



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2026 – 09:05 PM UTC

PDB ID : 6UX0 / pdb_00006ux0
Title : Isavuconazole bound complex of Acanthamoeba castellanii CYP51
Authors : Sharma, V.; Podust, L.M.
Deposited on : 2019-11-06
Resolution : 2.93 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 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

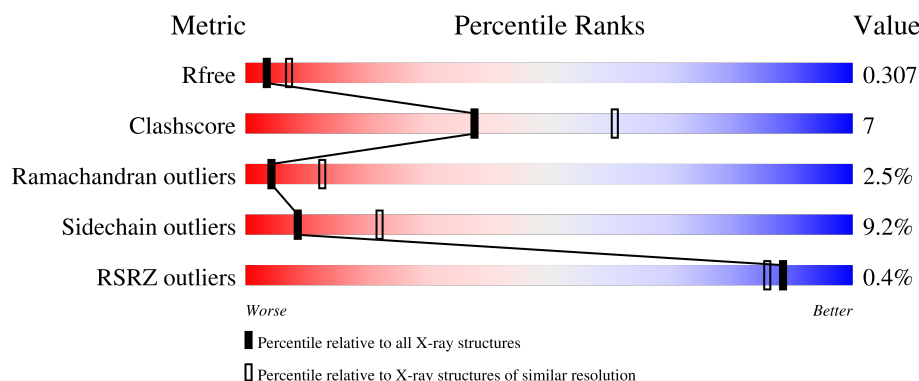
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.93 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	1159 (2.96-2.92)
Clashscore	190562	1184 (2.96-2.92)
Ramachandran outliers	187476	1131 (2.96-2.92)
Sidechain outliers	187428	1131 (2.96-2.92)
RSRZ outliers	180081	1159 (2.96-2.92)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	460	
1	B	460	
1	C	460	
1	D	460	
1	E	460	

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Mol	Chain	Length	Quality of chain
1	F	460	67% 21% • 10%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 19999 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 Obtusifoliol 14alphademethylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	413	Total	C	N	O	S	0	0	0
			3253	2099	540	596	18			
1	B	414	Total	C	N	O	S	0	0	0
			3262	2103	544	597	18			
1	C	414	Total	C	N	O	S	0	0	0
			3256	2103	541	594	18			
1	D	414	Total	C	N	O	S	0	0	0
			3268	2113	544	593	18			
1	E	413	Total	C	N	O	S	0	0	0
			3255	2101	542	594	18			
1	F	413	Total	C	N	O	S	0	0	0
			3258	2101	543	596	18			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	33	MET	-	expression tag	UNP L8GJB3
A	34	ALA	-	expression tag	UNP L8GJB3
A	35	LYS	-	expression tag	UNP L8GJB3
A	36	LYS	-	expression tag	UNP L8GJB3
A	37	THR	-	expression tag	UNP L8GJB3
A	38	SER	-	expression tag	UNP L8GJB3
A	39	SER	-	expression tag	UNP L8GJB3
A	40	LYS	-	expression tag	UNP L8GJB3
A	41	GLY	-	expression tag	UNP L8GJB3
A	42	LYS	-	expression tag	UNP L8GJB3
A	487	HIS	-	expression tag	UNP L8GJB3
A	488	HIS	-	expression tag	UNP L8GJB3
A	489	HIS	-	expression tag	UNP L8GJB3
A	490	HIS	-	expression tag	UNP L8GJB3
A	491	HIS	-	expression tag	UNP L8GJB3
A	492	HIS	-	expression tag	UNP L8GJB3
B	33	MET	-	expression tag	UNP L8GJB3

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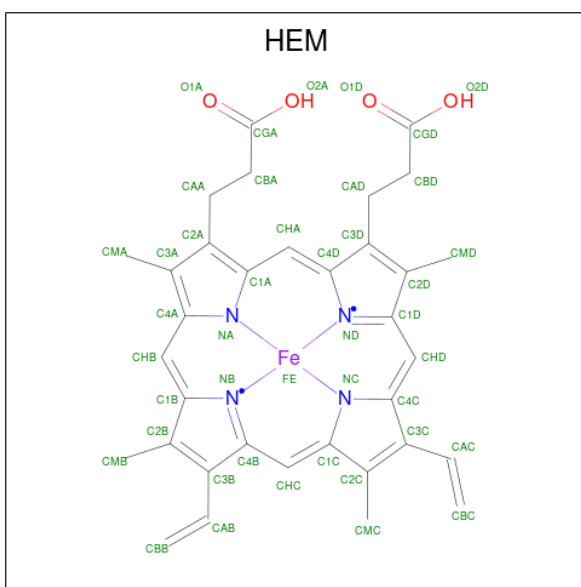
Chain	Residue	Modelled	Actual	Comment	Reference
B	34	ALA	-	expression tag	UNP L8GJB3
B	35	LYS	-	expression tag	UNP L8GJB3
B	36	LYS	-	expression tag	UNP L8GJB3
B	37	THR	-	expression tag	UNP L8GJB3
B	38	SER	-	expression tag	UNP L8GJB3
B	39	SER	-	expression tag	UNP L8GJB3
B	40	LYS	-	expression tag	UNP L8GJB3
B	41	GLY	-	expression tag	UNP L8GJB3
B	42	LYS	-	expression tag	UNP L8GJB3
B	487	HIS	-	expression tag	UNP L8GJB3
B	488	HIS	-	expression tag	UNP L8GJB3
B	489	HIS	-	expression tag	UNP L8GJB3
B	490	HIS	-	expression tag	UNP L8GJB3
B	491	HIS	-	expression tag	UNP L8GJB3
B	492	HIS	-	expression tag	UNP L8GJB3
C	33	MET	-	expression tag	UNP L8GJB3
C	34	ALA	-	expression tag	UNP L8GJB3
C	35	LYS	-	expression tag	UNP L8GJB3
C	36	LYS	-	expression tag	UNP L8GJB3
C	37	THR	-	expression tag	UNP L8GJB3
C	38	SER	-	expression tag	UNP L8GJB3
C	39	SER	-	expression tag	UNP L8GJB3
C	40	LYS	-	expression tag	UNP L8GJB3
C	41	GLY	-	expression tag	UNP L8GJB3
C	42	LYS	-	expression tag	UNP L8GJB3
C	487	HIS	-	expression tag	UNP L8GJB3
C	488	HIS	-	expression tag	UNP L8GJB3
C	489	HIS	-	expression tag	UNP L8GJB3
C	490	HIS	-	expression tag	UNP L8GJB3
C	491	HIS	-	expression tag	UNP L8GJB3
C	492	HIS	-	expression tag	UNP L8GJB3
D	33	MET	-	expression tag	UNP L8GJB3
D	34	ALA	-	expression tag	UNP L8GJB3
D	35	LYS	-	expression tag	UNP L8GJB3
D	36	LYS	-	expression tag	UNP L8GJB3
D	37	THR	-	expression tag	UNP L8GJB3
D	38	SER	-	expression tag	UNP L8GJB3
D	39	SER	-	expression tag	UNP L8GJB3
D	40	LYS	-	expression tag	UNP L8GJB3
D	41	GLY	-	expression tag	UNP L8GJB3
D	42	LYS	-	expression tag	UNP L8GJB3
D	487	HIS	-	expression tag	UNP L8GJB3

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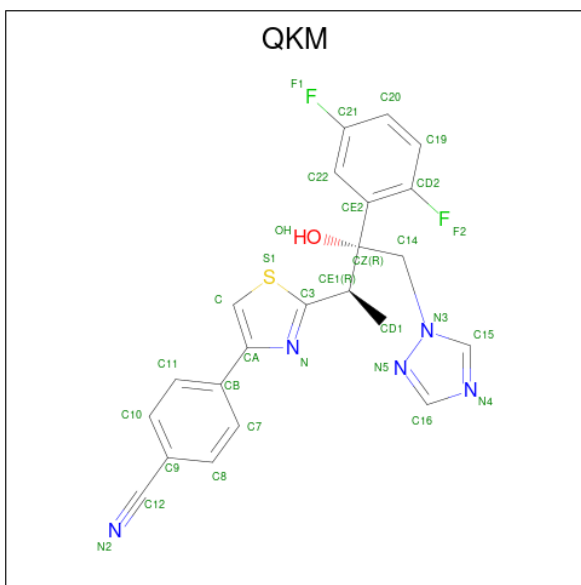
Chain	Residue	Modelled	Actual	Comment	Reference
D	488	HIS	-	expression tag	UNP L8GJB3
D	489	HIS	-	expression tag	UNP L8GJB3
D	490	HIS	-	expression tag	UNP L8GJB3
D	491	HIS	-	expression tag	UNP L8GJB3
D	492	HIS	-	expression tag	UNP L8GJB3
E	33	MET	-	expression tag	UNP L8GJB3
E	34	ALA	-	expression tag	UNP L8GJB3
E	35	LYS	-	expression tag	UNP L8GJB3
E	36	LYS	-	expression tag	UNP L8GJB3
E	37	THR	-	expression tag	UNP L8GJB3
E	38	SER	-	expression tag	UNP L8GJB3
E	39	SER	-	expression tag	UNP L8GJB3
E	40	LYS	-	expression tag	UNP L8GJB3
E	41	GLY	-	expression tag	UNP L8GJB3
E	42	LYS	-	expression tag	UNP L8GJB3
E	487	HIS	-	expression tag	UNP L8GJB3
E	488	HIS	-	expression tag	UNP L8GJB3
E	489	HIS	-	expression tag	UNP L8GJB3
E	490	HIS	-	expression tag	UNP L8GJB3
E	491	HIS	-	expression tag	UNP L8GJB3
E	492	HIS	-	expression tag	UNP L8GJB3
F	33	MET	-	expression tag	UNP L8GJB3
F	34	ALA	-	expression tag	UNP L8GJB3
F	35	LYS	-	expression tag	UNP L8GJB3
F	36	LYS	-	expression tag	UNP L8GJB3
F	37	THR	-	expression tag	UNP L8GJB3
F	38	SER	-	expression tag	UNP L8GJB3
F	39	SER	-	expression tag	UNP L8GJB3
F	40	LYS	-	expression tag	UNP L8GJB3
F	41	GLY	-	expression tag	UNP L8GJB3
F	42	LYS	-	expression tag	UNP L8GJB3
F	487	HIS	-	expression tag	UNP L8GJB3
F	488	HIS	-	expression tag	UNP L8GJB3
F	489	HIS	-	expression tag	UNP L8GJB3
F	490	HIS	-	expression tag	UNP L8GJB3
F	491	HIS	-	expression tag	UNP L8GJB3
F	492	HIS	-	expression tag	UNP L8GJB3

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	E	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	F	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 3 is 4-{2-[(2R,3R)-3-(2,5-difluorophenyl)-3-hydroxy-4-(1H-1,2,4-triazol-1-yl)butan-2-yl]-1,3-thiazol-4-yl}benzonitrile (CCD ID: QKM) (formula: C₂₂H₁₇F₂N₅OS) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	S	
			31	22	2	5	1	1	0
3	B	1	Total	C	F	N	O	S	
			31	22	2	5	1	1	0
3	C	1	Total	C	F	N	O	S	
			31	22	2	5	1	1	0
3	D	1	Total	C	F	N	O	S	
			31	22	2	5	1	1	0
3	E	1	Total	C	F	N	O	S	
			31	22	2	5	1	1	0
3	F	1	Total	C	F	N	O	S	
			31	22	2	5	1	1	0

- Molecule 4 is FE (III) ION (CCD ID: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Fe		
			1	1	0	0
4	F	1	Total	Fe		
			1	1	0	0

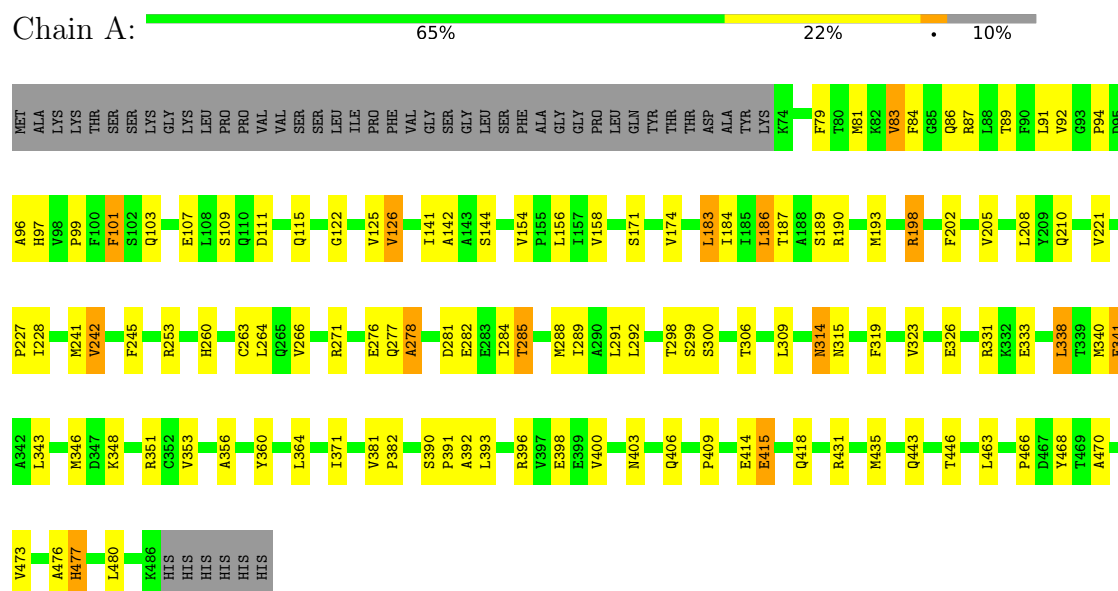
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	E	1	Total	O		
			1	1	0	0

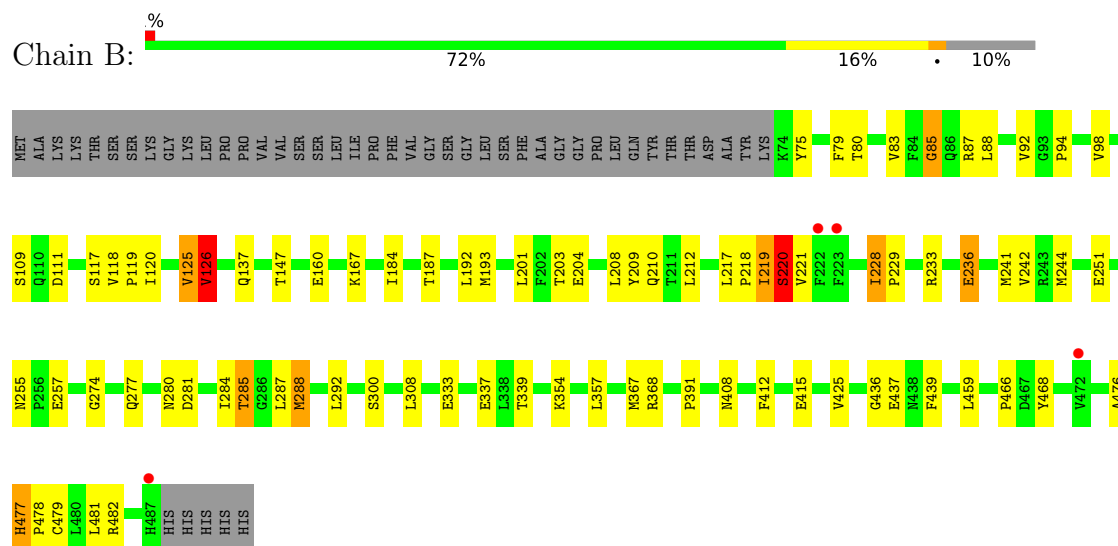
3 Residue-property plots

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.

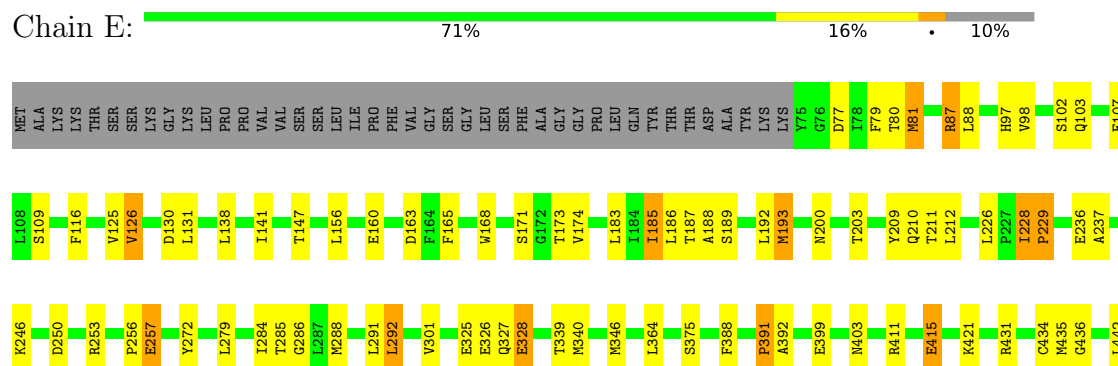
• Molecule 1: Obtusifoliol 14alphademethylase



• Molecule 1: Obtusifoliol 14alphademethylase



• Molecule 1: Obtusifoliol 14alphademethylase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	99.45Å 99.06Å 108.71Å 92.61° 96.20° 120.09°	Depositor
Resolution (Å)	107.35 – 2.93 107.35 – 2.93	Depositor EDS
% Data completeness (in resolution range)	94.0 (107.35-2.93) 93.9 (107.35-2.93)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.35 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.213 , 0.308 0.216 , 0.307	Depositor DCC
R_{free} test set	3622 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	90.4	Xtriage
Anisotropy	0.262	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 61.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.044 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	19999	wwPDB-VP
Average B, all atoms (Å ²)	101.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, QKM, FE

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	0.83	0/3333	1.11	7/4525 (0.2%)
1	B	0.80	0/3342	1.08	6/4536 (0.1%)
1	C	0.84	0/3337	1.08	9/4530 (0.2%)
1	D	0.82	0/3348	1.06	5/4541 (0.1%)
1	E	0.80	0/3334	1.01	0/4522
1	F	0.82	0/3338	1.08	6/4529 (0.1%)
All	All	0.82	0/20032	1.07	33/27183 (0.1%)

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
1	A	0	1
1	B	0	1
1	F	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	122	GLY	CA-C-N	7.10	127.50	119.83
1	A	122	GLY	C-N-CA	7.10	127.50	119.83
1	B	236	GLU	N-CA-C	-7.09	103.16	111.03
1	F	93	GLY	CA-C-N	6.63	127.17	119.47
1	F	93	GLY	C-N-CA	6.63	127.17	119.47

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	476	ALA	Peptide
1	B	476	ALA	Peptide
1	F	81	MET	Peptide

5.2 Too-close contacts

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	3253	0	3136	48	0
1	B	3262	0	3142	31	0
1	C	3256	0	3132	47	0
1	D	3268	0	3174	59	0
1	E	3255	0	3158	37	0
1	F	3258	0	3146	43	0
2	A	43	0	30	1	0
2	B	43	0	30	2	0
2	C	43	0	30	5	0
2	D	43	0	30	3	0
2	E	43	0	30	3	0
2	F	43	0	30	2	0
3	A	31	0	0	0	0
3	B	31	0	0	0	0
3	C	31	0	0	0	0
3	D	31	0	0	2	0
3	E	31	0	0	0	0
3	F	31	0	0	1	0
4	B	1	0	0	0	0
4	F	1	0	0	0	0
5	E	1	0	0	0	0
All	All	19999	0	19068	274	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 7.

The worst 5 of 274 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:364:LEU:HD21	1:D:473:VAL:HG21	1.57	0.87
1:A:309:LEU:HD23	1:A:463:LEU:HD11	1.64	0.79
1:A:245:PHE:CE1	1:A:288:MET:HE1	2.23	0.74
1:D:245:PHE:CD2	1:D:288:MET:HE1	2.24	0.71
2:D:501:HEM:HBC2	2:D:501:HEM:HMC2	1.71	0.71

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	411/460 (89%)	353 (86%)	47 (11%)	11 (3%)	4	11
1	B	412/460 (90%)	355 (86%)	46 (11%)	11 (3%)	4	11
1	C	412/460 (90%)	337 (82%)	64 (16%)	11 (3%)	4	11
1	D	412/460 (90%)	340 (82%)	61 (15%)	11 (3%)	4	11
1	E	411/460 (89%)	358 (87%)	46 (11%)	7 (2%)	7	20
1	F	411/460 (89%)	363 (88%)	37 (9%)	11 (3%)	4	11
All	All	2469/2760 (90%)	2106 (85%)	301 (12%)	62 (2%)	4	12

5 of 62 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	126	VAL
1	C	394	SER
1	C	404	ALA
1	C	405	ASP
1	D	466	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	336/397 (85%)	301 (90%)	35 (10%)	7	18
1	B	336/397 (85%)	307 (91%)	29 (9%)	10	24
1	C	334/397 (84%)	298 (89%)	36 (11%)	6	17
1	D	337/397 (85%)	311 (92%)	26 (8%)	12	28
1	E	337/397 (85%)	303 (90%)	34 (10%)	7	19
1	F	337/397 (85%)	312 (93%)	25 (7%)	13	30
All	All	2017/2382 (85%)	1832 (91%)	185 (9%)	8	22

5 of 185 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	331	ARG
1	E	210	GLN
1	D	399	GLU
1	E	102	SER
1	E	326	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	265	GLN
1	E	261	ASN
1	F	315	ASN
1	D	297	HIS
1	D	443	GLN

5.3.3 RNA ⓘ

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 14 ligands modelled in this entry, 2 are monoatomic - leaving 12 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	$\# Z > 2$
2	HEM	B	501	3,1	50,50,50	1.67	9 (18%)	67,82,82	1.55	13 (19%)
3	QKM	B	502	2	34,34,34	1.55	5 (14%)	46,49,49	2.29	22 (47%)
2	HEM	F	501	3,1	50,50,50	1.74	11 (22%)	67,82,82	1.49	11 (16%)
2	HEM	C	501	3,1	50,50,50	1.64	8 (16%)	67,82,82	1.96	12 (17%)
3	QKM	A	502	2	34,34,34	1.51	5 (14%)	46,49,49	2.21	17 (36%)
3	QKM	E	502	2	34,34,34	1.62	2 (5%)	46,49,49	1.72	11 (23%)
3	QKM	C	502	2	34,34,34	1.57	4 (11%)	46,49,49	1.76	10 (21%)
2	HEM	E	501	3,1	50,50,50	1.70	7 (14%)	67,82,82	1.68	16 (23%)
2	HEM	A	501	3,1	50,50,50	1.76	9 (18%)	67,82,82	1.70	16 (23%)
3	QKM	F	502	2	34,34,34	1.60	2 (5%)	46,49,49	1.49	7 (15%)
3	QKM	D	502	2	34,34,34	1.43	4 (11%)	46,49,49	1.85	8 (17%)
2	HEM	D	501	3,1	50,50,50	1.69	8 (16%)	67,82,82	1.81	12 (17%)

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
2	HEM	B	501	3,1	-	0/14/54/54	-
3	QKM	B	502	2	-	6/25/27/27	0/4/4/4
2	HEM	F	501	3,1	-	2/14/54/54	-
2	HEM	C	501	3,1	-	6/14/54/54	-
3	QKM	A	502	2	-	9/25/27/27	0/4/4/4
3	QKM	E	502	2	-	7/25/27/27	0/4/4/4
3	QKM	C	502	2	-	7/25/27/27	0/4/4/4
2	HEM	E	501	3,1	-	2/14/54/54	-
2	HEM	A	501	3,1	-	2/14/54/54	-
3	QKM	F	502	2	-	3/25/27/27	0/4/4/4
3	QKM	D	502	2	-	4/25/27/27	0/4/4/4
2	HEM	D	501	3,1	-	4/14/54/54	-

The worst 5 of 74 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	502	QKM	CA-N	6.93	1.51	1.39
3	F	502	QKM	CA-N	6.87	1.51	1.39
3	C	502	QKM	CA-N	6.00	1.49	1.39
3	A	502	QKM	CA-N	6.00	1.49	1.39
3	D	502	QKM	CA-N	5.99	1.49	1.39

The worst 5 of 155 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	501	HEM	CAD-C3D-C4D	6.37	135.80	124.70
2	D	501	HEM	CAD-C3D-C4D	6.35	135.77	124.70
3	D	502	QKM	C7-CB-CA	-5.69	114.50	120.87
3	A	502	QKM	OH-CZ-CE1	-5.64	100.64	110.64
3	A	502	QKM	C7-CB-CA	-5.38	114.84	120.87

There are no chirality outliers.

5 of 52 torsion outliers are listed below:

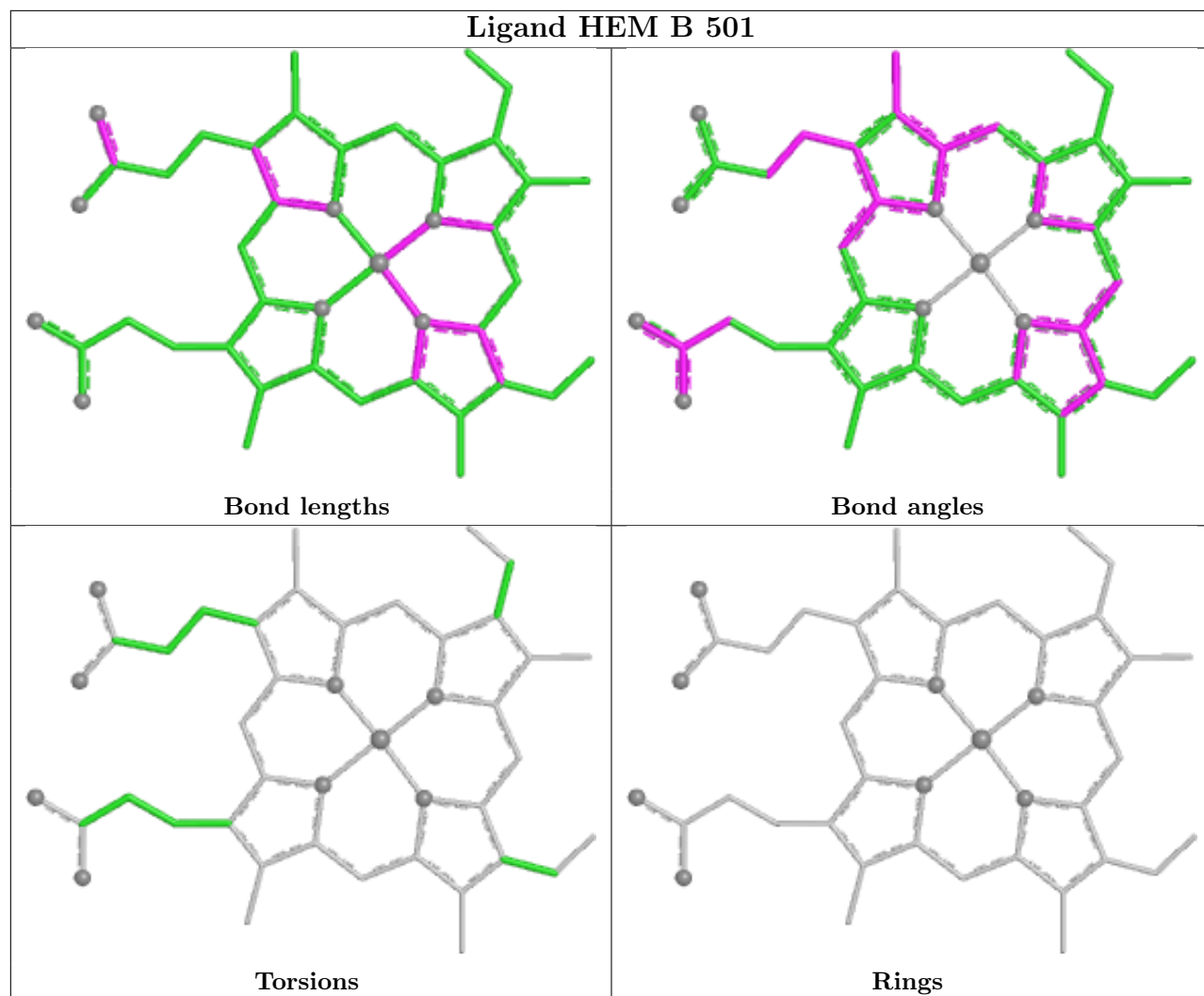
Mol	Chain	Res	Type	Atoms
2	C	501	HEM	C2D-C3D-CAD-CBD
2	C	501	HEM	C4D-C3D-CAD-CBD
2	D	501	HEM	C2D-C3D-CAD-CBD
2	D	501	HEM	C4D-C3D-CAD-CBD
3	A	502	QKM	N-CA-CB-C7

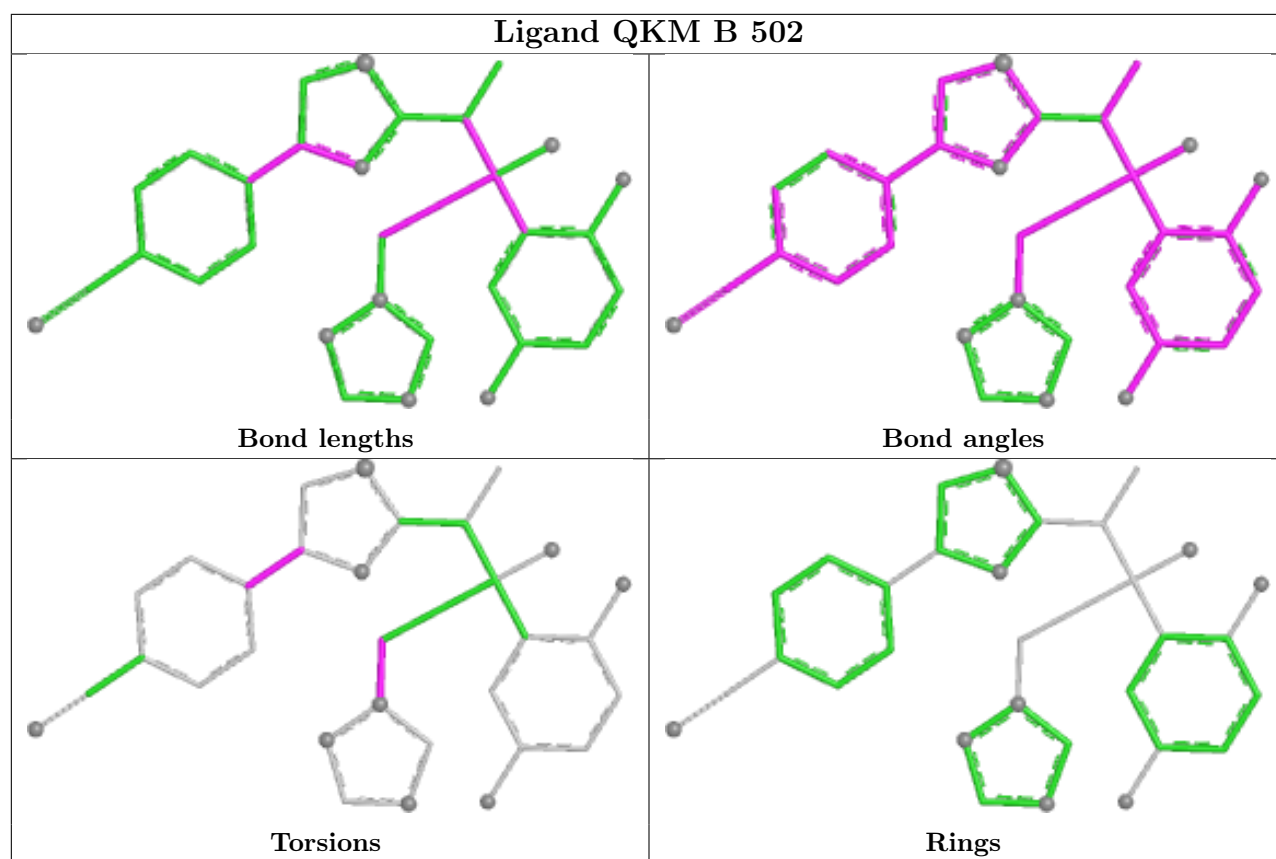
There are no ring outliers.

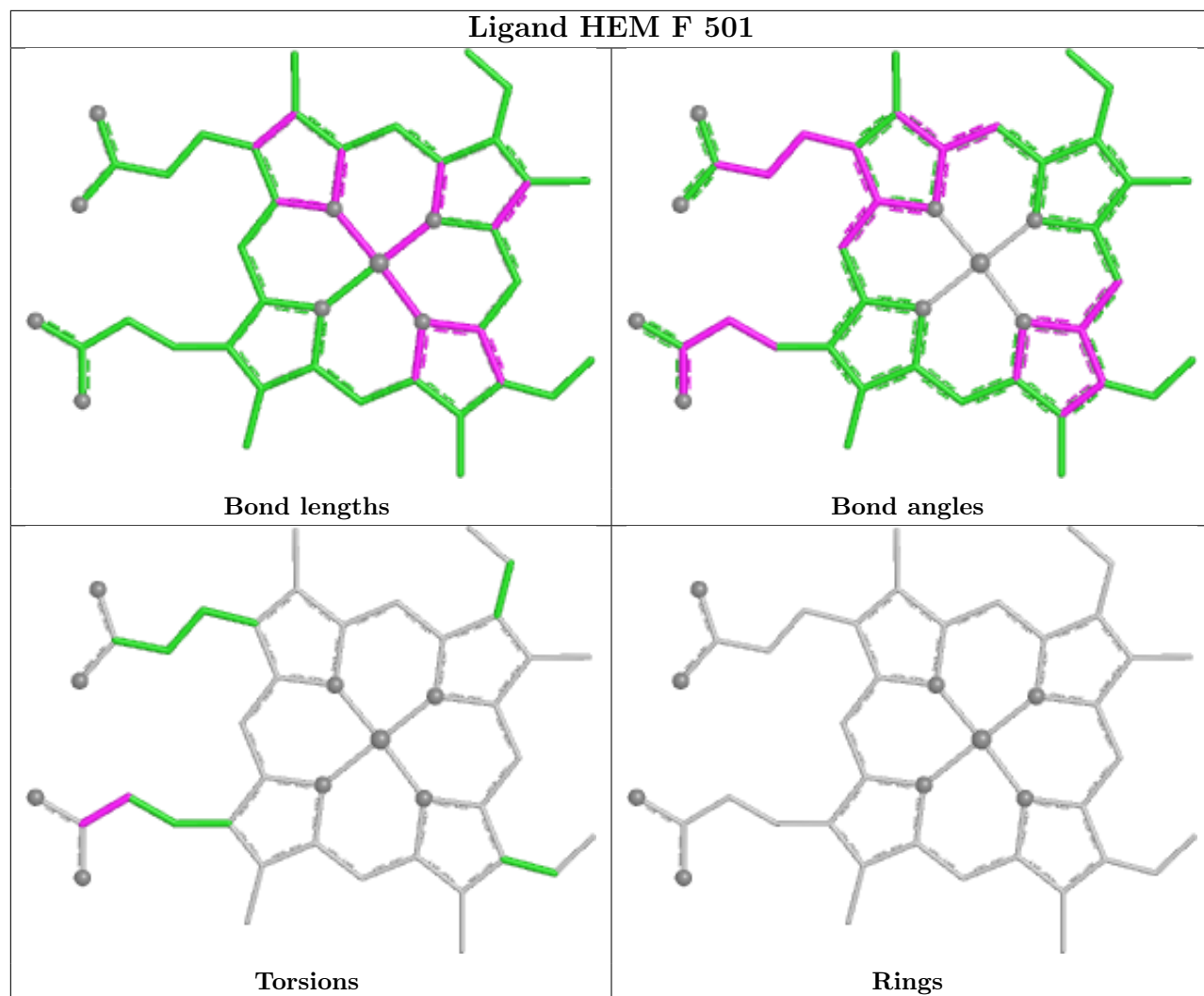
8 monomers are involved in 19 short contacts:

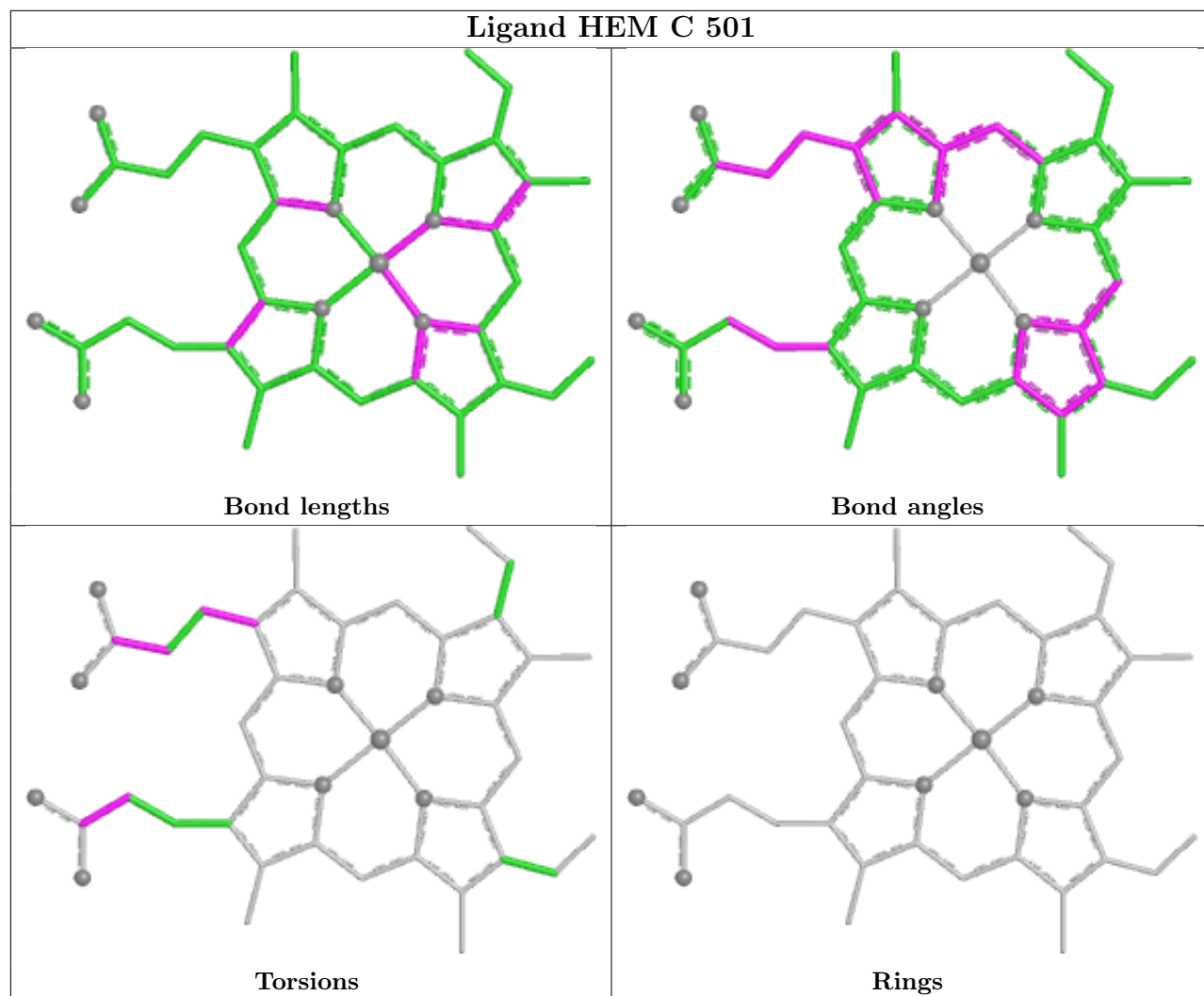
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	HEM	2	0
2	F	501	HEM	2	0
2	C	501	HEM	5	0
2	E	501	HEM	3	0
2	A	501	HEM	1	0
3	F	502	QKM	1	0
3	D	502	QKM	2	0
2	D	501	HEM	3	0

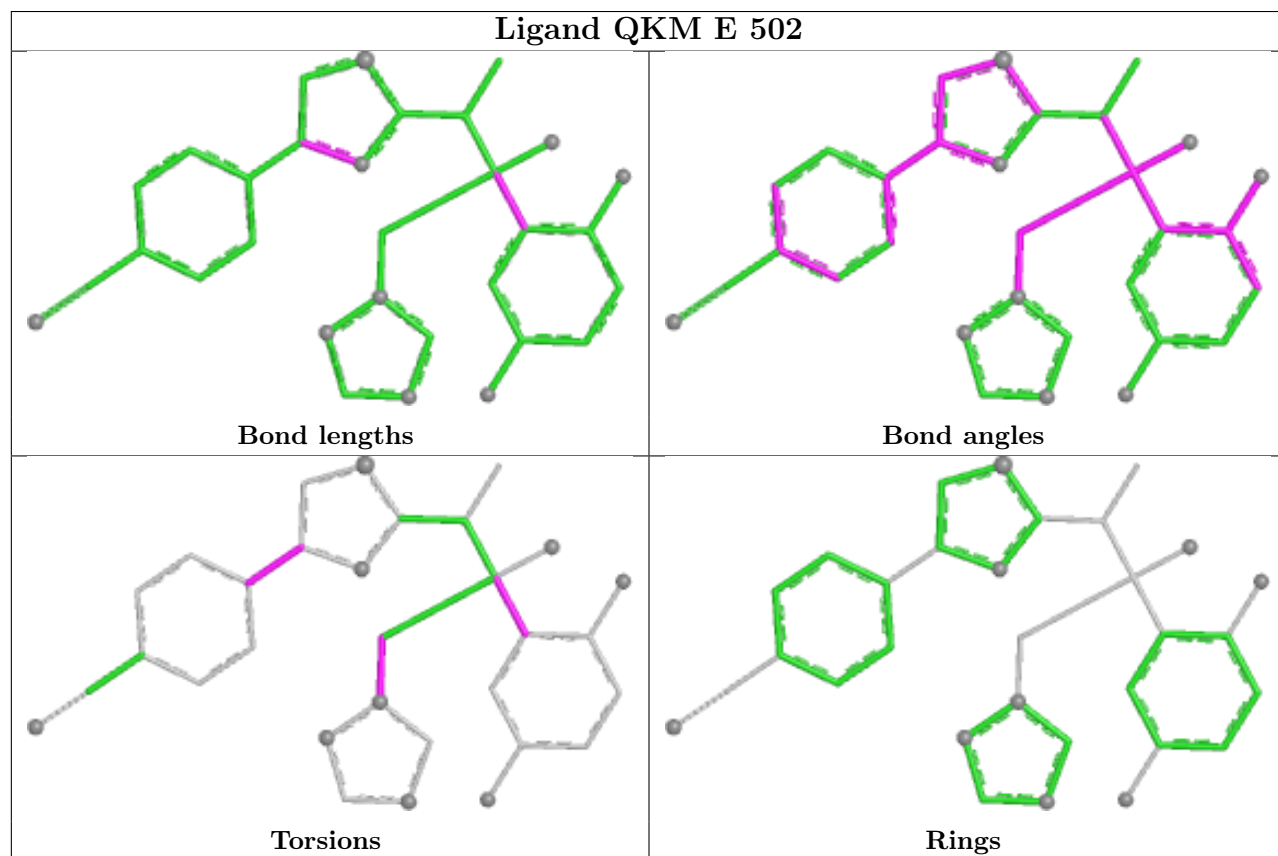
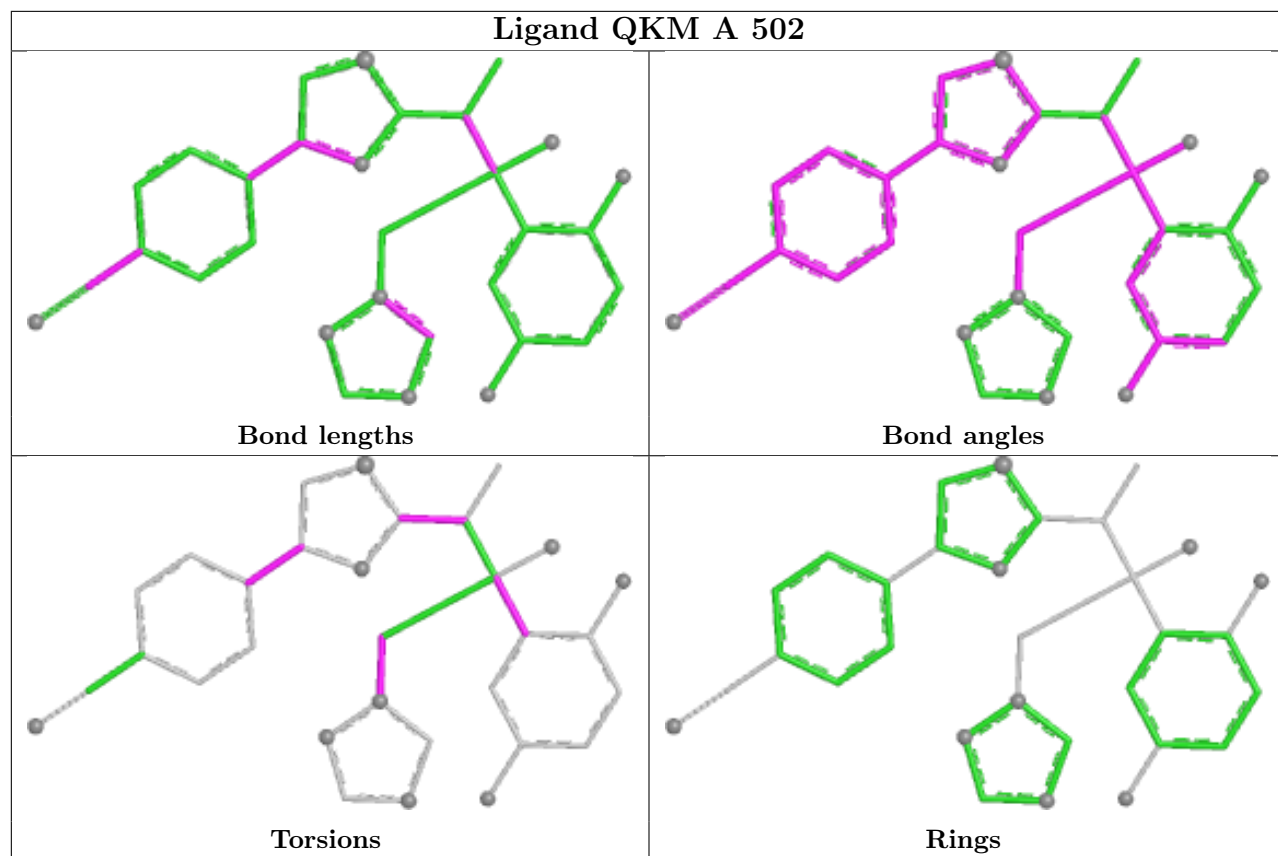
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

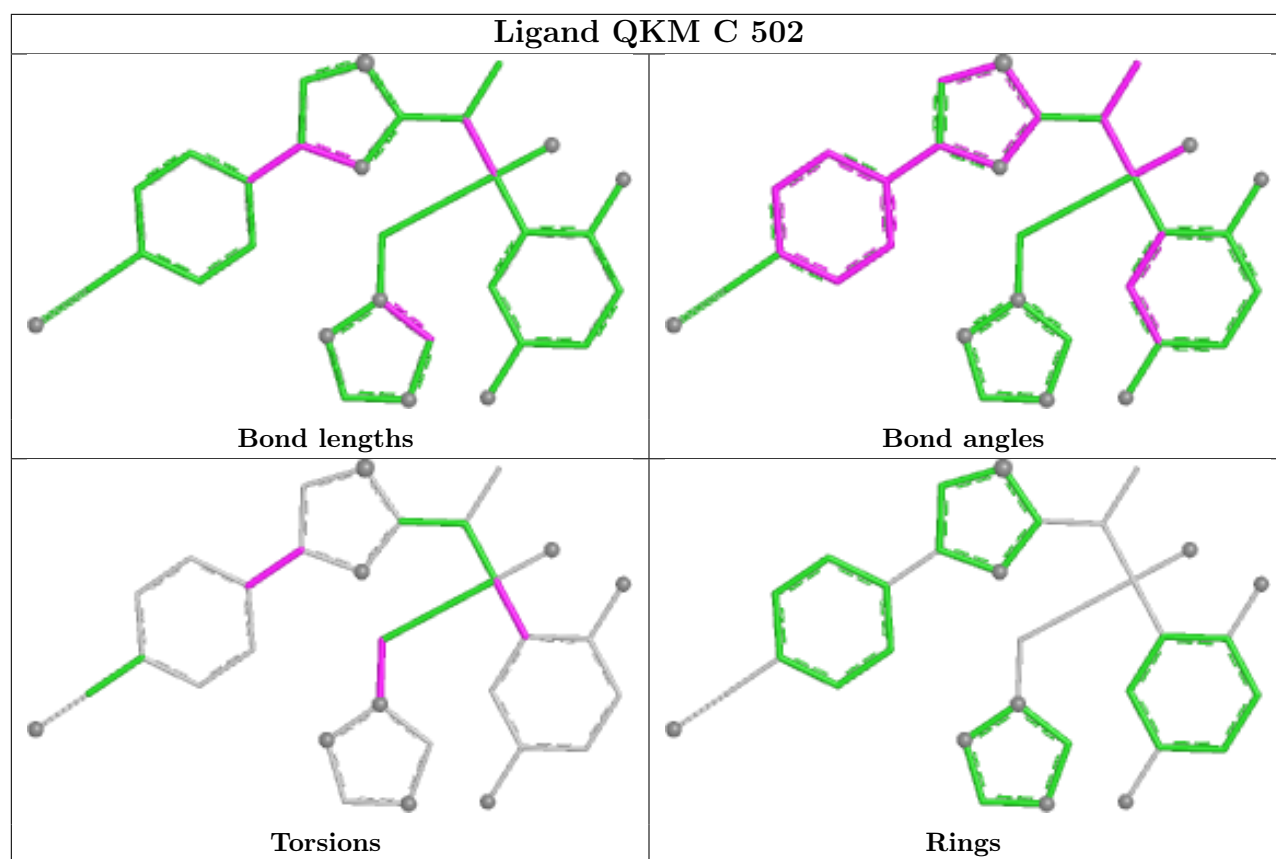


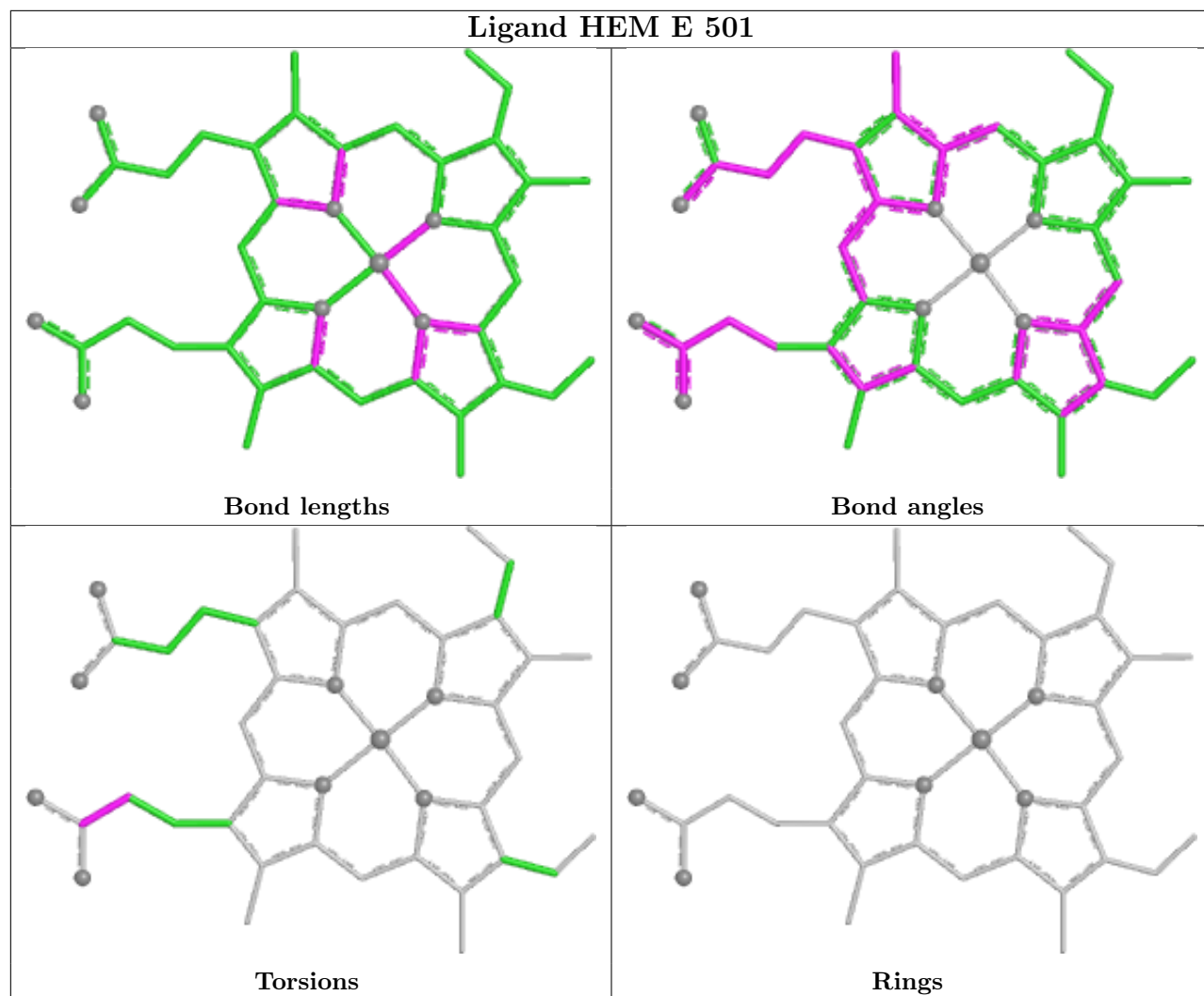


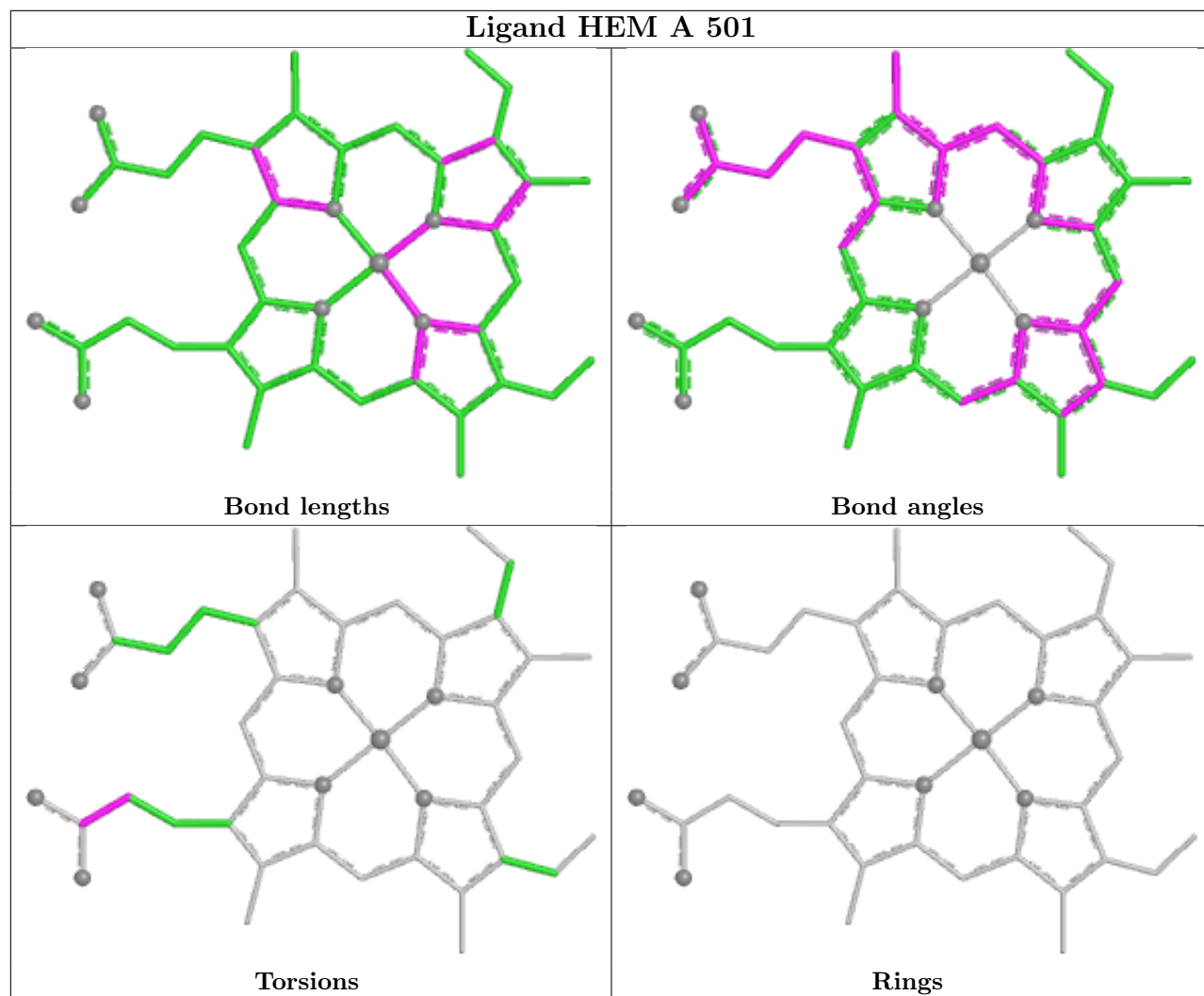


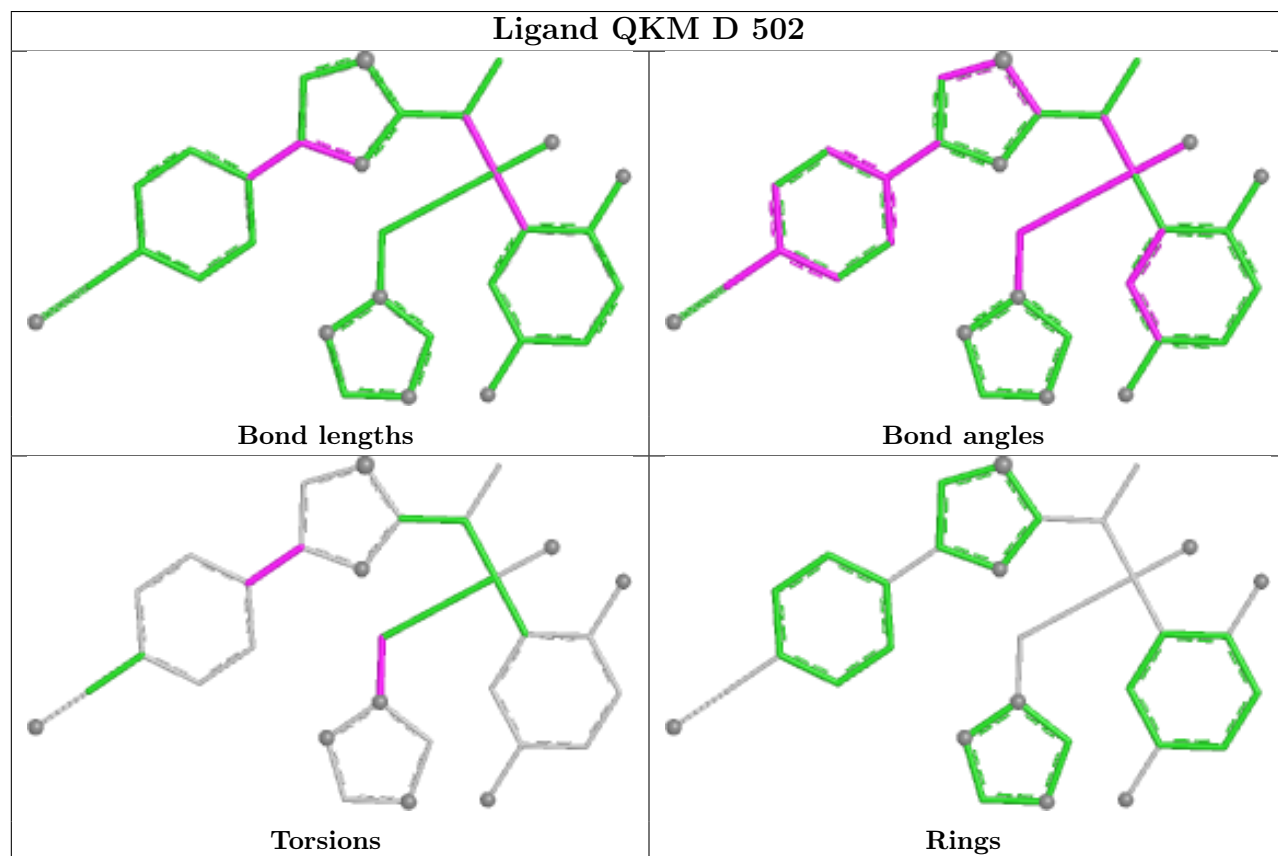
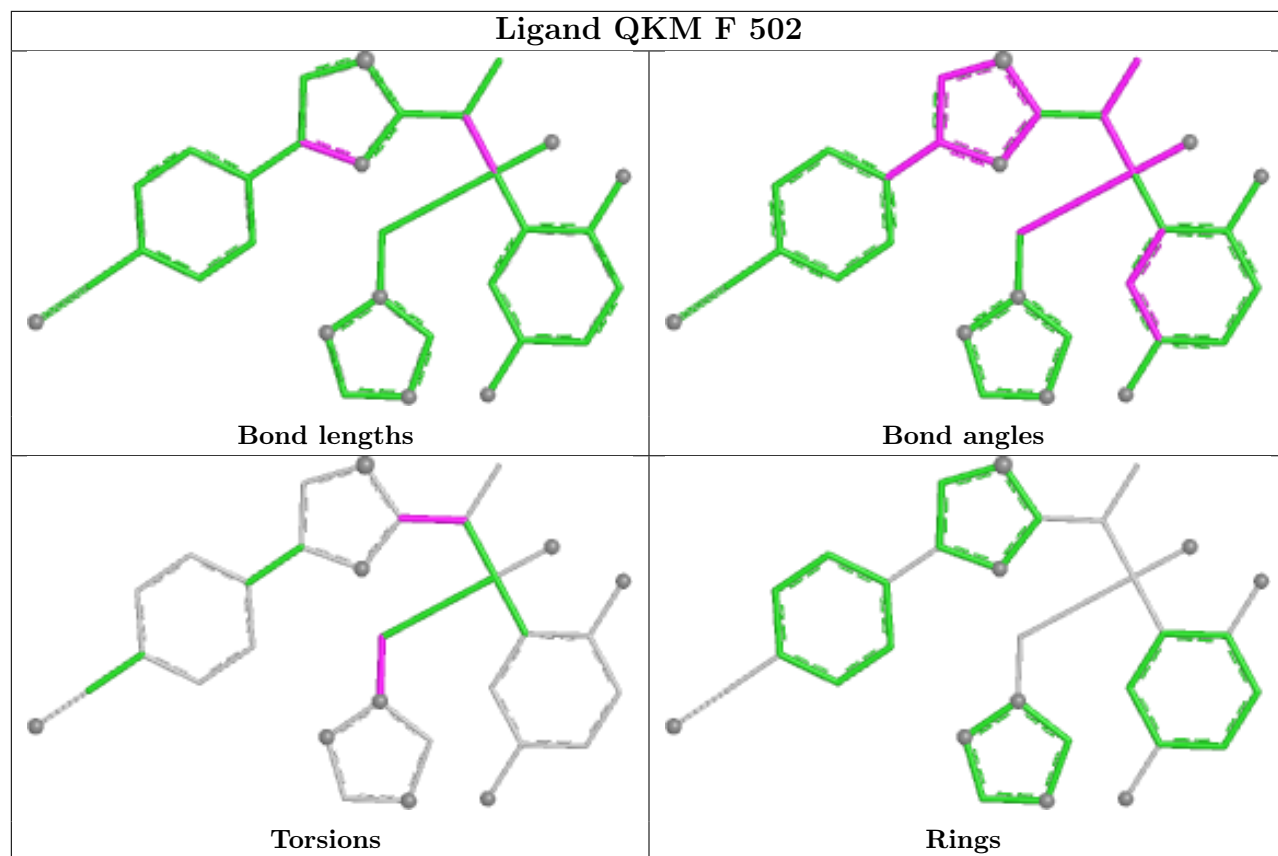


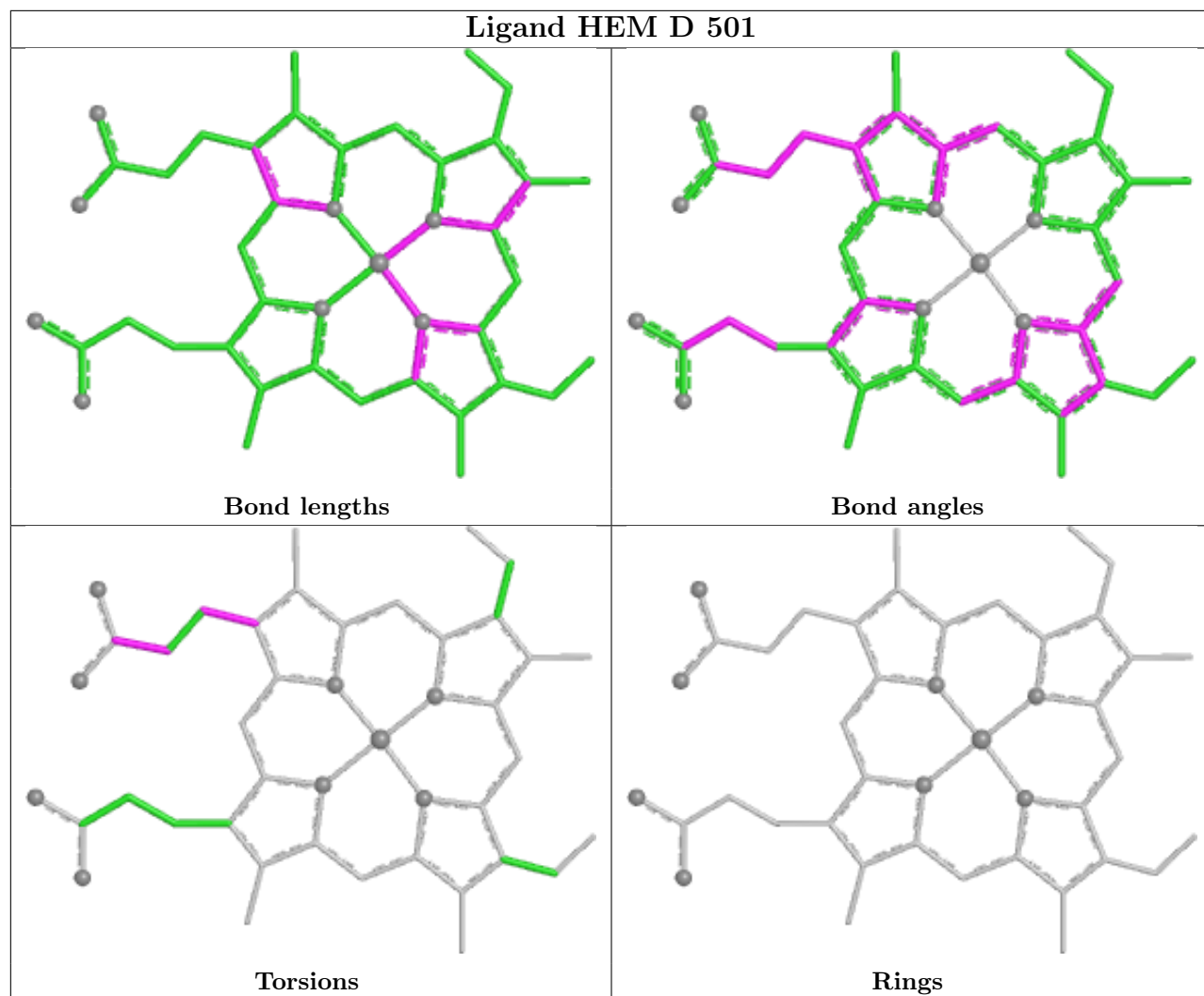












5.7 Other polymers [i](#)

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](#)

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, 95th 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 ²)	Q<0.9
1	A	413/460 (89%)	-0.40	0 100 100	57, 90, 132, 155	0
1	B	414/460 (90%)	-0.38	4 (0%) 79 74	58, 96, 132, 163	0
1	C	414/460 (90%)	-0.27	3 (0%) 84 79	59, 100, 145, 175	0
1	D	414/460 (90%)	-0.25	2 (0%) 87 83	66, 106, 145, 200	0
1	E	413/460 (89%)	-0.29	1 (0%) 91 89	63, 106, 155, 176	0
1	F	413/460 (89%)	-0.43	0 100 100	56, 93, 129, 172	0
All	All	2481/2760 (89%)	-0.34	10 (0%) 88 86	56, 98, 142, 200	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	223	PHE	3.1
1	B	472	VAL	3.1
1	D	487	HIS	3.0
1	C	380	TYR	2.9
1	B	487	HIS	2.8

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

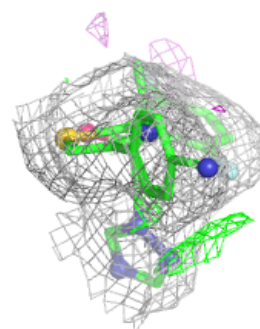
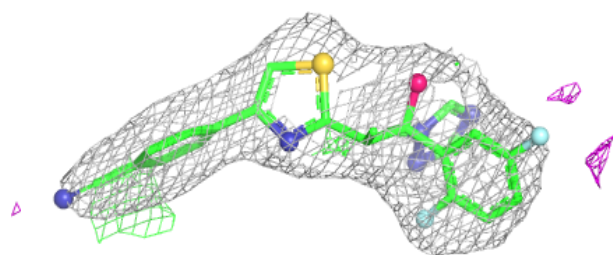
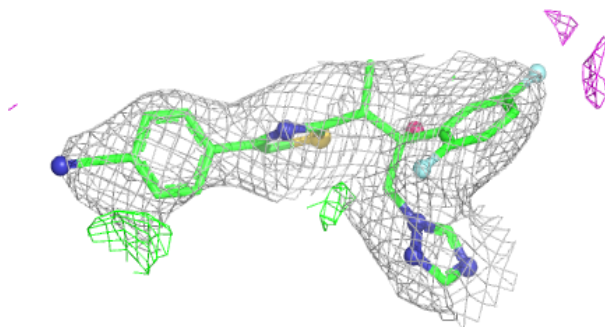
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	QKM	E	502	31/31	0.94	0.10	61,88,101,109	0
3	QKM	B	502	31/31	0.95	0.10	60,70,115,126	0
3	QKM	C	502	31/31	0.95	0.09	64,74,103,112	0
3	QKM	A	502	31/31	0.95	0.08	57,71,86,116	0
3	QKM	D	502	31/31	0.96	0.09	75,83,95,106	0
3	QKM	F	502	31/31	0.97	0.07	46,64,91,108	0
2	HEM	B	501	43/43	0.98	0.06	46,62,76,83	0
2	HEM	C	501	43/43	0.98	0.07	56,64,79,99	0
2	HEM	D	501	43/43	0.98	0.06	52,62,86,103	0
2	HEM	E	501	43/43	0.98	0.07	60,68,84,99	0
2	HEM	A	501	43/43	0.98	0.07	57,64,85,100	0
2	HEM	F	501	43/43	0.99	0.06	37,66,82,88	0
4	FE	B	503	1/1	0.99	0.07	76,76,76,76	0
4	FE	F	503	1/1	0.99	0.06	80,80,80,80	0

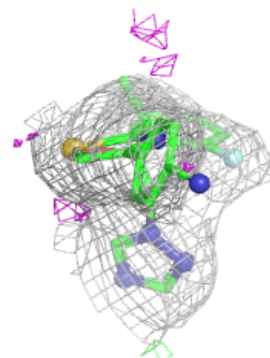
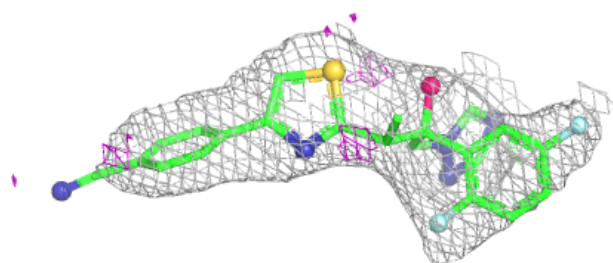
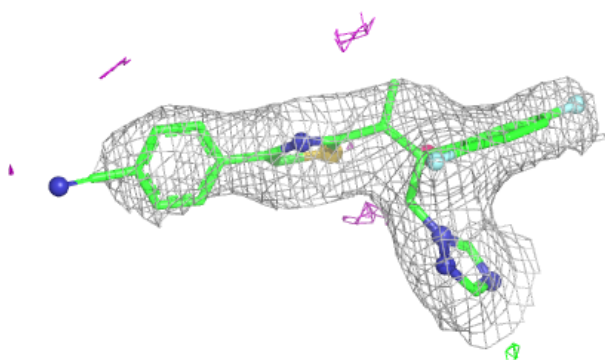
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around QKM E 502:

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

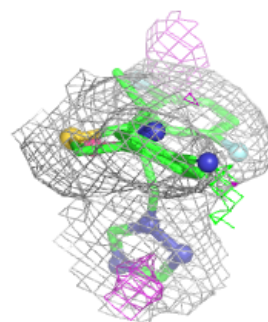
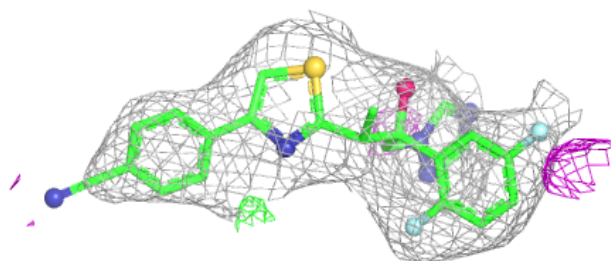
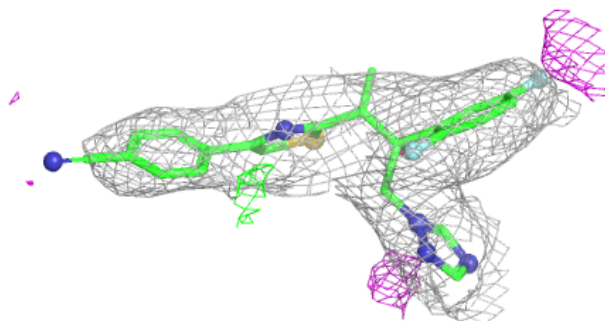
**Electron density around QKM B 502:**

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

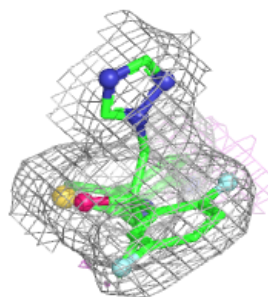
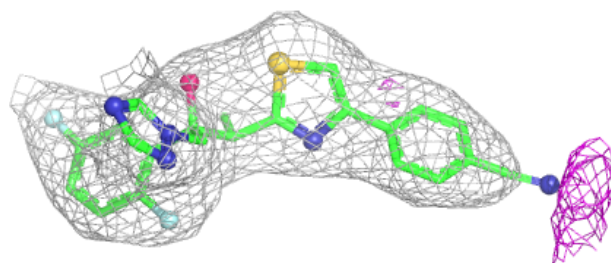
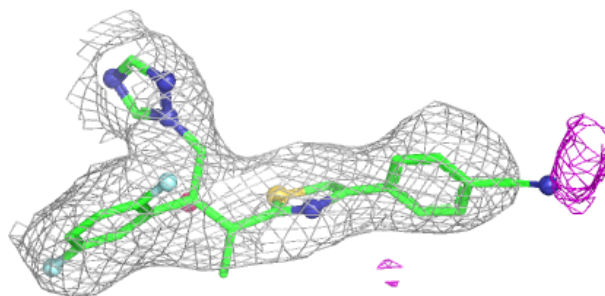


Electron density around QKM C 502:

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

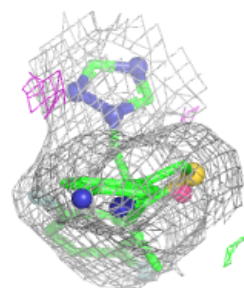
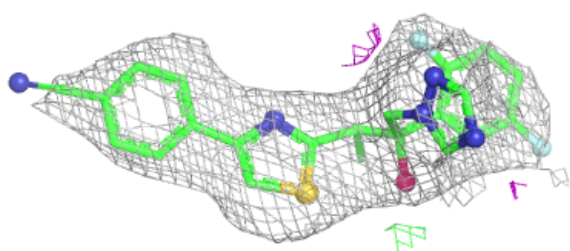
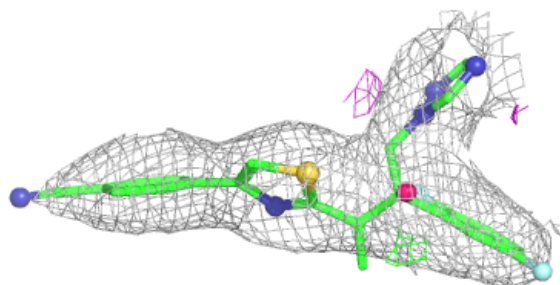
**Electron density around QKM A 502:**

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

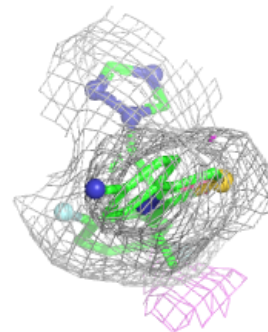
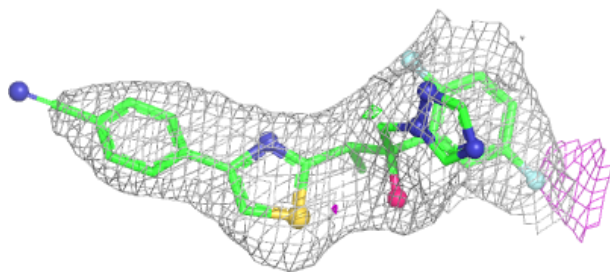
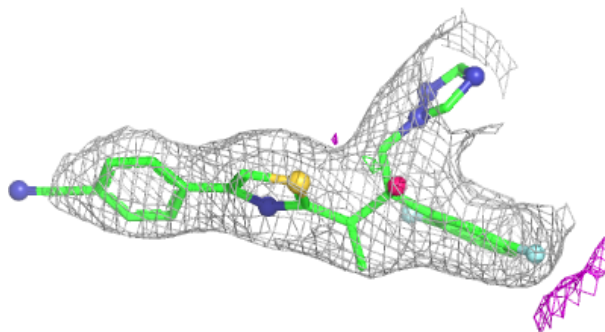


Electron density around QKM D 502:

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

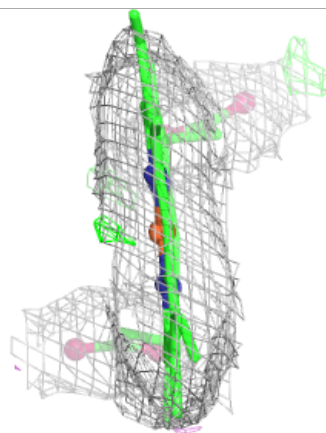
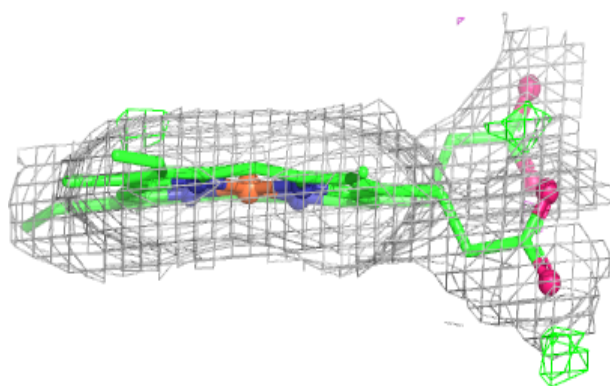
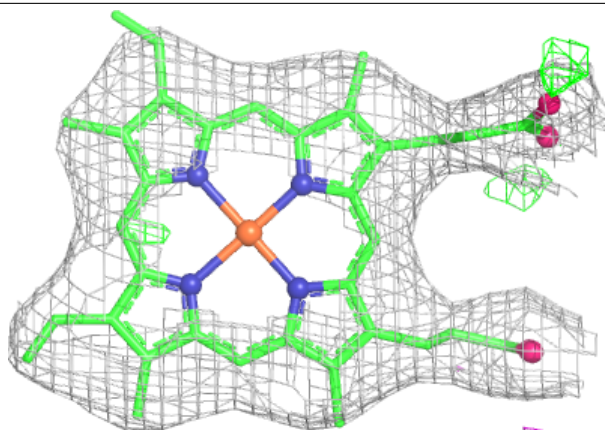
**Electron density around QKM F 502:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



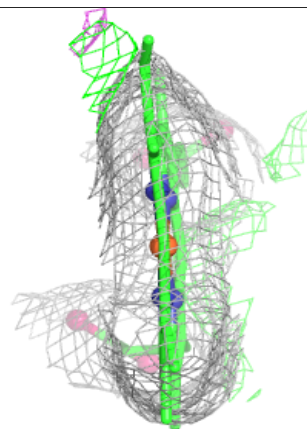
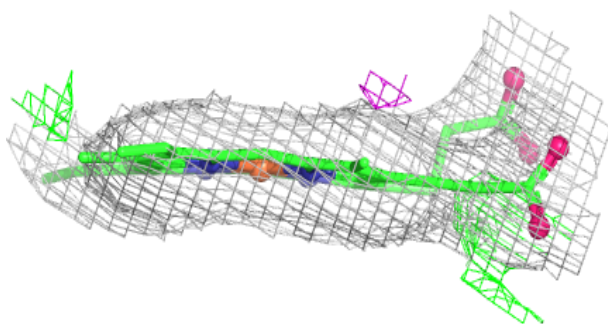
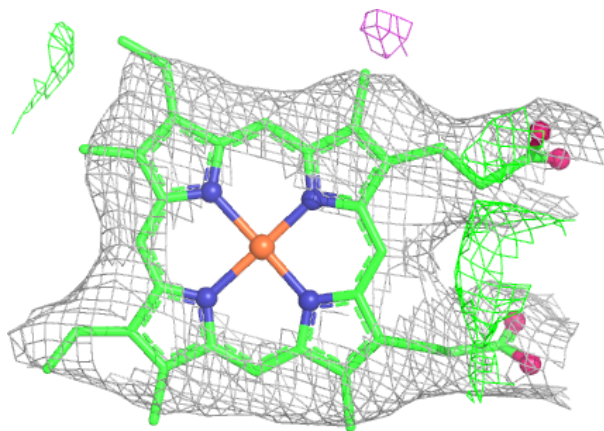
Electron density around HEM B 501:

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



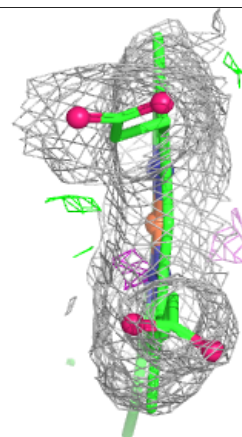
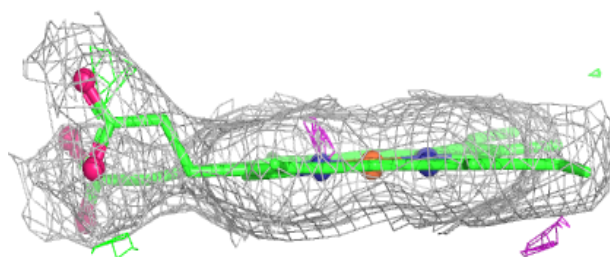
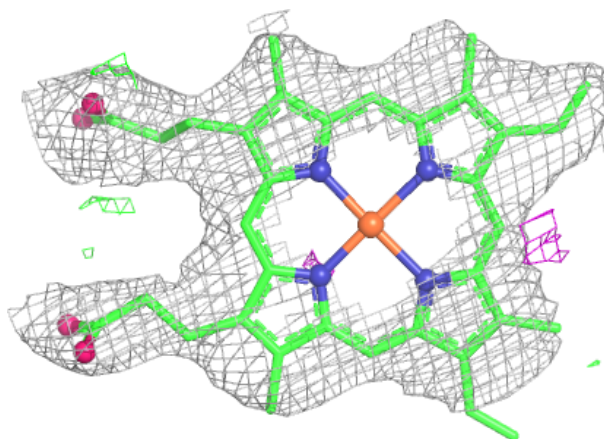
Electron density around HEM C 501:

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



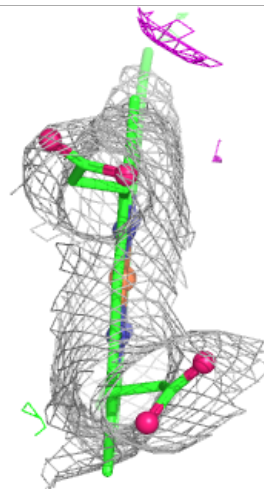
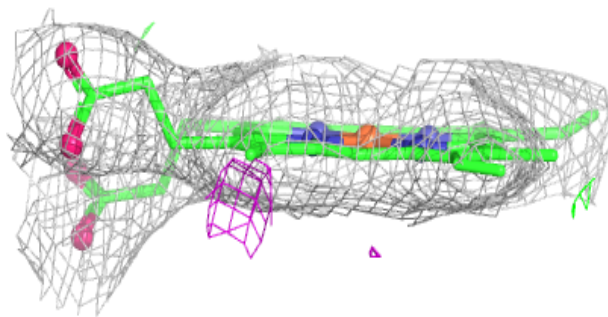
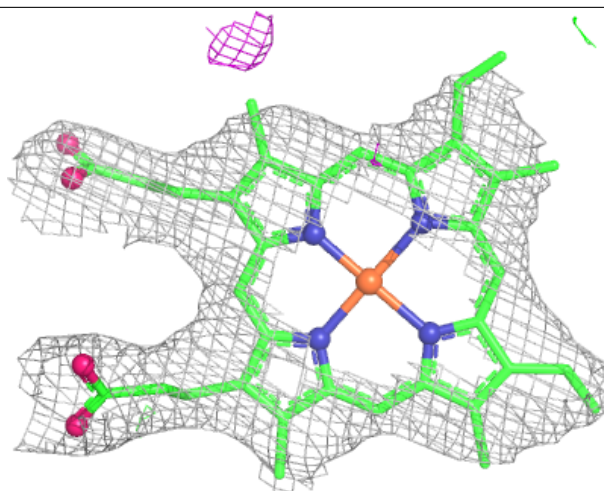
Electron density around HEM D 501:

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



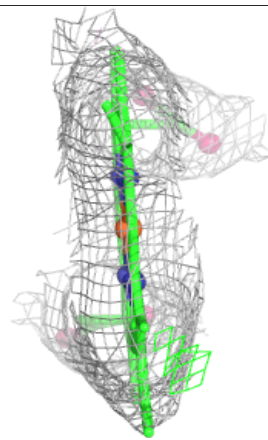
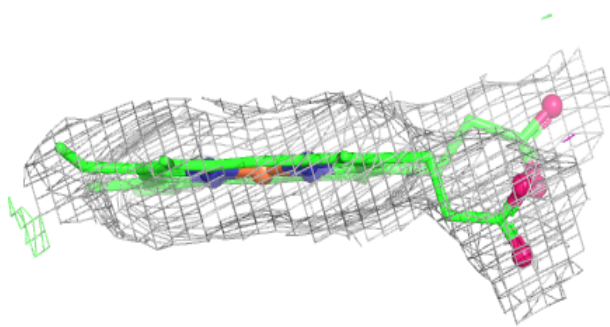
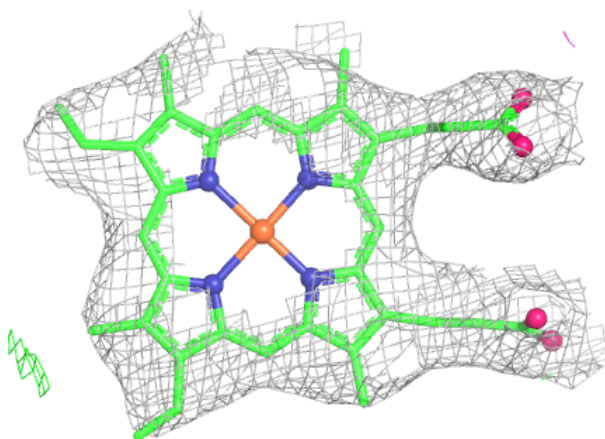
Electron density around HEM E 501:

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



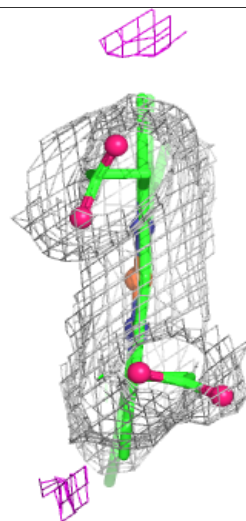
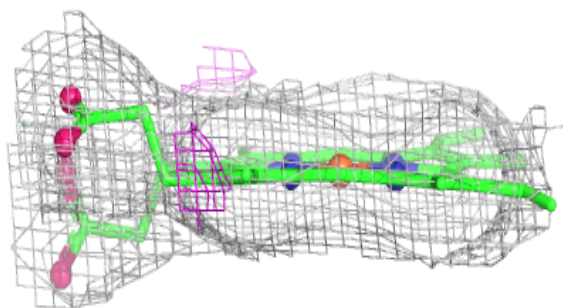
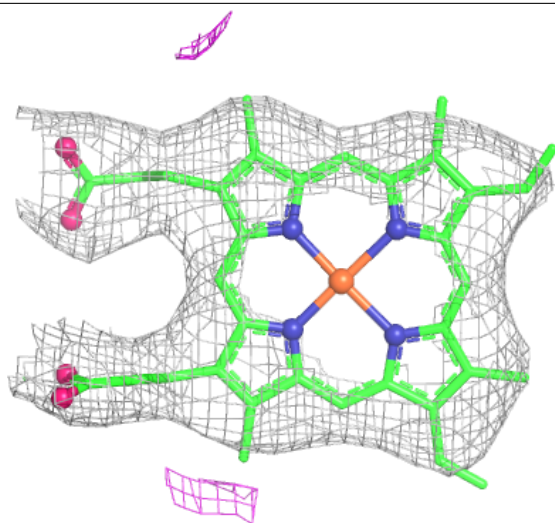
Electron density around HEM A 501:

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



Electron density around HEM F 501:

$2mF_o-DF_c$ (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.