



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 18, 2026 – 11:45 AM UTC

PDB ID : 1VF5 / pdb_00001vf5
Title : Crystal Structure of Cytochrome b6f Complex from M.laminosus
Authors : Kurisu, G.; Zhang, H.; Smith, J.L.; Cramer, W.A.
Deposited on : 2004-04-08
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

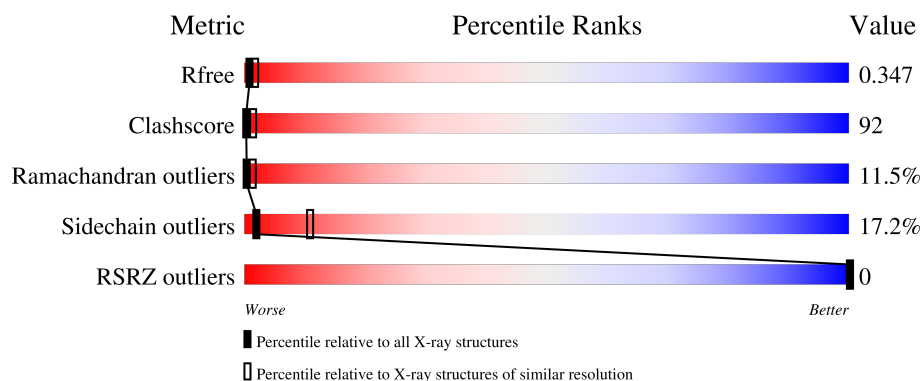
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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.



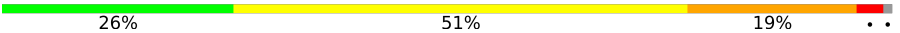
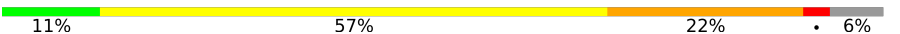
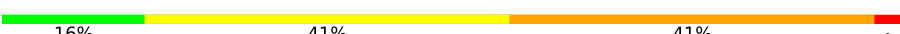
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	215	
1	N	215	
2	B	160	
2	O	160	
3	C	289	

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Mol	Chain	Length	Quality of chain
3	P	289	
4	D	179	
4	Q	179	
5	E	32	
5	R	32	
6	F	35	
6	S	35	
7	G	37	
7	T	37	
8	H	29	
8	U	29	

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	PL9	Q	1305	-	-	X	-
13	OPC	D	306	-	-	X	-
13	OPC	Q	1307	-	-	X	-
14	CLA	B	201	X	-	-	-
14	CLA	O	1201	X	-	-	-

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 15091 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 B6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	202	Total	C	N	O	S	0	0	0
			1593	1062	253	268	10			
1	N	202	Total	C	N	O	S	0	0	0
			1593	1062	253	268	10			

- Molecule 2 is a protein called SUBUNIT IV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	138	Total	C	N	O	S	0	0	0
			1075	727	165	178	5			
2	O	138	Total	C	N	O	S	0	0	0
			1075	727	165	178	5			

- Molecule 3 is a protein called CYTOCHROME F.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	286	Total	C	N	O	S	0	0	0
			2200	1406	366	421	7			
3	P	286	Total	C	N	O	S	0	0	0
			2200	1406	366	421	7			

- Molecule 4 is a protein called RIESKE IRON-SULFUR PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	168	Total	C	N	O	S	0	0	0
			1280	815	223	235	7			
4	Q	168	Total	C	N	O	S	0	0	0
			1280	815	223	235	7			

- Molecule 5 is a protein called PROTEIN PET L.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	32	Total	C	N	O	S	0	0	0
			248	179	34	34	1			
5	R	32	Total	C	N	O	S	0	0	0
			248	179	34	34	1			

- Molecule 6 is a protein called PROTEIN PET M.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	33	Total	C	N	O	S	0	0	0
			251	170	36	43	2			
6	S	35	Total	C	N	O	S	0	0	0
			270	181	39	48	2			

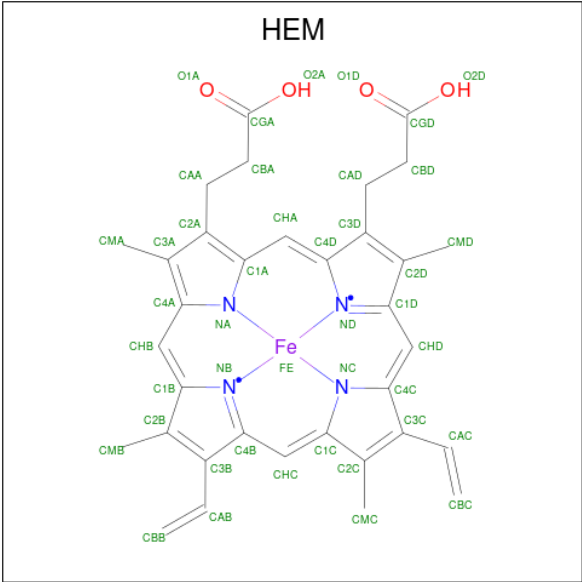
- Molecule 7 is a protein called PROTEIN PET G.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
7	G	23	Total	C	N	O	0	0	0
			184	126	29	29			
7	T	27	Total	C	N	O	0	0	0
			216	146	34	36			

- Molecule 8 is a protein called PROTEIN PET N.

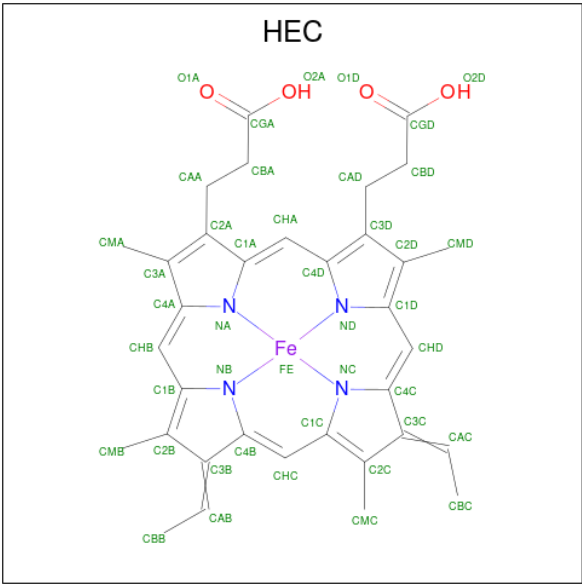
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	27	Total	C	N	O	S	0	0	0
			214	146	34	33	1			
8	U	27	Total	C	N	O	S	0	0	0
			214	146	34	33	1			

- Molecule 9 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



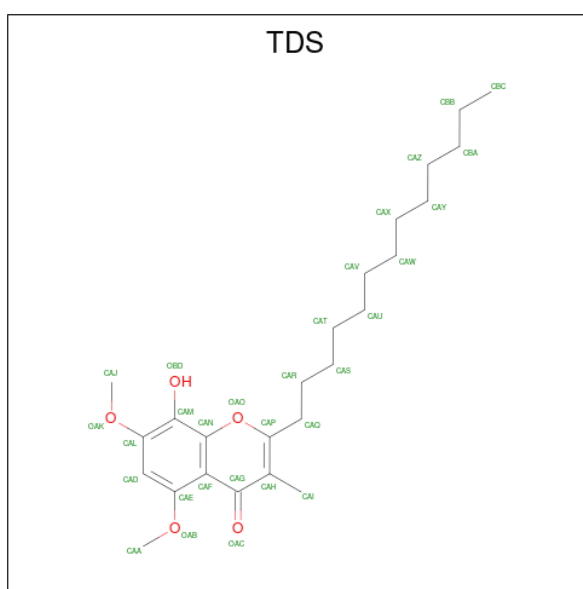
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
9	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
9	N	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
9	N	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 10 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



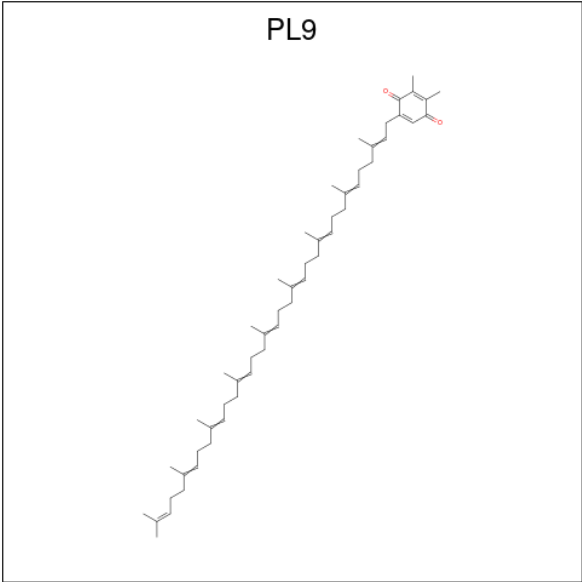
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	A	1	Total	C	Fe	N	O	
			43	34	1	4	4	
10	C	1	Total	C	Fe	N	O	
			43	34	1	4	4	
10	N	1	Total	C	Fe	N	O	
			43	34	1	4	4	
10	P	1	Total	C	Fe	N	O	
			43	34	1	4	4	

- Molecule 11 is 8-HYDROXY-5,7-DIMETHOXY-3-METHYL-2-TRIDECYL-4H-CHROME N-4-ONE (CCD ID: TDS) (formula: C₂₅H₃₈O₅).



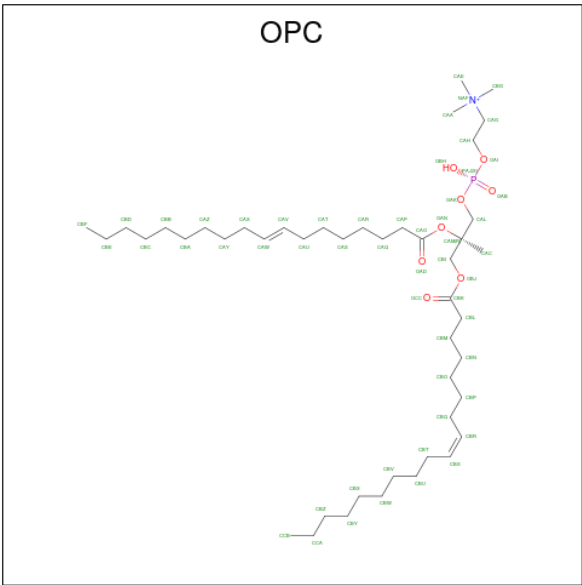
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O		
			30	25	5	0	0
11	N	1	Total	C	O		
			30	25	5	0	0

- Molecule 12 is 2,3-DIMETHYL-5-(3,7,11,15,19,23,27,31,35-NONAMETHYL-2,6,10,14,18,22,26,30,34-HEXATRIACONTANONAENYL-2,5-CYCLOHEXADIENE-1,4-DIONE-2,3-DIMETHYL-5-SOLANESYL-1,4-BENZOQUINONE (CCD ID: PL9) (formula: C₅₃H₈₀O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	A	1	Total	C	O	0	0
			55	53	2		
12	Q	1	Total	C	O	0	0
			55	53	2		

- Molecule 13 is (7R,17E)-4-HYDROXY-N,N,N,7-TETRAMETHYL-7-[(8E)-OCTADEC-8-ENOYLOXY]-10-OXO-3,5,9-TRIOXA-4-PHOSPHAHEPTACOS-17-EN-1-AMINIUM 4-OXIDE (CCD ID: OPC) (formula: C₄₅H₈₇NO₈P).



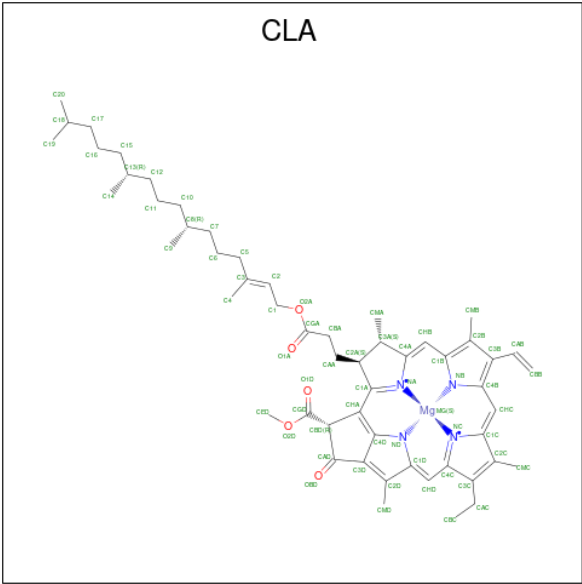
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
13	B	1	Total	C	N	O	P	0	0
			54	44	1	8	1		

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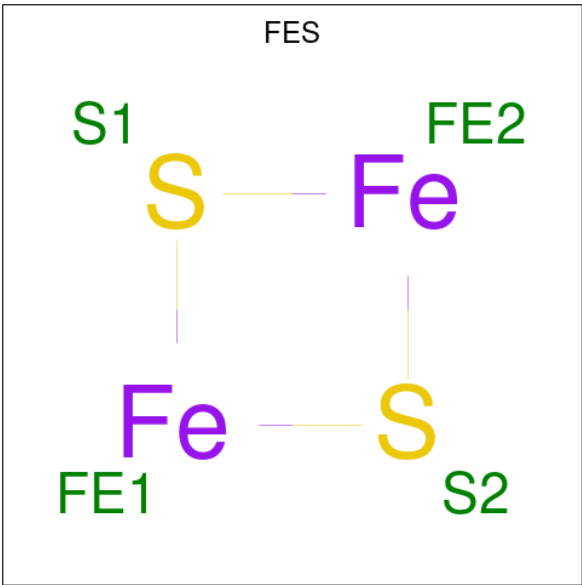
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
13	D	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
13	N	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
13	Q	1	Total	C	N	O	P	0	0
			54	44	1	8	1		

- Molecule 14 is CHLOROPHYLL A (CCD ID: CLA) (formula: $C_{55}H_{72}MgN_4O_5$).



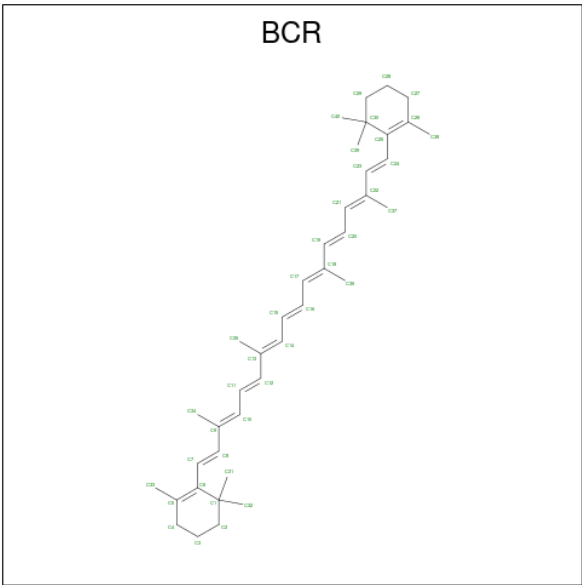
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
14	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
14	O	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		

- Molecule 15 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
15	D	1	Total	Fe	S	0	0
			4	2	2		
15	Q	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 16 is BETA-CAROTENE (CCD ID: BCR) (formula: C₄₀H₅₆).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	E	1	Total	C	0	0
			40	40		
16	R	1	Total	C	0	0
			40	40		

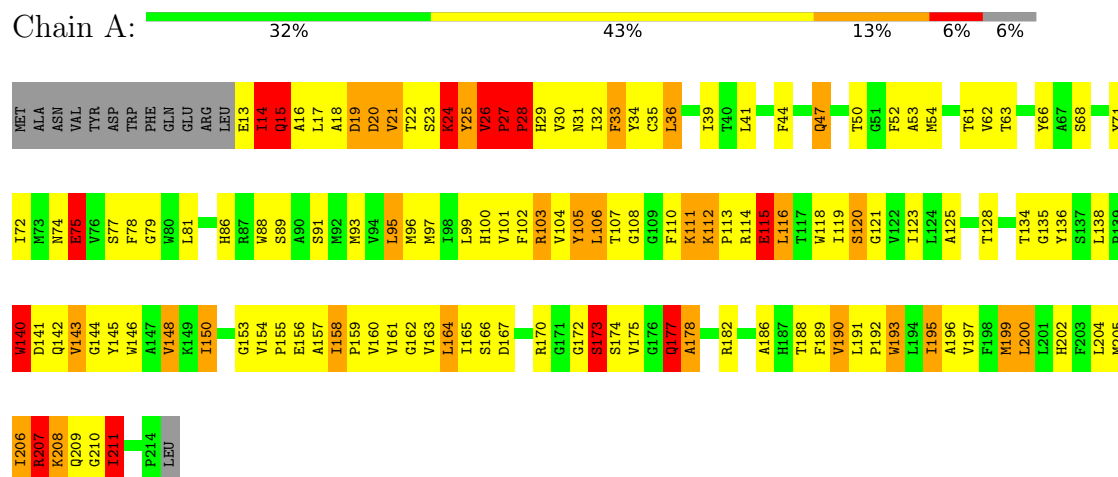
- Molecule 17 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	1	Total	O	0	0
			1	1		
17	N	1	Total	O	0	0
			1	1		

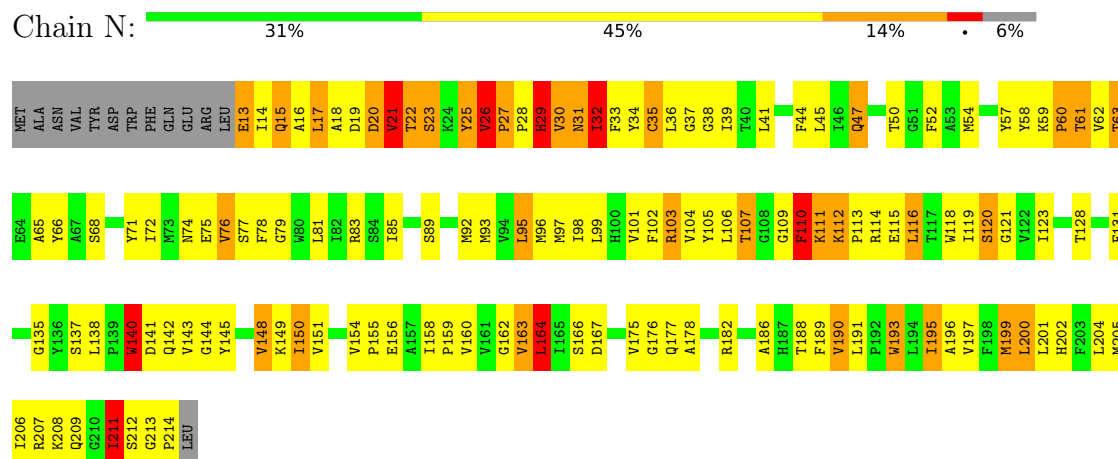
3 Residue-property plots

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.

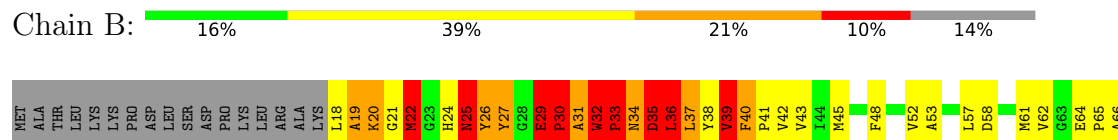
• Molecule 1: CYTOCHROME B6

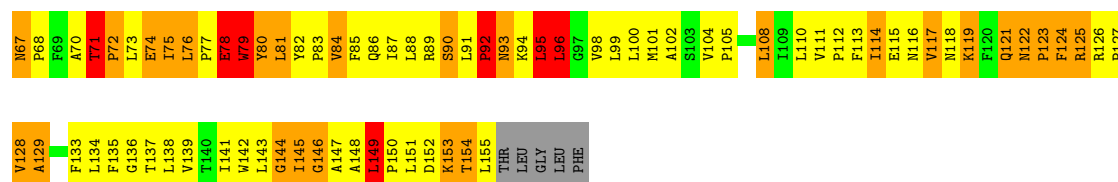


• Molecule 1: CYTOCHROME B6



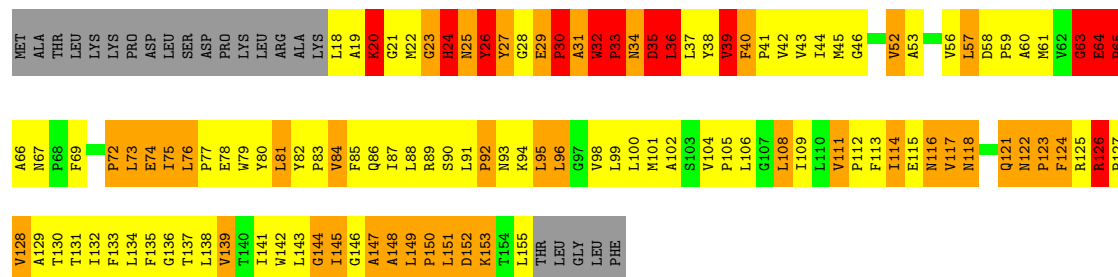
• Molecule 2: SUBUNIT IV





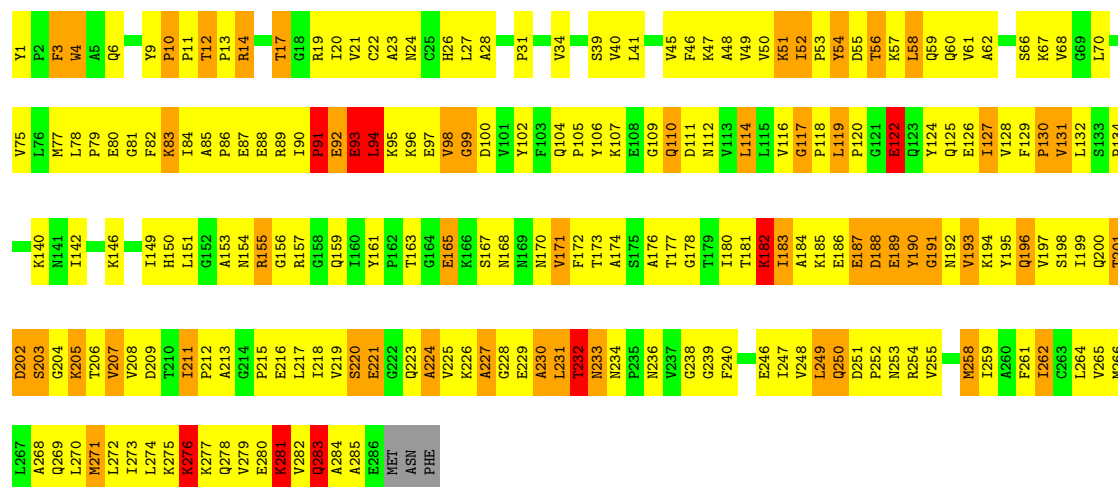
• Molecule 2: SUBUNIT IV

Chain O: 12% 41% 25% 8% 14%



• Molecule 3: CYTOCHROME F

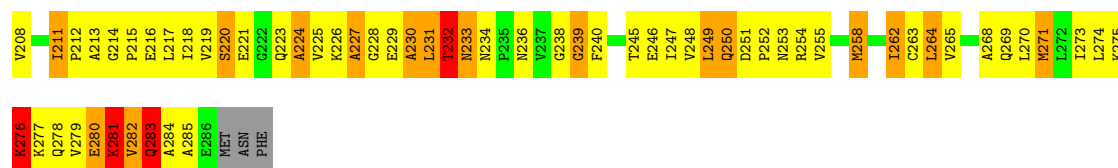
Chain C: 25% 53% 18% ..



• Molecule 3: CYTOCHROME F

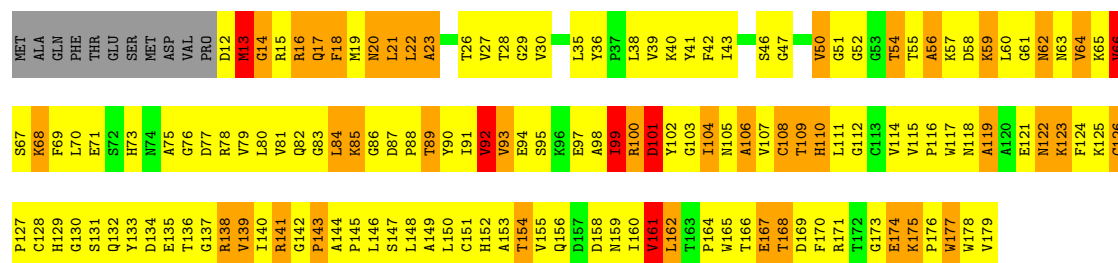
Chain P: 26% 51% 19% ..





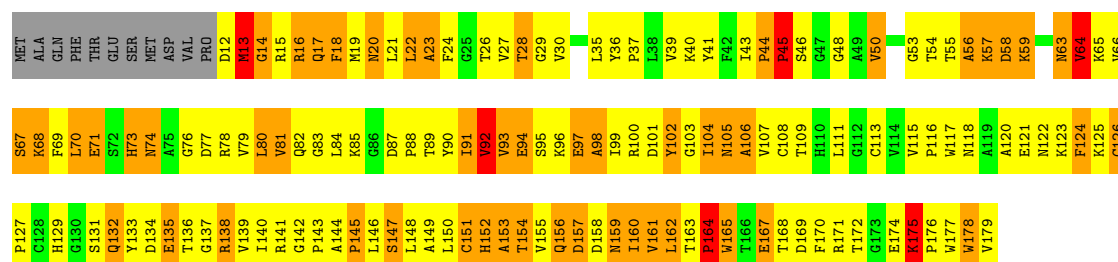
• Molecule 4: RIESKE IRON-SULFUR PROTEIN

Chain D: 11% 57% 22% 6%



• Molecule 4: RIESKE IRON-SULFUR PROTEIN

Chain Q: 14% 47% 29% 6%



• Molecule 5: PROTEIN PET L

Chain E: 12% 44% 41%



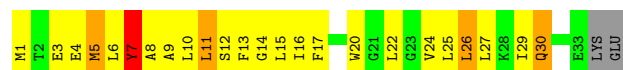
• Molecule 5: PROTEIN PET L

Chain R: 16% 41% 41%

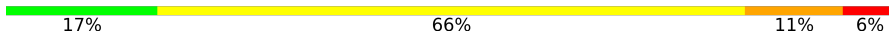


• Molecule 6: PROTEIN PET M

Chain F: 26% 54% 11% 6%

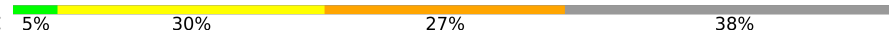


- Molecule 6: PROTEIN PET M

Chain S:  17% 66% 11% 6%



- Molecule 7: PROTEIN PET G

Chain G:  5% 30% 27% 38%

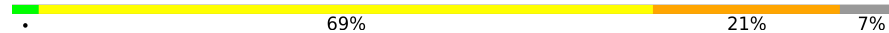


- Molecule 7: PROTEIN PET G

Chain T:  8% 30% 32% 27%



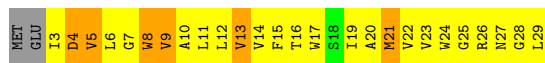
- Molecule 8: PROTEIN PET N

Chain H:  69% 21% 7%



- Molecule 8: PROTEIN PET N

Chain U:  69% 21% 7%



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	157.54Å 157.54Å 360.35Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.16 – 3.00 48.16 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.16-3.00) 99.8 (48.16-3.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.30 (at 3.01Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.258 , 0.346 0.259 , 0.347	Depositor DCC
R_{free} test set	2788 reflections (2.77%)	wwPDB-VP
Wilson B-factor (Å ²)	76.0	Xtriage
Anisotropy	0.238	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 141.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.499 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	15091	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.26% 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: HEC, HEM, CLA, PL9, TDS, BCR, OPC, FES

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.73	0/1641	1.28	20/2239 (0.9%)
1	N	0.75	0/1641	1.23	24/2239 (1.1%)
2	B	0.67	0/1110	1.49	28/1526 (1.8%)
2	O	0.77	1/1110 (0.1%)	1.52	30/1526 (2.0%)
3	C	0.54	0/2248	1.13	22/3061 (0.7%)
3	P	0.55	0/2248	1.10	22/3061 (0.7%)
4	D	0.63	0/1312	1.30	25/1786 (1.4%)
4	Q	0.65	0/1312	1.23	21/1786 (1.2%)
5	E	0.78	0/253	1.20	3/340 (0.9%)
5	R	0.79	0/253	1.22	4/340 (1.2%)
6	F	0.64	0/255	1.02	3/343 (0.9%)
6	S	0.59	0/274	0.98	2/366 (0.5%)
7	G	0.71	0/188	1.42	3/253 (1.2%)
7	T	0.71	0/221	1.45	6/299 (2.0%)
8	H	0.76	0/220	1.59	6/301 (2.0%)
8	U	0.71	0/220	1.51	5/301 (1.7%)
All	All	0.66	1/14506 (0.0%)	1.26	224/19767 (1.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	N	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	O	145	ILE	CA-CB	5.46	1.59	1.55

The worst 5 of 224 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	36	LEU	N-CA-C	-17.90	91.85	114.04
2	O	36	LEU	N-CA-C	-17.40	92.47	114.04
1	A	26	VAL	CA-C-N	15.65	136.50	120.38
1	A	26	VAL	C-N-CA	15.65	136.50	120.38
8	H	5	VAL	N-CA-C	-13.87	97.49	110.53

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	N	105	TYR	Sidechain

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	1593	0	1623	256	0
1	N	1593	0	1623	238	0
2	B	1075	0	1117	264	0
2	O	1075	0	1117	301	0
3	C	2200	0	2216	369	0
3	P	2200	0	2216	345	0
4	D	1280	0	1263	332	0
4	Q	1280	0	1263	395	0
5	E	248	0	284	77	0
5	R	248	0	284	114	0
6	F	251	0	266	41	0
6	S	270	0	285	45	0
7	G	184	0	190	108	0
7	T	216	0	220	70	0
8	H	214	0	221	45	0
8	U	214	0	221	49	0
9	A	86	0	60	15	0
9	N	86	0	60	14	0
10	A	43	0	31	4	0
10	C	43	0	29	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	N	43	0	31	4	0
10	P	43	0	29	1	0
11	A	30	0	37	13	0
11	N	30	0	37	12	0
12	A	55	0	80	19	0
12	Q	55	0	80	22	0
13	B	54	0	83	14	0
13	D	54	0	83	24	0
13	N	54	0	83	10	0
13	Q	54	0	83	30	0
14	B	65	0	70	8	0
14	O	65	0	70	19	0
15	D	4	0	0	1	0
15	Q	4	0	0	1	0
16	E	40	0	56	7	0
16	R	40	0	56	7	0
17	A	1	0	0	0	0
17	N	1	0	0	0	0
All	All	15091	0	15467	2802	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 92.

The worst 5 of 2802 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)
2:O:38:TYR:HB3	3:P:276:LYS:HG2	1.22	1.20
1:A:14:ILE:HA	1:A:17:LEU:HB2	1.26	1.18
1:N:214:PRO:HB3	5:R:29:ILE:HG22	1.19	1.17
4:D:166:THR:HA	4:D:179:VAL:HG13	1.22	1.17
2:B:71:THR:HB	2:B:72:PRO:HD3	1.28	1.15

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	200/215 (93%)	152 (76%)	29 (14%)	19 (10%)	0	2
1	N	200/215 (93%)	155 (78%)	32 (16%)	13 (6%)	1	5
2	B	136/160 (85%)	80 (59%)	31 (23%)	25 (18%)	0	0
2	O	136/160 (85%)	67 (49%)	38 (28%)	31 (23%)	0	0
3	C	284/289 (98%)	206 (72%)	47 (16%)	31 (11%)	0	1
3	P	284/289 (98%)	213 (75%)	44 (16%)	27 (10%)	0	2
4	D	166/179 (93%)	123 (74%)	25 (15%)	18 (11%)	0	1
4	Q	166/179 (93%)	85 (51%)	49 (30%)	32 (19%)	0	0
5	E	30/32 (94%)	22 (73%)	6 (20%)	2 (7%)	1	5
5	R	30/32 (94%)	23 (77%)	5 (17%)	2 (7%)	1	5
6	F	31/35 (89%)	25 (81%)	5 (16%)	1 (3%)	3	18
6	S	33/35 (94%)	25 (76%)	5 (15%)	3 (9%)	0	2
7	G	21/37 (57%)	15 (71%)	5 (24%)	1 (5%)	2	11
7	T	25/37 (68%)	18 (72%)	6 (24%)	1 (4%)	2	14
8	H	25/29 (86%)	18 (72%)	7 (28%)	0	100	100
8	U	25/29 (86%)	19 (76%)	6 (24%)	0	100	100
All	All	1792/1952 (92%)	1246 (70%)	340 (19%)	206 (12%)	0	1

5 of 206 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	25	TYR
1	A	28	PRO
1	A	111	LYS
1	A	160	VAL
1	A	173	SER

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	172/184 (94%)	144 (84%)	28 (16%)	2	12
1	N	172/184 (94%)	150 (87%)	22 (13%)	4	19
2	B	117/136 (86%)	92 (79%)	25 (21%)	1	6
2	O	117/136 (86%)	96 (82%)	21 (18%)	2	10
3	C	240/243 (99%)	205 (85%)	35 (15%)	3	15
3	P	240/243 (99%)	202 (84%)	38 (16%)	2	13
4	D	136/146 (93%)	117 (86%)	19 (14%)	3	16
4	Q	136/146 (93%)	116 (85%)	20 (15%)	3	15
5	E	25/25 (100%)	14 (56%)	11 (44%)	0	0
5	R	25/25 (100%)	13 (52%)	12 (48%)	0	0
6	F	25/27 (93%)	22 (88%)	3 (12%)	5	22
6	S	27/27 (100%)	23 (85%)	4 (15%)	3	15
7	G	17/28 (61%)	9 (53%)	8 (47%)	0	0
7	T	21/28 (75%)	12 (57%)	9 (43%)	0	0
8	H	22/24 (92%)	19 (86%)	3 (14%)	3	17
8	U	22/24 (92%)	19 (86%)	3 (14%)	3	17
All	All	1514/1626 (93%)	1253 (83%)	261 (17%)	2	11

5 of 261 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	Q	175	LYS
5	R	15	PHE
8	U	21	MET
4	D	101	ASP
4	D	93	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
2	O	116	ASN
3	P	223	GLN
8	U	27	ASN
2	O	121	GLN
3	P	60	GLN

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 ⓘ

22 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
10	HEC	P	301	3	46,50,50	1.78	8 (17%)	58,82,82	1.33	8 (13%)
9	HEM	A	302	1	50,50,50	1.76	14 (28%)	67,82,82	1.99	10 (14%)
9	HEM	N	302	1	50,50,50	1.79	8 (16%)	67,82,82	2.01	12 (17%)
11	TDS	N	1304	-	31,31,31	2.82	9 (29%)	37,40,40	2.05	9 (24%)
15	FES	Q	1200	4	0,4,4	-	-	-	-	-
9	HEM	A	301	1	50,50,50	1.77	11 (22%)	67,82,82	1.39	10 (14%)
12	PL9	A	305	-	55,55,55	3.41	21 (38%)	68,69,69	2.30	18 (26%)
11	TDS	A	304	-	31,31,31	2.83	9 (29%)	37,40,40	1.96	9 (24%)
16	BCR	E	101	-	41,41,41	2.16	8 (19%)	56,56,56	2.51	23 (41%)
13	OPC	Q	1307	-	53,53,54	1.43	9 (16%)	59,61,64	1.19	3 (5%)
13	OPC	B	307	-	53,53,54	1.43	9 (16%)	59,61,64	1.07	4 (6%)
16	BCR	R	1101	-	41,41,41	2.08	9 (21%)	56,56,56	2.52	22 (39%)
13	OPC	N	1306	-	53,53,54	1.42	9 (16%)	59,61,64	1.37	6 (10%)
10	HEC	C	301	3	46,50,50	1.73	6 (13%)	58,82,82	1.31	5 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	PL9	Q	1305	-	55,55,55	3.40	21 (38%)	68,69,69	2.39	16 (23%)
14	CLA	B	201	-	69,73,73	1.61	9 (13%)	82,113,113	2.22	17 (20%)
13	OPC	D	306	-	53,53,54	1.43	9 (16%)	59,61,64	1.17	5 (8%)
10	HEC	A	303	17,1	46,50,50	1.81	6 (13%)	58,82,82	2.09	14 (24%)
15	FES	D	200	4	0,4,4	-	-	-	-	-
9	HEM	N	301	1	50,50,50	1.81	11 (22%)	67,82,82	1.37	8 (11%)
10	HEC	N	303	17,1	46,50,50	1.80	7 (15%)	58,82,82	1.85	11 (18%)
14	CLA	O	1201	-	69,73,73	1.55	11 (15%)	82,113,113	2.31	15 (18%)

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
10	HEC	P	301	3	-	5/14/54/54	-
9	HEM	A	302	1	-	4/14/54/54	-
9	HEM	N	302	1	-	4/14/54/54	-
11	TDS	N	1304	-	-	7/17/17/17	0/2/2/2
15	FES	Q	1200	4	-	-	0/1/1/1
9	HEM	A	301	1	-	6/14/54/54	-
12	PL9	A	305	-	-	28/53/73/73	0/1/1/1
11	TDS	A	304	-	-	6/17/17/17	0/2/2/2
16	BCR	E	101	-	-	5/29/63/63	0/2/2/2
13	OPC	Q	1307	-	-	11/57/57/60	-
13	OPC	B	307	-	-	14/57/57/60	-
16	BCR	R	1101	-	-	5/29/63/63	0/2/2/2
13	OPC	N	1306	-	-	11/57/57/60	-
10	HEC	C	301	3	-	5/14/54/54	-
12	PL9	Q	1305	-	-	30/53/73/73	0/1/1/1
14	CLA	B	201	-	3/3/15/20	18/39/115/115	-
13	OPC	D	306	-	-	10/57/57/60	-
10	HEC	A	303	17,1	-	6/14/54/54	-
15	FES	D	200	4	-	-	0/1/1/1
9	HEM	N	301	1	-	9/14/54/54	-
10	HEC	N	303	17,1	-	5/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
14	CLA	O	1201	-	4/4/15/20	10/39/115/115	-

The worst 5 of 204 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	N	1304	TDS	CAL-CAM	9.34	1.53	1.40
11	A	304	TDS	CAL-CAM	9.33	1.53	1.40
12	A	305	PL9	C13-C14	8.98	1.53	1.33
12	A	305	PL9	C33-C34	8.92	1.53	1.33
12	A	305	PL9	C18-C19	8.91	1.53	1.33

The worst 5 of 225 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	O	1201	CLA	C4A-NA-C1A	10.47	111.46	106.68
9	N	302	HEM	CBA-CAA-C2A	-9.63	85.90	112.53
9	A	302	HEM	CBA-CAA-C2A	-9.44	86.43	112.53
14	B	201	CLA	C4A-NA-C1A	8.89	110.73	106.68
14	O	1201	CLA	C4D-C3D-CAD	8.28	117.10	108.11

5 of 7 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
14	B	201	CLA	C8
14	B	201	CLA	C3A
14	B	201	CLA	ND
14	O	1201	CLA	C2A
14	O	1201	CLA	C8

5 of 199 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	A	301	HEM	C2B-C3B-CAB-CBB
9	A	301	HEM	C4B-C3B-CAB-CBB
9	A	302	HEM	C2C-C3C-CAC-CBC
9	A	302	HEM	C4C-C3C-CAC-CBC
9	N	301	HEM	C2B-C3B-CAB-CBB

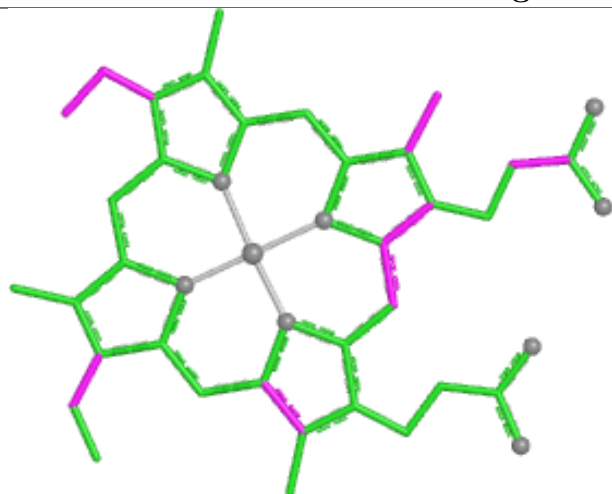
There are no ring outliers.

21 monomers are involved in 202 short contacts:

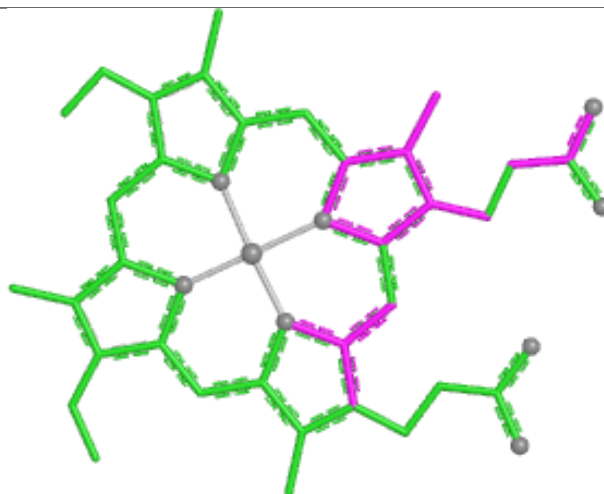
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	P	301	HEC	1	0
9	A	302	HEM	5	0
9	N	302	HEM	5	0
11	N	1304	TDS	12	0
15	Q	1200	FES	1	0
9	A	301	HEM	10	0
12	A	305	PL9	19	0
11	A	304	TDS	13	0
16	E	101	BCR	7	0
13	Q	1307	OPC	30	0
13	B	307	OPC	14	0
16	R	1101	BCR	7	0
13	N	1306	OPC	10	0
12	Q	1305	PL9	22	0
14	B	201	CLA	8	0
13	D	306	OPC	24	0
10	A	303	HEC	4	0
15	D	200	FES	1	0
9	N	301	HEM	9	0
10	N	303	HEC	4	0
14	O	1201	CLA	19	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.

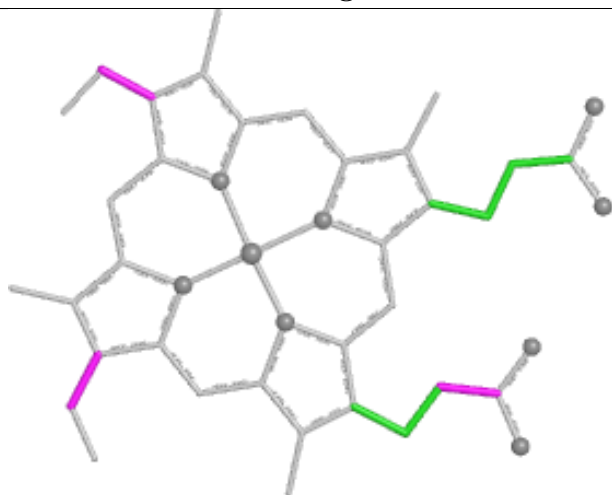
Ligand HEC P 301



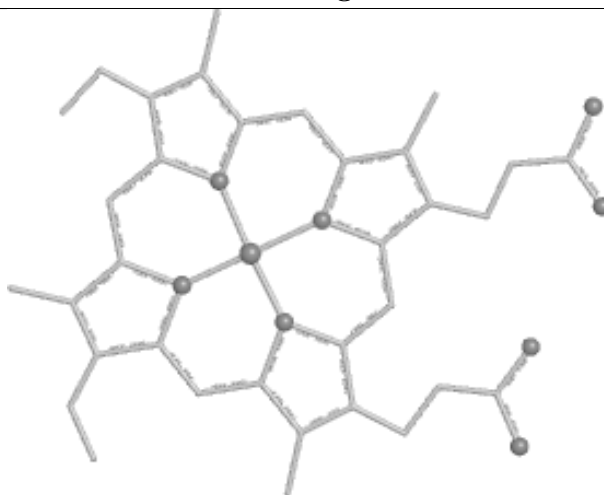
Bond lengths



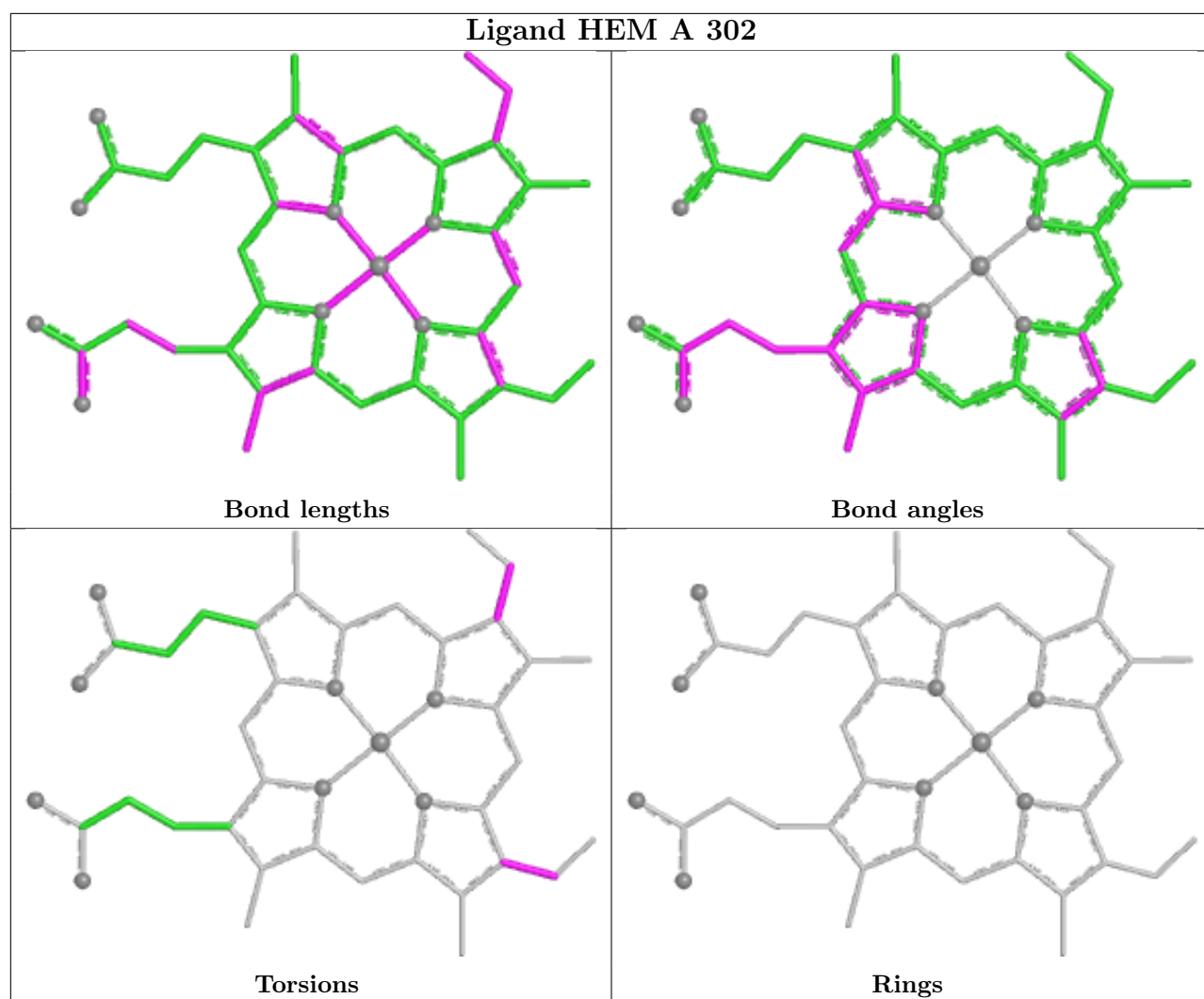
Bond angles

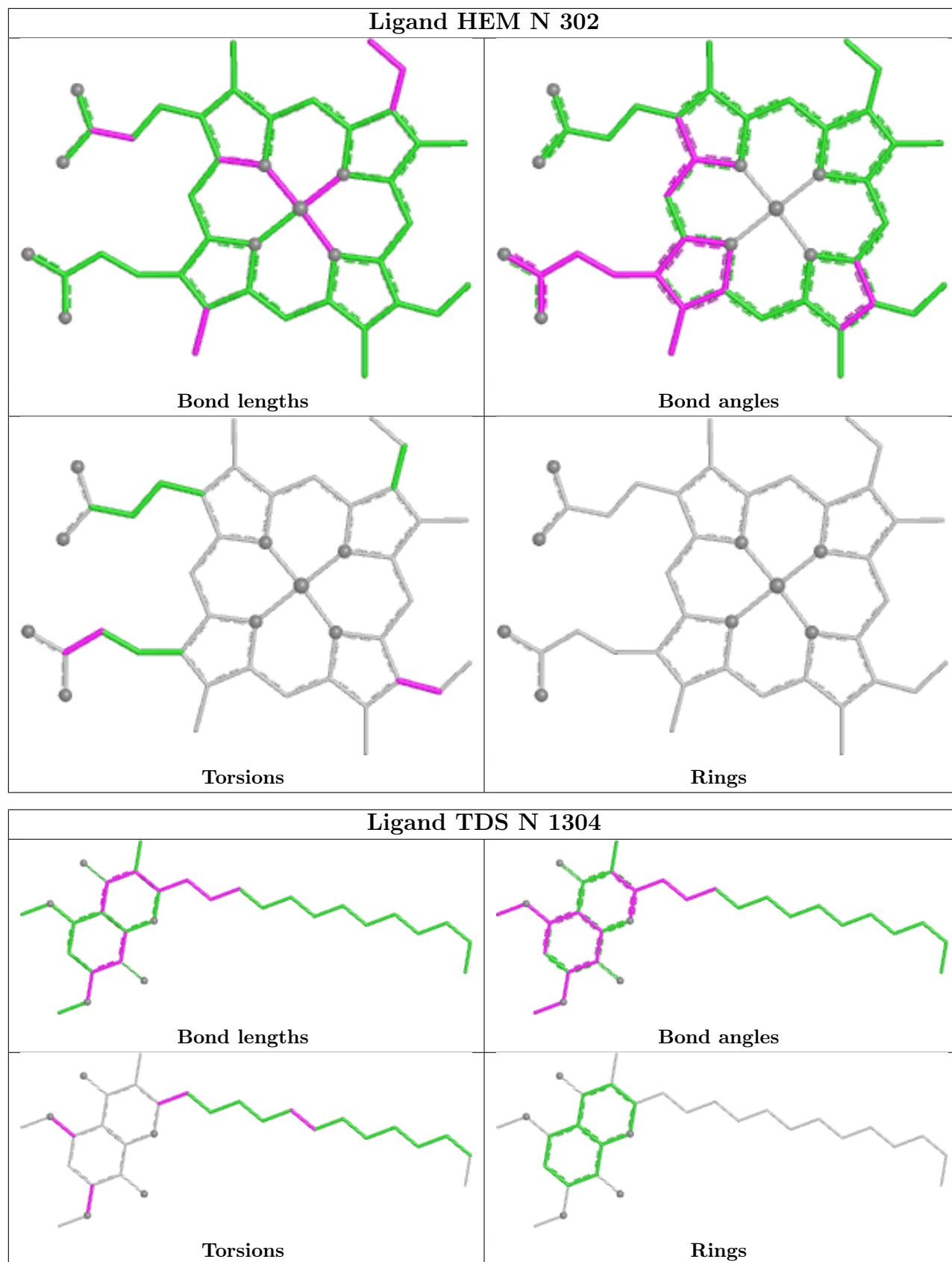


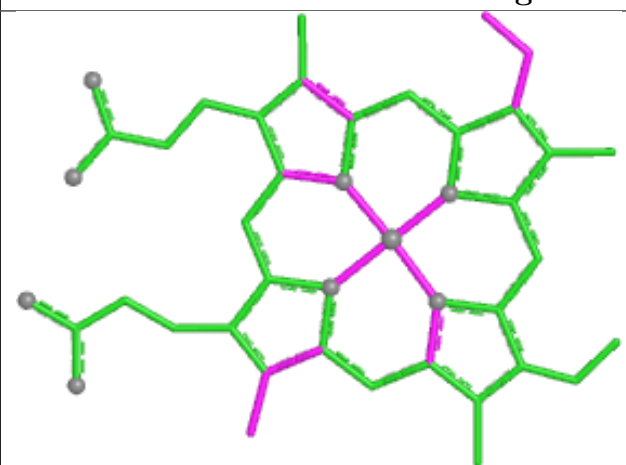
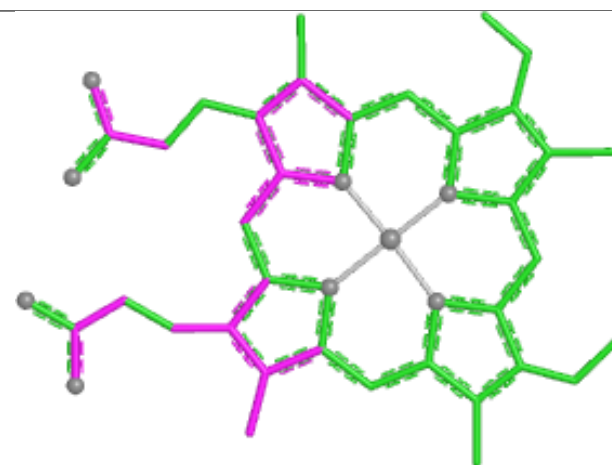
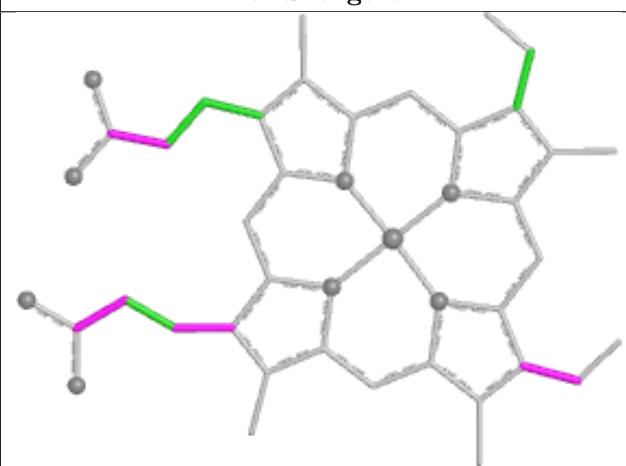
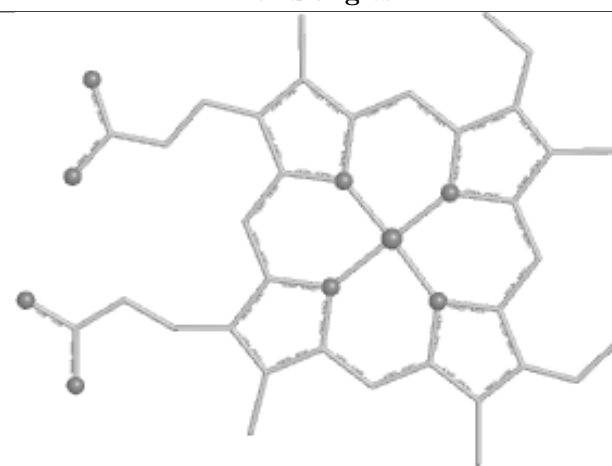
Torsions

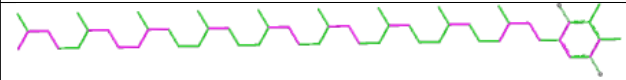
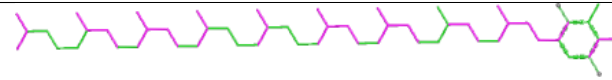
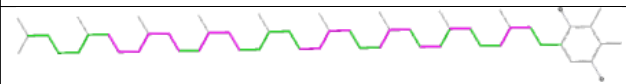
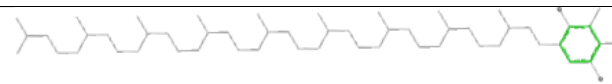


Rings

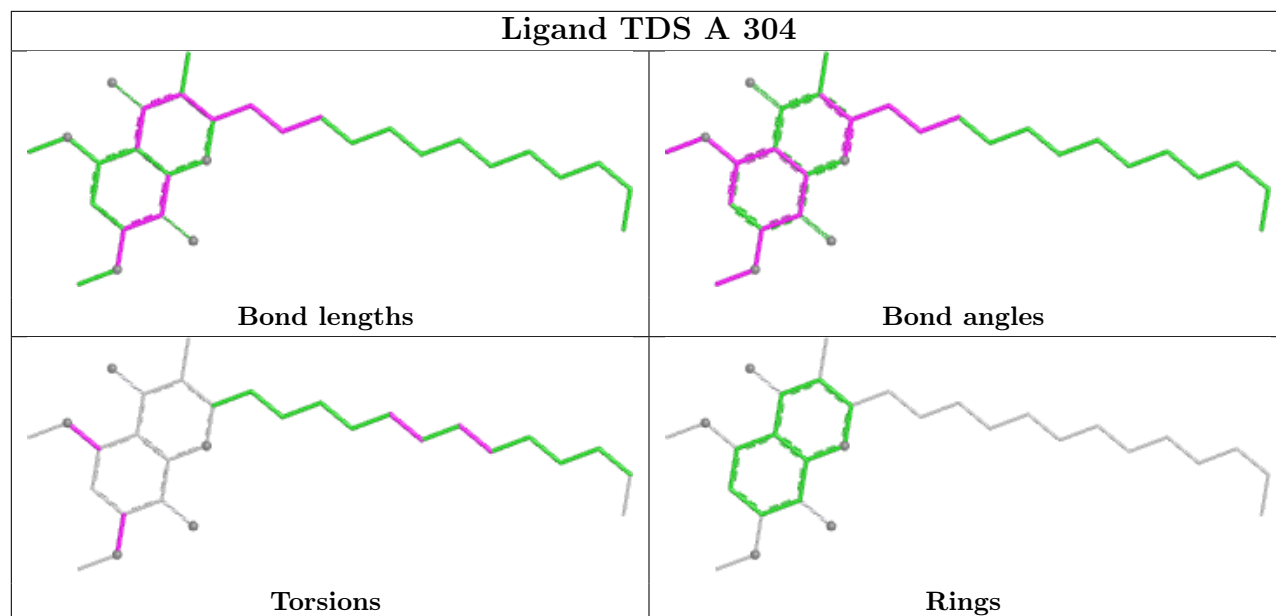




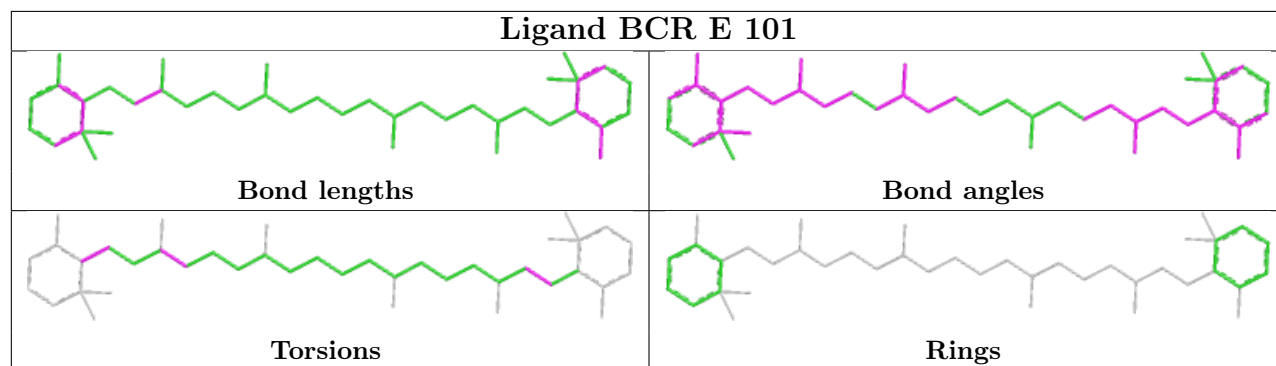
Ligand HEM A 301	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand PL9 A 305	
	
Bond lengths	Bond angles
	
Torsions	Rings

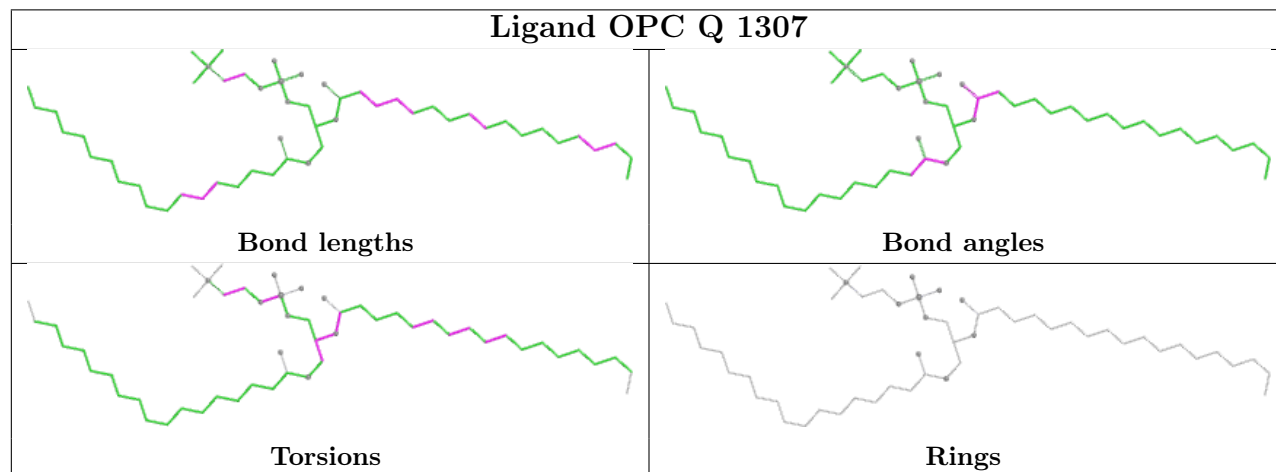
Ligand TDS A 304

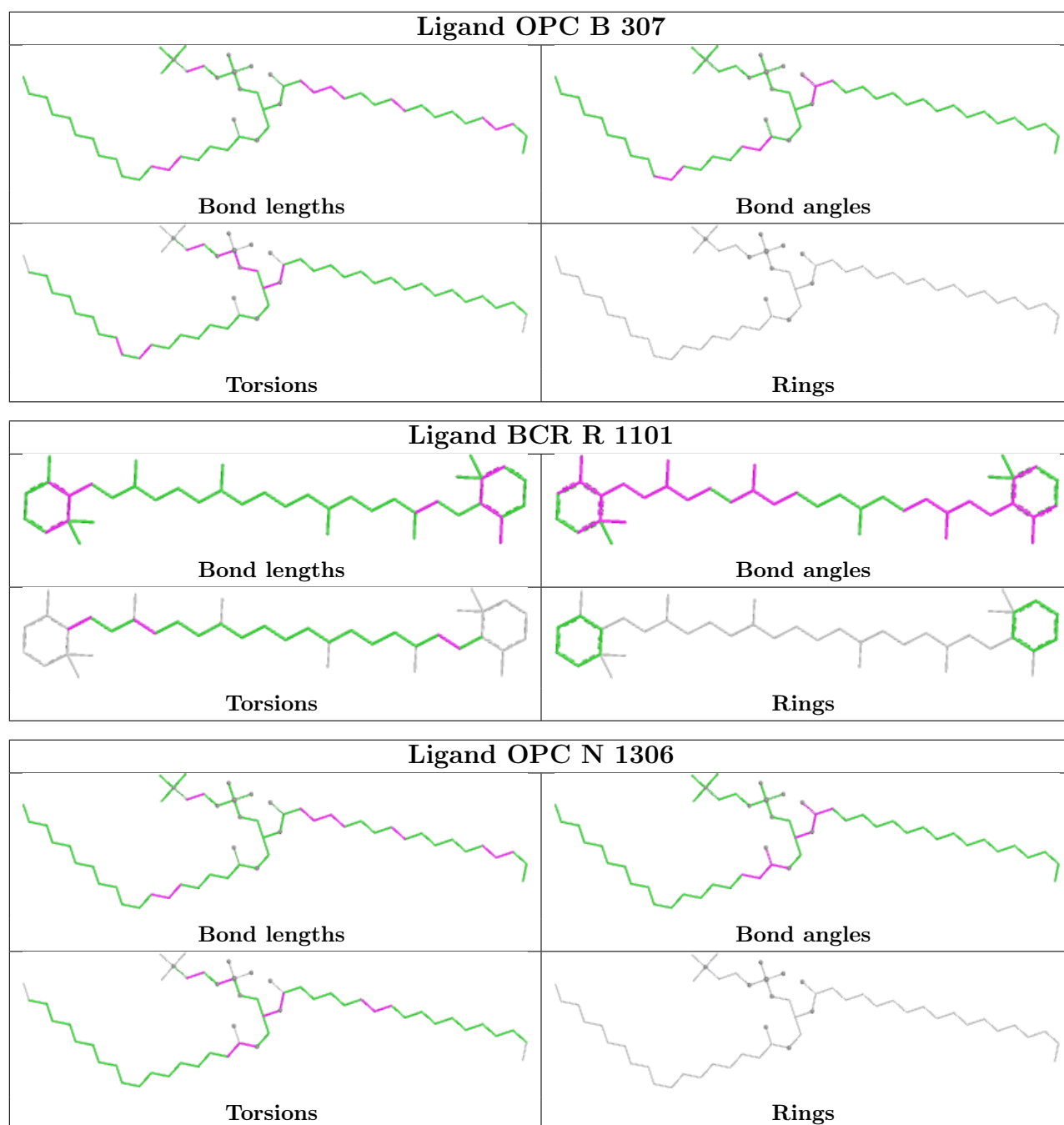


Ligand BCR E 101

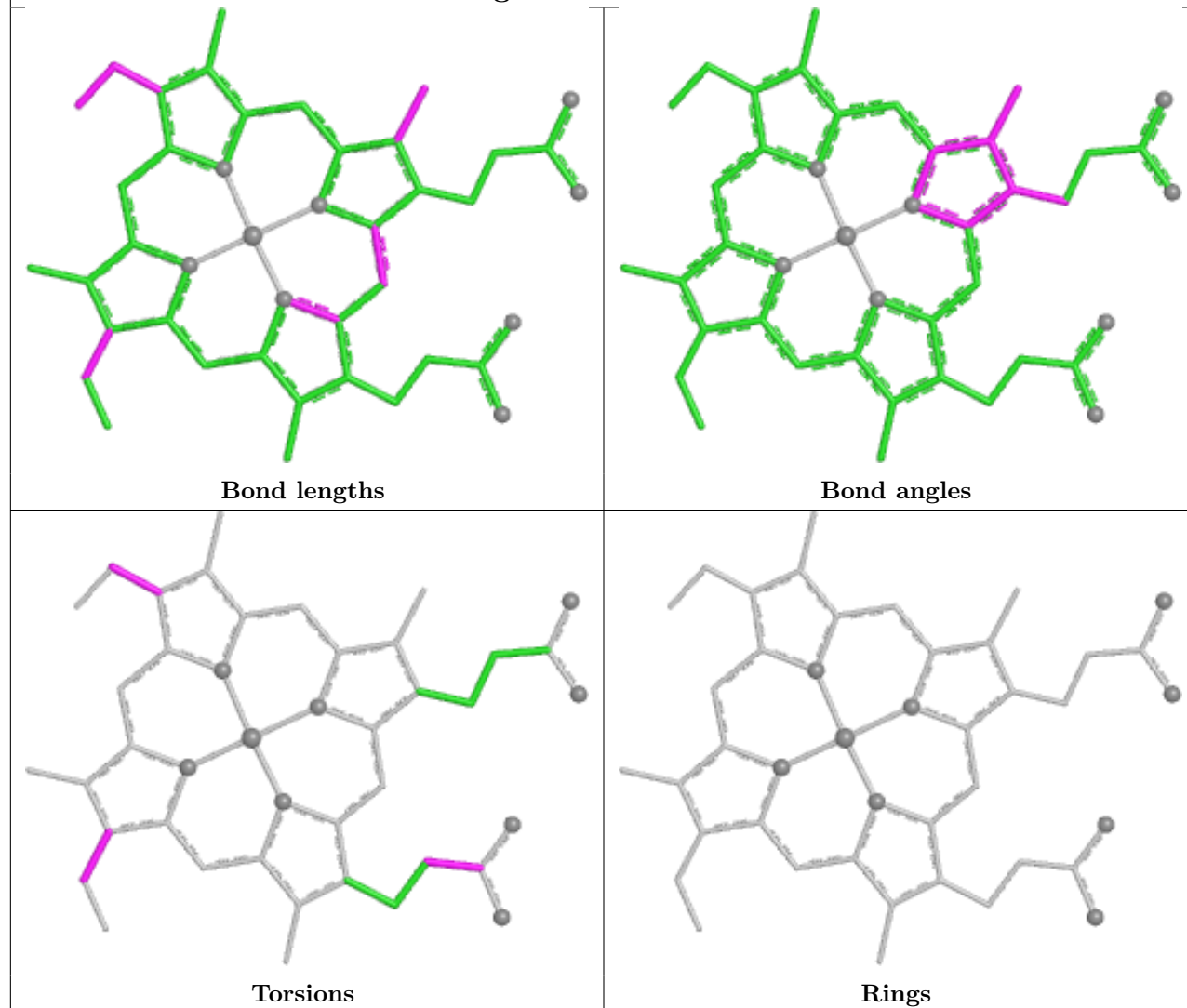


Ligand OPC Q 1307



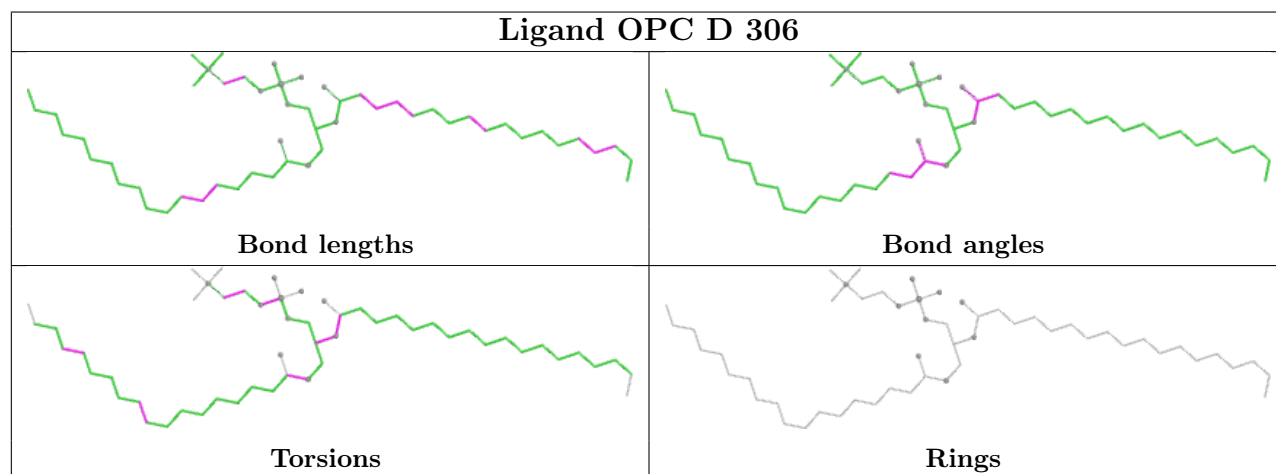
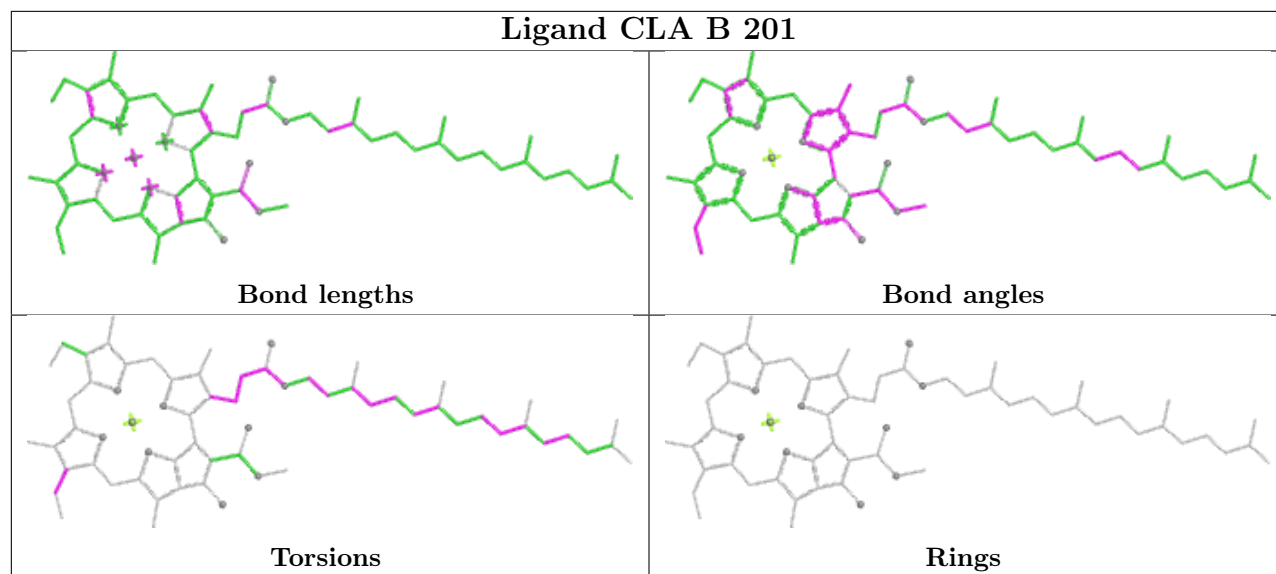


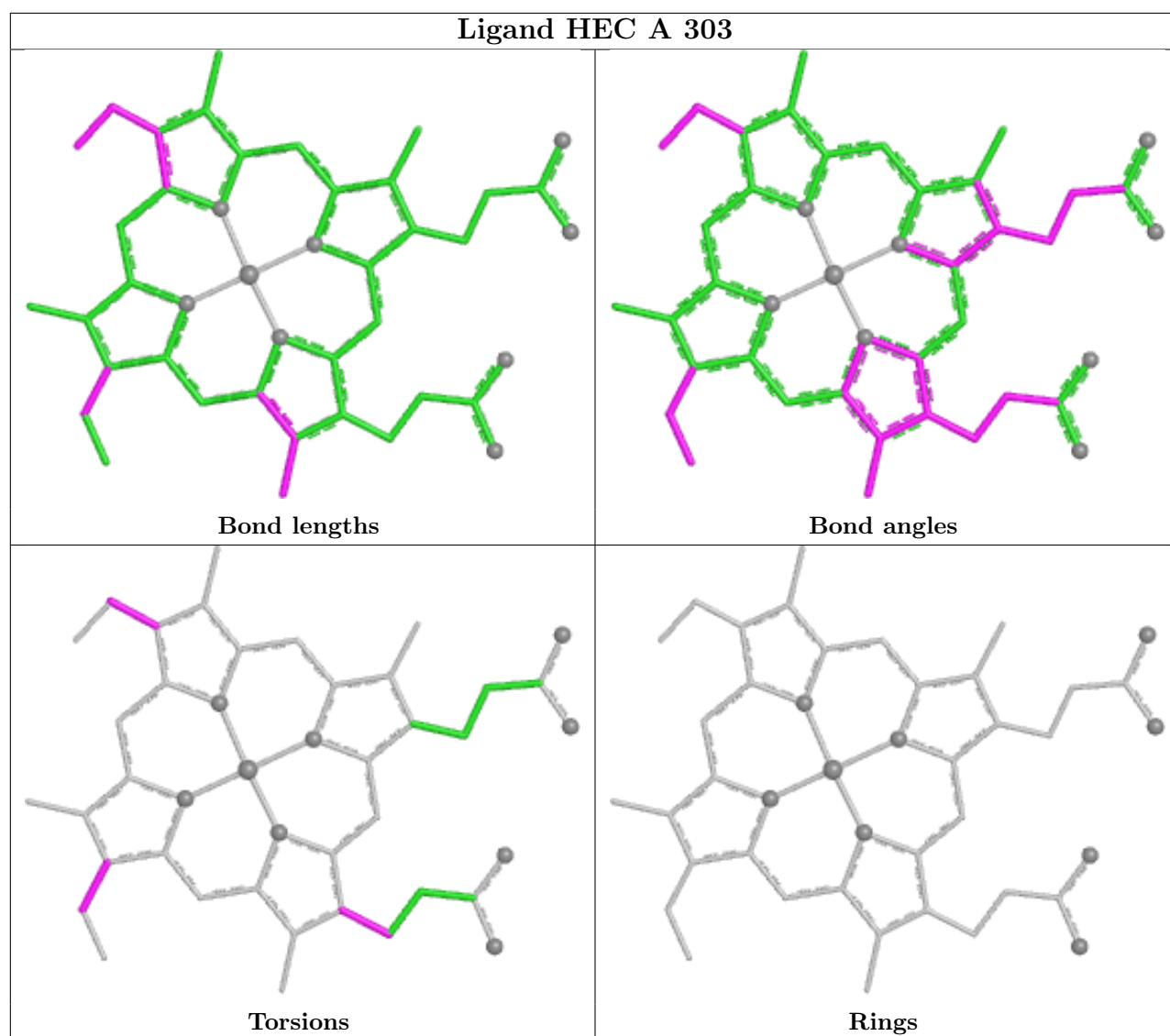
Ligand HEC C 301

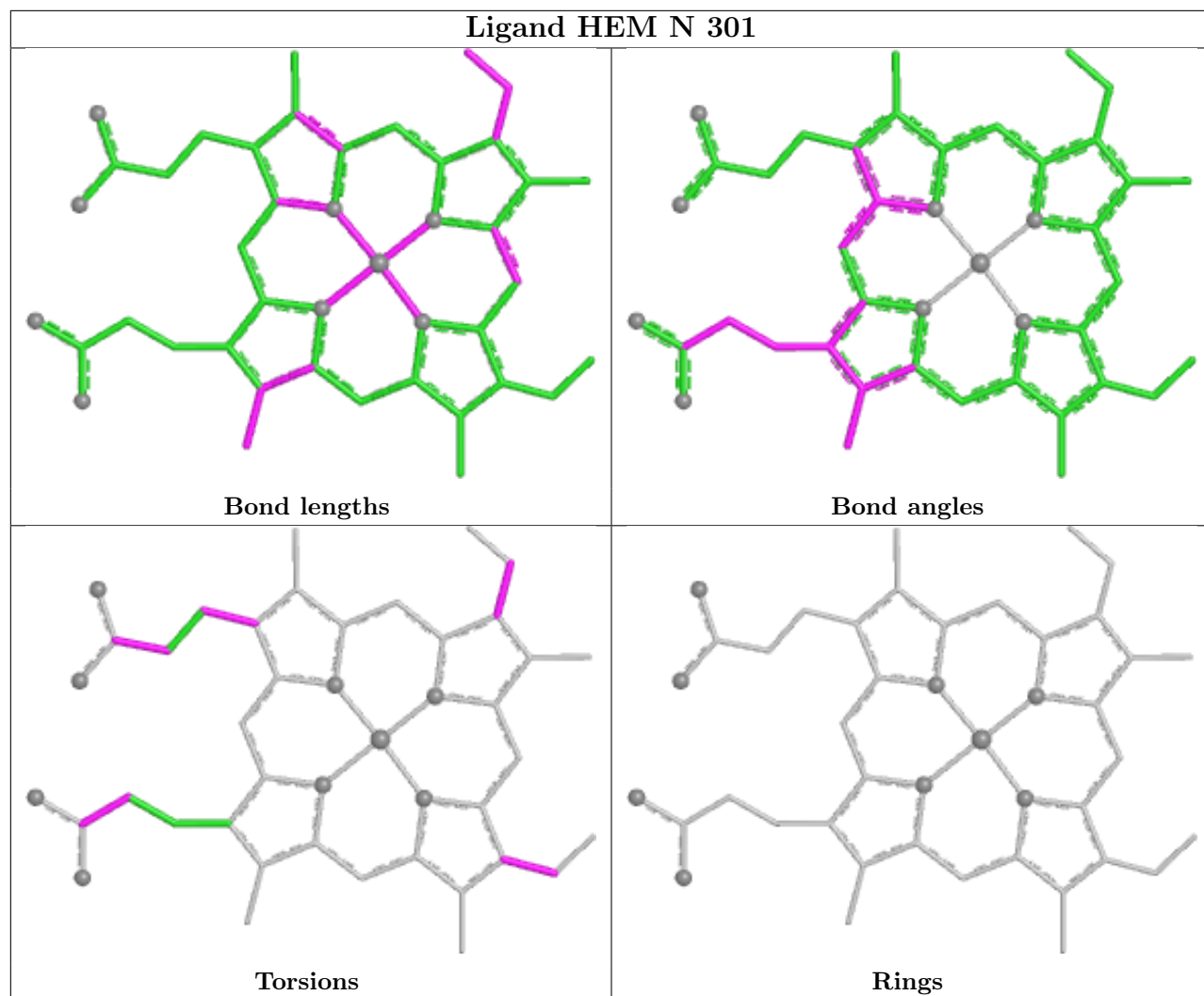


Ligand PL9 Q 1305

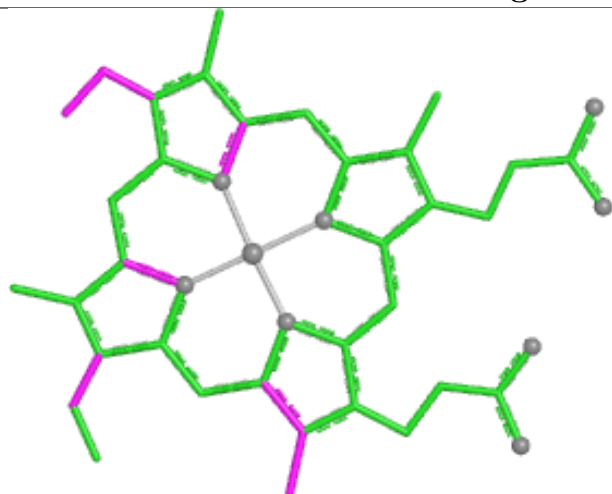




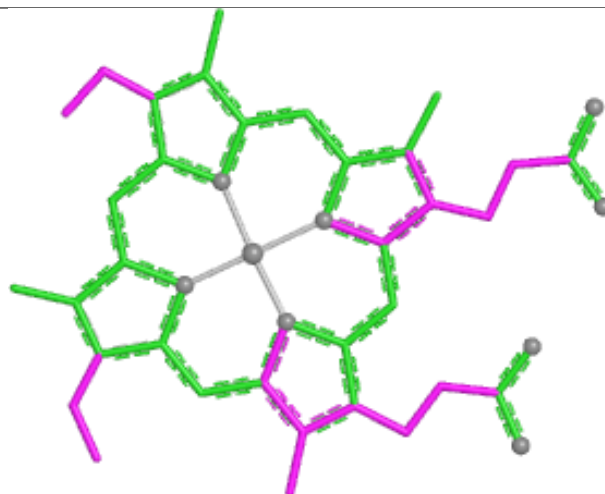




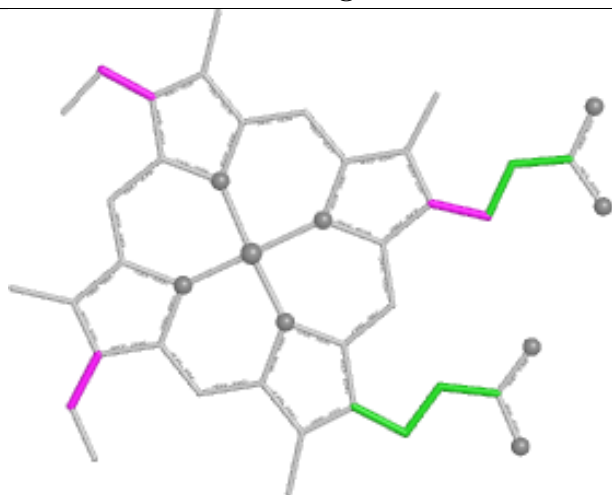
Ligand HEC N 303



Bond lengths



Bond angles

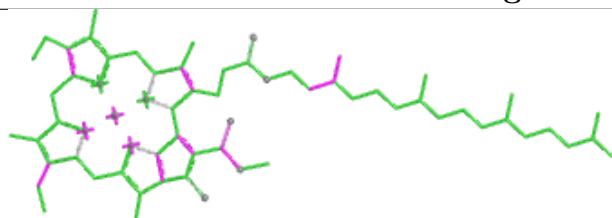


Torsions

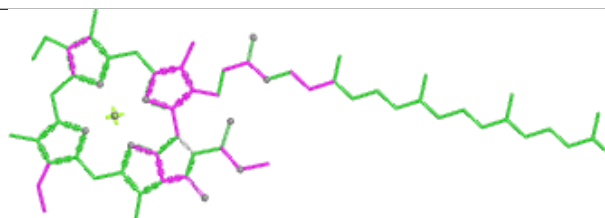


Rings

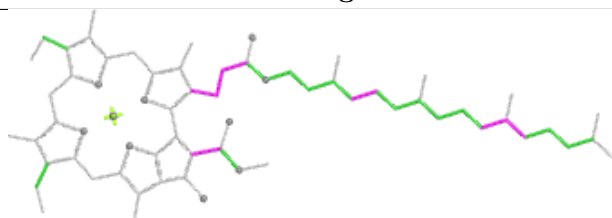
Ligand CLA O 1201



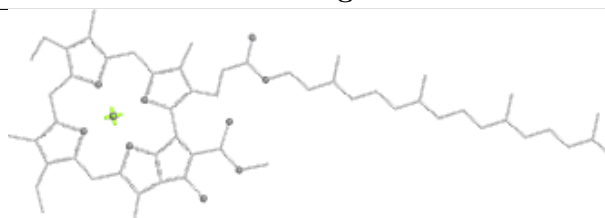
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	202/215 (93%)	-1.46	0 100 100	22, 55, 101, 174	0
1	N	202/215 (93%)	-1.50	0 100 100	19, 53, 86, 121	0
2	B	138/160 (86%)	-1.35	0 100 100	24, 65, 122, 194	0
2	O	138/160 (86%)	-1.31	0 100 100	28, 62, 139, 184	0
3	C	286/289 (98%)	-1.21	0 100 100	3, 82, 153, 200	1 (0%)
3	P	286/289 (98%)	-1.24	0 100 100	7, 85, 154, 200	1 (0%)
4	D	168/179 (93%)	-1.09	0 100 100	36, 117, 179, 200	0
4	Q	168/179 (93%)	-1.12	0 100 100	33, 109, 165, 192	0
5	E	32/32 (100%)	-1.14	0 100 100	30, 76, 149, 177	0
5	R	32/32 (100%)	-1.23	0 100 100	37, 81, 149, 171	0
6	F	33/35 (94%)	-1.27	0 100 100	39, 63, 140, 177	0
6	S	35/35 (100%)	-1.12	0 100 100	41, 78, 152, 167	0
7	G	23/37 (62%)	-1.45	0 100 100	33, 71, 128, 171	0
7	T	27/37 (72%)	-1.36	0 100 100	37, 65, 100, 152	0
8	H	27/29 (93%)	-1.29	0 100 100	33, 71, 130, 165	0
8	U	27/29 (93%)	-1.13	0 100 100	46, 81, 152, 157	0
All	All	1824/1952 (93%)	-1.28	0 100 100	3, 74, 155, 200	2 (0%)

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

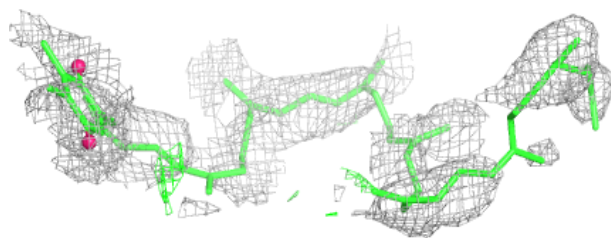
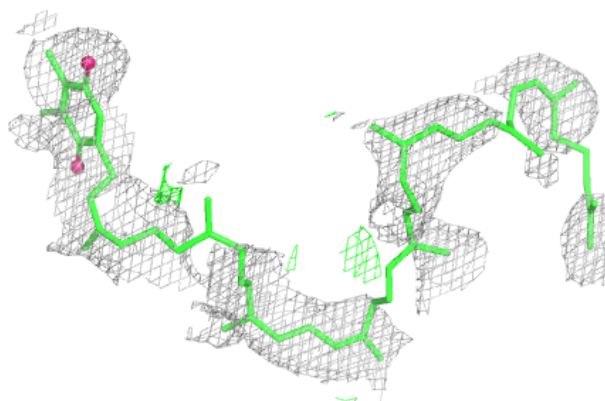
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
12	PL9	A	305	55/55	0.98	0.08	98,98,98,98	0
12	PL9	Q	1305	55/55	0.98	0.06	85,85,85,85	0
13	OPC	B	307	54/55	0.98	0.06	84,84,84,84	0
13	OPC	N	1306	54/55	0.98	0.07	87,87,87,87	0
11	TDS	A	304	30/30	0.99	0.06	52,52,52,52	0
13	OPC	D	306	54/55	0.99	0.06	86,86,86,86	0
11	TDS	N	1304	30/30	0.99	0.07	80,80,80,80	0
13	OPC	Q	1307	54/55	0.99	0.05	72,72,72,72	0
14	CLA	B	201	65/65	0.99	0.04	45,56,56,56	0
14	CLA	O	1201	65/65	0.99	0.05	22,72,72,72	0
16	BCR	E	101	40/40	0.99	0.06	77,77,77,77	0
16	BCR	R	1101	40/40	0.99	0.07	91,91,91,91	0
10	HEC	A	303	43/43	1.00	0.04	55,81,81,81	0
10	HEC	C	301	43/43	1.00	0.04	62,83,83,83	0
10	HEC	N	303	43/43	1.00	0.03	61,61,61,64	0
10	HEC	P	301	43/43	1.00	0.03	47,56,56,56	0
9	HEM	A	301	43/43	1.00	0.04	45,45,45,45	0
9	HEM	A	302	43/43	1.00	0.04	62,62,62,62	0
15	FES	D	200	4/4	1.00	0.04	144,144,170,170	0
15	FES	Q	1200	4/4	1.00	0.04	94,94,98,98	0
9	HEM	N	301	43/43	1.00	0.04	41,50,50,50	0
9	HEM	N	302	43/43	1.00	0.03	48,56,56,56	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.

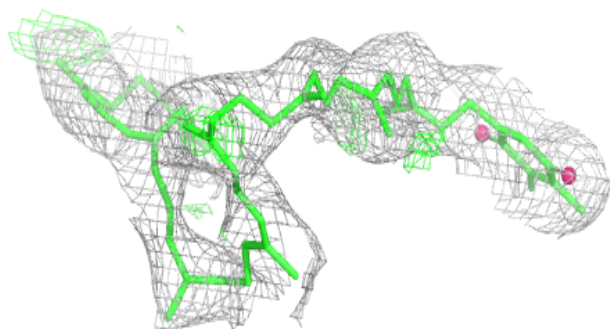
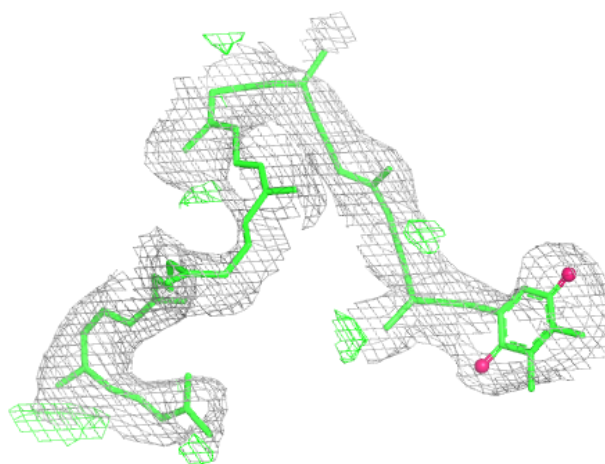
Electron density around PL9 A 305:

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



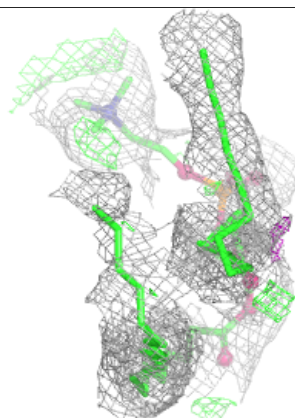
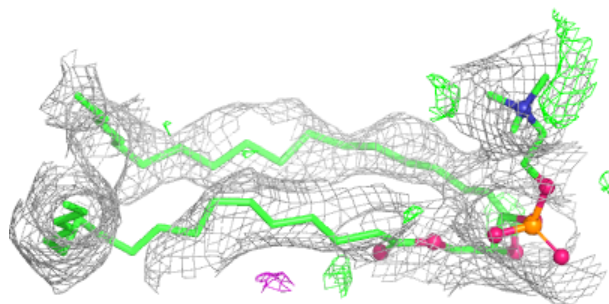
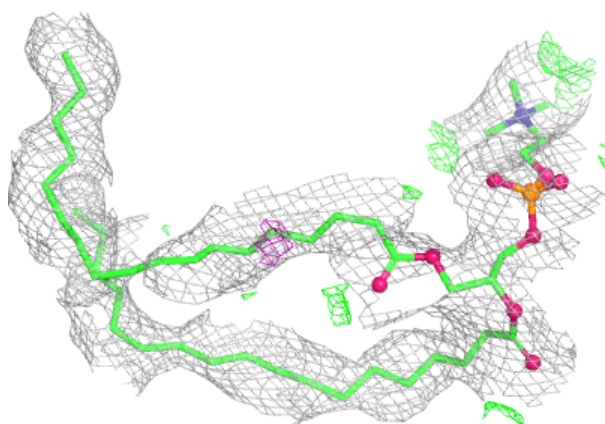
Electron density around PL9 Q 1305:

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

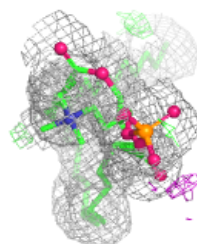
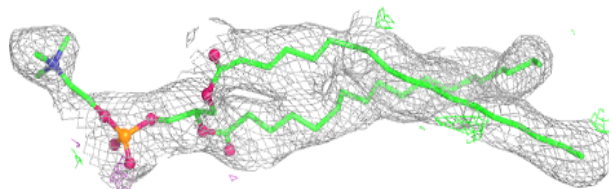
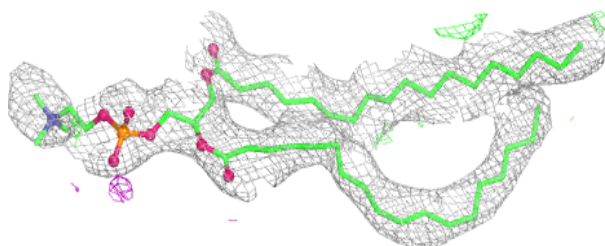


Electron density around OPC B 307:

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

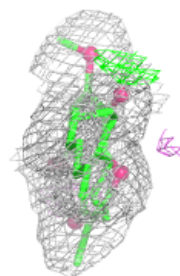
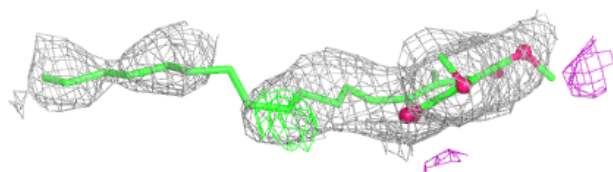
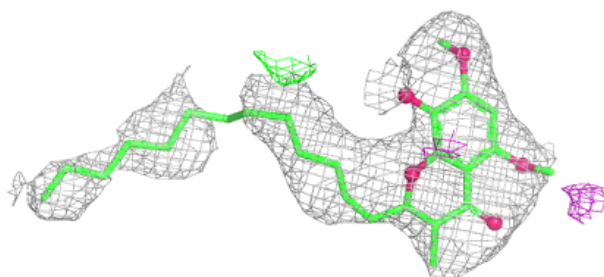
**Electron density around OPC N 1306:**

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

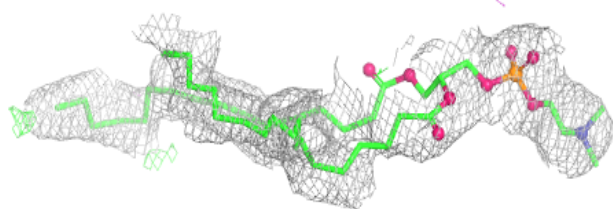
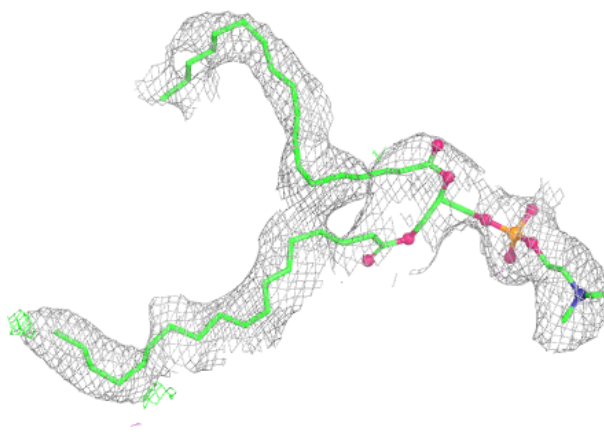


Electron density around TDS A 304:

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

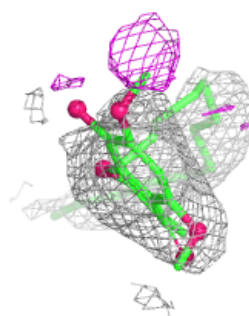
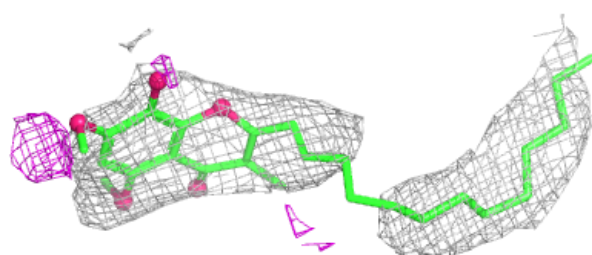
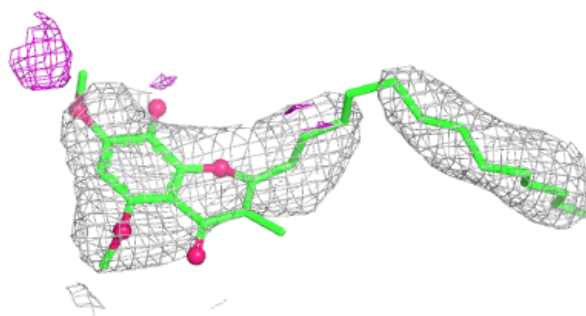
**Electron density around OPC D 306:**

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and green (positive)

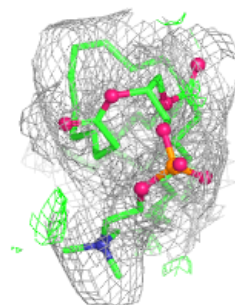
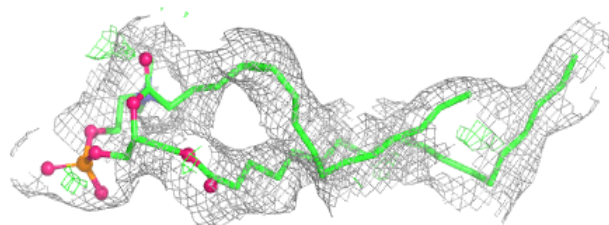
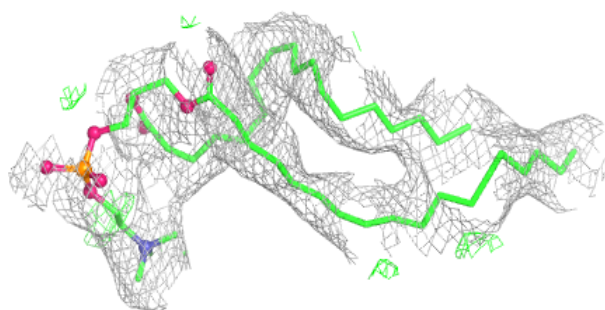


Electron density around TDS N 1304:

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

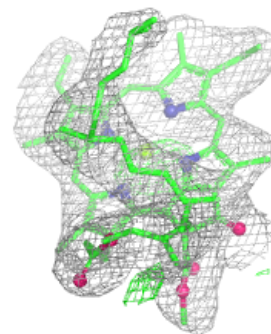
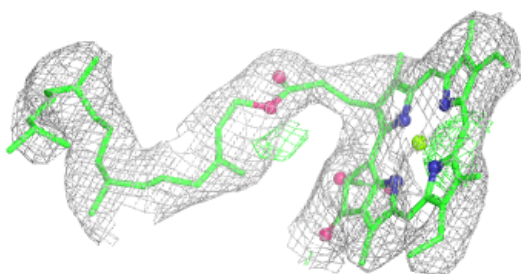
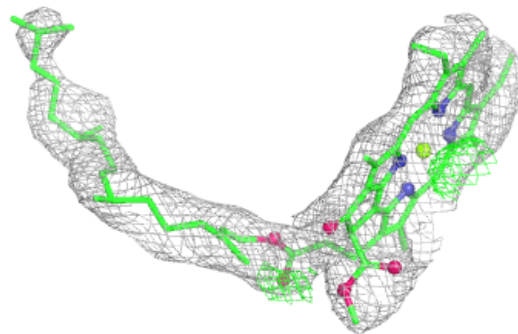
**Electron density around OPC Q 1307:**

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

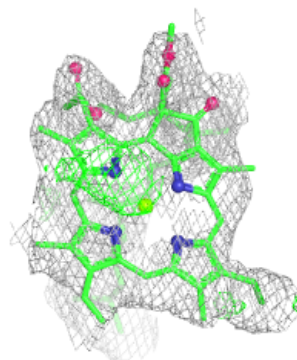
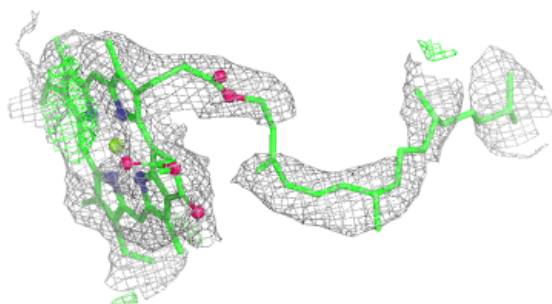
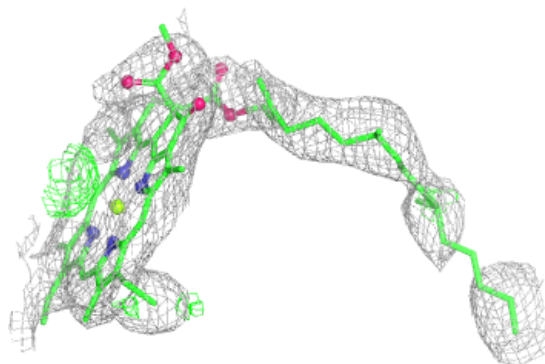


Electron density around CLA B 201:

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

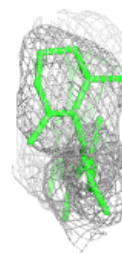
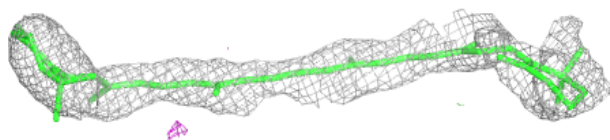
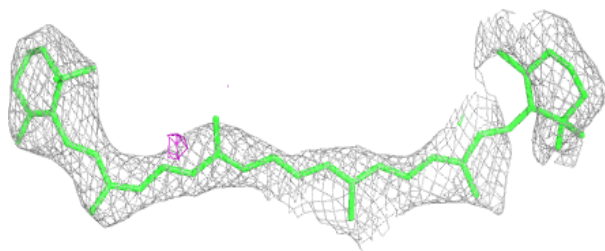
**Electron density around CLA O 1201:**

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

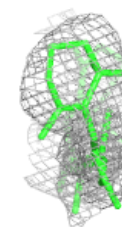
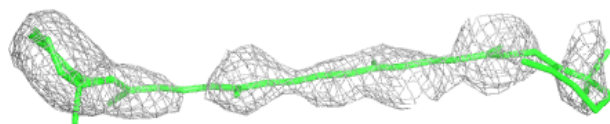
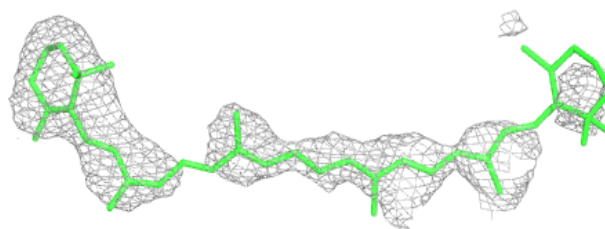


Electron density around BCR E 101:

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

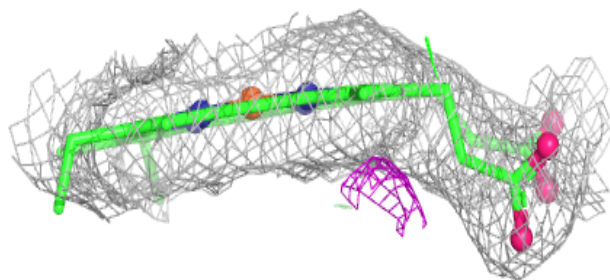
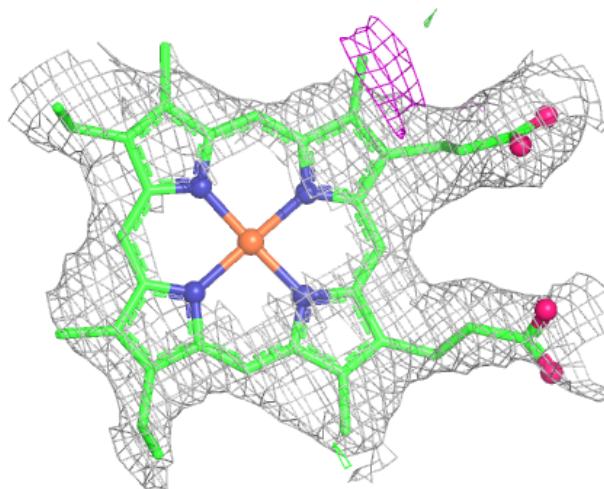
**Electron density around BCR R 1101:**

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



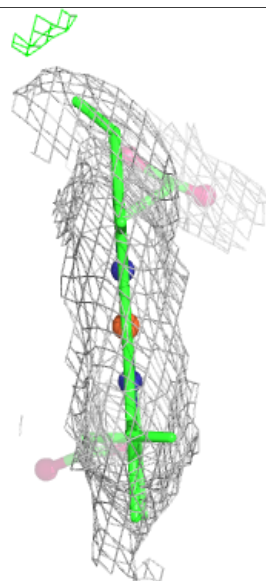
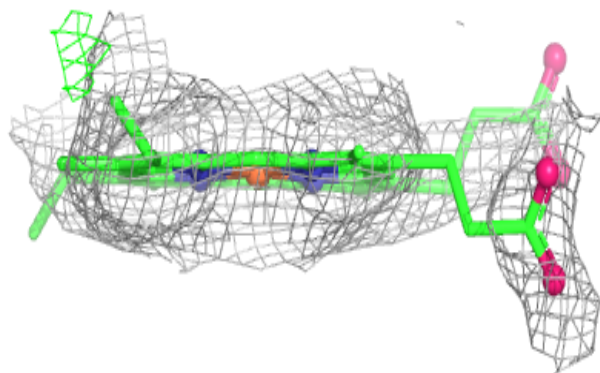
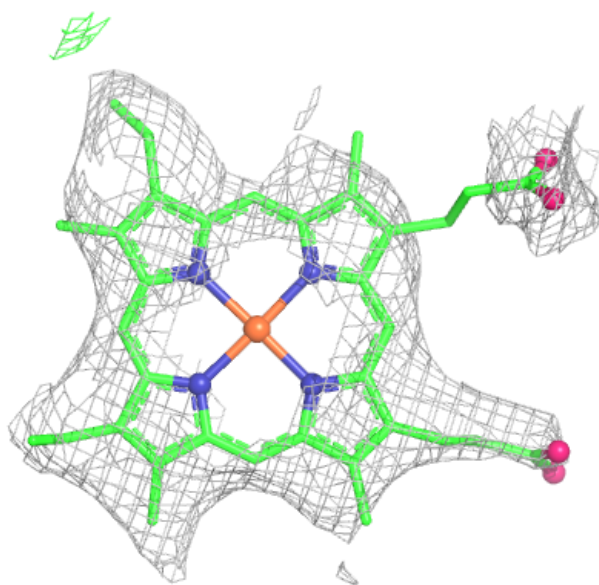
Electron density around HEC A 303:

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and green (positive)



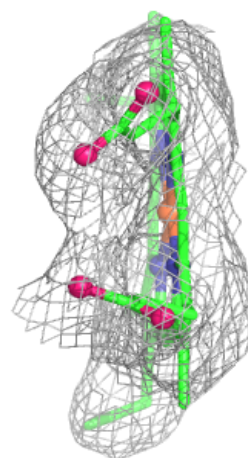
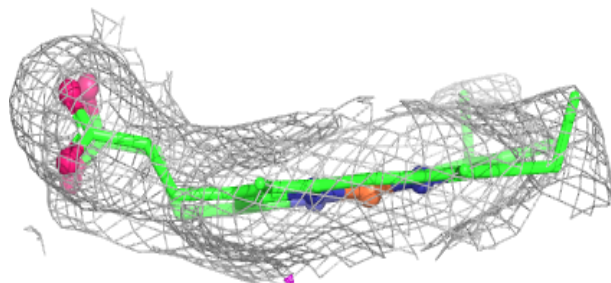
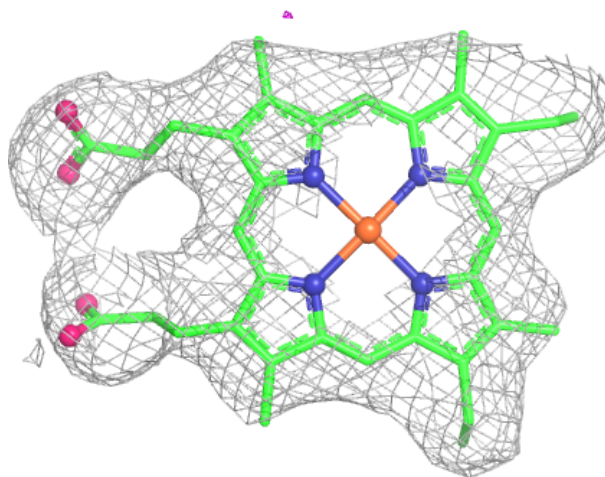
Electron density around HEC C 301:

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and green (positive)



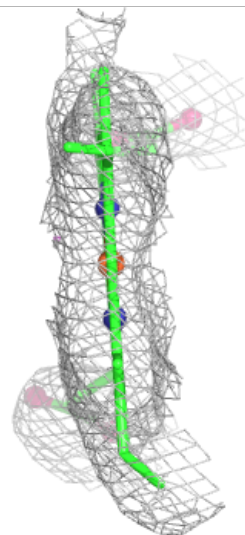
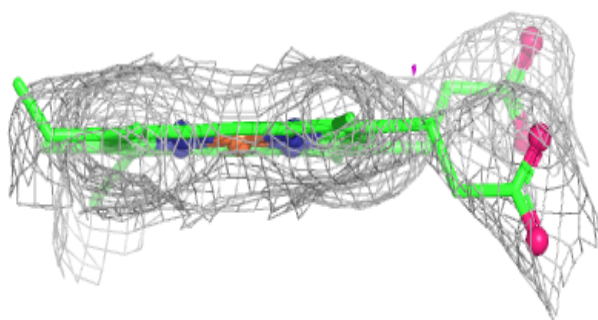
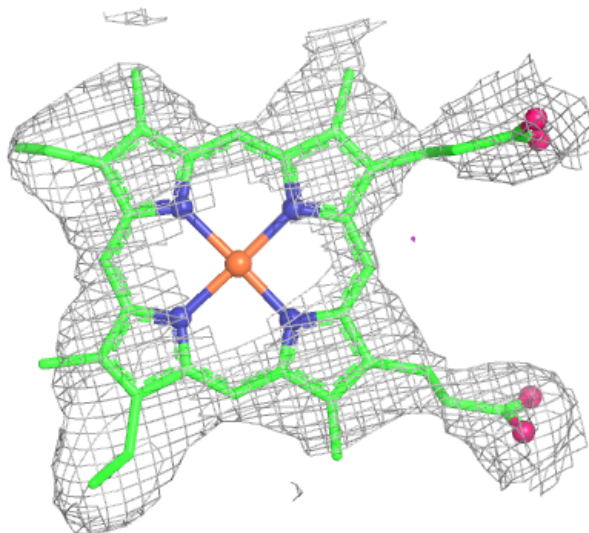
Electron density around HEC N 303:

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and green (positive)



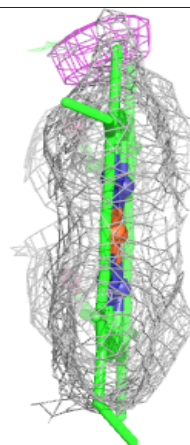
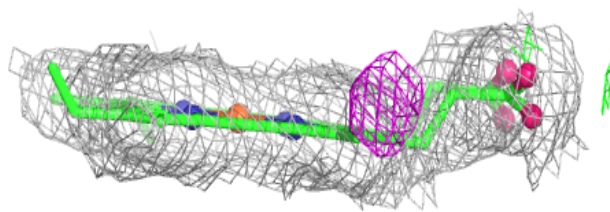
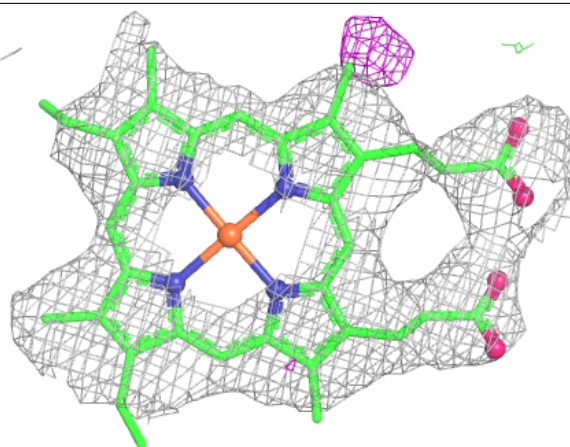
Electron density around HEC P 301:

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



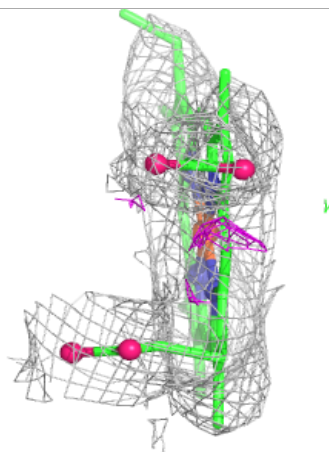
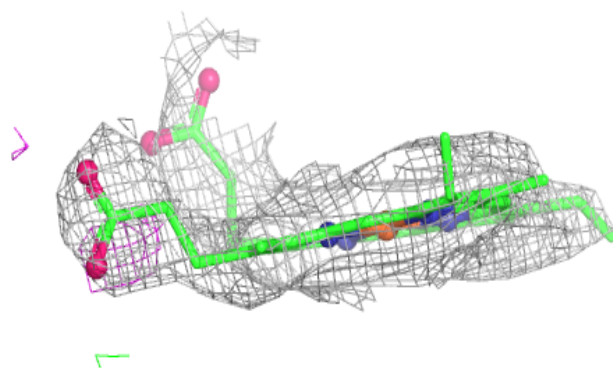
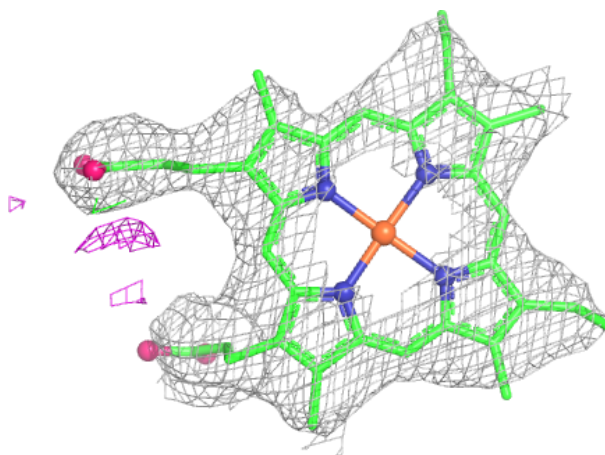
Electron density around HEM A 301:

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and green (positive)



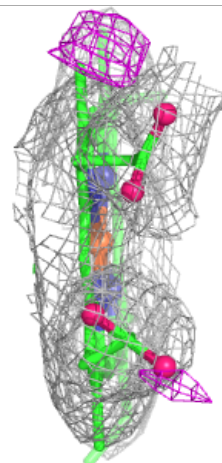
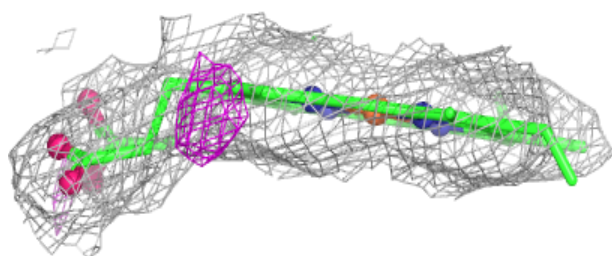
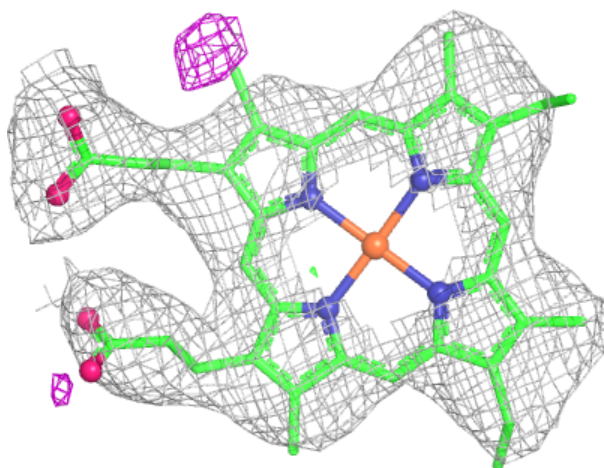
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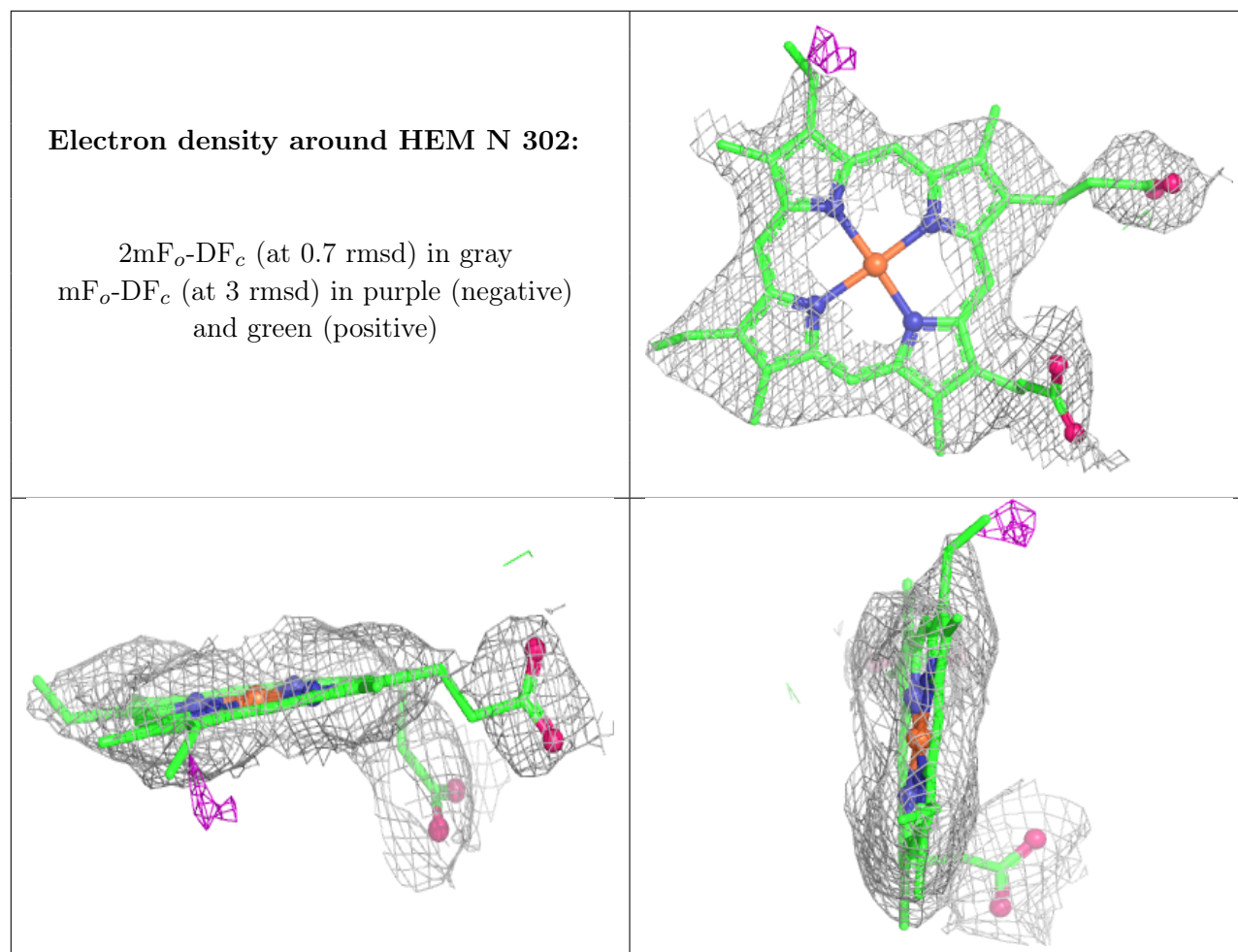
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM N 301:

$2mF_o-DF_c$ (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.