



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 15, 2024 – 07:21 pm GMT

PDB ID : 6ZFU
Title : Crystal structure of bovine cytochrome bc1 in complex with quinolone inhibitor RKA066
Authors : Amporndanai, K.; O'Neill, P.M.; Hong, W.D.; Amewu, R.K.; Pidathala, C.; Berry, N.G.; Biagini, G.A.; Leung, S.C.; Hasnain, S.S.; Antonyuk, S.V.
Deposited on : 2020-06-17
Resolution : 3.50 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

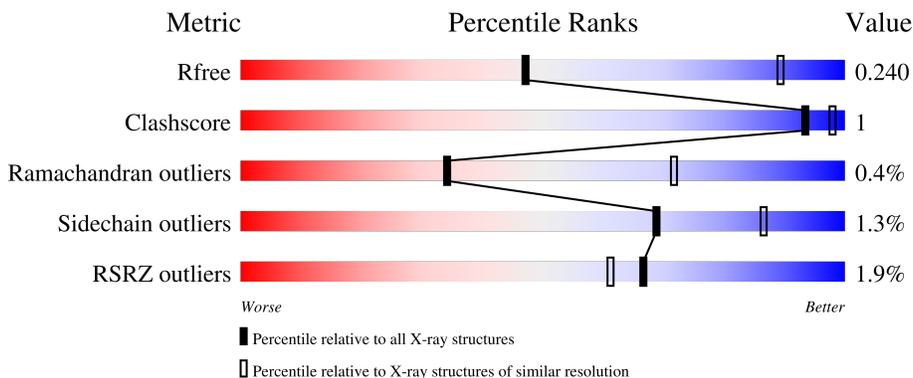
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

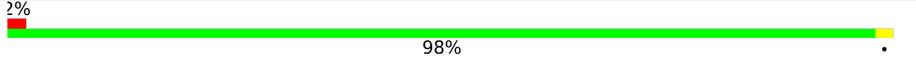
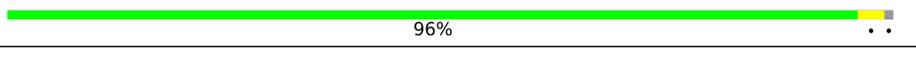
The reported resolution of this entry is 3.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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	444	 2% 98%
2	B	420	 96%
3	C	378	 93% 7%
4	D	239	 4% 96%

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Mol	Chain	Length	Quality of chain
5	E	196	 %
6	F	99	 %
7	G	74	 3%
8	H	65	 11%
9	I	46	 2%
10	J	59	 3%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
11	PG4	C	404	-	-	-	X
11	PG4	C	405	-	-	-	X
16	PEE	C	407	X	-	-	-
16	PEE	E	203	X	-	-	-
19	PO4	D	502	-	-	-	X
19	PO4	F	501	-	-	-	X
19	PO4	G	102	-	-	-	X

2 Entry composition [i](#)

There are 22 unique types of molecules in this entry. The entry contains 16290 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 Cytochrome b-c1 complex subunit 1, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	444	3417	2133	603	661	20	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	226	GLU	ASP	conflict	UNP P31800
A	227	THR	ALA	conflict	UNP P31800

- Molecule 2 is a protein called Cytochrome b-c1 complex subunit 2, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	415	3106	1952	550	597	7	0	0	0

- Molecule 3 is a protein called Cytochrome b.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	378	2990	2004	468	500	18	0	0	0

- Molecule 4 is a protein called Cytochrome c1, heme protein, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	239	1872	1198	321	338	15	0	0	0

- Molecule 5 is a protein called Cytochrome b-c1 complex subunit Rieske, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	E	196	1509	950	263	288	8	0	0	0

- Molecule 6 is a protein called Cytochrome b-c1 complex subunit 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	F	99	859	545	157	155	2	0	0	0

- Molecule 7 is a protein called Cytochrome b-c1 complex subunit 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
7	G	74	616	403	115	97	1	0	0	0

- Molecule 8 is a protein called Cytochrome b-c1 complex subunit 6, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
8	H	65	507	307	93	102	5	0	0	0

- Molecule 9 is a protein called Cytochrome b-c1 complex subunit Rieske, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
9	I	46	332	206	61	64	1	0	0	0

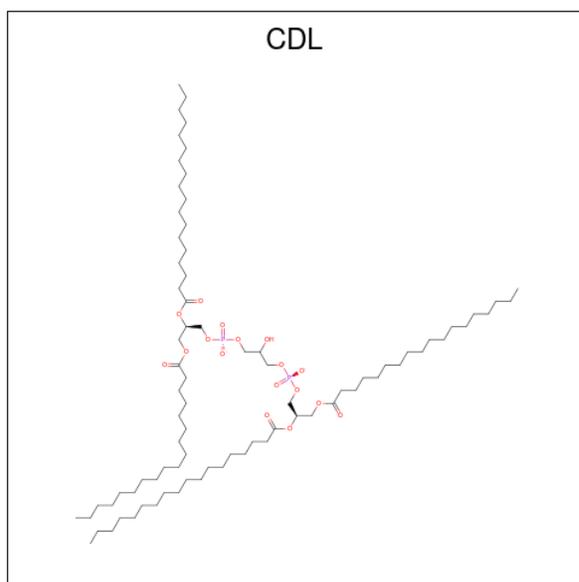
- Molecule 10 is a protein called Cytochrome b-c1 complex subunit 9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
10	J	59	480	314	83	83	0	0	0

- Molecule 11 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C₈H₁₈O₅).

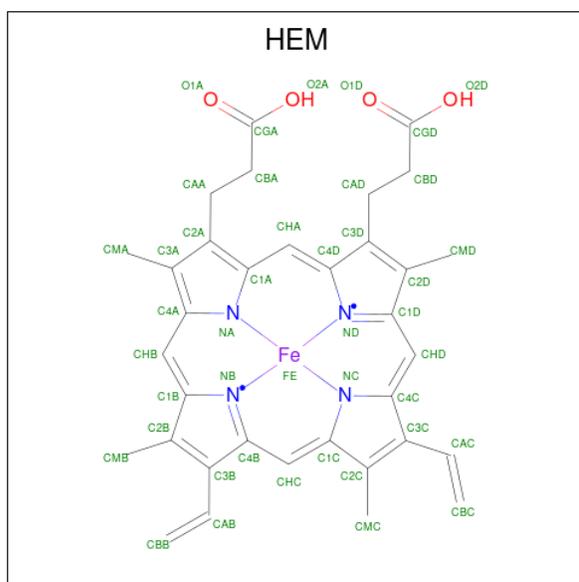
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
12	A	1	23	13	1	8	1	0	0

- Molecule 13 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



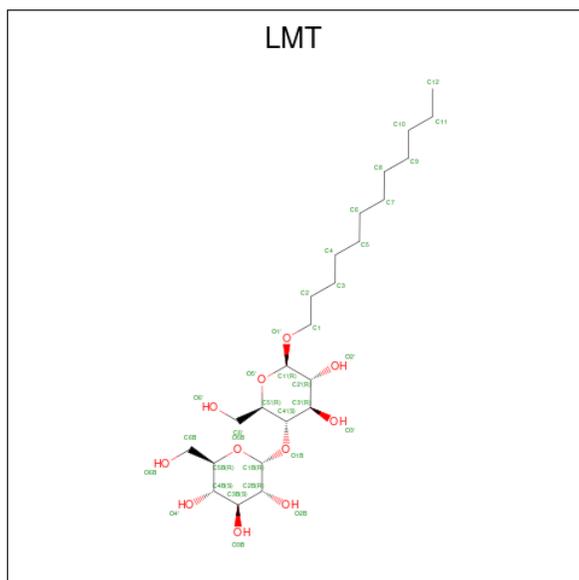
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
13	A	1	34	17	15	2	0	0
13	C	1	44	25	17	2	0	0
13	D	1	54	35	17	2	0	0
13	E	1	60	41	17	2	0	0

- Molecule 14 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).

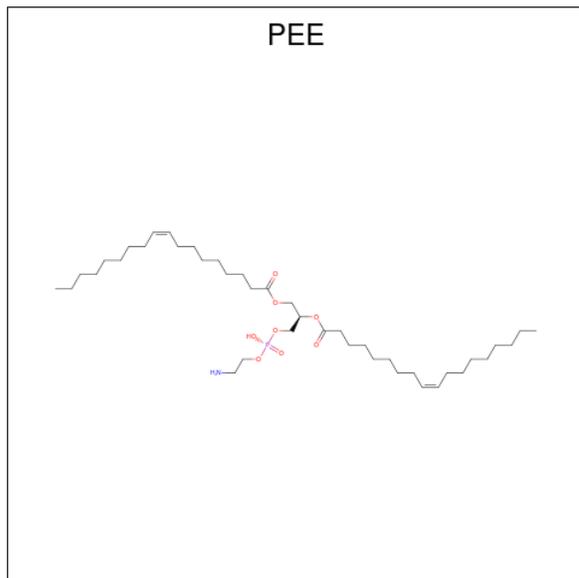


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
14	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
14	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 15 is DODECYL-BETA-D-MALTOSE (three-letter code: LMT) (formula: $C_{24}H_{46}O_{11}$).

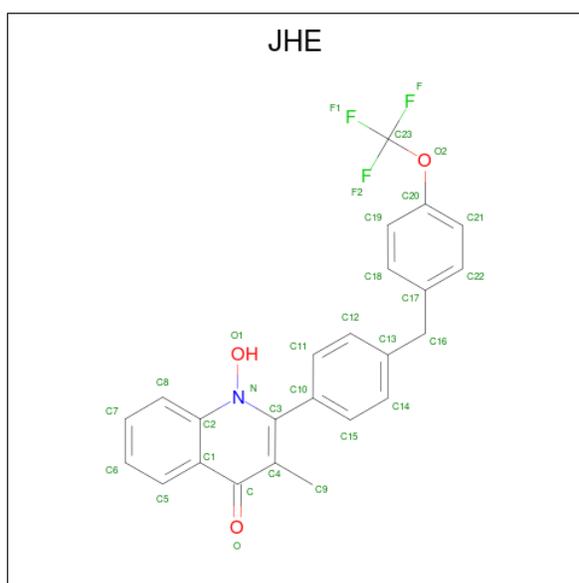


- Molecule 16 is 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (three-letter code: PEE) (formula: $C_{41}H_{78}NO_8P$).



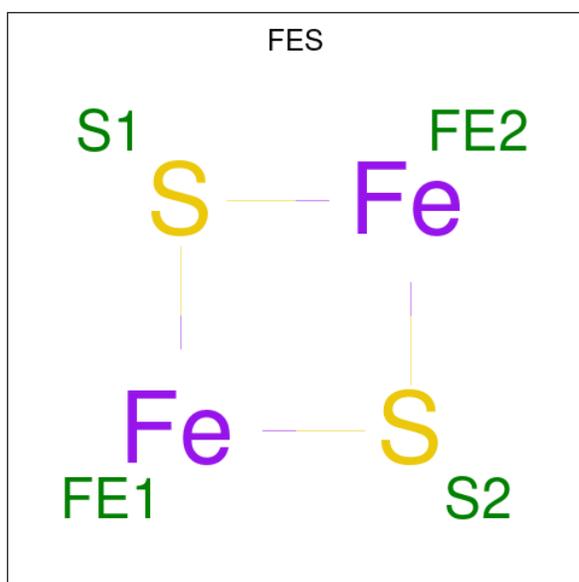
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	N	O	P			
16	C	1	Total	40	30	1	8	1	0	0
16	E	1	Total	41	31	1	8	1	0	0

- Molecule 17 is 3-methyl-1-oxidanyl-2-[4-[[4-(trifluoromethoxy)phenyl]methyl]phenyl]quinolin-4-one (three-letter code: JHE) (formula: $C_{24}H_{18}F_3NO_3$) (labeled as "Ligand of Interest" by depositor).



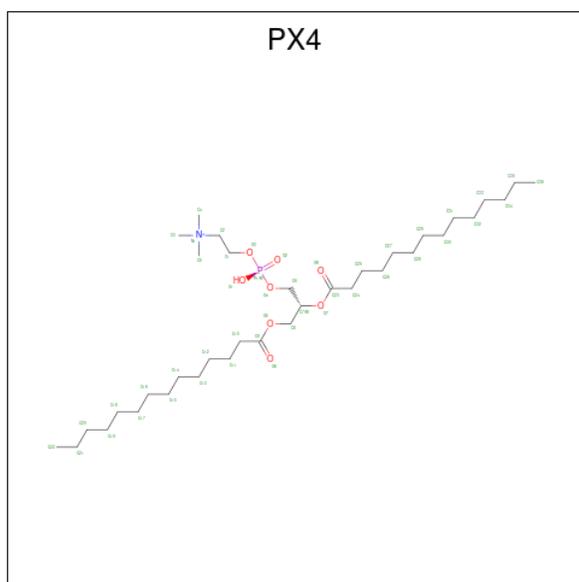
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
19	D	1	Total O P 5 4 1	0	0
19	F	1	Total O P 5 4 1	0	0
19	G	1	Total O P 5 4 1	0	0
19	G	1	Total O P 5 4 1	0	0
19	G	1	Total O P 5 4 1	0	0

- Molecule 20 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



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

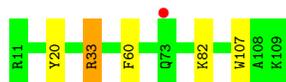
- Molecule 21 is 1,2-DIMYRISTOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: PX4) (formula: C₃₆H₇₃NO₈P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
21	E	1	37	27	1	8	1	0	0

- Molecule 22 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
22	A	3	Total O 3 3	0	0
22	C	1	Total O 1 1	0	0
22	G	1	Total O 1 1	0	0
22	I	1	Total O 1 1	0	0



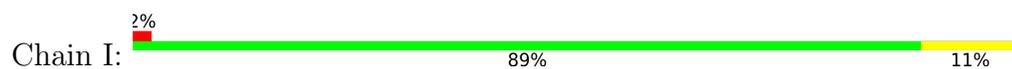
- Molecule 7: Cytochrome b-c1 complex subunit 8



- Molecule 8: Cytochrome b-c1 complex subunit 6, mitochondrial



- Molecule 9: Cytochrome b-c1 complex subunit Rieske, mitochondrial



- Molecule 10: Cytochrome b-c1 complex subunit 9



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	210.74Å 210.74Å 343.94Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	89.85 – 3.50 89.85 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.9 (89.85-3.50) 99.9 (89.85-3.50)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.41 (at 3.49Å)	Xtrriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.221 , 0.238 0.225 , 0.240	Depositor DCC
R_{free} test set	2924 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	96.2	Xtrriage
Anisotropy	0.215	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 124.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	16290	wwPDB-VP
Average B, all atoms (Å ²)	140.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.99% 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: PEE, CDL, HEM, PX4, PG4, PO4, FES, LMT, HEC, 6PE, JHE

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	0.46	0/3488	0.69	0/4738
2	B	0.47	0/3163	0.66	0/4292
3	C	0.49	0/3086	0.66	0/4224
4	D	0.46	0/1931	0.69	0/2627
5	E	0.50	0/1542	0.67	0/2085
6	F	0.50	0/878	0.70	0/1181
7	G	0.54	0/637	0.70	0/864
8	H	0.45	0/512	0.72	0/692
9	I	0.63	0/336	0.95	0/457
10	J	0.51	0/493	0.65	0/667
All	All	0.48	0/16066	0.68	0/21827

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	3417	0	3296	6	0
2	B	3106	0	3074	5	0
3	C	2990	0	3047	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	1872	0	1785	11	0
5	E	1509	0	1495	2	0
6	F	859	0	838	3	0
7	G	616	0	613	2	0
8	H	507	0	468	0	0
9	I	332	0	345	2	0
10	J	480	0	467	0	0
11	A	13	0	18	0	0
11	C	26	0	36	0	0
12	A	23	0	19	2	0
13	A	34	0	24	3	0
13	C	44	0	32	0	0
13	D	54	0	52	0	0
13	E	60	0	64	1	0
14	C	86	0	60	6	0
15	C	35	0	46	0	0
16	C	40	0	54	0	0
16	E	41	0	59	1	0
17	C	31	0	0	0	0
18	D	43	0	32	5	0
19	D	5	0	0	0	0
19	F	5	0	0	0	0
19	G	15	0	0	0	0
20	E	4	0	0	0	0
21	E	37	0	51	0	0
22	A	3	0	0	0	0
22	C	1	0	0	0	0
22	G	1	0	0	0	0
22	I	1	0	0	0	0
All	All	16290	0	15975	45	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 1.

The worst 5 of 45 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)
4:D:37:CYS:SG	18:D:501:HEC:CAB	2.74	0.75
4:D:211:MET:HA	4:D:211:MET:HE2	1.69	0.74
4:D:116:ILE:HG12	18:D:501:HEC:HMA3	1.70	0.73
1:A:336:PHE:CZ	3:C:3:ASN:HB3	2.24	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:C:402:HEM:HMC2	14:C:402:HEM:HBC2	1.79	0.65

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	442/444 (100%)	424 (96%)	18 (4%)	0	100	100
2	B	411/420 (98%)	399 (97%)	11 (3%)	1 (0%)	47	81
3	C	376/378 (100%)	363 (96%)	12 (3%)	1 (0%)	41	75
4	D	237/239 (99%)	225 (95%)	12 (5%)	0	100	100
5	E	194/196 (99%)	179 (92%)	11 (6%)	4 (2%)	7	38
6	F	97/99 (98%)	95 (98%)	2 (2%)	0	100	100
7	G	72/74 (97%)	72 (100%)	0	0	100	100
8	H	63/65 (97%)	58 (92%)	5 (8%)	0	100	100
9	I	44/46 (96%)	43 (98%)	0	1 (2%)	6	36
10	J	57/59 (97%)	55 (96%)	2 (4%)	0	100	100
All	All	1993/2020 (99%)	1913 (96%)	73 (4%)	7 (0%)	34	72

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	171	ALA
3	C	155	TYR
5	E	162	GLY
9	I	41	PRO
5	E	155	GLY

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	363/369 (98%)	361 (99%)	2 (1%)	86	94
2	B	323/329 (98%)	319 (99%)	4 (1%)	71	87
3	C	324/326 (99%)	318 (98%)	6 (2%)	57	80
4	D	194/204 (95%)	193 (100%)	1 (0%)	88	94
5	E	166/168 (99%)	165 (99%)	1 (1%)	86	94
6	F	88/91 (97%)	85 (97%)	3 (3%)	37	68
7	G	64/66 (97%)	63 (98%)	1 (2%)	62	83
8	H	56/62 (90%)	56 (100%)	0	100	100
9	I	37/38 (97%)	35 (95%)	2 (5%)	22	55
10	J	47/49 (96%)	46 (98%)	1 (2%)	53	79
All	All	1662/1702 (98%)	1641 (99%)	21 (1%)	69	86

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	F	33	ARG
7	G	46	LEU
10	J	33	ARG
9	I	50	LEU
6	F	107	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	15	ASN
4	D	225	HIS
8	H	23	GLN
7	G	12	HIS
2	B	400	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

22 ligands are modelled in this entry.

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
14	HEM	C	401	3	41,50,50	1.41	7 (17%)	45,82,82	1.59	11 (24%)
19	PO4	G	103	-	4,4,4	0.85	0	6,6,6	0.57	0
11	PG4	C	405	-	12,12,12	0.49	0	11,11,11	0.43	0
21	PX4	E	202	-	36,36,45	1.33	2 (5%)	42,44,53	1.20	5 (11%)
14	HEM	C	402	3	41,50,50	1.34	7 (17%)	45,82,82	1.47	10 (22%)
18	HEC	D	501	4	32,50,50	2.51	12 (37%)	24,82,82	2.30	7 (29%)
13	CDL	A	503	-	33,33,99	1.28	2 (6%)	37,43,111	1.35	4 (10%)
19	PO4	G	101	-	4,4,4	0.74	0	6,6,6	0.84	0
19	PO4	G	102	-	4,4,4	0.91	0	6,6,6	0.50	0
11	PG4	C	404	-	12,12,12	0.69	0	11,11,11	0.63	0
19	PO4	D	502	-	4,4,4	1.07	0	6,6,6	0.36	0
12	6PE	A	502	-	22,22,26	1.54	2 (9%)	25,27,31	1.40	3 (12%)
11	PG4	A	501	-	12,12,12	0.56	0	11,11,11	0.39	0
13	CDL	E	204	-	59,59,99	1.27	4 (6%)	65,71,111	1.18	7 (10%)
16	PEE	E	203	-	40,40,50	1.28	3 (7%)	43,45,55	1.10	2 (4%)
15	LMT	C	403	-	36,36,36	0.82	1 (2%)	47,47,47	1.21	4 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
17	JHE	C	408	-	34,34,34	2.39	5 (14%)	44,50,50	1.03	3 (6%)
16	PEE	C	407	-	39,39,50	1.25	3 (7%)	42,44,55	1.15	2 (4%)
20	FES	E	201	-	0,4,4	-	-	-	-	-
13	CDL	D	503	-	53,53,99	1.40	4 (7%)	59,65,111	1.22	6 (10%)
19	PO4	F	501	-	4,4,4	0.88	0	6,6,6	0.43	0
13	CDL	C	406	-	43,43,99	1.58	4 (9%)	49,55,111	1.55	6 (12%)

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
14	HEM	C	402	3	-	4/12/54/54	-
15	LMT	C	403	-	-	9/21/61/61	0/2/2/2
13	CDL	A	503	-	-	18/41/41/110	-
18	HEC	D	501	4	-	2/10/54/54	-
14	HEM	C	401	3	-	5/12/54/54	-
20	FES	E	201	-	-	-	0/1/1/1
11	PG4	C	404	-	-	5/10/10/10	-
13	CDL	D	503	-	-	24/63/63/110	-
13	CDL	E	204	-	-	36/69/69/110	-
13	CDL	C	406	-	-	16/52/52/110	-
11	PG4	C	405	-	-	5/10/10/10	-
17	JHE	C	408	-	-	2/13/13/13	0/4/4/4
12	6PE	A	502	-	-	12/26/26/30	-
11	PG4	A	501	-	-	6/10/10/10	-
16	PEE	C	407	-	1/1/4/8	18/43/43/54	-
16	PEE	E	203	-	1/1/4/8	29/44/44/54	-
21	PX4	E	202	-	-	15/40/40/49	-

The worst 5 of 56 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	C	408	JHE	C3-C4	11.23	1.49	1.36
18	D	501	HEC	C3C-C2C	7.72	1.48	1.40
18	D	501	HEC	C2B-C3B	6.75	1.47	1.40
17	C	408	JHE	C1-C2	5.79	1.50	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	C	406	CDL	OA6-CA5	5.61	1.47	1.35

The worst 5 of 70 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	C	406	CDL	OA6-CA5-C11	6.08	122.27	111.09
18	D	501	HEC	C1D-C2D-C3D	-5.95	102.85	107.00
18	D	501	HEC	CMB-C2B-C3B	5.04	131.74	125.82
12	A	502	6PE	O6-C10-C11	4.59	121.40	111.50
18	D	501	HEC	CMC-C2C-C3C	4.57	131.20	125.82

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
16	C	407	PEE	C2
16	E	203	PEE	C2

5 of 206 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	A	502	6PE	C1-O3-P1-O1
12	A	502	6PE	C11-C10-O6-C2
12	A	502	6PE	O8-C16-C17-N1
13	A	503	CDL	CA3-OA5-PA1-OA4
13	A	503	CDL	CB2-OB2-PB2-OB3

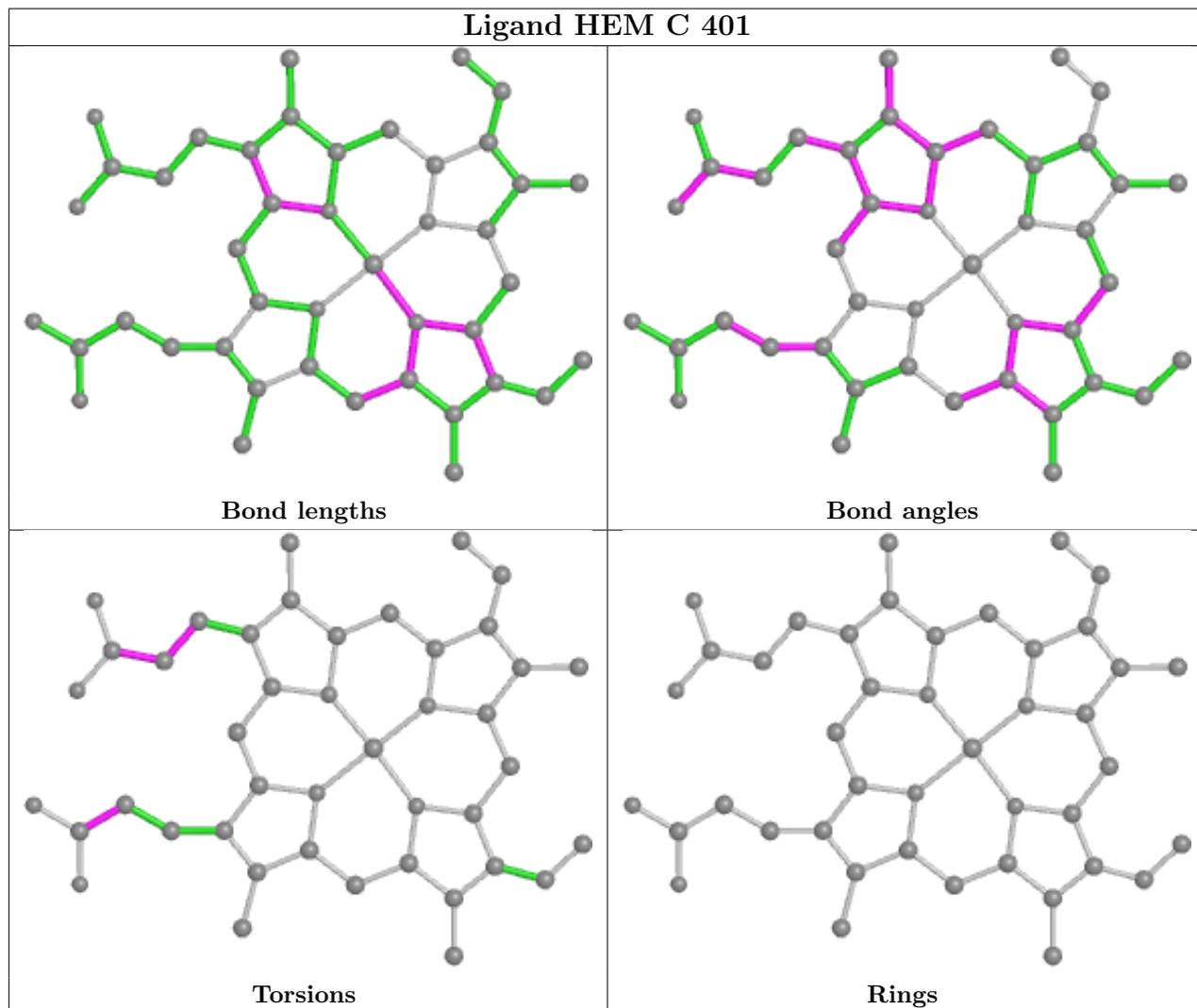
There are no ring outliers.

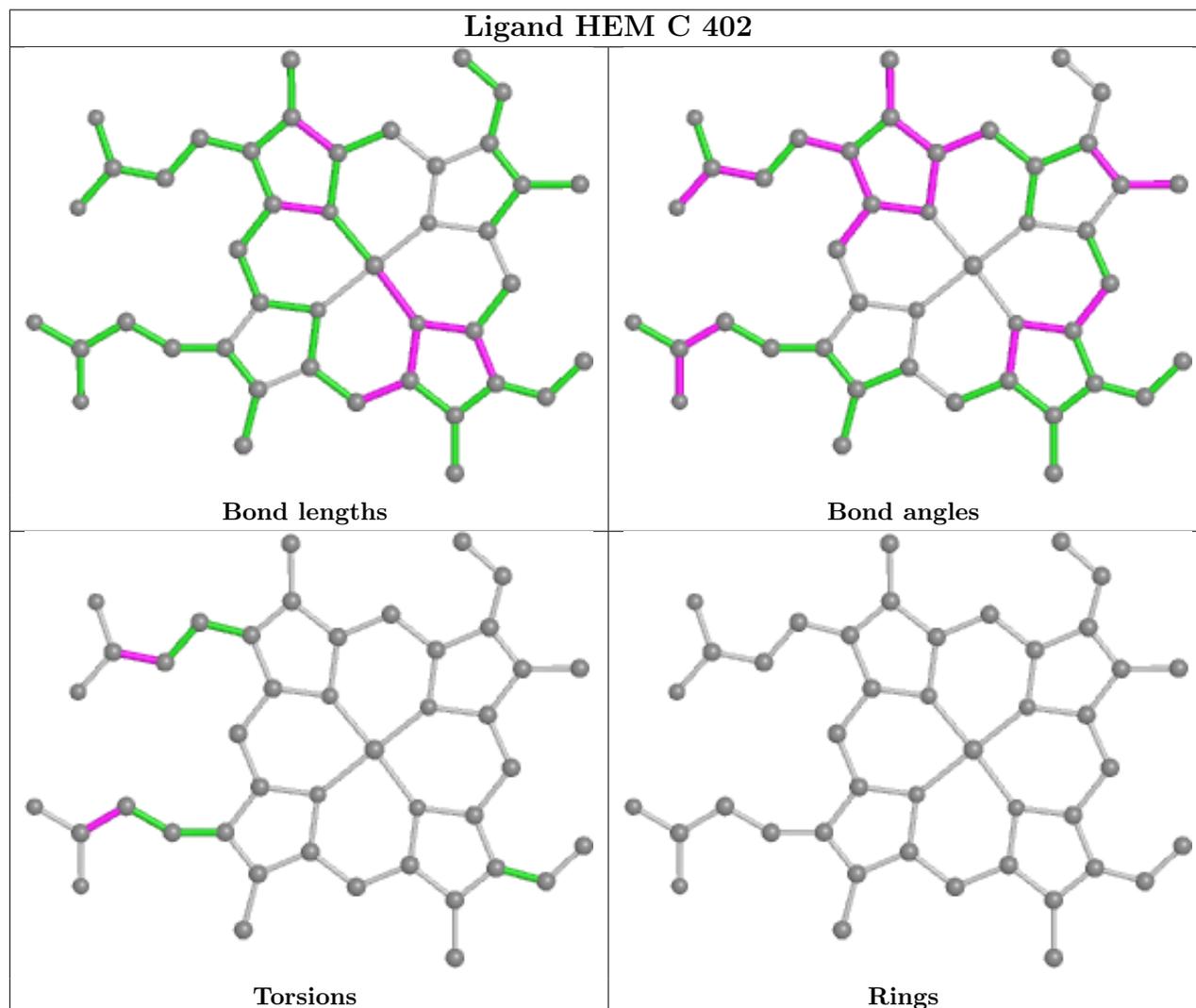
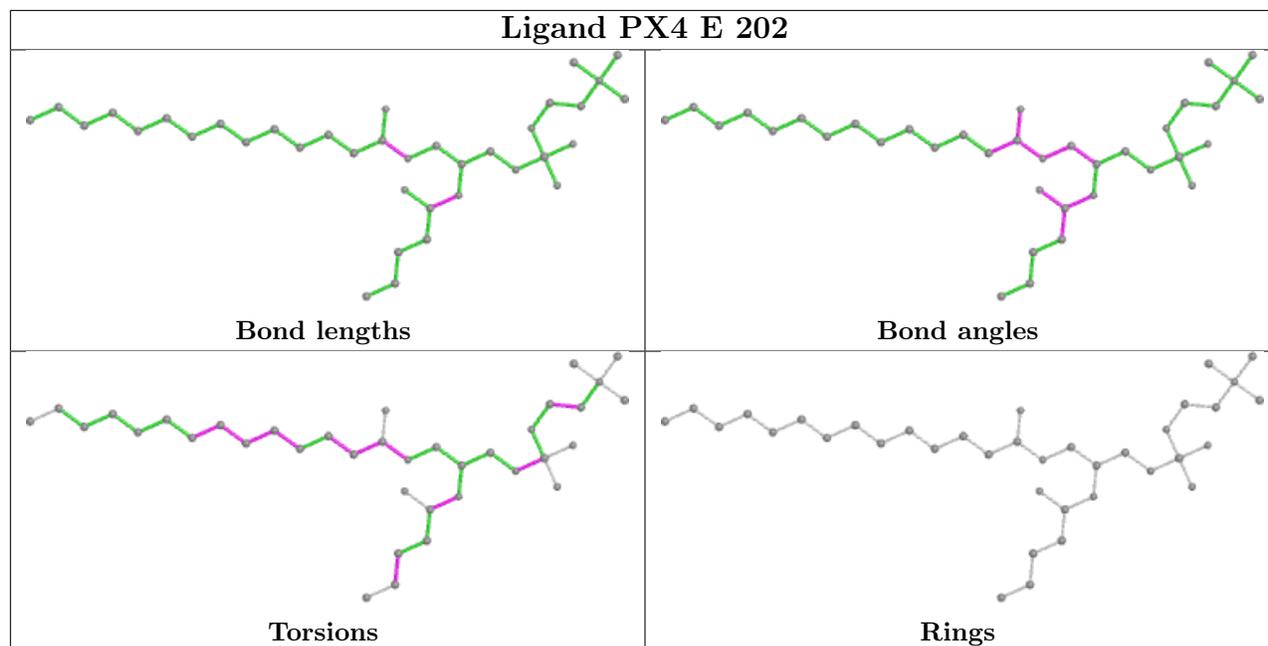
7 monomers are involved in 16 short contacts:

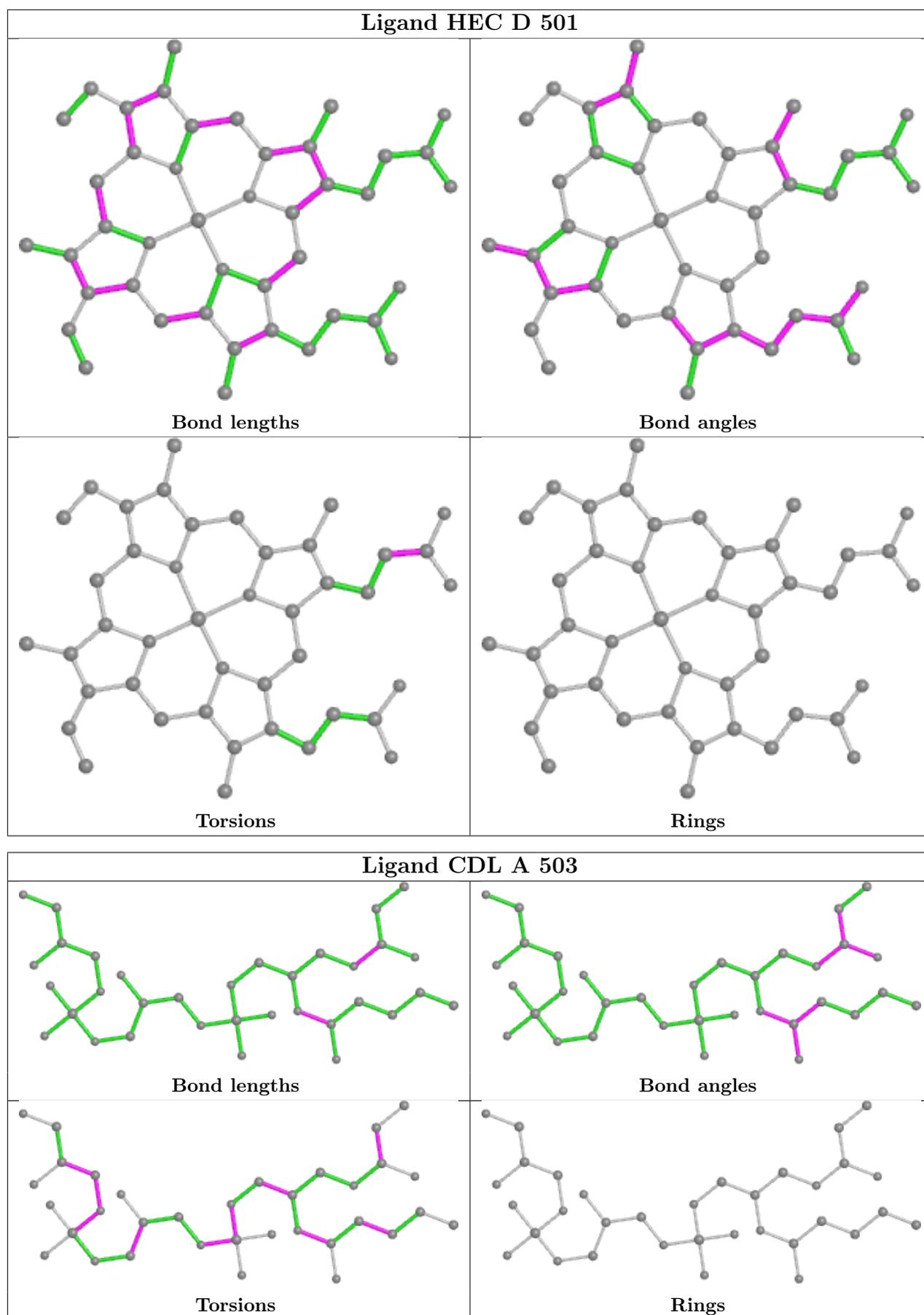
Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	C	401	HEM	2	0
14	C	402	HEM	4	0
18	D	501	HEC	5	0
13	A	503	CDL	3	0
12	A	502	6PE	2	0
13	E	204	CDL	1	0
16	E	203	PEE	1	0

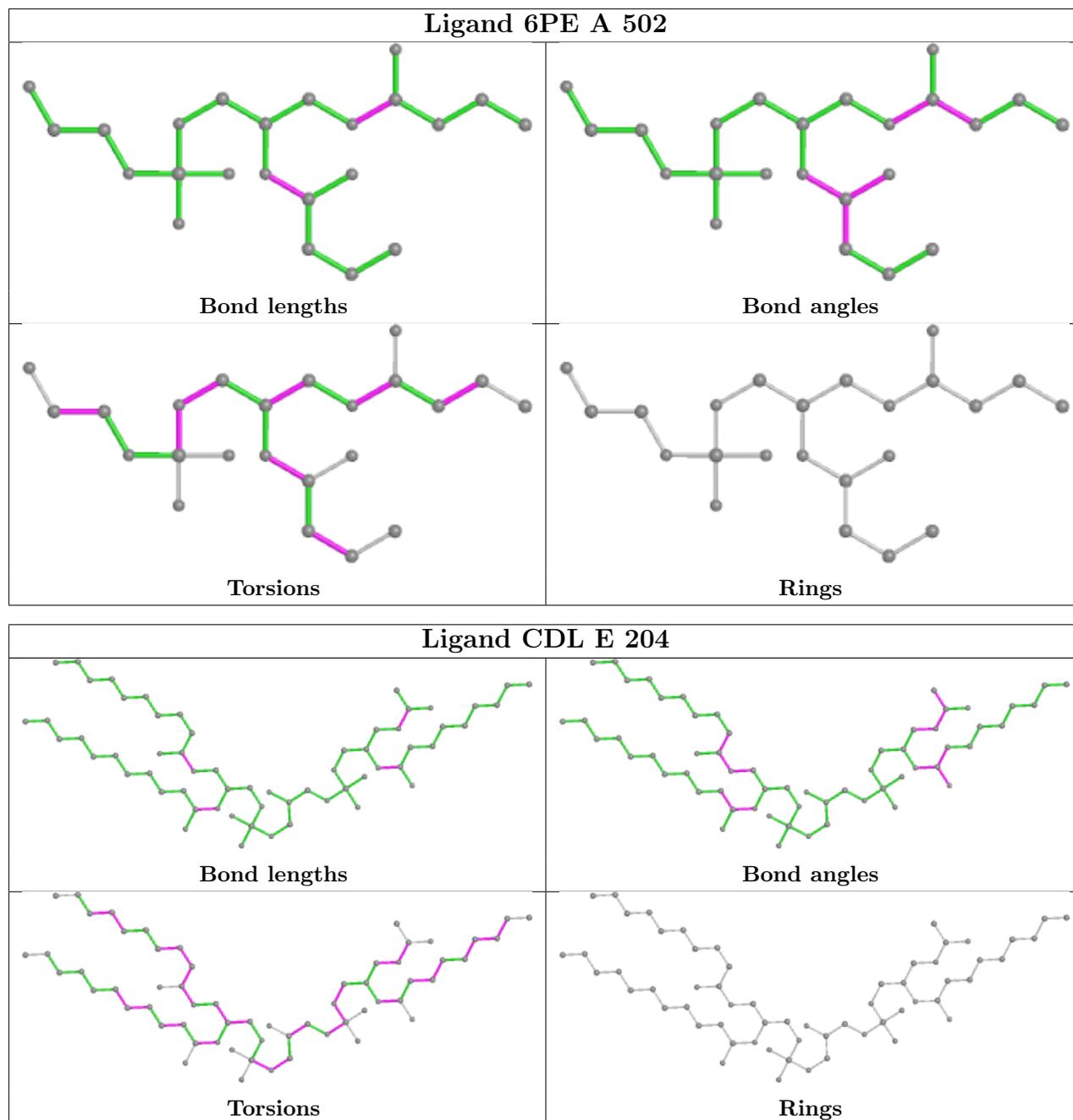
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

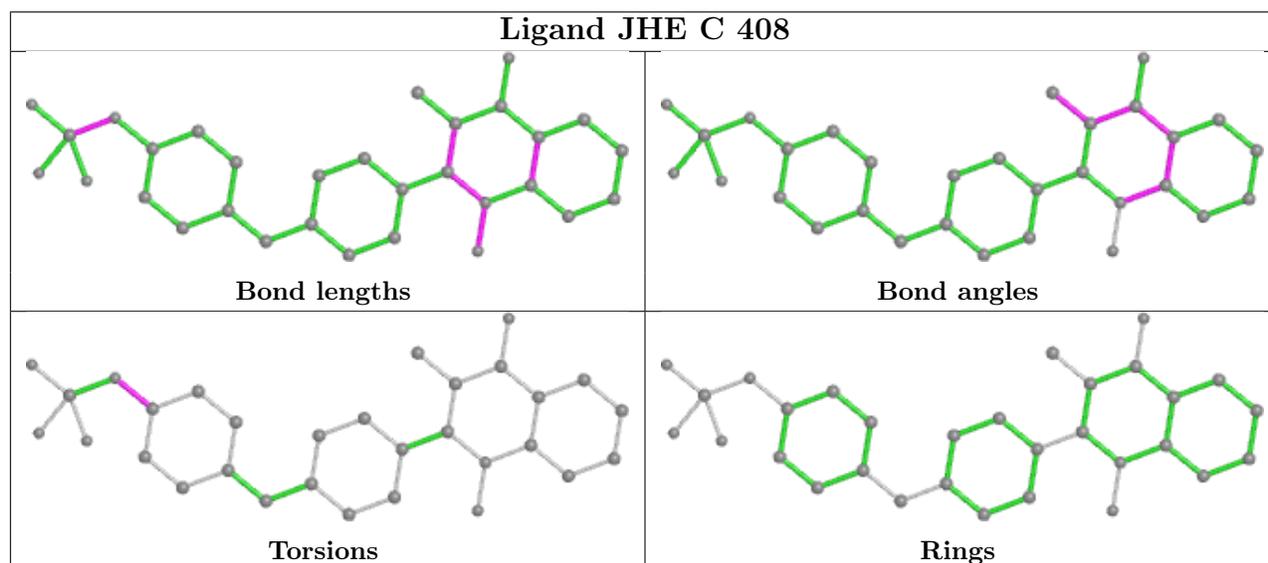
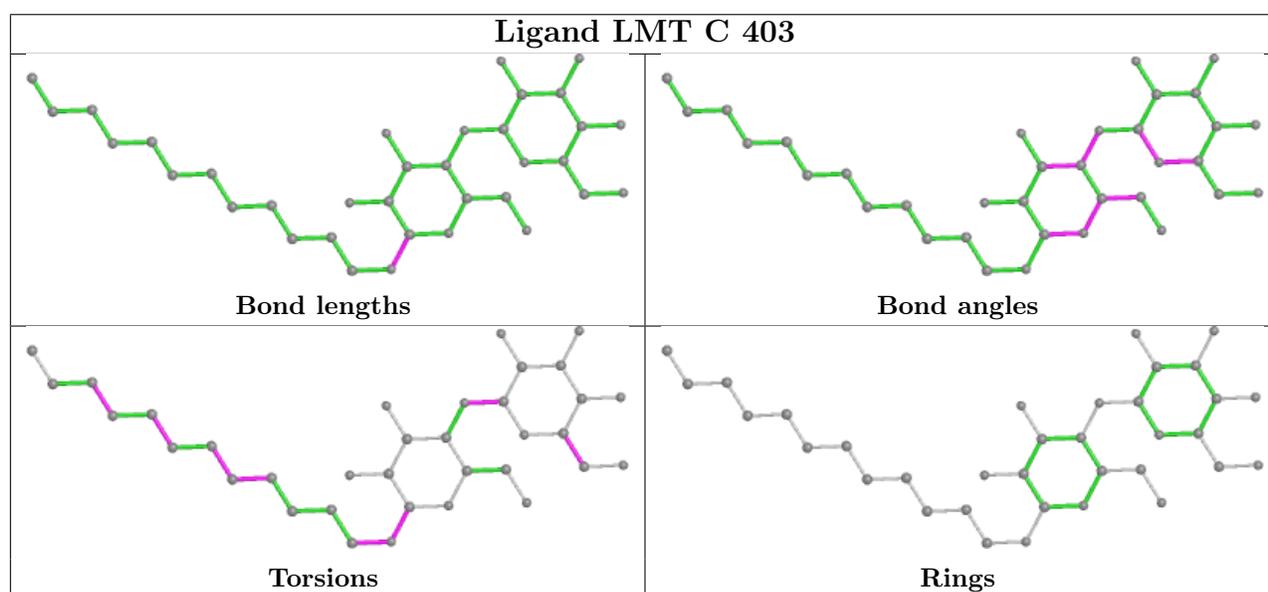
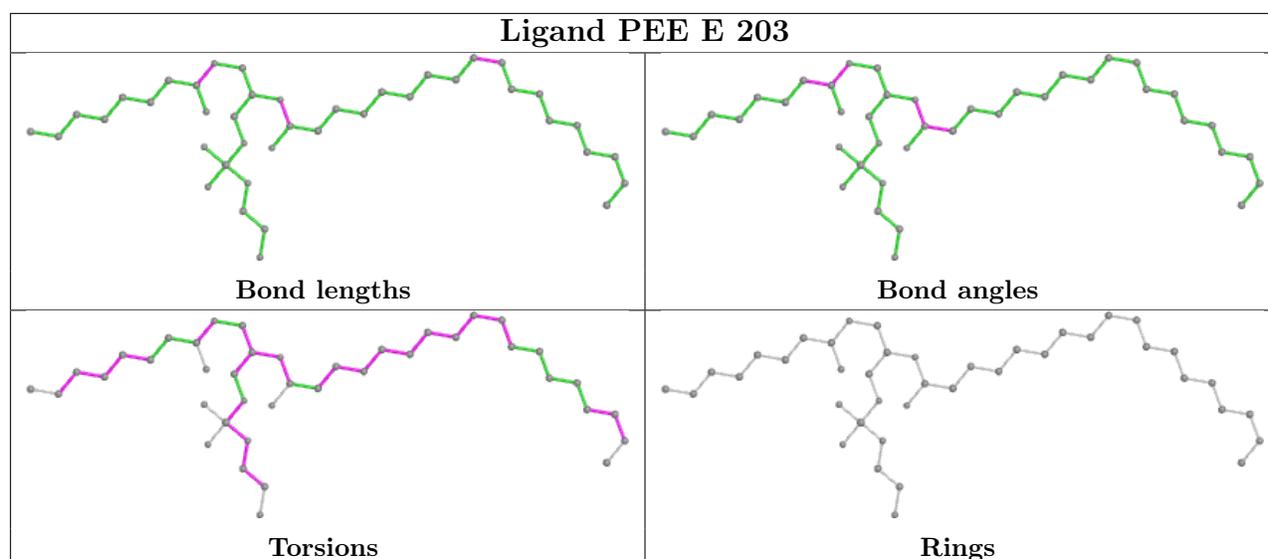
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question 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.

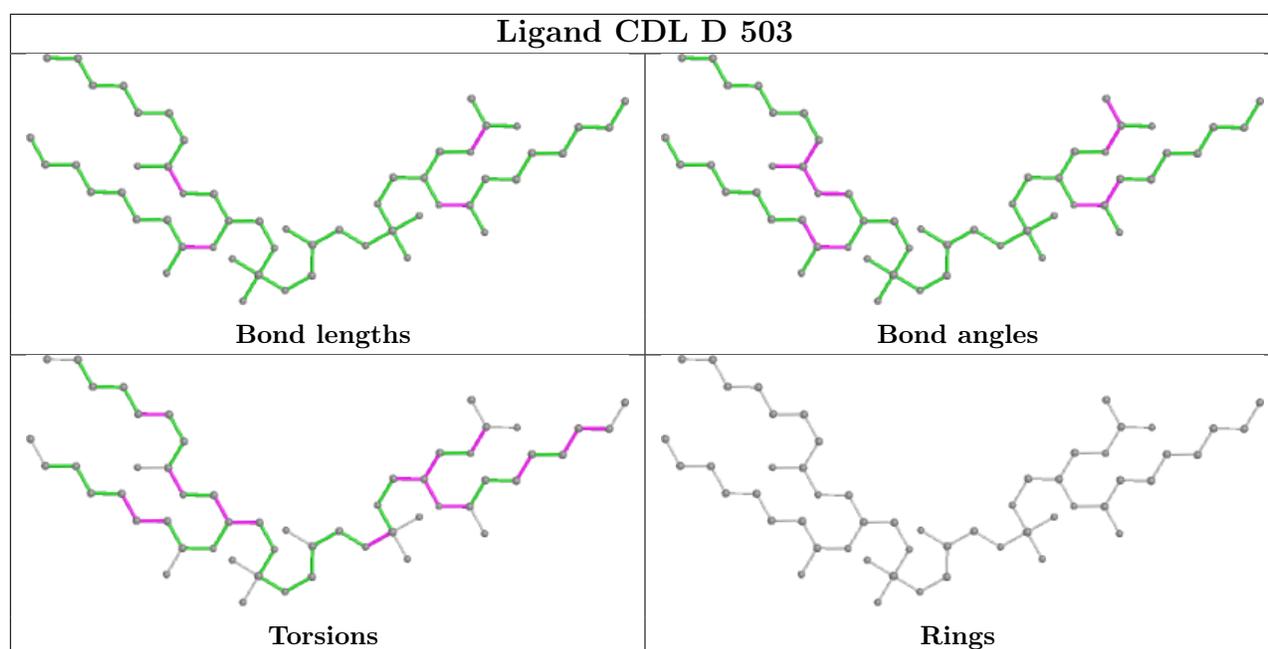
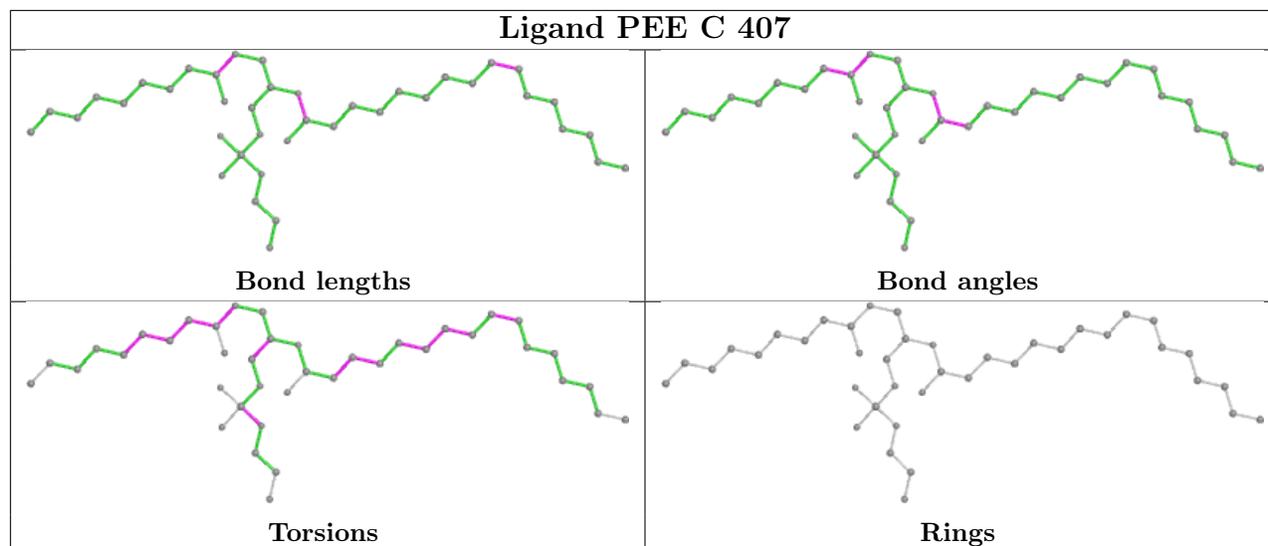


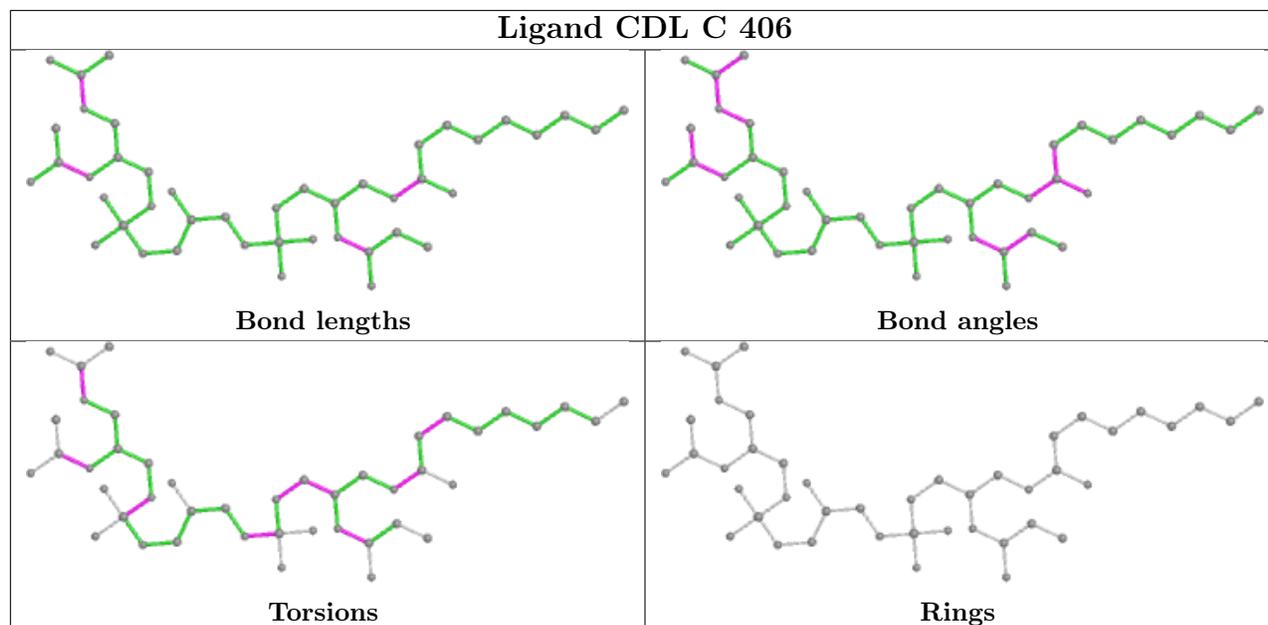












5.7 Other polymers [i](#)

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, 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	444/444 (100%)	0.37	11 (2%) 57 51	91, 128, 164, 240	0
2	B	415/420 (98%)	0.07	2 (0%) 91 88	98, 132, 164, 226	0
3	C	378/378 (100%)	-0.15	0 100 100	88, 116, 152, 188	0
4	D	239/239 (100%)	0.43	10 (4%) 36 32	115, 154, 182, 203	0
5	E	196/196 (100%)	0.03	2 (1%) 82 77	106, 189, 242, 279	0
6	F	99/99 (100%)	0.05	1 (1%) 82 77	73, 125, 162, 198	0
7	G	74/74 (100%)	0.16	2 (2%) 54 48	99, 133, 179, 195	0
8	H	65/65 (100%)	0.99	7 (10%) 5 6	183, 200, 216, 227	0
9	I	46/46 (100%)	0.39	1 (2%) 62 56	142, 187, 205, 211	0
10	J	59/59 (100%)	0.23	2 (3%) 45 40	115, 141, 189, 209	0
All	All	2015/2020 (99%)	0.18	38 (1%) 66 61	73, 134, 205, 279	0

The worst 5 of 38 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	198	HIS	3.6
1	A	414	TYR	3.3
8	H	61	PHE	3.1
4	D	21	LEU	3.1
5	E	159	PRO	2.9

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](#)

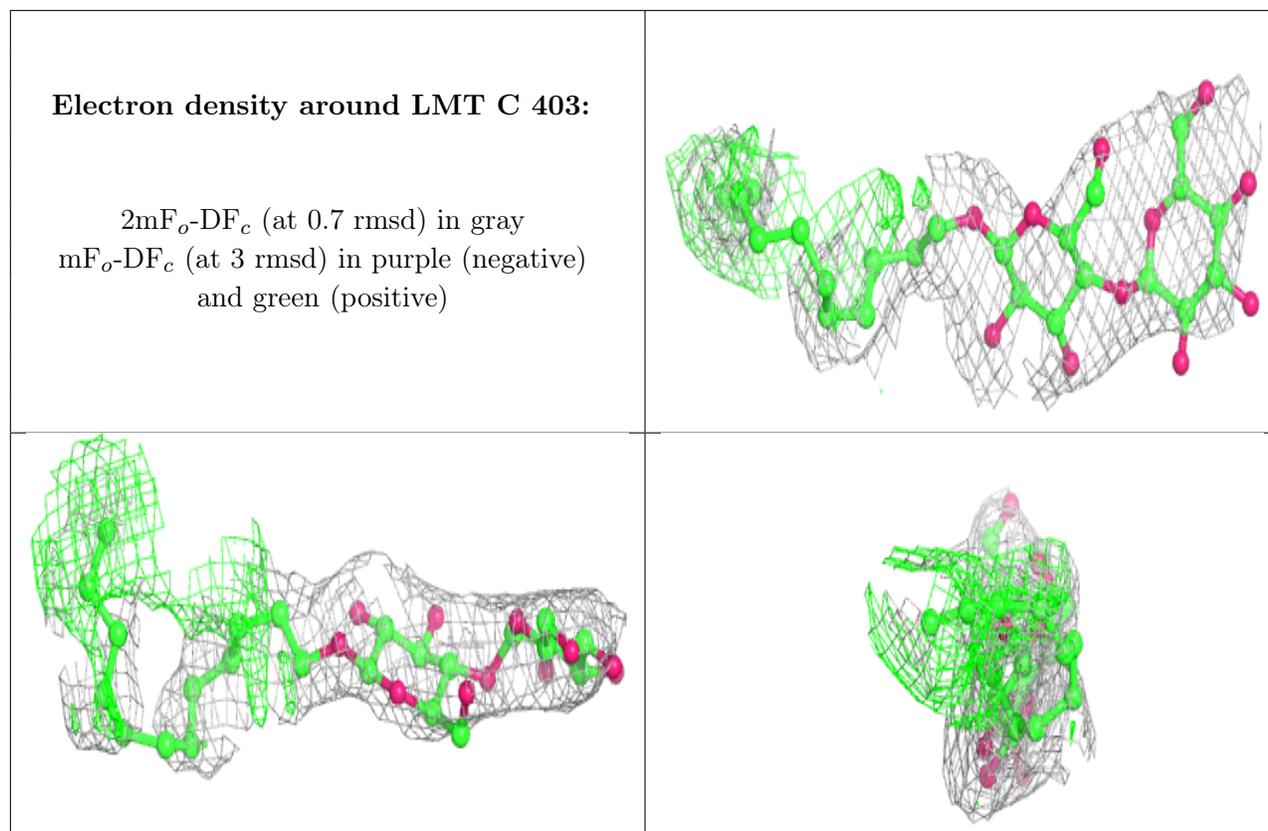
There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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.

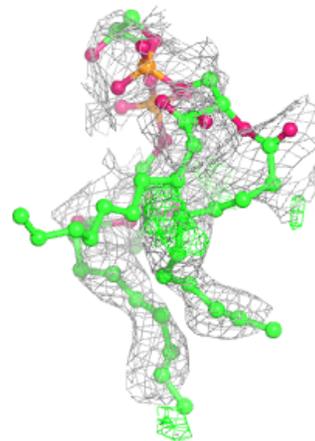
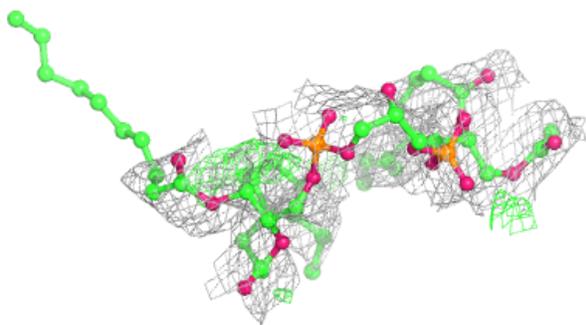
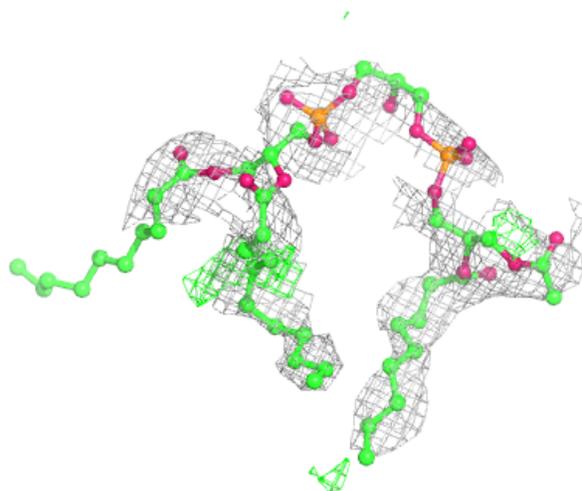
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
19	PO4	G	102	5/5	0.38	0.42	239,242,243,249	0
19	PO4	D	502	5/5	0.54	0.46	211,212,216,218	0
19	PO4	F	501	5/5	0.63	0.46	203,206,209,209	0
15	LMT	C	403	35/35	0.63	0.31	170,207,219,222	0
13	CDL	E	204	60/100	0.65	0.31	150,185,246,250	0
19	PO4	G	101	5/5	0.72	0.35	168,168,171,172	0
19	PO4	G	103	5/5	0.72	0.24	191,192,195,198	0
11	PG4	A	501	13/13	0.73	0.27	150,169,181,182	0
11	PG4	C	405	13/13	0.74	0.48	126,134,144,146	0
11	PG4	C	404	13/13	0.74	0.57	125,128,135,135	0
13	CDL	A	503	34/100	0.81	0.29	143,166,179,181	0
21	PX4	E	202	37/46	0.81	0.40	122,143,153,155	0
13	CDL	D	503	54/100	0.82	0.49	106,145,185,193	0
16	PEE	E	203	41/51	0.83	0.46	122,128,140,142	0
20	FES	E	201	4/4	0.90	0.11	288,291,295,306	0
13	CDL	C	406	44/100	0.91	0.29	124,134,144,149	0
12	6PE	A	502	23/27	0.93	0.28	133,157,178,183	0
17	JHE	C	408	31/31	0.96	0.24	66,75,121,132	0
16	PEE	C	407	40/51	0.96	0.40	107,113,119,123	0
18	HEC	D	501	43/43	0.97	0.35	147,155,164,168	0
14	HEM	C	401	43/43	0.98	0.33	103,106,112,114	0
14	HEM	C	402	43/43	0.98	0.30	96,100,106,110	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.



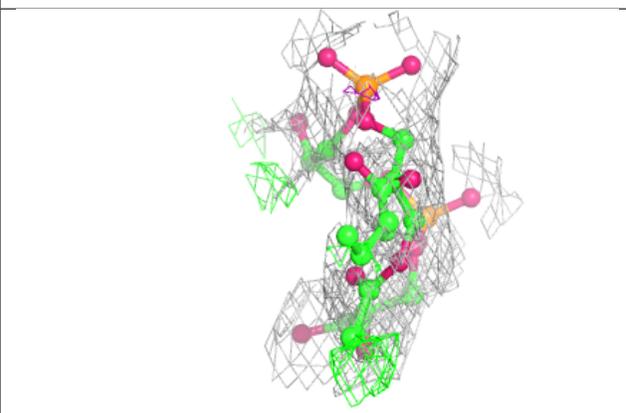
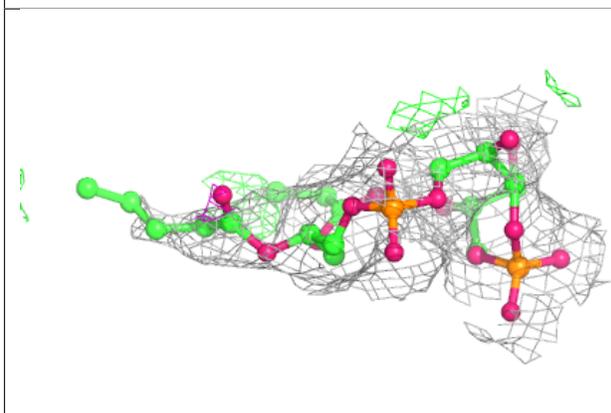
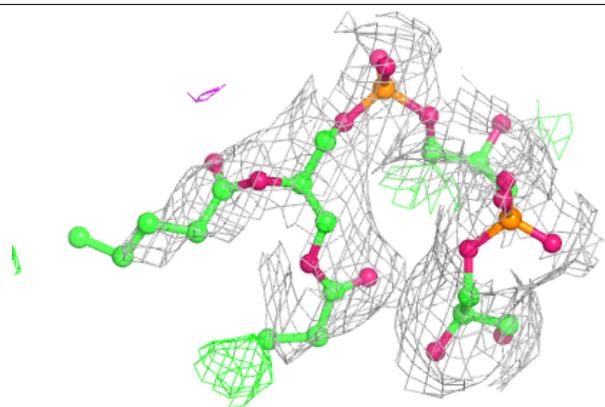
Electron density around CDL E 204:

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

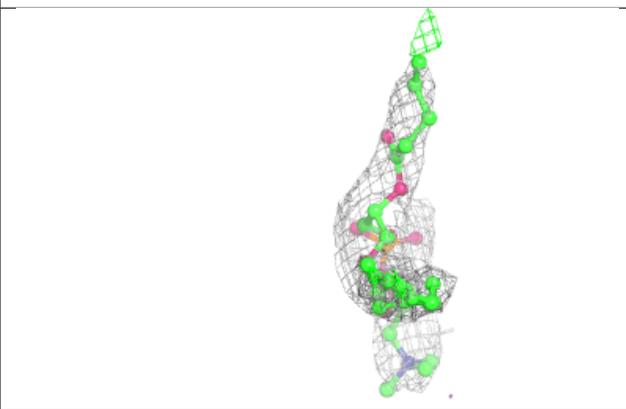
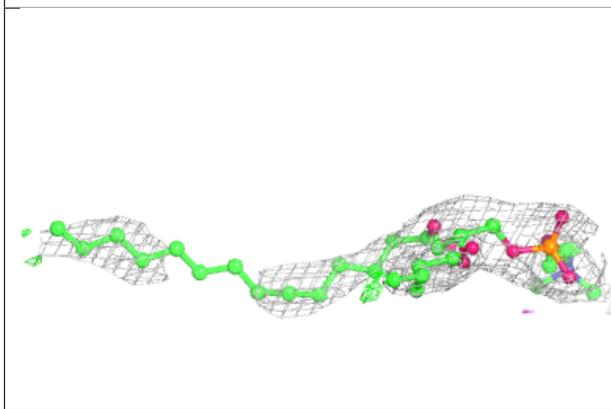
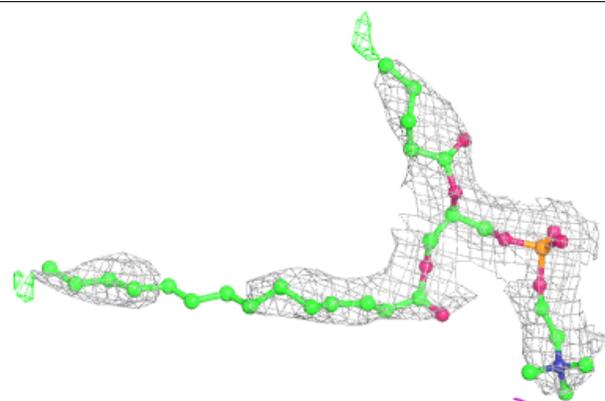


Electron density around CDL A 503:

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

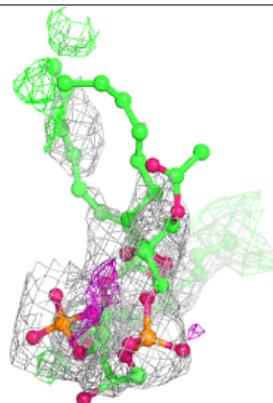
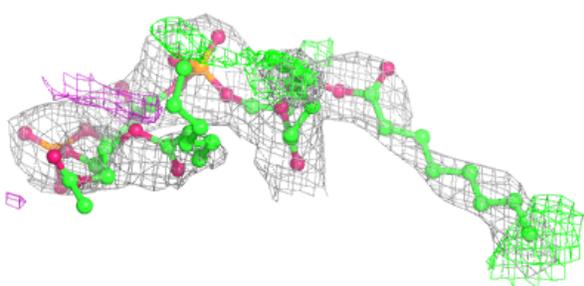
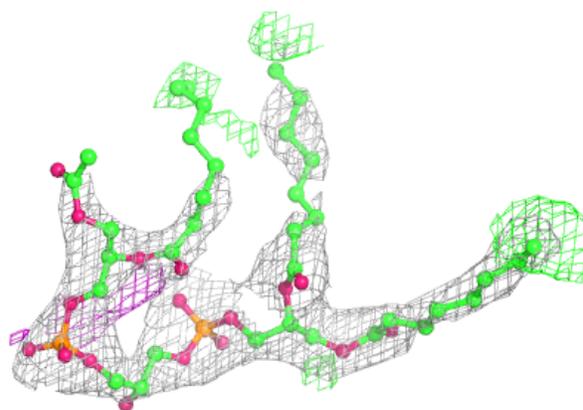
**Electron density around PX4 E 202:**

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

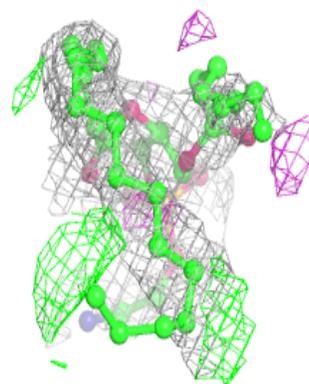
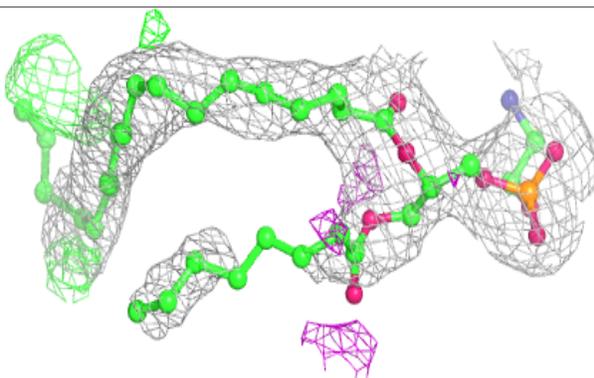
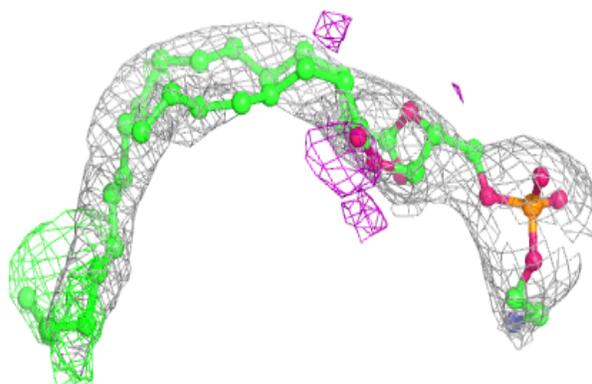


Electron density around CDL D 503:

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

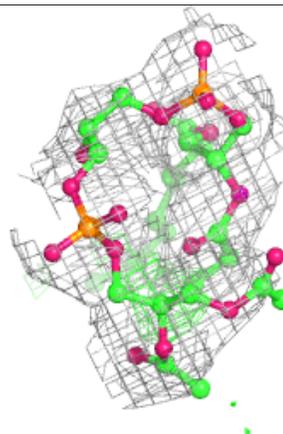
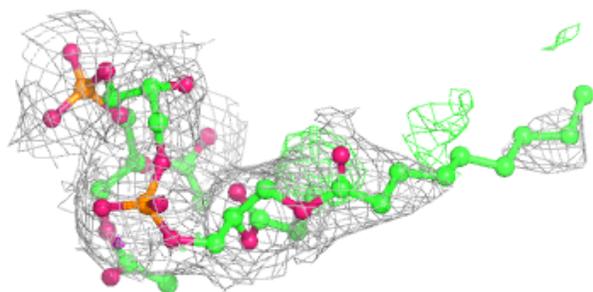
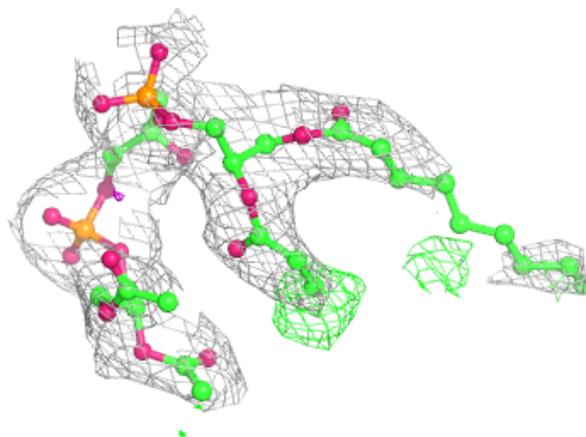
**Electron density around PEE E 203:**

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



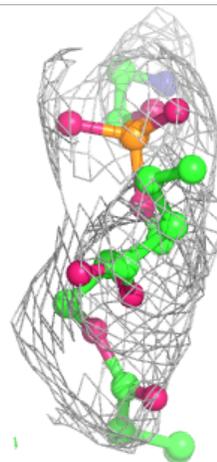
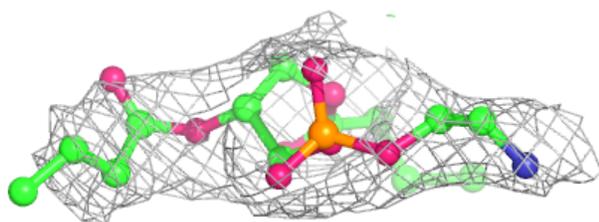
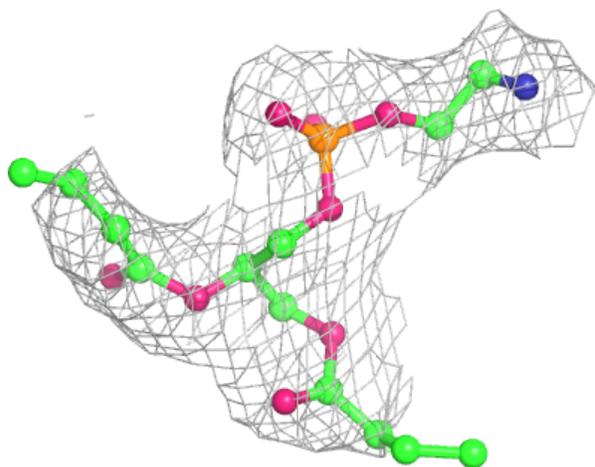
Electron density around CDL C 406:

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



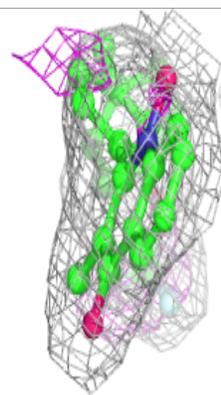
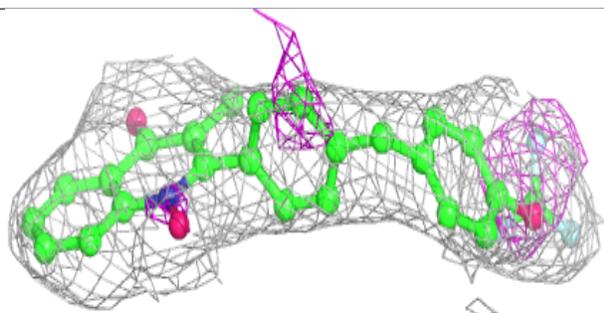
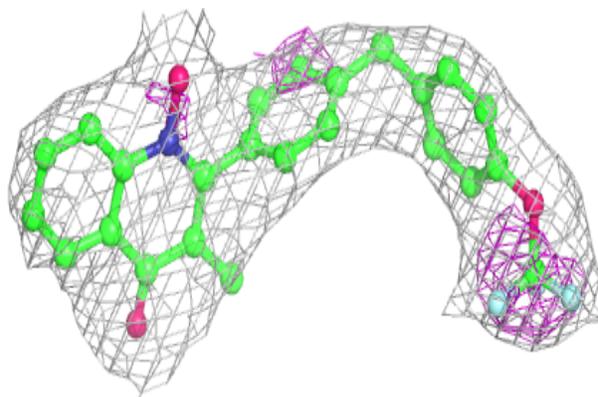
Electron density around 6PE A 502:

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

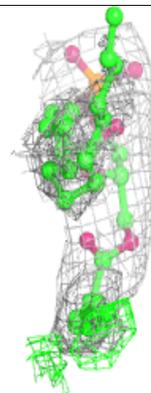
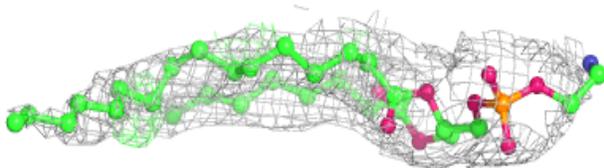
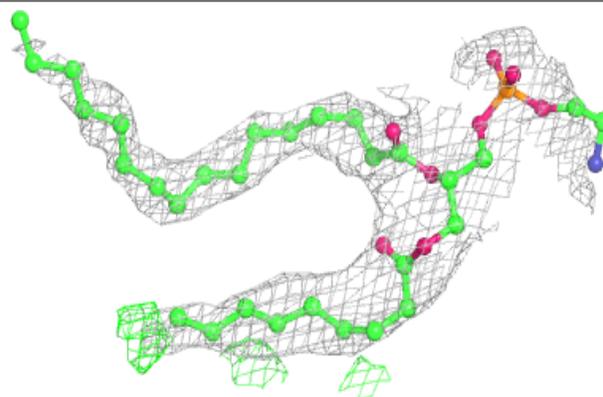


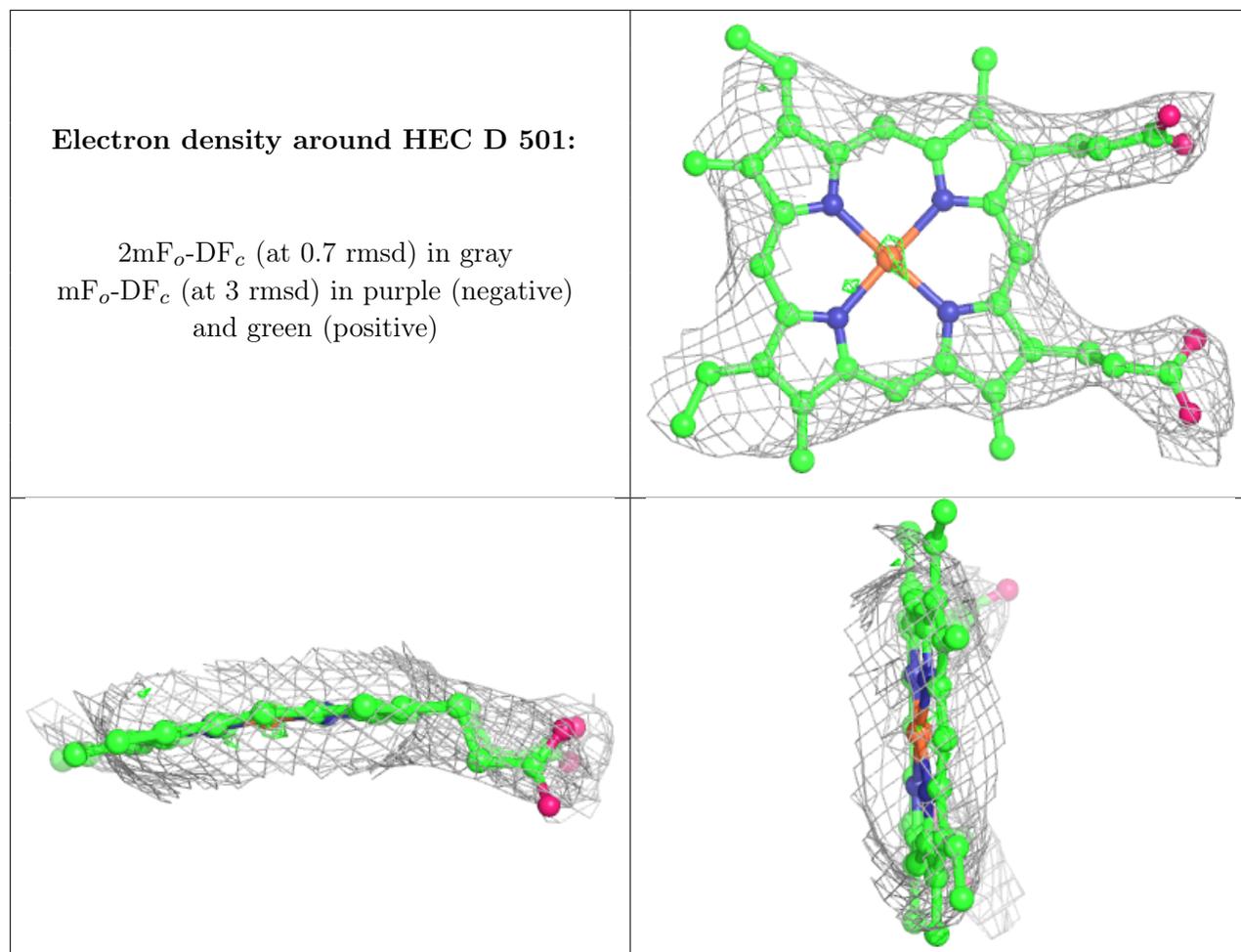
Electron density around JHE C 408:

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

**Electron density around PEE C 407:**

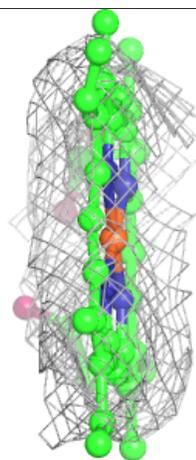
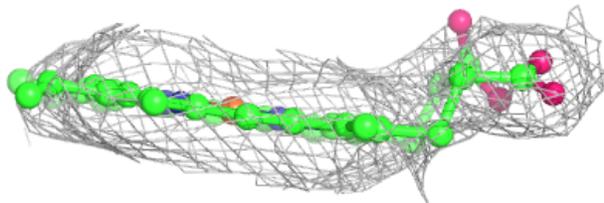
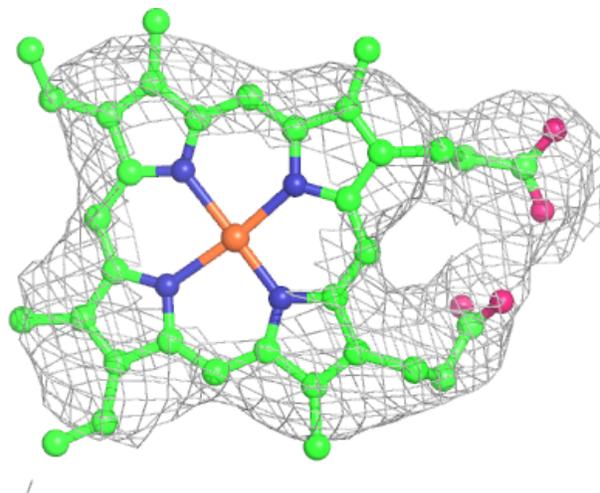
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

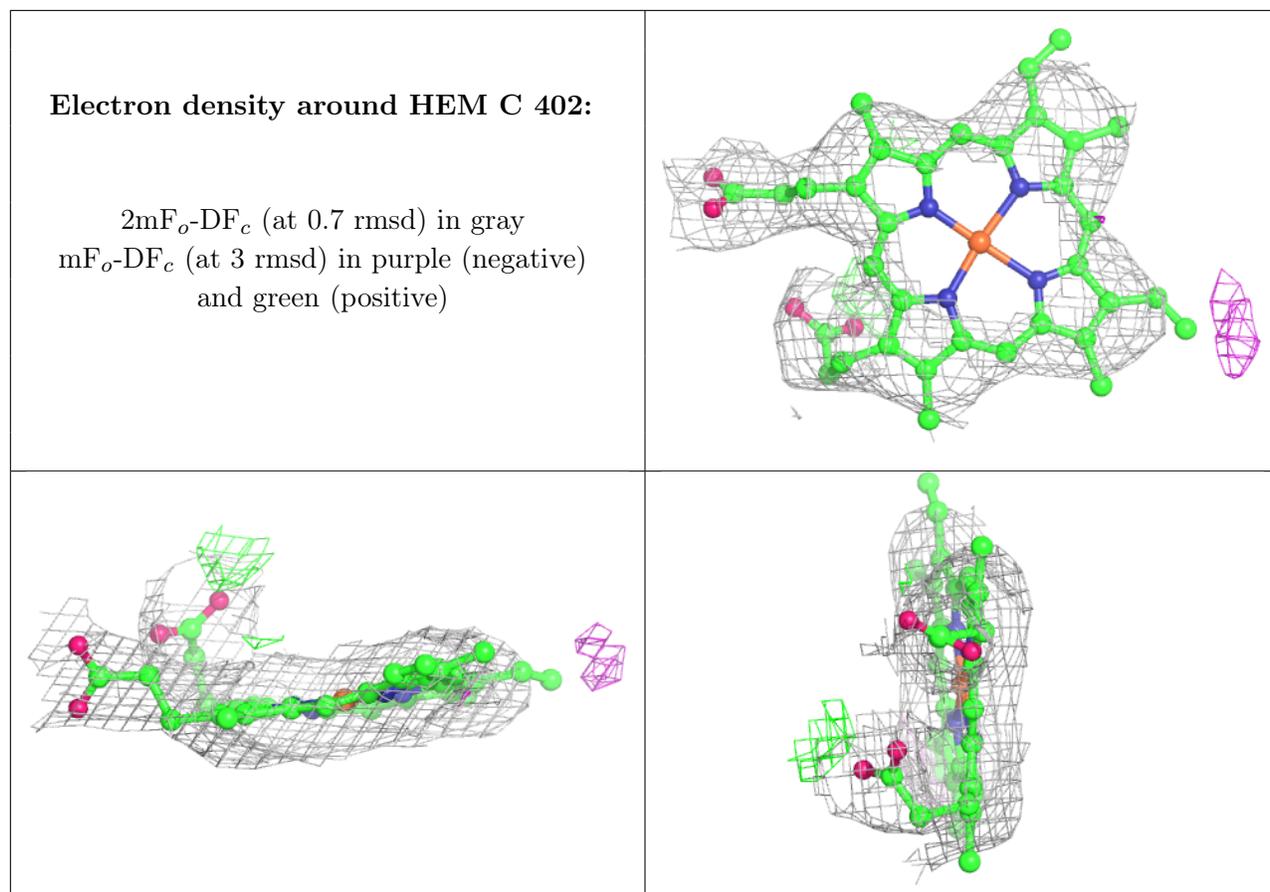




Electron density around HEM C 401:

$2mF_o-DF_c$ (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.