



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 04:59 PM UTC

PDB ID : 1QLB / pdb\_00001qlb  
Title : respiratory complex II-like fumarate reductase from Wolinella succinogenes  
Authors : Lancaster, C.R.D.; Kroeger, A.; Auer, M.; Michel, H.  
Deposited on : 1999-08-25  
Resolution : 2.33 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
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

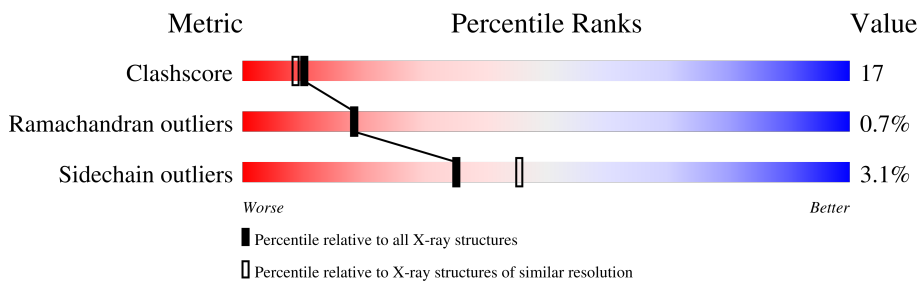
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.33 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	3127 (2.36-2.32)
Ramachandran outliers	187476	3095 (2.36-2.32)
Sidechain outliers	187428	3095 (2.36-2.32)

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  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	656	73% 25% .
1	D	656	73% 25% .
2	B	239	72% 27% .
2	E	239	71% 28% .
3	C	256	63% 32% . .
3	F	256	62% 34% . .

## 2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 19056 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 FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	655	5101	3194	913	962	32	88	0	0
1	D	655	5101	3194	913	962	32	88	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	281	ASP	ARG	conflict	UNP P17412
A	282	VAL	CYS	conflict	UNP P17412
A	283	ASP	GLY	conflict	UNP P17412
A	284	GLY	TRP	conflict	UNP P17412
A	285	HIS	THR	conflict	UNP P17412
A	286	ARG	PRO	conflict	UNP P17412
A	287	PHE	ILE	conflict	UNP P17412
A	288	MET	HIS	conflict	UNP P17412
A	289	PRO	ALA	conflict	UNP P17412
D	281	ASP	ARG	conflict	UNP P17412
D	282	VAL	CYS	conflict	UNP P17412
D	283	ASP	GLY	conflict	UNP P17412
D	284	GLY	TRP	conflict	UNP P17412
D	285	HIS	THR	conflict	UNP P17412
D	286	ARG	PRO	conflict	UNP P17412
D	287	PHE	ILE	conflict	UNP P17412
D	288	MET	HIS	conflict	UNP P17412
D	289	PRO	ALA	conflict	UNP P17412

- Molecule 2 is a protein called FUMARATE REDUCTASE IRON-SULFUR PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	239	1893	1194	322	354	23	0	0	0

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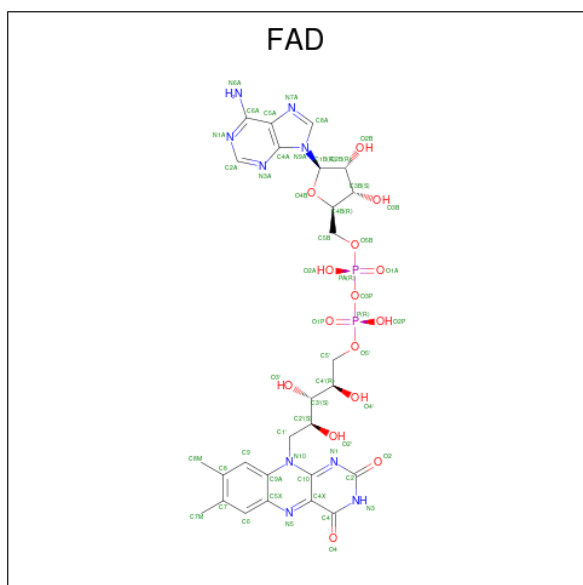
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	E	239	Total 1893	C 1194	N 322	O 354	S 23	0	0	0

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

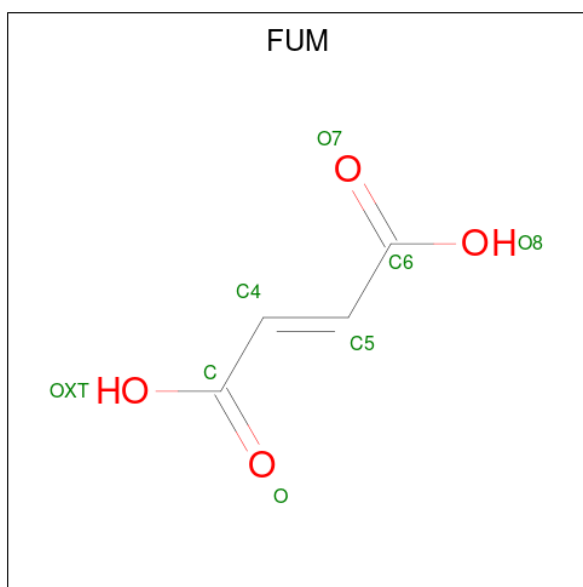
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	254	Total 2080	C 1388	N 333	O 345	S 14	111	0	0
3	F	254	Total 2080	C 1388	N 333	O 345	S 14	111	0	0

- Molecule 4 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



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

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

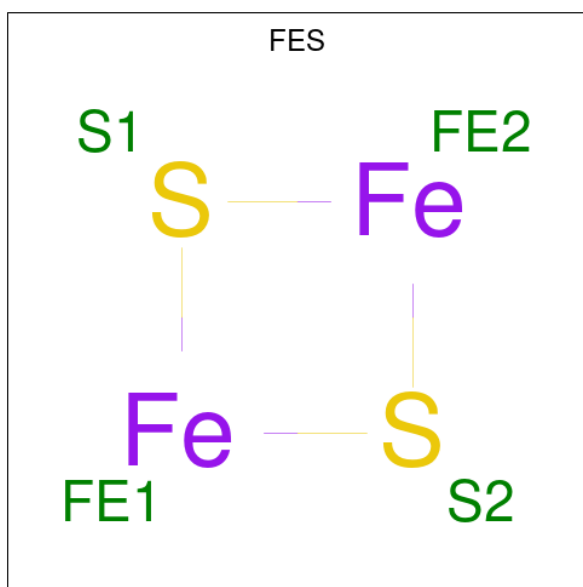


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 8 4 4	0	0
5	D	1	Total C O 8 4 4	0	0

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

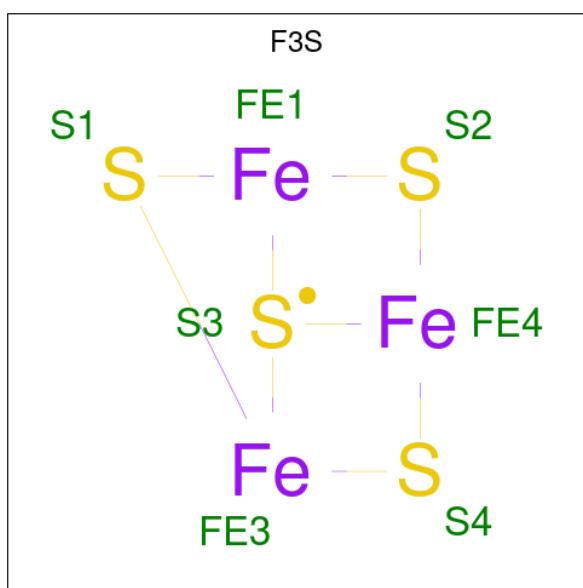
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Ca 1 1	0	0
6	D	1	Total Ca 1 1	0	0

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



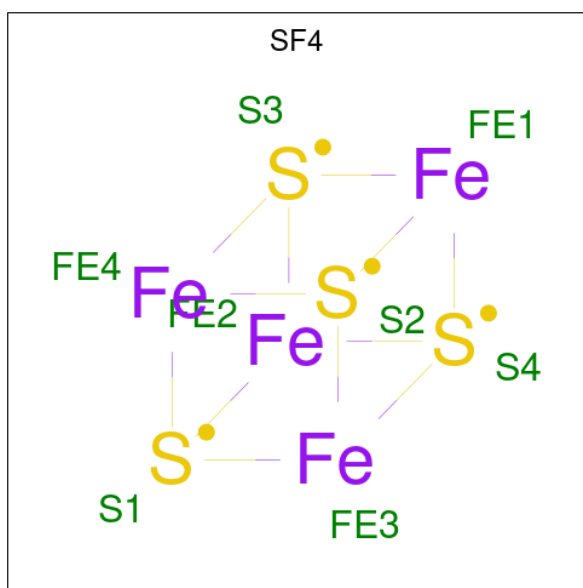
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	Fe	S	0	0
			4	2	2		
7	E	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 8 is FE3-S4 CLUSTER (CCD ID: F3S) (formula:  $\text{Fe}_3\text{S}_4$ ).



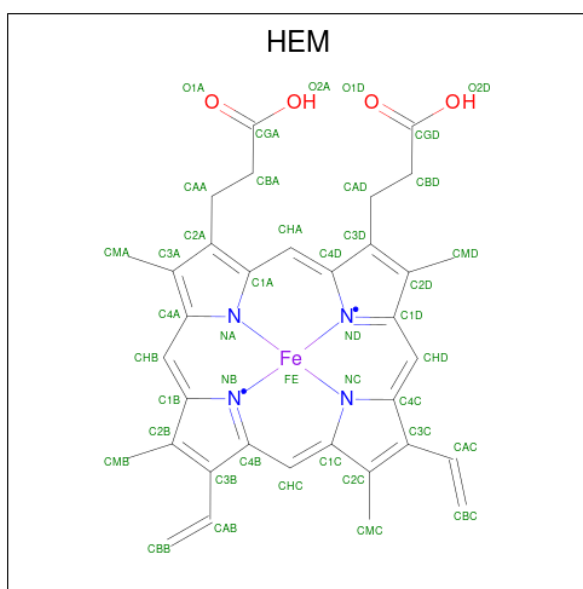
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	Fe	S	0	0
			7	3	4		
8	E	1	Total	Fe	S	0	0
			7	3	4		

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



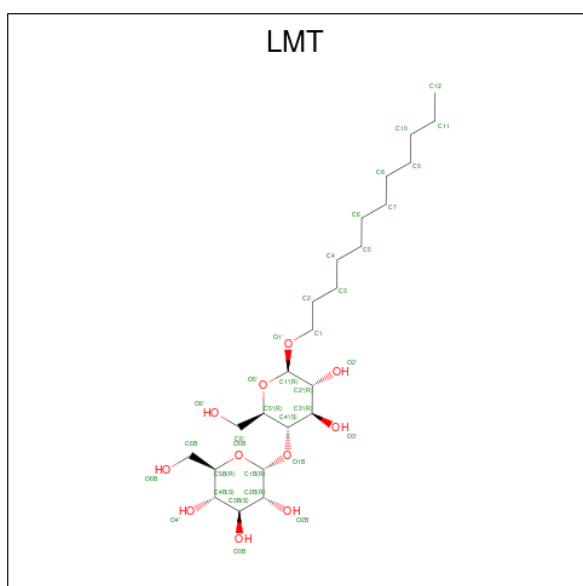
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	B	1	Total Fe S 8 4 4	0	0
9	E	1	Total Fe S 8 4 4	0	0

- Molecule 10 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: C<sub>34</sub>H<sub>32</sub>FeN<sub>4</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
10	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
10	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
10	F	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
10	F	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 11 is DODECYL-BETA-D-MALTOSE (CCD ID: LMT) (formula: C<sub>24</sub>H<sub>46</sub>O<sub>11</sub>).



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	149	Total	O	0	0
			149	149		
12	B	79	Total	O	0	0
			79	79		
12	C	23	Total	O	0	0
			23	23		
12	D	148	Total	O	0	0
			148	148		

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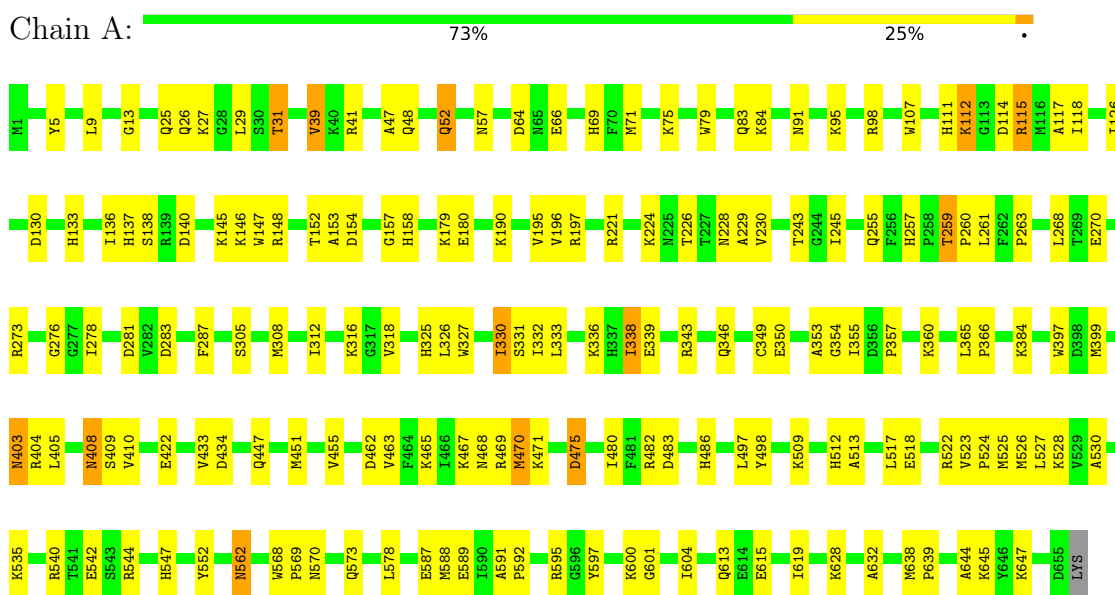
<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
12	E	83	Total	O	0	0
			83	83		
12	F	22	Total	O	0	0
			22	22		

### 3 Residue-property plots

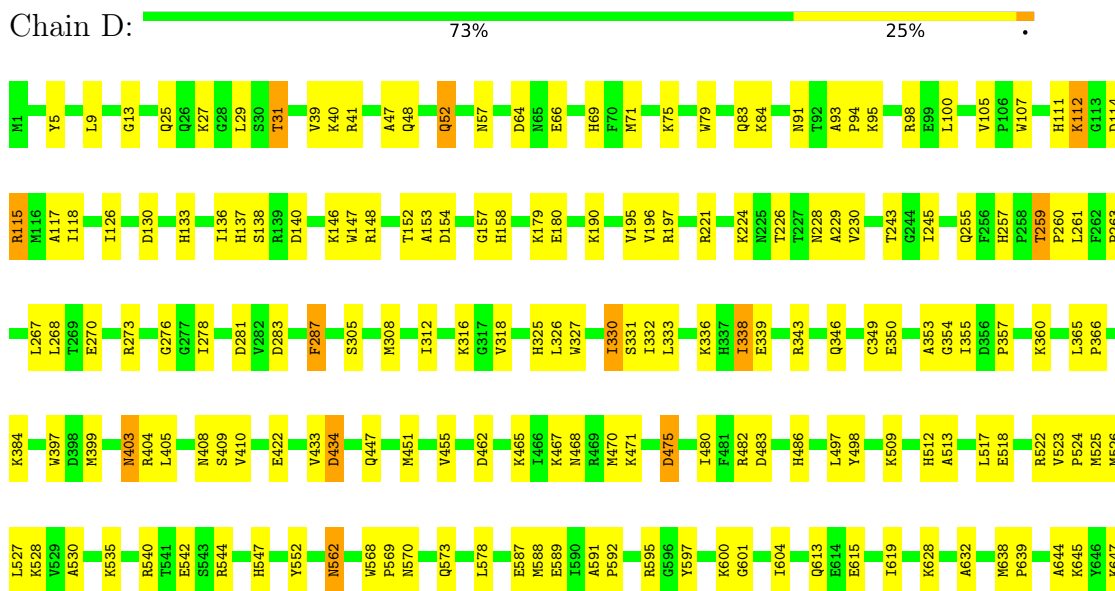
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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 was not executed.

- Molecule 1: FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT



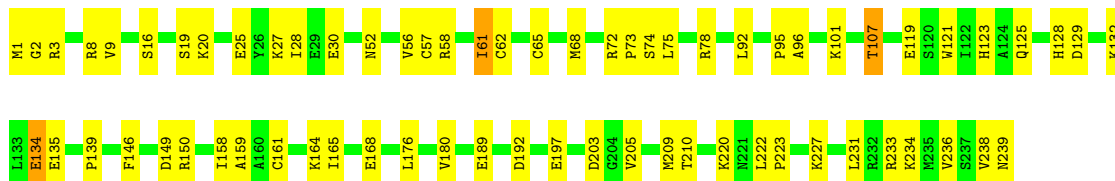
- Molecule 1: FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT



D655  
LYS

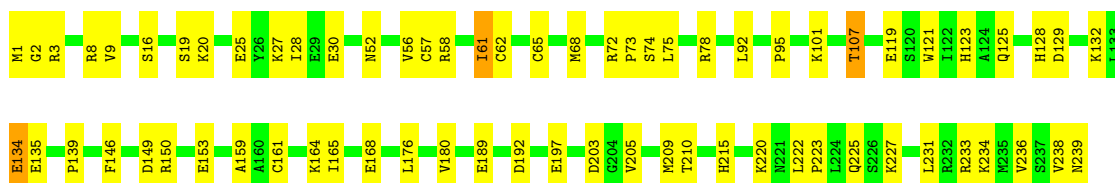
• Molecule 2: FUMARATE REDUCTASE IRON-SULFUR PROTEIN

Chain B:  72% 27%



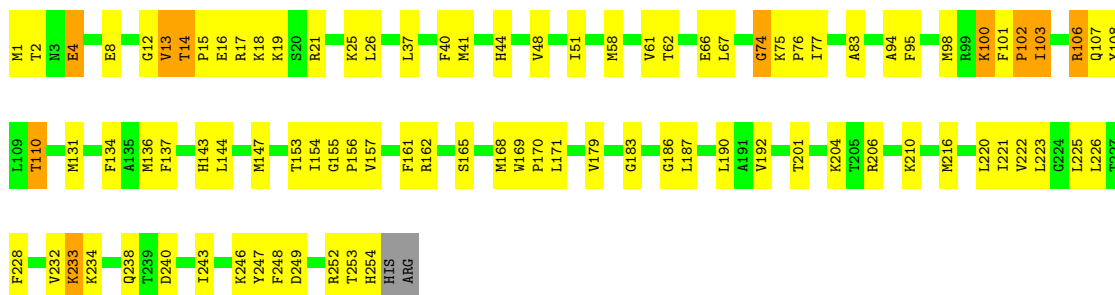
• Molecule 2: FUMARATE REDUCTASE IRON-SULFUR PROTEIN

Chain E:  71% 28%



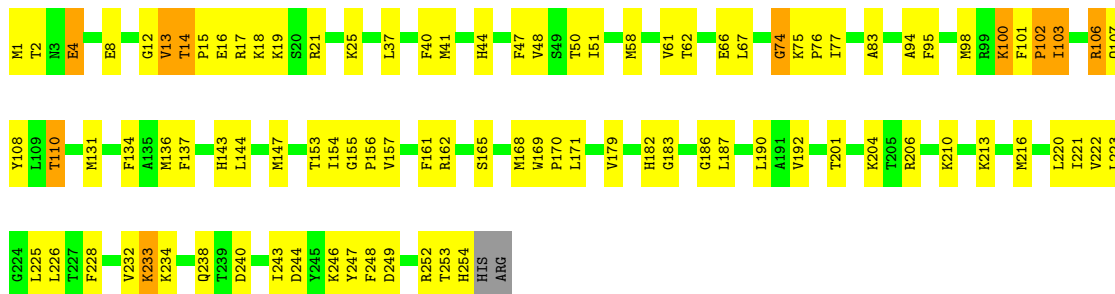
• Molecule 3: FUMARATE REDUCTASE CYTOCHROME B SUBUNIT

Chain C:  63% 32%



• Molecule 3: FUMARATE REDUCTASE CYTOCHROME B SUBUNIT

Chain F:  62% 34%



## 4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	118.40Å 85.05Å 188.85Å 90.00° 96.46° 90.00°	Depositor
Resolution (Å)	38.87 – 2.33	Depositor
% Data completeness (in resolution range)	95.8 (38.87-2.33)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
Refinement program	CNS 0.5	Depositor
R, $R_{free}$	0.213 , 0.223	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	19056	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

## 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, HEM, FAD, FUM, LMT, CA, FES

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	0.41	1/5197 (0.0%)	0.91	13/7006 (0.2%)
1	D	0.39	0/5197	0.91	12/7006 (0.2%)
2	B	0.41	0/1930	0.90	7/2604 (0.3%)
2	E	0.40	0/1930	0.90	6/2604 (0.2%)
3	C	0.34	0/2146	0.83	3/2904 (0.1%)
3	F	0.34	0/2146	0.83	3/2904 (0.1%)
All	All	0.39	1/18546 (0.0%)	0.89	44/25028 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	470	MET	SD-CE	-5.13	1.66	1.79

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	397	TRP	N-CA-C	-10.52	99.89	111.36
1	A	397	TRP	N-CA-C	-10.47	99.95	111.36
3	C	102	PRO	N-CA-C	-9.15	96.82	111.19
3	F	102	PRO	N-CA-C	-9.13	96.85	111.19
1	A	399	MET	N-CA-C	-7.78	102.87	113.30

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	5101	0	5079	165	0
1	D	5101	0	5079	163	0
2	B	1893	0	1861	63	0
2	E	1893	0	1861	65	0
3	C	2080	0	2101	103	0
3	F	2080	0	2101	105	0
4	A	53	0	29	1	0
4	D	53	0	29	1	0
5	A	8	0	1	2	0
5	D	8	0	1	1	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	7	0
10	F	86	0	60	8	0
11	C	35	0	46	7	0
11	F	35	0	46	8	0
12	A	149	0	0	9	0
12	B	79	0	0	2	0
12	C	23	0	0	0	0
12	D	148	0	0	7	0
12	E	83	0	0	3	0
12	F	22	0	0	0	0
All	All	19056	0	18354	618	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 17.

The worst 5 of 618 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:253:THR:HG22	3:F:254:HIS:H	1.25	0.99
3:C:253:THR:HG22	3:C:254:HIS:H	1.25	0.98
2:B:239:ASN:ND2	3:C:21:ARG:HH21	1.64	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:239:ASN:ND2	3:F:21:ARG:HH21	1.64	0.95
2:E:239:ASN:HD22	3:F:21:ARG:HH21	1.15	0.91

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	586/656 (89%)	549 (94%)	32 (6%)	5 (1%)	14	13
1	D	653/656 (100%)	615 (94%)	33 (5%)	5 (1%)	16	16
2	B	237/239 (99%)	229 (97%)	8 (3%)	0	100	100
2	E	237/239 (99%)	229 (97%)	8 (3%)	0	100	100
3	C	252/256 (98%)	234 (93%)	15 (6%)	3 (1%)	10	8
3	F	252/256 (98%)	235 (93%)	14 (6%)	3 (1%)	10	8
All	All	2217/2302 (96%)	2091 (94%)	110 (5%)	16 (1%)	18	18

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	117	ALA
1	A	338	ILE
3	C	67	LEU
1	D	117	ALA
1	D	338	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	534/535 (100%)	517 (97%)	17 (3%)	34	44
1	D	534/535 (100%)	517 (97%)	17 (3%)	34	44
2	B	211/211 (100%)	207 (98%)	4 (2%)	50	63
2	E	211/211 (100%)	207 (98%)	4 (2%)	50	63
3	C	221/223 (99%)	212 (96%)	9 (4%)	27	35
3	F	221/223 (99%)	212 (96%)	9 (4%)	27	35
All	All	1932/1938 (100%)	1872 (97%)	60 (3%)	35	45

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

Mol	Chain	Res	Type
3	C	110	THR
3	F	58	MET
1	D	112	LYS
3	F	14	THR
3	F	233	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 61 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	238	GLN
2	E	177	ASN
1	D	158	HIS
2	E	123	HIS
3	F	238	GLN

### 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
11	LMT	F	1257	-	36,36,36	1.11	2 (5%)	47,47,47	1.27	4 (8%)
9	SF4	B	1242	2	0,12,12	-	-	-		
9	SF4	E	1242	2	0,12,12	-	-	-		
7	FES	E	1240	2	0,4,4	-	-	-		
11	LMT	C	1257	-	36,36,36	1.10	2 (5%)	47,47,47	1.27	4 (8%)
7	FES	B	1240	2	0,4,4	-	-	-		
8	F3S	B	1241	2	0,9,9	-	-	-		
10	HEM	C	1256	3	50,50,50	1.36	7 (14%)	67,82,82	1.00	4 (5%)
4	FAD	D	1656	1	58,58,58	1.96	13 (22%)	85,89,89	1.26	9 (10%)
5	FUM	D	1657	-	7,7,7	1.60	2 (28%)	8,8,8	0.79	0
5	FUM	A	1657	-	7,7,7	1.61	2 (28%)	8,8,8	0.79	0
4	FAD	A	1656	1	58,58,58	2.03	16 (27%)	85,89,89	1.26	9 (10%)
10	HEM	F	1256	3	50,50,50	1.34	7 (14%)	67,82,82	0.99	4 (5%)
10	HEM	F	1255	3	50,50,50	1.40	7 (14%)	67,82,82	0.80	0
8	F3S	E	1241	2	0,9,9	-	-	-		
10	HEM	C	1255	3	50,50,50	1.39	7 (14%)	67,82,82	0.79	0

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
11	LMT	F	1257	-	-	10/21/61/61	0/2/2/2

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

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1656	FAD	P-O3P	-8.05	1.50	1.59
4	D	1656	FAD	P-O3P	-7.93	1.50	1.59
4	A	1656	FAD	C1'-C2'	4.19	1.58	1.52
4	A	1656	FAD	O5'-C5'	4.11	1.60	1.44
4	D	1656	FAD	C1'-C2'	4.10	1.58	1.52

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	C	1257	LMT	C1-O1'-C1'	4.93	122.11	113.68
11	F	1257	LMT	C1-O1'-C1'	4.89	122.03	113.68
4	A	1656	FAD	C1'-N10-C9A	-4.37	112.15	120.63
4	D	1656	FAD	C1'-N10-C9A	-4.33	112.22	120.63
4	D	1656	FAD	O4B-C1B-N9A	-3.50	101.36	108.09

There are no chirality outliers.

5 of 43 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1656	FAD	PA-O3P-P-O5'

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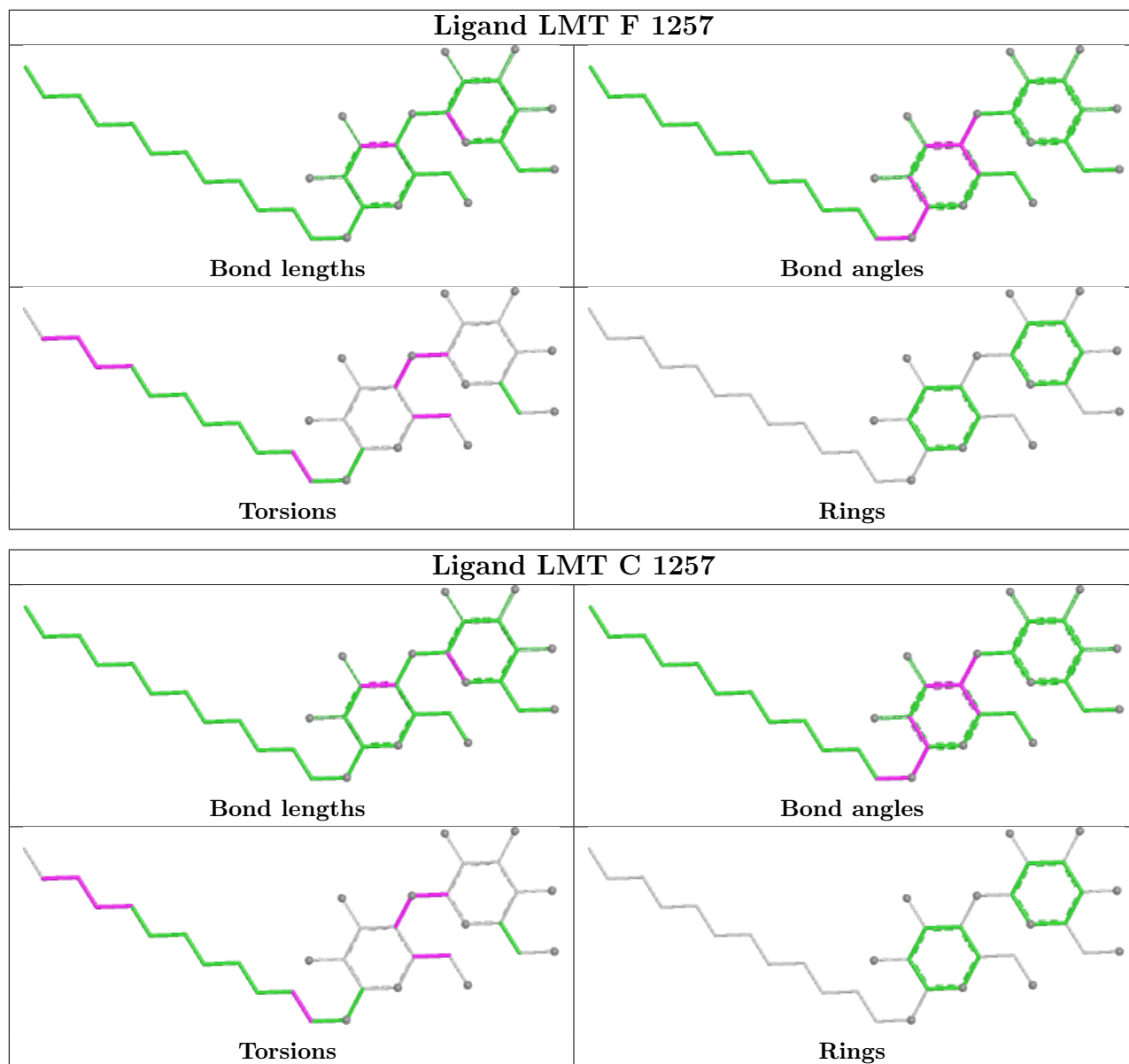
Mol	Chain	Res	Type	Atoms
4	D	1656	FAD	PA-O3P-P-O5'
10	C	1255	HEM	C2B-C3B-CAB-CBB
10	C	1255	HEM	C4B-C3B-CAB-CBB
10	C	1255	HEM	C2C-C3C-CAC-CBC

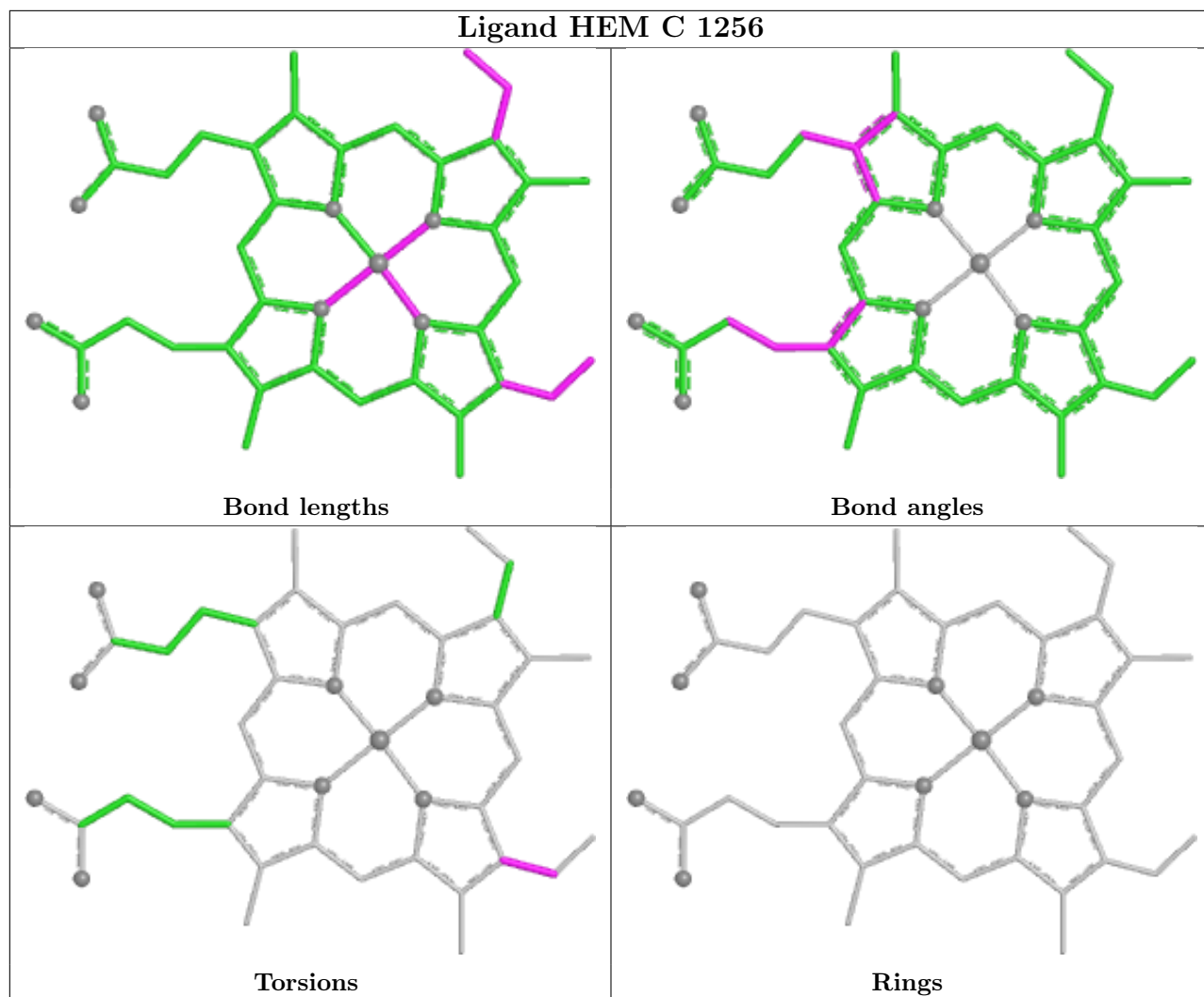
There are no ring outliers.

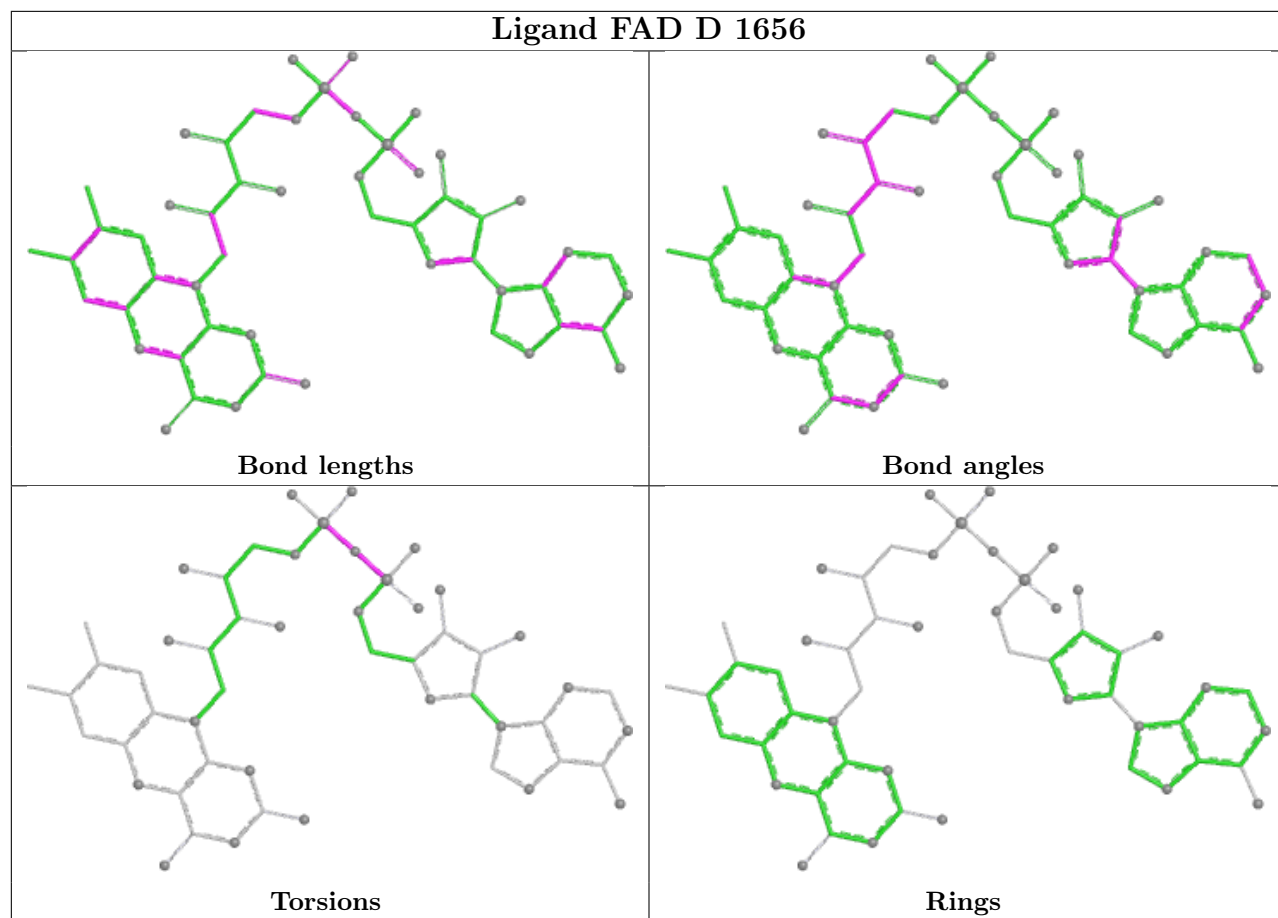
10 monomers are involved in 35 short contacts:

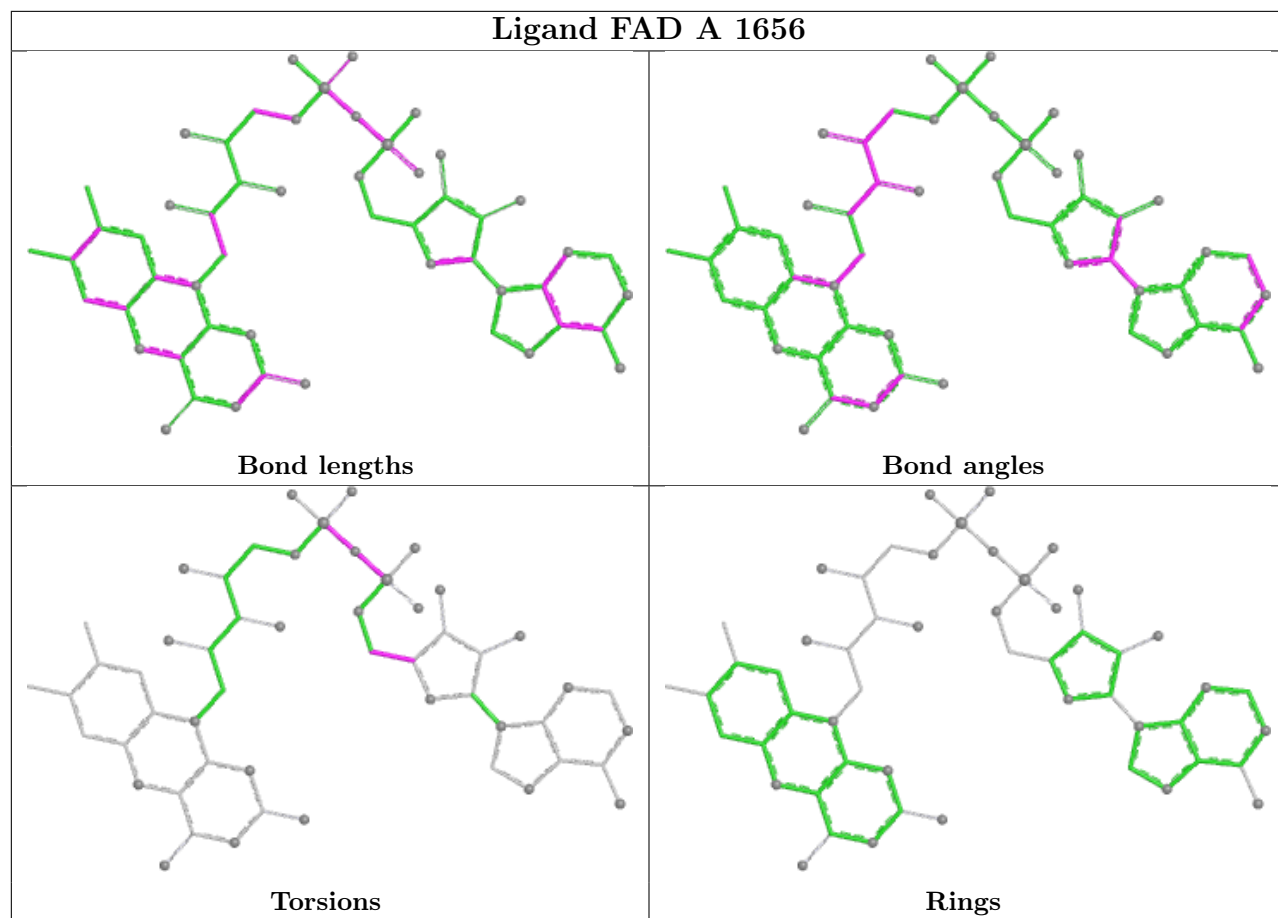
Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	F	1257	LMT	8	0
11	C	1257	LMT	7	0
10	C	1256	HEM	4	0
4	D	1656	FAD	1	0
5	D	1657	FUM	1	0
5	A	1657	FUM	2	0
4	A	1656	FAD	1	0
10	F	1256	HEM	4	0
10	F	1255	HEM	4	0
10	C	1255	HEM	3	0

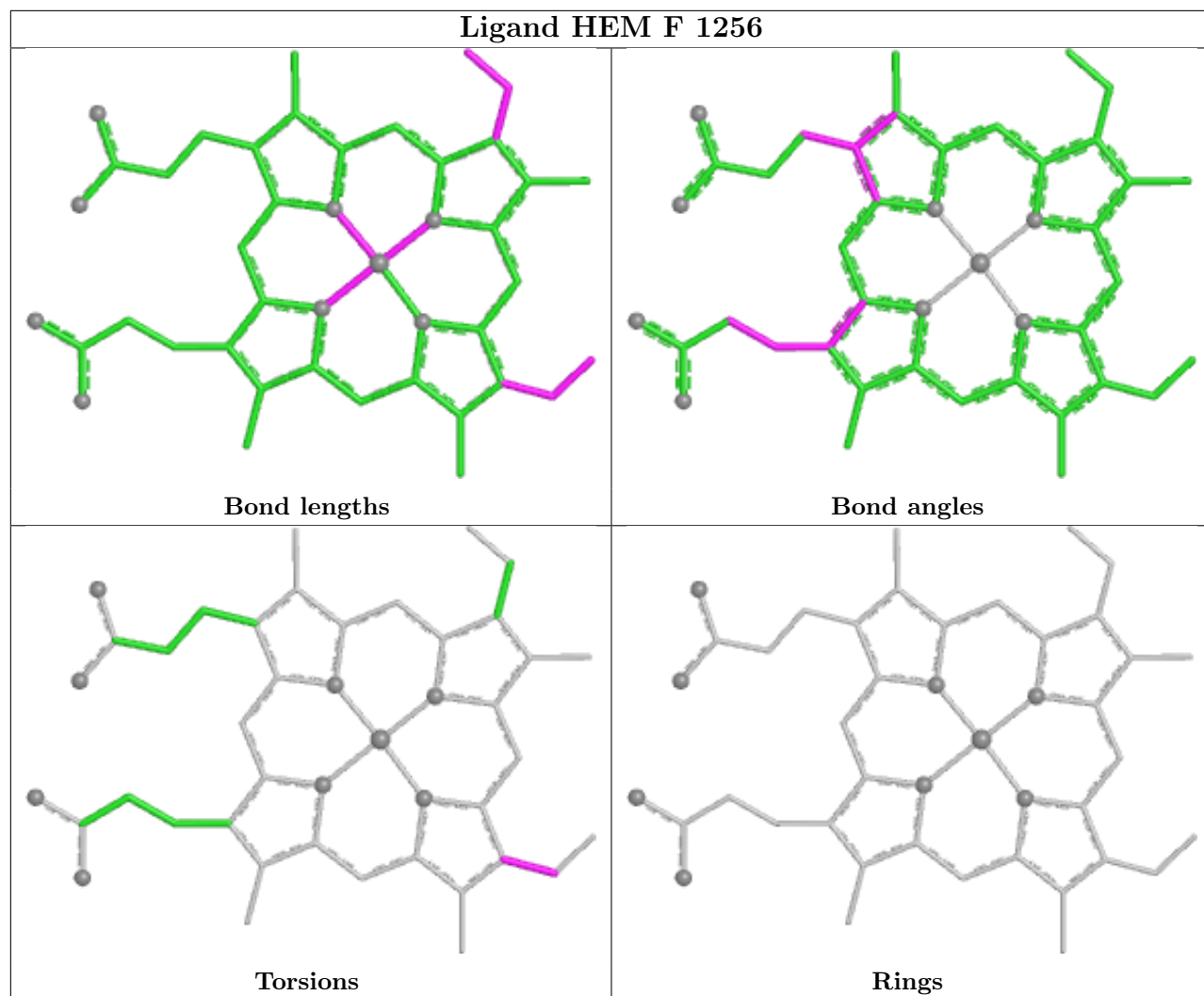
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

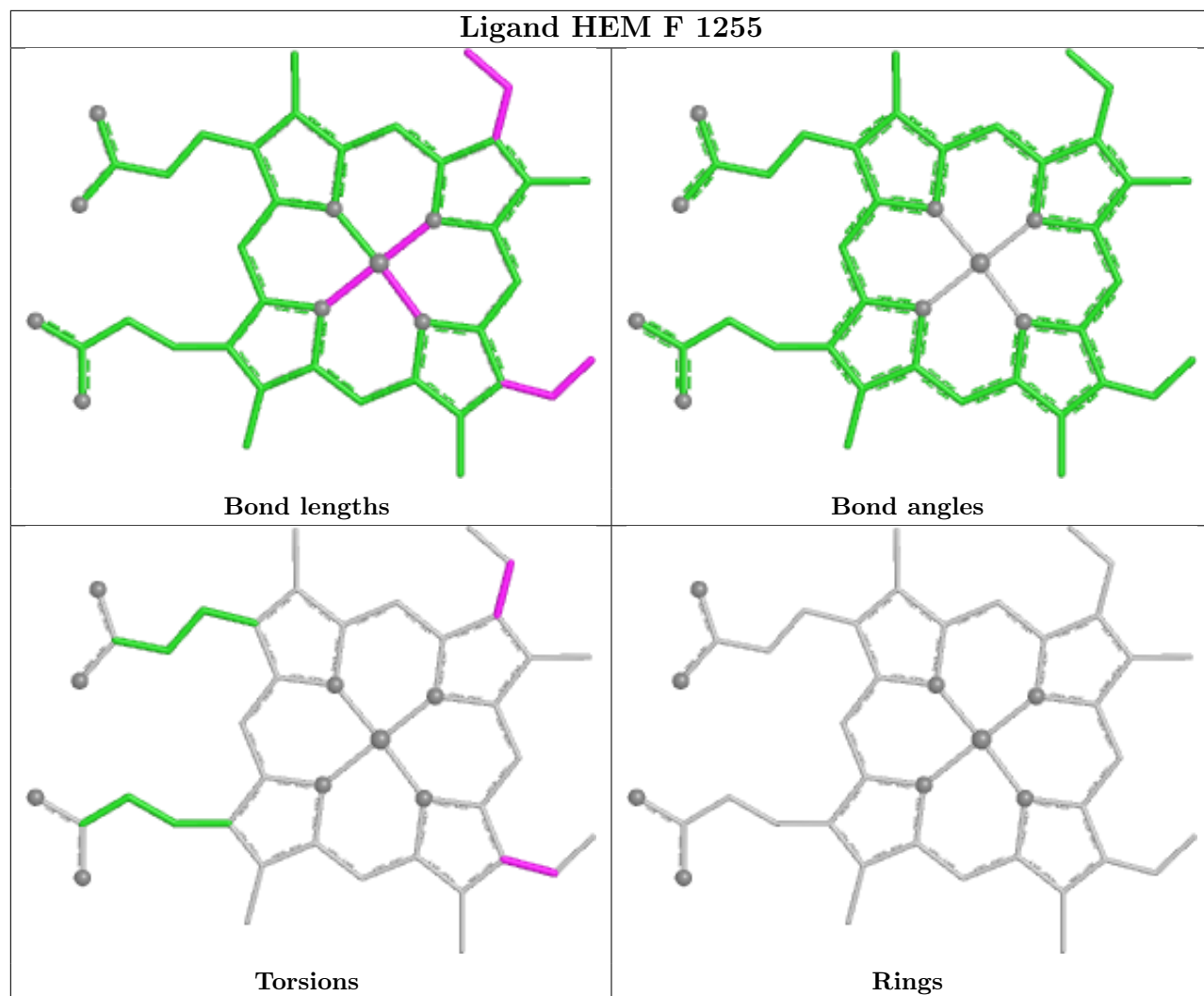


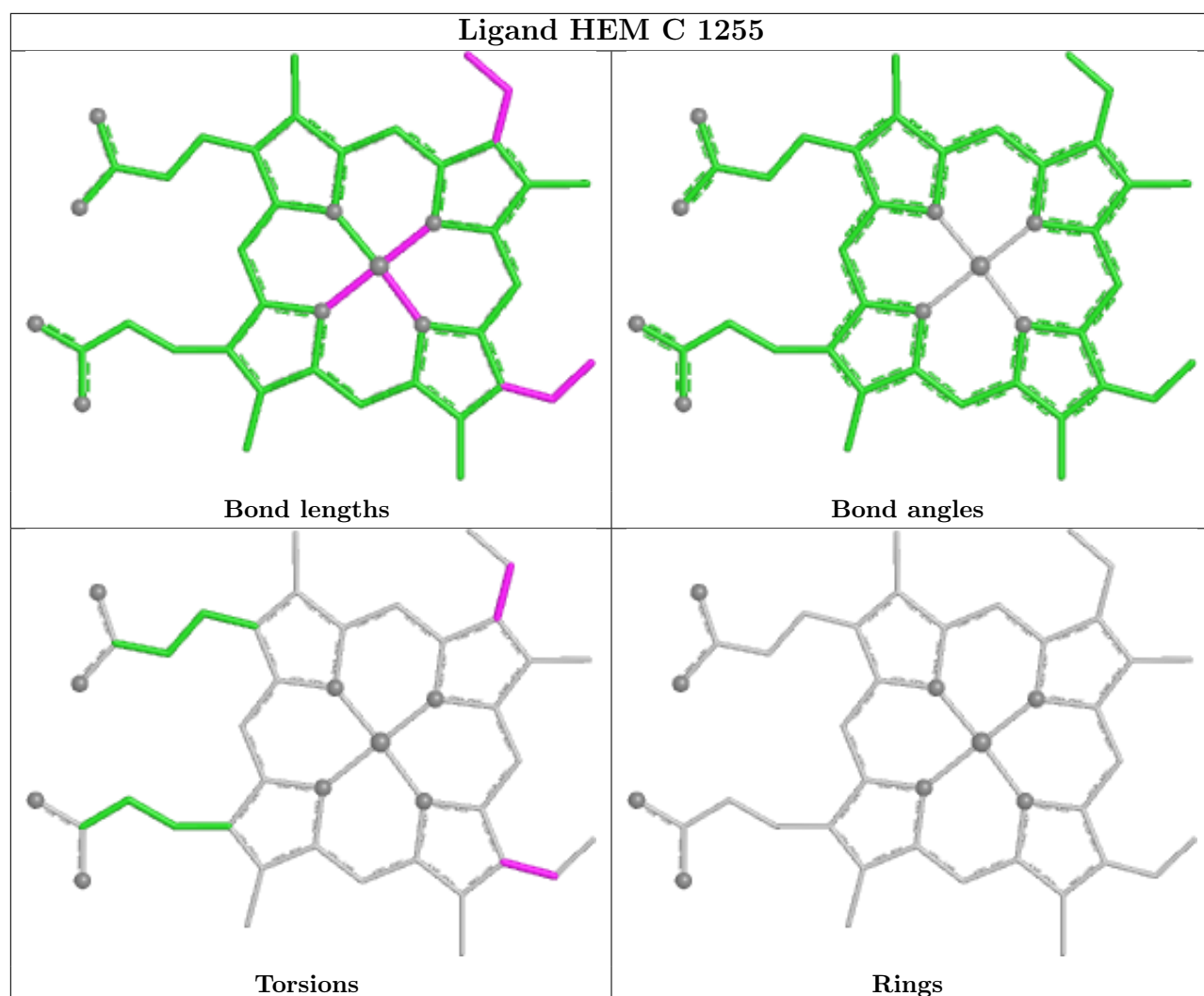












## 5.7 Other polymers [i](#)

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](#)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.