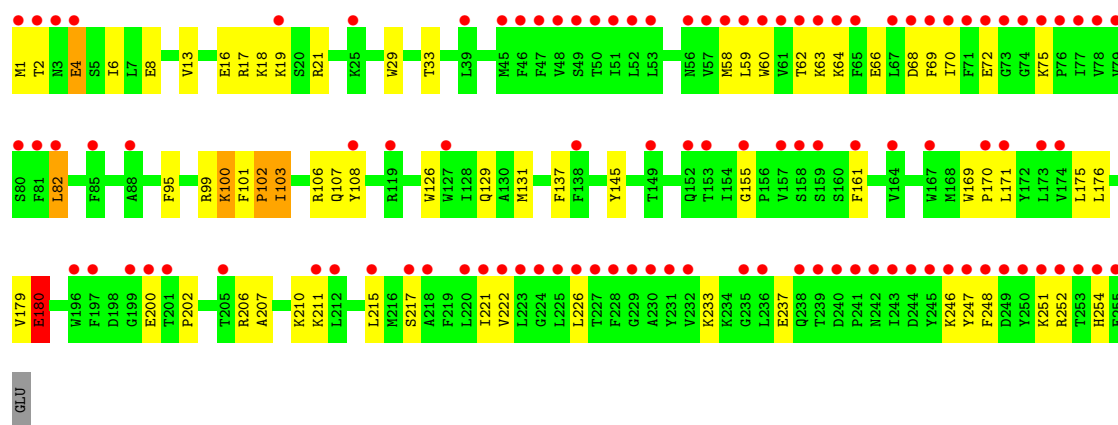
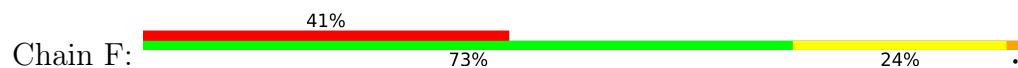


● Molecule 3: QUINOL-FUMARATE REDUCTASE DIHEME CYTOCHROME B SUBUNIT C





• Molecule 3: QUINOL-FUMARATE REDUCTASE DIHEME CYTOCHROME B SUBUNIT C



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	85.10Å 188.77Å 117.82Å 90.00° 104.47° 90.00°	Depositor
Resolution (Å)	28.70 – 1.78 28.70 – 1.78	Depositor EDS
% Data completeness (in resolution range)	92.5 (28.70-1.78) 92.6 (28.70-1.78)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.25 (at 1.78Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.229 , 0.237 0.224 , 0.230	Depositor DCC
$R_{free}$ test set	4488 reflections (1.41%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.2	Xtrriage
Anisotropy	0.185	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 55.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	19666	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.55% of the height of the origin peak. No significant pseudotranslation is detected.*

<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: SF4, F3S, FES, FAD, HEM, LMT, FUM, NA

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	1.69	3/5241 (0.1%)	0.90	15/7063 (0.2%)
1	D	0.38	1/5221 (0.0%)	0.89	14/7038 (0.2%)
2	B	0.42	1/1939 (0.1%)	0.86	4/2616 (0.2%)
2	E	0.42	1/1939 (0.1%)	0.87	3/2616 (0.1%)
3	C	1.40	3/2165 (0.1%)	0.98	5/2930 (0.2%)
3	F	2.13	7/2165 (0.3%)	1.55	9/2930 (0.3%)
All	All	1.28	16/18670 (0.1%)	1.00	50/25193 (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
3	C	0	1
3	F	0	1
All	All	0	2

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2[A]	LYS	CE-NZ	84.19	4.01	1.49
1	A	2[B]	LYS	CE-NZ	84.19	4.01	1.49
3	F	180[A]	GLU	CD-OE2	63.88	2.46	1.25
3	F	180[B]	GLU	CD-OE2	63.88	2.46	1.25
3	C	180[A]	GLU	CD-OE2	44.56	2.10	1.25

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	180[A]	GLU	OE1-CD-OE2	-36.76	34.68	122.90
3	F	180[B]	GLU	OE1-CD-OE2	-36.76	34.68	122.90
3	F	180[A]	GLU	CG-CD-OE1	-25.83	58.98	118.40
3	F	180[B]	GLU	CG-CD-OE1	-25.83	58.98	118.40
3	F	180[A]	GLU	CG-CD-OE2	-22.90	65.73	118.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	180[A]	GLU	Sidechain
3	F	180[A]	GLU	Sidechain

## 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	5145	0	5124	132	0
1	D	5125	0	5100	133	0
2	B	1902	0	1869	48	0
2	E	1902	0	1869	51	0
3	C	2099	0	2111	57	0
3	F	2099	0	2111	68	0
4	A	53	0	29	3	0
4	D	53	0	29	3	0
5	A	8	0	1	0	0
5	D	8	0	1	0	0
6	A	1	0	0	0	0
6	D	1	0	0	0	0
7	B	4	0	0	0	0
7	E	4	0	0	0	0
8	B	7	0	0	0	0
8	E	7	0	0	0	0
9	B	8	0	0	0	0
9	E	8	0	0	0	0
10	C	86	0	60	1	0
10	F	86	0	60	1	0
11	C	35	0	46	8	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	F	35	0	46	9	0
12	A	273	0	0	9	0
12	B	155	0	0	3	0
12	C	55	0	0	1	0
12	D	287	0	0	5	0
12	E	164	0	0	2	0
12	F	56	0	0	1	0
All	All	19666	0	18456	462	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 13.

The worst 5 of 462 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:F:180[B]:GLU:CD	3:F:180[B]:GLU:CG	1.80	1.54
3:F:180[A]:GLU:OE1	3:F:180[A]:GLU:CD	1.70	1.33
3:F:180[B]:GLU:OE1	3:F:180[B]:GLU:HG2	1.47	1.11
3:F:180[A]:GLU:CD	3:F:180[A]:GLU:HB2	1.84	1.03
2:B:1:MET:HG2	2:B:2:GLY:H	1.24	1.01

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	659/660 (100%)	634 (96%)	21 (3%)	4 (1%)	21	9
1	D	657/660 (100%)	631 (96%)	22 (3%)	4 (1%)	21	9
2	B	239/241 (99%)	227 (95%)	8 (3%)	4 (2%)	7	1
2	E	239/241 (99%)	227 (95%)	8 (3%)	4 (2%)	7	1

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	255/256 (100%)	247 (97%)	7 (3%)	1 (0%)	30	16
3	F	255/256 (100%)	247 (97%)	7 (3%)	1 (0%)	30	16
All	All	2304/2314 (100%)	2213 (96%)	73 (3%)	18 (1%)	16	6

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	121	ALA
2	B	86	ASP
3	C	72	GLU
1	D	121	ALA
2	E	86	ASP

### 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	537/537 (100%)	524 (98%)	13 (2%)	43	24
1	D	535/537 (100%)	524 (98%)	11 (2%)	47	27
2	B	212/213 (100%)	210 (99%)	2 (1%)	70	59
2	E	212/213 (100%)	210 (99%)	2 (1%)	70	59
3	C	223/223 (100%)	218 (98%)	5 (2%)	45	26
3	F	223/223 (100%)	218 (98%)	5 (2%)	45	26
All	All	1942/1946 (100%)	1904 (98%)	38 (2%)	50	29

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	562	ASN
3	F	82	LEU
1	D	611	LYS
2	E	193	GLU
3	F	106	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	57	ASN
1	D	257	HIS
2	E	123	HIS
1	D	91	ASN
1	D	225	ASN

### 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 oligosaccharides 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	$\# Z  > 2$
9	SF4	E	1242	2	0,12,12	-	-	-		
8	F3S	B	1241	2	0,9,9	-	-	-		
7	FES	E	1240	2	0,4,4	-	-	-		
10	HEM	C	1255	3	50,50,50	1.35	7 (14%)	67,82,82	0.74	0
5	FUM	A	1657	-	7,7,7	1.18	1 (14%)	8,8,8	0.71	0
10	HEM	F	1255	3	50,50,50	1.34	8 (16%)	67,82,82	0.76	1 (1%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
8	F3S	E	1241	2	0,9,9	-	-	-		
7	FES	B	1240	2	0,4,4	-	-	-		
4	FAD	A	1656	1	58,58,58	2.02	15 (25%)	85,89,89	1.23	7 (8%)
11	LMT	F	1257	-	36,36,36	1.10	2 (5%)	47,47,47	1.29	4 (8%)
11	LMT	C	1257	-	36,36,36	1.09	2 (5%)	47,47,47	1.28	4 (8%)
10	HEM	F	1256	3	50,50,50	1.33	7 (14%)	67,82,82	0.93	3 (4%)
5	FUM	D	1657	-	7,7,7	1.17	0	8,8,8	0.69	0
4	FAD	D	1656	1	58,58,58	1.98	12 (20%)	85,89,89	1.23	6 (7%)
9	SF4	B	1242	2	0,12,12	-	-	-		
10	HEM	C	1256	3	50,50,50	1.35	7 (14%)	67,82,82	0.93	3 (4%)

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
9	SF4	E	1242	2	-	-	0/6/5/5
8	F3S	B	1241	2	-	-	0/3/3/3
10	HEM	F	1255	3	-	0/14/54/54	-
10	HEM	C	1255	3	-	0/14/54/54	-
5	FUM	A	1657	-	-	0/5/5/5	-
7	FES	E	1240	2	-	-	0/1/1/1
8	F3S	E	1241	2	-	-	0/3/3/3
7	FES	B	1240	2	-	-	0/1/1/1
4	FAD	A	1656	1	-	3/34/50/50	0/6/6/6
11	LMT	F	1257	-	-	12/21/61/61	0/2/2/2
11	LMT	C	1257	-	-	12/21/61/61	0/2/2/2
10	HEM	F	1256	3	-	4/14/54/54	-
5	FUM	D	1657	-	-	0/5/5/5	-
4	FAD	D	1656	1	-	3/34/50/50	0/6/6/6
9	SF4	B	1242	2	-	-	0/6/5/5
10	HEM	C	1256	3	-	4/14/54/54	-

The worst 5 of 61 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1656	FAD	P-O3P	-9.22	1.49	1.59
4	A	1656	FAD	P-O3P	-8.86	1.49	1.59
4	D	1656	FAD	C1'-C2'	4.01	1.58	1.52

*Continued on next page...*

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1656	FAD	PA-O2A	-3.89	1.37	1.55
4	A	1656	FAD	C1'-C2'	3.87	1.58	1.52

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	F	1257	LMT	C1-O1'-C1'	4.94	122.11	113.68
11	C	1257	LMT	C1-O1'-C1'	4.88	122.02	113.68
4	D	1656	FAD	C1'-N10-C9A	-4.32	112.23	120.63
4	A	1656	FAD	C1'-N10-C9A	-4.30	112.27	120.63
10	F	1256	HEM	CAD-C3D-C4D	3.71	131.16	124.70

There are no chirality outliers.

5 of 38 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1656	FAD	PA-O3P-P-O5'
4	D	1656	FAD	PA-O3P-P-O5'
11	C	1257	LMT	C2'-C1'-O1'-C1
11	F	1257	LMT	C2'-C1'-O1'-C1
11	C	1257	LMT	C4'-C5'-C6'-O6'

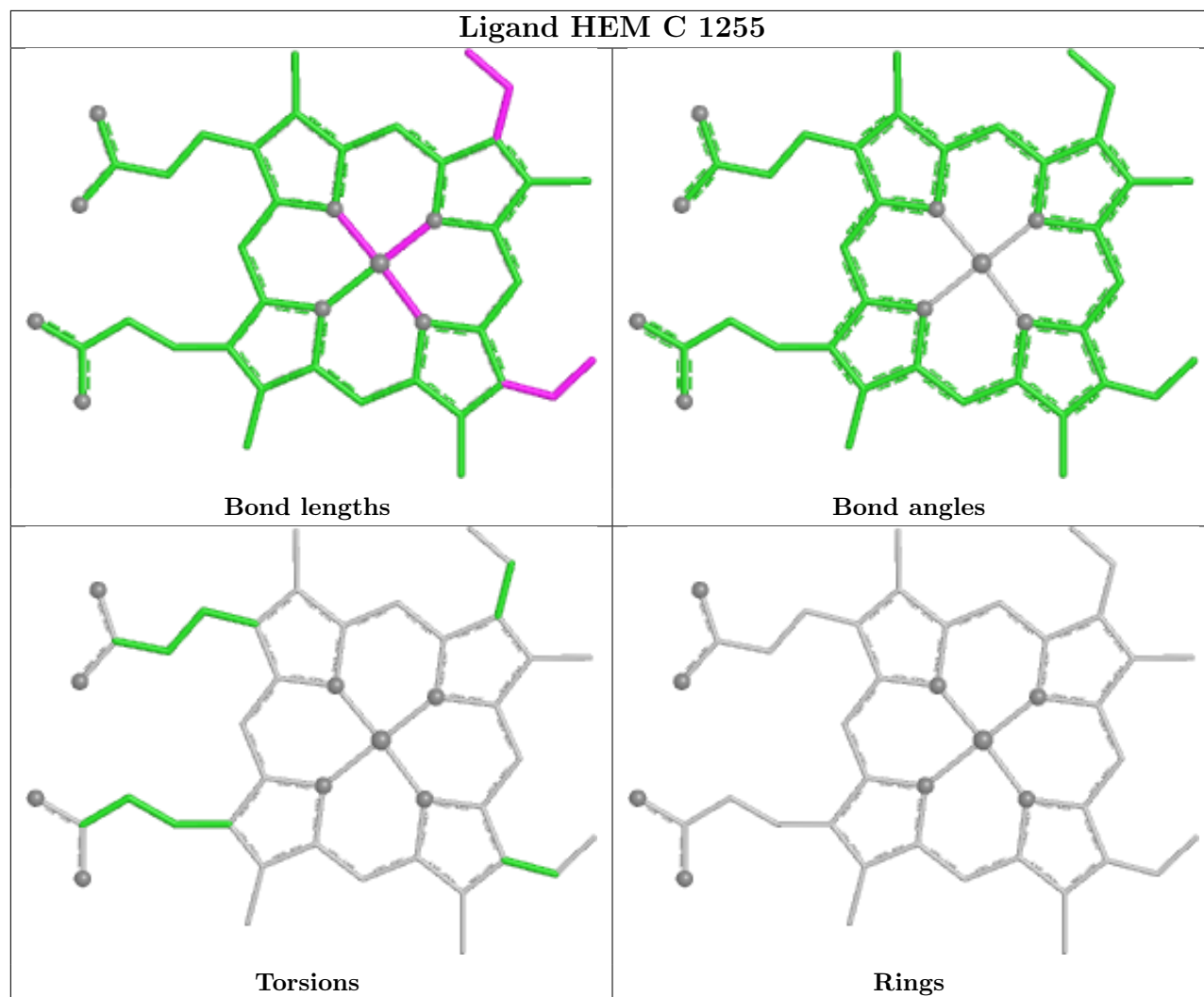
There are no ring outliers.

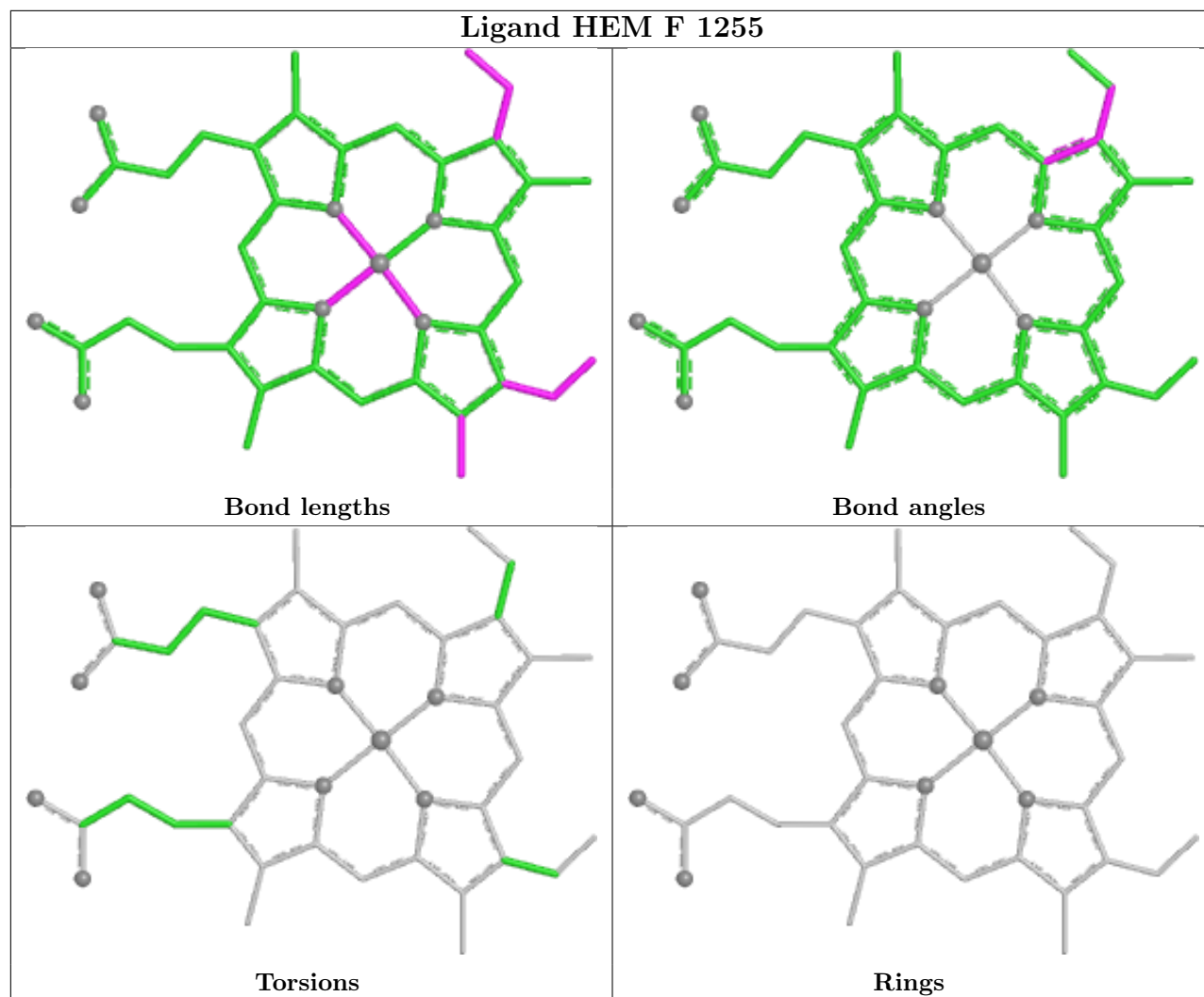
6 monomers are involved in 25 short contacts:

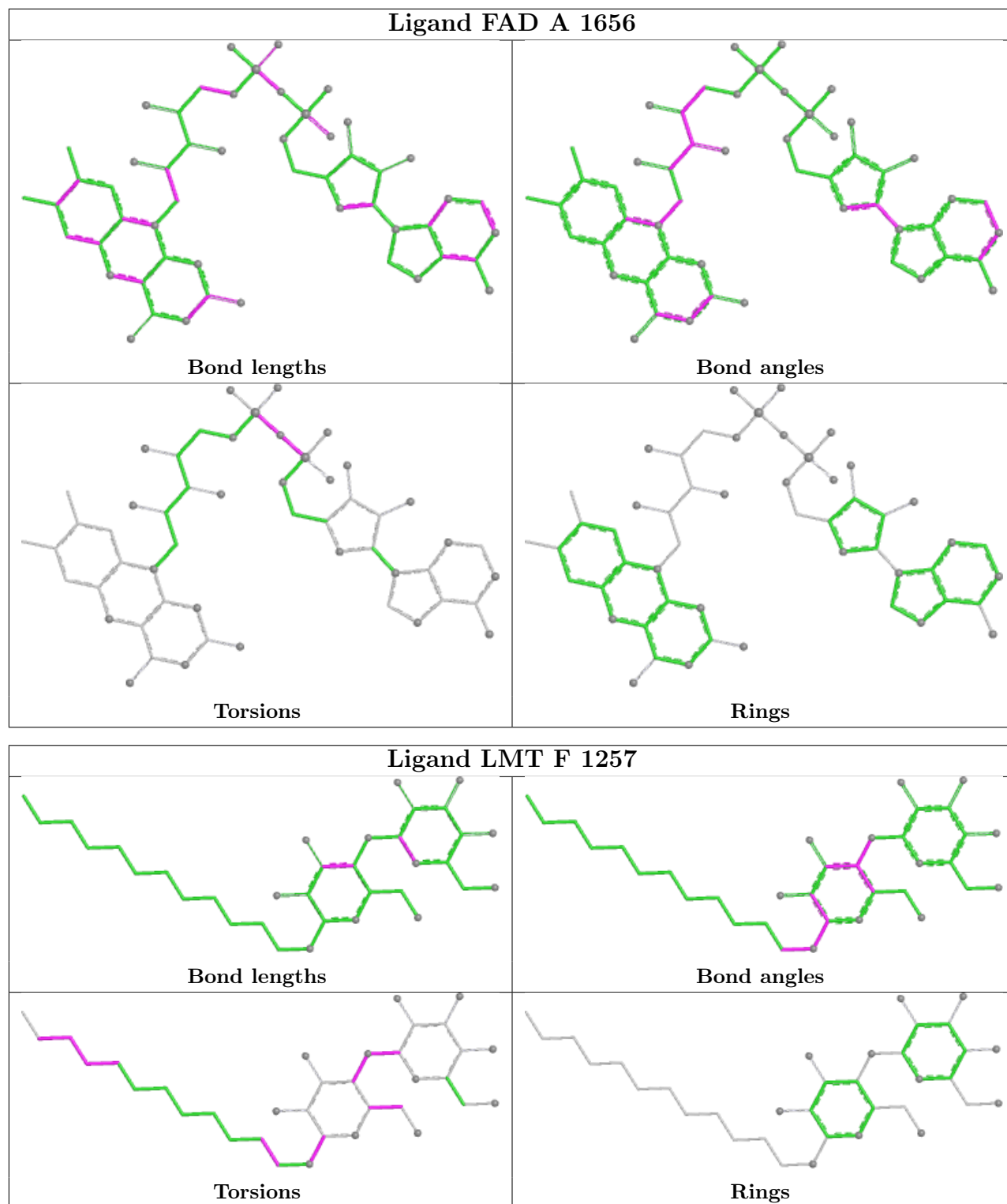
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1656	FAD	3	0
11	F	1257	LMT	9	0
11	C	1257	LMT	8	0
10	F	1256	HEM	1	0
4	D	1656	FAD	3	0
10	C	1256	HEM	1	0

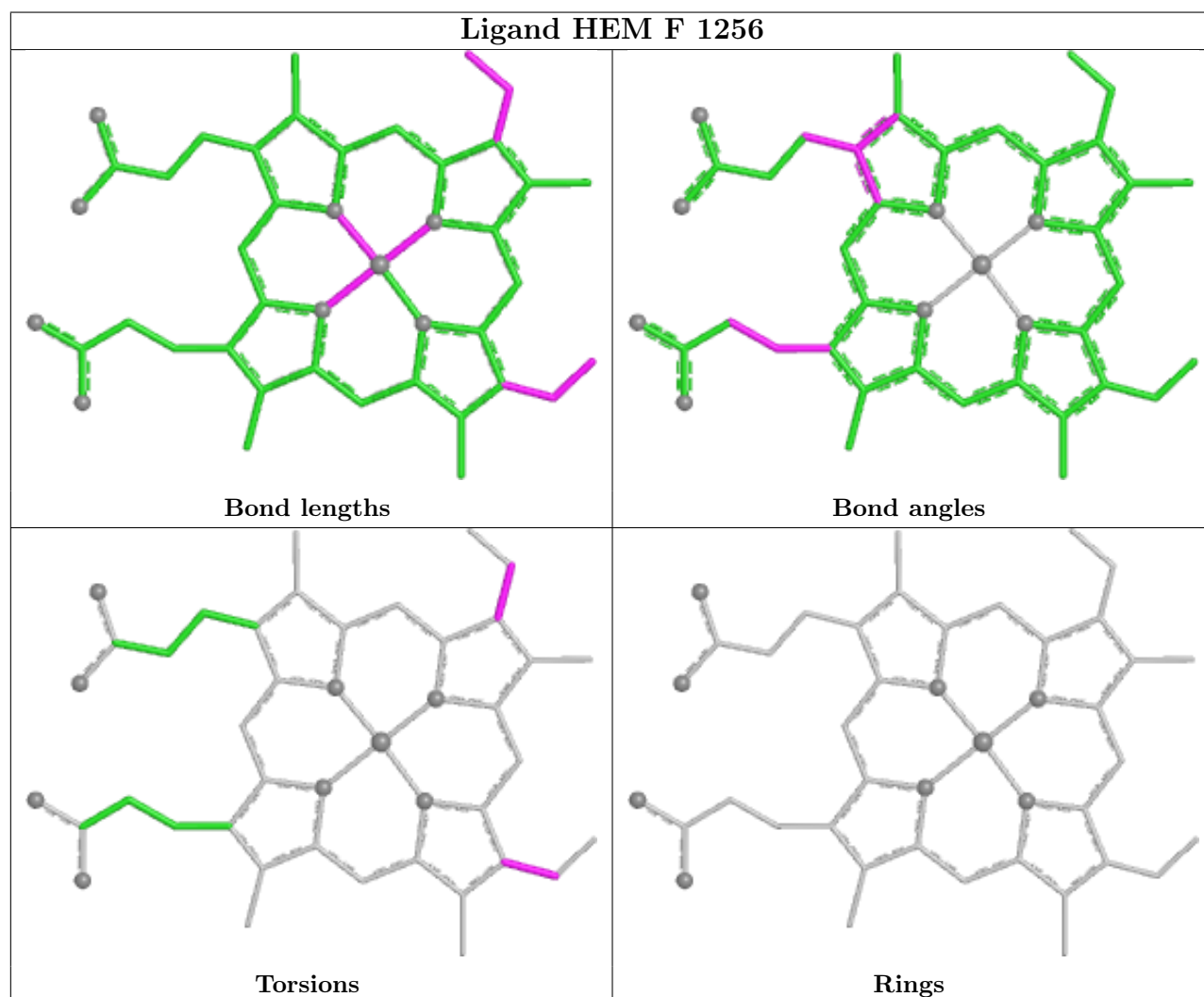
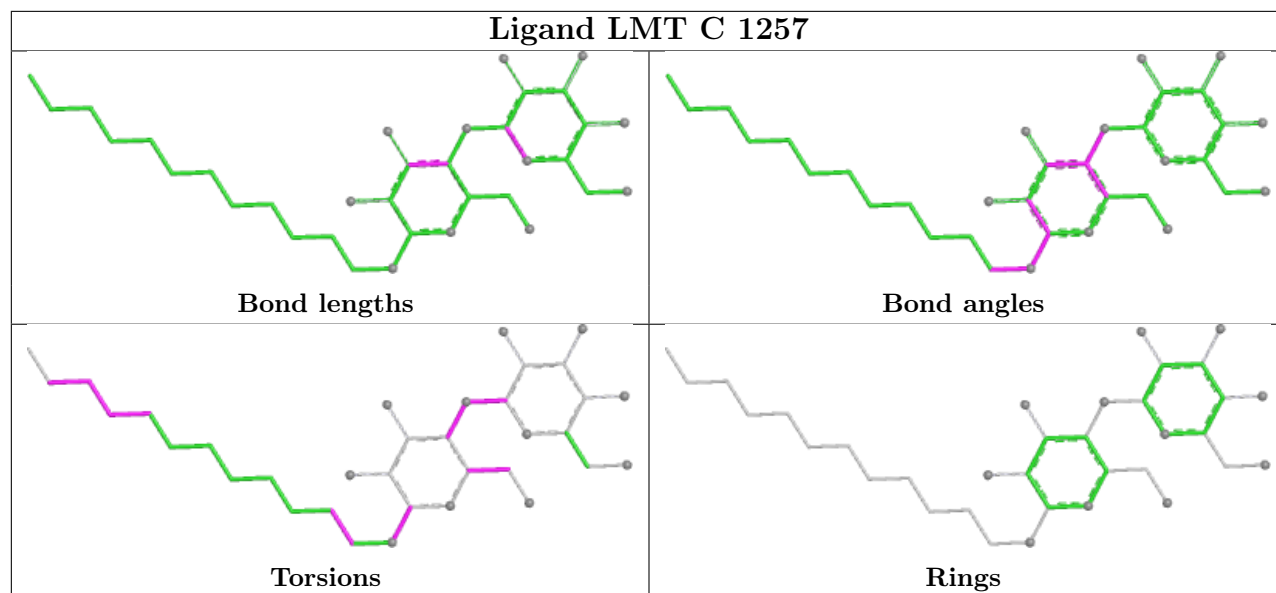
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

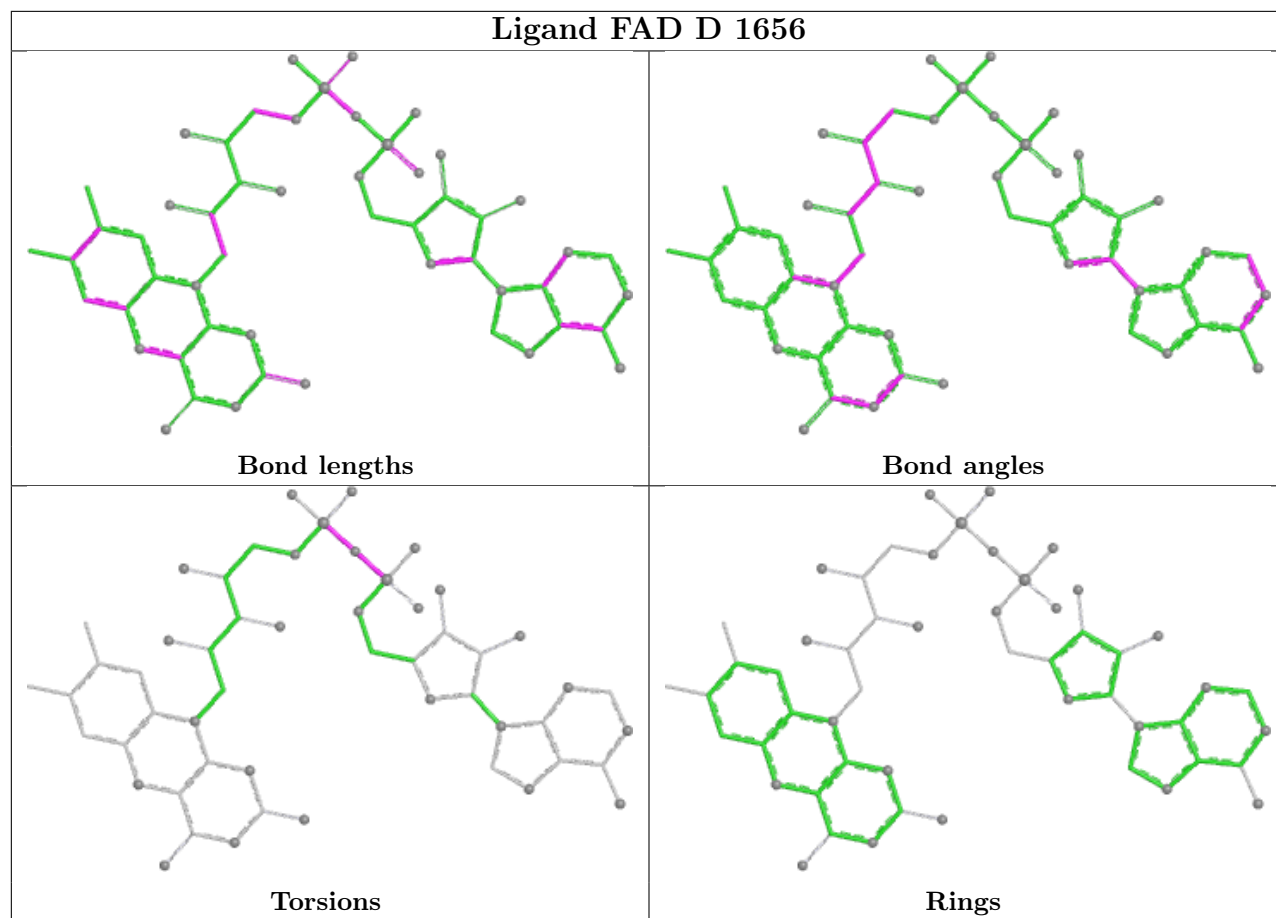
any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

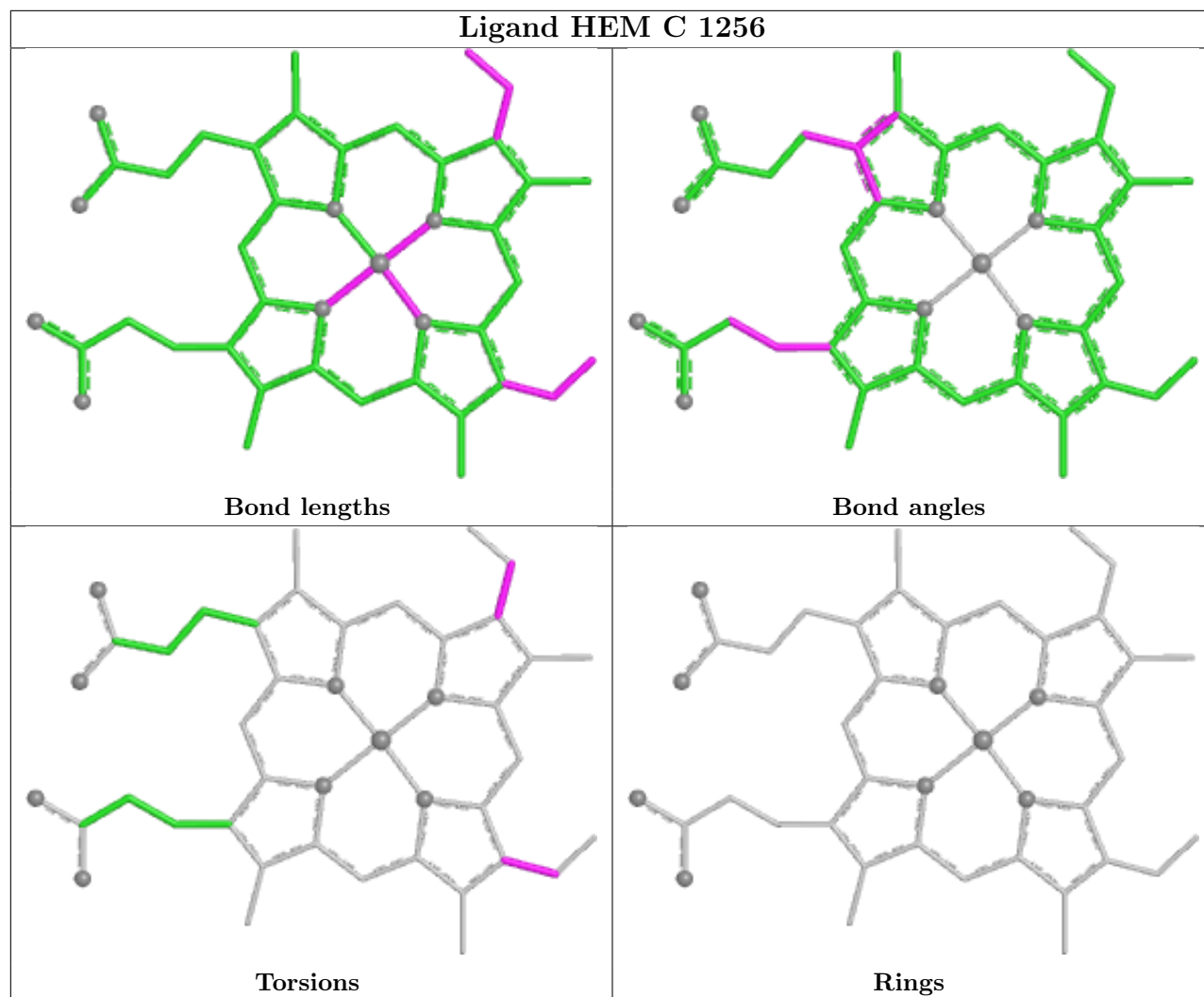












## 5.7 Other polymers [i](#)

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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	656/660 (99%)	1.18	141 (21%) 2 2	16, 33, 68, 80	19 (2%)
1	D	656/660 (99%)	1.27	151 (23%) 2 2	16, 33, 68, 80	19 (2%)
2	B	240/241 (99%)	0.76	25 (10%) 11 13	11, 29, 50, 74	3 (1%)
2	E	240/241 (99%)	0.78	35 (14%) 6 6	11, 28, 50, 74	3 (1%)
3	C	255/256 (99%)	2.07	114 (44%) 0 0	20, 43, 75, 91	13 (5%)
3	F	255/256 (99%)	2.00	106 (41%) 0 0	19, 42, 75, 90	12 (4%)
All	All	2302/2314 (99%)	1.31	572 (24%) 2 2	11, 33, 68, 91	69 (2%)

The worst 5 of 572 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	338	ILE	10.7
1	D	342	LEU	9.7
2	B	2	GLY	9.0
3	F	253	THR	8.6
1	D	121	ALA	7.9

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

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

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 6.4 Ligands

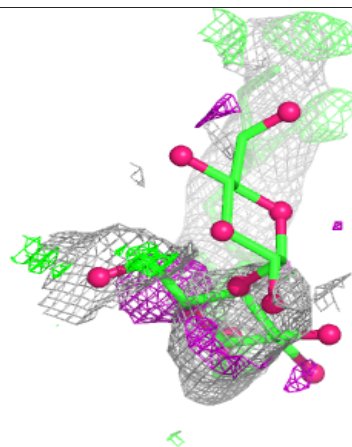
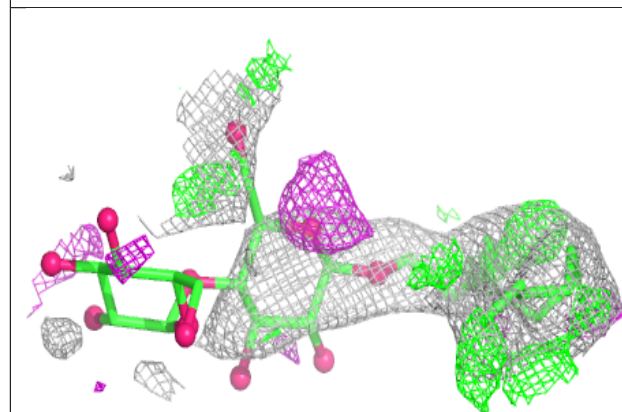
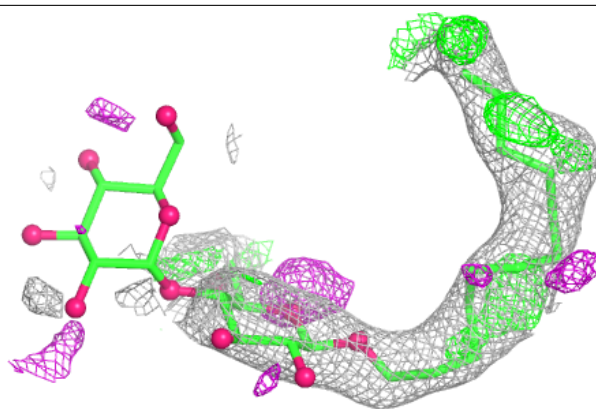
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
11	LMT	C	1257	35/35	0.68	0.30	59,63,68,69	16
11	LMT	F	1257	35/35	0.74	0.26	59,63,69,69	16
5	FUM	A	1657	8/8	0.75	0.18	42,46,48,50	0
5	FUM	D	1657	8/8	0.81	0.16	43,46,47,48	0
10	HEM	C	1256	43/43	0.94	0.12	38,40,43,45	0
6	NA	D	1658	1/1	0.95	0.07	26,26,26,26	0
10	HEM	F	1256	43/43	0.95	0.10	36,40,43,45	0
4	FAD	D	1656	53/53	0.96	0.07	18,22,25,25	0
10	HEM	C	1255	43/43	0.96	0.09	26,31,34,38	0
10	HEM	F	1255	43/43	0.97	0.09	26,32,35,38	0
4	FAD	A	1656	53/53	0.98	0.05	16,22,25,27	0
8	F3S	E	1241	7/7	0.98	0.04	23,24,25,25	0
7	FES	B	1240	4/4	0.99	0.04	22,22,23,24	0
7	FES	E	1240	4/4	0.99	0.03	21,21,21,23	0
8	F3S	B	1241	7/7	0.99	0.04	24,25,26,27	0
6	NA	A	1658	1/1	0.99	0.04	26,26,26,26	0
9	SF4	B	1242	8/8	0.99	0.03	22,24,25,25	0
9	SF4	E	1242	8/8	0.99	0.03	21,23,23,24	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.

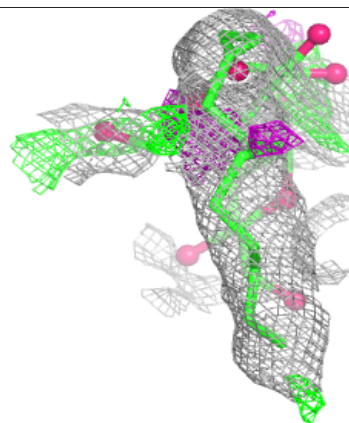
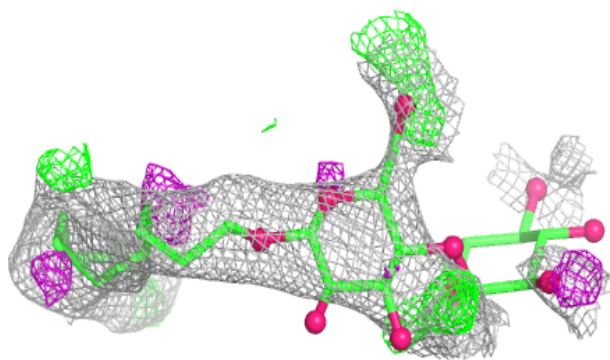
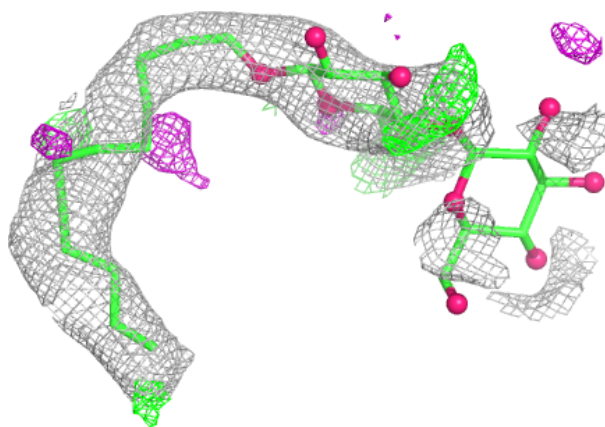
**Electron density around LMT C 1257:**

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



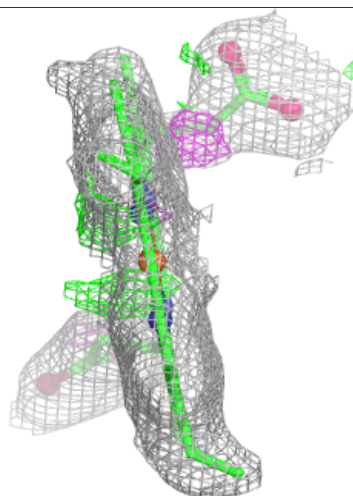
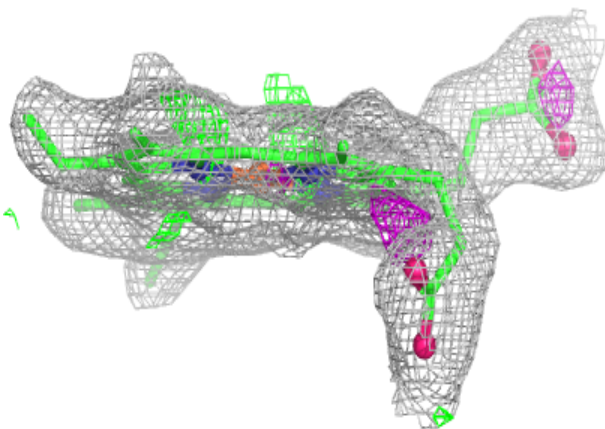
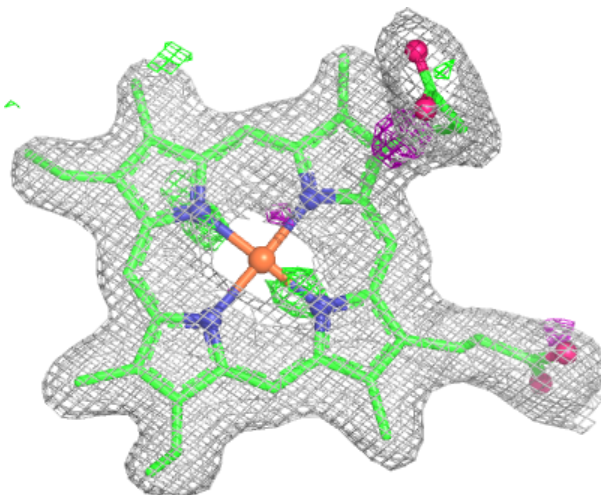
**Electron density around LMT F 1257:**

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



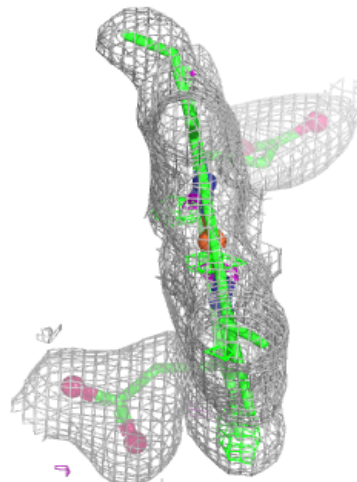
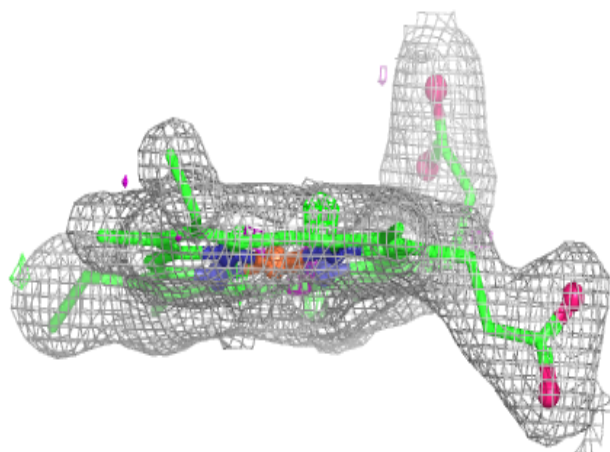
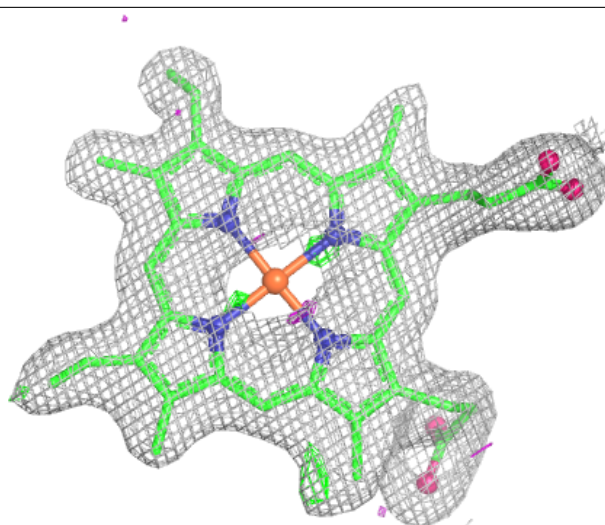
**Electron density around HEM C 1256:**

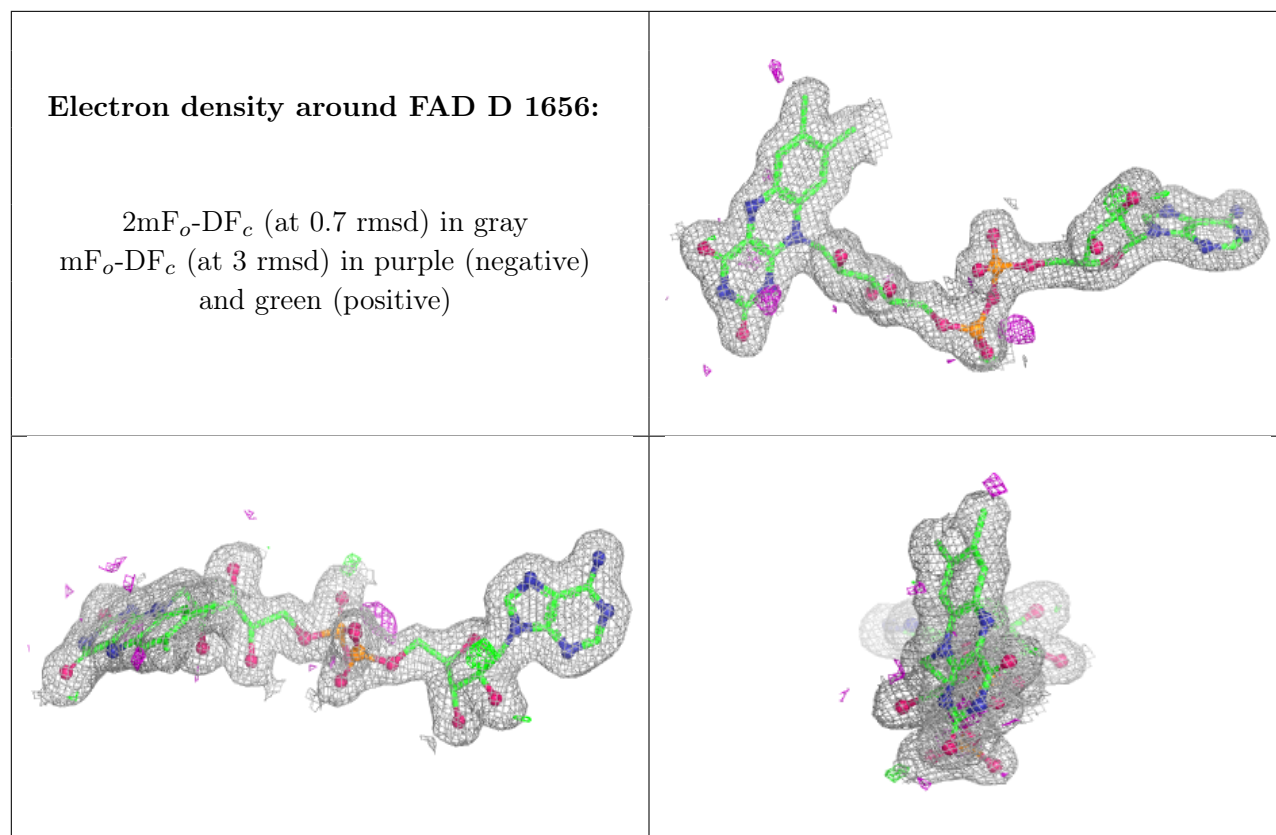
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around HEM F 1256:**

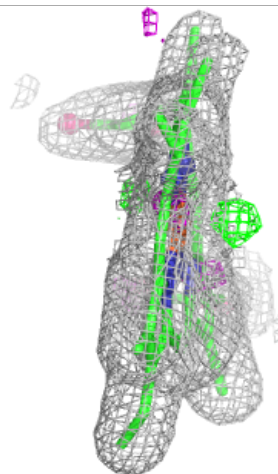
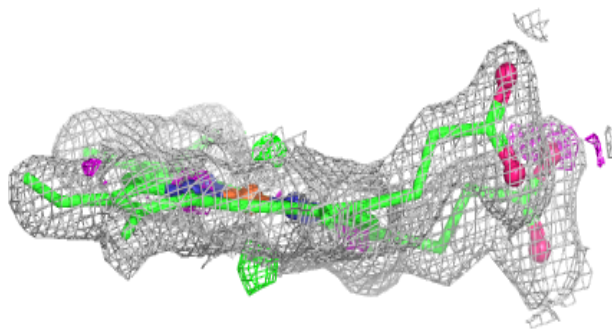
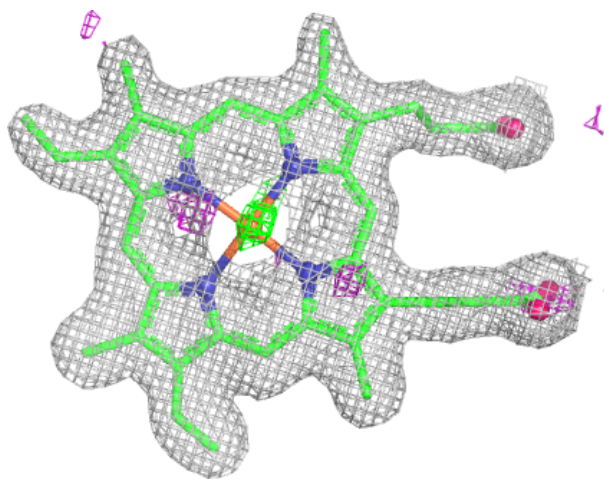
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





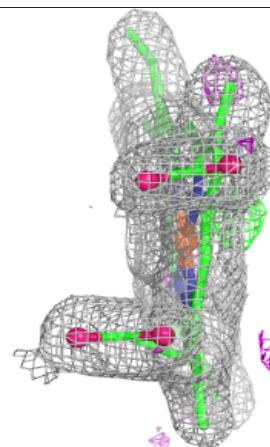
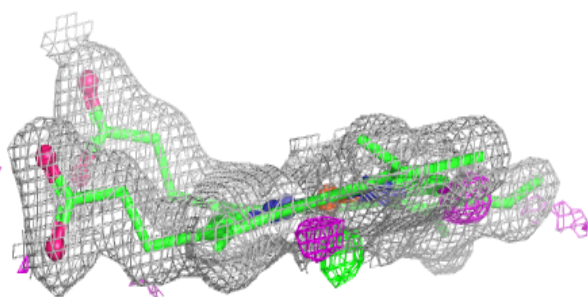
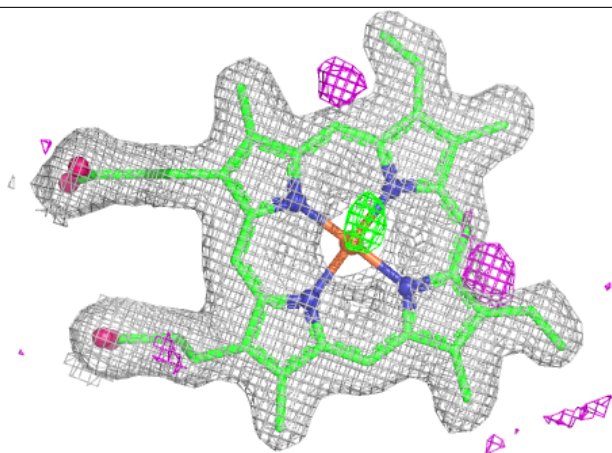
**Electron density around HEM C 1255:**

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

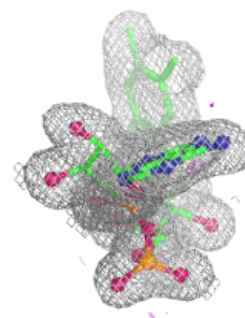
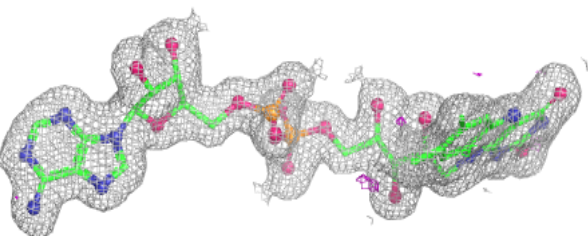
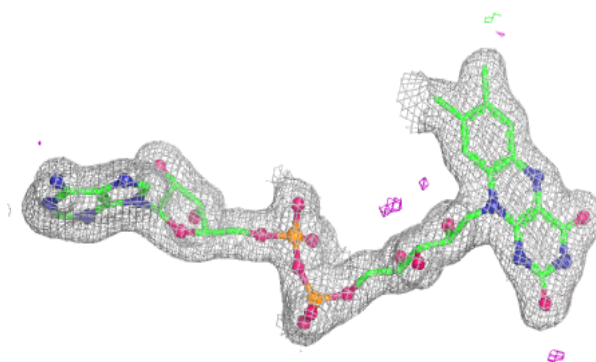


**Electron density around HEM F 1255:**

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

**Electron density around FAD A 1656:**

$2mF_o-DF_c$  (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.