



wwPDB X-ray Structure Validation Summary Report ⓘ

May 14, 2020 – 08:27 am BST

PDB ID : 1QLB
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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

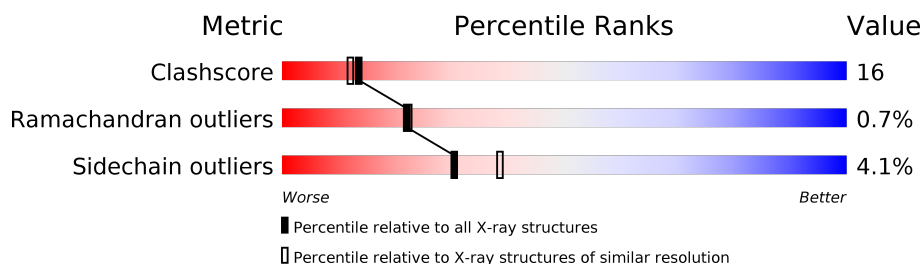
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.33 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	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (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 on 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 was not executed.

Mol	Chain	Length	Quality of chain
1	A	656	75% 23% .
1	D	656	74% 24% .
2	B	239	74% 24% .
2	E	239	74% 24% .
3	C	256	65% 31% ..
3	F	256	63% 34% ..

2 Entry composition

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
1	A	655	Total	C	N	O	S	88	0	0
			5101	3194	913	962	32			
1	D	655	Total	C	N	O	S	88	0	0
			5101	3194	913	962	32			

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
2	B	239	Total	C	N	O	S	0	0	0
			1893	1194	322	354	23			

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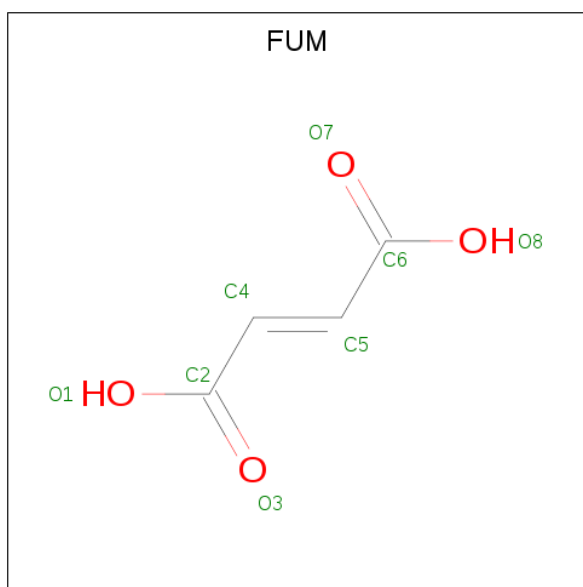
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	239	Total	C	N	O	S	0	0	0
			1893	1194	322	354	23			

- | Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|---------------|-----------|----------|----------|---------|---------|---------|-------|
| 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 |

- # FAD
-
- The image displays the chemical structure of Flavin Adenine Dinucleotide (FAD), a crucial coenzyme. It is composed of three main parts: a ribitol chain, an isoalloxazine ring system (flavin), and an adenine ring system.
- Ribitol Chain:** A five-carbon chain (C58-C68) that serves as the backbone. It features a hydroxyl group (OH) at C58, a phosphate group (P) at C60, and another phosphate group (P) at C62. The chain ends with a hydroxyl group (OH) at C68.
 - Flavin Ring System:** A bicyclic system consisting of a pyrimidine ring fused to an imidazole ring. The pyrimidine ring has nitrogen atoms at N7A and N3A, and carbon atoms at C6A, C5A, C4A, and C8A. The imidazole ring has nitrogen atoms at N1A and N9A, and carbon atoms at C2A and C7A. The ribitol chain is attached to the C5A position.
 - Adenine Ring System:** A purine ring system consisting of a pyrimidine ring fused to an imidazole ring. The pyrimidine ring has nitrogen atoms at N1 and N3, and carbon atoms at C2, C4, C6, and C8. The imidazole ring has nitrogen atoms at N7 and N9, and carbon atoms at C5 and C8. The ribitol chain is attached to the C9 position.
- The structure is shown in a 3D representation, with atoms labeled with their respective element symbols and bond types. The ribitol chain is highlighted in red, and the adenine ring system is highlighted in blue.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
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

- 



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 CALCIUM ION (three-letter code: CA) (formula: Ca).

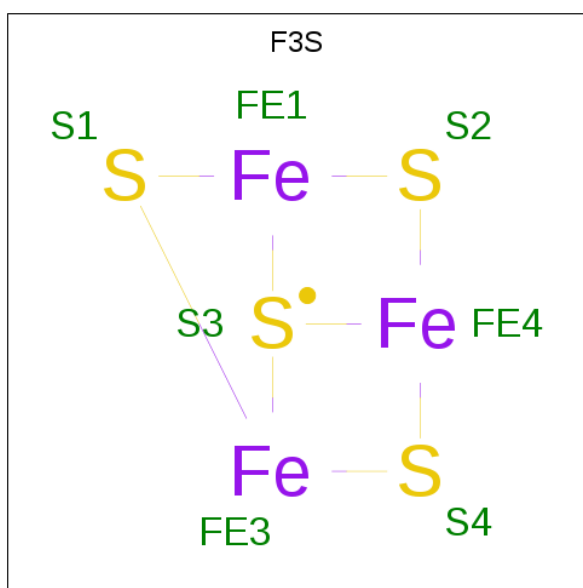
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Ca	0	0
			1	1		
6	D	1	Total	Ca	0	0
			1	1		

- Molecule 7 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



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		

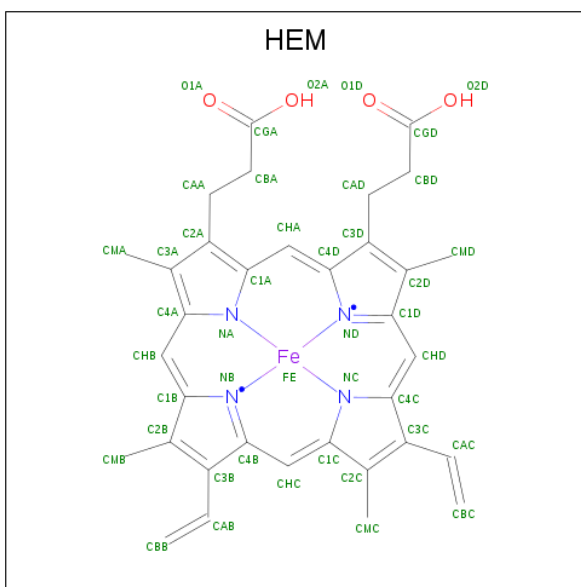
- Molecule 8 is FE3-S4 CLUSTER (three-letter code: F3S) (formula: Fe_3S_4).



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		

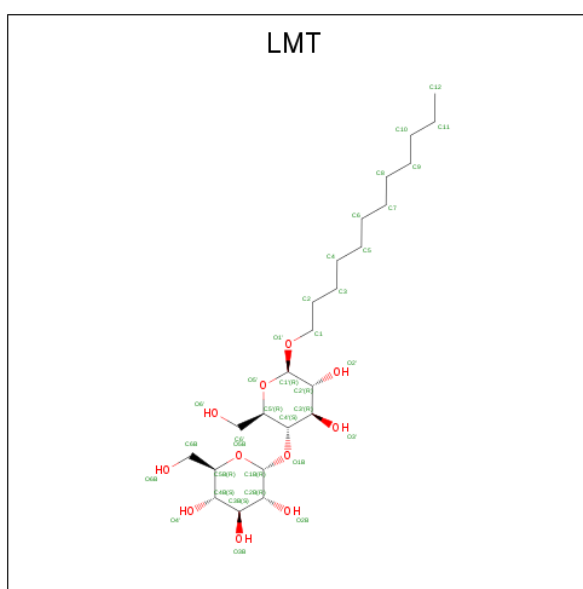
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- Molecule 10 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

- Molecule 11 is DODECYL-BETA-D-MALTOSE (three-letter code: LMT) (formula: $C_{24}H_{46}O_{11}$).



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		

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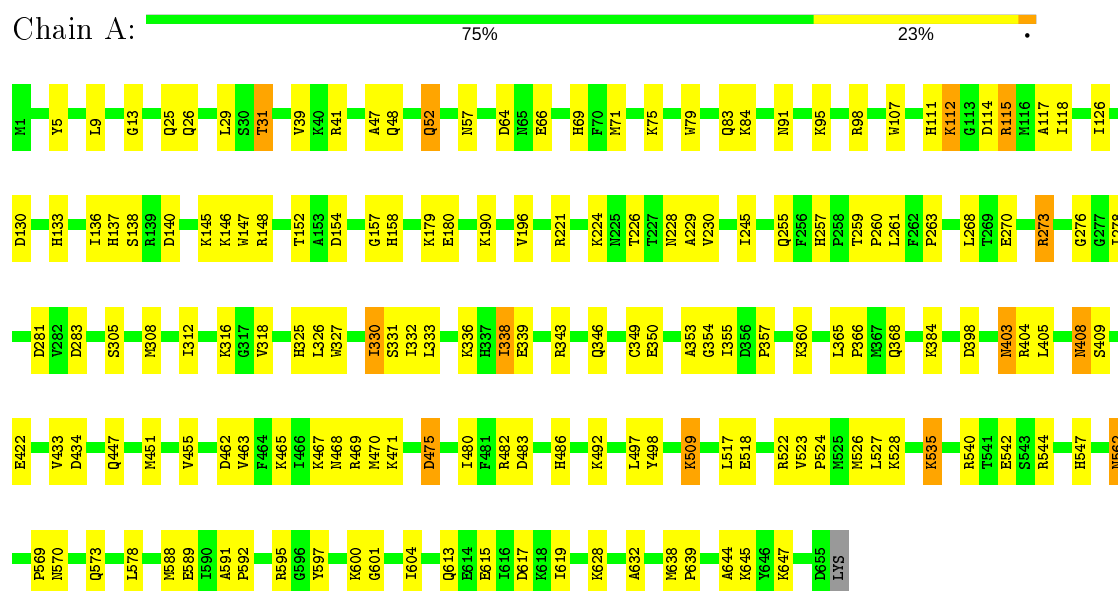
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	D	148	Total 148	O 148	0	0
12	E	83	Total 83	O 83	0	0
12	F	22	Total 22	O 22	0	0

3 Residue-property plots [i](#)

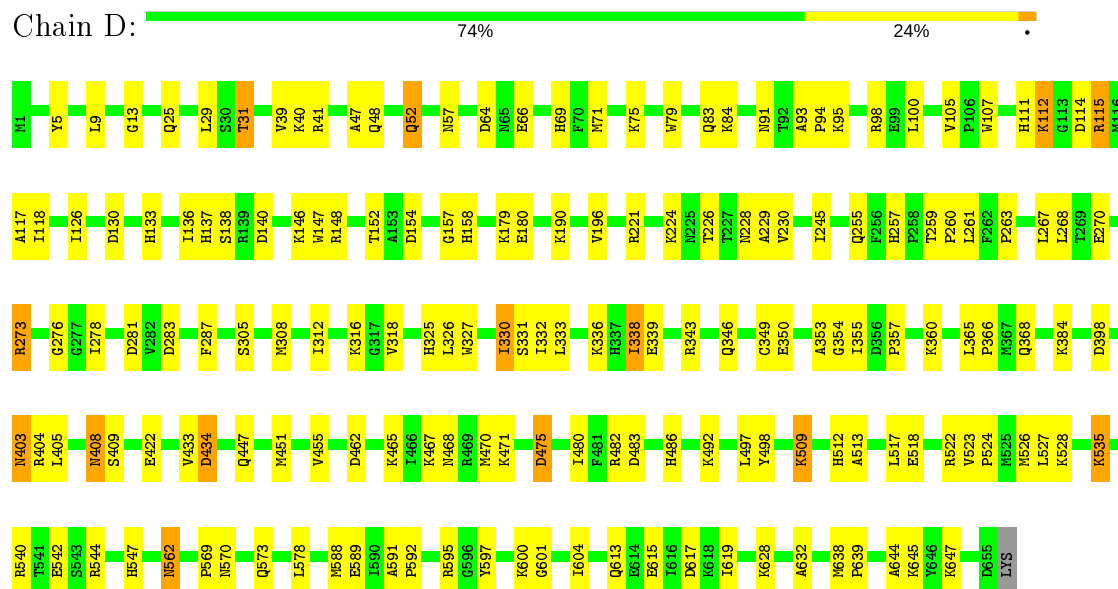
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according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

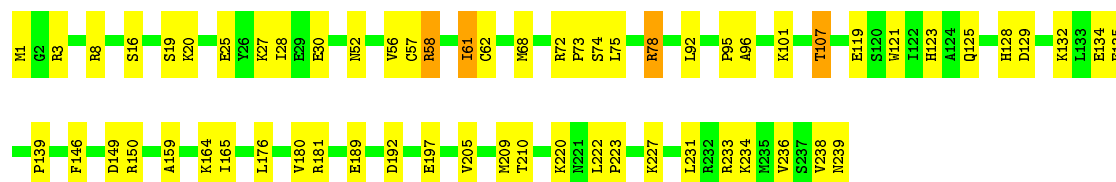


• Molecule 1: FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT



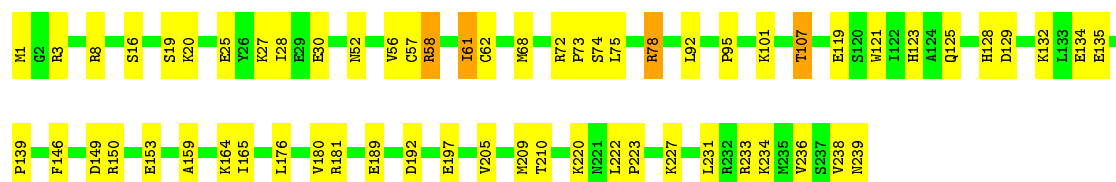
• Molecule 2: FUMARATE REDUCTASE IRON-SULFUR PROTEIN

Chain B: 



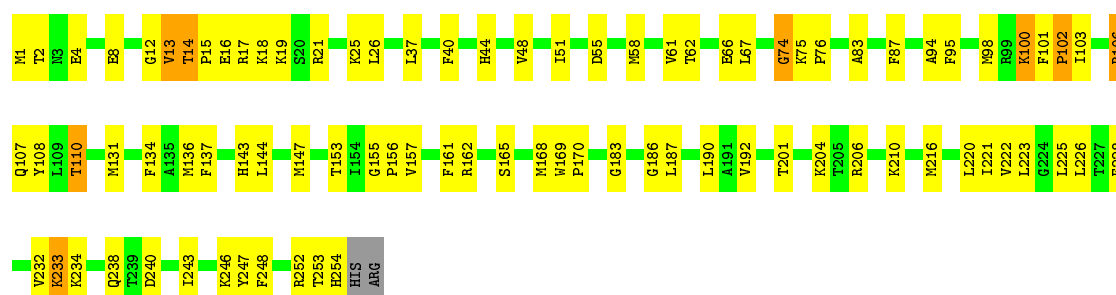
• Molecule 2: FUMARATE REDUCTASE IRON-SULFUR PROTEIN

Chain E: 



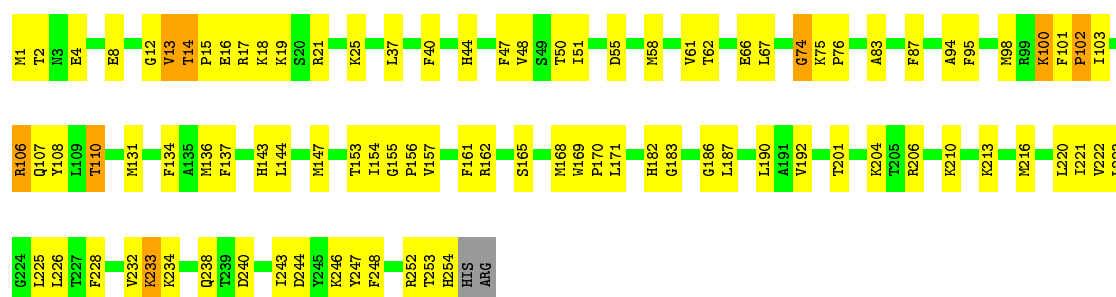
• Molecule 3: FUMARATE REDUCTASE CYTOCHROME B SUBUNIT

Chain C: 



• Molecule 3: FUMARATE REDUCTASE CYTOCHROME B SUBUNIT

Chain F: 



4 Data and refinement statistics

Xtriage (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, α , β , γ	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.	Xtriage
Total number of atoms	19056	wwPDB-VP
Average B, all atoms (Å ²)	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, LMT, F3S, FES, HEM, FUM, CA, FAD

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	0.32	0/5197	0.60	0/7006
1	D	0.32	0/5197	0.60	0/7006
2	B	0.35	0/1930	0.59	0/2604
2	E	0.34	0/1930	0.59	0/2604
3	C	0.32	0/2146	0.50	1/2904 (0.0%)
3	F	0.33	0/2146	0.50	1/2904 (0.0%)
All	All	0.33	0/18546	0.58	2/25028 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	102	PRO	N-CA-C	-5.88	96.82	112.10
3	F	102	PRO	N-CA-C	-5.86	96.85	112.10

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	148	0
1	D	5101	0	5079	149	0
2	B	1893	0	1861	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	1893	0	1861	63	0
3	C	2080	0	2101	98	0
3	F	2080	0	2101	103	0
4	A	53	0	29	1	0
4	D	53	0	29	1	0
5	A	8	0	2	2	0
5	D	8	0	2	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	8	0
12	B	79	0	0	2	0
12	C	23	0	0	0	0
12	D	148	0	0	6	0
12	E	83	0	0	3	0
12	F	22	0	0	0	0
All	All	19056	0	18356	576	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 16.

The worst 5 of 576 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
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	653/656 (100%)	615 (94%)	33 (5%)	5 (1%)	19	20
1	D	653/656 (100%)	615 (94%)	33 (5%)	5 (1%)	19	20
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%)	13	11
3	F	252/256 (98%)	235 (93%)	14 (6%)	3 (1%)	13	11
All	All	2284/2302 (99%)	2157 (94%)	111 (5%)	16 (1%)	22	22

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%)	511 (96%)	23 (4%)	29	36
1	D	534/535 (100%)	510 (96%)	24 (4%)	27	34
2	B	211/211 (100%)	205 (97%)	6 (3%)	43	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	211/211 (100%)	205 (97%)	6 (3%)	43	53
3	C	221/223 (99%)	211 (96%)	10 (4%)	27	34
3	F	221/223 (99%)	211 (96%)	10 (4%)	27	34
All	All	1932/1938 (100%)	1853 (96%)	79 (4%)	30	38

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	100	LYS
1	D	115	ARG
3	F	58	MET
3	C	106	ARG
1	D	31	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	208	ASN
1	D	133	HIS
3	F	3	ASN
3	C	238	GLN
1	D	48	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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	0.00	-	-		
10	HEM	F	1256	3	27,50,50	1.69	6 (22%)	17,82,82	1.17	1 (5%)
4	FAD	D	1656	1	51,58,58	2.30	15 (29%)	60,89,89	2.28	13 (21%)
11	LMT	C	1257	-	36,36,36	1.11	2 (5%)	47,47,47	1.26	4 (8%)
10	HEM	C	1255	3	27,50,50	1.72	6 (22%)	17,82,82	1.11	1 (5%)
11	LMT	F	1257	-	36,36,36	1.12	2 (5%)	47,47,47	1.25	4 (8%)
4	FAD	A	1656	1	51,58,58	2.35	14 (27%)	60,89,89	2.29	13 (21%)
7	FES	B	1240	2	0,4,4	0.00	-	-		
10	HEM	C	1256	3	27,50,50	1.70	6 (22%)	17,82,82	1.17	1 (5%)
5	FUM	A	1657	-	1,7,7	1.75	0	2,8,8	0.66	0
9	SF4	B	1242	2	0,12,12	0.00	-	-		
8	F3S	B	1241	2	0,9,9	0.00	-	-		
8	F3S	E	1241	2	0,9,9	0.00	-	-		
10	HEM	F	1255	3	27,50,50	1.72	6 (22%)	17,82,82	1.11	1 (5%)
7	FES	E	1240	2	0,4,4	0.00	-	-		
5	FUM	D	1657	-	1,7,7	1.76	0	2,8,8	0.67	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	C	1257	-	-	10/21/61/61	0/2/2/2
10	HEM	F	1256	3	-	0/6/54/54	-
4	FAD	D	1656	1	-	4/30/50/50	0/6/6/6
11	LMT	F	1257	-	-	10/21/61/61	0/2/2/2
4	FAD	A	1656	1	-	4/30/50/50	0/6/6/6
7	FES	B	1240	2	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	F3S	B	1241	2	-	-	0/3/3/3
10	HEM	C	1256	3	-	0/6/54/54	-
5	FUM	A	1657	-	-	0/0/5/5	-
9	SF4	B	1242	2	-	-	0/6/5/5
10	HEM	C	1255	3	-	0/6/54/54	-
9	SF4	E	1242	2	-	-	0/6/5/5
8	F3S	E	1241	2	-	-	0/3/3/3
10	HEM	F	1255	3	-	0/6/54/54	-
7	FES	E	1240	2	-	-	0/1/1/1
5	FUM	D	1657	-	-	0/0/5/5	-

The worst 5 of 57 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1656	FAD	C4X-C10	9.50	1.48	1.38
4	D	1656	FAD	C4X-C10	8.92	1.47	1.38
4	D	1656	FAD	C9A-N10	5.11	1.45	1.38
4	A	1656	FAD	C9A-N10	4.73	1.44	1.38
10	F	1256	HEM	C3B-CAB	-4.55	1.38	1.47

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1656	FAD	C1'-N10-C10	9.18	126.63	118.41
4	D	1656	FAD	C1'-N10-C10	9.01	126.48	118.41
4	A	1656	FAD	C1'-N10-C9A	-7.81	112.15	118.29
4	D	1656	FAD	C1'-N10-C9A	-7.72	112.22	118.29
4	D	1656	FAD	C4-N3-C2	7.68	121.62	115.14

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

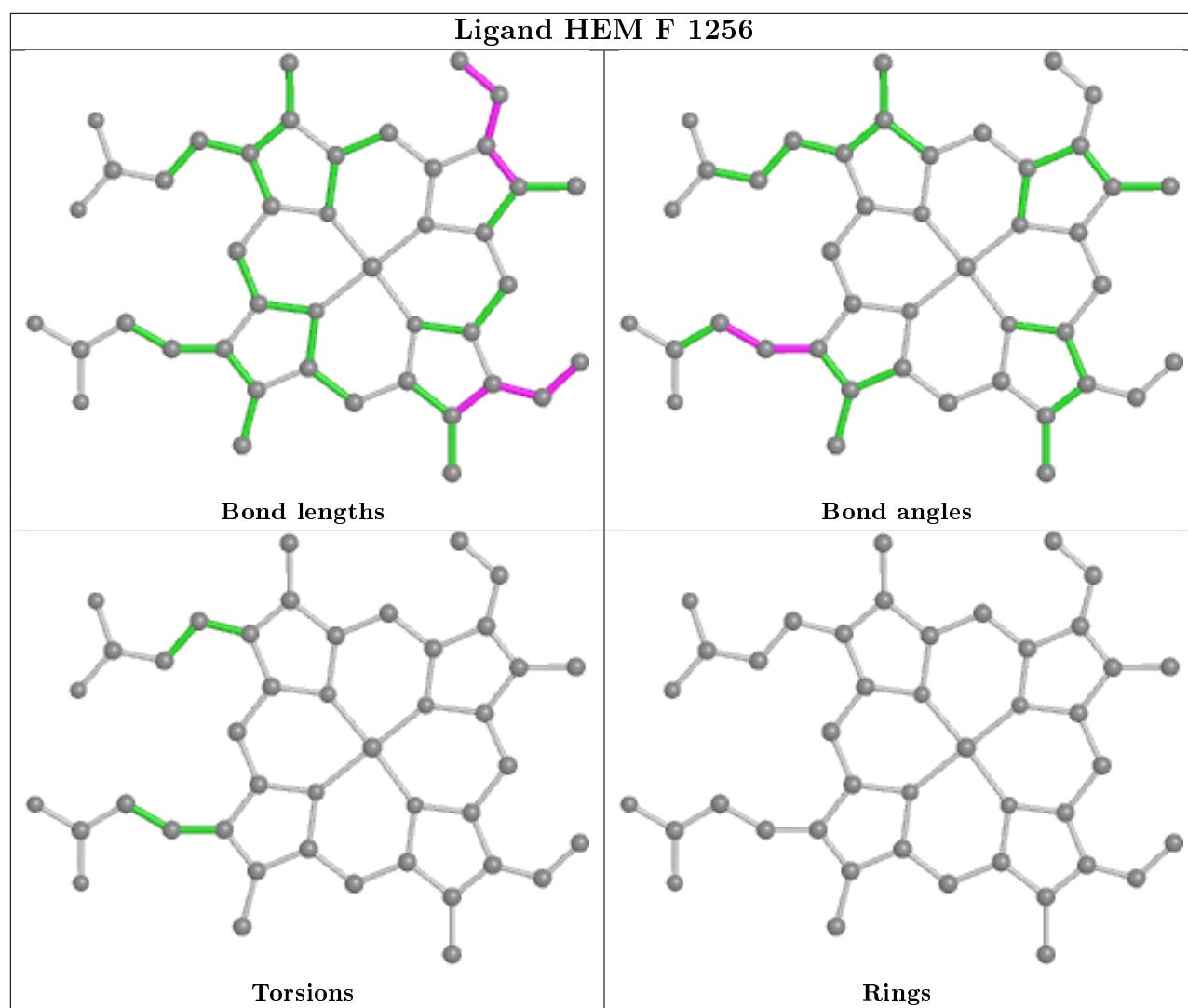
Mol	Chain	Res	Type	Atoms
4	D	1656	FAD	PA-O3P-P-O5'
4	A	1656	FAD	PA-O3P-P-O5'
11	F	1257	LMT	O5'-C5'-C6'-O6'
11	C	1257	LMT	O5'-C5'-C6'-O6'
11	F	1257	LMT	C4'-C5'-C6'-O6'

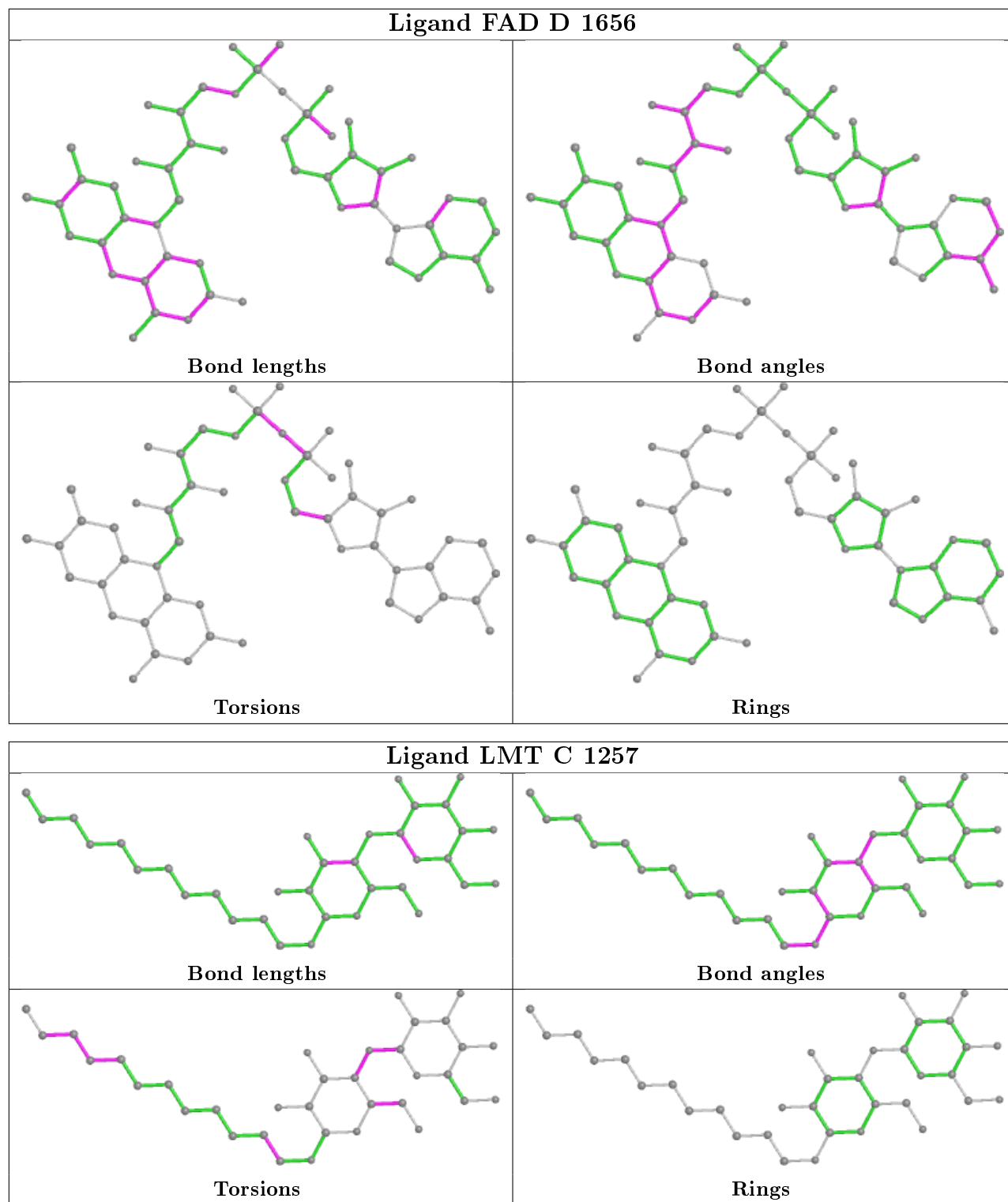
There are no ring outliers.

10 monomers are involved in 35 short contacts:

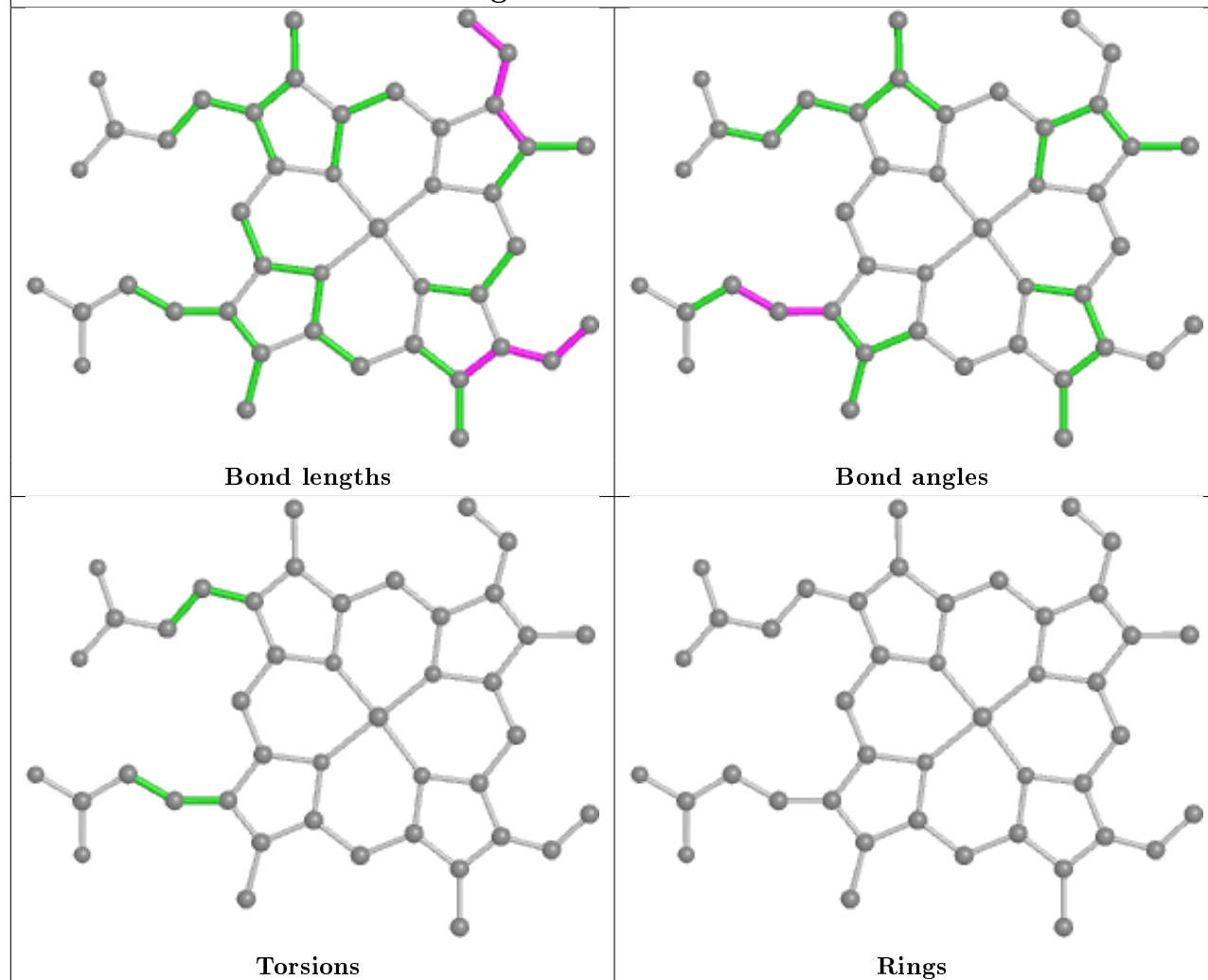
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	F	1256	HEM	4	0
4	D	1656	FAD	1	0
11	C	1257	LMT	7	0
10	C	1255	HEM	3	0
11	F	1257	LMT	8	0
4	A	1656	FAD	1	0
10	C	1256	HEM	4	0
5	A	1657	FUM	2	0
10	F	1255	HEM	4	0
5	D	1657	FUM	1	0

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.

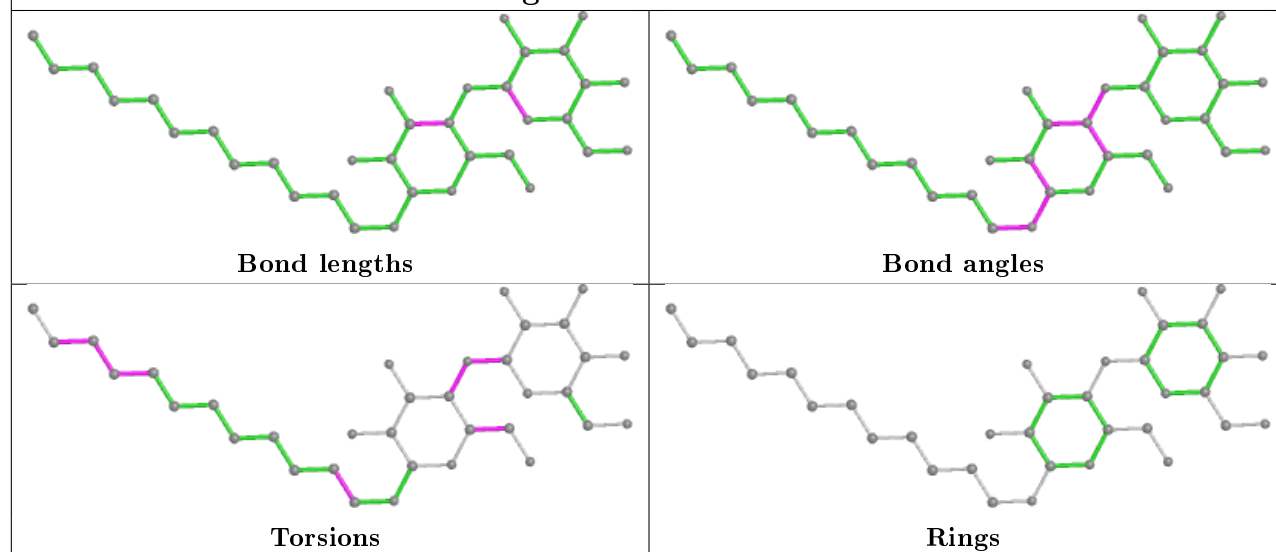


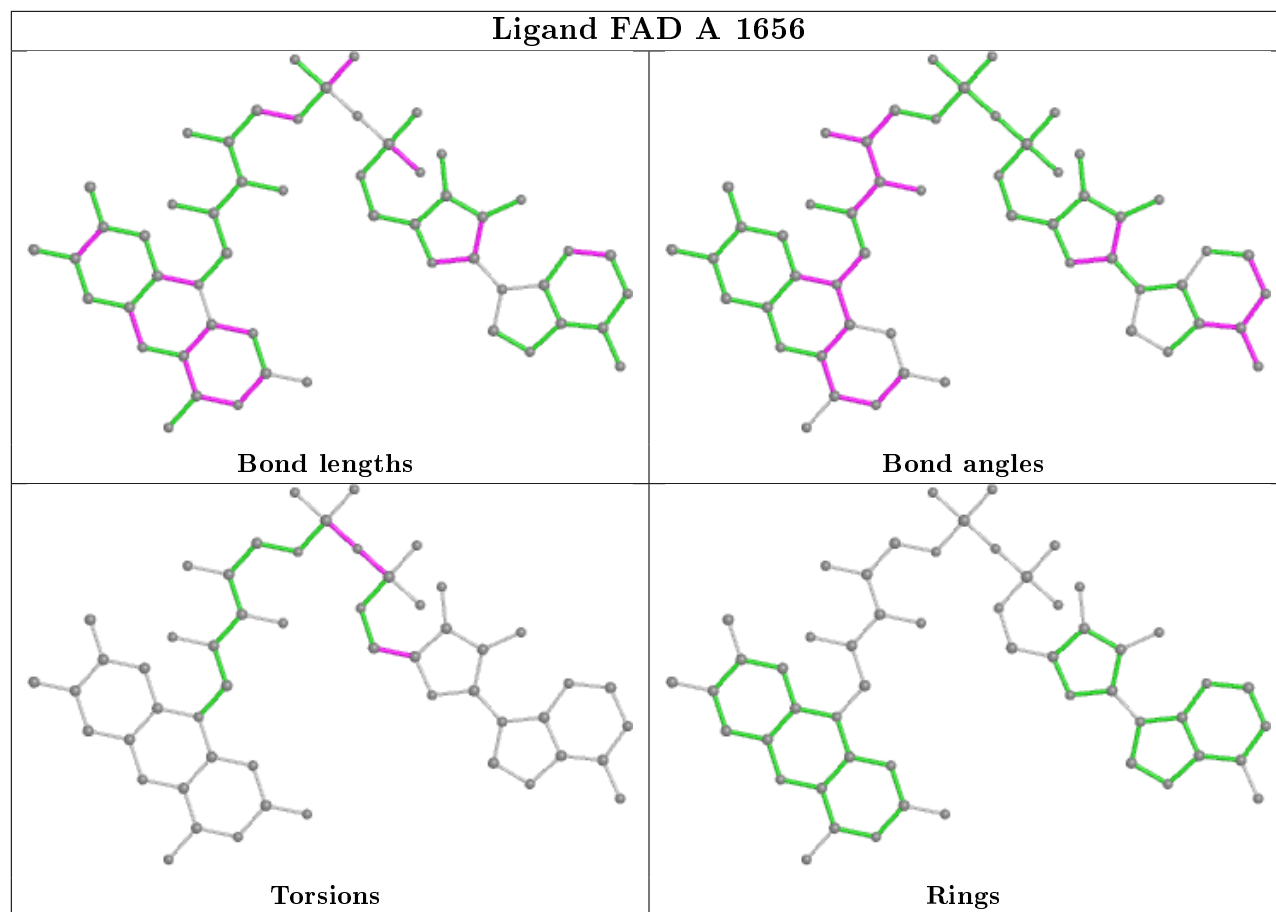


Ligand HEM C 1255

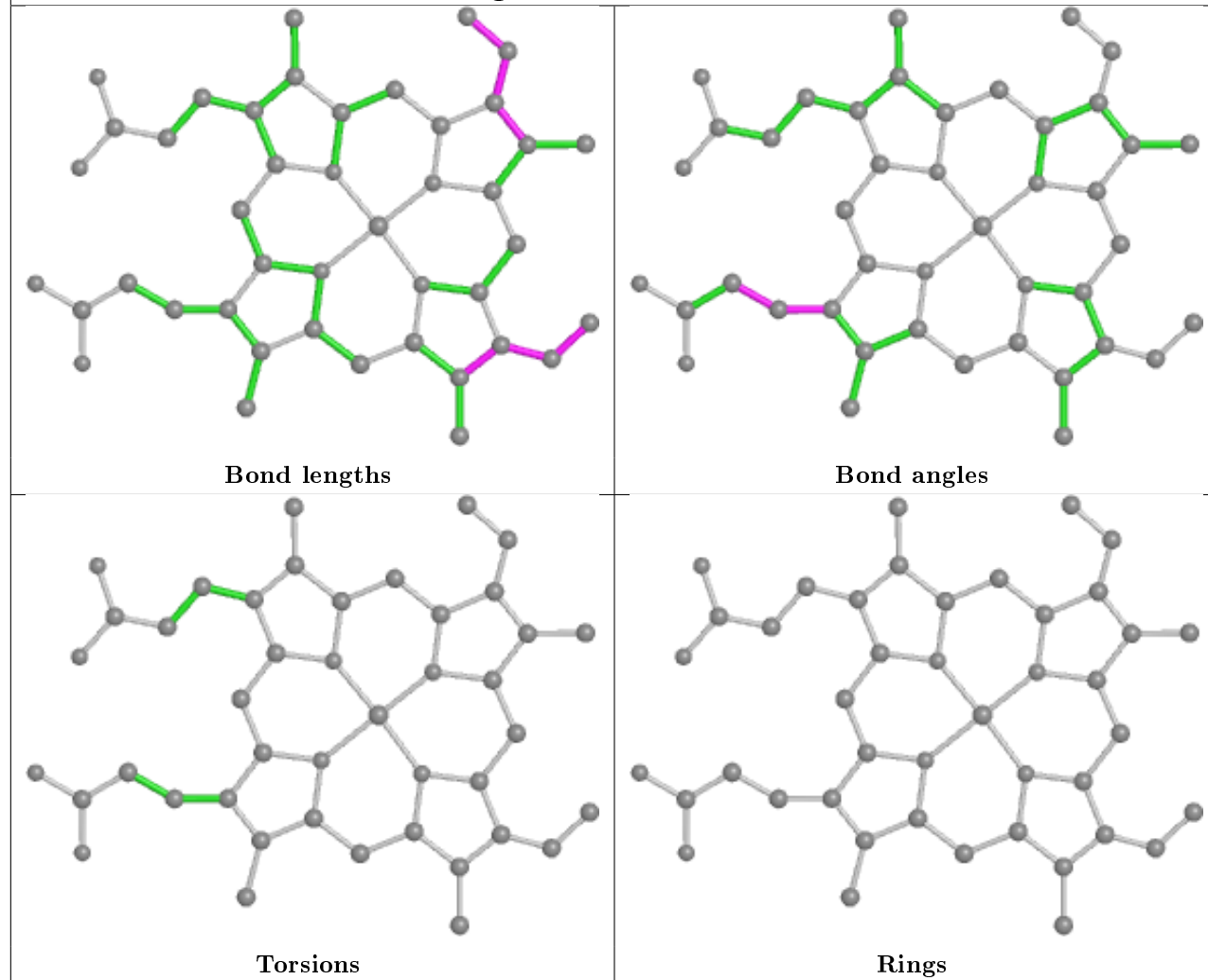


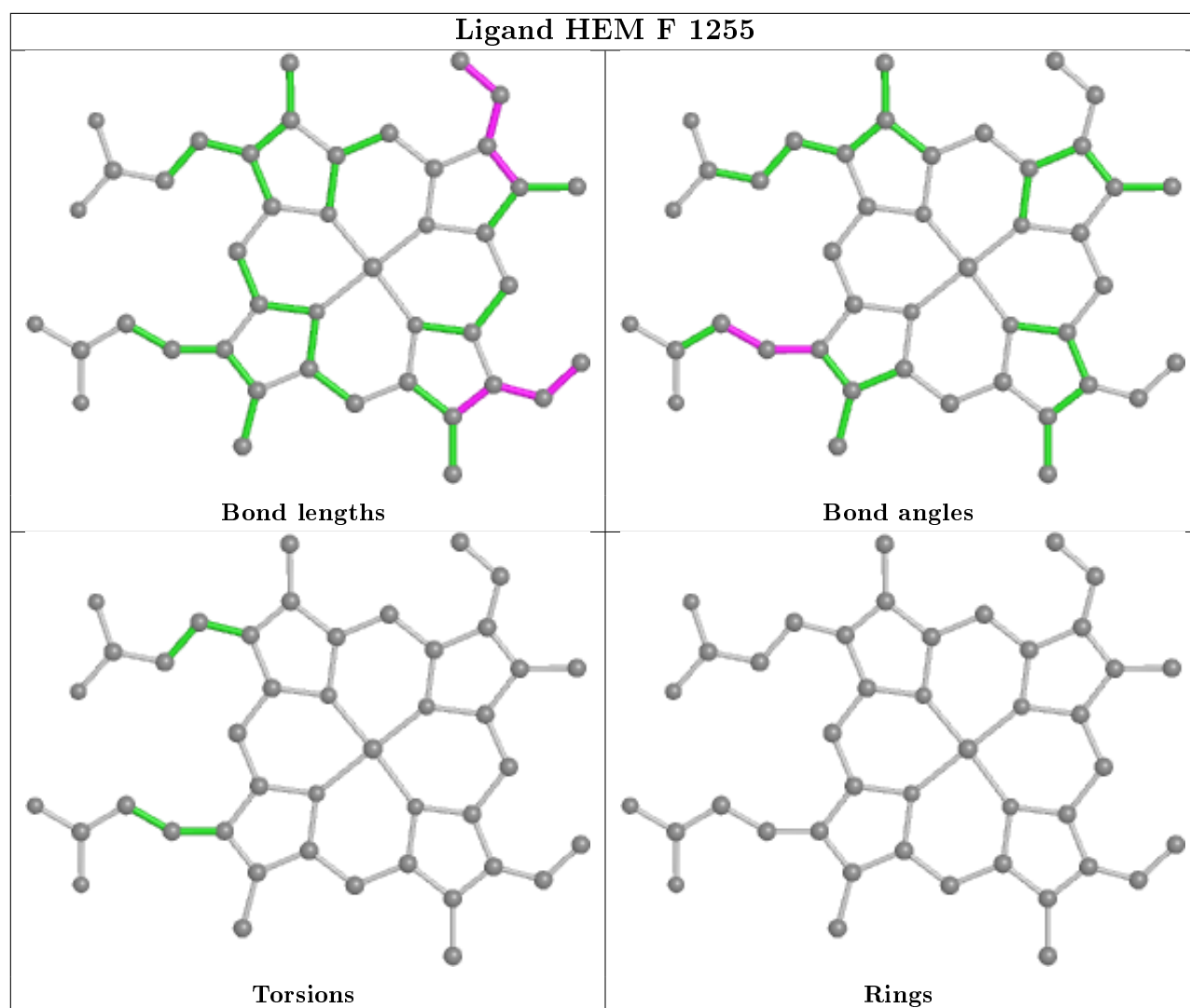
Ligand LMT F 1257





Ligand HEM C 1256





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 was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.