



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 2, 2025 – 12:45 am BST

PDB ID : 5NMI / pdb_00005nmi
Title : Cytochrome bc1 bound to the inhibitor MJM170
Authors : Capper, N.J.; Antonyuk, S.V.; Hasnain, S.S.
Deposited on : 2017-04-05
Resolution : 3.50 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.003 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

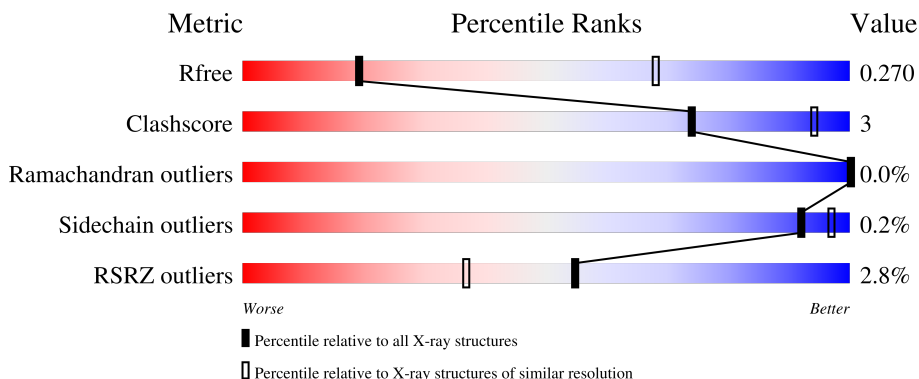
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	1094 (3.56-3.44)
Clashscore	180529	1045 (3.54-3.46)
Ramachandran outliers	177936	1032 (3.54-3.46)
Sidechain outliers	177891	1033 (3.54-3.46)
RSRZ outliers	164620	1093 (3.56-3.44)

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	<div> <div>3%</div> <div>96%</div> <div>.</div> </div>
1	N	444	<div> <div>4%</div> <div>97%</div> <div>.</div> </div>
2	B	423	<div> <div>2%</div> <div>96%</div> <div>.</div> </div>
2	O	423	<div> <div>4%</div> <div>94%</div> <div>6%</div> <div>.</div> </div>
3	C	372	<div> <div>%</div> <div>96%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
3	P	372	
4	D	240	
4	Q	240	
5	E	274	
5	I	274	
5	R	274	
5	V	274	
6	F	111	
6	S	111	
7	G	82	
7	T	82	
8	H	91	
8	U	91	
9	J	64	
9	W	64	
10	K	22	
10	X	22	

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
12	MJM	C	503	X	-	-	-
12	MJM	P	404	X	-	-	-
13	PEE	D	502	X	-	-	-
13	PEE	E	502	X	-	-	-
13	PEE	R	201	X	-	-	-
13	PEE	R	202	X	-	-	-

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 31648 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	444	Total	C	N	O	S	48	0	0
			3440	2148	607	665	20			
1	N	444	Total	C	N	O	S	45	0	0
			3440	2148	607	665	20			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	423	Total	C	N	O	S	27	0	0
			3172	1993	562	610	7			
2	O	423	Total	C	N	O	S	8	0	0
			3172	1993	562	610	7			

- Molecule 3 is a protein called Cytochrome b.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	372	Total	C	N	O	S	0	0	0
			2954	1984	460	492	18			
3	P	372	Total	C	N	O	S	0	0	0
			2954	1984	460	492	18			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	240	Total	C	N	O	S	0	0	0
			1913	1222	329	347	15			
4	Q	240	Total	C	N	O	S	5	0	0
			1913	1222	329	347	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
			1519	957	263	291	8			
5	I	30	Total	C	N	O	S	9	0	0
			221	137	44	39	1			
5	R	72	Total	C	N	O	S	0	0	0
			540	335	90	113	2			
5	V	30	Total	C	N	O	S	0	0	0
			221	137	44	39	1			

- 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
			870	553	157	158	2			
6	S	99	Total	C	N	O	S	4	0	0
			870	553	157	158	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
			623	407	117	98	1			
7	T	80	Total	C	N	O	S	0	0	0
			677	439	127	110	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	66	Total	C	N	O	S	3	0	0
			539	327	98	109	5			
8	U	68	Total	C	N	O	S	0	0	0
			557	337	100	115	5			

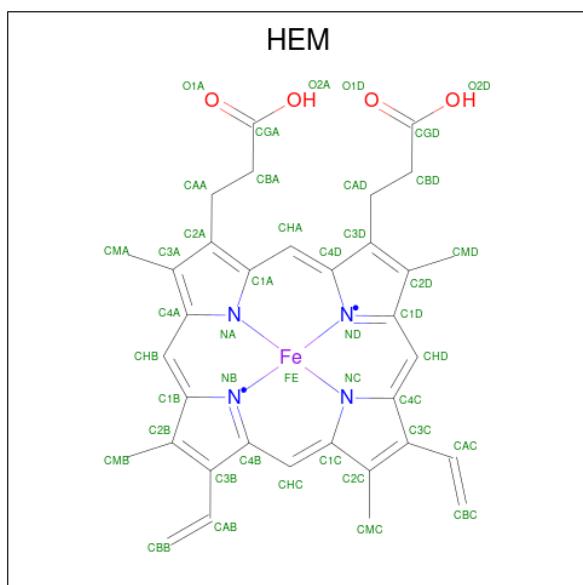
- Molecule 9 is a protein called Cytochrome b-c1 complex subunit 9.

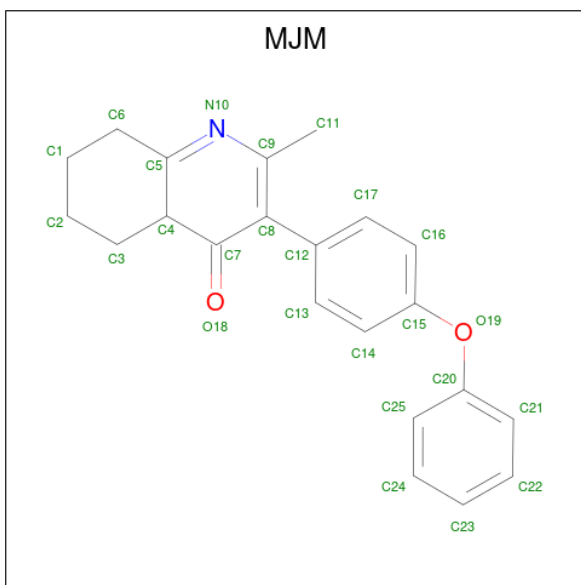
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	J	59	Total	C	N	O	0	0	0
			492	322	86	84			
9	W	59	Total	C	N	O	0	0	0
			487	320	84	83			

- Molecule 10 is a protein called ARG-ASN-TRP-VAL-PRO-THR-ALA-GLN-LEU-TRP-GLY-ALA-VAL-GLY-ALA-VAL-GLY-LEU-VAL-SER-ALA-THR.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	K	22	Total	C	N	O	0	0	0
			159	103	29	27			
10	X	22	Total	C	N	O	12	0	0
			159	103	29	27			

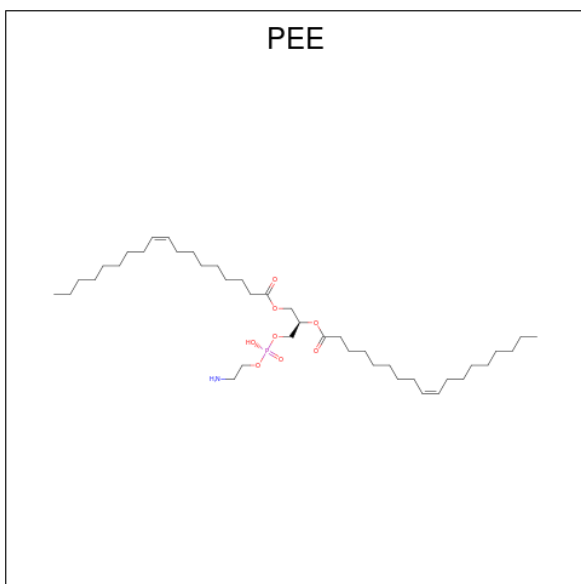
- Molecule 11 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	C	1	Total	C	N	O	0	0
			25	22	1	2		
12	P	1	Total	C	N	O	0	0
			25	22	1	2		

- Molecule 13 is 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (CCD ID: PEE) (formula: $C_{41}H_{78}NO_8P$).



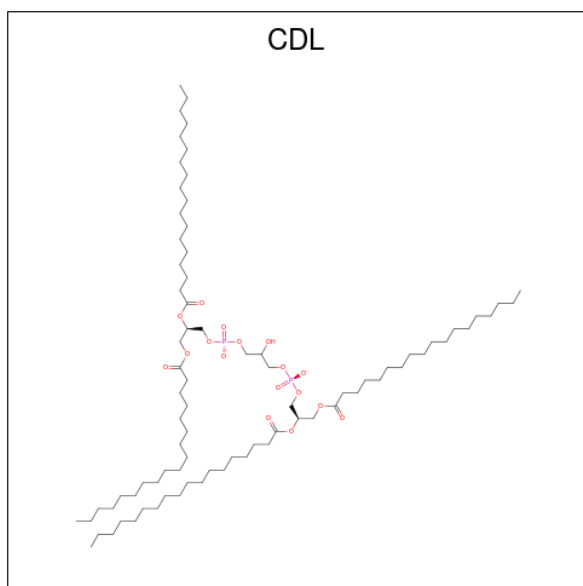
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
13	C	1	Total	C	N	O	P	0	0
			28	19	1	7	1		

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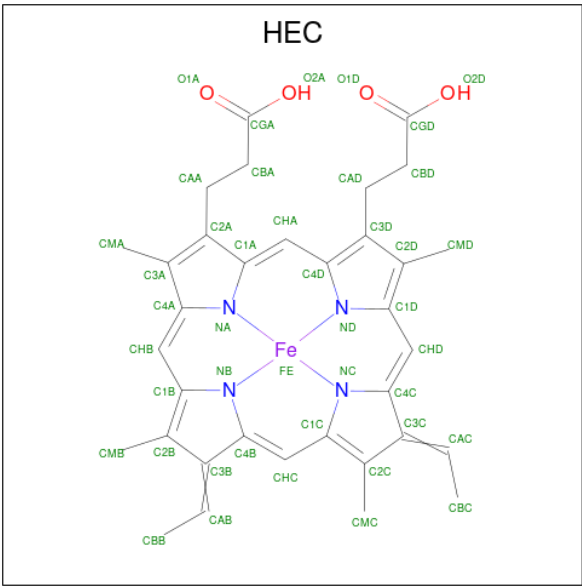
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
13	D	1	Total	C	N	O	P	0	0
			42	32	1	8	1		
13	E	1	Total	C	N	O	P	0	0
			29	19	1	8	1		
13	P	1	Total	C	N	O	P	0	0
			38	28	1	8	1		
13	R	1	Total	C	N	O	P	0	0
			34	24	1	8	1		
13	R	1	Total	C	N	O	P	0	0
			24	14	1	8	1		

- Molecule 14 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



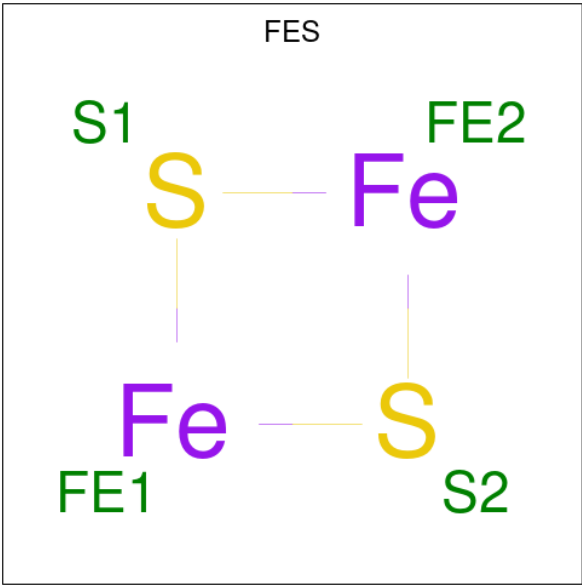
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
14	C	1	Total	C	O	P	0	0
			42	23	17	2		
14	C	1	Total	C	O	P	0	0
			37	18	17	2		
14	D	1	Total	C	O	P	0	0
			44	27	15	2		
14	P	1	Total	C	O	P	0	0
			42	27	13	2		
14	P	1	Total	C	O	P	0	0
			46	28	16	2		
14	P	1	Total	C	O	P	0	0
			38	19	17	2		

- Molecule 15 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



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

- Molecule 16 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).

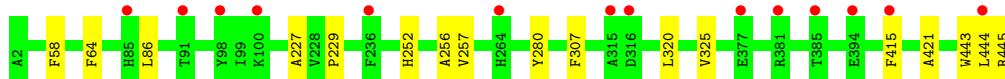


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
16	E	1	Total	Fe	S	0	0
			4	2	2		

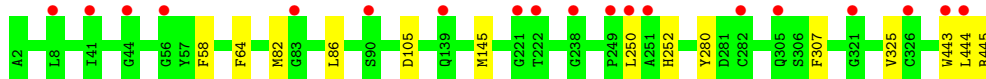
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

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



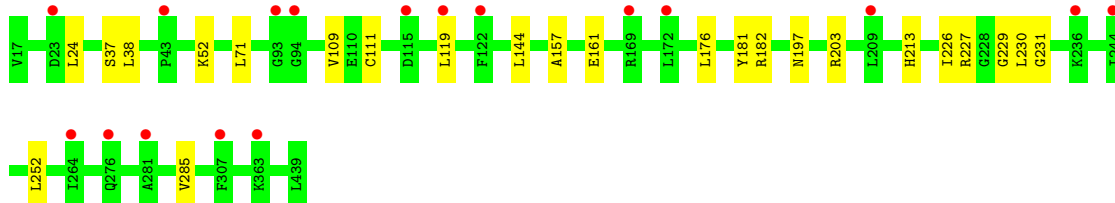
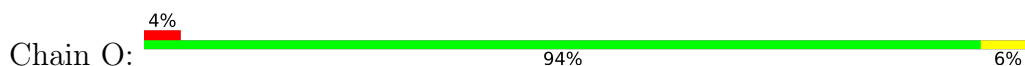
- Molecule 1: Cytochrome b-c1 complex subunit 1, mitochondrial



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



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



- Molecule 3: Cytochrome b

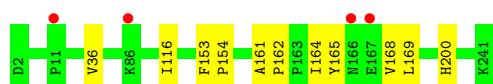




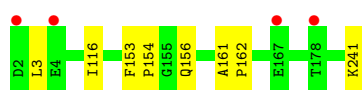
• Molecule 3: Cytochrome b



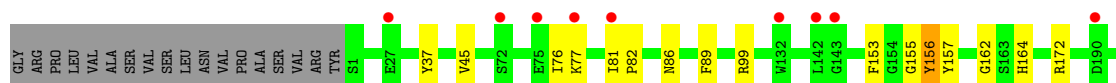
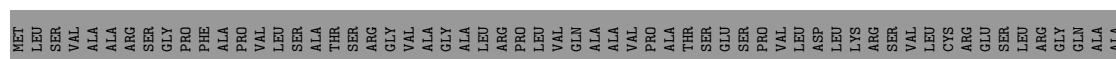
• Molecule 4: Cytochrome c1, heme protein, mitochondrial



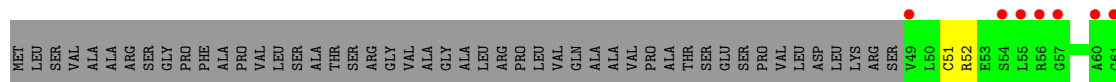
• Molecule 4: Cytochrome c1, heme protein, mitochondrial

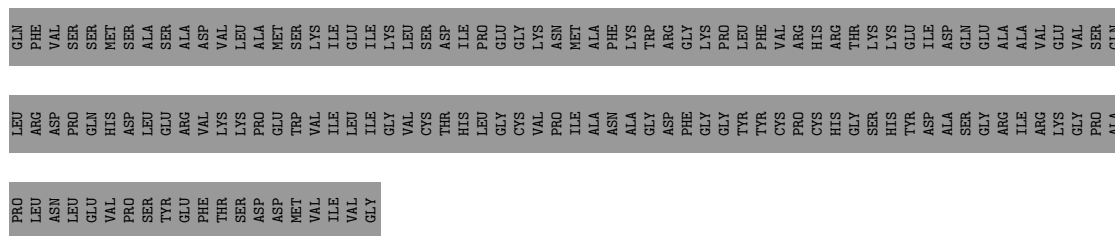


• Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial

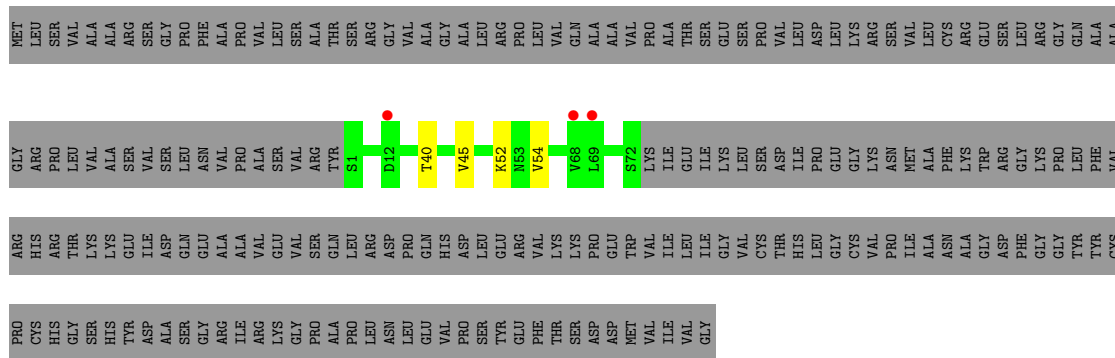


• Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial





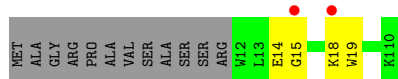
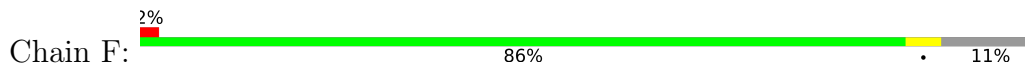
- Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial



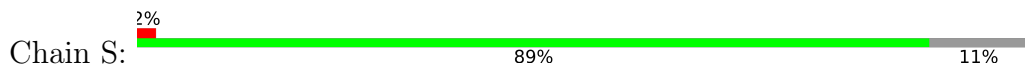
- Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial

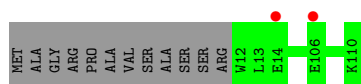


- Molecule 6: Cytochrome b-c1 complex subunit 7



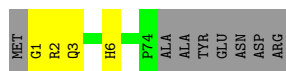
- Molecule 6: Cytochrome b-c1 complex subunit 7





- Molecule 7: Cytochrome b-c1 complex subunit 8

Chain G: 85% 5% 10%



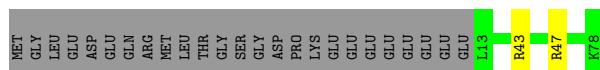
- Molecule 7: Cytochrome b-c1 complex subunit 8

Chain T: 4% 94% . .



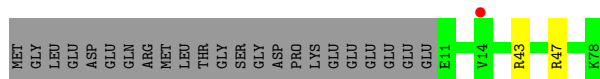
- Molecule 8: Cytochrome b-c1 complex subunit 6, mitochondrial

Chain H: 70% . 27%



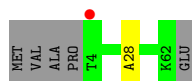
- Molecule 8: Cytochrome b-c1 complex subunit 6, mitochondrial

Chain U: % 73% . 25%



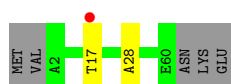
- Molecule 9: Cytochrome b-c1 complex subunit 9

Chain J: 2% 91% . 8%

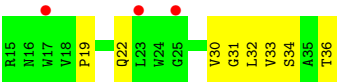


- Molecule 9: Cytochrome b-c1 complex subunit 9

Chain W: 2% 89% . 8%



- Molecule 10: ARG-ASN-TRP-VAL-PRO-THR-ALA-GLN-LEU-TRP-GLY-ALA-VAL-GLY-ALA-VAL-GLY-LEU-VAL-SER-ALA-THR



● Molecule 10: ARG-ASN-TRP-VAL-PRO-THR-ALA-GLN-LEU-TRP-GLY-ALA-VAL-GLY-ALA-VAL-GLY-LEU-VAL-SER-ALA-THR



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	129.48Å 129.48Å 720.29Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	64.74 – 3.50 64.74 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.5 (64.74-3.50) 99.5 (64.74-3.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 3.49Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.248 , 0.268 0.250 , 0.270	Depositor DCC
R_{free} test set	4365 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	78.7	Xtriage
Anisotropy	0.335	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 53.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.096 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	31648	wwPDB-VP
Average B, all atoms (Å ²)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.82% 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: CDL, PEE, HEC, FES, HEM, MJM

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	0.35	0/3512	0.60	0/4766
1	N	0.37	0/3512	0.60	0/4766
2	B	0.36	0/3232	0.56	0/4386
2	O	0.36	0/3232	0.56	0/4386
3	C	0.37	1/3051 (0.0%)	0.53	0/4177
3	P	0.37	0/3051	0.53	0/4177
4	D	0.36	0/1972	0.58	0/2676
4	Q	0.41	1/1972 (0.1%)	0.59	1/2676 (0.0%)
5	E	0.37	0/1553	0.61	0/2100
5	I	0.49	0/223	0.82	0/302
5	R	0.35	0/548	0.53	0/741
5	V	0.41	0/223	0.73	0/302
6	F	0.36	0/889	0.58	0/1191
6	S	0.36	0/889	0.57	0/1191
7	G	0.40	0/644	0.62	0/871
7	T	0.40	0/699	0.61	0/946
8	H	0.34	0/544	0.59	0/729
8	U	0.34	0/562	0.61	0/753
9	J	0.37	0/504	0.55	0/678
9	W	0.37	0/500	0.56	0/675
10	K	0.46	0/163	0.56	0/225
10	X	0.69	1/163 (0.6%)	0.56	0/225
All	All	0.37	3/31638 (0.0%)	0.58	1/42939 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	Q	241	LYS	CA-CB	-8.75	1.34	1.53
10	X	17	TRP	CB-CG	7.05	1.62	1.50
3	C	183	PHE	CG-CD2	-5.48	1.30	1.38

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	Q	241	LYS	CB-CA-C	-5.13	100.14	110.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3440	0	3337	20	0
1	N	3440	0	3337	13	0
2	B	3172	0	3152	9	0
2	O	3172	0	3152	20	0
3	C	2954	0	3010	29	0
3	P	2954	0	3010	32	0
4	D	1913	0	1860	10	0
4	Q	1913	0	1860	5	0
5	E	1519	0	1503	21	0
5	I	221	0	234	2	0
5	R	540	0	534	5	0
5	V	221	0	234	5	0
6	F	870	0	864	3	0
6	S	870	0	864	0	0
7	G	623	0	631	7	0
7	T	677	0	673	2	0
8	H	539	0	524	1	0
8	U	557	0	536	2	0
9	J	492	0	494	1	0
9	W	487	0	487	2	0
10	K	159	0	159	11	0
10	X	159	0	159	0	0
11	C	86	0	60	15	0
11	P	86	0	60	14	0
12	C	25	0	0	0	0
12	P	25	0	0	1	0
13	C	28	0	32	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	D	42	0	57	5	0
13	E	29	0	32	1	0
13	P	38	0	50	0	0
13	R	58	0	64	3	0
14	C	79	0	46	1	0
14	D	44	0	40	0	0
14	P	126	0	101	3	0
15	D	43	0	31	1	0
15	Q	43	0	31	1	0
16	E	4	0	0	0	0
All	All	31648	0	31218	190	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 3.

The worst 5 of 190 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)
13:D:502:PEE:C1	13:D:502:PEE:C2	2.00	1.39
3:C:183:PHE:CE1	11:C:501:HEM:HBC1	1.89	1.08
3:C:183:PHE:CD2	3:P:183:PHE:CD1	2.44	1.06
2:O:197:ASN:O	2:O:230:LEU:HD12	1.62	0.98
3:C:183:PHE:CE2	3:P:183:PHE:CD1	2.55	0.94

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	442/444 (100%)	422 (96%)	20 (4%)	0	100	100
1	N	442/444 (100%)	417 (94%)	25 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	421/423 (100%)	396 (94%)	25 (6%)	0	100	100
2	O	421/423 (100%)	393 (93%)	27 (6%)	1 (0%)	44	75
3	C	370/372 (100%)	356 (96%)	14 (4%)	0	100	100
3	P	370/372 (100%)	356 (96%)	14 (4%)	0	100	100
4	D	238/240 (99%)	227 (95%)	11 (5%)	0	100	100
4	Q	238/240 (99%)	228 (96%)	10 (4%)	0	100	100
5	E	194/274 (71%)	182 (94%)	12 (6%)	0	100	100
5	I	28/274 (10%)	24 (86%)	4 (14%)	0	100	100
5	R	70/274 (26%)	70 (100%)	0	0	100	100
5	V	28/274 (10%)	26 (93%)	2 (7%)	0	100	100
6	F	97/111 (87%)	95 (98%)	2 (2%)	0	100	100
6	S	97/111 (87%)	96 (99%)	1 (1%)	0	100	100
7	G	72/82 (88%)	66 (92%)	6 (8%)	0	100	100
7	T	78/82 (95%)	71 (91%)	7 (9%)	0	100	100
8	H	64/91 (70%)	63 (98%)	1 (2%)	0	100	100
8	U	66/91 (72%)	66 (100%)	0	0	100	100
9	J	57/64 (89%)	54 (95%)	3 (5%)	0	100	100
9	W	57/64 (89%)	54 (95%)	3 (5%)	0	100	100
10	K	20/22 (91%)	19 (95%)	1 (5%)	0	100	100
10	X	20/22 (91%)	20 (100%)	0	0	100	100
All	All	3890/4794 (81%)	3701 (95%)	188 (5%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	O	231	GLY

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	368/368 (100%)	366 (100%)	2 (0%)	86	93
1	N	368/368 (100%)	366 (100%)	2 (0%)	86	93
2	B	332/332 (100%)	332 (100%)	0	100	100
2	O	332/332 (100%)	332 (100%)	0	100	100
3	C	320/320 (100%)	320 (100%)	0	100	100
3	P	320/320 (100%)	320 (100%)	0	100	100
4	D	205/205 (100%)	205 (100%)	0	100	100
4	Q	205/205 (100%)	205 (100%)	0	100	100
5	E	168/228 (74%)	167 (99%)	1 (1%)	84	91
5	I	24/228 (10%)	24 (100%)	0	100	100
5	R	62/228 (27%)	62 (100%)	0	100	100
5	V	24/228 (10%)	24 (100%)	0	100	100
6	F	91/99 (92%)	91 (100%)	0	100	100
6	S	91/99 (92%)	91 (100%)	0	100	100
7	G	66/72 (92%)	66 (100%)	0	100	100
7	T	71/72 (99%)	71 (100%)	0	100	100
8	H	63/85 (74%)	63 (100%)	0	100	100
8	U	65/85 (76%)	65 (100%)	0	100	100
9	J	50/54 (93%)	50 (100%)	0	100	100
9	W	49/54 (91%)	49 (100%)	0	100	100
10	K	15/15 (100%)	15 (100%)	0	100	100
10	X	15/15 (100%)	15 (100%)	0	100	100
All	All	3304/4012 (82%)	3299 (100%)	5 (0%)	92	97

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	58	PHE
1	A	443	TRP
5	E	156	TYR
1	N	58	PHE
1	N	443	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

21 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	$\# Z > 2$
11	HEM	P	402	3	41,50,50	1.45	7 (17%)	45,82,82	1.90	13 (28%)
14	CDL	D	503	-	42,42,99	1.02	2 (4%)	44,51,111	1.00	2 (4%)
11	HEM	C	501	3	41,50,50	1.37	6 (14%)	45,82,82	1.79	12 (26%)
15	HEC	D	501	4	32,50,50	2.19	11 (34%)	24,82,82	2.08	7 (29%)
12	MJM	C	503	-	27,28,28	1.58	2 (7%)	30,39,39	1.02	2 (6%)
11	HEM	P	403	3	41,50,50	1.39	5 (12%)	45,82,82	1.69	10 (22%)
14	CDL	P	406	-	45,45,99	1.14	3 (6%)	50,56,111	1.49	7 (14%)
15	HEC	Q	501	4	32,50,50	2.17	7 (21%)	24,82,82	2.20	6 (25%)
14	CDL	P	401	-	41,41,99	1.01	2 (4%)	45,50,111	1.19	3 (6%)
11	HEM	C	502	3	41,50,50	1.40	6 (14%)	45,82,82	1.66	8 (17%)
16	FES	E	501	5	0,4,4	-	-	-	-	-
13	PEE	E	502	-	28,28,50	1.16	2 (7%)	31,33,55	1.13	2 (6%)
14	CDL	P	407	-	37,37,99	1.35	4 (10%)	43,49,111	1.24	2 (4%)
14	CDL	C	506	-	36,36,99	1.36	4 (11%)	42,48,111	1.45	4 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
13	PEE	R	201	-	33,33,50	1.33	3 (9%)	36,38,55	1.26	5 (13%)
13	PEE	P	405	-	37,37,50	1.20	4 (10%)	40,42,55	0.62	0
12	MJM	P	404	-	27,28,28	1.58	2 (7%)	30,39,39	1.24	3 (10%)
13	PEE	C	504	-	27,27,50	1.16	2 (7%)	29,31,55	0.56	0
13	PEE	D	502	-	41,41,50	4.15	7 (17%)	44,46,55	3.20	8 (18%)
13	PEE	R	202	-	23,23,50	1.24	2 (8%)	26,28,55	1.10	3 (11%)
14	CDL	C	505	-	41,41,99	1.48	4 (9%)	47,53,111	1.54	5 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	HEM	P	402	3	-	5/12/54/54	-
14	CDL	D	503	-	-	18/48/48/110	-
11	HEM	C	501	3	-	5/12/54/54	-
15	HEC	D	501	4	-	4/10/54/54	-
12	MJM	C	503	-	1/1/5/5	0/8/35/35	0/4/4/4
11	HEM	P	403	3	-	4/12/54/54	-
14	CDL	P	406	-	-	25/55/55/110	-
15	HEC	Q	501	4	-	4/10/54/54	-
14	CDL	P	401	-	-	22/48/48/110	-
11	HEM	C	502	3	-	4/12/54/54	-
16	FES	E	501	5	-	-	0/1/1/1
13	PEE	E	502	-	1/1/4/8	13/32/32/54	-
14	CDL	P	407	-	-	20/45/45/110	-
14	CDL	C	506	-	-	22/44/44/110	-
13	PEE	R	201	-	1/1/4/8	15/37/37/54	-
13	PEE	P	405	-	-	11/41/41/54	-
12	MJM	P	404	-	1/1/5/5	0/8/35/35	0/4/4/4
13	PEE	C	504	-	-	10/30/30/54	-
13	PEE	D	502	-	1/1/4/8	18/45/45/54	-
13	PEE	R	202	-	1/1/4/8	8/27/27/54	-
14	CDL	C	505	-	-	28/49/49/110	-

The worst 5 of 85 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	D	502	PEE	O2-C2	-19.41	0.97	1.46
13	D	502	PEE	C1-C2	16.21	2.00	1.50
15	Q	501	HEC	C2B-C3B	6.22	1.47	1.40
15	D	501	HEC	C2B-C3B	5.91	1.46	1.40
15	D	501	HEC	C3C-C2C	5.58	1.46	1.40

The worst 5 of 102 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	D	502	PEE	O2-C2-C3	15.35	163.99	108.40
13	D	502	PEE	O3-C3-C2	-8.52	83.62	108.43
13	D	502	PEE	C3-C2-C1	-8.27	92.24	111.79
14	C	505	CDL	CB4-OB6-CB5	-5.59	107.47	117.90
14	C	505	CDL	OB6-CB5-C51	5.40	121.03	111.09

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
12	C	503	MJM	C4
12	P	404	MJM	C4
13	D	502	PEE	C2
13	E	502	PEE	C2
13	R	201	PEE	C2

5 of 236 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	C	504	PEE	C4-O4P-P-O1P
13	D	502	PEE	C11-C10-O2-C2
13	D	502	PEE	O2-C2-C3-O3
13	D	502	PEE	C4-O4P-P-O2P
13	E	502	PEE	C4-O4P-P-O3P

There are no ring outliers.

13 monomers are involved in 44 short contacts:

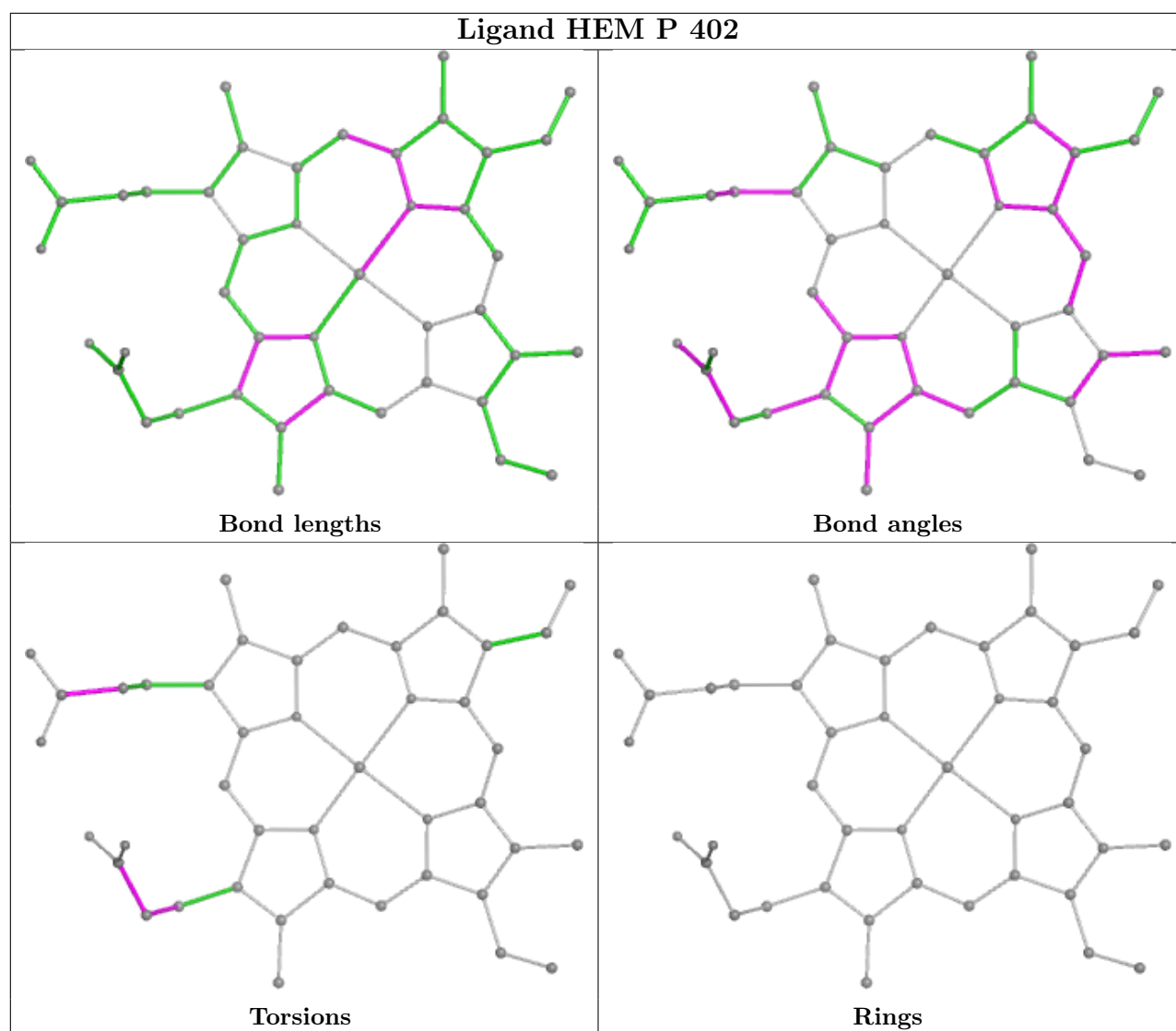
Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	P	402	HEM	6	0
11	C	501	HEM	13	0
15	D	501	HEC	1	0
11	P	403	HEM	8	0
14	P	406	CDL	3	0

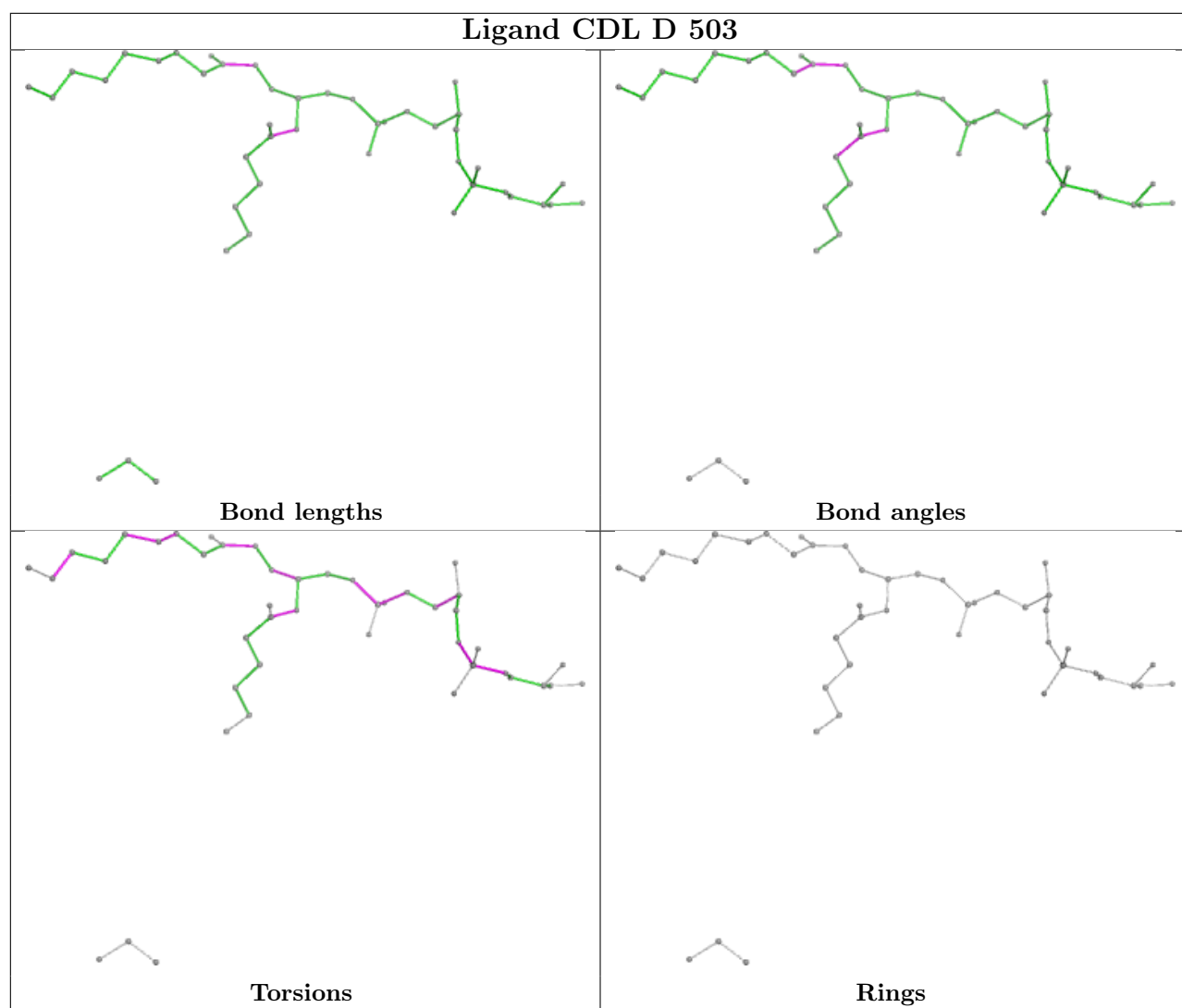
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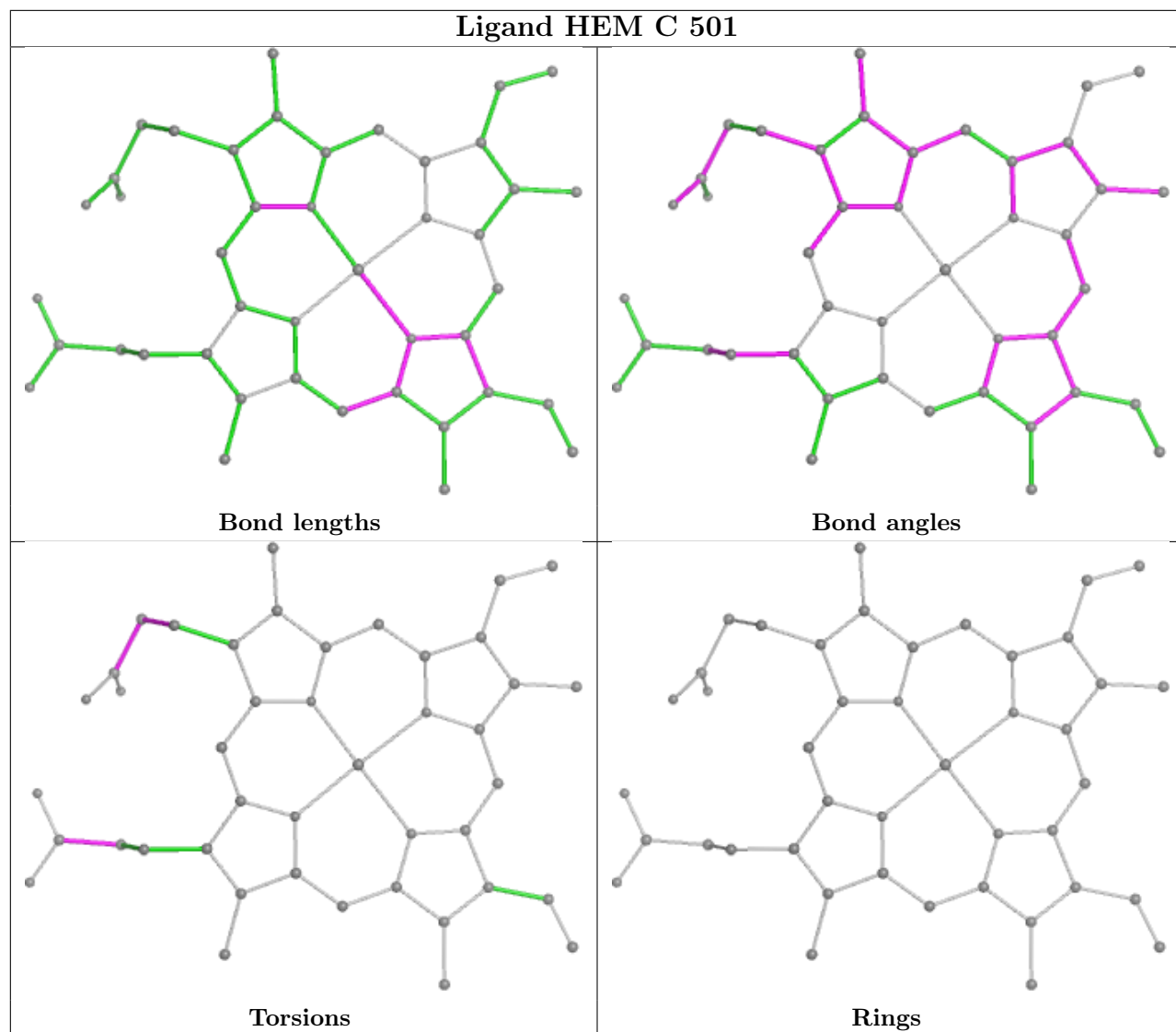
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	Q	501	HEC	1	0
11	C	502	HEM	2	0
13	E	502	PEE	1	0
13	R	201	PEE	2	0
12	P	404	MJM	1	0
13	D	502	PEE	5	0
13	R	202	PEE	1	0
14	C	505	CDL	1	0

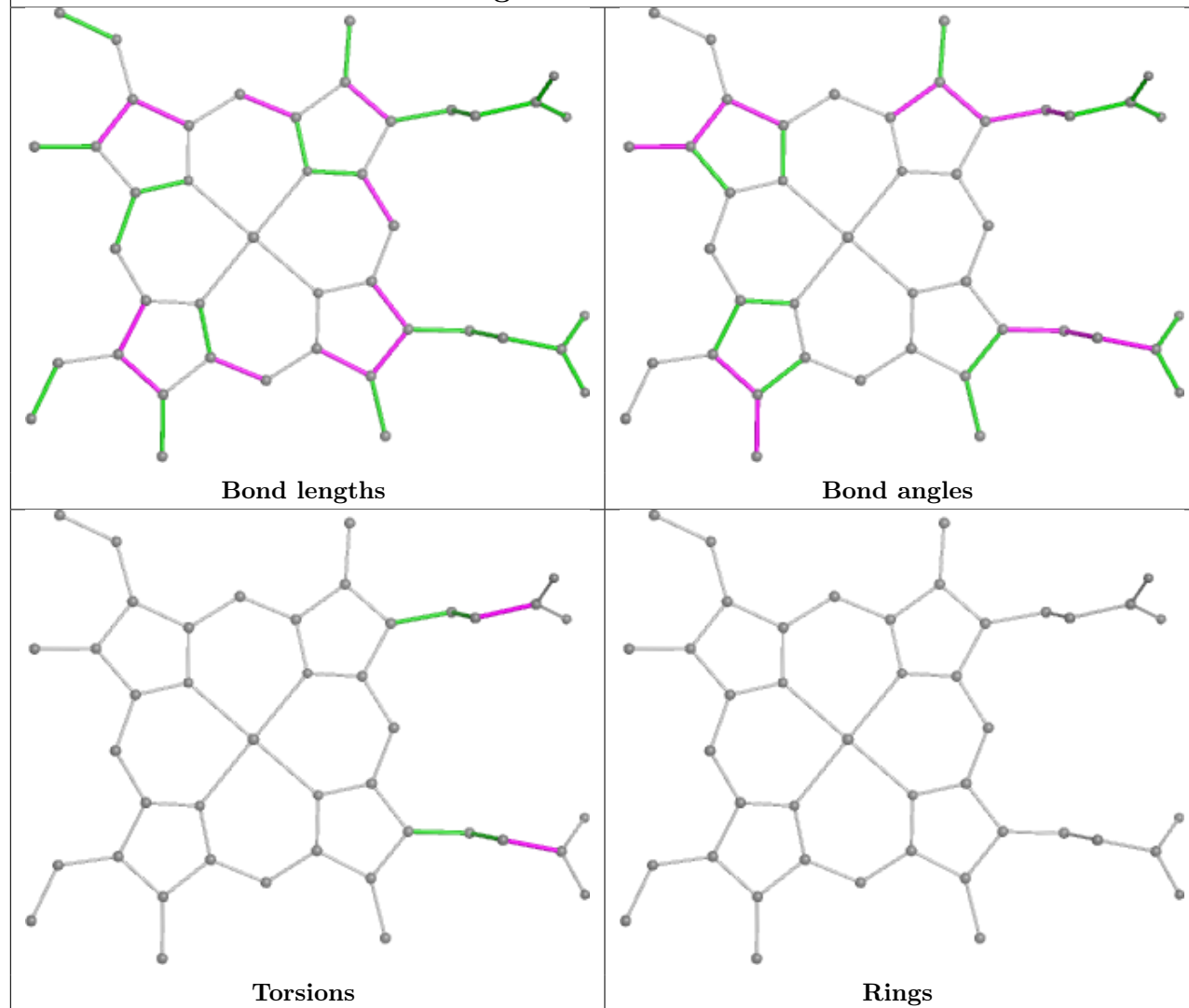
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



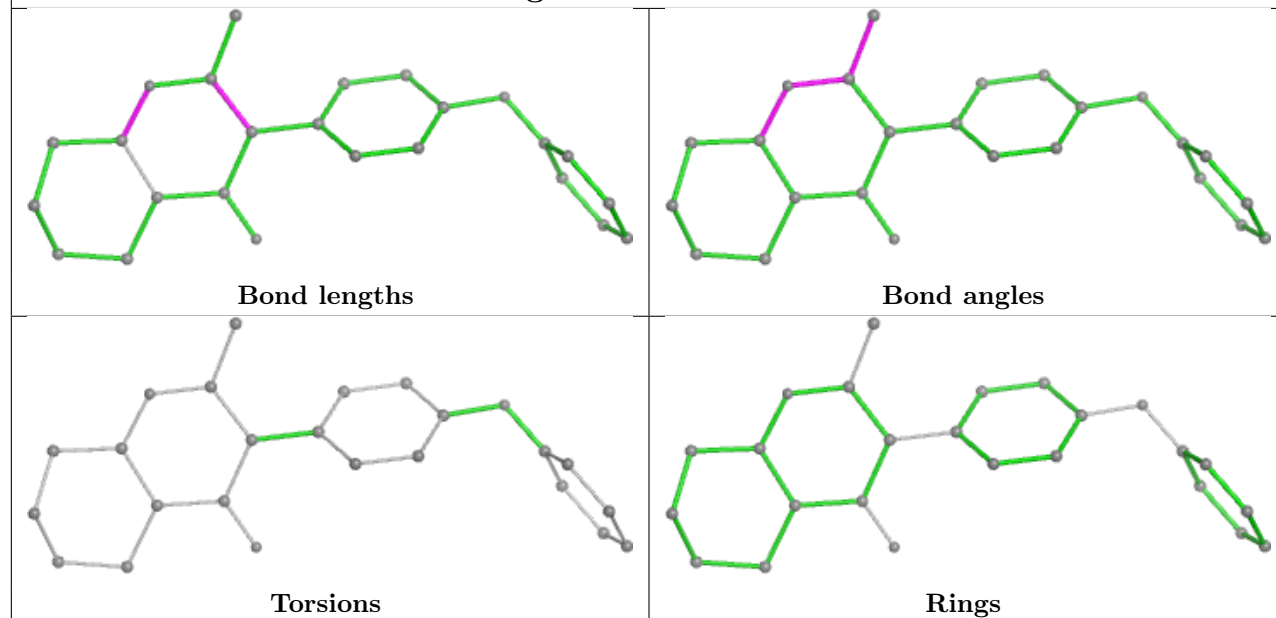


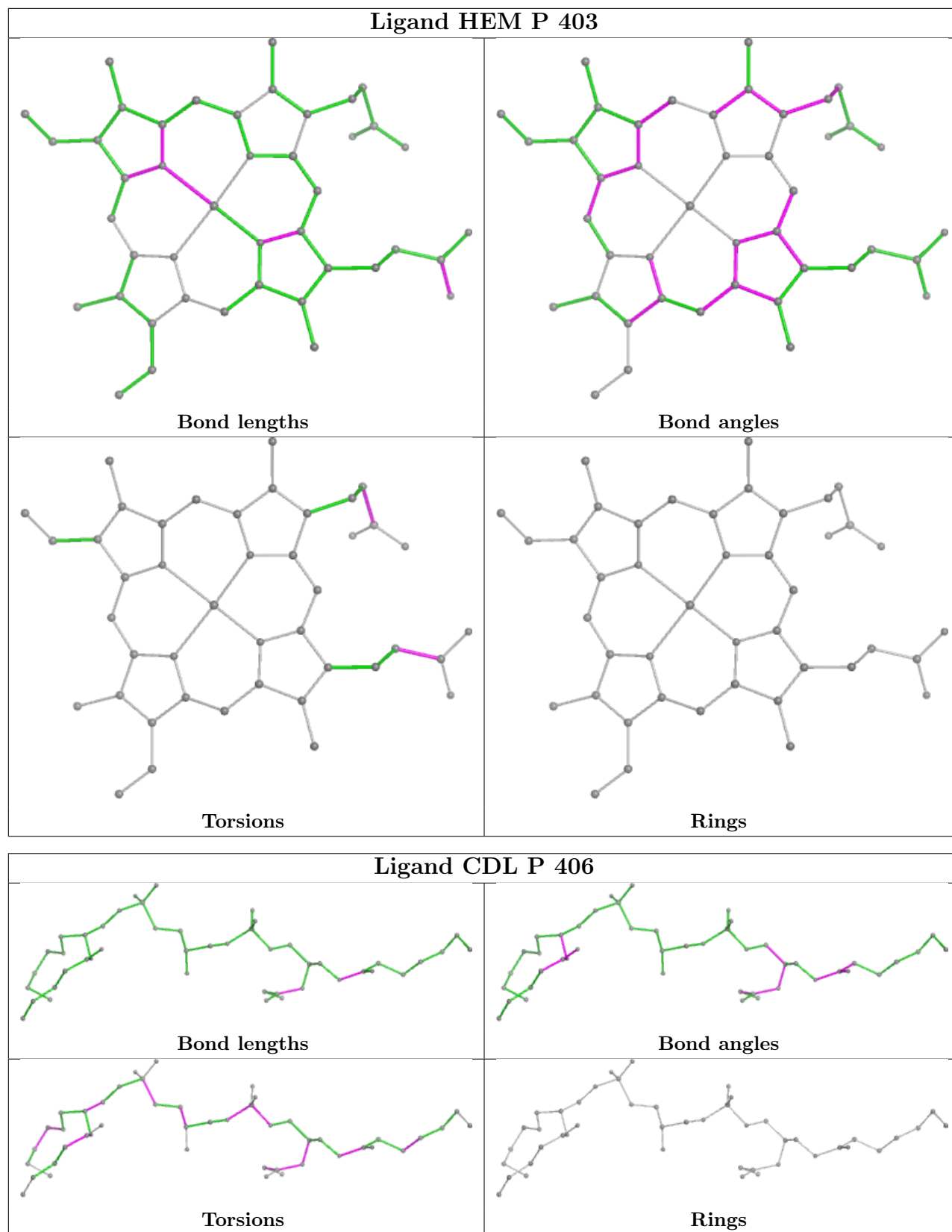


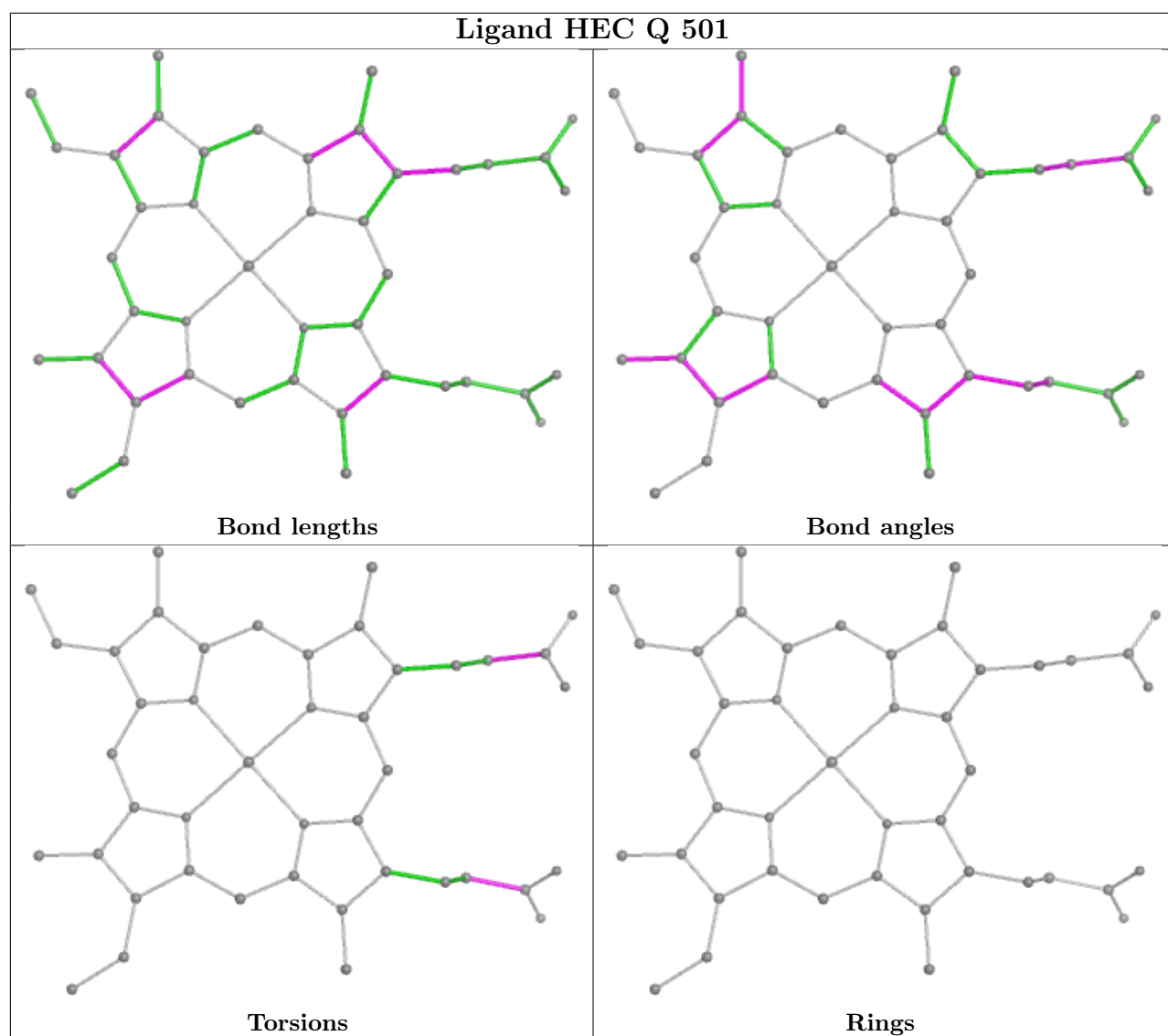
Ligand HEC D 501

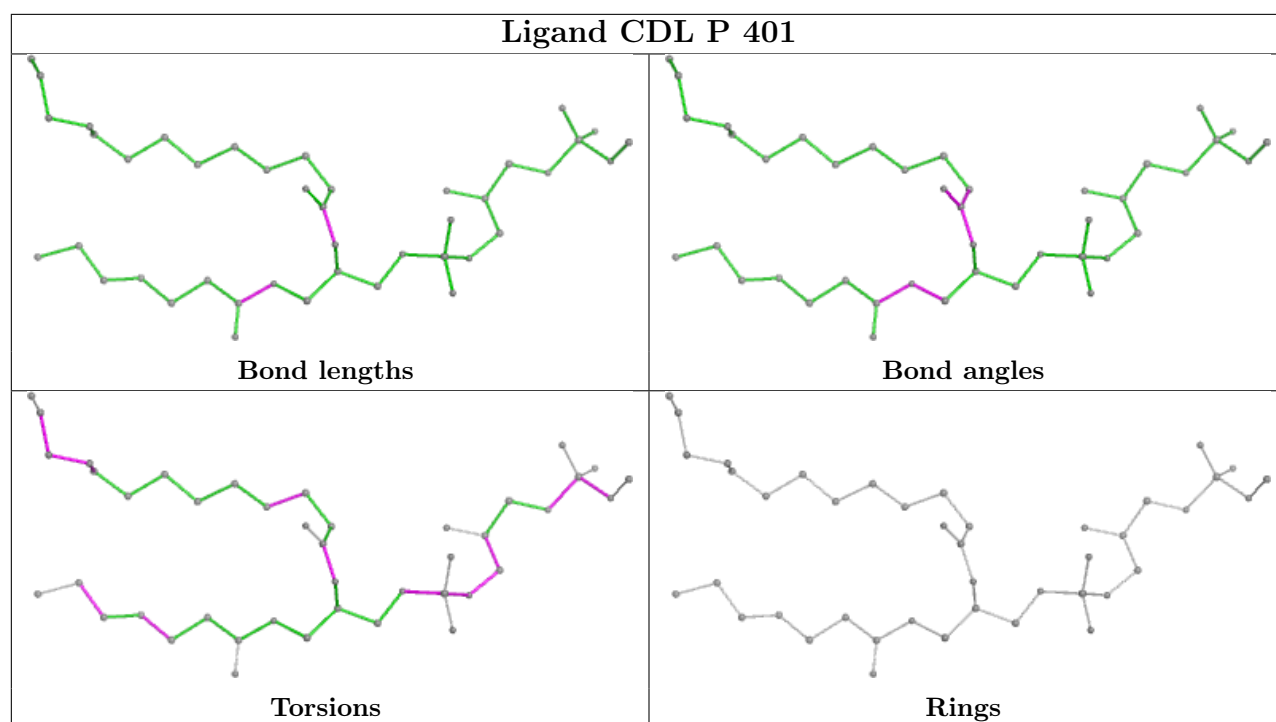


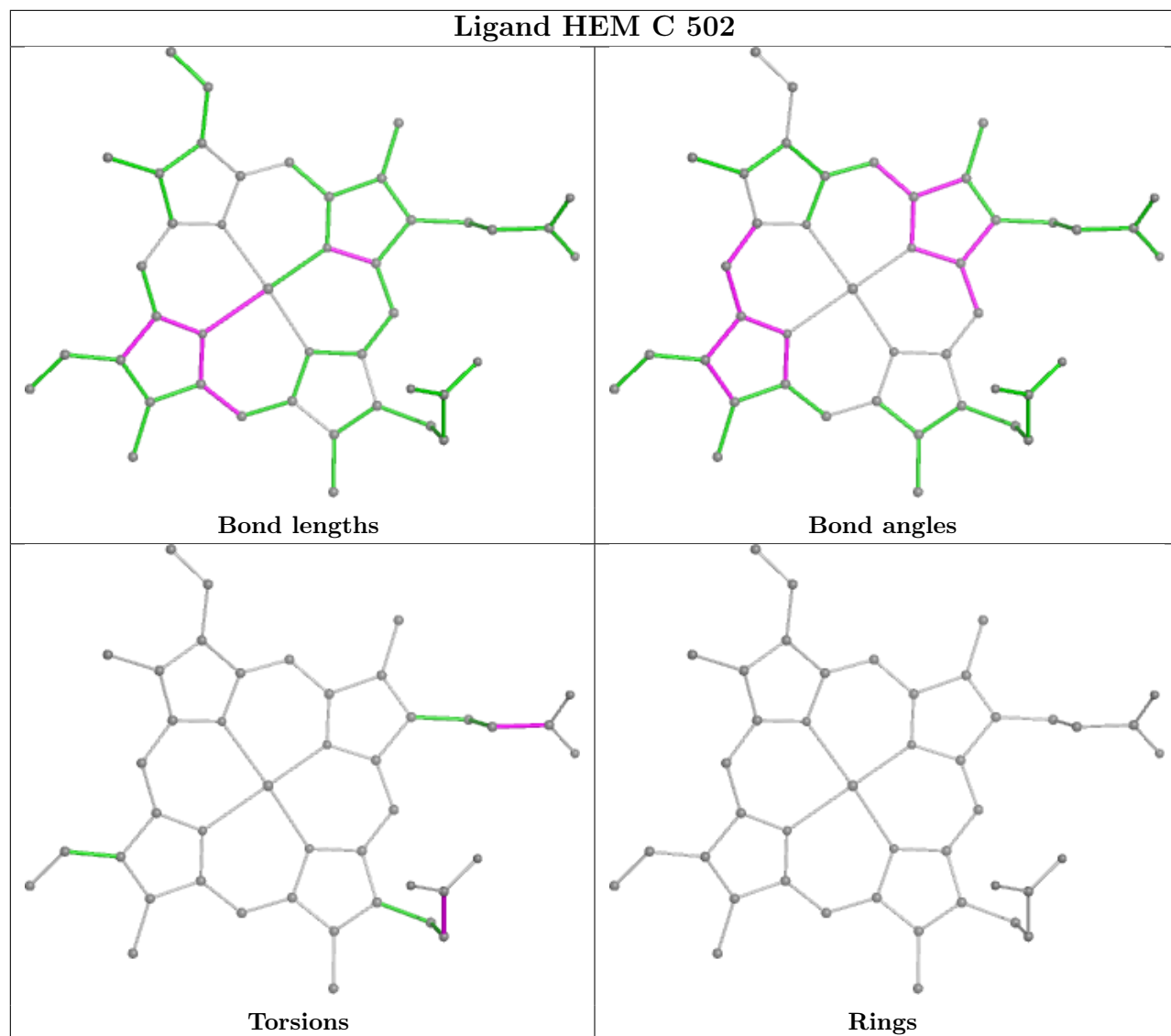
Ligand MJM C 503

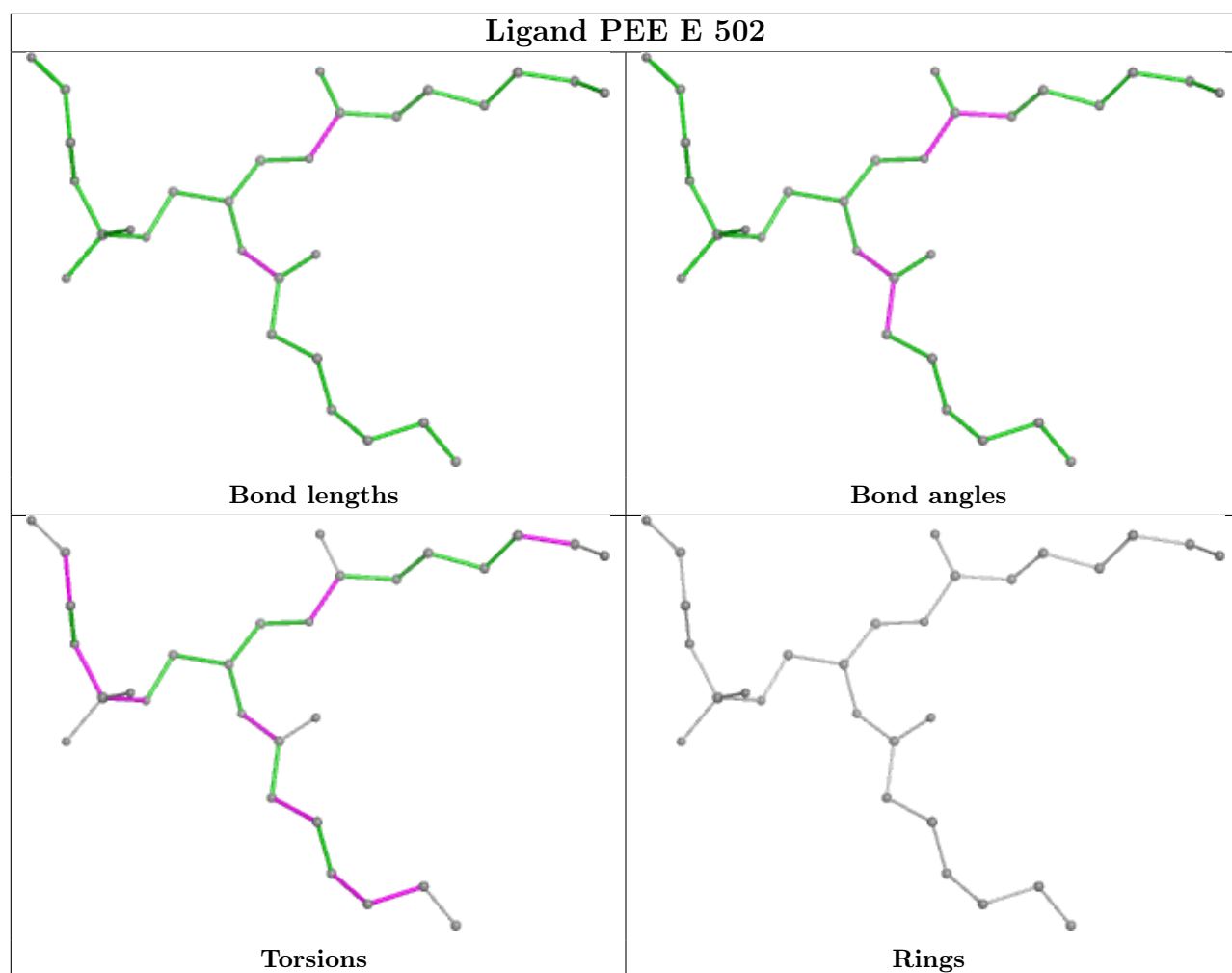


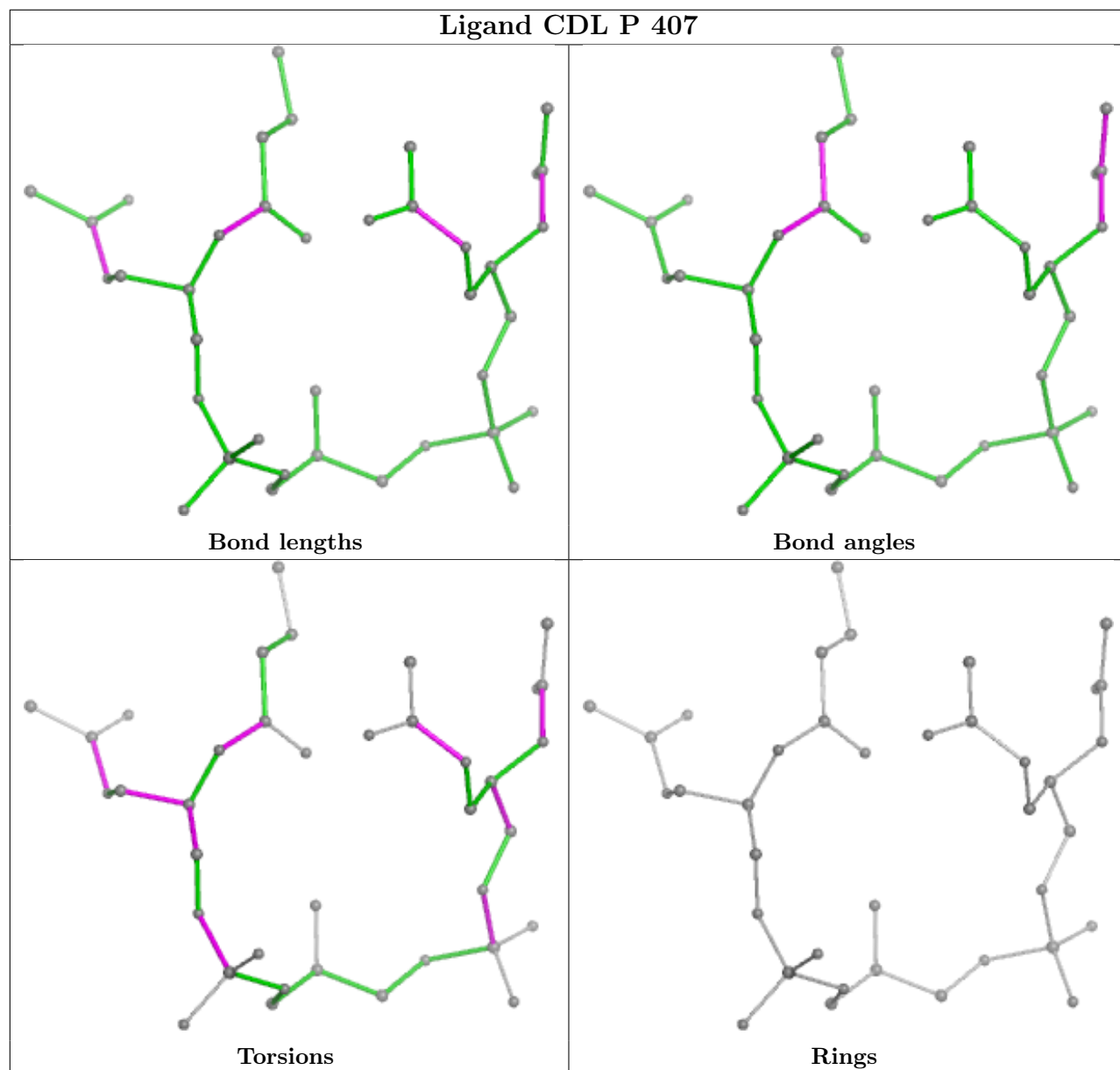


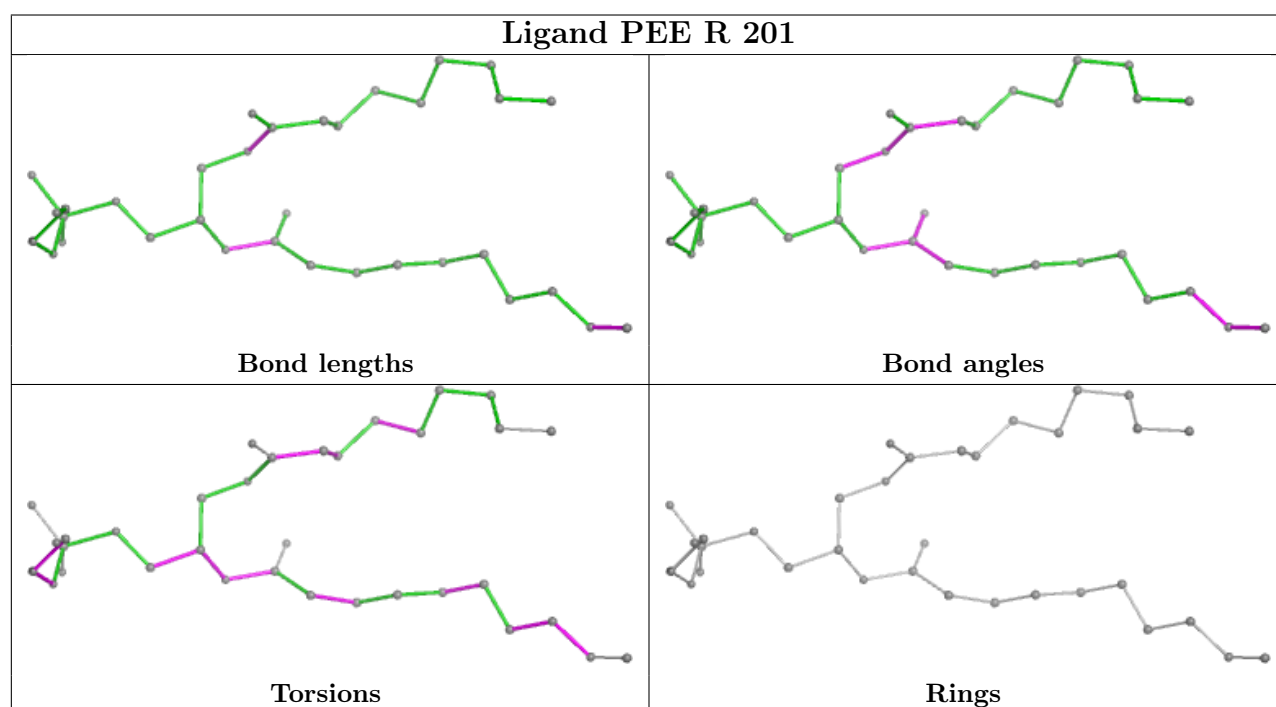
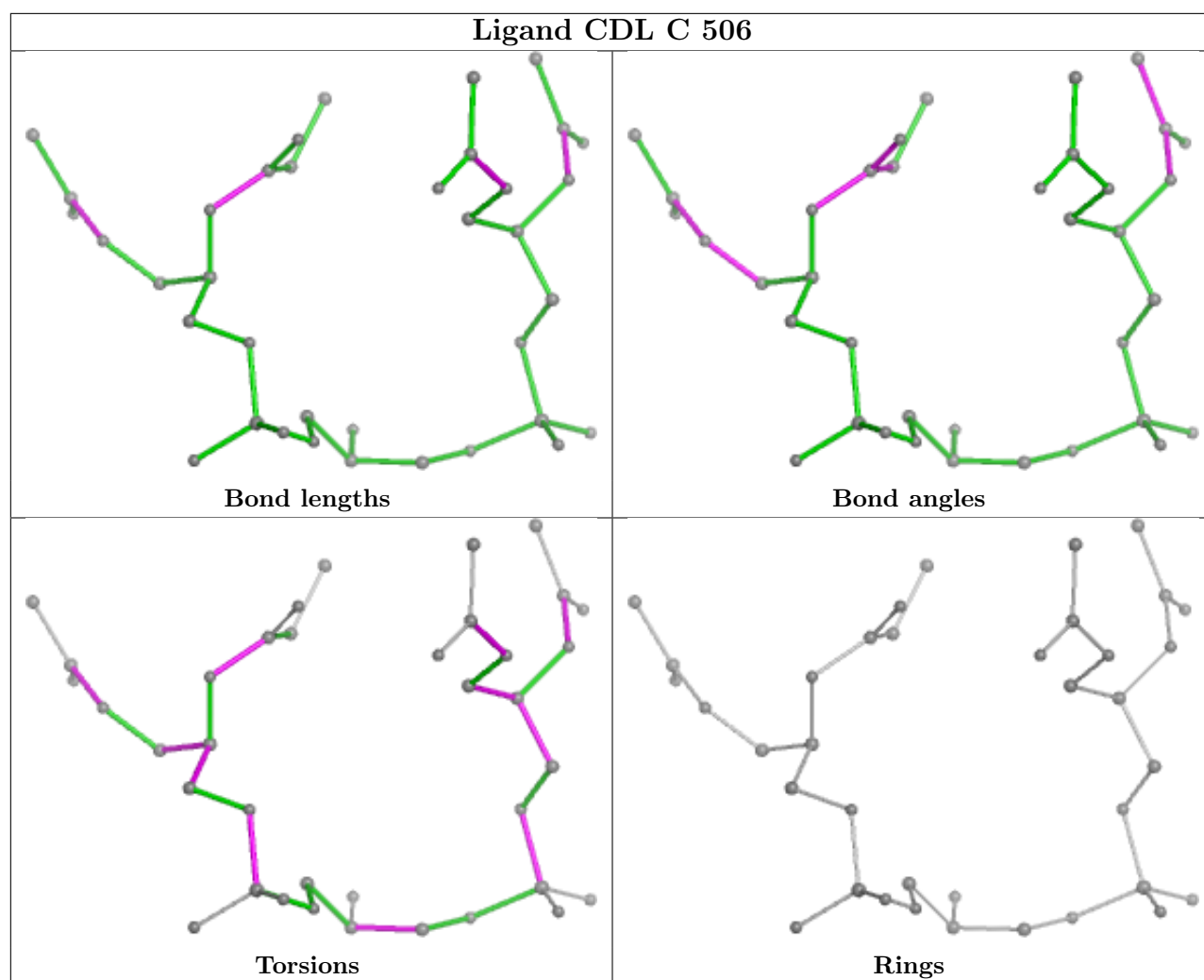


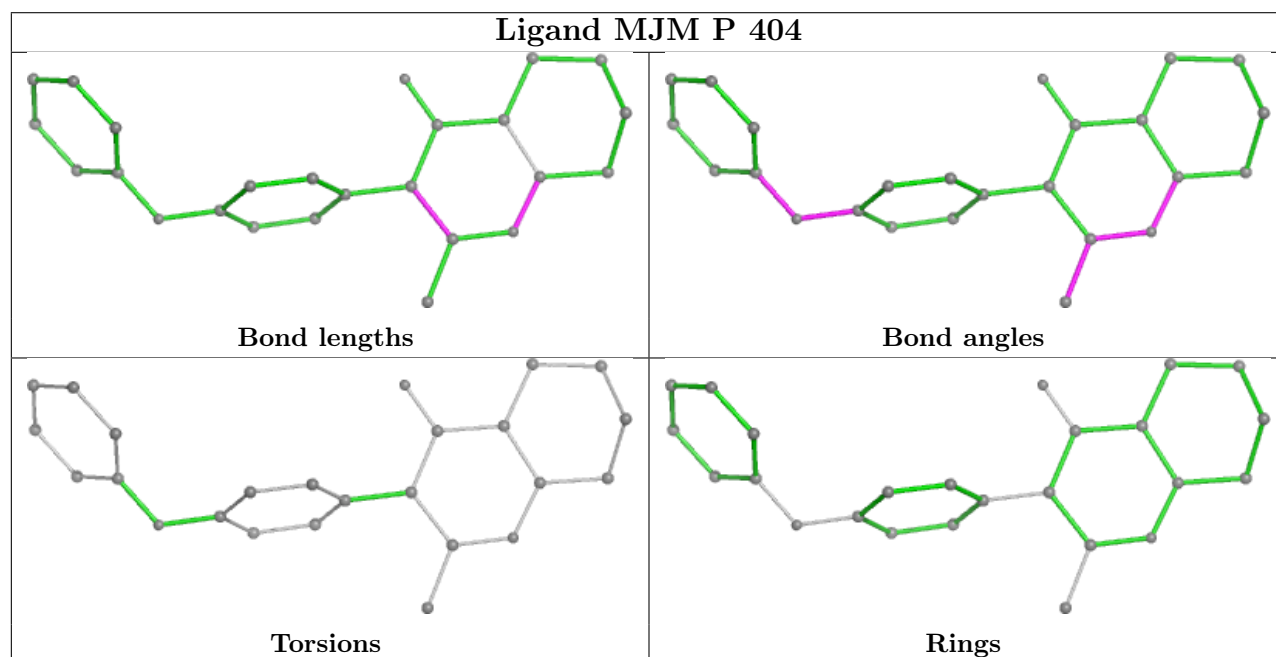
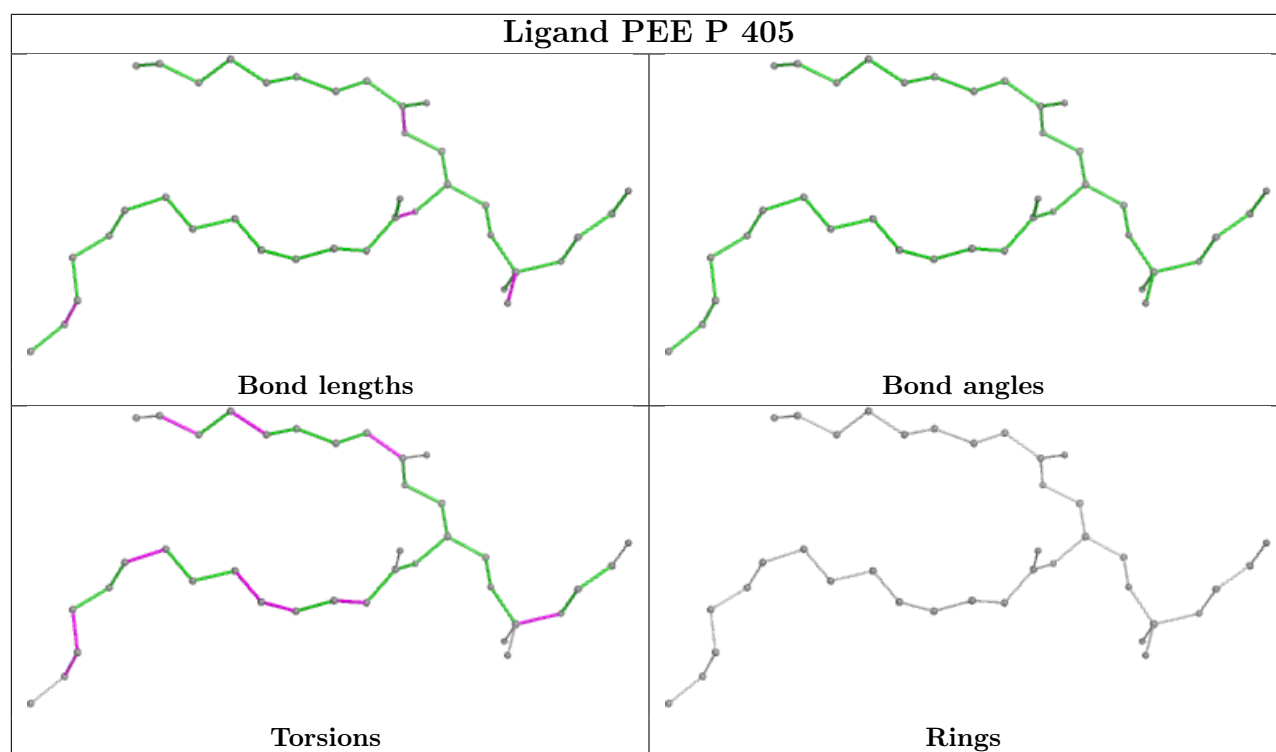


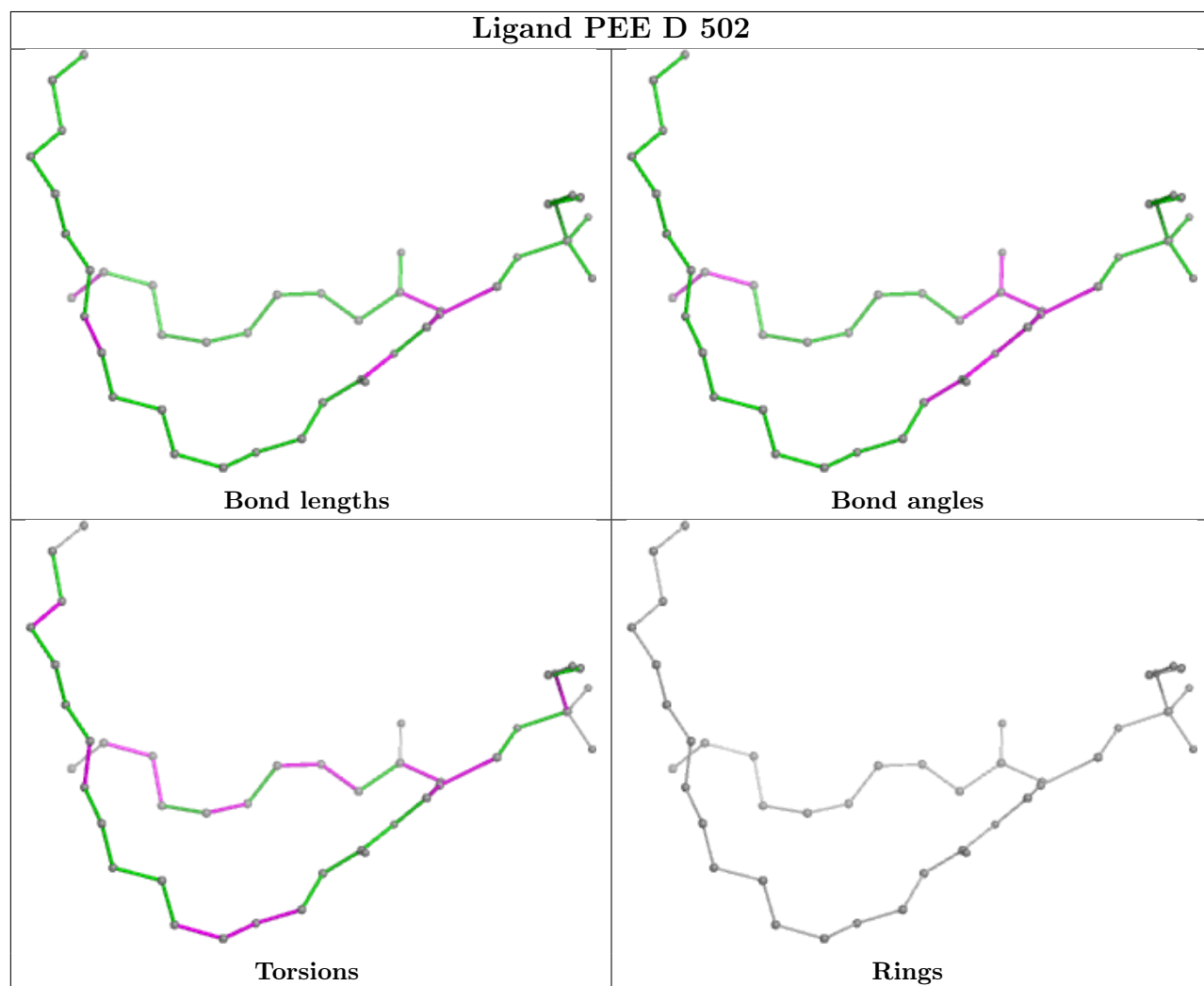
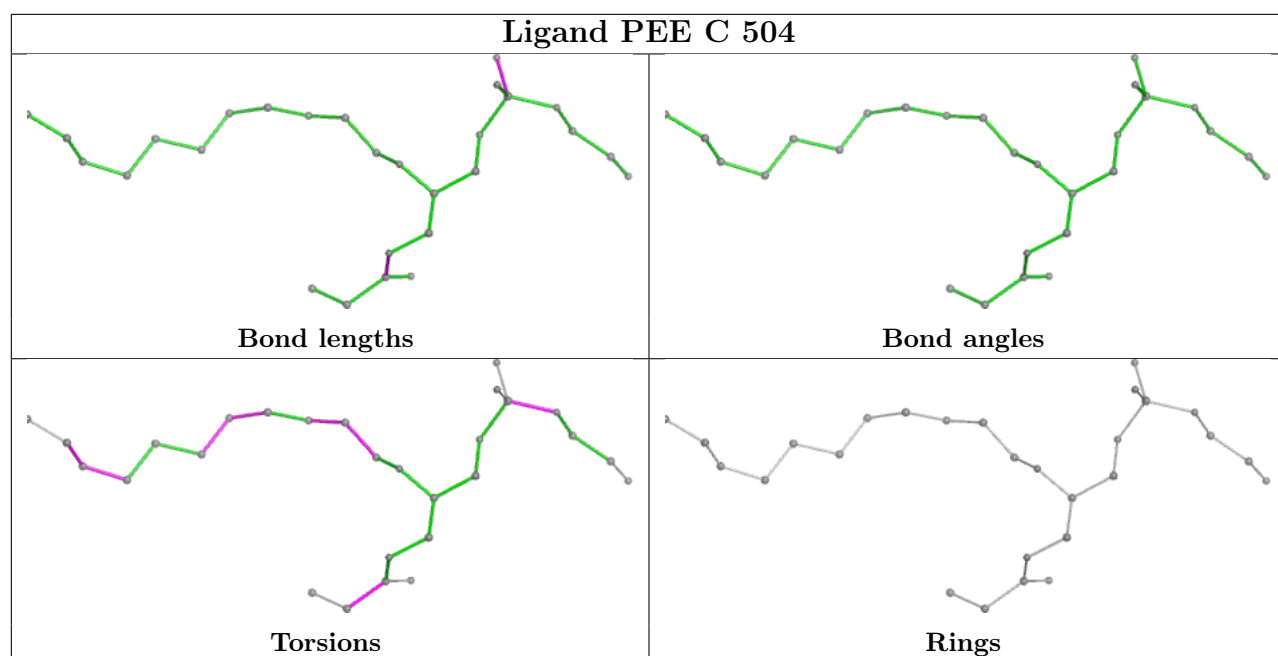




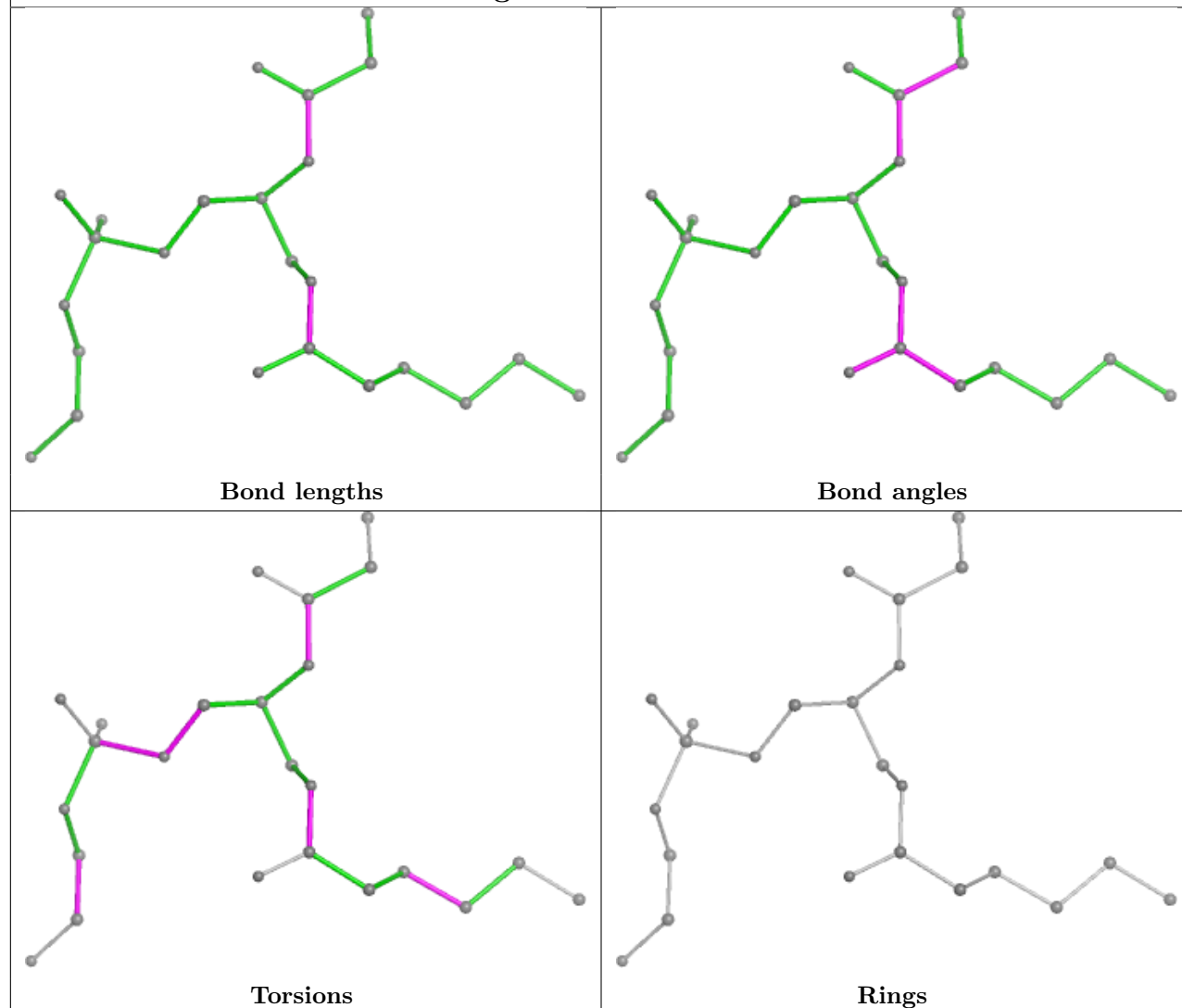




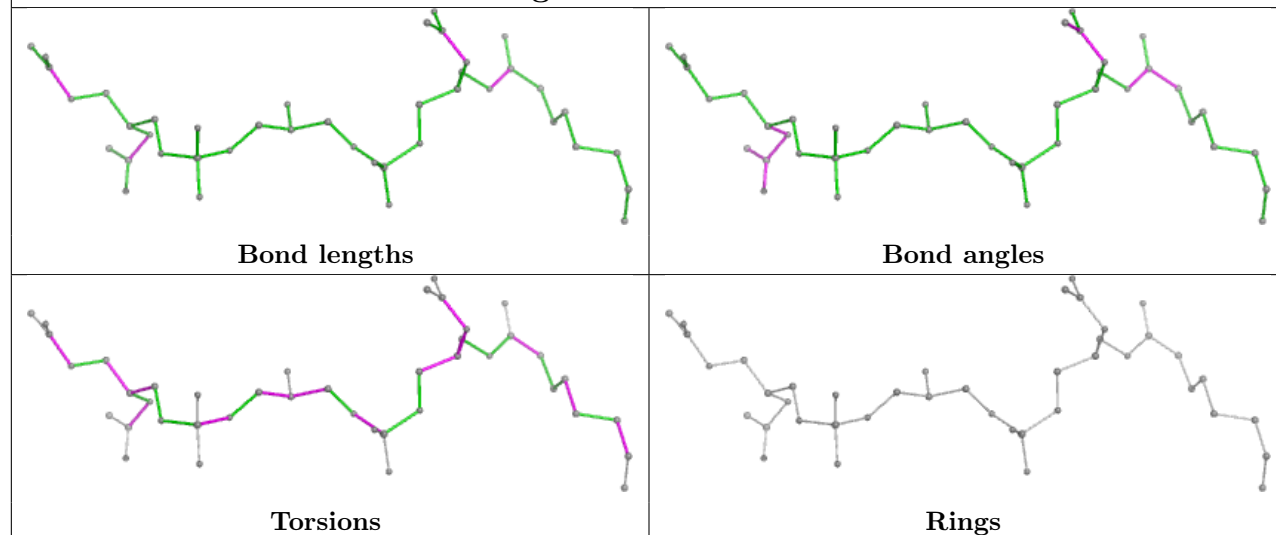




Ligand PEE R 202



Ligand CDL C 505



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	438/444 (98%)	0.08	14 (3%) 50 34	47, 92, 130, 166	0
1	N	439/444 (98%)	0.27	19 (4%) 40 27	56, 108, 152, 181	2 (0%)
2	B	418/423 (98%)	0.10	7 (1%) 69 49	64, 106, 143, 196	0
2	O	422/423 (99%)	0.36	17 (4%) 43 29	71, 115, 151, 203	0
3	C	372/372 (100%)	-0.18	4 (1%) 77 59	46, 73, 105, 141	0
3	P	372/372 (100%)	-0.17	4 (1%) 77 59	33, 62, 92, 127	0
4	D	240/240 (100%)	0.05	4 (1%) 69 49	56, 96, 132, 181	0
4	Q	240/240 (100%)	0.13	4 (1%) 69 49	52, 82, 120, 138	1 (0%)
5	E	196/274 (71%)	0.26	9 (4%) 38 27	48, 107, 143, 166	0
5	I	29/274 (10%)	1.73	9 (31%) 1 1	84, 130, 157, 166	0
5	R	72/274 (26%)	0.10	3 (4%) 41 28	55, 84, 118, 130	0
5	V	30/274 (10%)	1.09	4 (13%) 8 7	89, 132, 168, 208	0
6	F	99/111 (89%)	-0.02	2 (2%) 64 45	50, 78, 127, 141	0
6	S	99/111 (89%)	-0.03	2 (2%) 64 45	53, 81, 115, 128	1 (1%)
7	G	74/82 (90%)	-0.07	0 100 100	54, 85, 127, 147	0
7	T	80/82 (97%)	0.07	3 (3%) 44 30	57, 82, 129, 161	0
8	H	66/91 (72%)	0.23	0 100 100	68, 135, 156, 182	1 (1%)
8	U	68/91 (74%)	0.26	1 (1%) 71 53	64, 95, 126, 141	0
9	J	59/64 (92%)	-0.15	1 (1%) 69 49	57, 83, 123, 138	0
9	W	59/64 (92%)	-0.22	1 (1%) 69 49	60, 95, 126, 141	0
10	K	22/22 (100%)	1.07	3 (13%) 8 7	123, 151, 173, 200	0
10	X	22/22 (100%)	0.09	0 100 100	59, 128, 140, 155	2 (9%)
All	All	3916/4794 (81%)	0.11	111 (2%) 55 37	33, 93, 143, 208	7 (0%)

The worst 5 of 111 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	I	54	SER	6.4
1	A	98	TYR	4.5
5	I	57	GLY	4.4
2	O	119	LEU	4.4
3	C	168	PHE	4.4

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 monosaccharides 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.

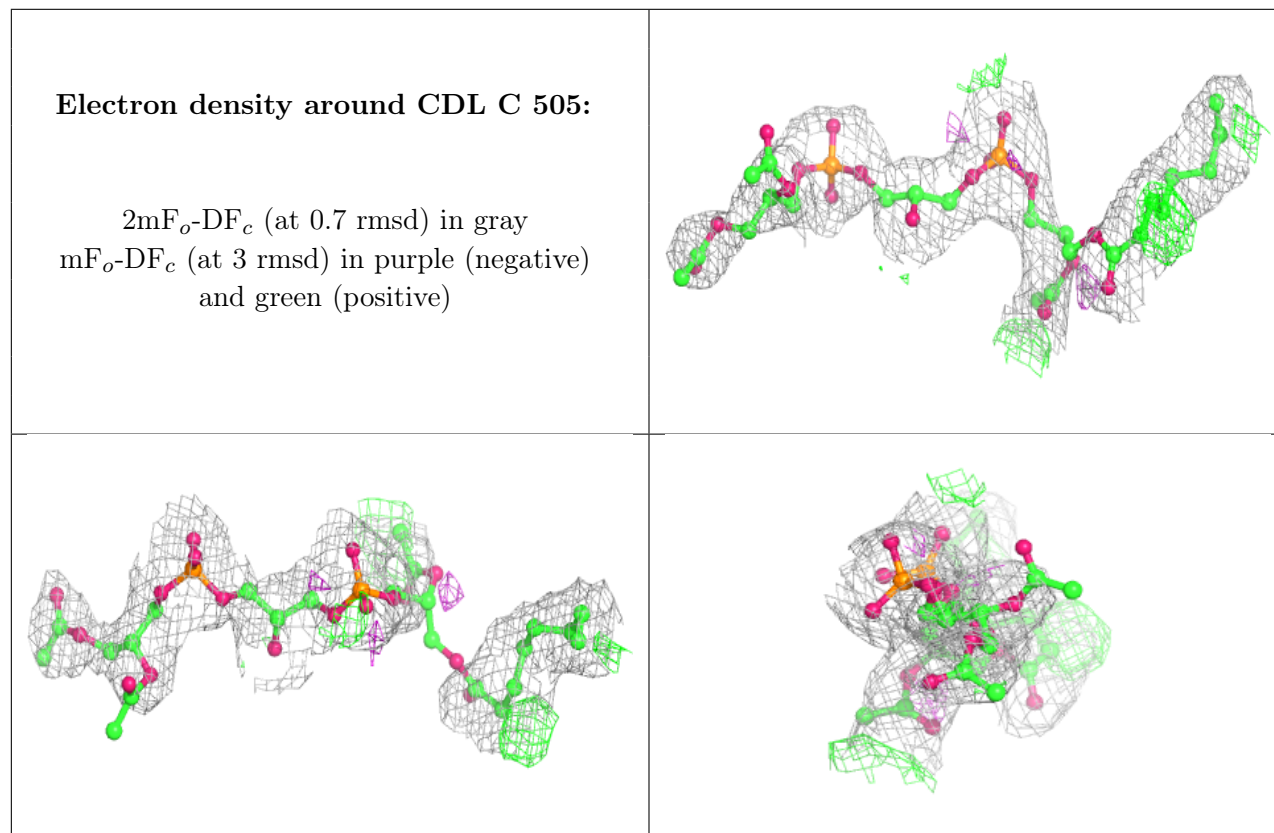
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
14	CDL	C	505	42/100	0.80	0.19	45,88,122,130	0
12	MJM	P	404	25/25	0.82	0.19	49,56,64,69	0
14	CDL	P	401	42/100	0.85	0.20	53,90,135,159	0
14	CDL	P	406	46/100	0.86	0.16	70,106,125,128	0
13	PEE	R	202	24/51	0.88	0.15	26,37,52,55	0
14	CDL	D	503	44/100	0.88	0.17	42,86,112,116	0
13	PEE	E	502	29/51	0.89	0.18	47,83,98,103	0
13	PEE	C	504	28/51	0.89	0.16	35,45,57,59	0
12	MJM	C	503	25/25	0.91	0.13	49,56,68,69	0
13	PEE	P	405	38/51	0.92	0.16	41,56,81,81	0
14	CDL	C	506	37/100	0.93	0.12	59,73,108,108	0
13	PEE	D	502	42/51	0.94	0.15	60,79,102,111	0
14	CDL	P	407	38/100	0.94	0.13	53,71,87,90	0
15	HEC	D	501	43/43	0.94	0.12	66,84,109,147	0
15	HEC	Q	501	43/43	0.95	0.14	59,79,111,145	0
13	PEE	R	201	34/51	0.96	0.12	57,78,91,101	0
11	HEM	C	501	43/43	0.96	0.11	51,59,77,90	0
16	FES	E	501	4/4	0.96	0.07	104,106,122,144	0
11	HEM	P	403	43/43	0.97	0.10	52,55,60,61	0

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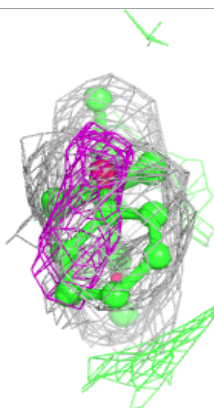
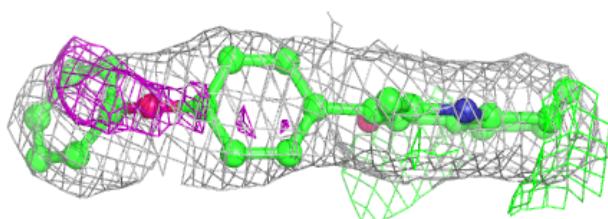
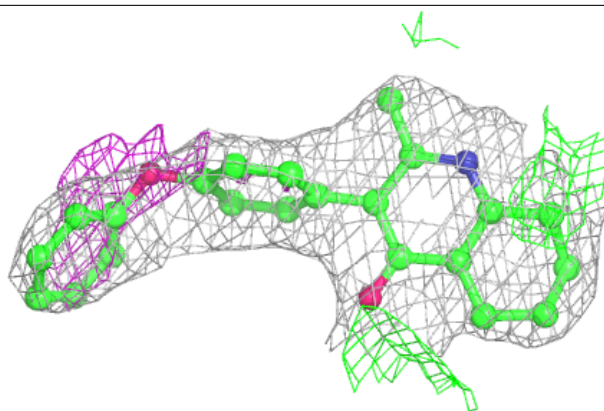
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
11	HEM	C	502	43/43	0.97	0.09	45,53,71,76	0
11	HEM	P	402	43/43	0.97	0.10	43,55,60,74	0

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.

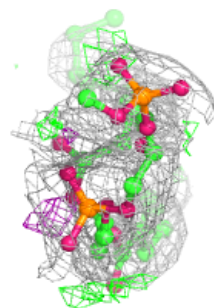
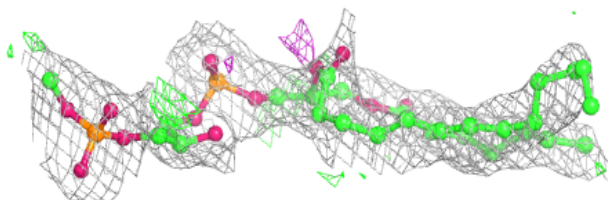
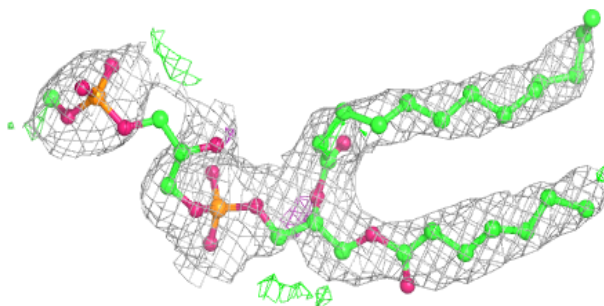


Electron density around MJM P 404:

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

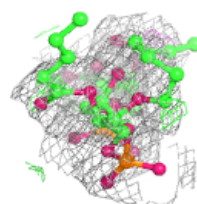
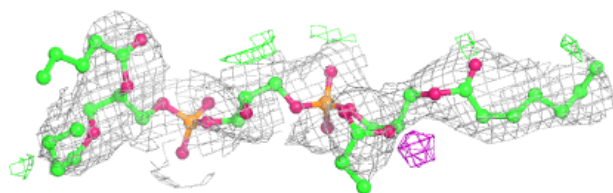
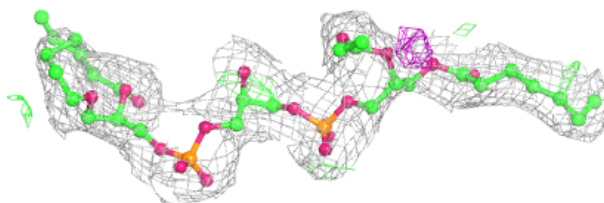
**Electron density around CDL P 401:**

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



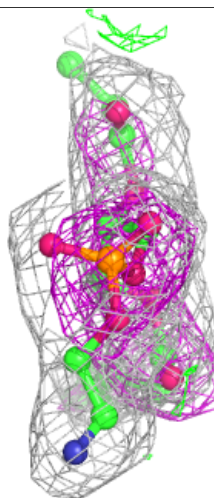
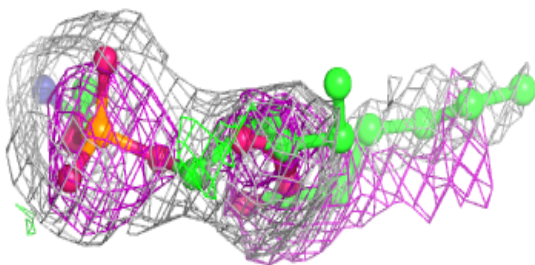
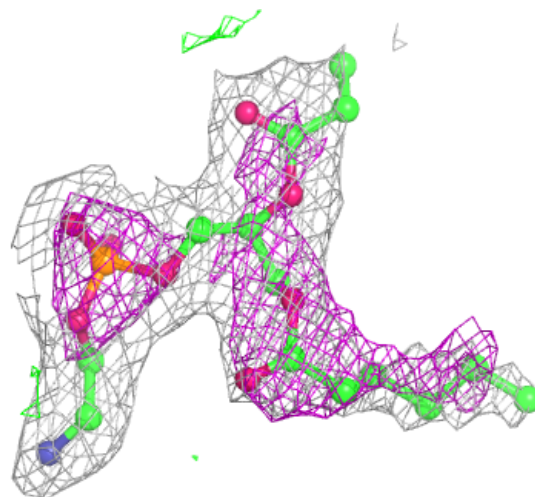
Electron density around CDL P 406:

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



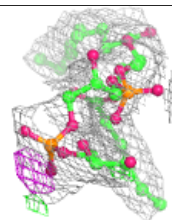
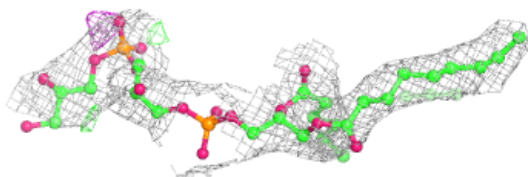
Electron density around PEE R 202:

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



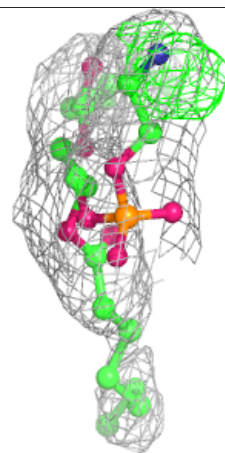
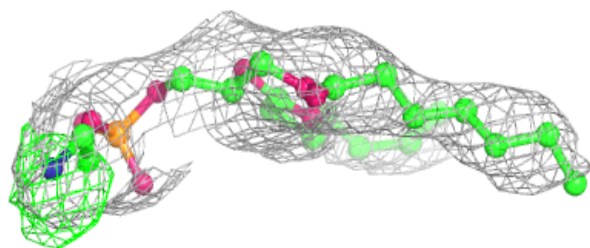
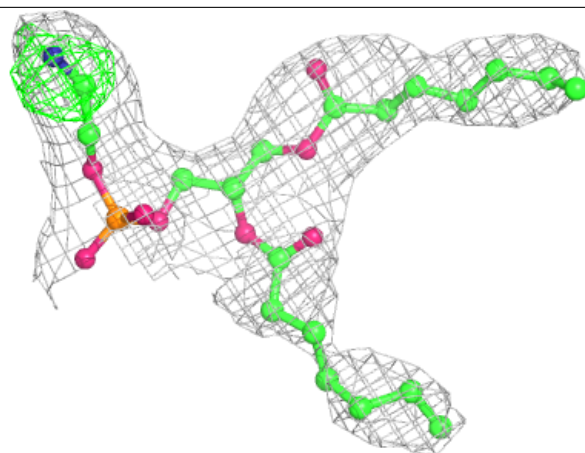
Electron density around CDL D 503:

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

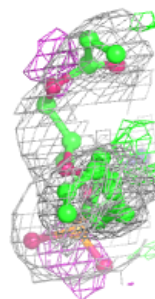
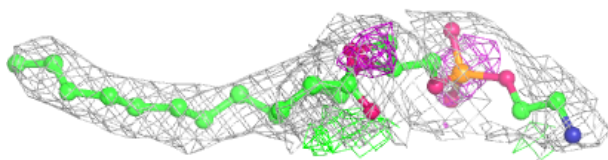
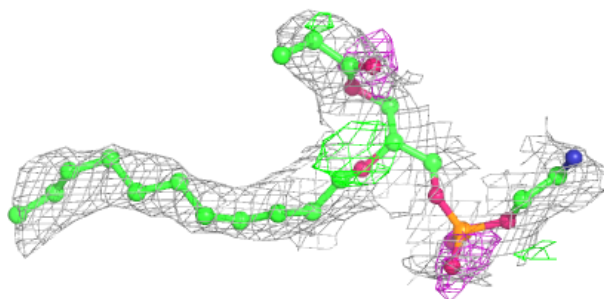


Electron density around PEE E 502:

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

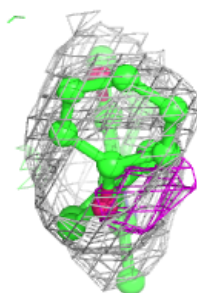
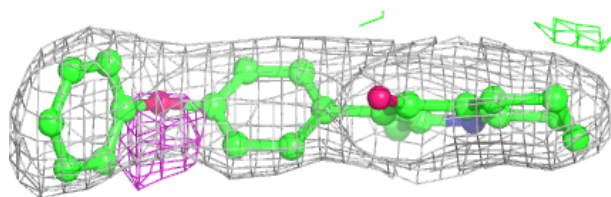
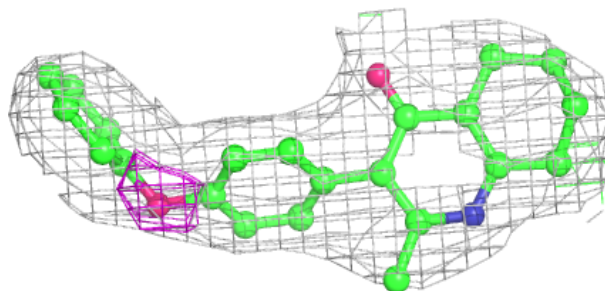
**Electron density around PEE C 504:**

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

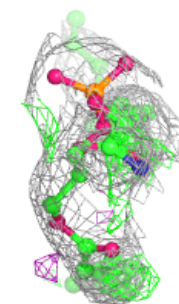
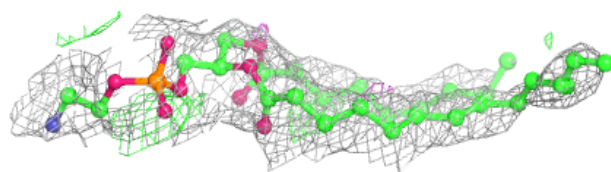
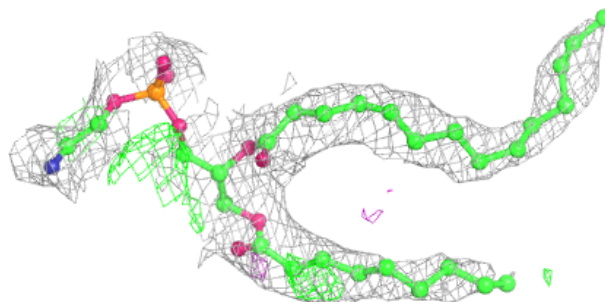


Electron density around MJM C 503:

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

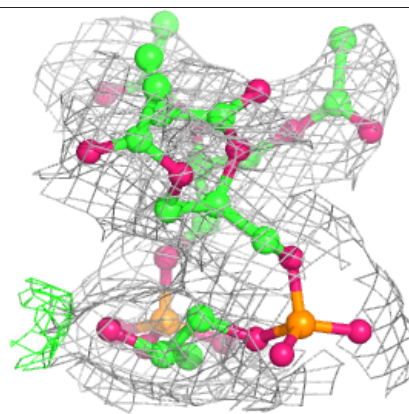
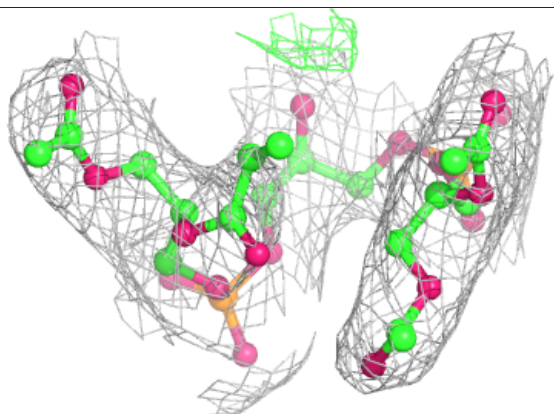
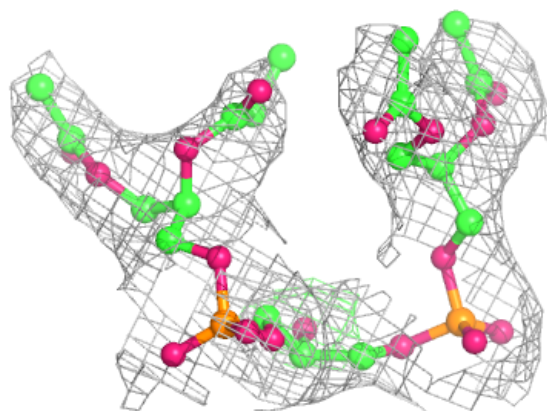
**Electron density around PEE P 405:**

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



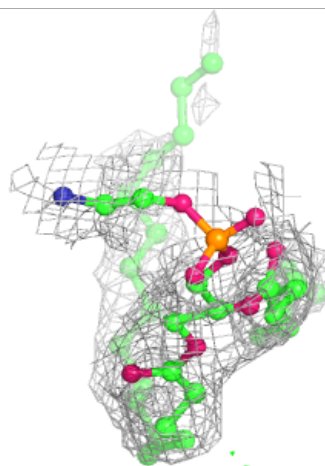
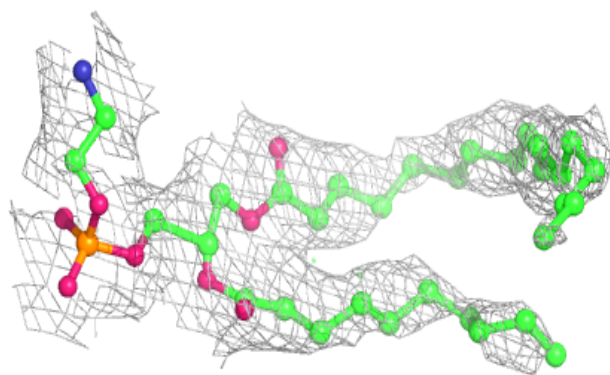
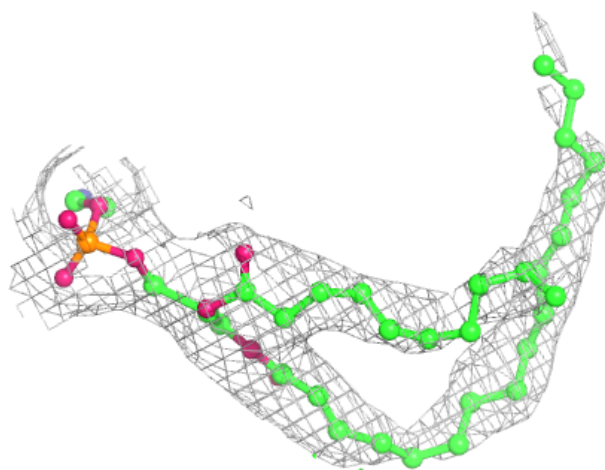
Electron density around CDL C 506:

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



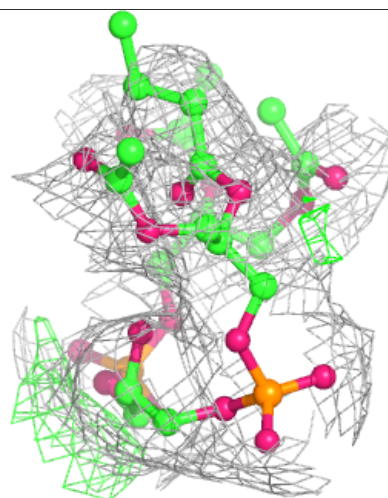
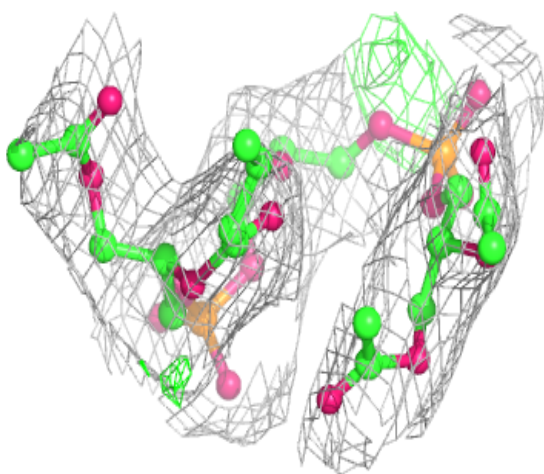
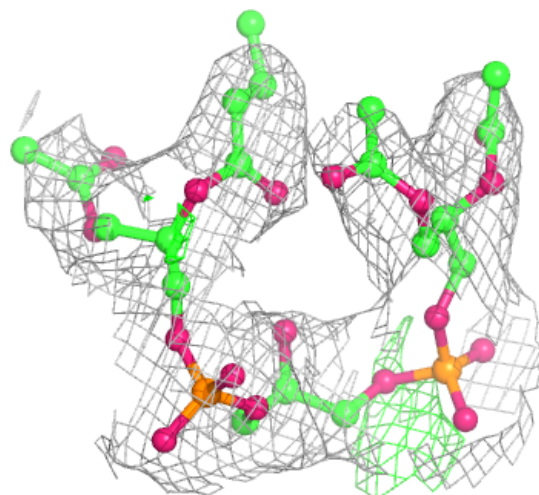
Electron density around PEE D 502:

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



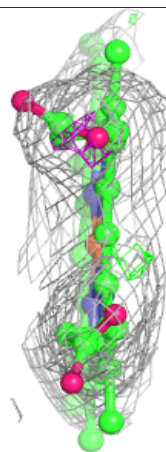
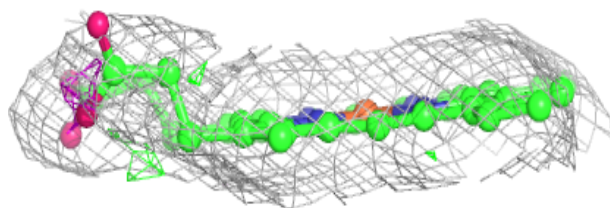
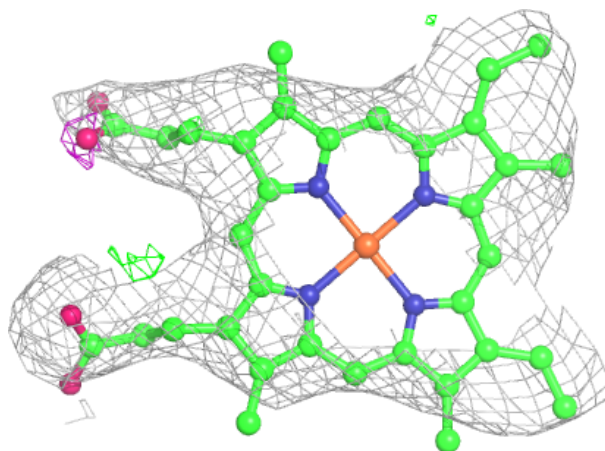
Electron density around CDL P 407:

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



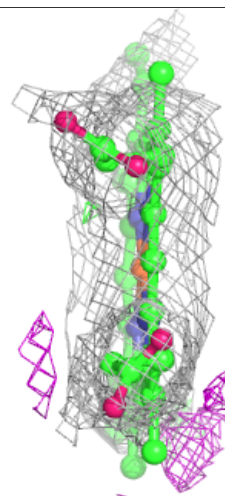
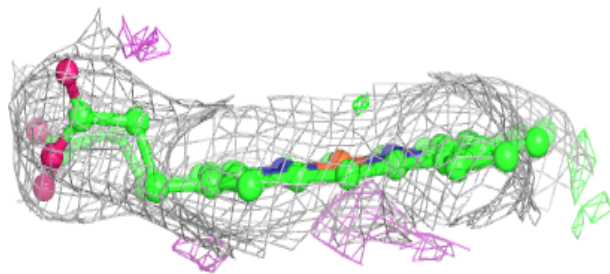
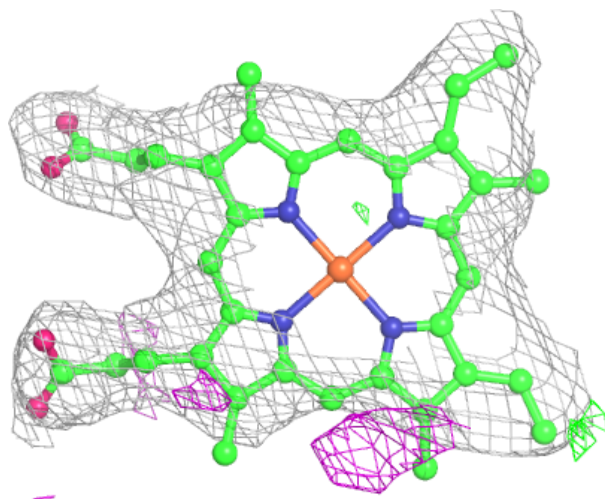
Electron density around HEC D 501:

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



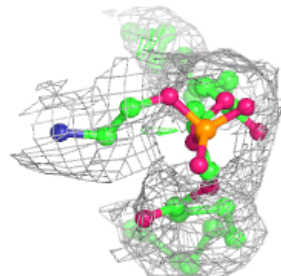
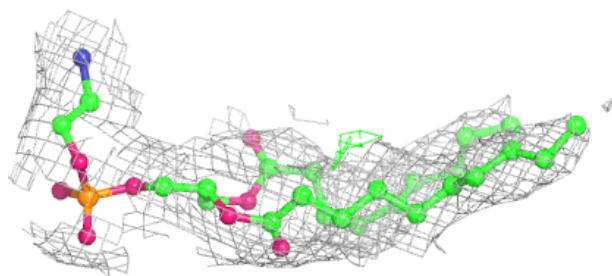
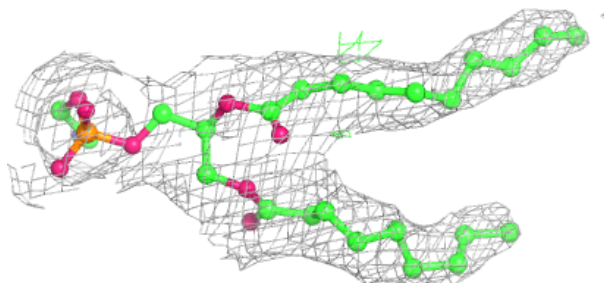
Electron density around HEC Q 501:

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



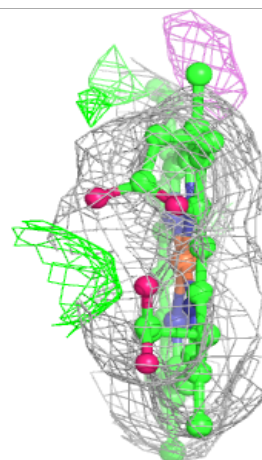
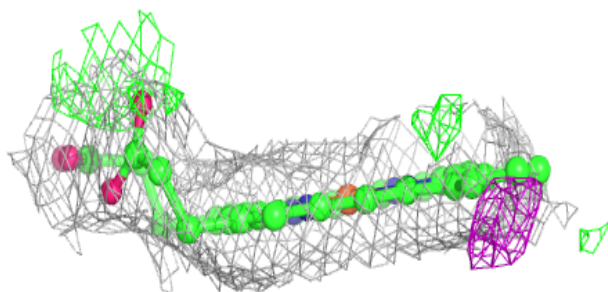
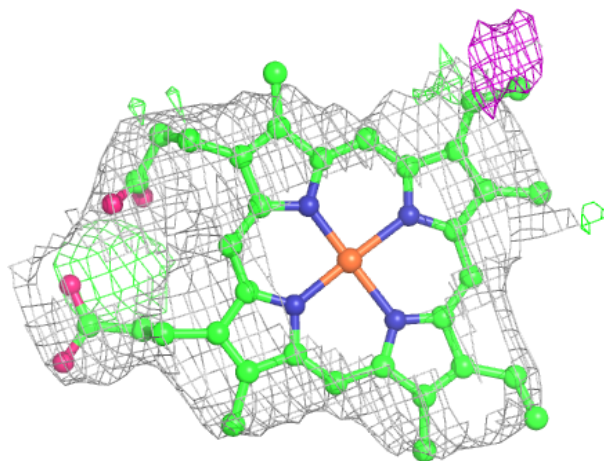
Electron density around PEE R 201:

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



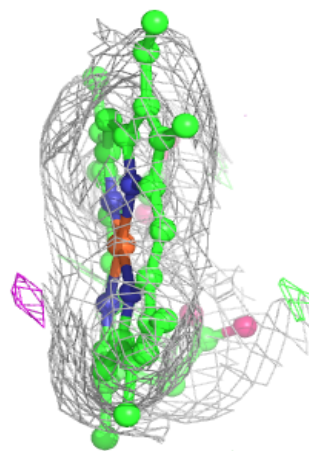
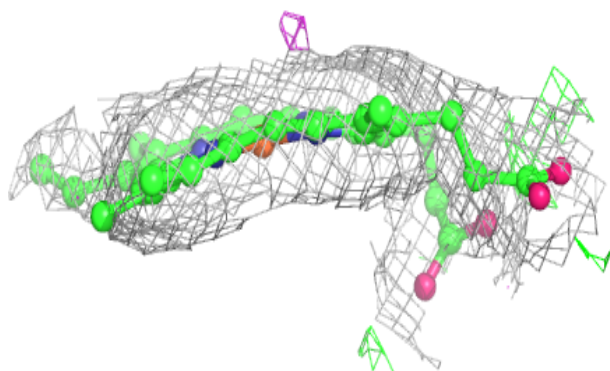
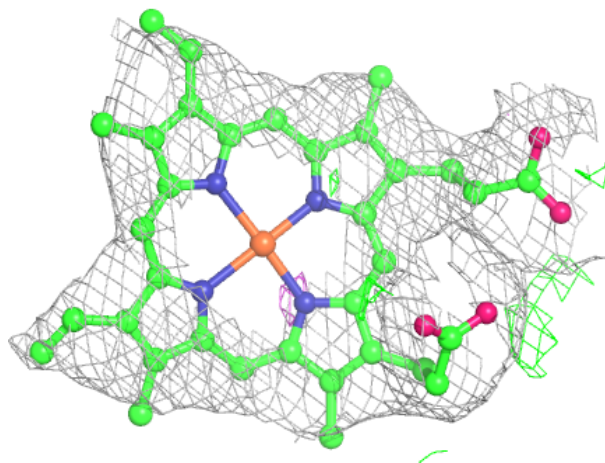
Electron density around HEM C 501:

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



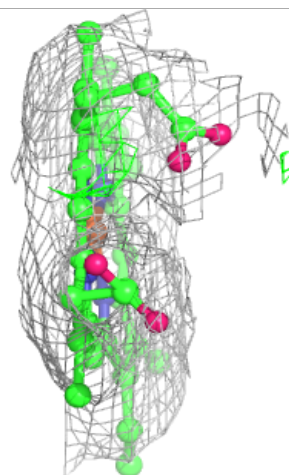
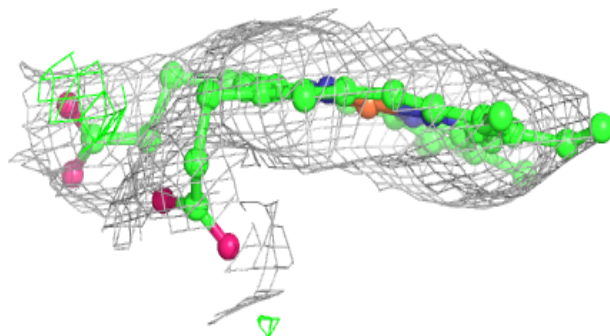
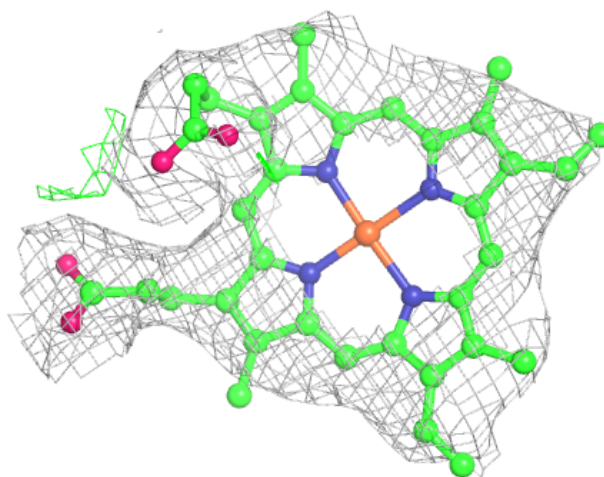
Electron density around HEM P 403:

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



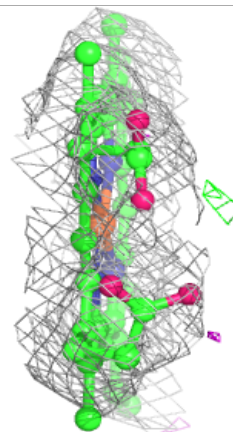
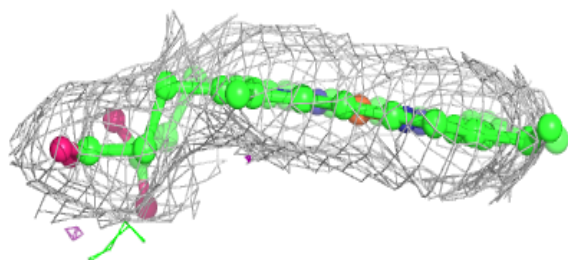
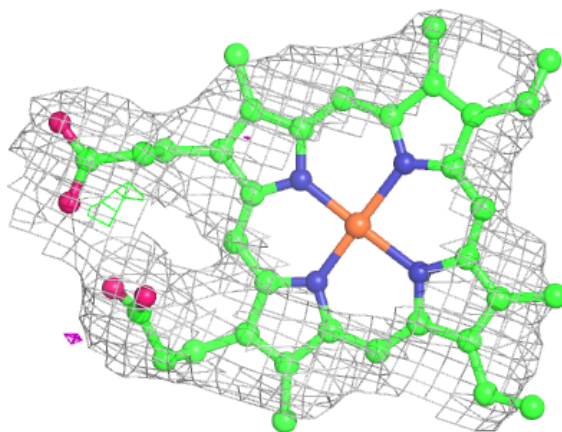
Electron density around HEM C 502:

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



Electron density around HEM P 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.