



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 18, 2026 – 01:48 pm BST

PDB ID : 5OKD / pdb_00005okd
Title : Crystal structure of bovine Cytochrome bc1 in complex with inhibitor SCR0911.
Authors : Amporndanai, K.; O'Neill, P.M.; Hasnain, S.S.; Antonyuk, S.V.
Deposited on : 2017-07-25
Resolution : 3.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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:

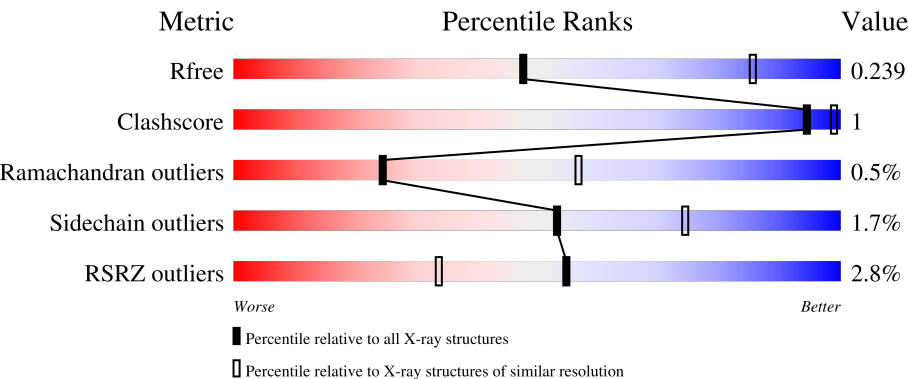
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	480	88% 7%
2	B	453	88% 8%
3	C	379	97% ..
4	D	325	70% 26%
5	E	196	11% 96% .

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Mol	Chain	Length	Quality of chain
6	F	111	
7	G	82	
8	H	91	
9	I	47	
10	J	64	

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
17	PEE	C	409	X	-	-	-
17	PEE	E	204	X	-	-	-
18	HEC	D	501	X	-	-	-

2 Entry composition

There are 22 unique types of molecules in this entry. The entry contains 16469 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	445	Total	C	N	O	S	0	0	0
			3449	2157	608	664	20			

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
2	B	415	Total	C	N	O	S	0	0	0
			3116	1957	553	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
			1884	1205	321	343	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
			1512	951	263	290	8			

- 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
			859	545	156	156	2			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	56	ASP	ASN	conflict	UNP P00129

- 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
			525	318	95	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
			338	209	64	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).

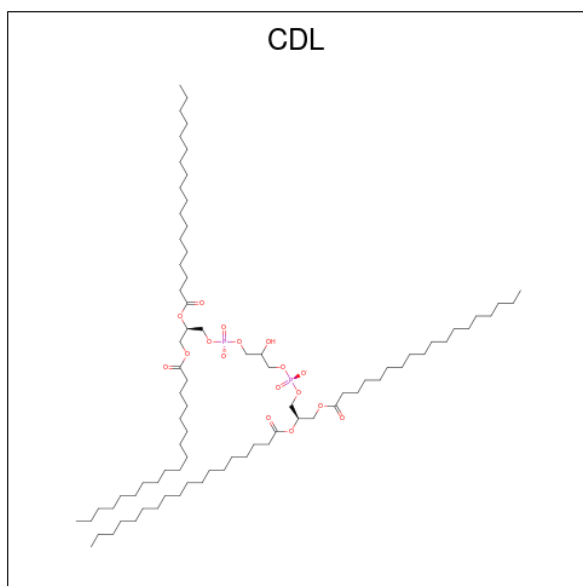


- Molecule 12 is 1,2-DIHEXANOYL-SN-GLYCERO-3-PHOSPHOETHANOLAMINE (CCD ID: 6PE) (formula: $C_{17}H_{33}NO_8P$).



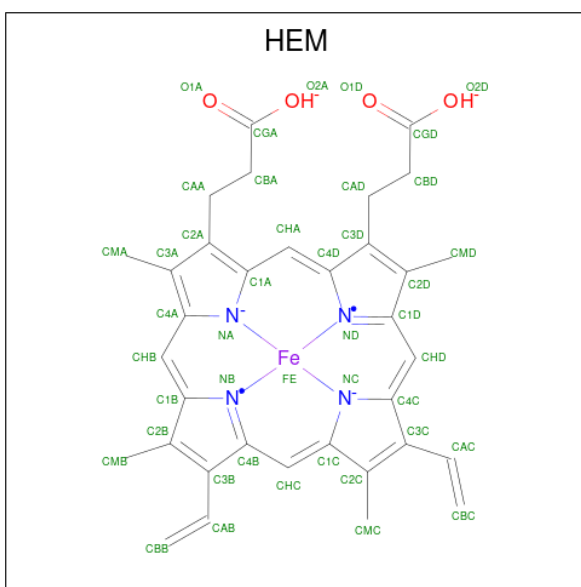
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
12	A	1	Total	C	N	O	P	0	0
			23	13	1	8	1		

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



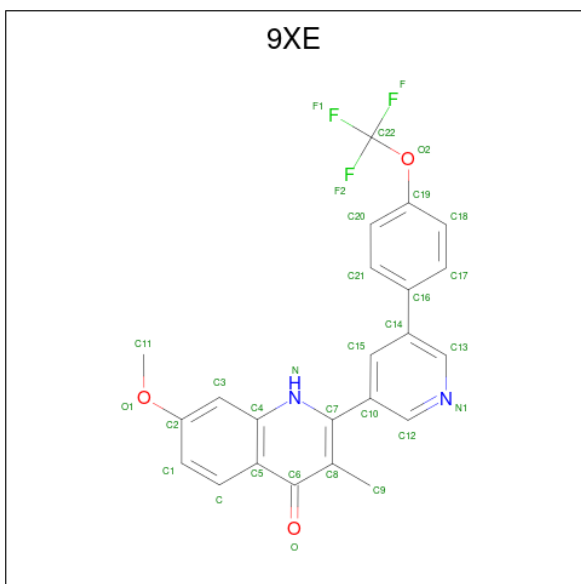
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
13	C	1	Total	C	O	P	0	0
			34	17	15	2		
13	C	1	Total	C	O	P	0	0
			44	25	17	2		
13	D	1	Total	C	O	P	0	0
			54	35	17	2		
13	E	1	Total	C	O	P	0	0
			60	41	17	2		

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



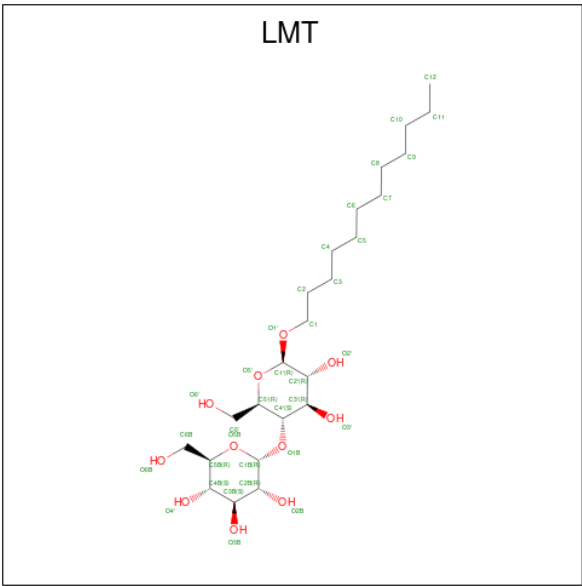
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
14	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
14	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 15 is 7-methoxy-3-methyl-2-[5-[4-(trifluoromethoxy)phenyl]pyridin-3-yl]-1 {H}-quinolin-4-one (CCD ID: 9XE) (formula: $C_{23}H_{17}F_3N_2O_3$).



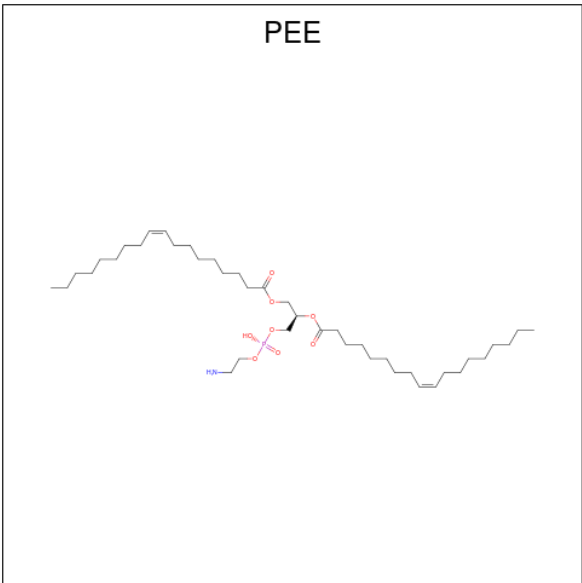
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
15	C	1	Total	C	F	N	O	0	0
			31	23	3	2	3		

- 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).



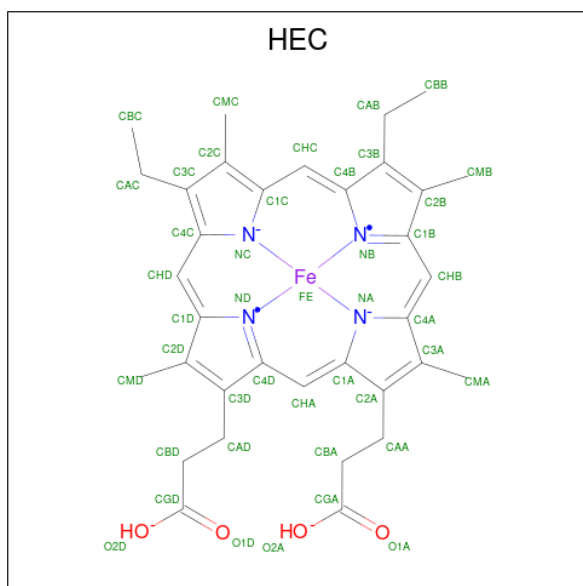
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
17	C	1	Total	C	N	O	P	0	0
			40	30	1	8	1		

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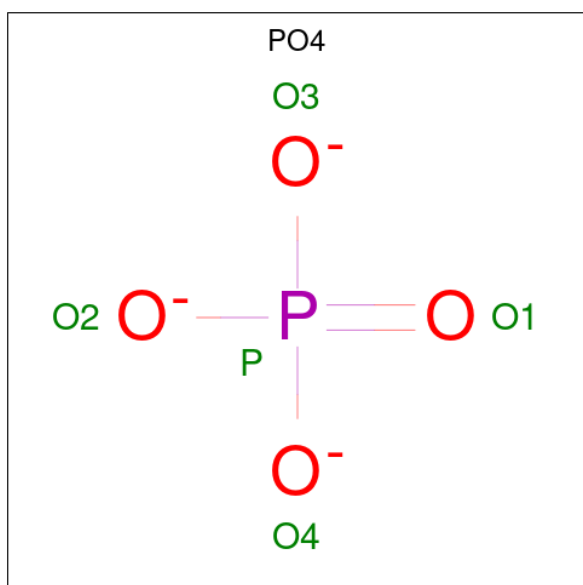
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
17	E	1	Total	C	N	O	P	0	0
			41	31	1	8	1		

- Molecule 18 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{36}FeN_4O_4$).



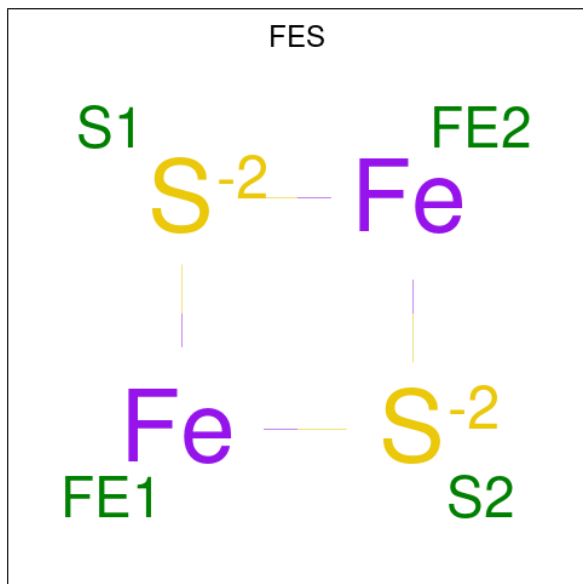
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
18	D	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 19 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



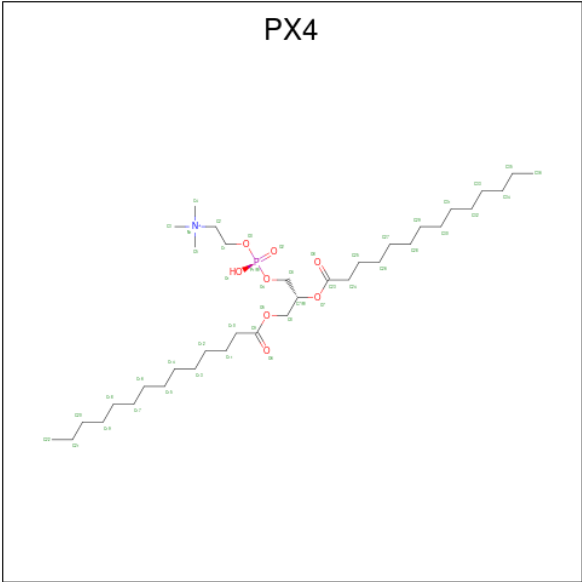
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
19	D	1	Total O P 5 4 1	0	0
19	E	1	Total O P 5 4 1	0	0
19	F	1	Total O P 5 4 1	0	0
19	G	1	Total O P 5 4 1	0	0
19	G	1	Total O P 5 4 1	0	0
19	G	1	Total O P 5 4 1	0	0

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



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 (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		

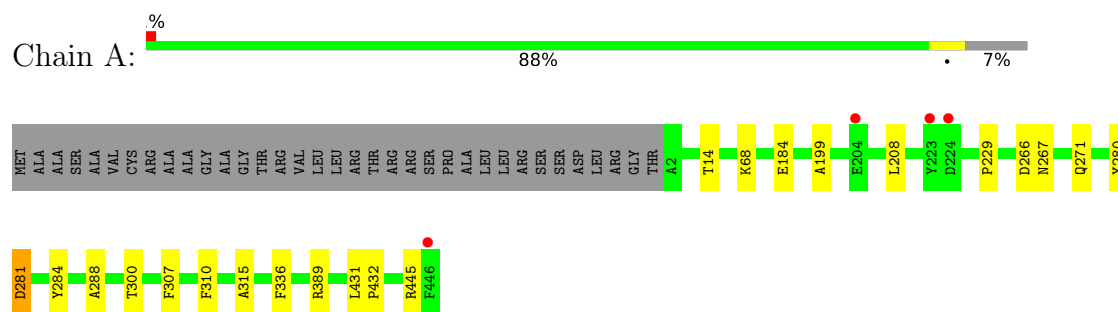
- Molecule 22 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	A	15	Total	O	0	0
			15	15		
22	B	12	Total	O	0	0
			12	12		
22	C	27	Total	O	0	0
			27	27		
22	D	5	Total	O	0	0
			5	5		
22	E	6	Total	O	0	0
			6	6		
22	F	8	Total	O	0	0
			8	8		
22	G	5	Total	O	0	0
			5	5		
22	H	1	Total	O	0	0
			1	1		
22	J	3	Total	O	0	0
			3	3		

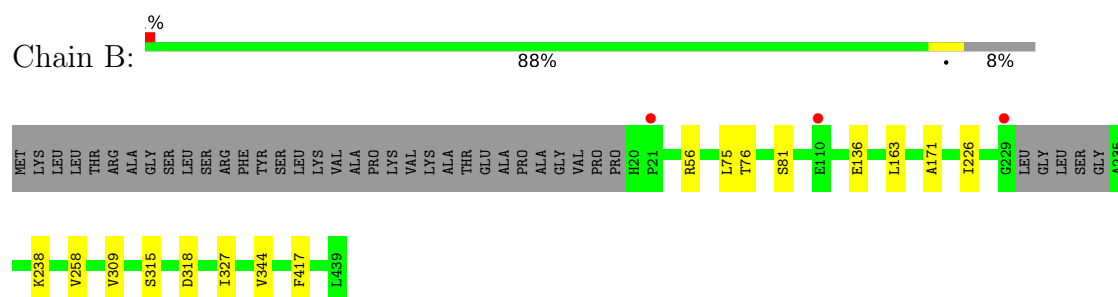
3 Residue-property plots [i](#)

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.

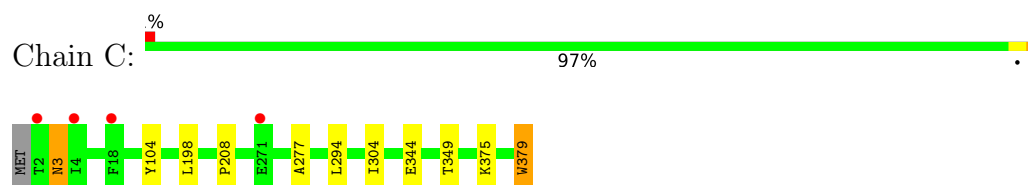
- Molecule 1: Cytochrome b-c1 complex subunit 1, mitochondrial



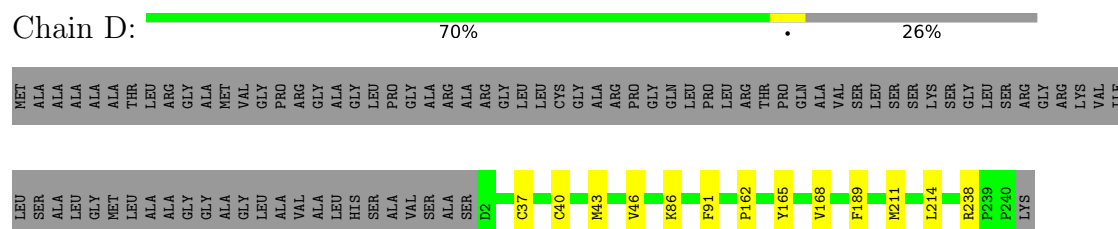
- Molecule 2: Cytochrome b-c1 complex subunit 2, mitochondrial



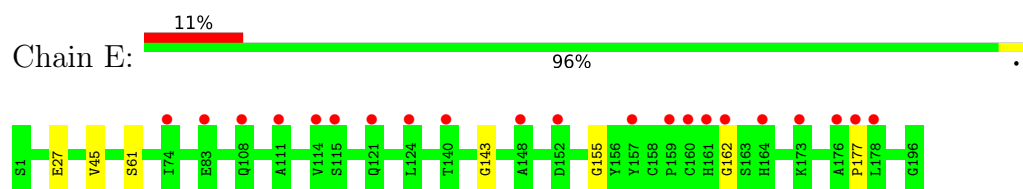
- Molecule 3: Cytochrome b



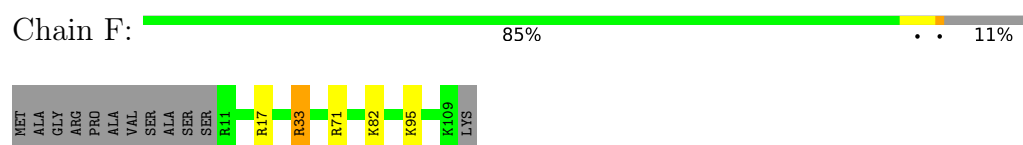
- Molecule 4: Cytochrome c1, heme protein, mitochondrial



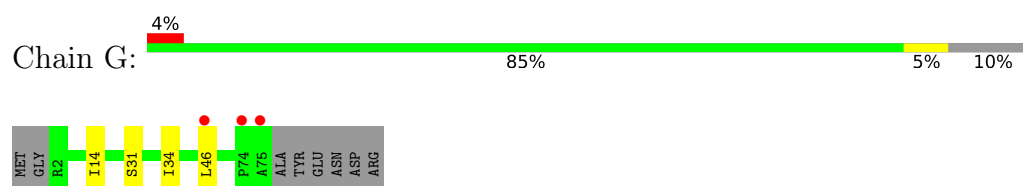
- Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial



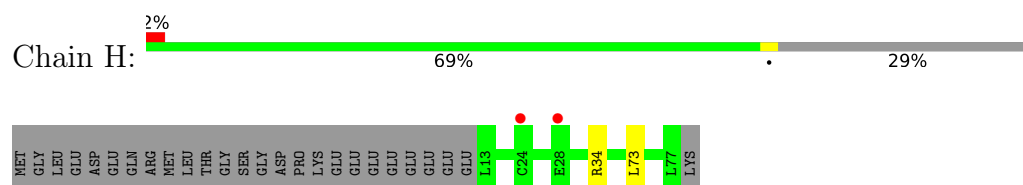
- Molecule 6: Cytochrome b-c1 complex subunit 7



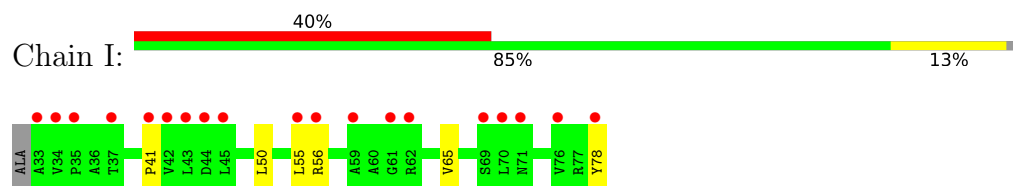
- Molecule 7: Cytochrome b-c1 complex subunit 8



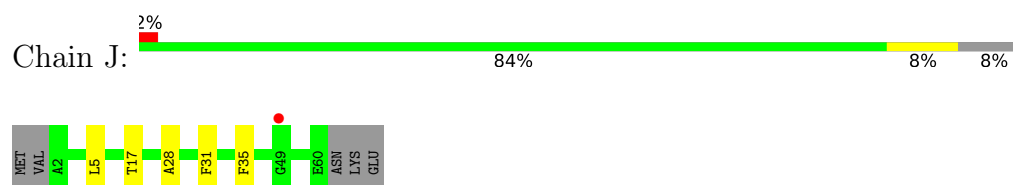
- Molecule 8: Cytochrome b-c1 complex subunit 6, mitochondrial



- 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	209.87Å 209.87Å 342.10Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	31.76 – 3.10 31.76 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.0 (31.76-3.10) 99.0 (31.76-3.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.205 , 0.240 0.207 , 0.239	Depositor DCC
R_{free} test set	4037 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	91.4	Xtriage
Anisotropy	0.123	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 45.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	16469	wwPDB-VP
Average B, all atoms (Å ²)	103.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.79% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PG4, 6PE, HEC, FES, PEE, LMT, 9XE, CDL, HEM, PO4, PX4

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	0.54	0/3522	0.81	1/4781 (0.0%)
2	B	0.54	0/3173	0.84	0/4304
3	C	0.57	1/3092 (0.0%)	0.86	1/4231 (0.0%)
4	D	0.57	0/1943	0.81	0/2642
5	E	0.59	0/1545	0.79	0/2089
6	F	0.52	0/878	0.84	0/1181
7	G	0.59	1/641 (0.2%)	0.84	0/868
8	H	0.59	0/530	0.83	0/714
9	I	0.75	0/342	0.91	0/464
10	J	0.57	0/500	0.86	0/675
All	All	0.56	2/16166 (0.0%)	0.83	2/21949 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	304	ILE	CA-CB	5.15	1.56	1.54
7	G	34	ILE	CA-CB	5.08	1.56	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	304	ILE	CB-CA-C	-5.30	108.66	113.70
1	A	310	PHE	N-CA-C	5.21	121.89	110.80

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	3449	0	3346	9	0
2	B	3116	0	3089	8	0
3	C	2996	0	3058	6	0
4	D	1884	0	1814	15	0
5	E	1512	0	1498	1	0
6	F	859	0	836	2	0
7	G	620	0	624	1	0
8	H	525	0	500	0	0
9	I	338	0	356	2	0
10	J	487	0	487	4	0
11	A	13	0	18	0	0
11	C	26	0	36	0	0
12	A	23	0	19	0	0
13	C	78	0	56	0	0
13	D	54	0	52	0	0
13	E	60	0	64	0	0
14	C	86	0	60	3	0
15	C	31	0	0	0	0
16	C	35	0	46	0	0
17	C	40	0	54	0	0
17	E	41	0	59	0	0
18	D	43	0	32	5	0
19	D	5	0	0	0	0
19	E	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	15	0	0	0	0
22	B	12	0	0	0	0
22	C	27	0	0	0	0
22	D	5	0	0	0	0
22	E	6	0	0	0	0
22	F	8	0	0	0	0
22	G	5	0	0	0	0
22	H	1	0	0	0	0
22	J	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	16469	0	16155	41	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.

All (41) 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	2.70	0.79
14:C:402:HEM:HMC1	14:C:402:HEM:HBC2	1.85	0.58
14:C:403:HEM:HMC2	14:C:403:HEM:HBC2	1.87	0.57
4:D:37:CYS:SG	18:D:501:HEC:C3B	2.94	0.56
4:D:43:MET:HE3	4:D:46:VAL:HG21	1.89	0.55
2:B:163:LEU:HD11	2:B:258:VAL:HG22	1.89	0.54
4:D:43:MET:HE1	4:D:189:PHE:CZ	2.43	0.53
4:D:211:MET:HE1	10:J:31:PHE:CZ	2.45	0.52
4:D:211:MET:HE1	10:J:31:PHE:HZ	1.75	0.52
3:C:375:LYS:O	6:F:17:ARG:NH1	2.44	0.51
14:C:402:HEM:HMB1	14:C:402:HEM:HBB2	1.94	0.50
2:B:75:LEU:HD22	2:B:136:GLU:HB3	1.94	0.49
4:D:211:MET:HA	4:D:211:MET:HE2	1.94	0.48
4:D:37:CYS:SG	18:D:501:HEC:HBB3	2.53	0.48
4:D:211:MET:HE3	10:J:35:PHE:CE1	2.49	0.48
4:D:40:CYS:SG	18:D:501:HEC:HBC3	2.54	0.47
1:A:280:TYR:HA	1:A:284:TYR:CE2	2.50	0.47
2:B:309:VAL:O	9:I:56:ARG:NH1	2.47	0.47
4:D:37:CYS:SG	18:D:501:HEC:CBB	3.03	0.46
4:D:238:ARG:HG3	7:G:14:ILE:HD12	1.97	0.46
1:A:199:ALA:HB3	1:A:208:LEU:HD22	1.98	0.45
2:B:327:ILE:HG21	9:I:55:LEU:HD11	1.97	0.45
2:B:344:VAL:HG11	2:B:417:PHE:CD2	2.52	0.45
3:C:104:TYR:CD1	3:C:208:PRO:HA	2.52	0.45
1:A:281:ASP:OD1	1:A:281:ASP:C	2.60	0.44
4:D:43:MET:HE1	4:D:189:PHE:CE2	2.54	0.43
3:C:277:ALA:HB1	3:C:294:LEU:CD1	2.47	0.43
1:A:288:ALA:HB2	1:A:300:THR:HG22	2.01	0.43
4:D:43:MET:HE2	4:D:91:PHE:CD2	2.54	0.42
1:A:267:ASN:O	1:A:271:GLN:HG2	2.20	0.42
3:C:277:ALA:HB1	3:C:294:LEU:HD12	2.02	0.42
4:D:165:TYR:CZ	4:D:168:VAL:HG23	2.54	0.42
2:B:76:THR:HG23	2:B:81:SER:HA	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:56:ARG:HB2	2:B:171:ALA:HB1	2.01	0.41
1:A:280:TYR:HB3	1:A:307:PHE:CE2	2.55	0.41
5:E:45:VAL:HG13	10:J:28:ALA:HA	2.03	0.41
1:A:431:LEU:HD12	1:A:432:PRO:HD2	2.03	0.41
1:A:14:THR:OG1	1:A:389:ARG:NH1	2.54	0.41
1:A:336:PHE:CZ	3:C:3:ASN:HB3	2.57	0.40
2:B:56:ARG:NH1	2:B:318:ASP:OD1	2.54	0.40
3:C:379:TRP:CZ2	6:F:33:ARG:HD3	2.56	0.40

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	443/480 (92%)	422 (95%)	17 (4%)	4 (1%)	14	44
2	B	411/453 (91%)	398 (97%)	13 (3%)	0	100	100
3	C	376/379 (99%)	362 (96%)	14 (4%)	0	100	100
4	D	237/325 (73%)	228 (96%)	8 (3%)	1 (0%)	30	61
5	E	194/196 (99%)	183 (94%)	7 (4%)	4 (2%)	5	25
6	F	97/111 (87%)	95 (98%)	2 (2%)	0	100	100
7	G	72/82 (88%)	70 (97%)	2 (3%)	0	100	100
8	H	63/91 (69%)	58 (92%)	5 (8%)	0	100	100
9	I	44/47 (94%)	43 (98%)	0	1 (2%)	5	23
10	J	57/64 (89%)	56 (98%)	1 (2%)	0	100	100
All	All	1994/2228 (90%)	1915 (96%)	69 (4%)	10 (0%)	24	57

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	266	ASP
5	E	162	GLY
5	E	177	PRO
9	I	41	PRO
1	A	315	ALA
1	A	445	ARG
4	D	162	PRO
5	E	143	GLY
5	E	155	GLY
1	A	229	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	369/395 (93%)	366 (99%)	3 (1%)	73	81
2	B	325/355 (92%)	322 (99%)	3 (1%)	70	80
3	C	325/327 (99%)	320 (98%)	5 (2%)	57	75
4	D	200/257 (78%)	198 (99%)	2 (1%)	68	79
5	E	167/168 (99%)	165 (99%)	2 (1%)	63	78
6	F	88/99 (89%)	84 (96%)	4 (4%)	24	56
7	G	65/72 (90%)	63 (97%)	2 (3%)	35	64
8	H	61/85 (72%)	59 (97%)	2 (3%)	33	63
9	I	38/38 (100%)	35 (92%)	3 (8%)	11	37
10	J	49/54 (91%)	47 (96%)	2 (4%)	27	59
All	All	1687/1850 (91%)	1659 (98%)	28 (2%)	53	74

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	68	LYS
1	A	184	GLU
1	A	281	ASP
2	B	226	ILE

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Mol	Chain	Res	Type
2	B	238	LYS
2	B	315	SER
3	C	3	ASN
3	C	198	LEU
3	C	344	GLU
3	C	349	THR
3	C	379	TRP
4	D	86	LYS
4	D	214	LEU
5	E	27	GLU
5	E	61	SER
6	F	33	ARG
6	F	71	ARG
6	F	82	LYS
6	F	95	LYS
7	G	31	SER
7	G	46	LEU
8	H	34	ARG
8	H	73	LEU
9	I	50	LEU
9	I	65	VAL
9	I	78	TYR
10	J	5	LEU
10	J	17	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	53	ASN
1	A	87	ASN
1	A	165	GLN
1	A	213	GLN
1	A	240	GLN
1	A	267	ASN
1	A	271	GLN
1	A	311	ASN
1	A	328	HIS
2	B	158	HIS
2	B	400	GLN
3	C	15	ASN
3	C	345	HIS
3	C	352	GLN

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Mol	Chain	Res	Type
4	D	6	HIS
4	D	71	GLN
4	D	166	ASN
4	D	225	HIS
5	E	122	HIS
5	E	149	ASN
6	F	38	HIS
6	F	79	GLN
8	H	23	GLN
10	J	57	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

23 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$
13	CDL	C	408	-	43,43,99	1.50	4 (9%)	49,55,111	1.30	5 (10%)
15	9XE	C	404	-	34,34,34	1.62	3 (8%)	47,50,50	1.17	5 (10%)
17	PEE	C	409	-	39,39,50	1.19	3 (7%)	42,44,55	0.91	2 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
14	HEM	C	402	3	50,50,50	1.56	6 (12%)	66,82,82	1.55	12 (18%)
19	PO4	F	501	-	4,4,4	0.89	0	6,6,6	0.45	0
19	PO4	E	203	-	4,4,4	0.92	0	6,6,6	0.70	0
12	6PE	A	502	-	22,22,26	1.46	2 (9%)	25,27,31	1.23	2 (8%)
16	LMT	C	405	-	36,36,36	0.65	1 (2%)	47,47,47	1.06	2 (4%)
13	CDL	E	205	-	59,59,99	1.18	4 (6%)	65,71,111	1.06	4 (6%)
19	PO4	G	103	-	4,4,4	0.89	0	6,6,6	0.45	0
19	PO4	G	101	-	4,4,4	0.90	0	6,6,6	0.26	0
20	FES	E	201	-	0,4,4	-	-	-	-	-
11	PG4	C	407	-	12,12,12	0.55	0	11,11,11	0.40	0
11	PG4	C	406	-	12,12,12	0.56	0	11,11,11	0.52	0
21	PX4	E	202	-	36,36,45	1.25	2 (5%)	42,44,53	1.03	2 (4%)
19	PO4	D	502	-	4,4,4	0.86	0	6,6,6	0.50	0
17	PEE	E	204	-	40,40,50	1.20	3 (7%)	43,45,55	1.06	2 (4%)
19	PO4	G	102	-	4,4,4	0.92	0	6,6,6	0.43	0
14	HEM	C	403	3	50,50,50	1.58	8 (16%)	66,82,82	1.42	10 (15%)
11	PG4	A	501	-	12,12,12	0.55	0	11,11,11	0.29	0
13	CDL	D	503	-	53,53,99	1.28	4 (7%)	59,65,111	1.12	4 (6%)
18	HEC	D	501	4	50,50,50	2.93	30 (60%)	68,82,82	2.49	28 (41%)
13	CDL	C	401	-	33,33,99	1.24	2 (6%)	37,43,111	1.28	3 (8%)

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	-	5/14/54/54	-
11	PG4	C	406	-	-	5/10/10/10	-
12	6PE	A	502	-	-	12/26/26/30	-
13	CDL	C	408	-	-	19/52/52/110	-
16	LMT	C	405	-	-	10/21/61/61	0/2/2/2
13	CDL	C	401	-	-	21/41/41/110	-
13	CDL	E	205	-	-	34/69/69/110	-
21	PX4	E	202	-	-	17/40/40/49	-
15	9XE	C	404	-	-	5/15/15/15	0/4/4/4
17	PEE	E	204	-	1/1/4/8	27/44/44/54	-
14	HEM	C	403	3	-	2/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
17	PEE	C	409	-	1/1/4/8	17/43/43/54	-
11	PG4	A	501	-	-	5/10/10/10	-
20	FES	E	201	-	-	-	0/1/1/1
11	PG4	C	407	-	-	5/10/10/10	-
13	CDL	D	503	-	-	24/63/63/110	-
18	HEC	D	501	4	1/1/3/7	7/14/54/54	-

All (72) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	C	404	9XE	C7-C8	6.31	1.50	1.37
18	D	501	HEC	FE-NB	5.42	2.11	1.94
13	C	408	CDL	OA6-CA5	5.23	1.47	1.35
15	C	404	9XE	C5-C4	5.23	1.49	1.41
14	C	402	HEM	FE-NB	5.19	2.10	1.94
18	D	501	HEC	C2A-C3A	5.16	1.47	1.36
18	D	501	HEC	FE-ND	5.02	2.10	1.94
18	D	501	HEC	CHA-C1A	5.00	1.48	1.38
13	C	408	CDL	OB6-CB5	4.98	1.48	1.34
18	D	501	HEC	CHB-C4A	4.96	1.48	1.38
18	D	501	HEC	C3B-C2B	4.94	1.47	1.36
14	C	403	HEM	FE-NB	4.91	2.10	1.94
18	D	501	HEC	C3D-C2D	4.84	1.47	1.36
21	E	202	PX4	O7-C23	4.72	1.47	1.34
13	D	503	CDL	OA8-CA7	4.70	1.47	1.33
13	C	408	CDL	OB8-CB7	4.67	1.47	1.33
21	E	202	PX4	O5-C9	4.64	1.46	1.33
13	D	503	CDL	OA6-CA5	4.62	1.47	1.34
13	C	401	CDL	OB8-CB7	4.62	1.46	1.33
13	E	205	CDL	OA8-CA7	4.61	1.46	1.33
13	D	503	CDL	OB6-CB5	4.54	1.47	1.34
18	D	501	HEC	CHD-C1D	4.53	1.47	1.38
12	A	502	6PE	O6-C10	4.52	1.47	1.34
13	E	205	CDL	OA6-CA5	4.52	1.47	1.34
18	D	501	HEC	FE-NC	4.46	2.10	1.95
18	D	501	HEC	FE-NA	4.42	2.10	1.95
18	D	501	HEC	CHC-C4B	4.40	1.47	1.38
12	A	502	6PE	O4-C4	4.38	1.46	1.33
13	C	401	CDL	OB6-CB5	4.31	1.46	1.34
17	C	409	PEE	O3-C30	4.30	1.45	1.33
17	E	204	PEE	O2-C10	4.29	1.46	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	E	205	CDL	OB6-CB5	4.27	1.46	1.34
14	C	403	HEM	FE-NC	4.19	2.09	1.95
17	E	204	PEE	O3-C30	4.13	1.45	1.33
14	C	402	HEM	FE-NC	4.12	2.09	1.95
17	C	409	PEE	O2-C10	4.05	1.45	1.34
18	D	501	HEC	CHD-C4C	3.86	1.48	1.39
14	C	403	HEM	C1B-NB	-3.85	1.33	1.40
18	D	501	HEC	CHB-C1B	3.78	1.47	1.39
18	D	501	HEC	CHC-C1C	3.74	1.47	1.39
17	C	409	PEE	C18-C19	3.69	1.53	1.31
17	E	204	PEE	C18-C19	3.67	1.53	1.31
18	D	501	HEC	CHA-C4D	3.63	1.47	1.39
18	D	501	HEC	C3C-C2C	3.49	1.48	1.38
14	C	402	HEM	C1B-NB	-3.45	1.34	1.40
18	D	501	HEC	C4B-NB	-3.34	1.34	1.40
18	D	501	HEC	C1D-ND	-3.10	1.35	1.40
14	C	403	HEM	C4D-ND	-2.88	1.35	1.40
14	C	402	HEM	C4D-ND	-2.86	1.35	1.40
15	C	404	9XE	C4-N	-2.78	1.35	1.39
13	C	408	CDL	OA8-CA7	2.78	1.47	1.33
18	D	501	HEC	C1C-C2C	2.66	1.49	1.43
13	E	205	CDL	OB8-CB7	2.60	1.46	1.33
16	C	405	LMT	O1'-C1'	2.58	1.44	1.40
14	C	403	HEM	C4B-NB	-2.58	1.33	1.38
18	D	501	HEC	C1B-C2B	2.54	1.49	1.44
18	D	501	HEC	C1C-NC	-2.53	1.34	1.39
13	D	503	CDL	OB8-CB7	2.53	1.45	1.33
18	D	501	HEC	C4A-NA	-2.53	1.34	1.39
18	D	501	HEC	C1D-C2D	2.52	1.49	1.44
14	C	402	HEM	C3B-C4B	2.46	1.49	1.44
18	D	501	HEC	C4C-C3C	2.44	1.49	1.44
18	D	501	HEC	C1A-C2A	2.42	1.49	1.45
14	C	402	HEM	C4B-NB	-2.37	1.33	1.38
18	D	501	HEC	C4C-NC	-2.26	1.35	1.39
18	D	501	HEC	C4D-C3D	2.22	1.48	1.45
14	C	403	HEM	C3B-C4B	2.18	1.49	1.44
18	D	501	HEC	C1A-NA	-2.18	1.35	1.39
18	D	501	HEC	C4A-C3A	2.15	1.49	1.45
18	D	501	HEC	C4B-C3B	2.13	1.48	1.45
14	C	403	HEM	C1D-ND	-2.13	1.34	1.38
14	C	403	HEM	C1D-C2D	2.03	1.48	1.44

All (81) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	D	501	HEC	C1B-C2B-C3B	-5.66	101.00	106.96
18	D	501	HEC	C3D-C4D-ND	5.36	115.55	110.36
18	D	501	HEC	C2A-C1A-NA	5.16	115.34	110.32
18	D	501	HEC	C2B-C1B-NB	5.12	116.02	109.88
13	C	401	CDL	OB6-CB5-C51	4.71	121.66	111.50
18	D	501	HEC	CBC-CAC-C3C	4.71	125.41	112.43
14	C	402	HEM	C1B-NB-C4B	4.69	109.92	105.07
18	D	501	HEC	C1C-C2C-C3C	-4.69	101.35	106.83
18	D	501	HEC	C2D-C1D-ND	4.54	115.22	109.84
13	C	408	CDL	OA6-CA5-C11	4.46	119.29	111.09
18	D	501	HEC	CBB-CAB-C3B	4.43	124.66	112.43
21	E	202	PX4	O7-C23-C24	4.28	120.72	111.50
14	C	403	HEM	C1B-NB-C4B	4.20	109.41	105.07
13	E	205	CDL	OB6-CB5-C51	4.08	120.29	111.50
17	E	204	PEE	O2-C10-C11	4.03	120.19	111.50
13	D	503	CDL	OA6-CA5-C11	4.02	120.16	111.50
18	D	501	HEC	C1D-C2D-C3D	-4.02	102.73	106.96
13	D	503	CDL	OB6-CB5-C51	4.01	120.13	111.50
13	C	401	CDL	OB8-CB7-C71	3.97	121.79	111.38
12	A	502	6PE	O6-C10-C11	3.94	119.99	111.50
18	D	501	HEC	C2C-C1C-NC	3.89	116.00	110.08
13	E	205	CDL	OA6-CA5-C11	3.87	119.83	111.50
18	D	501	HEC	C1A-C2A-C3A	-3.77	102.22	107.13
16	C	405	LMT	C1B-O5B-C5B	3.76	121.06	113.69
18	D	501	HEC	C3B-C4B-NB	3.72	114.31	110.17
14	C	402	HEM	CHC-C4B-NB	3.56	128.28	124.42
14	C	403	HEM	CHC-C4B-NB	3.52	128.25	124.42
14	C	403	HEM	C4C-NC-C1C	3.50	108.78	105.35
18	D	501	HEC	C3C-C4C-NC	3.46	114.02	110.15
14	C	402	HEM	CHD-C1D-ND	3.46	128.18	124.42
15	C	404	9XE	C13-N1-C12	3.45	122.19	117.48
14	C	402	HEM	C4C-NC-C1C	3.37	108.65	105.35
13	C	408	CDL	OB6-CB5-C51	3.28	119.95	110.80
18	D	501	HEC	CMD-C2D-C1D	3.21	129.94	125.04
13	D	503	CDL	OA8-CA7-C31	3.14	121.76	111.91
14	C	402	HEM	CHD-C1D-C2D	-3.14	120.08	124.98
13	C	408	CDL	OB8-CB7-C71	3.09	121.62	111.91
16	C	405	LMT	C1-O1'-C1'	3.05	118.89	113.84
14	C	403	HEM	CHD-C1D-ND	2.98	127.65	124.42
18	D	501	HEC	C4D-C3D-C2D	-2.93	102.63	106.90
18	D	501	HEC	CAD-C3D-C4D	2.88	129.70	124.66
18	D	501	HEC	C3A-C4A-NA	2.79	114.83	109.69
18	D	501	HEC	CMC-C2C-C3C	2.76	131.58	125.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	C	409	PEE	O3-C30-C31	2.76	120.57	111.91
14	C	402	HEM	CAD-C3D-C4D	2.72	129.41	124.66
21	E	202	PX4	O5-C9-C10	2.71	120.41	111.91
14	C	402	HEM	CMD-C2D-C1D	2.69	129.13	125.04
18	D	501	HEC	CAA-C2A-C1A	2.64	129.88	124.89
18	D	501	HEC	CHA-C4D-C3D	-2.63	120.97	124.84
14	C	403	HEM	CHA-C4D-ND	2.60	127.58	124.37
17	C	409	PEE	O2-C10-C11	2.56	117.02	111.50
13	E	205	CDL	OA8-CA7-C31	2.55	119.90	111.91
18	D	501	HEC	C4A-C3A-C2A	-2.54	103.23	106.94
14	C	403	HEM	CHA-C4D-C3D	-2.53	120.57	125.33
14	C	402	HEM	CHA-C4D-ND	2.53	127.49	124.37
18	D	501	HEC	CMB-C2B-C1B	2.50	128.85	125.04
17	E	204	PEE	O3-C30-C31	2.46	119.64	111.91
12	A	502	6PE	O4-C4-C5	2.46	119.62	111.91
18	D	501	HEC	CHC-C1C-C2C	-2.43	120.38	127.24
14	C	402	HEM	O2D-CGD-CBD	2.42	121.82	114.03
14	C	403	HEM	CHD-C1D-C2D	-2.42	121.20	124.98
15	C	404	9XE	C9-C8-C6	2.38	120.21	116.27
18	D	501	HEC	CHB-C1B-C2B	-2.37	121.28	124.98
13	D	503	CDL	OA8-CA7-OA9	-2.36	117.64	123.59
14	C	403	HEM	O2A-CGA-CBA	2.32	121.49	114.03
18	D	501	HEC	CAA-CBA-CGA	-2.31	108.62	113.60
18	D	501	HEC	CHA-C1A-C2A	-2.30	121.21	124.94
13	C	408	CDL	CA6-OA8-CA7	2.28	122.83	117.10
15	C	404	9XE	C11-O1-C2	2.27	122.44	117.51
18	D	501	HEC	CMA-C3A-C4A	2.23	128.65	124.71
14	C	402	HEM	CHA-C4D-C3D	-2.21	121.17	125.33
13	C	401	CDL	OB6-CB5-OB7	-2.20	118.38	123.70
15	C	404	9XE	C5-C4-N	2.20	121.22	119.49
15	C	404	9XE	C10-C12-N1	-2.14	120.33	123.49
13	C	408	CDL	OA8-CA7-C31	2.14	121.69	112.38
14	C	402	HEM	CBA-CAA-C2A	-2.13	106.72	112.63
14	C	403	HEM	O2A-CGA-O1A	-2.12	118.01	123.30
14	C	403	HEM	O2D-CGD-CBD	2.10	120.79	114.03
18	D	501	HEC	CBD-CAD-C3D	-2.06	106.89	112.63
14	C	402	HEM	O2A-CGA-CBA	2.01	120.50	114.03
13	E	205	CDL	OB8-CB7-C71	2.01	121.14	112.38

All (3) chirality outliers are listed below:

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Mol	Chain	Res	Type	Atom
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Mol	Chain	Res	Type	Atom
17	C	409	PEE	C2
17	E	204	PEE	C2
18	D	501	HEC	NA

All (215) 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	CB3-OB5-PB2-OB4
13	C	401	CDL	C51-CB5-OB6-CB4
13	C	408	CDL	CA3-OA5-PA1-OA4
13	D	503	CDL	CB2-OB2-PB2-OB3
13	D	503	CDL	OB7-CB5-OB6-CB4
13	D	503	CDL	C51-CB5-OB6-CB4
13	E	205	CDL	CB3-OB5-PB2-OB3
13	E	205	CDL	C51-CB5-OB6-CB4
15	C	404	9XE	F-C22-O2-C19
16	C	405	LMT	C2'-C1'-O1'-C1
16	C	405	LMT	O5'-C1'-O1'-C1
17	C	409	PEE	C4-O4P-P-O3P
17	C	409	PEE	C4-O4P-P-O2P
17	C	409	PEE	C4-O4P-P-O1P
17	E	204	PEE	C4-O4P-P-O1P
17	E	204	PEE	O4P-C4-C5-N
21	E	202	PX4	C6-O4-P1-O1
21	E	202	PX4	C24-C23-O7-C7
13	C	408	CDL	C11-CA5-OA6-CA4
18	D	501	HEC	C4B-C3B-CAB-CBB
18	D	501	HEC	C2B-C3B-CAB-CBB
17	C	409	PEE	O5-C30-O3-C3
18	D	501	HEC	C4C-C3C-CAC-CBC
13	D	503	CDL	OB9-CB7-OB8-CB6
18	D	501	HEC	C2C-C3C-CAC-CBC
12	A	502	6PE	O7-C10-O6-C2
13	C	401	CDL	OB7-CB5-OB6-CB4
13	E	205	CDL	OB7-CB5-OB6-CB4
21	E	202	PX4	O8-C23-O7-C7
13	D	503	CDL	C31-CA7-OA8-CA6
17	C	409	PEE	C31-C30-O3-C3

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Mol	Chain	Res	Type	Atoms
17	E	204	PEE	C31-C30-O3-C3
21	E	202	PX4	C10-C9-O5-C8
13	D	503	CDL	C71-CB7-OB8-CB6
17	C	409	PEE	C17-C18-C19-C20
13	D	503	CDL	OA9-CA7-OA8-CA6
17	E	204	PEE	O5-C30-O3-C3
13	C	408	CDL	OA7-CA5-OA6-CA4
13	E	205	CDL	CB4-CB6-OB8-CB7
13	C	401	CDL	OA5-CA3-CA4-OA6
13	E	205	CDL	O1-C1-CB2-OB2
11	C	406	PG4	O2-C3-C4-O3
13	E	205	CDL	CB4-CB3-OB5-PB2
21	E	202	PX4	O6-C9-O5-C8
13	C	408	CDL	C31-CA7-OA8-CA6
11	C	407	PG4	O2-C3-C4-O3
15	C	404	9XE	F2-C22-O2-C19
13	E	205	CDL	C71-CB7-OB8-CB6
13	C	401	CDL	CB5-C51-C52-C53
13	D	503	CDL	CA5-C11-C12-C13
11	A	501	PG4	O1-C1-C2-O2
13	C	408	CDL	OA9-CA7-OA8-CA6
12	A	502	6PE	C1-O3-P1-O8
13	C	401	CDL	CA3-OA5-PA1-OA2
13	C	408	CDL	CA3-OA5-PA1-OA2
13	D	503	CDL	CB2-OB2-PB2-OB5
13	E	205	CDL	CB3-OB5-PB2-OB2
21	E	202	PX4	C9-C10-C11-C12
13	C	401	CDL	OA5-CA3-CA4-CA6
15	C	404	9XE	F1-C22-O2-C19
11	C	406	PG4	O3-C5-C6-O4
17	C	409	PEE	C31-C32-C33-C34
17	E	204	PEE	C33-C34-C35-C36
17	C	409	PEE	C13-C14-C15-C16
13	C	408	CDL	C71-CB7-OB8-CB6
17	C	409	PEE	C14-C15-C16-C17
13	E	205	CDL	C51-C52-C53-C54
13	E	205	CDL	OA7-CA5-OA6-CA4
13	E	205	CDL	C11-CA5-OA6-CA4
16	C	405	LMT	C4-C5-C6-C7
13	E	205	CDL	C13-C14-C15-C16
13	D	503	CDL	C11-C12-C13-C14
16	C	405	LMT	C2-C1-O1'-C1'

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Mol	Chain	Res	Type	Atoms
17	C	409	PEE	C10-C11-C12-C13
13	D	503	CDL	C51-C52-C53-C54
21	E	202	PX4	C12-C13-C14-C15
13	E	205	CDL	CA3-CA4-CA6-OA8
17	E	204	PEE	C11-C10-O2-C2
16	C	405	LMT	C7-C8-C9-C10
12	A	502	6PE	C4-C5-C6-C7
13	C	408	CDL	OB9-CB7-OB8-CB6
17	E	204	PEE	O4-C10-O2-C2
11	A	501	PG4	O4-C7-C8-O5
12	A	502	6PE	C5-C4-O4-C3
16	C	405	LMT	C11-C10-C9-C8
13	D	503	CDL	C53-C54-C55-C56
13	C	408	CDL	C51-CB5-OB6-CB4
13	D	503	CDL	OA5-CA3-CA4-OA6
13	C	408	CDL	OB7-CB5-OB6-CB4
13	E	205	CDL	OB9-CB7-OB8-CB6
17	E	204	PEE	C20-C21-C22-C23
13	E	205	CDL	CA5-C11-C12-C13
13	C	408	CDL	CB4-CB3-OB5-PB2
13	C	401	CDL	OB5-CB3-CB4-CB6
13	C	408	CDL	OB5-CB3-CB4-CB6
13	E	205	CDL	CA2-C1-CB2-OB2
13	D	503	CDL	C31-C32-C33-C34
12	A	502	6PE	O5-C4-O4-C3
11	C	406	PG4	O1-C1-C2-O2
13	D	503	CDL	CA3-CA4-CA6-OA8
17	E	204	PEE	C34-C35-C36-C37
17	E	204	PEE	C31-C32-C33-C34
16	C	405	LMT	O5B-C5B-C6B-O6B
13	C	401	CDL	C51-C52-C53-C54
13	E	205	CDL	C35-C36-C37-C38
13	D	503	CDL	CB6-CB4-OB6-CB5
13	E	205	CDL	CA7-C31-C32-C33
17	E	204	PEE	C23-C24-C25-C26
13	D	503	CDL	OA5-CA3-CA4-CA6
17	C	409	PEE	O3P-C1-C2-C3
13	C	408	CDL	C75-C76-C77-C78
15	C	404	9XE	C3-C2-O1-C11
17	E	204	PEE	C12-C13-C14-C15
21	E	202	PX4	C23-C24-C25-C26
17	E	204	PEE	C24-C25-C26-C27

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Mol	Chain	Res	Type	Atoms
15	C	404	9XE	C1-C2-O1-C11
13	C	408	CDL	OB5-CB3-CB4-OB6
17	C	409	PEE	O3P-C1-C2-O2
12	A	502	6PE	C2-C1-O3-P1
13	E	205	CDL	C1-CA2-OA2-PA1
21	E	202	PX4	C24-C25-C26-C27
21	E	202	PX4	C16-C17-C18-C19
17	C	409	PEE	C11-C12-C13-C14
13	D	503	CDL	OB5-CB3-CB4-CB6
11	A	501	PG4	O2-C3-C4-O3
13	E	205	CDL	C53-C54-C55-C56
21	E	202	PX4	C10-C11-C12-C13
11	C	406	PG4	C3-C4-O3-C5
12	A	502	6PE	C1-C2-C3-O4
17	E	204	PEE	O3P-C1-C2-O2
13	E	205	CDL	OA6-CA4-CA6-OA8
13	C	408	CDL	CB7-C71-C72-C73
17	E	204	PEE	C13-C14-C15-C16
11	C	407	PG4	C1-C2-O2-C3
13	E	205	CDL	C17-C18-C19-C20
17	E	204	PEE	C4-O4P-P-O3P
21	E	202	PX4	C6-O4-P1-O3
13	C	401	CDL	CA3-OA5-PA1-OA3
13	D	503	CDL	CB2-OB2-PB2-OB4
13	E	205	CDL	CB3-OB5-PB2-OB4
21	E	202	PX4	C6-O4-P1-O2
17	E	204	PEE	O3P-C1-C2-C3
14	C	402	HEM	C3D-CAD-CBD-CGD
11	A	501	PG4	C3-C4-O3-C5
11	C	407	PG4	C6-C5-O3-C4
21	E	202	PX4	C13-C14-C15-C16
13	C	401	CDL	OB5-CB3-CB4-OB6
13	D	503	CDL	OB5-CB3-CB4-OB6
21	E	202	PX4	O3-C1-C2-N1
12	A	502	6PE	O6-C2-C3-O4
13	D	503	CDL	OA6-CA4-CA6-OA8
11	A	501	PG4	C5-C6-O4-C7
16	C	405	LMT	C1-C2-C3-C4
13	E	205	CDL	CB5-C51-C52-C53
17	E	204	PEE	C10-C11-C12-C13
17	E	204	PEE	C3-C2-O2-C10
11	C	406	PG4	C4-C3-O2-C2

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Mol	Chain	Res	Type	Atoms
13	C	401	CDL	CA4-CA3-OA5-PA1
11	C	407	PG4	O1-C1-C2-O2
17	E	204	PEE	O2-C2-C3-O3
13	C	408	CDL	CB2-OB2-PB2-OB5
13	E	205	CDL	CA2-OA2-PA1-OA5
13	E	205	CDL	CB2-OB2-PB2-OB5
17	E	204	PEE	C1-O3P-P-O4P
16	C	405	LMT	C2-C3-C4-C5
13	E	205	CDL	C52-C53-C54-C55
14	C	403	HEM	CAA-CBA-CGA-O1A
14	C	403	HEM	CAA-CBA-CGA-O2A
13	E	205	CDL	C54-C55-C56-C57
13	C	401	CDL	CB3-OB5-PB2-OB2
17	E	204	PEE	C2-C3-O3-C30
13	C	408	CDL	OA6-CA4-CA6-OA8
13	D	503	CDL	C54-C55-C56-C57
17	E	204	PEE	C14-C15-C16-C17
13	E	205	CDL	C12-C13-C14-C15
14	C	402	HEM	CAD-CBD-CGD-O2D
11	C	407	PG4	C3-C4-O3-C5
14	C	402	HEM	CAA-CBA-CGA-O2A
16	C	405	LMT	O5B-C1B-O1B-C4'
13	E	205	CDL	C32-C31-CA7-OA8
17	E	204	PEE	C15-C16-C17-C18
14	C	402	HEM	CAA-CBA-CGA-O1A
17	C	409	PEE	C34-C35-C36-C37
18	D	501	HEC	CAA-CBA-CGA-O2A
14	C	402	HEM	CAD-CBD-CGD-O1D
18	D	501	HEC	CAA-CBA-CGA-O1A
17	E	204	PEE	C11-C12-C13-C14
17	C	409	PEE	O3-C30-C31-C32
17	C	409	PEE	C33-C34-C35-C36
13	E	205	CDL	C16-C17-C18-C19
21	E	202	PX4	C11-C10-C9-O5
13	D	503	CDL	C13-C14-C15-C16
13	E	205	CDL	C32-C31-CA7-OA9
13	C	401	CDL	CB2-C1-CA2-OA2
13	E	205	CDL	C32-C33-C34-C35
13	C	401	CDL	C52-C51-CB5-OB6
13	C	401	CDL	CA3-OA5-PA1-OA4
13	C	401	CDL	CB2-OB2-PB2-OB3
13	C	401	CDL	CB3-OB5-PB2-OB3

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Mol	Chain	Res	Type	Atoms
13	C	408	CDL	CB2-OB2-PB2-OB3
13	E	205	CDL	CA2-OA2-PA1-OA3
17	E	204	PEE	C22-C23-C24-C25
13	C	408	CDL	C72-C71-CB7-OB8
12	A	502	6PE	O4-C4-C5-C6
17	C	409	PEE	O5-C30-C31-C32
17	E	204	PEE	C5-C4-O4P-P
13	C	401	CDL	O1-C1-CA2-OA2
21	E	202	PX4	O7-C23-C24-C25
13	C	401	CDL	C72-C71-CB7-OB8
13	C	401	CDL	C52-C51-CB5-OB7
18	D	501	HEC	CAD-CBD-CGD-O1D
13	D	503	CDL	C12-C13-C14-C15

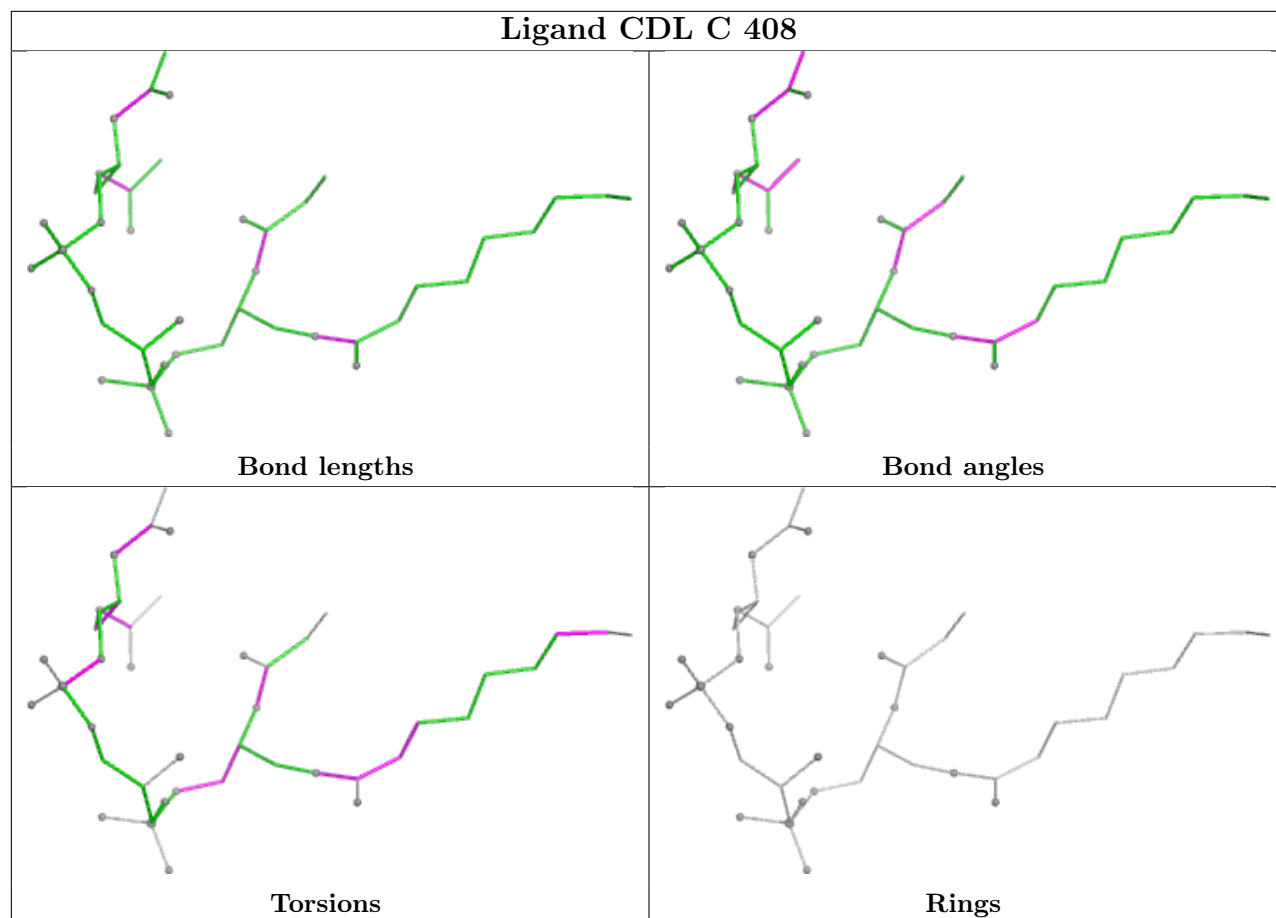
There are no ring outliers.

3 monomers are involved in 8 short contacts:

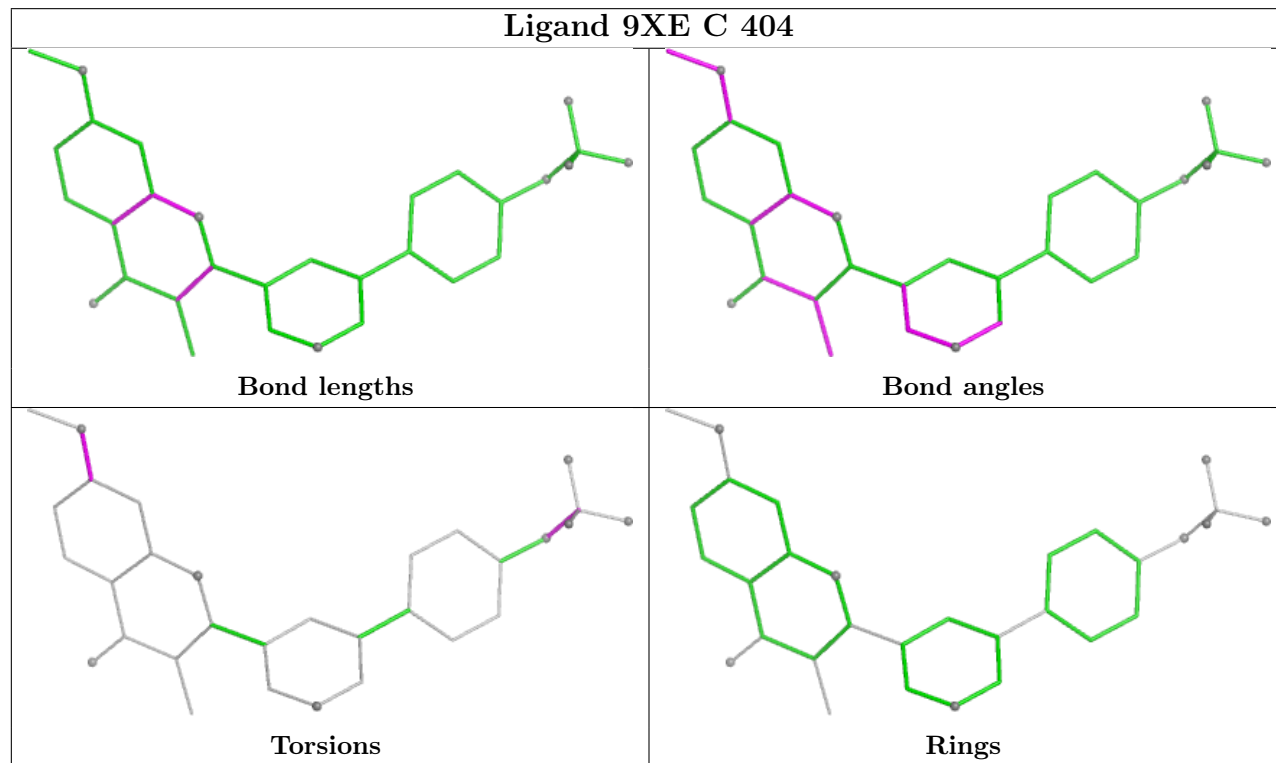
Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	C	402	HEM	2	0
14	C	403	HEM	1	0
18	D	501	HEC	5	0

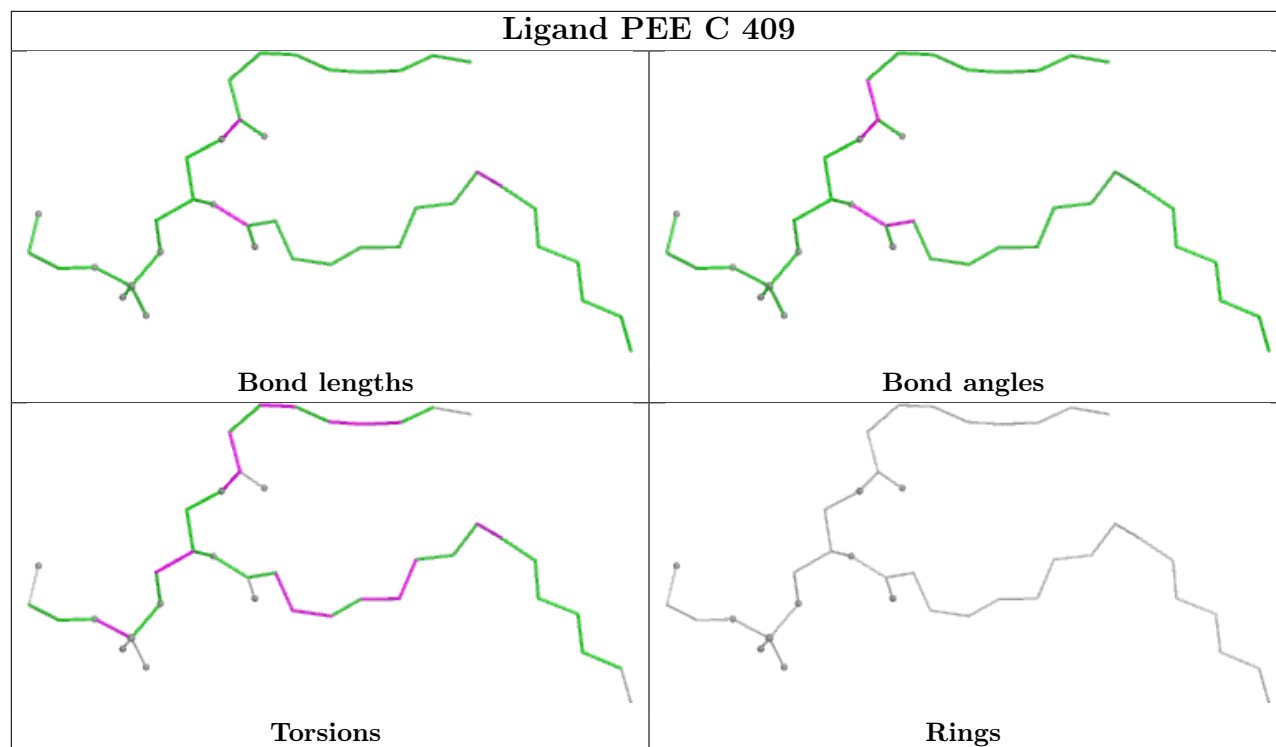
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

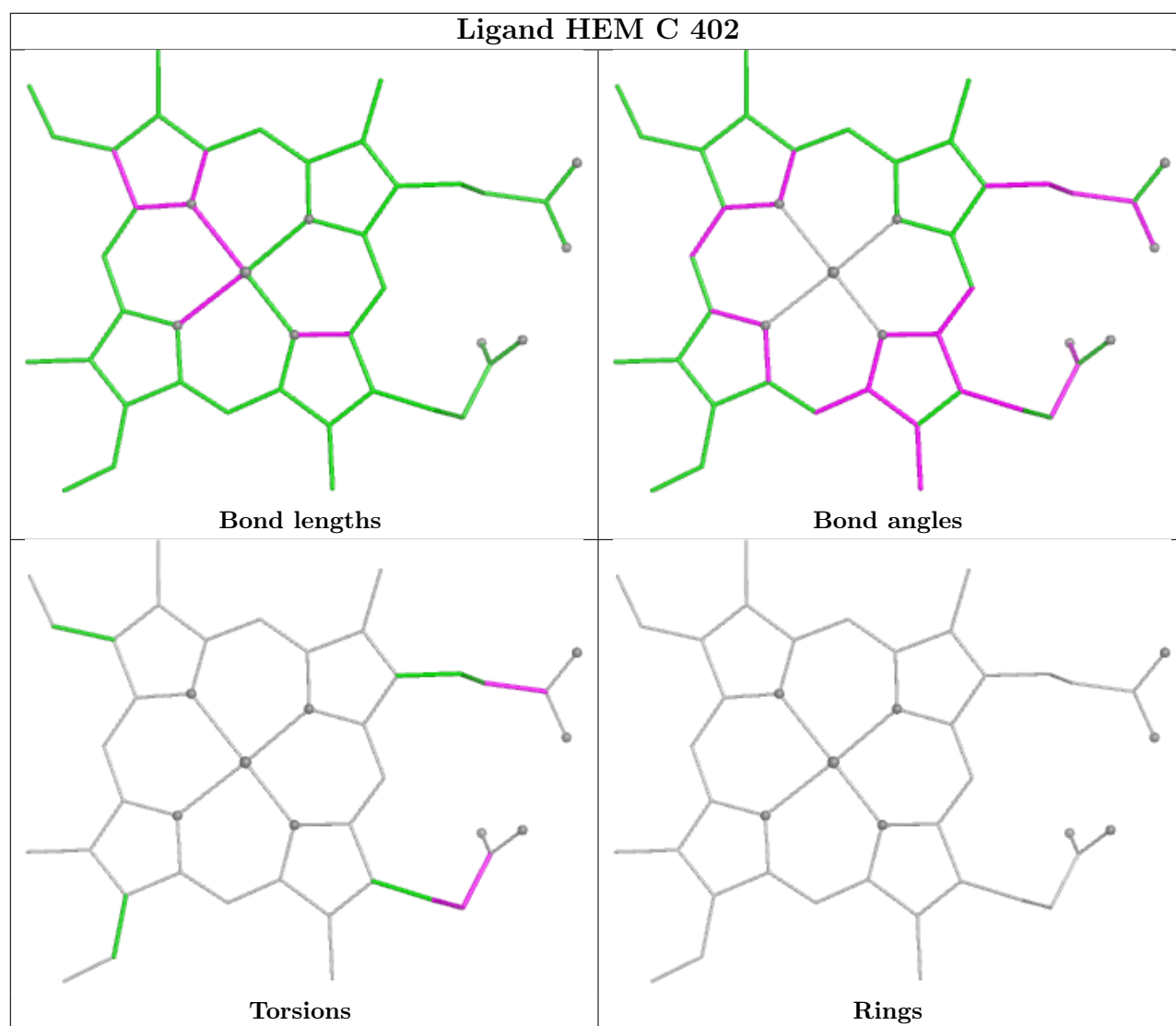
Ligand CDL C 408



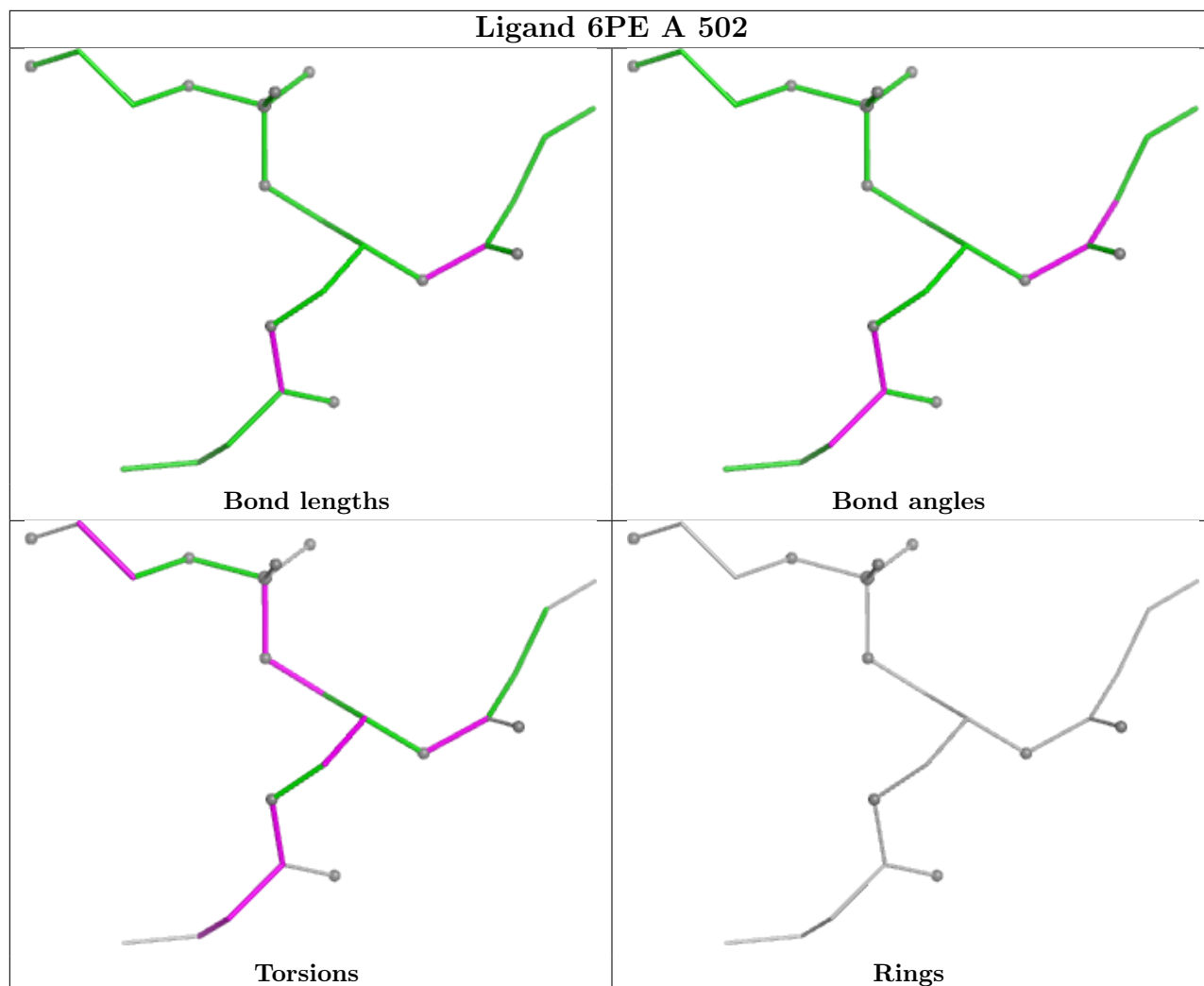
Ligand 9XE C 404



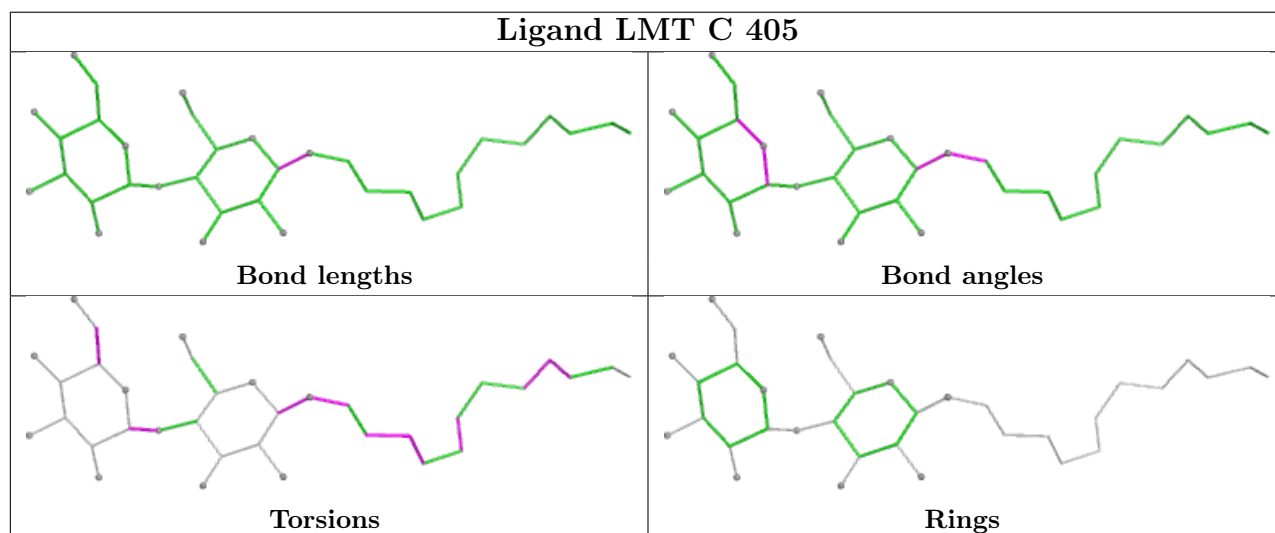


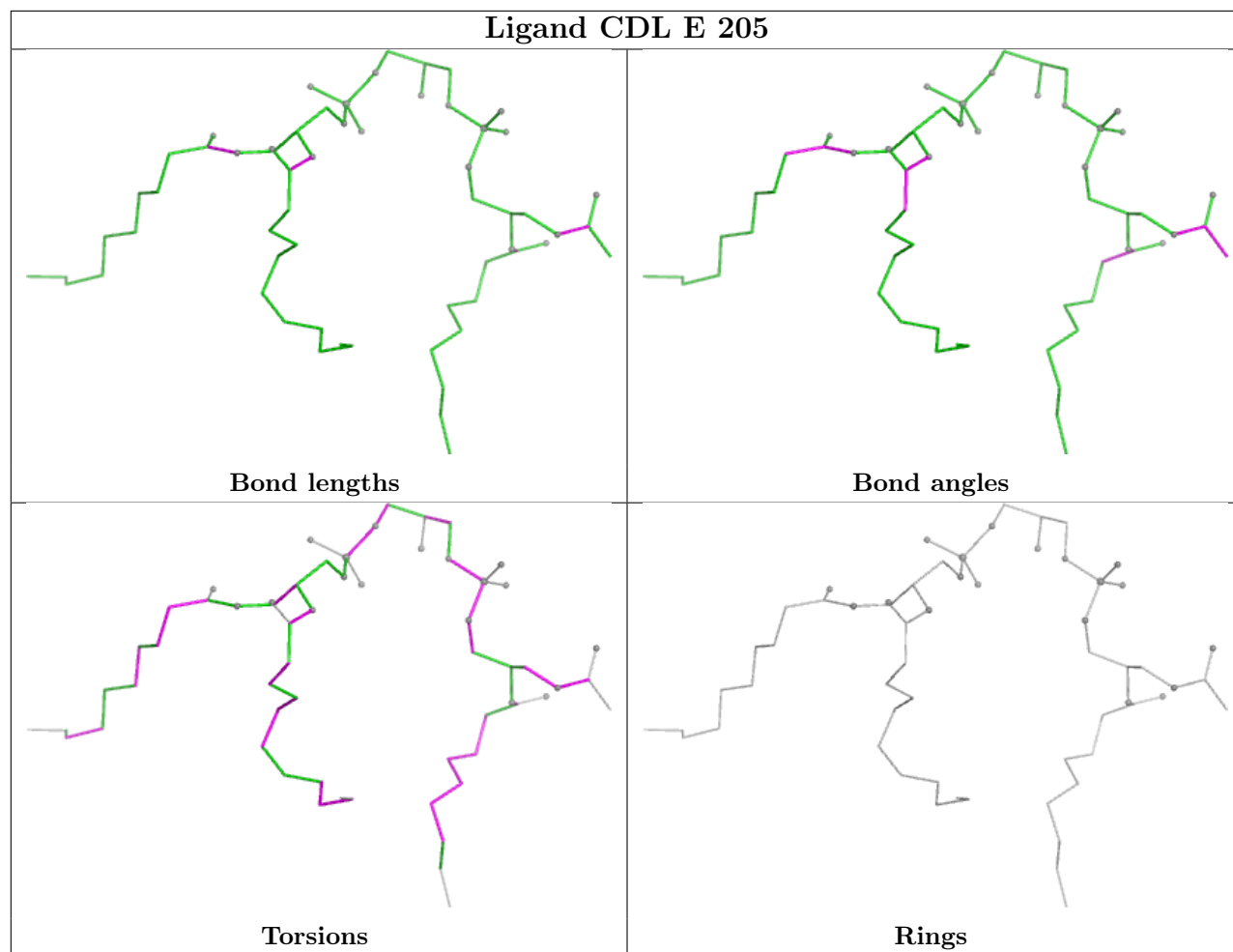


Ligand 6PE A 502

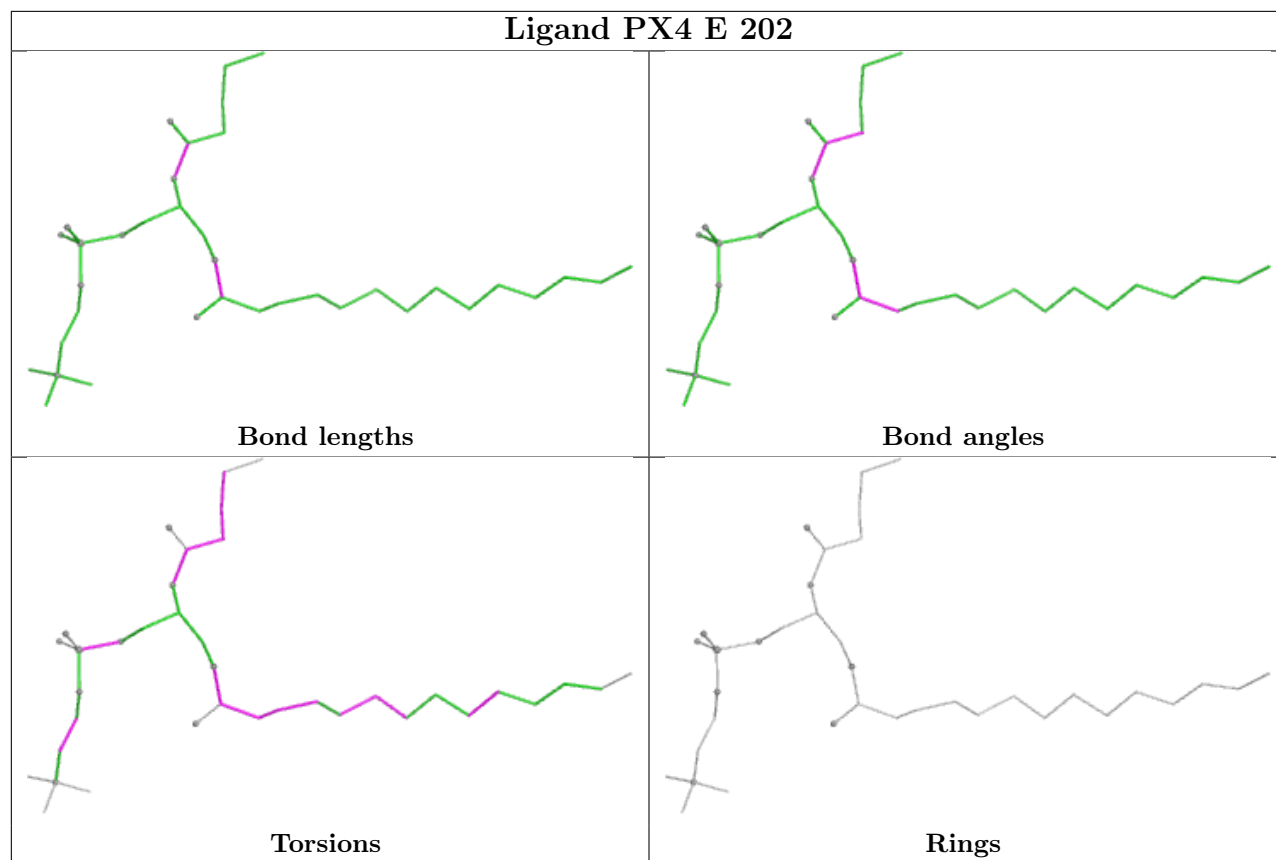


Ligand LMT C 405

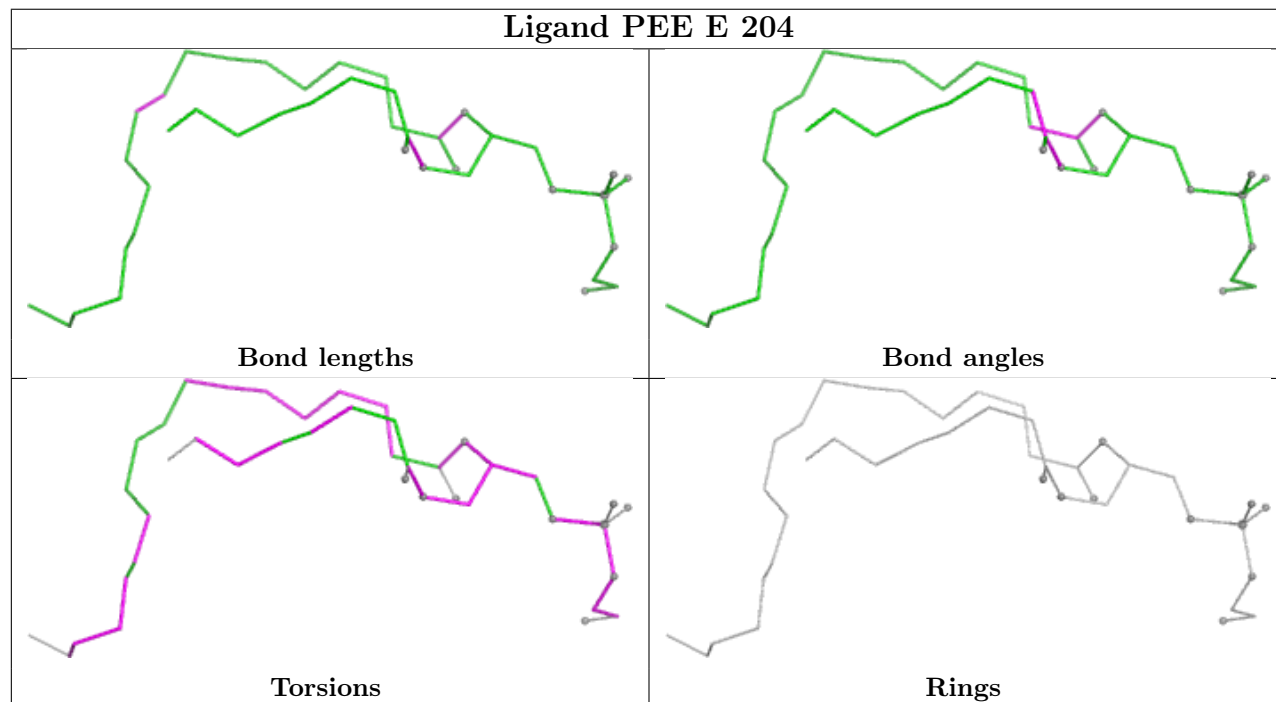


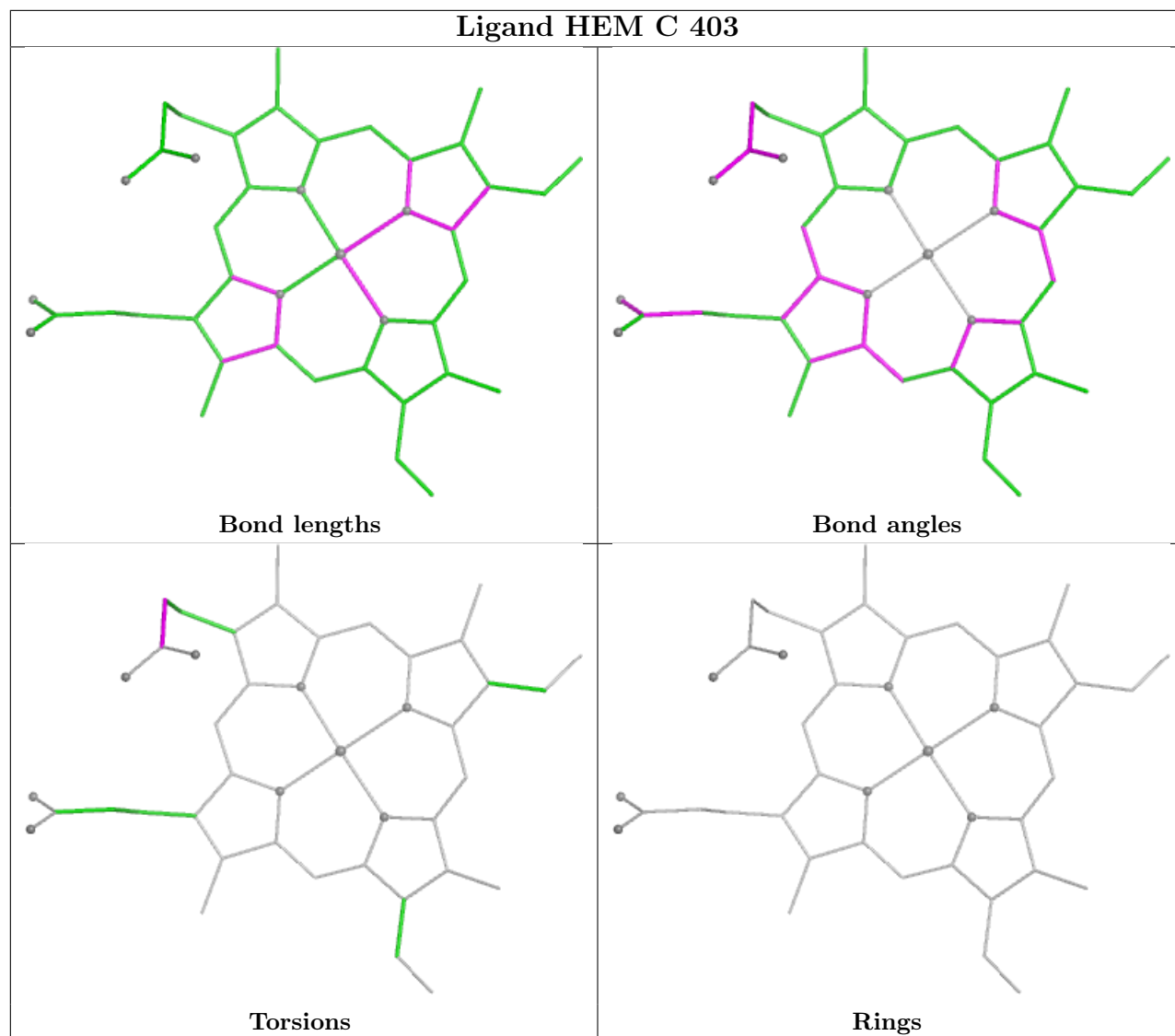


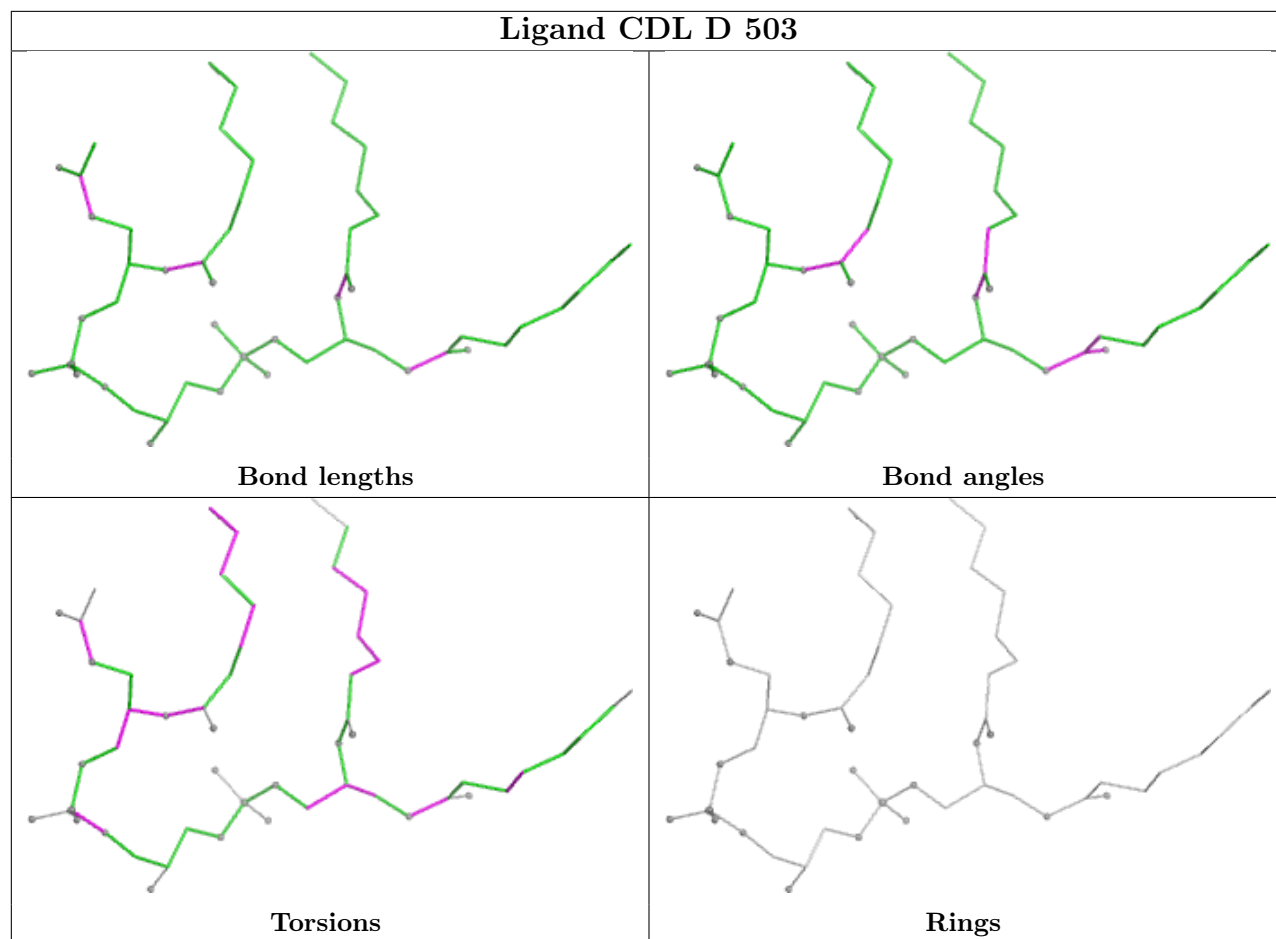
Ligand PX4 E 202

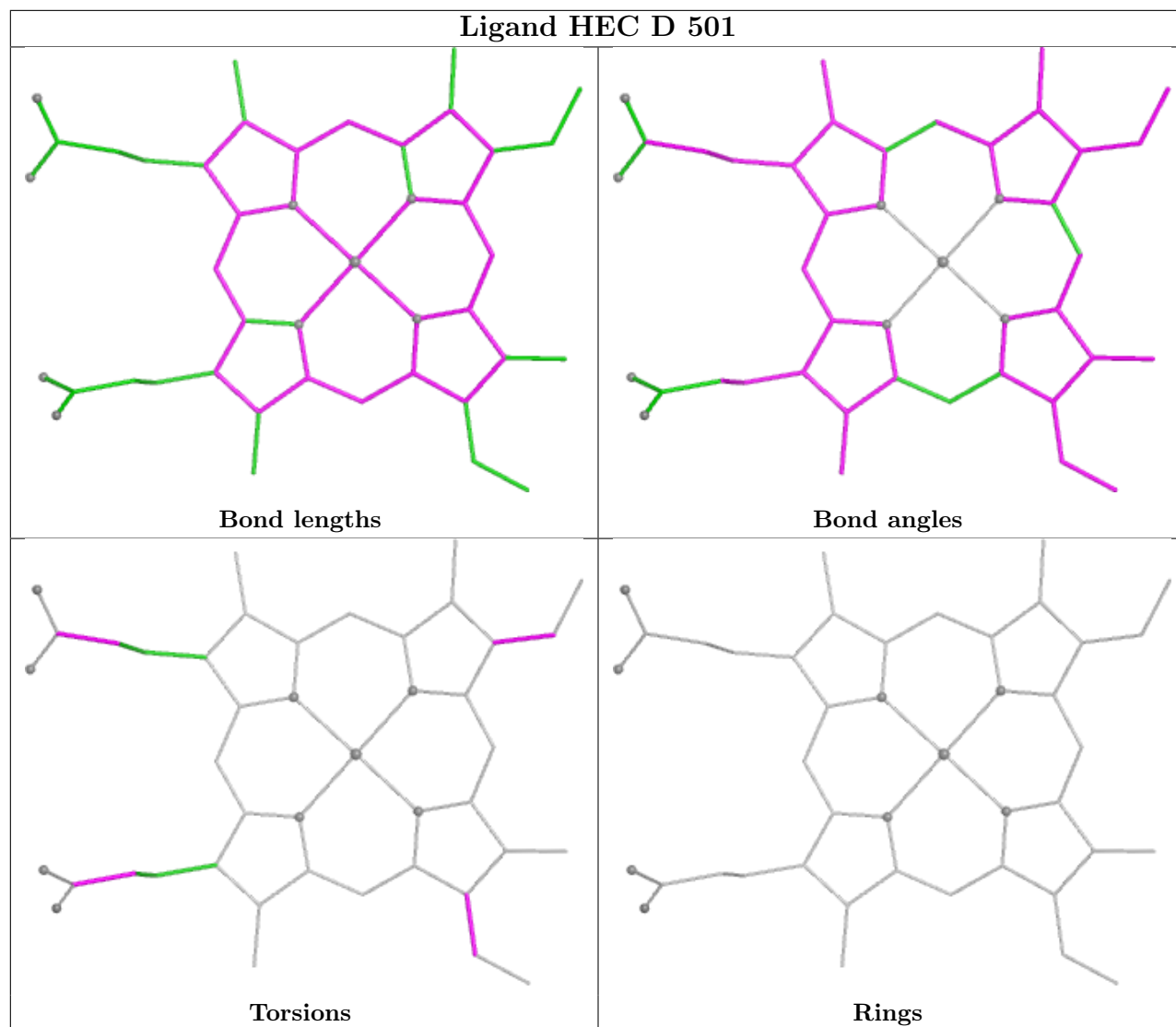


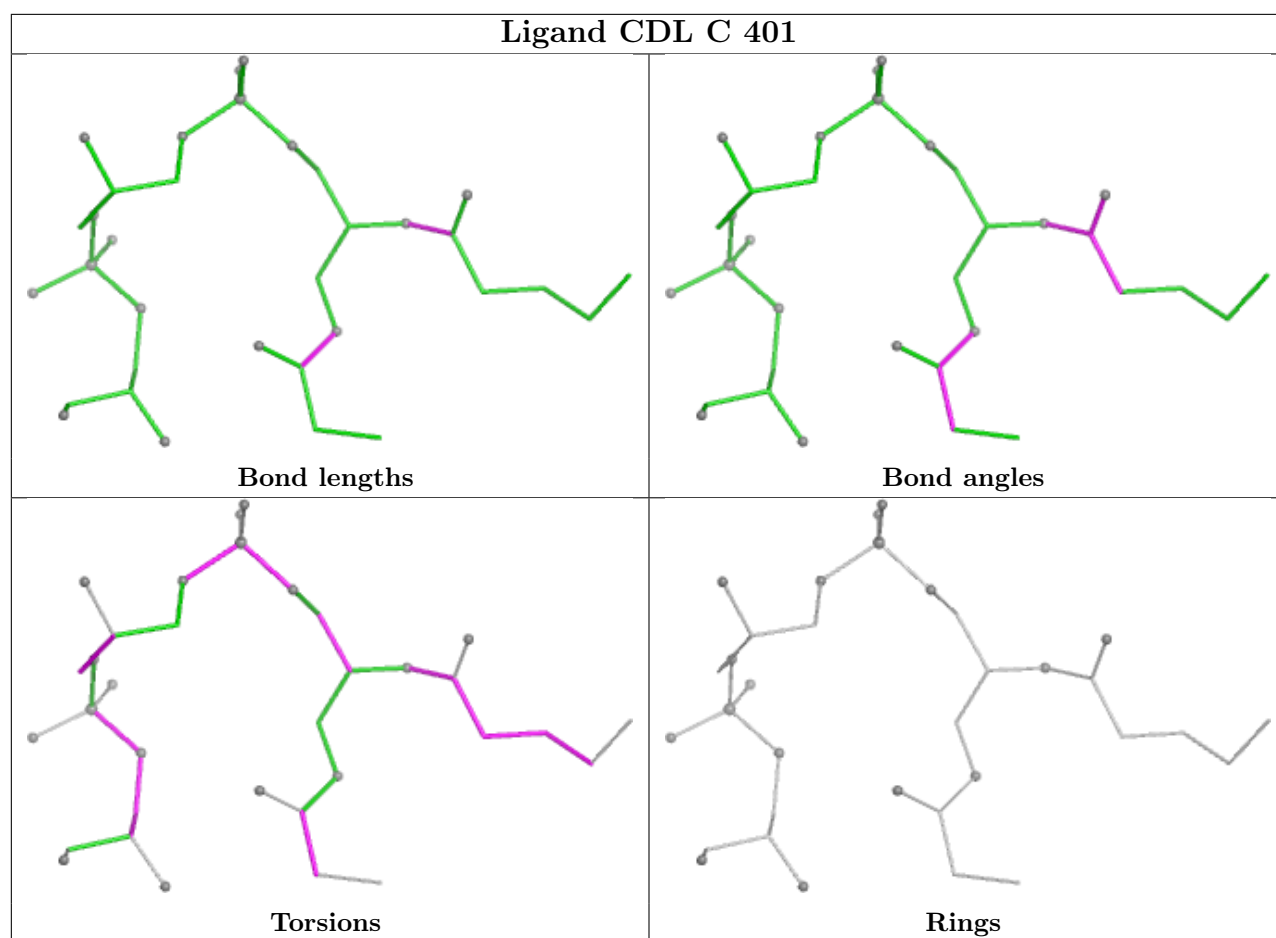
Ligand PEE E 204











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	445/480 (92%)	-0.25	4 (0%) 81 63	62, 92, 126, 188	0
2	B	415/453 (91%)	-0.29	3 (0%) 84 68	68, 95, 122, 179	0
3	C	378/379 (99%)	-0.18	4 (1%) 78 59	63, 84, 123, 152	0
4	D	239/325 (73%)	-0.04	0 100 100	76, 118, 144, 158	0
5	E	196/196 (100%)	0.57	21 (10%) 11 6	77, 141, 182, 194	0
6	F	99/111 (89%)	-0.17	0 100 100	67, 85, 123, 155	0
7	G	74/82 (90%)	-0.13	3 (4%) 41 23	64, 96, 142, 152	0
8	H	65/91 (71%)	0.41	2 (3%) 51 30	124, 143, 161, 168	0
9	I	46/47 (97%)	2.05	19 (41%) 0 0	98, 135, 152, 161	0
10	J	59/64 (92%)	-0.09	1 (1%) 69 48	88, 102, 138, 152	0
All	All	2016/2228 (90%)	-0.06	57 (2%) 55 34	62, 97, 155, 194	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
9	I	33	ALA	7.4
9	I	43	LEU	5.9
5	E	178	LEU	5.1
5	E	159	PRO	4.7
5	E	152	ASP	4.4
9	I	41	PRO	4.3
9	I	42	VAL	4.0
7	G	75	ALA	4.0
1	A	446	PHE	3.9
9	I	35	PRO	3.8
10	J	49	GLY	3.5
9	I	62	ARG	3.5
5	E	114	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
9	I	70	LEU	3.5
5	E	111	ALA	3.3
8	H	24	CYS	3.3
9	I	71	ASN	3.2
9	I	56	ARG	3.2
9	I	45	LEU	3.0
5	E	161	HIS	3.0
5	E	177	PRO	2.9
9	I	78	TYR	2.9
9	I	76	VAL	2.8
8	H	28	GLU	2.8
5	E	162	GLY	2.7
5	E	124	LEU	2.7
9	I	61	GLY	2.6
5	E	160	CYS	2.6
5	E	157	TYR	2.5
5	E	83	GLU	2.5
5	E	74	ILE	2.5
5	E	140	THR	2.5
1	A	223	TYR	2.4
9	I	44	ASP	2.4
5	E	176	ALA	2.3
2	B	110	GLU	2.3
5	E	148	ALA	2.3
9	I	37	THR	2.3
9	I	34	VAL	2.3
5	E	115	SER	2.2
3	C	271	GLU	2.2
3	C	2	THR	2.2
5	E	164	HIS	2.2
2	B	21	PRO	2.1
7	G	74	PRO	2.1
5	E	173	LYS	2.1
5	E	108	GLN	2.1
2	B	229	GLY	2.1
1	A	224	ASP	2.1
3	C	4	ILE	2.1
9	I	59	ALA	2.1
5	E	121	GLN	2.1
1	A	204	GLU	2.1
9	I	69	SER	2.0
7	G	46	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
3	C	18	PHE	2.0
9	I	55	LEU	2.0

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 [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
13	CDL	E	205	60/100	0.62	0.25	127,151,185,192	0
16	LMT	C	405	35/35	0.64	0.21	151,166,170,171	0
19	PO4	E	203	5/5	0.69	0.19	156,156,161,161	0
19	PO4	G	102	5/5	0.78	0.12	153,154,156,161	0
19	PO4	D	502	5/5	0.79	0.12	168,169,170,170	0
13	CDL	C	401	34/100	0.83	0.19	144,157,168,169	0
11	PG4	A	501	13/13	0.84	0.15	114,130,142,143	0
19	PO4	G	103	5/5	0.84	0.10	132,134,137,137	0
13	CDL	D	503	54/100	0.88	0.19	94,117,141,142	0
17	PEE	E	204	41/51	0.88	0.21	85,103,111,119	0
11	PG4	C	407	13/13	0.88	0.20	110,116,119,120	0
12	6PE	A	502	23/27	0.90	0.17	96,124,142,145	0
19	PO4	F	501	5/5	0.90	0.18	124,129,132,132	0
21	PX4	E	202	37/46	0.91	0.20	112,129,138,139	0
13	CDL	C	408	44/100	0.92	0.15	84,102,125,127	0
15	9XE	C	404	31/31	0.94	0.10	75,79,90,92	0
17	PEE	C	409	40/51	0.94	0.15	79,91,104,108	0
20	FES	E	201	4/4	0.94	0.06	217,217,217,218	0
19	PO4	G	101	5/5	0.94	0.08	106,107,113,113	0
11	PG4	C	406	13/13	0.95	0.13	98,104,115,115	0
18	HEC	D	501	43/43	0.97	0.11	111,114,120,123	0

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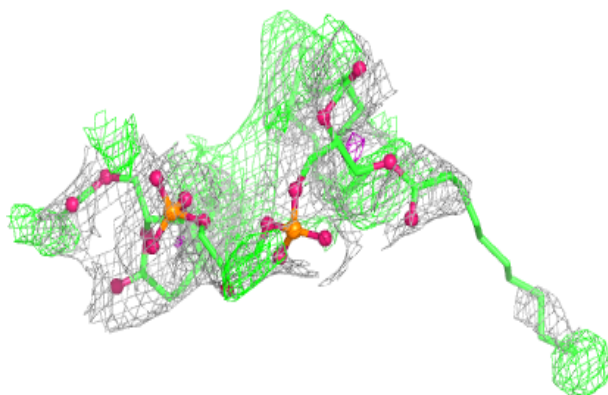
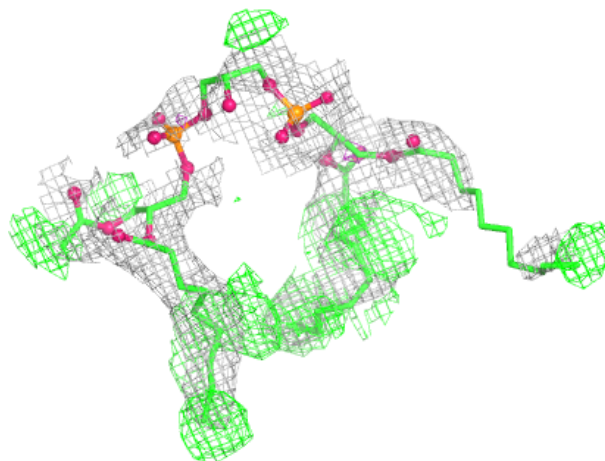
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
14	HEM	C	403	43/43	0.98	0.08	62,65,67,68	0
14	HEM	C	402	43/43	0.98	0.08	68,71,75,79	0

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.

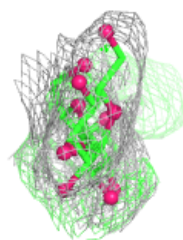
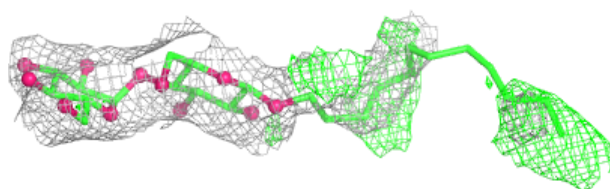
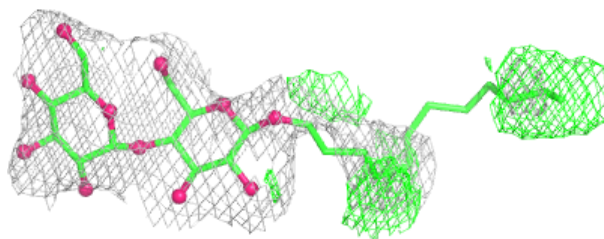
Electron density around CDL E 205:

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

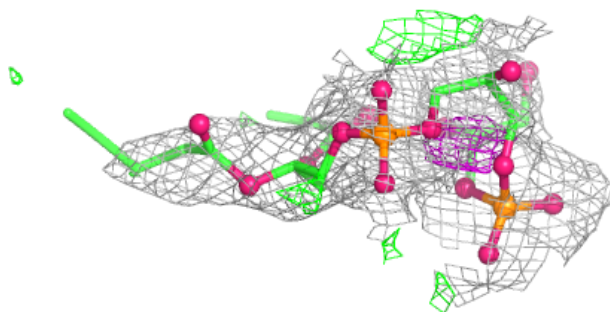
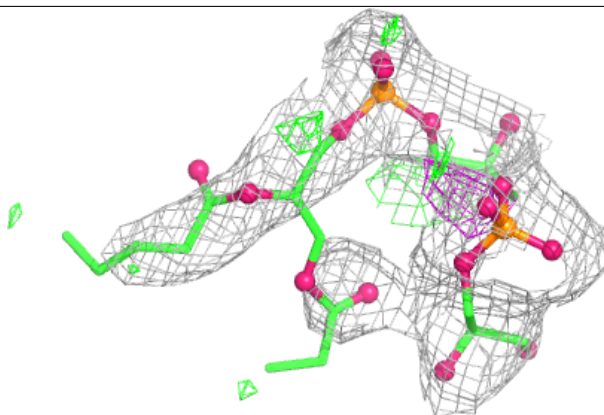


Electron density around LMT C 405:

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

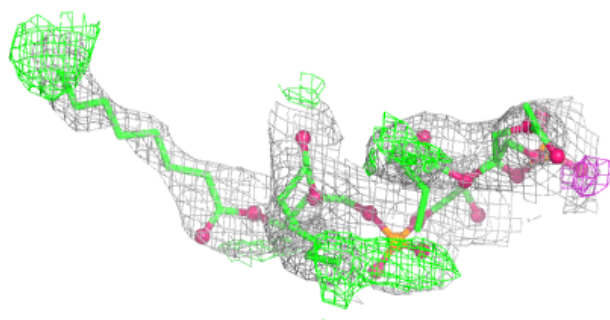
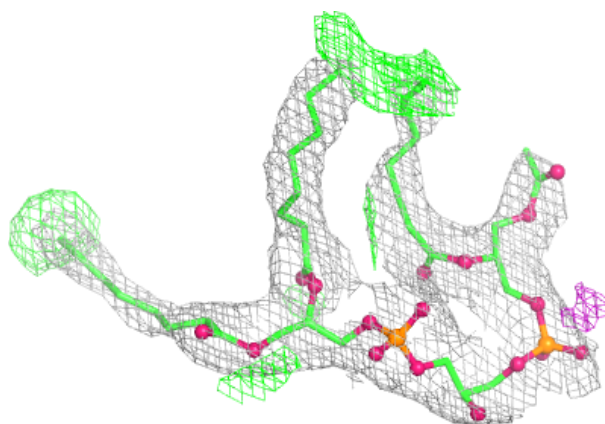
**Electron density around CDL C 401:**

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

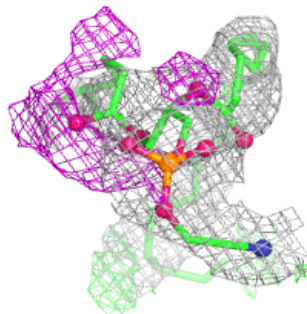
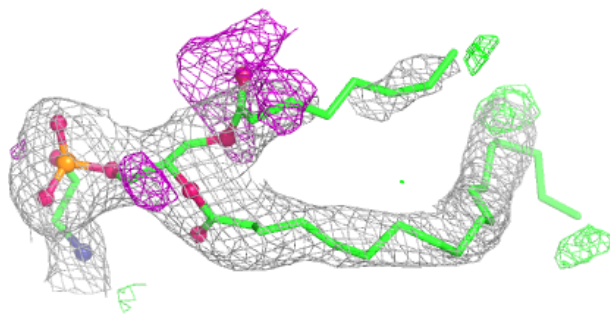
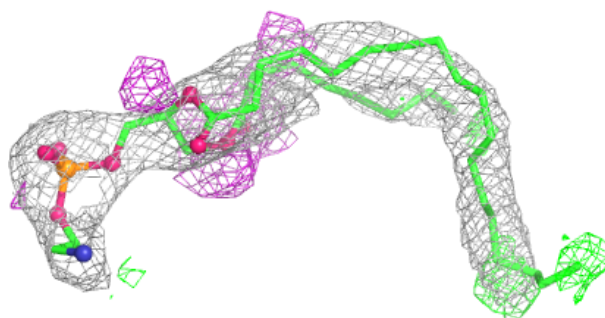


Electron density around CDL D 503:

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

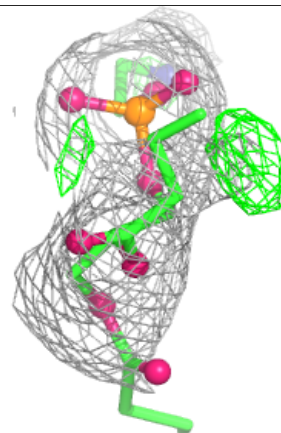
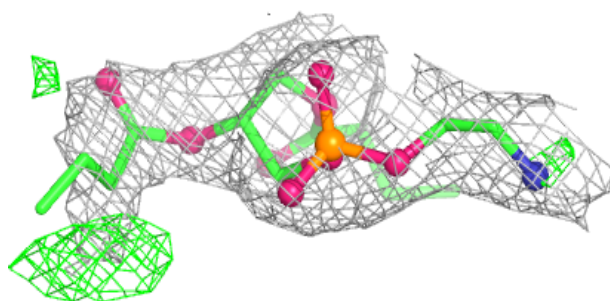
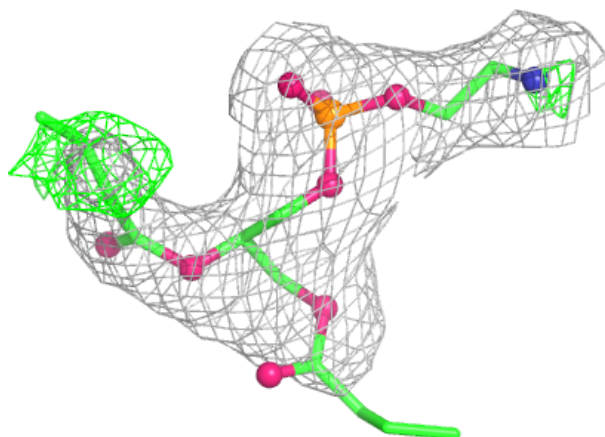
**Electron density around PEE E 204:**

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

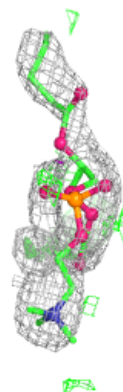
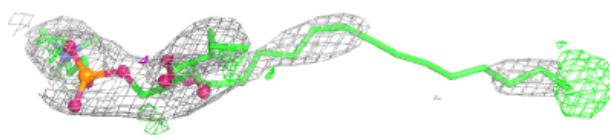
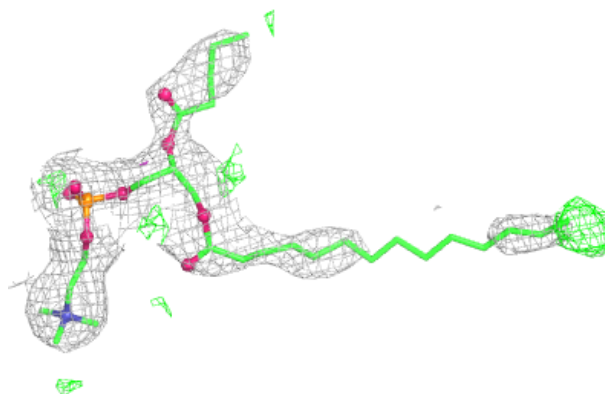


Electron density around 6PE A 502:

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

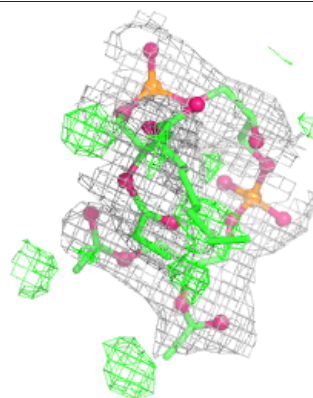
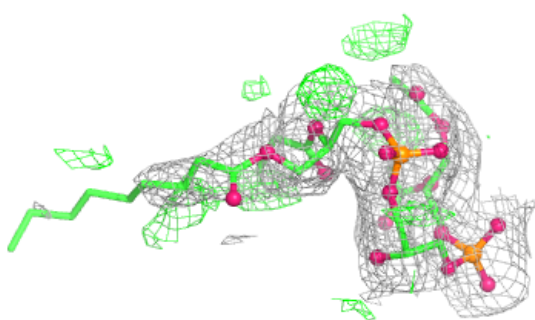
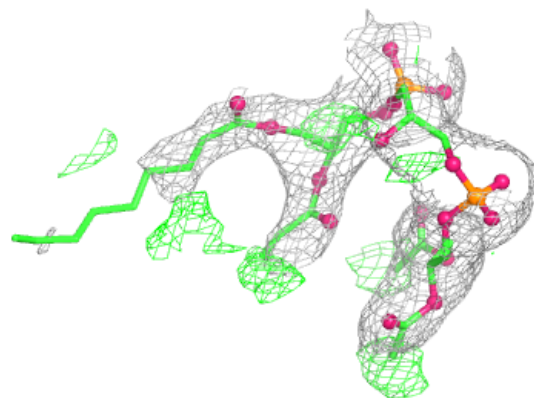
**Electron density around PX4 E 202:**

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

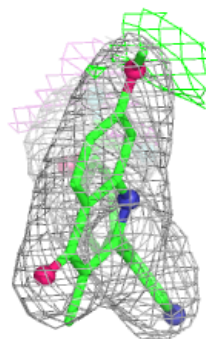
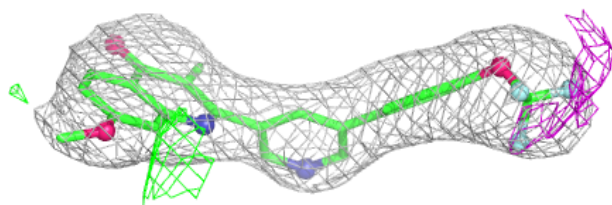
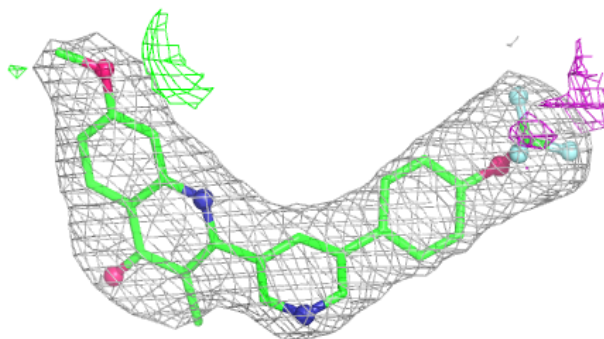


Electron density around CDL C 408:

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

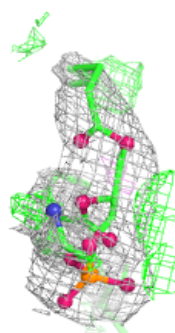
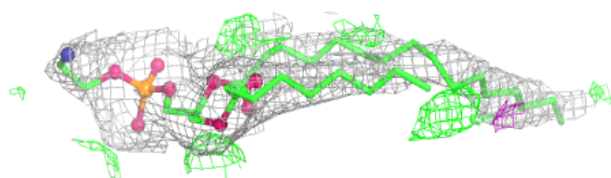
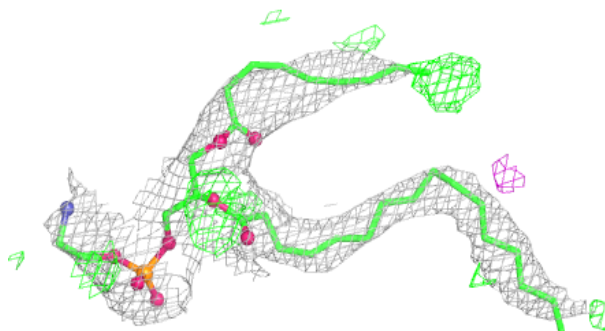
**Electron density around 9XE C 404:**

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

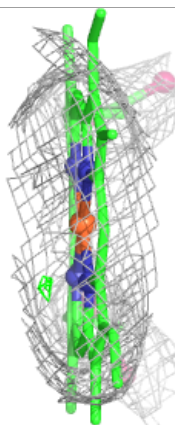
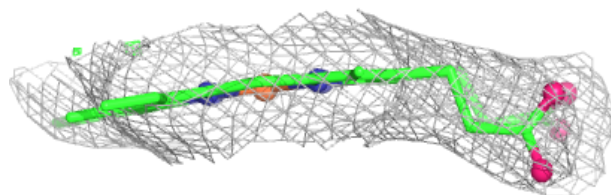
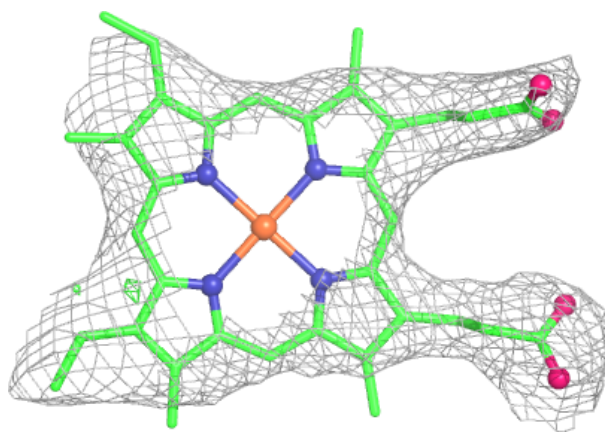


Electron density around PEE C 409:

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

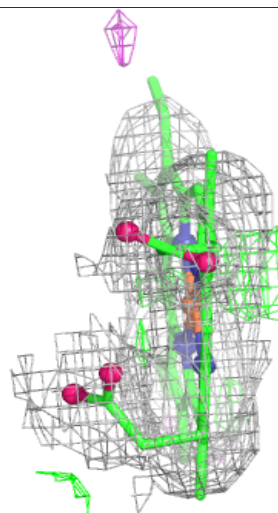
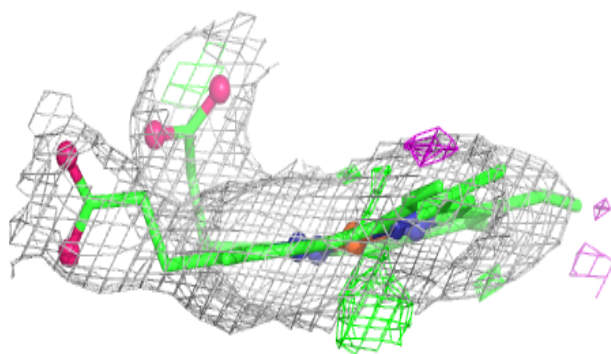
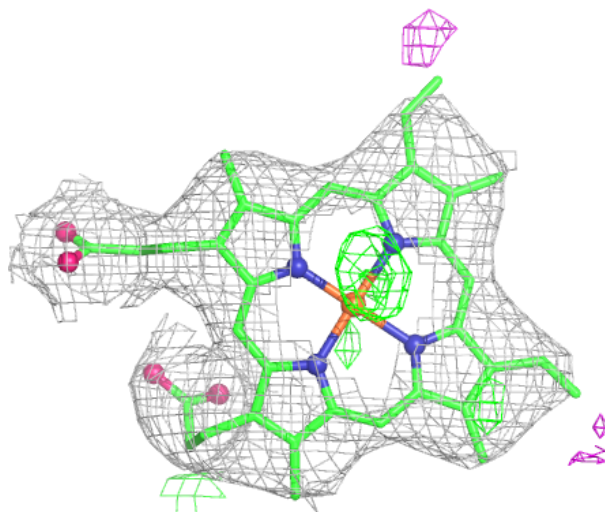
**Electron density around HEC D 501:**

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



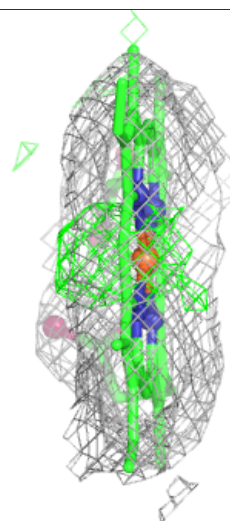
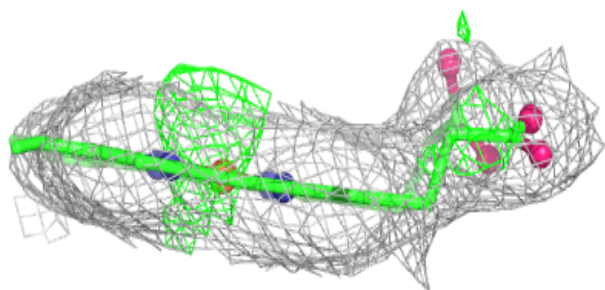
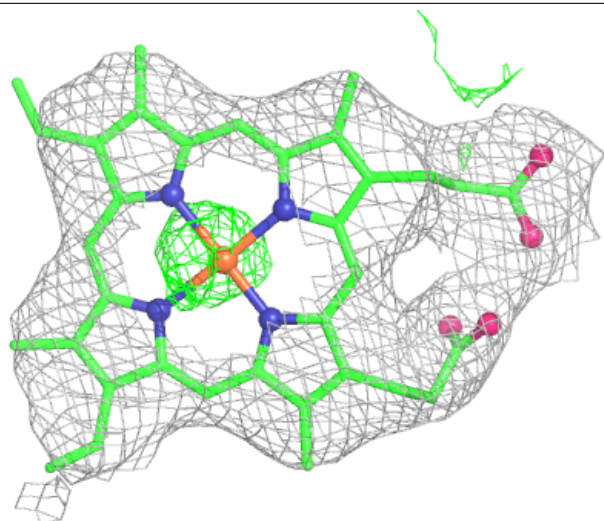
Electron density around HEM C 403:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
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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)



6.5 Other polymers [i](#)

There are no such residues in this entry.