



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 26, 2026 – 03:01 am BST

PDB ID : 6ZFT / pdb_00006zft
Title : Crystal structure of bovine cytochrome bc1 in complex with quinolone inhibitor CK-2-68
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 : 3.30 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	:	1.8.4, CSD as541be (2020)
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	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

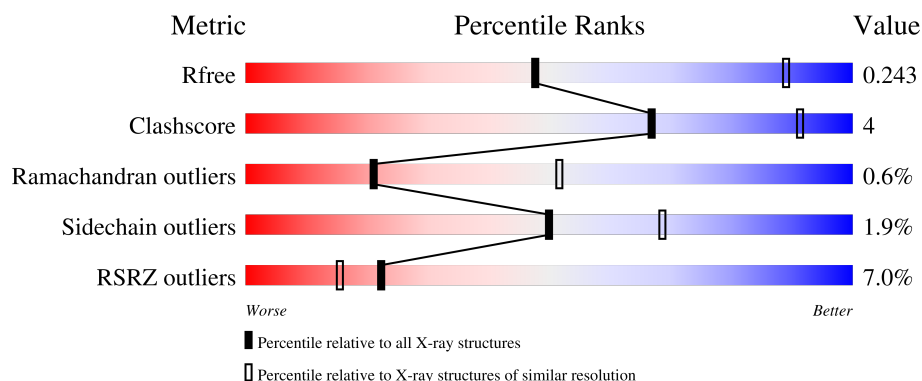
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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	5% 88% 10% .
2	B	420	5% 89% 9% ..
3	C	378	6% 89% 10% .
4	D	239	6% 91% 9%

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

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	A	503	-	-	X	-
17	PEE	C	409	X	-	-	-
17	PEE	D	503	X	-	-	-
19	HEC	D	501	X	-	-	-

2 Entry composition

There are 22 unique types of molecules in this entry. The entry contains 16262 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
1	A	439	Total	C	N	O	S	0	0	0
			3391	2121	600	650	20			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
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
2	B	415	Total	C	N	O	S	0	0	0
			3108	1951	551	599	7			

- Molecule 3 is a protein called Cytochrome b.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	378	Total	C	N	O	S	0	0	0
			2996	2007	471	500	18			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	239	Total	C	N	O	S	0	0	0
			1876	1201	321	339	15			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	196	Total	C	N	O	S	0	0	0
			1474	923	258	286	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	99	Total	C	N	O	S	0	0	0
			848	537	156	153	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	74	Total	C	N	O	S	0	0	0
			620	406	116	97	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	65	Total	C	N	O	S	0	0	0
			517	313	92	107	5			

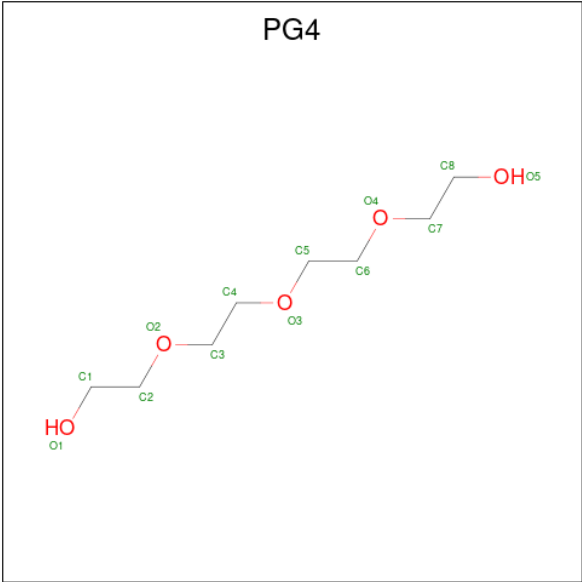
- Molecule 9 is a protein called Cytochrome b-c1 complex subunit Rieske, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	46	Total	C	N	O	S	0	0	0
			324	201	58	64	1			

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

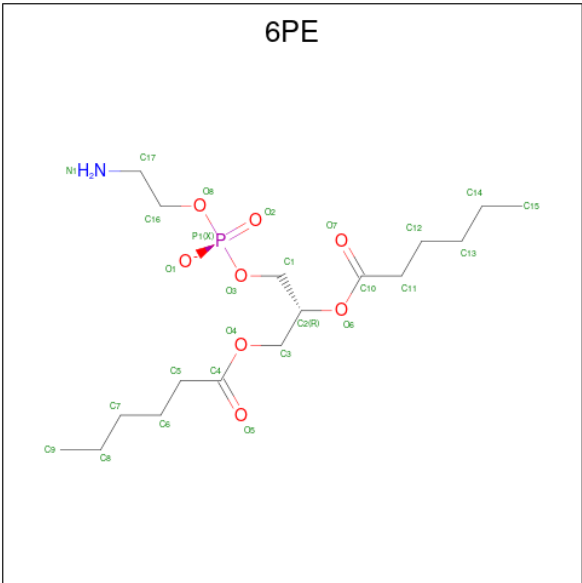
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	J	59	Total	C	N	O	0	0	0
			487	320	84	83			

- Molecule 11 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C₈H₁₈O₅).



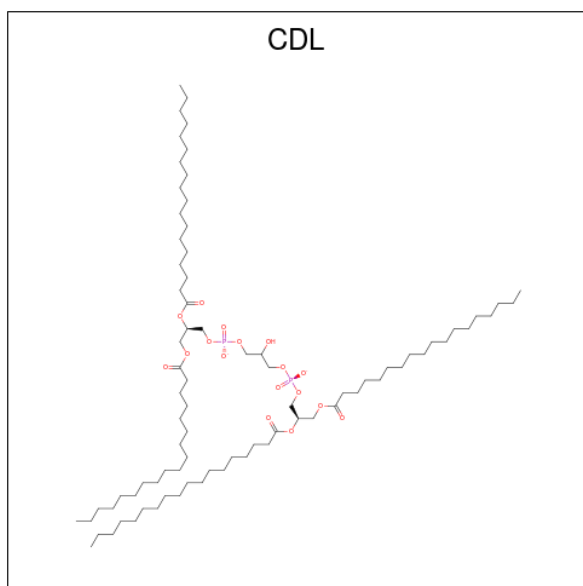
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O	0	0
			13	8	5		
11	A	1	Total	C	O	0	0
			13	8	5		
11	C	1	Total	C	O	0	0
			13	8	5		
11	C	1	Total	C	O	0	0
			13	8	5		

- Molecule 12 is 1,2-DIHEXANOYL-SN-GLYCERO-3-PHOSPHOETHANOLAMINE (CCD ID: 6PE) (formula: C₁₇H₃₃NO₈P).



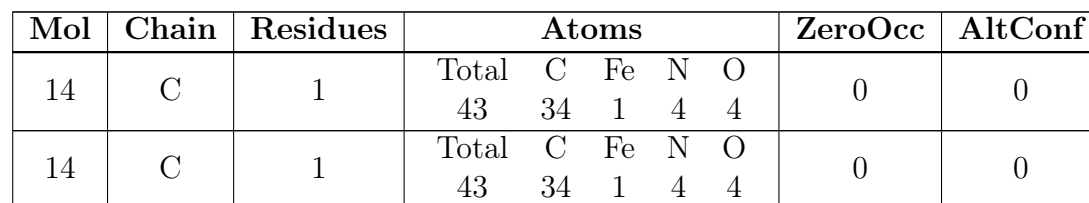
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
12	A	1	Total	C	N	O	P	0	0
			23	13	1	8	1		

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

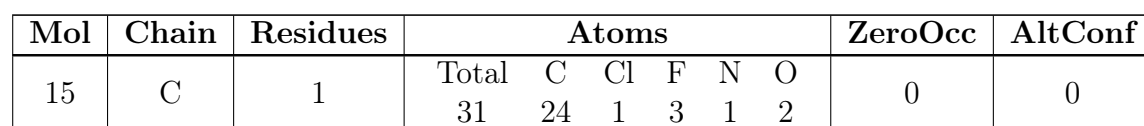


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
13	C	1	Total	C	O	P	0	0
			34	17	15	2		
13	C	1	Total	C	O	P	0	0
			44	25	17	2		
13	D	1	Total	C	O	P	0	0
			54	35	17	2		
13	E	1	Total	C	O	P	0	0
			60	41	17	2		

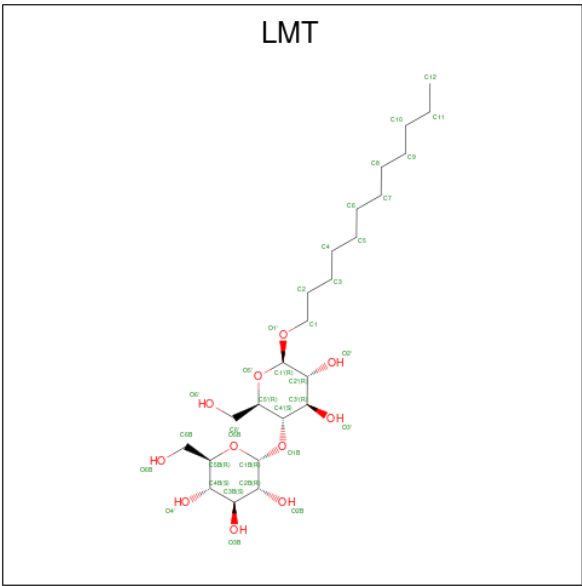
- Molecule 14 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



- Molecule 15 is 7-chloranyl-3-methyl-2-[4-[[4-(trifluoromethoxy)phenyl]methyl]phenyl]-1 {H}-quinolin-4-one (CCD ID: JHB) (formula: $C_{24}H_{17}ClF_3NO_2$) (labeled as "Ligand of Interest" by depositor).

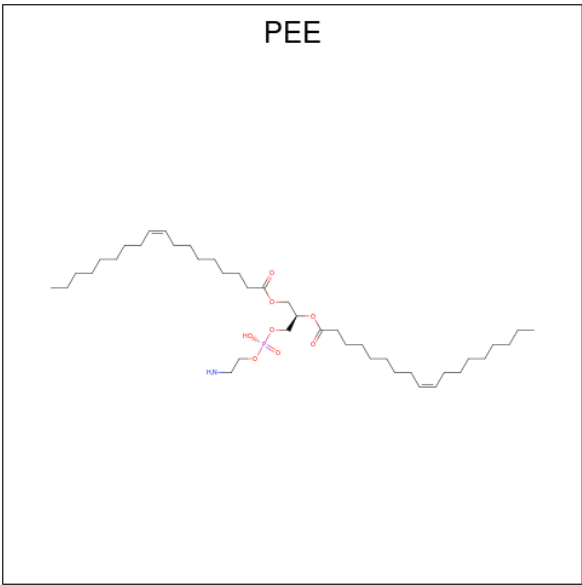


- Molecule 16 is DODECYL-BETA-D-MALTOSE (CCD ID: LMT) (formula: C₂₄H₄₆O₁₁).



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

- Molecule 17 is 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (CCD ID: PEE) (formula: C₄₁H₇₈NO₈P).



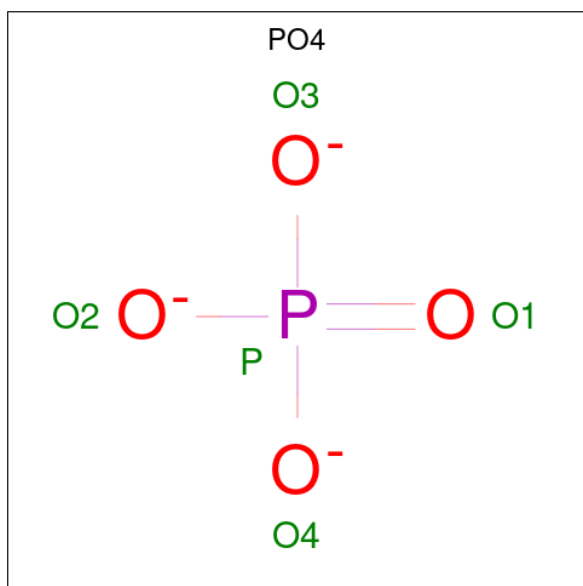
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
17	C	1	Total	C	N	O	P	0	0
			40	30	1	8	1		

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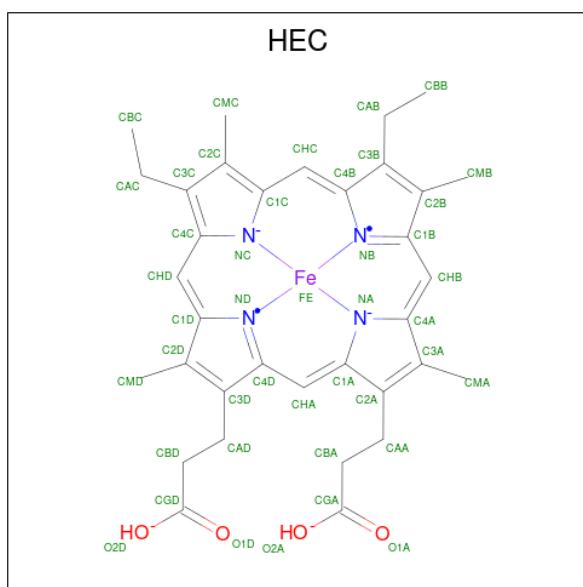
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
17	D	1	Total	C	N	O	P	0	0
			37	27	1	8	1		

- Molecule 18 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



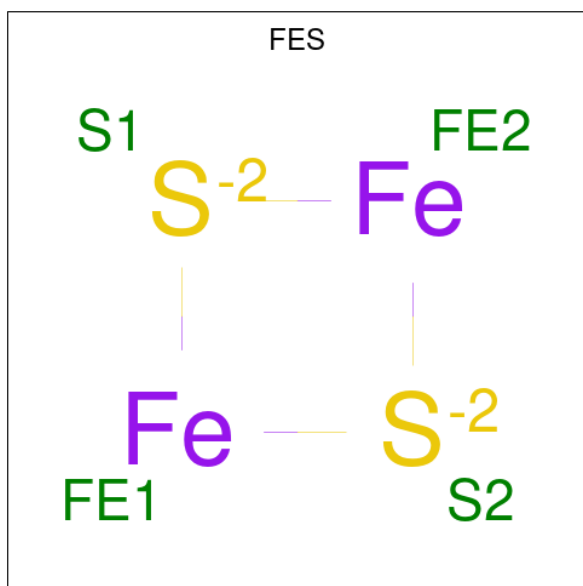
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
18	C	1	Total	O	P	0	0
			5	4	1		
18	F	1	Total	O	P	0	0
			5	4	1		
18	G	1	Total	O	P	0	0
			5	4	1		
18	G	1	Total	O	P	0	0
			5	4	1		
18	G	1	Total	O	P	0	0
			5	4	1		
18	H	1	Total	O	P	0	0
			5	4	1		

- Molecule 19 is HEME C (CCD ID: HEC) (formula: C₃₄H₃₆FeN₄O₄).



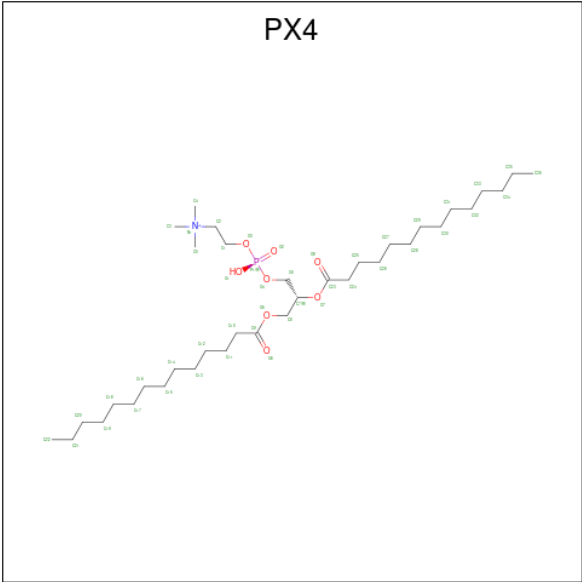
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
19	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 20 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



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

- Molecule 21 is 1,2-DIMYRISTOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PX4) (formula: $\text{C}_{36}\text{H}_{73}\text{NO}_8\text{P}$).



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

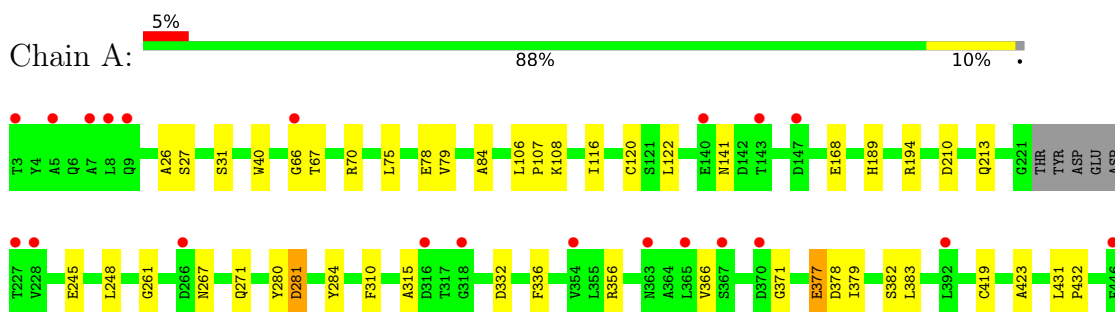
- Molecule 22 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	A	3	Total	O	0	0
			3	3		
22	B	1	Total	O	0	0
			1	1		
22	C	4	Total	O	0	0
			4	4		
22	D	2	Total	O	0	0
			2	2		
22	F	1	Total	O	0	0
			1	1		

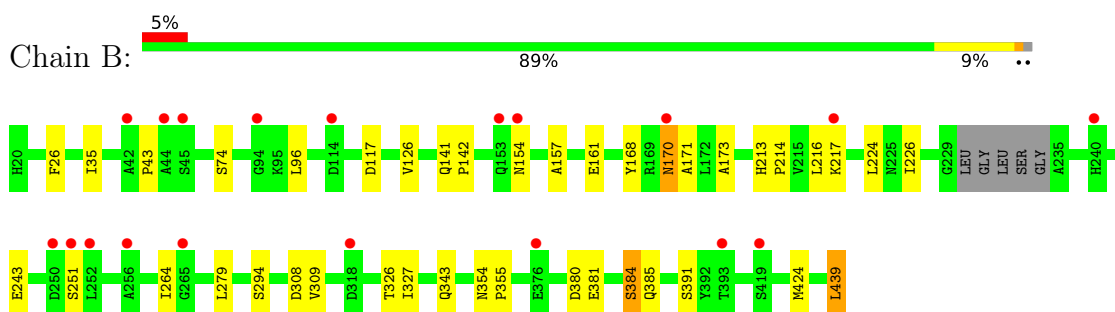
3 Residue-property plots [i](#)

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.

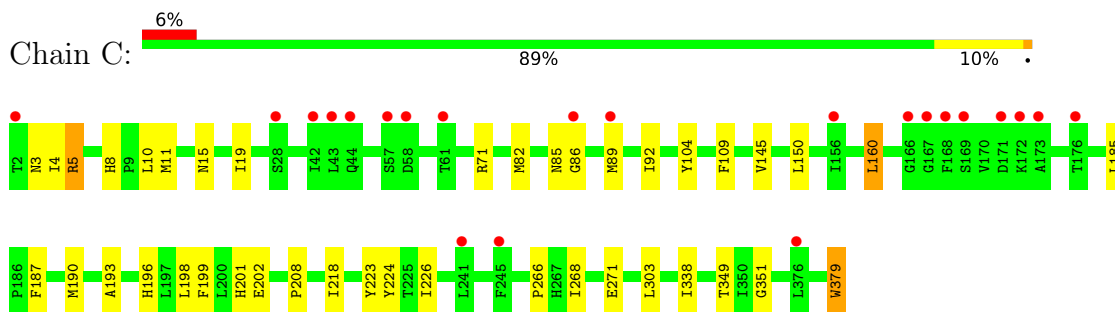
- Molecule 1: Cytochrome b-c1 complex subunit 1, mitochondrial



- Molecule 2: Cytochrome b-c1 complex subunit 2, mitochondrial

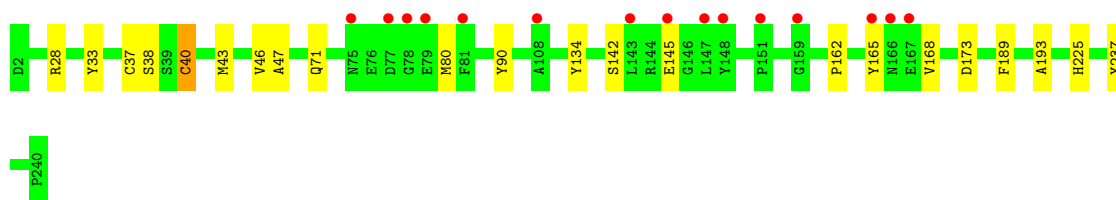


- Molecule 3: Cytochrome b

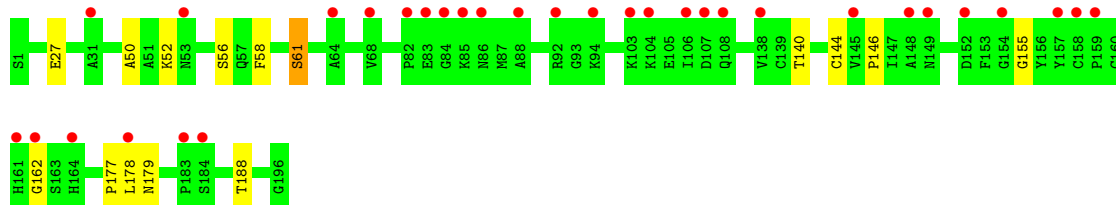
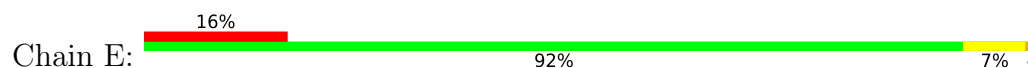


- Molecule 4: Cytochrome c1, heme protein, mitochondrial

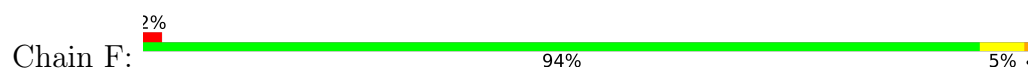




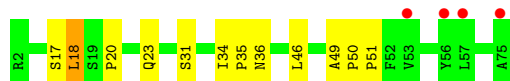
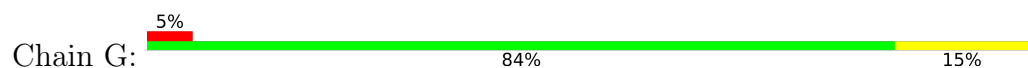
- Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial



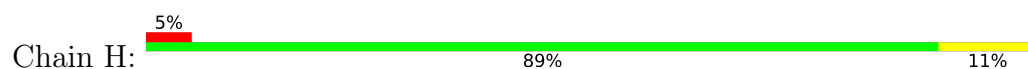
- Molecule 6: Cytochrome b-c1 complex subunit 7



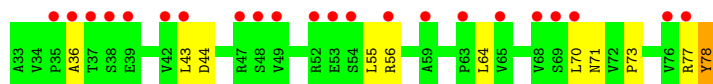
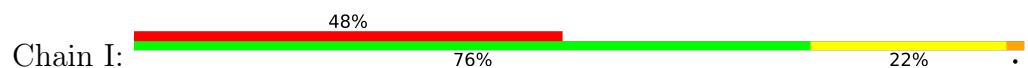
- Molecule 7: Cytochrome b-c1 complex subunit 8



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

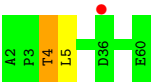


- Molecule 9: Cytochrome b-c1 complex subunit Rieske, mitochondrial



- 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	212.36Å 212.36Å 345.91Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	60.92 – 3.30 60.92 – 3.30	Depositor EDS
% Data completeness (in resolution range)	69.5 (60.92-3.30) 69.5 (60.92-3.30)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.42 (at 3.33Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.214 , 0.244 0.217 , 0.243	Depositor DCC
R_{free} test set	2445 reflections (3.51%)	wwPDB-VP
Wilson B-factor (Å ²)	89.9	Xtriage
Anisotropy	0.231	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 65.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	16262	wwPDB-VP
Average B, all atoms (Å ²)	109.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.78% 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: PO4, JHB, CDL, HEC, 6PE, PG4, PX4, LMT, PEE, HEM, FES

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	1.08	0/3462	1.52	6/4700 (0.1%)
2	B	1.09	0/3165	1.54	0/4296
3	C	1.02	0/3092	1.53	2/4231 (0.0%)
4	D	1.03	0/1935	1.47	0/2632
5	E	1.11	0/1507	1.52	0/2044
6	F	1.00	0/867	1.54	0/1168
7	G	1.03	0/641	1.46	0/868
8	H	1.06	0/522	1.60	0/704
9	I	1.25	0/328	1.67	1/447 (0.2%)
10	J	1.01	0/500	1.60	0/675
All	All	1.06	0/16019	1.53	9/21765 (0.0%)

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
2	B	0	1
8	H	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	44	ASP	CA-CB-CG	6.22	118.82	112.60
1	A	423	ALA	CA-C-N	5.70	125.53	121.65
1	A	423	ALA	C-N-CA	5.70	125.53	121.65
1	A	66	GLY	CA-C-O	-5.58	118.59	122.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	371	GLY	CA-C-O	-5.52	118.42	122.23

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	170	ASN	Peptide
8	H	49	GLN	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	3391	0	3286	31	0
2	B	3108	0	3067	24	0
3	C	2996	0	3058	21	0
4	D	1876	0	1806	17	0
5	E	1474	0	1401	5	0
6	F	848	0	814	5	0
7	G	620	0	624	7	0
8	H	517	0	482	2	0
9	I	324	0	327	8	0
10	J	487	0	487	1	0
11	A	26	0	36	9	0
11	C	26	0	36	0	0
12	A	23	0	19	1	0
13	C	78	0	56	2	0
13	D	54	0	52	1	0
13	E	60	0	64	0	0
14	C	86	0	60	6	0
15	C	31	0	0	3	0
16	C	35	0	46	0	0
17	C	40	0	54	0	0
17	D	37	0	48	1	0
18	C	5	0	0	0	0
18	F	5	0	0	0	0
18	G	15	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	H	5	0	0	0	0
19	D	43	0	32	6	0
20	E	4	0	0	0	0
21	E	37	0	51	0	0
22	A	3	0	0	1	0
22	B	1	0	0	0	0
22	C	4	0	0	0	0
22	D	2	0	0	0	0
22	F	1	0	0	0	0
All	All	16262	0	15906	118	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 4.

The worst 5 of 118 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	19:D:501:HEC:CAB	2.19	1.29
4:D:37:CYS:SG	19:D:501:HEC:C3B	2.54	0.94
4:D:37:CYS:SG	19:D:501:HEC:CBB	2.59	0.91
1:A:432:PRO:CG	11:A:503:PG4:H51	2.10	0.82
4:D:37:CYS:SG	19:D:501:HEC:HBB3	2.19	0.82

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	435/444 (98%)	410 (94%)	23 (5%)	2 (0%)	24 55
2	B	411/420 (98%)	388 (94%)	22 (5%)	1 (0%)	43 71

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	C	376/378 (100%)	353 (94%)	21 (6%)	2 (0%)	24 55
4	D	237/239 (99%)	217 (92%)	18 (8%)	2 (1%)	16 45
5	E	194/196 (99%)	176 (91%)	14 (7%)	4 (2%)	5 26
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%)	41 (93%)	2 (4%)	1 (2%)	5 25
10	J	57/59 (97%)	54 (95%)	3 (5%)	0	100 100
All	All	1986/2020 (98%)	1864 (94%)	110 (6%)	12 (1%)	21 52

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	31	SER
1	A	315	ALA
4	D	145	GLU
5	E	177	PRO
4	D	142	SER

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	362/370 (98%)	358 (99%)	4 (1%)	65 76
2	B	323/329 (98%)	316 (98%)	7 (2%)	45 66
3	C	325/326 (100%)	318 (98%)	7 (2%)	45 66
4	D	198/204 (97%)	197 (100%)	1 (0%)	81 83
5	E	155/168 (92%)	152 (98%)	3 (2%)	50 68
6	F	85/91 (93%)	82 (96%)	3 (4%)	32 58
7	G	65/66 (98%)	62 (95%)	3 (5%)	24 53
8	H	59/62 (95%)	57 (97%)	2 (3%)	32 59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	I	35/38 (92%)	34 (97%)	1 (3%)	37	62
10	J	49/49 (100%)	48 (98%)	1 (2%)	48	68
All	All	1656/1703 (97%)	1624 (98%)	32 (2%)	50	68

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	H	27	LEU
8	H	39	LEU
3	C	185	LEU
3	C	160	LEU
9	I	78	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	263	ASN
4	D	50	HIS
8	H	23	GLN
4	D	6	HIS
4	D	71	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

24 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$
12	6PE	A	502	-	22,22,26	0.41	0	25,27,31	0.65	0
18	PO4	G	102	-	4,4,4	0.66	0	6,6,6	0.43	0
20	FES	E	201	5	0,4,4	-	-	-	-	-
16	LMT	C	405	-	36,36,36	0.73	1 (2%)	47,47,47	1.42	7 (14%)
17	PEE	C	409	-	39,39,50	0.69	1 (2%)	42,44,55	0.63	0
11	PG4	A	503	-	12,12,12	0.44	0	11,11,11	0.33	0
11	PG4	C	406	-	12,12,12	0.27	0	11,11,11	0.22	0
13	CDL	E	203	-	59,59,99	0.38	0	65,71,111	0.61	1 (1%)
18	PO4	G	103	-	4,4,4	0.46	0	6,6,6	0.56	0
11	PG4	C	407	-	12,12,12	0.30	0	11,11,11	0.15	0
13	CDL	C	408	-	43,43,99	0.49	0	49,55,111	0.84	2 (4%)
18	PO4	H	101	-	4,4,4	0.76	0	6,6,6	0.37	0
21	PX4	E	202	-	36,36,45	0.42	0	42,44,53	0.68	1 (2%)
15	JHB	C	404	-	34,34,34	2.00	5 (14%)	48,50,50	1.29	4 (8%)
14	HEM	C	403	3	50,50,50	1.55	9 (18%)	66,82,82	1.53	13 (19%)
14	HEM	C	402	3	50,50,50	1.61	10 (20%)	66,82,82	1.52	10 (15%)
13	CDL	D	502	-	53,53,99	0.42	0	59,65,111	0.59	0
13	CDL	C	401	-	33,33,99	0.51	0	37,43,111	0.81	1 (2%)
18	PO4	C	410	-	4,4,4	0.74	0	6,6,6	0.41	0
18	PO4	F	501	-	4,4,4	0.63	0	6,6,6	0.47	0
11	PG4	A	501	-	12,12,12	0.23	0	11,11,11	0.14	0
19	HEC	D	501	4	50,50,50	2.83	29 (58%)	68,82,82	2.55	32 (47%)
17	PEE	D	503	-	36,36,50	0.79	1 (2%)	39,41,55	0.67	1 (2%)
18	PO4	G	101	-	4,4,4	0.73	0	6,6,6	0.41	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
12	6PE	A	502	-	-	13/26/26/30	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	CDL	D	502	-	-	25/63/63/110	-
17	PEE	C	409	-	1/1/4/8	17/43/43/54	-
13	CDL	C	401	-	-	21/41/41/110	-
11	PG4	A	503	-	-	6/10/10/10	-
13	CDL	C	408	-	-	21/52/52/110	-
11	PG4	A	501	-	-	6/10/10/10	-
11	PG4	C	406	-	-	5/10/10/10	-
13	CDL	E	203	-	-	34/69/69/110	-
14	HEM	C	403	3	-	4/14/54/54	-
21	PX4	E	202	-	-	21/40/40/49	-
19	HEC	D	501	4	1/1/3/7	7/14/54/54	-
17	PEE	D	503	-	1/1/4/8	23/40/40/54	-
20	FES	E	201	5	-	-	0/1/1/1
11	PG4	C	407	-	-	4/10/10/10	-
15	JHB	C	404	-	-	0/13/13/13	0/4/4/4
14	HEM	C	402	3	-	6/14/54/54	-
16	LMT	C	405	-	-	11/21/61/61	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	C	404	JHB	C5-C4	7.02	1.52	1.41
15	C	404	JHB	C7-C8	6.57	1.51	1.37
19	D	501	HEC	FE-ND	5.18	2.10	1.94
19	D	501	HEC	C2A-C3A	5.14	1.47	1.36
19	D	501	HEC	CHB-C4A	4.97	1.48	1.38

The worst 5 of 72 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	D	501	HEC	C3D-C4D-ND	6.06	116.23	110.36
19	D	501	HEC	C1B-C2B-C3B	-5.65	101.01	106.96
19	D	501	HEC	C2A-C1A-NA	5.54	115.71	110.32
19	D	501	HEC	C2B-C1B-NB	5.44	116.40	109.88
19	D	501	HEC	C2D-C1D-ND	5.35	116.18	109.84

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
17	C	409	PEE	C2
17	D	503	PEE	C2
19	D	501	HEC	NA

5 of 224 torsion outliers are listed below:

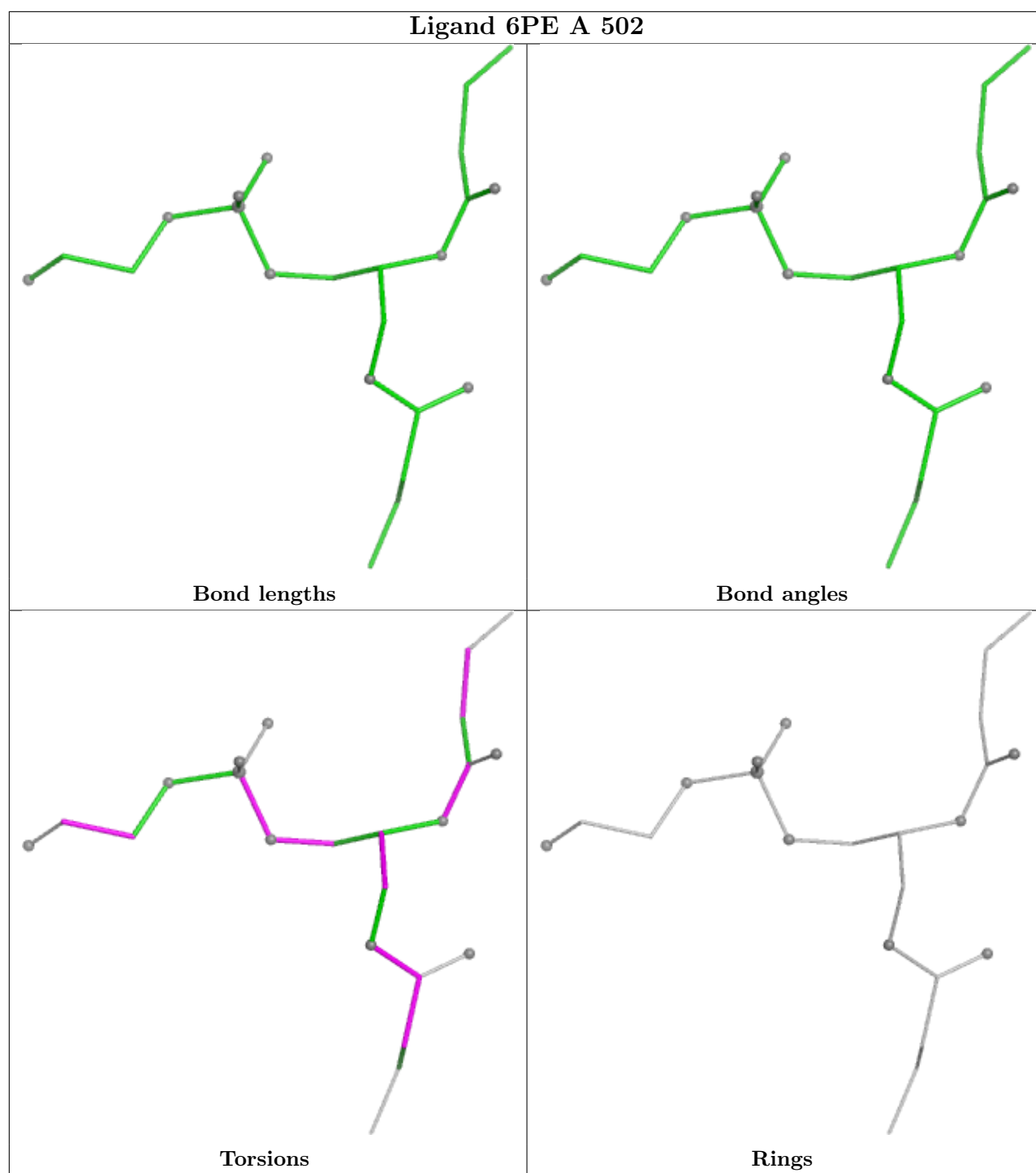
Mol	Chain	Res	Type	Atoms
12	A	502	6PE	C1-O3-P1-O1
12	A	502	6PE	C11-C10-O6-C2
12	A	502	6PE	O8-C16-C17-N1
13	C	401	CDL	CB2-OB2-PB2-OB3
13	C	401	CDL	CB3-OB5-PB2-OB4

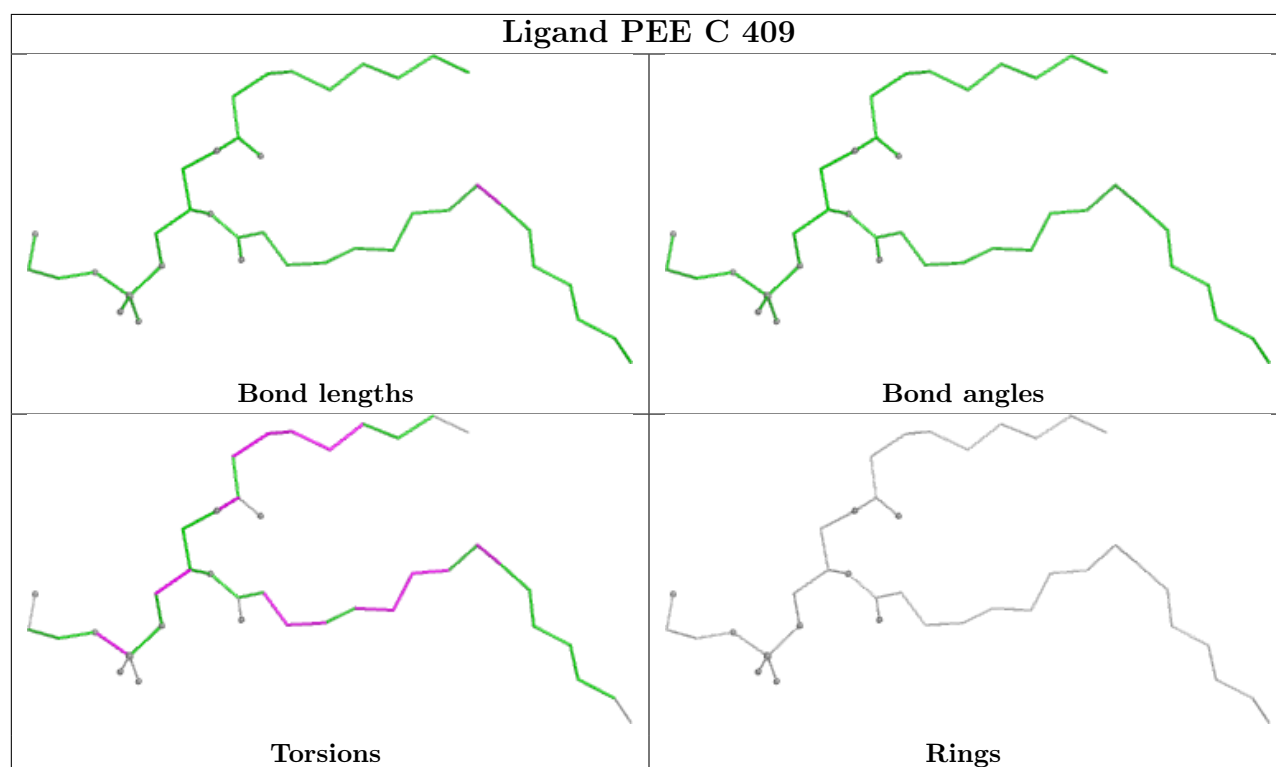
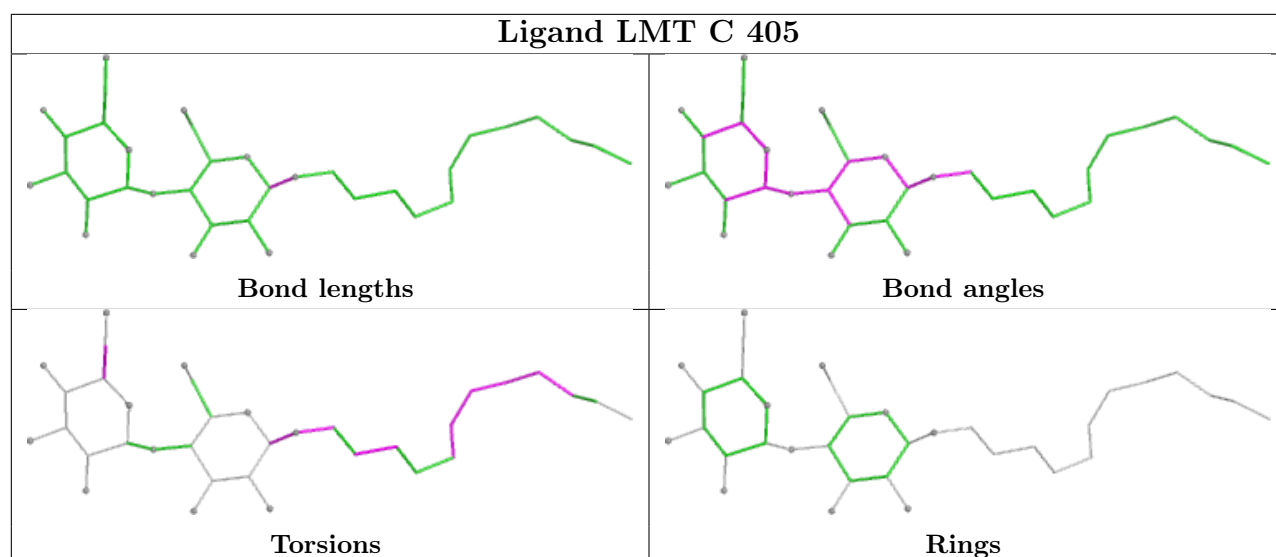
There are no ring outliers.

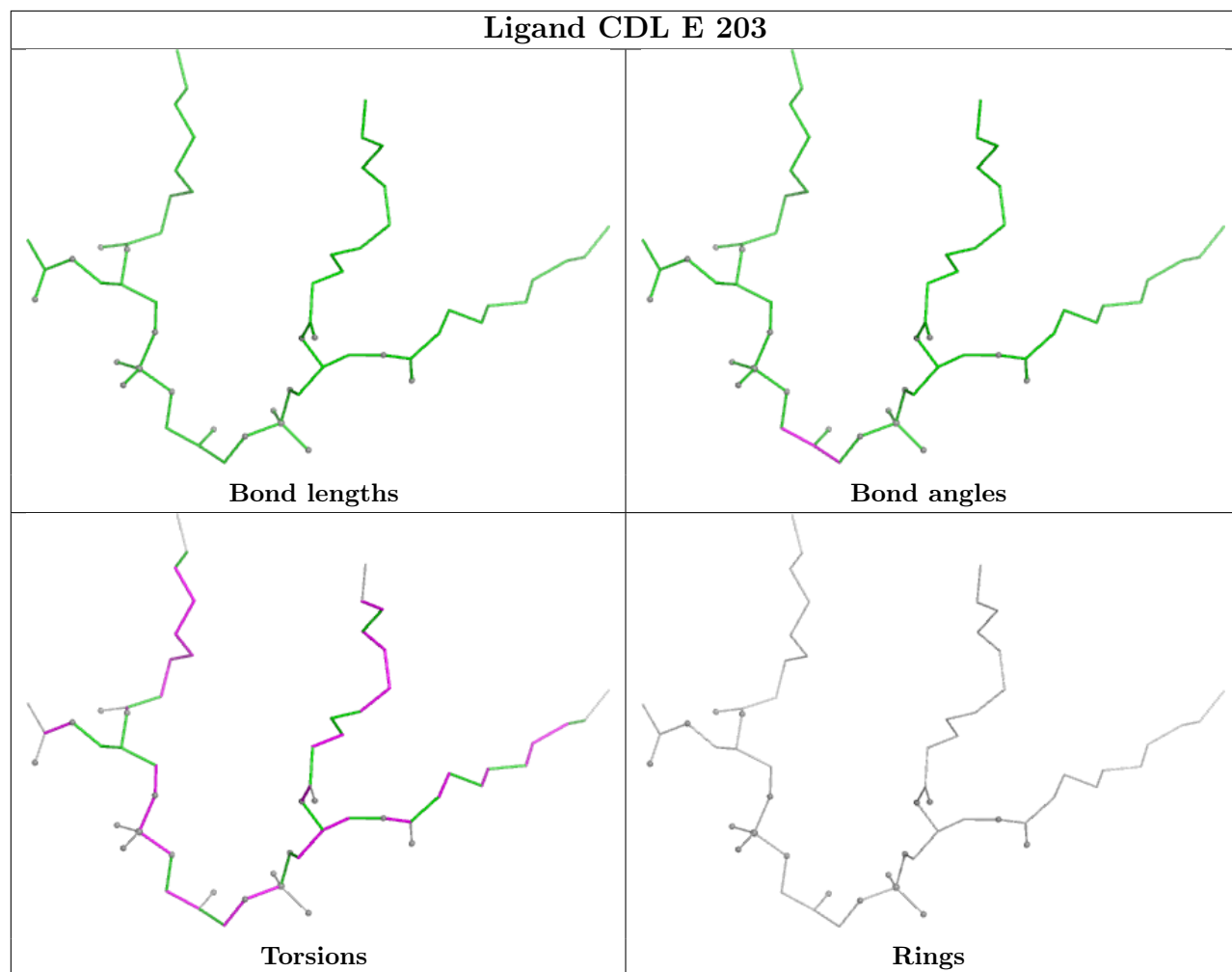
9 monomers are involved in 28 short contacts:

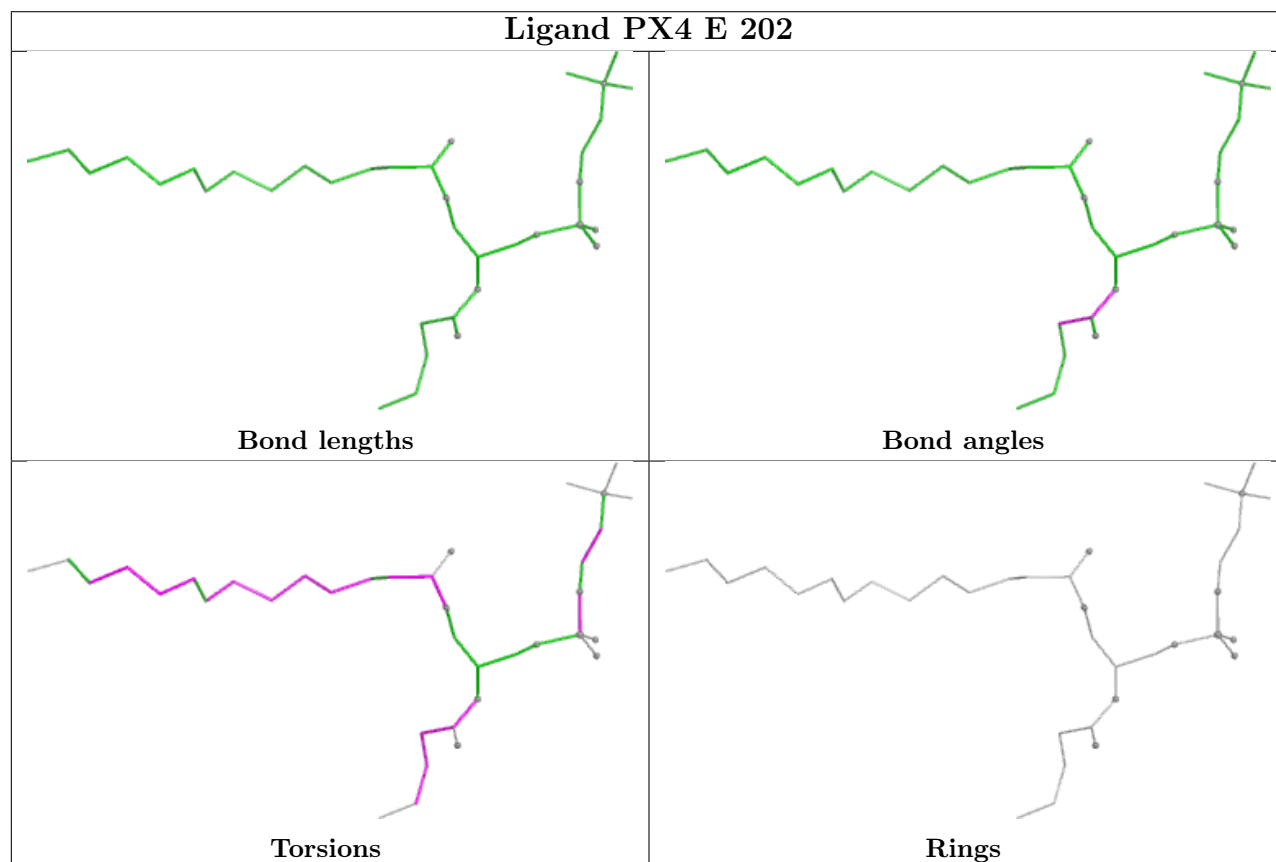
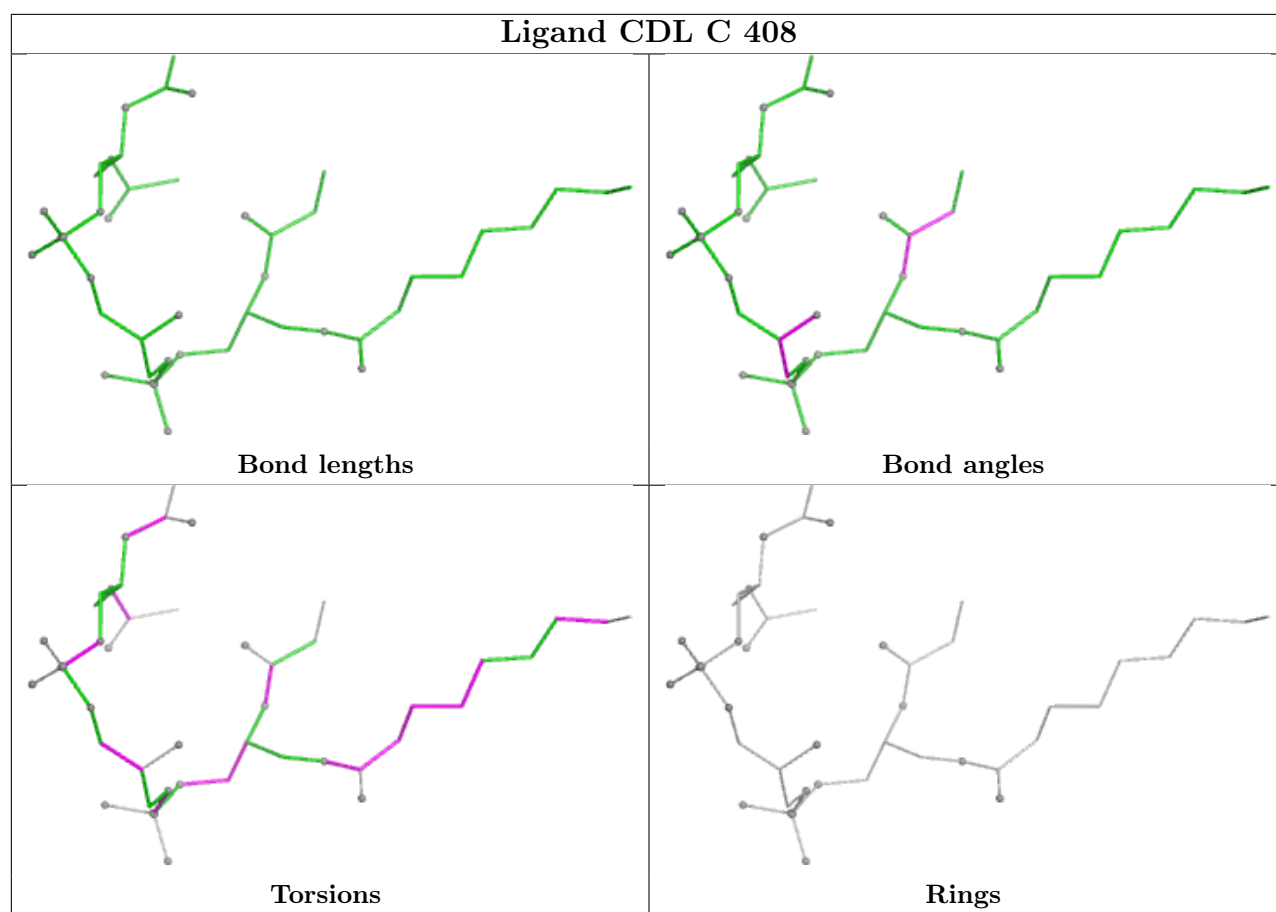
Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	A	502	6PE	1	0
11	A	503	PG4	9	0
15	C	404	JHB	3	0
14	C	403	HEM	4	0
14	C	402	HEM	2	0
13	D	502	CDL	1	0
13	C	401	CDL	2	0
19	D	501	HEC	6	0
17	D	503	PEE	1	0

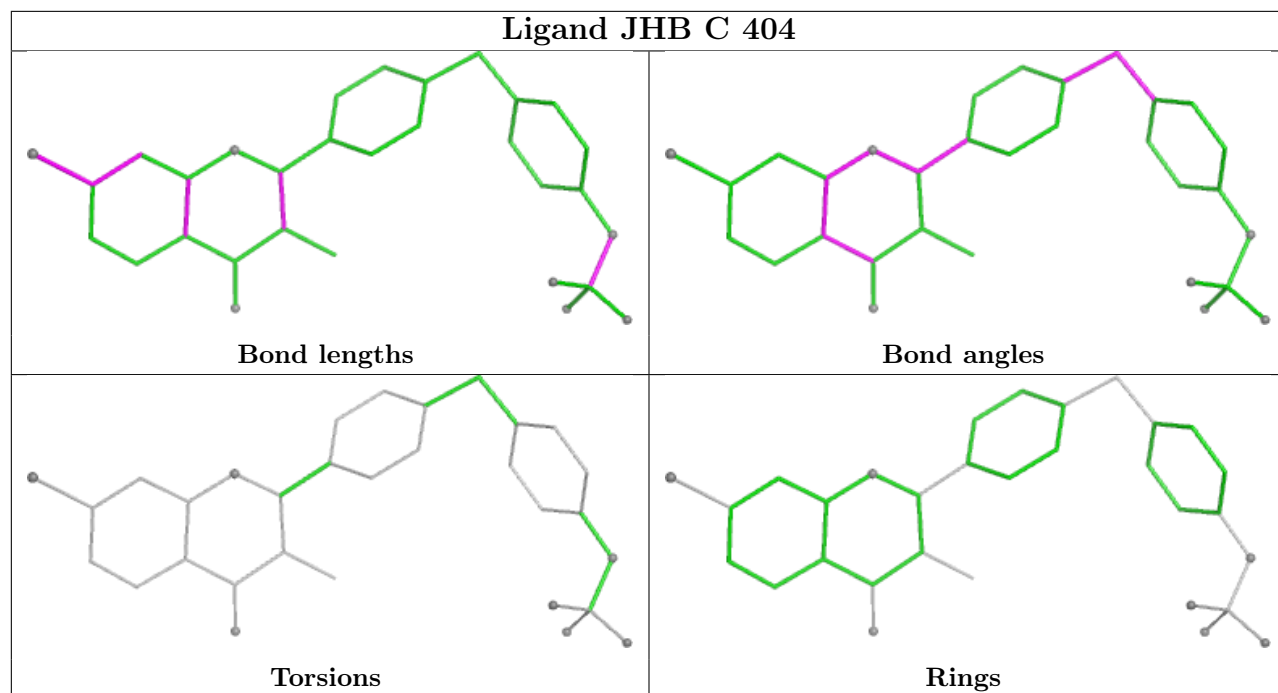
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

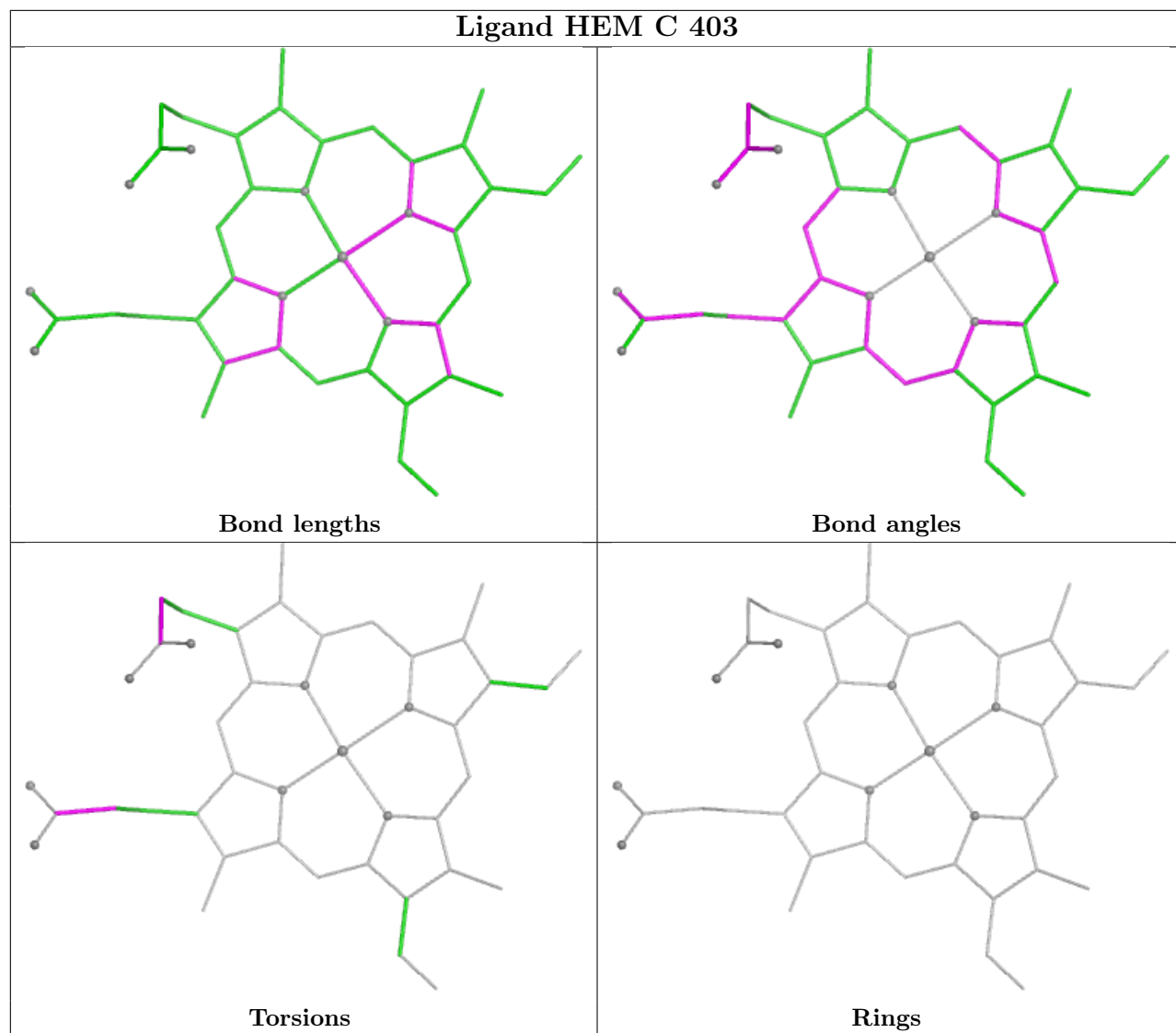


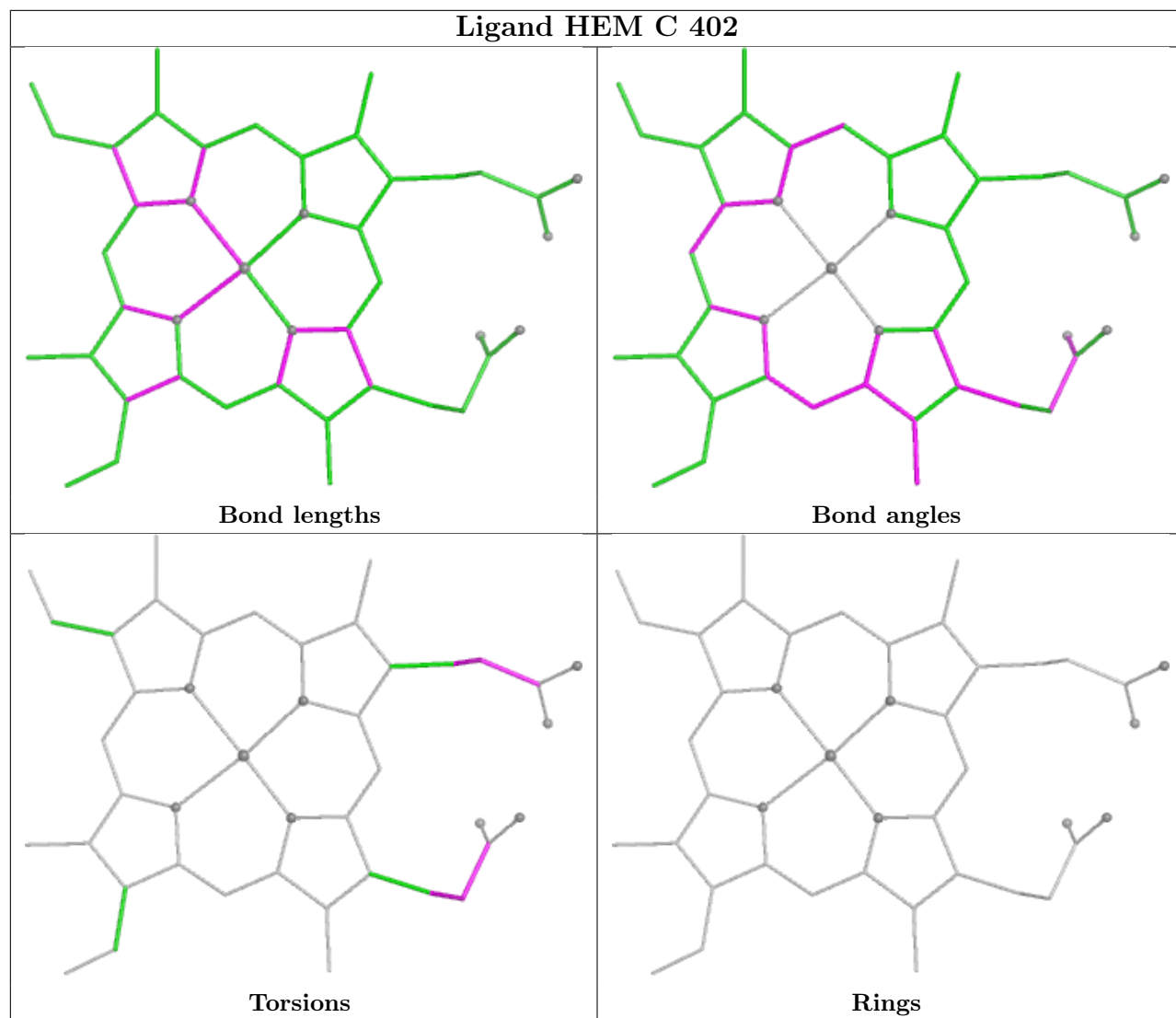


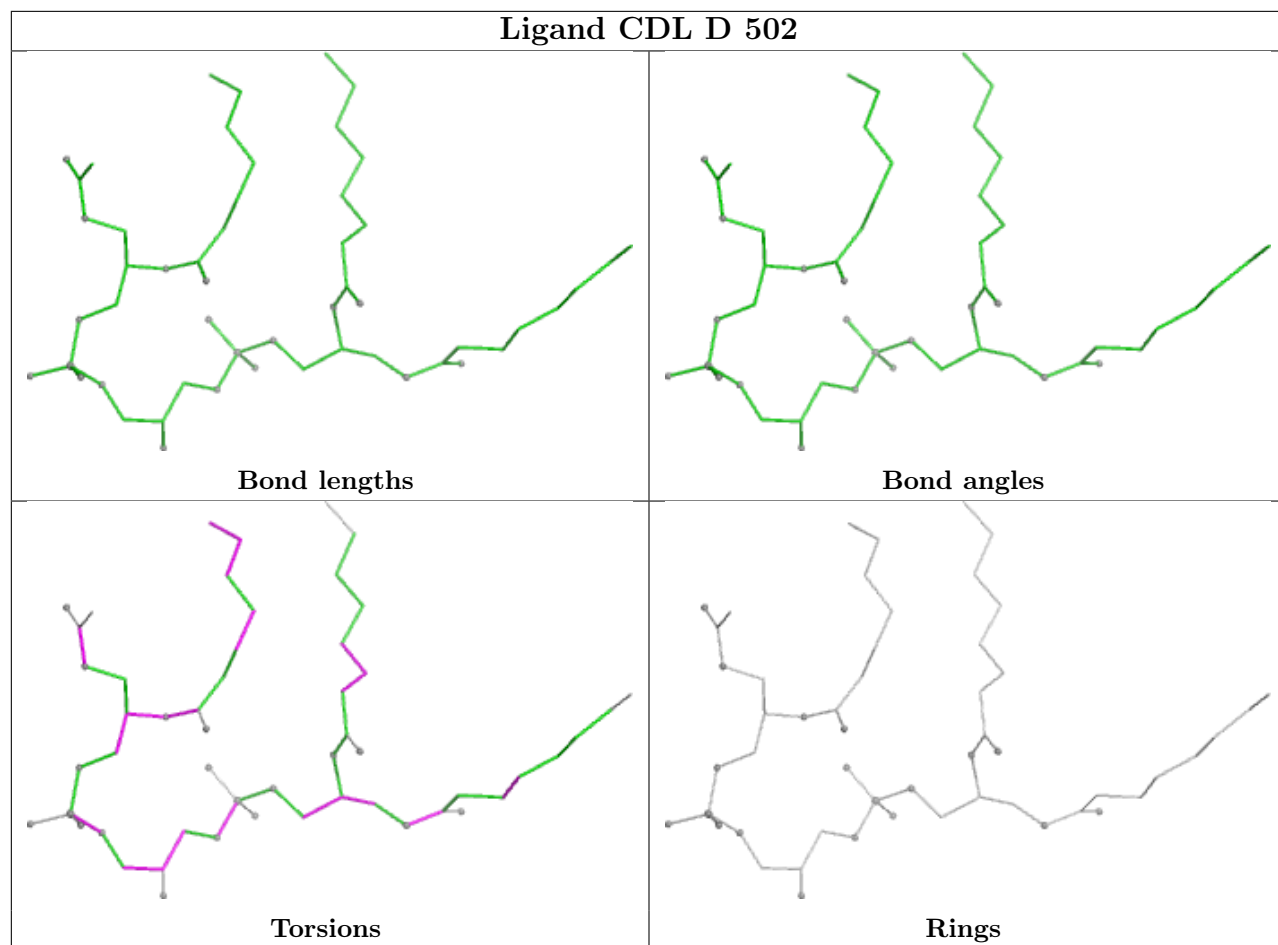


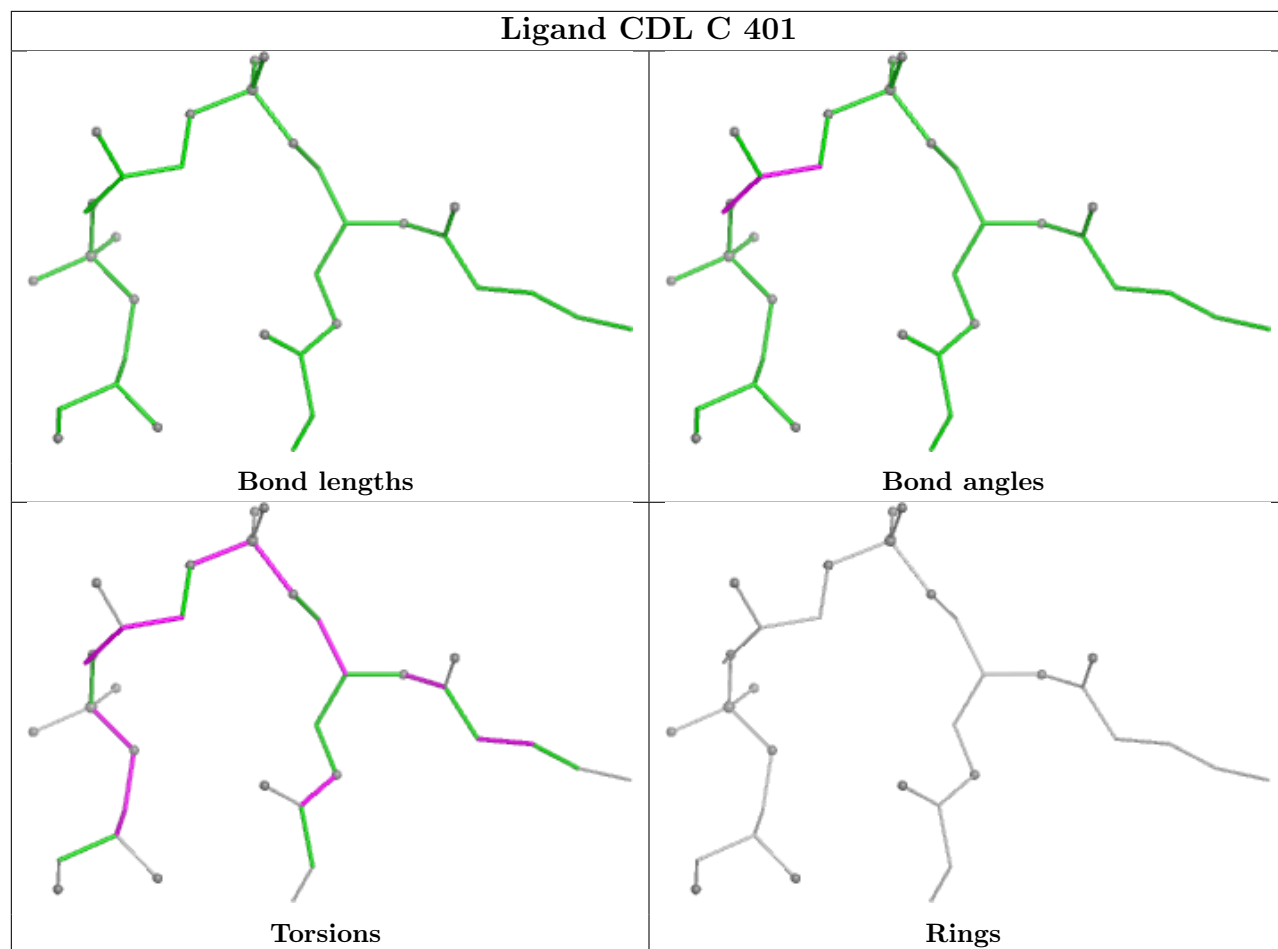


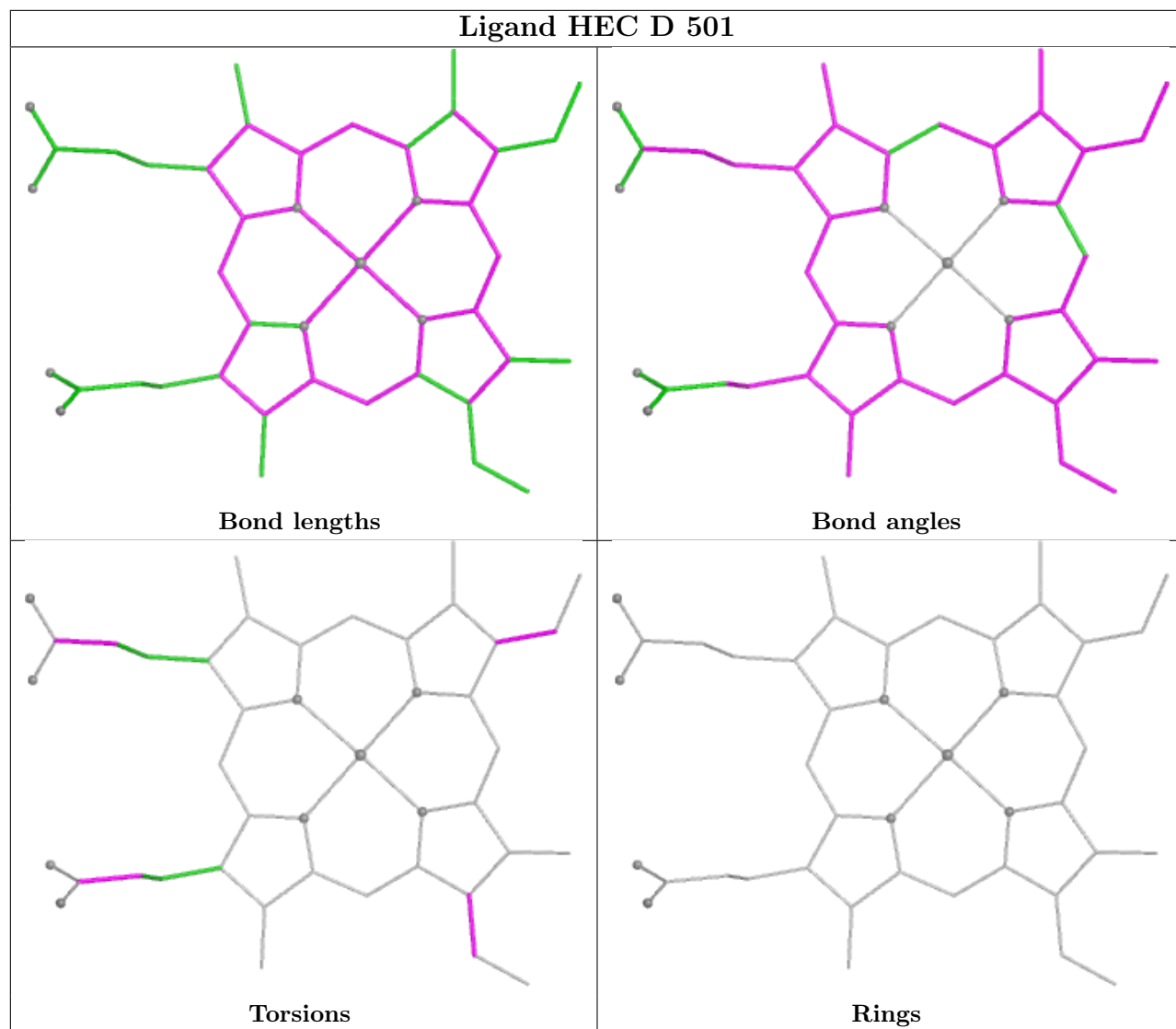


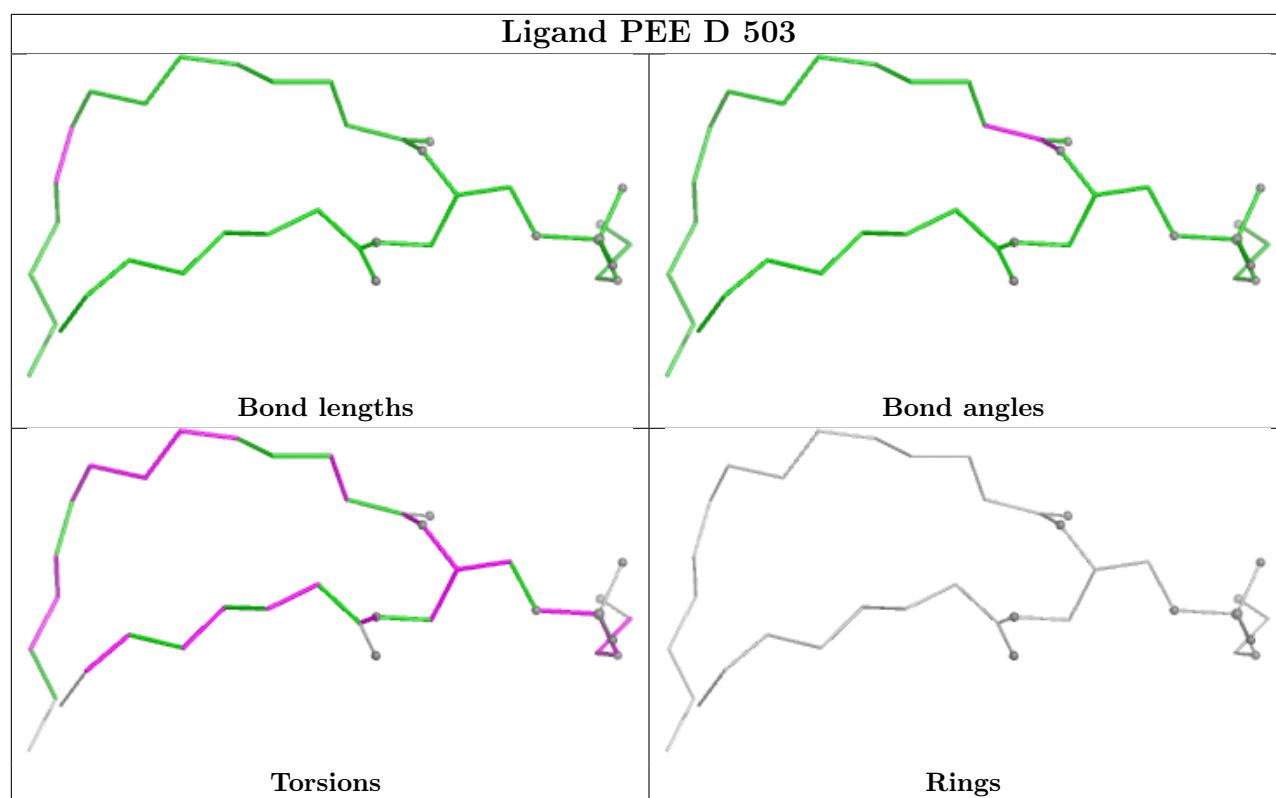












5.7 Other polymers [i](#)

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	439/444 (98%)	-0.01	21 (4%)	35	24	72, 96, 128, 161	0
2	B	415/420 (98%)	0.08	19 (4%)	37	25	72, 98, 129, 178	0
3	C	378/378 (100%)	0.15	22 (5%)	29	19	72, 86, 116, 137	0
4	D	239/239 (100%)	0.22	15 (6%)	26	17	109, 135, 160, 186	0
5	E	196/196 (100%)	0.82	32 (16%)	4	4	82, 143, 179, 195	0
6	F	99/99 (100%)	-0.07	2 (2%)	65	46	80, 98, 141, 185	0
7	G	74/74 (100%)	0.09	4 (5%)	31	21	74, 98, 151, 157	0
8	H	65/65 (100%)	0.12	3 (4%)	37	25	143, 166, 184, 189	0
9	I	46/46 (100%)	2.20	22 (47%)	0	0	122, 144, 165, 176	0
10	J	59/59 (100%)	0.01	1 (1%)	69	50	90, 106, 151, 157	0
All	All	2010/2020 (99%)	0.20	141 (7%)	22	15	72, 104, 164, 195	0

The worst 5 of 141 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
9	I	37	THR	9.0
4	D	77	ASP	6.5
5	E	159	PRO	6.3
5	E	83	GLU	5.9
9	I	38	SER	5.4

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

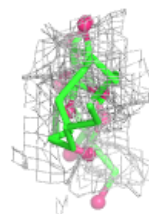
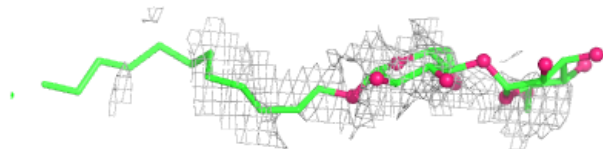
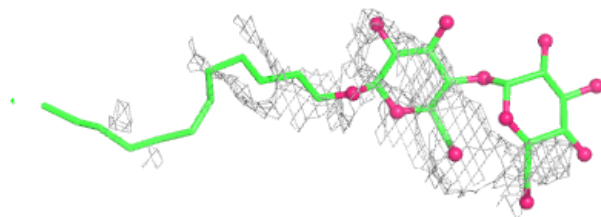
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
16	LMT	C	405	35/35	0.44	0.17	155,168,174,175	0
13	CDL	E	203	60/100	0.64	0.16	130,164,197,201	0
18	PO4	G	102	5/5	0.72	0.09	175,175,177,181	0
11	PG4	A	501	13/13	0.81	0.13	127,137,143,144	0
18	PO4	H	101	5/5	0.82	0.11	209,210,213,216	0
18	PO4	G	101	5/5	0.84	0.10	127,128,130,131	0
18	PO4	G	103	5/5	0.85	0.20	134,134,134,135	0
15	JHB	C	404	31/31	0.85	0.19	90,97,124,128	0
13	CDL	C	401	34/100	0.88	0.13	116,129,138,139	0
17	PEE	D	503	37/51	0.91	0.14	89,106,110,110	0
18	PO4	F	501	5/5	0.91	0.30	153,156,156,157	0
12	6PE	A	502	23/27	0.91	0.15	109,122,132,132	0
21	PX4	E	202	37/46	0.91	0.24	119,132,142,144	0
11	PG4	A	503	13/13	0.93	0.15	47,57,70,71	0
11	PG4	C	406	13/13	0.93	0.13	91,93,96,96	0
13	CDL	D	502	54/100	0.93	0.12	112,152,177,180	0
18	PO4	C	410	5/5	0.93	0.10	159,161,162,162	0
11	PG4	C	407	13/13	0.93	0.11	105,108,113,114	0
20	FES	E	201	4/4	0.95	0.05	214,214,217,220	0
17	PEE	C	409	40/51	0.96	0.11	82,84,85,85	0
13	CDL	C	408	44/100	0.96	0.11	86,92,96,96	0
19	HEC	D	501	43/43	0.98	0.07	126,132,135,138	0
14	HEM	C	402	43/43	0.98	0.08	76,77,79,79	0
14	HEM	C	403	43/43	0.98	0.08	73,73,73,74	0

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

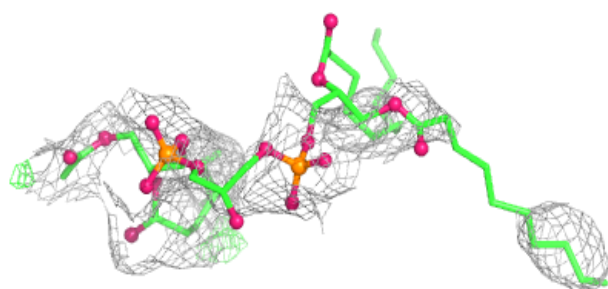
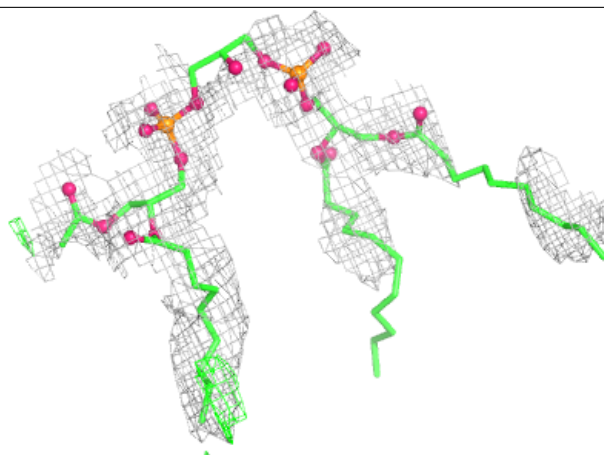
Electron density around LMT C 405:

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

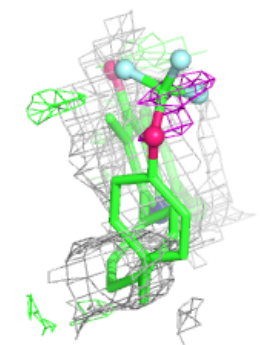
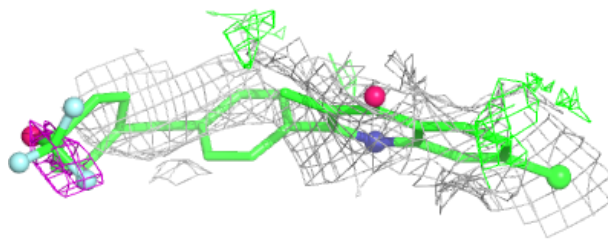
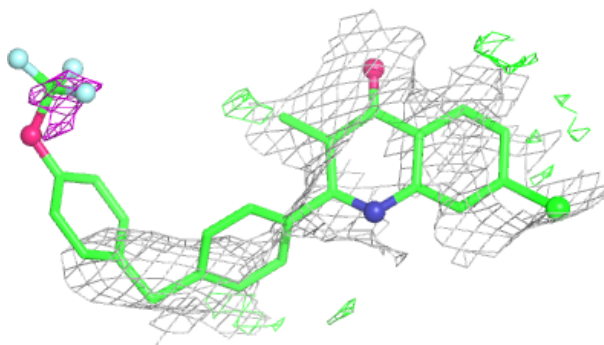


Electron density around CDL E 203:

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

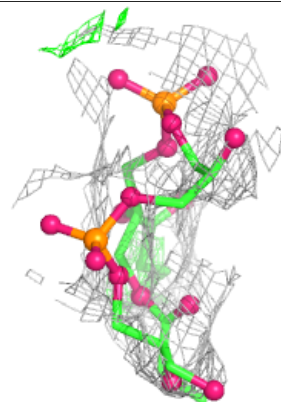
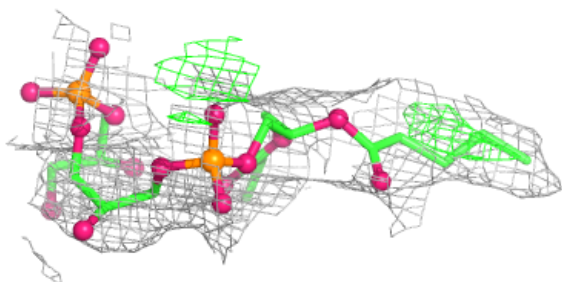
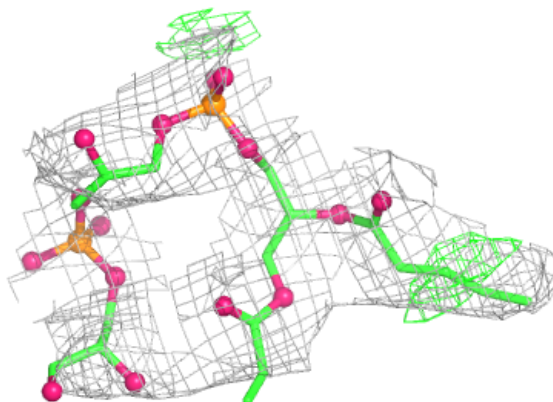
**Electron density around JHB C 404:**

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

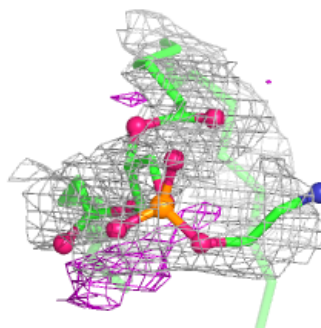
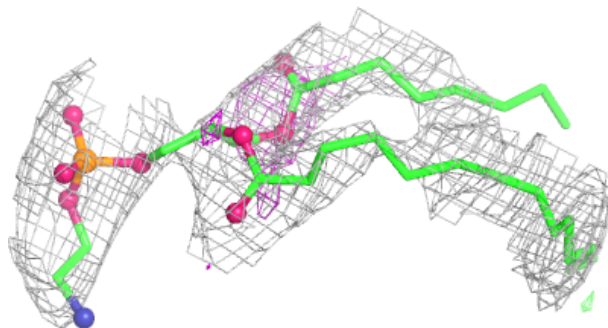
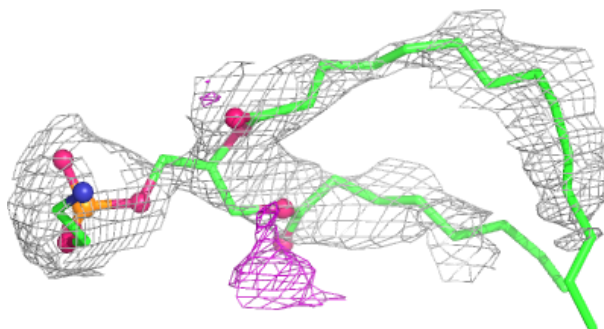


Electron density around CDL C 401:

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

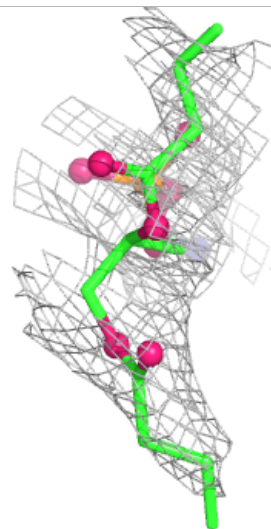
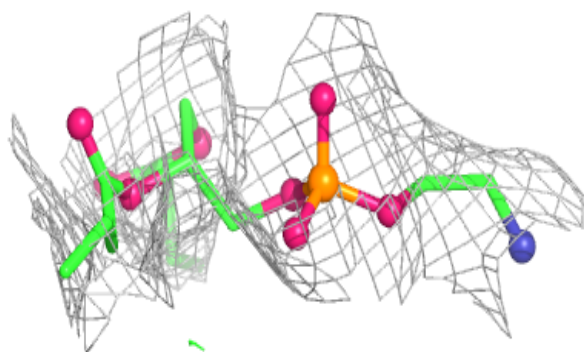
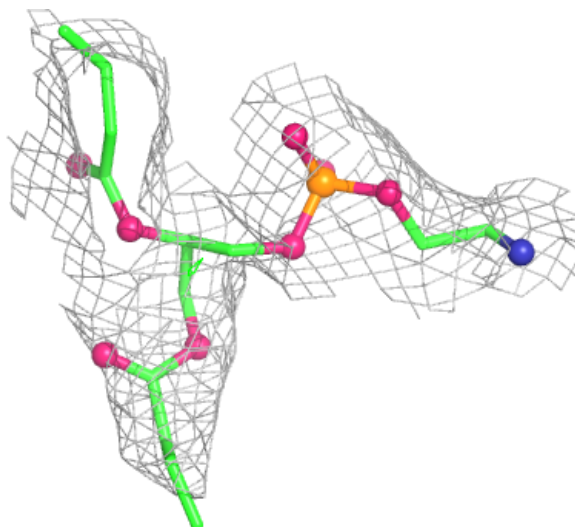
**Electron density around PEE D 503:**

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



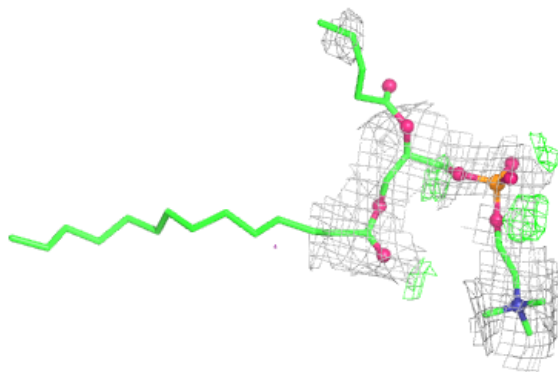
Electron density around 6PE A 502:

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

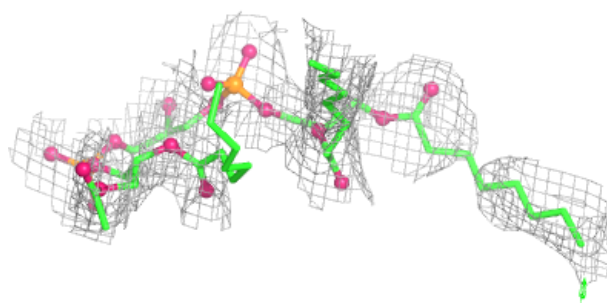
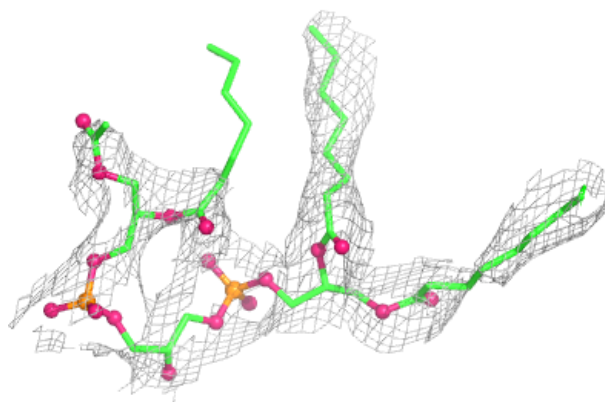


Electron density around PX4 E 202:

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

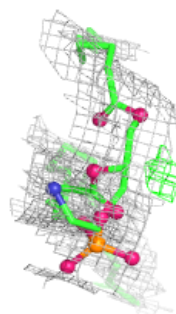
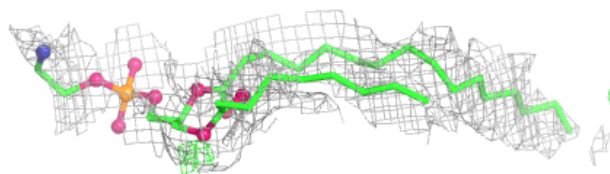
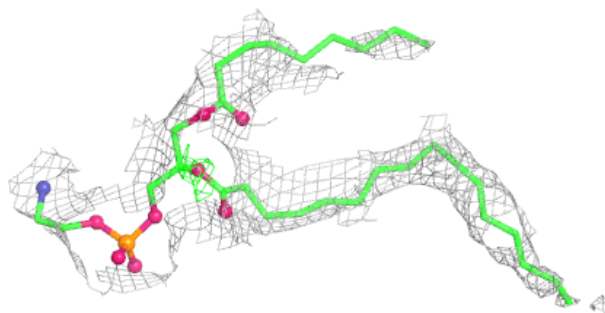
**Electron density around CDL D 502:**

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

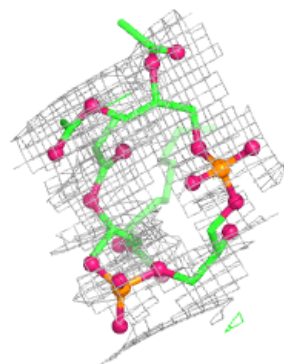
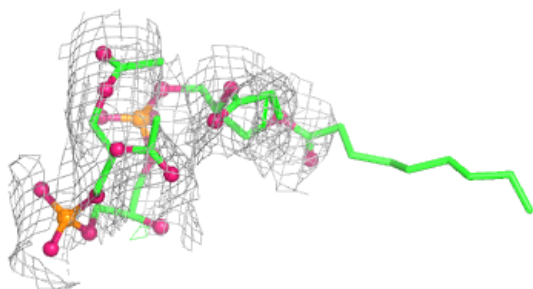
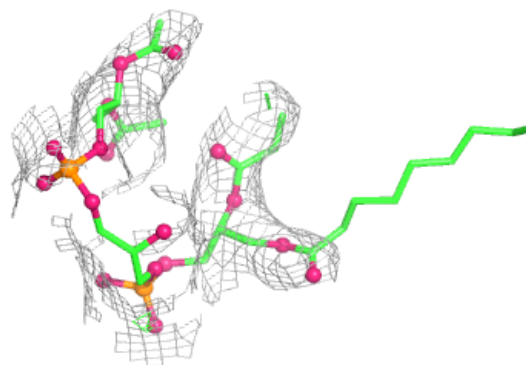


Electron density around PEE C 409:

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

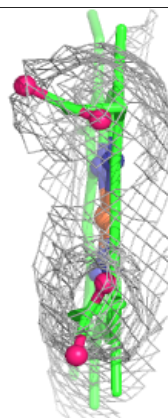
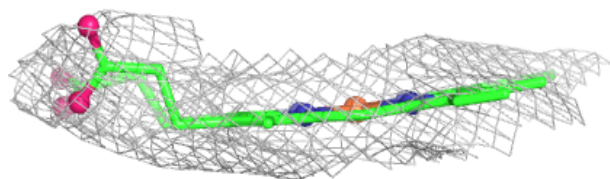
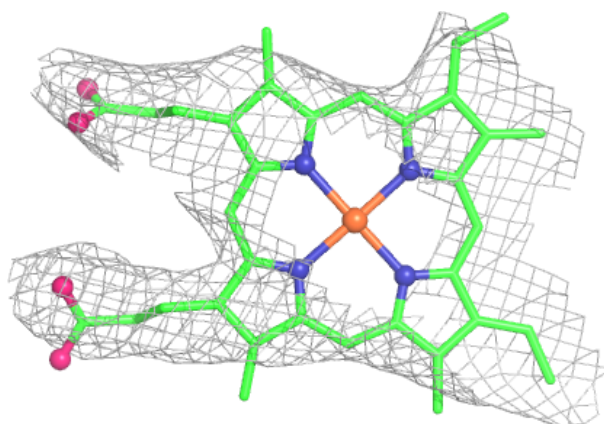
**Electron density around CDL C 408:**

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



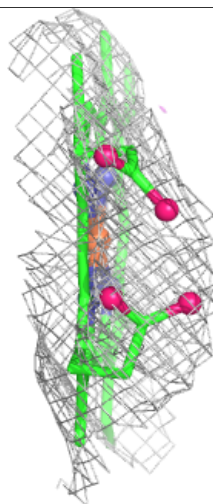
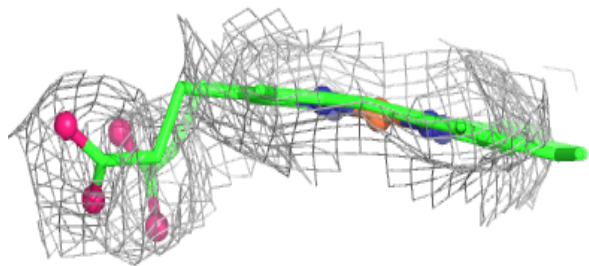
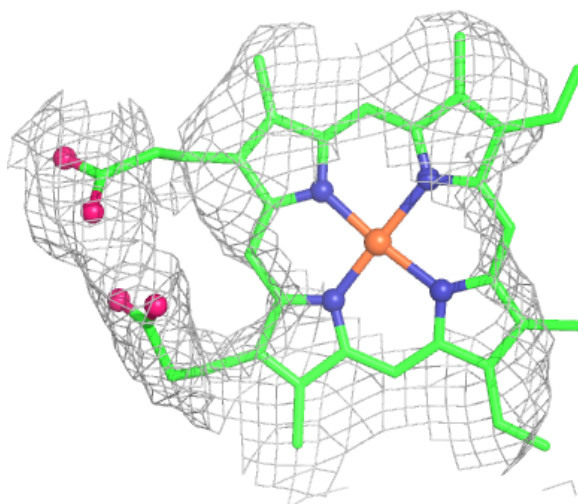
Electron density around HEC D 501:

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



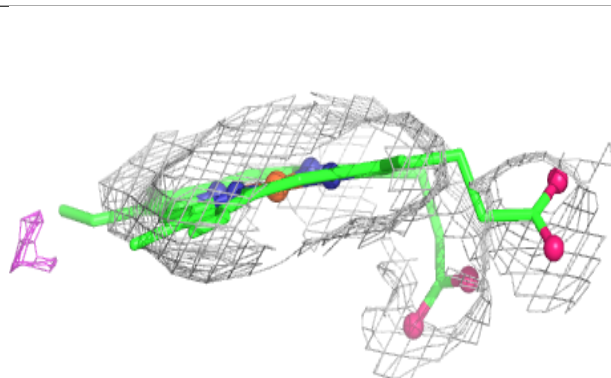
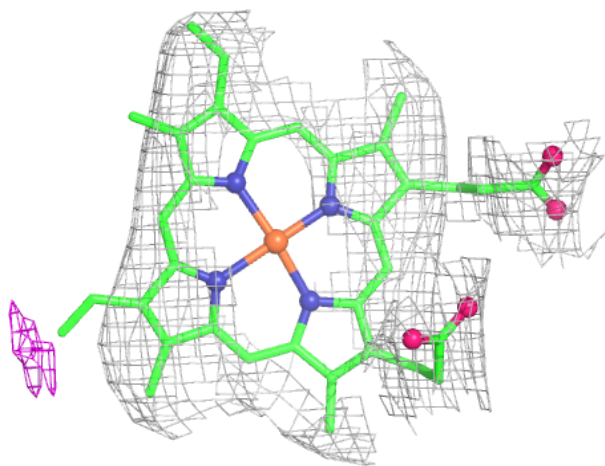
Electron density around HEM C 402:

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



Electron density around HEM C 403:

$2mF_o-DF_c$ (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.