



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 4, 2026 – 10:41 PM EDT

PDB ID : 1VCR / pdb_00001vcr
Title : An icosahedral assembly of light-harvesting chlorophyll a/b protein complex from pea thylakoid membranes
Authors : Hino, T.; Kanamori, E.; Shen, J.-R.; Kouyama, T.
Deposited on : 2004-03-10
Resolution : 9.50 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	:	4-5-2 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	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

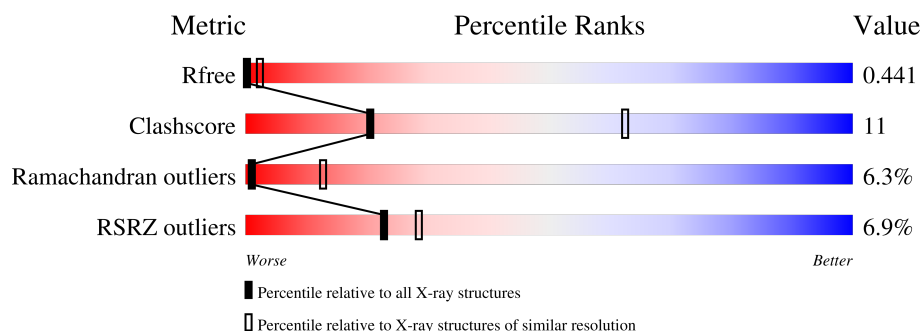
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 9.50 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}	180053	1168 (11.50-4.00)
Clashscore	190562	1001 (11.50-4.06)
Ramachandran outliers	187476	1055 (11.50-4.00)
RSRZ outliers	180081	1162 (11.50-4.00)

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	232	

2 Entry composition [i](#)

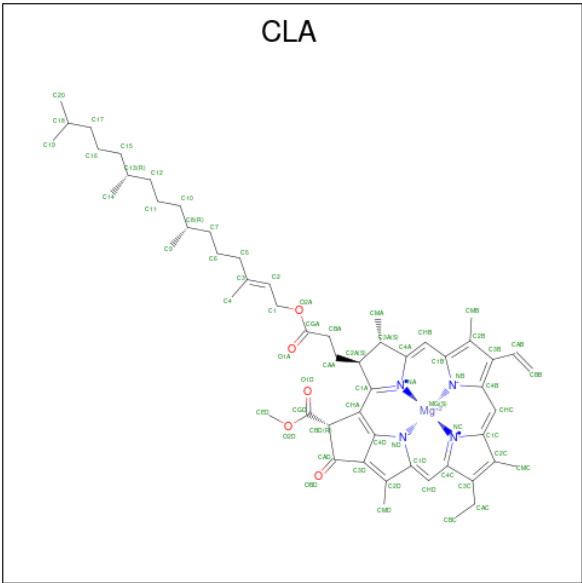
There are 3 unique types of molecules in this entry. The entry contains 796 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Chlorophyll a-b binding protein AB80.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	101	Total	C	N	O	0	0	0
			496	294	101	101			

- Molecule 2 is CHLOROPHYLL A (CCD ID: CLA) (formula: C₅₅H₇₂MgN₄O₅).



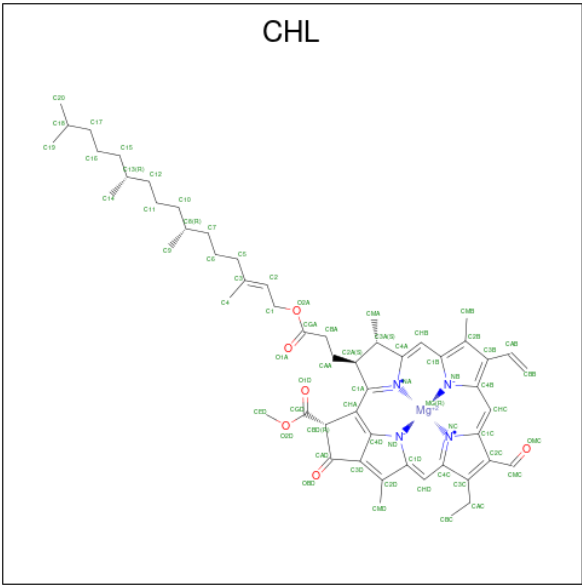
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	Mg	N	0	0
			25	20	1	4		
2	A	1	Total	C	Mg	N	0	0
			25	20	1	4		
2	A	1	Total	C	Mg	N	0	0
			25	20	1	4		
2	A	1	Total	C	Mg	N	0	0
			25	20	1	4		
2	A	1	Total	C	Mg	N	0	0
			25	20	1	4		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	Mg	N	0	0
			25	20	1	4		
2	A	1	Total	C	Mg	N	0	0
			25	20	1	4		

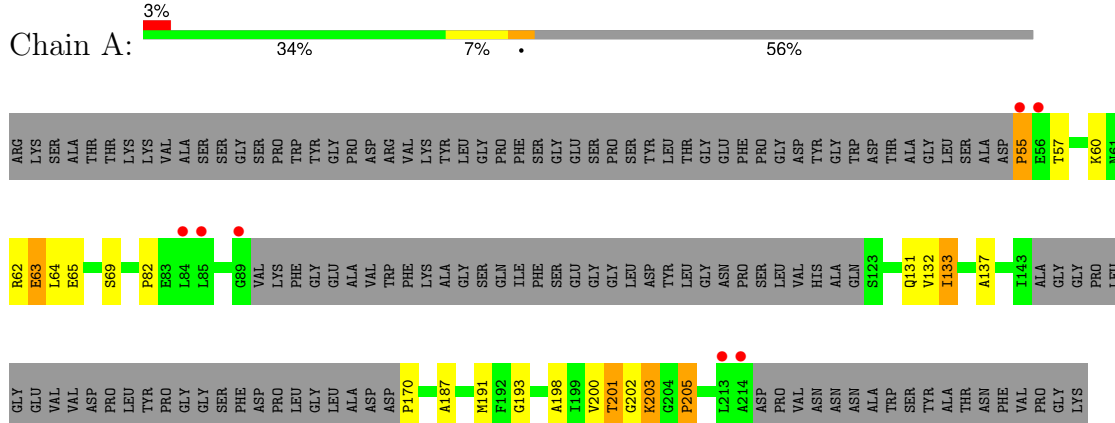
- Molecule 3 is CHLOROPHYLL B (CCD ID: CHL) (formula: C₅₅H₇₀MgN₄O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	Mg	N	0	0
			25	20	1	4		
3	A	1	Total	C	Mg	N	0	0
			25	20	1	4		
3	A	1	Total	C	Mg	N	0	0
			25	20	1	4		
3	A	1	Total	C	Mg	N	0	0
			25	20	1	4		
3	A	1	Total	C	Mg	N	0	0
			25	20	1	4		

i

- Molecule 1: Chlorophyll a-b binding protein AB80



4 Data and refinement statistics

Property	Value	Source
Space group	F 2 3	Depositor
Cell constants a, b, c, α , β , γ	360.65Å 360.65Å 360.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 9.50 20.00 – 9.50	Depositor EDS
% Data completeness (in resolution range)	86.3 (20.00-9.50) 100.0 (20.00-9.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	9.13 (at 9.99Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.379 , 0.353 0.424 , 0.441	Depositor DCC
R_{free} test set	241 reflections (9.52%)	wwPDB-VP
Wilson B-factor (Å ²)	281.9	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 162.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.16$, $\langle L^2 \rangle = 0.04$	Xtriage
Estimated twinning fraction	0.459 for k,h,-l	Xtriage
F_o, F_c correlation	0.32	EDS
Total number of atoms	796	wwPDB-VP
Average B, all atoms (Å ²)	296.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.97% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CHL, CLA

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.46	0/493	1.15	7/680 (1.0%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	205	PRO	N-CA-CB	6.41	109.98	103.25
1	A	55	PRO	N-CA-CB	6.36	109.99	103.00
1	A	170	PRO	N-CA-CB	6.26	109.89	103.00
1	A	82	PRO	N-CA-CB	5.85	109.85	103.30
1	A	64	LEU	N-CA-C	-5.26	106.12	113.37

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	496	0	239	12	0
2	A	175	0	21	0	0
3	A	125	0	15	0	0
All	All	796	0	275	12	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 11.

The worst 5 of 12 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)
1:A:63:GLU:C	1:A:65:GLU:H	1.97	0.72
1:A:55:PRO:C	1:A:57:THR:H	2.03	0.65
1:A:200:VAL:O	1:A:201:THR:CB	2.50	0.58
1:A:191:MET:C	1:A:193:GLY:H	2.13	0.55
1:A:198:ALA:HA	1:A:203:LYS:O	2.10	0.52

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	95/232 (41%)	79 (83%)	10 (10%)	6 (6%)	1 13

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	201	THR
1	A	203	LYS
1	A	205	PRO
1	A	132	VAL
1	A	202	GLY

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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 ⓘ

12 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	$\# Z > 2$
3	CHL	A	265	-	24,32,74	3.02	10 (41%)	31,54,114	2.33	8 (25%)
2	CLA	A	252	-	24,32,73	3.05	10 (41%)	31,54,113	2.34	8 (25%)
2	CLA	A	257	-	24,32,73	3.01	11 (45%)	31,54,113	2.39	8 (25%)
2	CLA	A	251	-	24,32,73	2.98	10 (41%)	31,54,113	2.33	8 (25%)
2	CLA	A	253	-	24,32,73	3.08	10 (41%)	31,54,113	2.35	8 (25%)
2	CLA	A	254	-	24,32,73	3.02	12 (50%)	31,54,113	2.33	8 (25%)
3	CHL	A	262	-	24,32,74	3.03	10 (41%)	31,54,114	2.34	8 (25%)
2	CLA	A	255	-	24,32,73	3.05	10 (41%)	31,54,113	2.34	8 (25%)
3	CHL	A	266	-	24,32,74	2.97	10 (41%)	31,54,114	2.36	8 (25%)
3	CHL	A	263	-	24,32,74	3.04	10 (41%)	31,54,114	2.33	8 (25%)
3	CHL	A	261	-	24,32,74	3.03	10 (41%)	31,54,114	2.35	8 (25%)
2	CLA	A	256	-	24,32,73	3.00	10 (41%)	31,54,113	2.32	8 (25%)

The worst 5 of 123 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	254	CLA	C3C-C2C	8.58	1.54	1.35
2	A	253	CLA	C3C-C2C	8.50	1.54	1.35
2	A	252	CLA	C3C-C2C	8.44	1.54	1.35
2	A	255	CLA	C3C-C2C	8.42	1.54	1.35
3	A	261	CHL	C3C-C2C	8.41	1.54	1.35

The worst 5 of 96 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	257	CLA	CHA-C4D-ND	7.42	135.32	124.84
3	A	266	CHL	CHA-C4D-ND	7.32	135.18	124.84
2	A	252	CLA	CHA-C4D-ND	7.29	135.14	124.84
2	A	255	CLA	CHA-C4D-ND	7.29	135.13	124.84
3	A	262	CHL	CHA-C4D-ND	7.28	135.12	124.84

There are no chirality outliers.

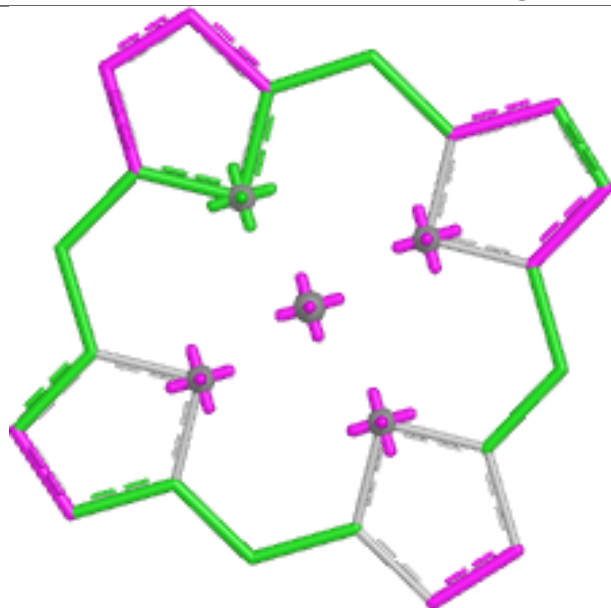
There are no torsion outliers.

There are no ring outliers.

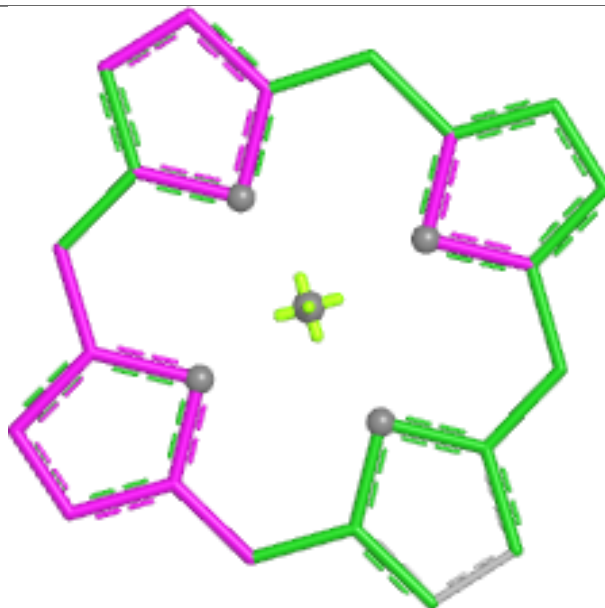
No monomer is involved in short contacts.

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.

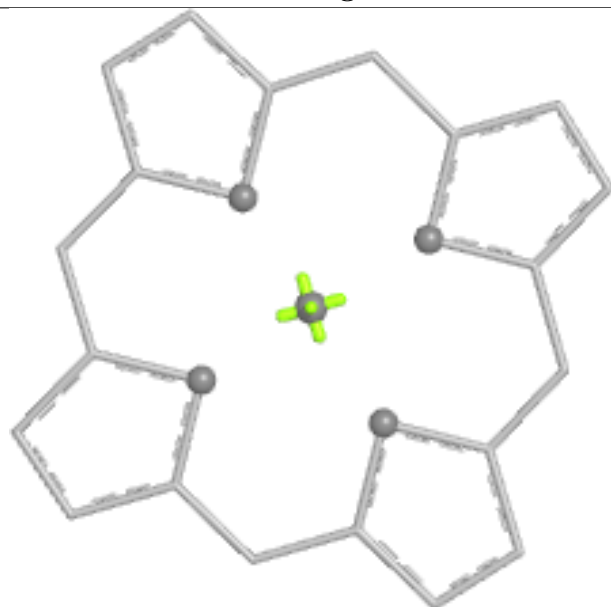
Ligand CHL A 265



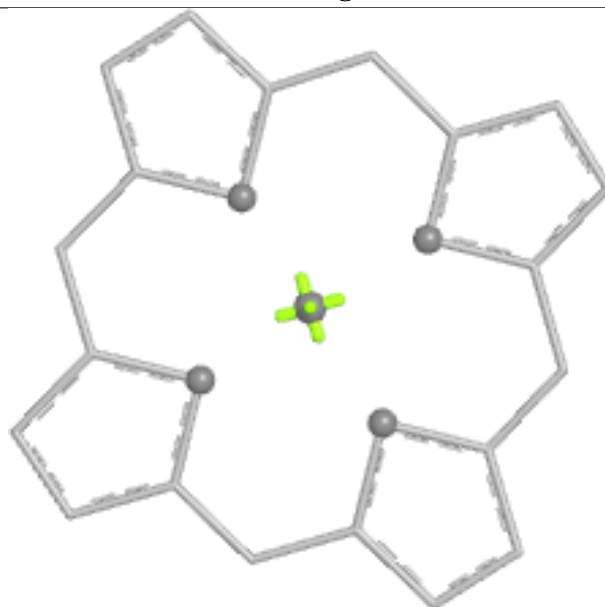
Bond lengths



Bond angles

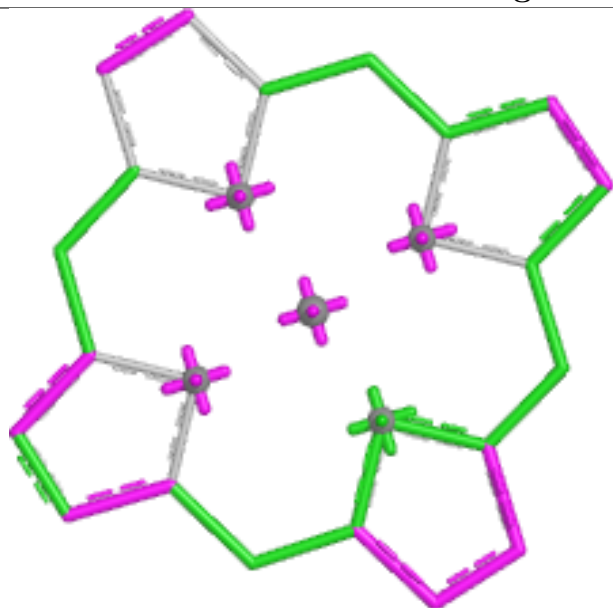


Torsions

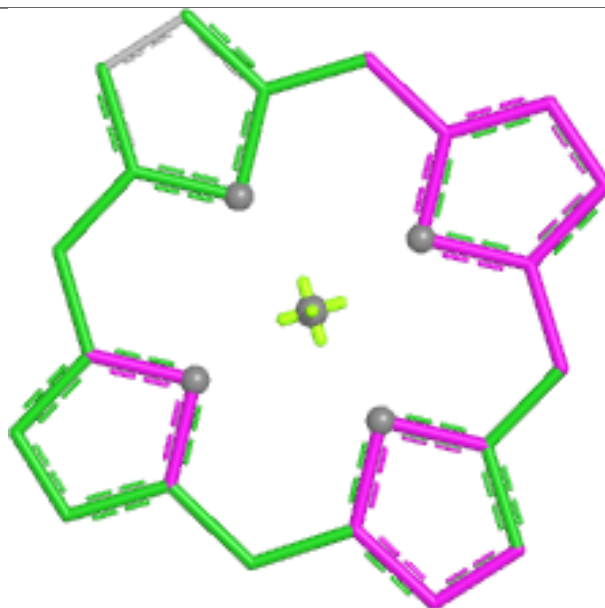


Rings

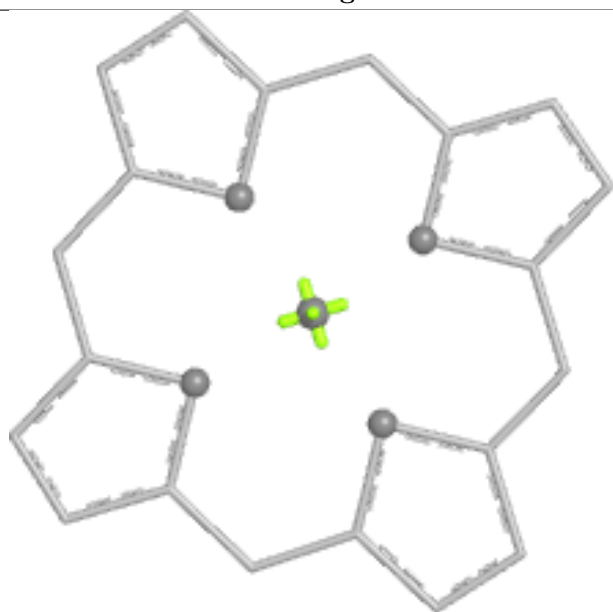
Ligand CLA A 252



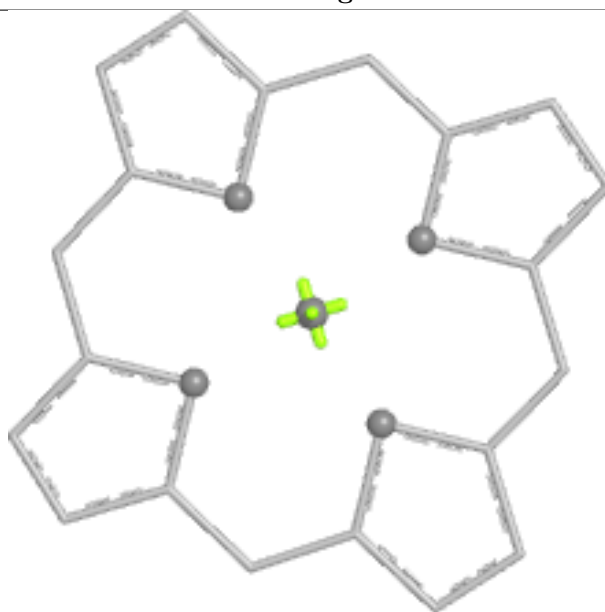
Bond lengths



Bond angles

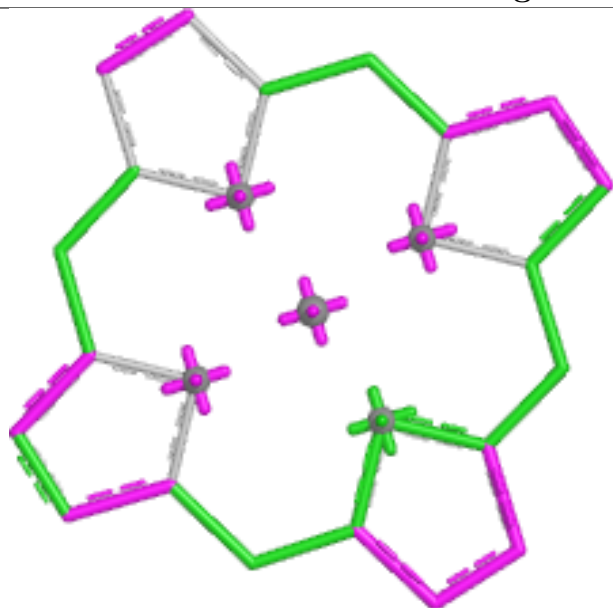


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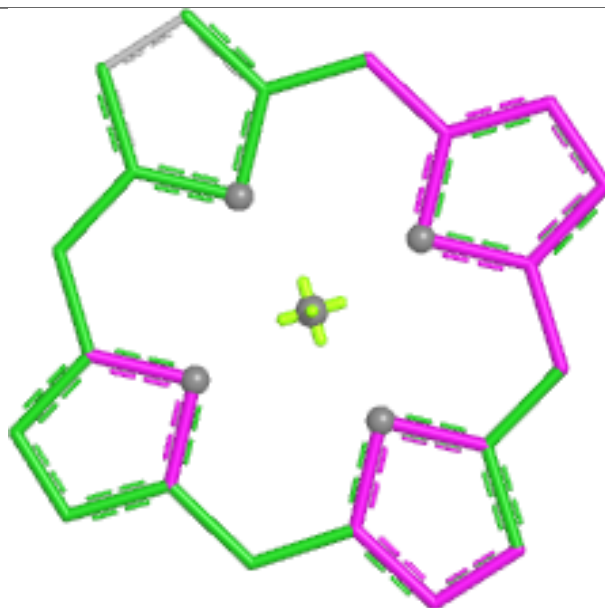


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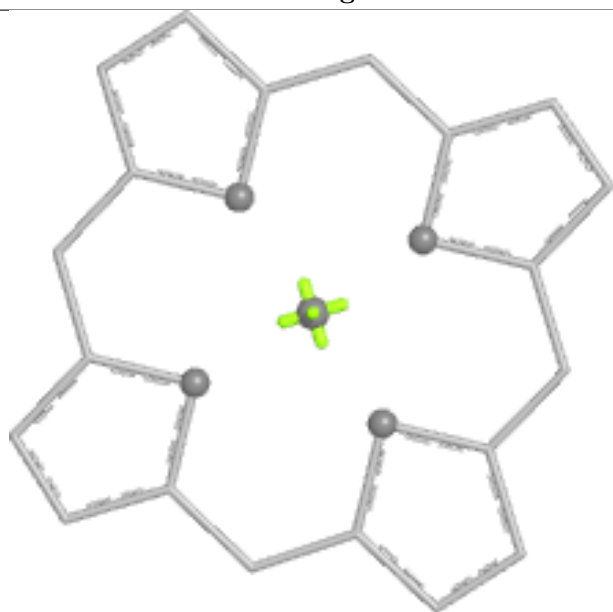
Ligand CLA A 257



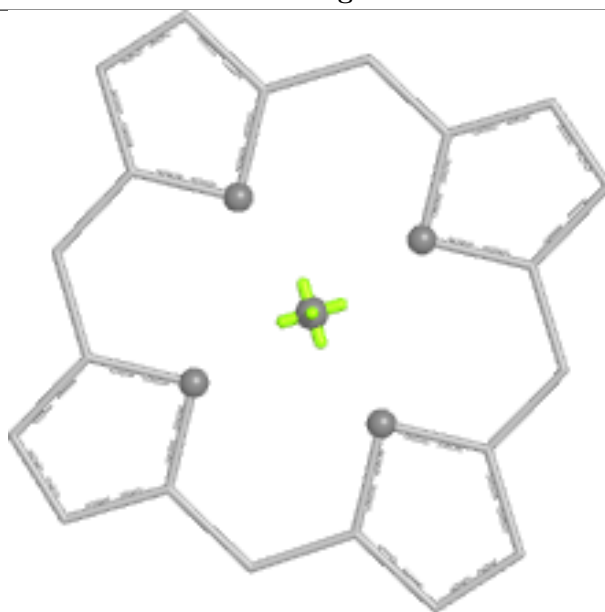
Bond lengths



Bond angles

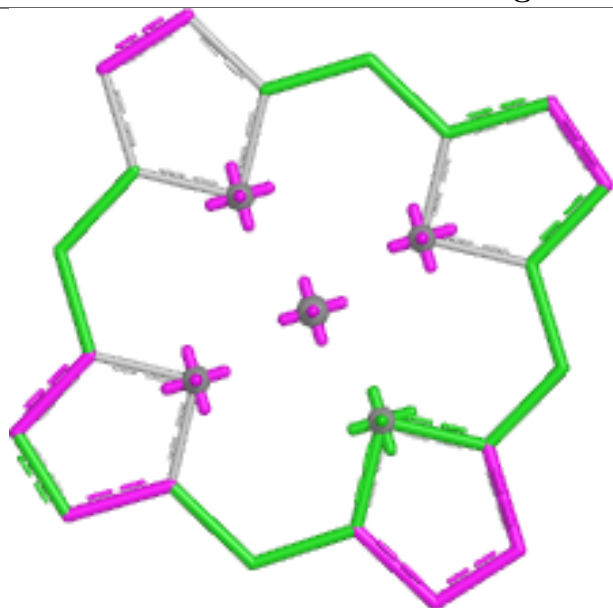


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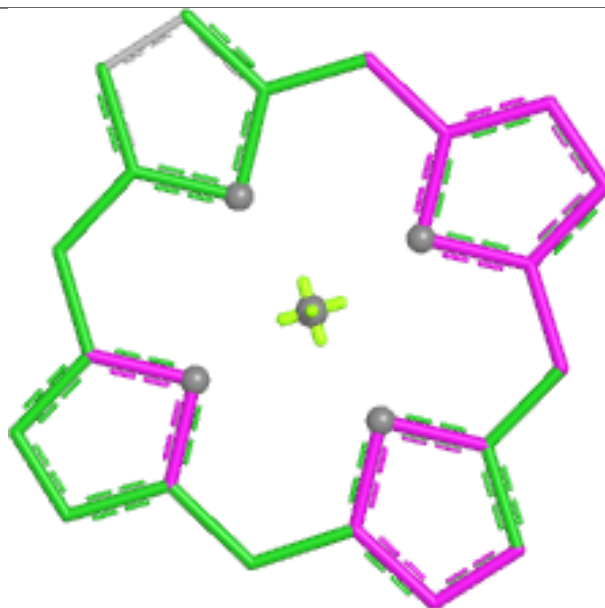


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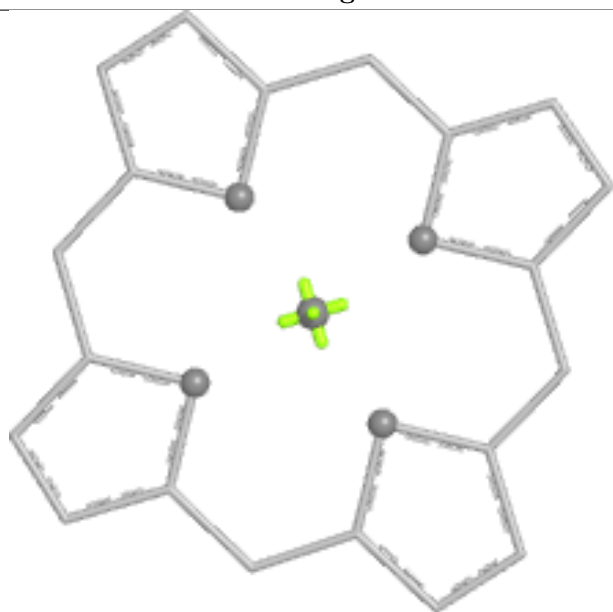
Ligand CLA A 251



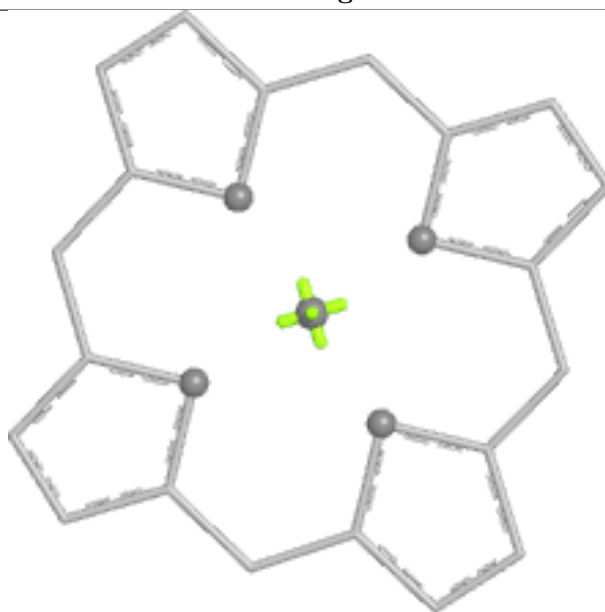
Bond lengths



Bond angles

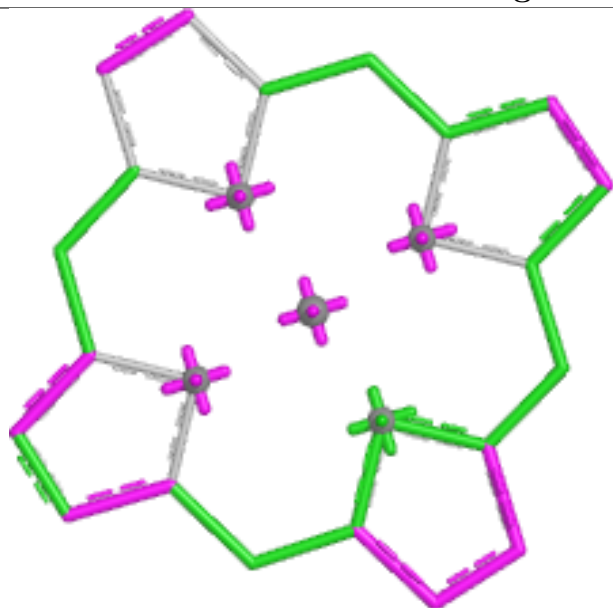


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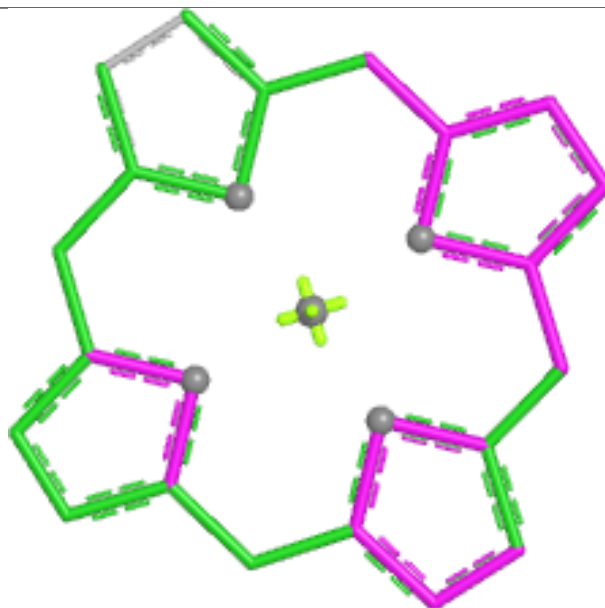


Rings

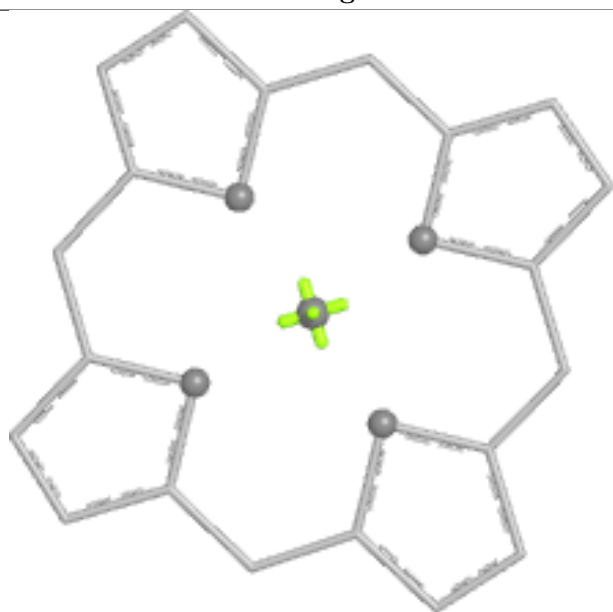
Ligand CLA A 253



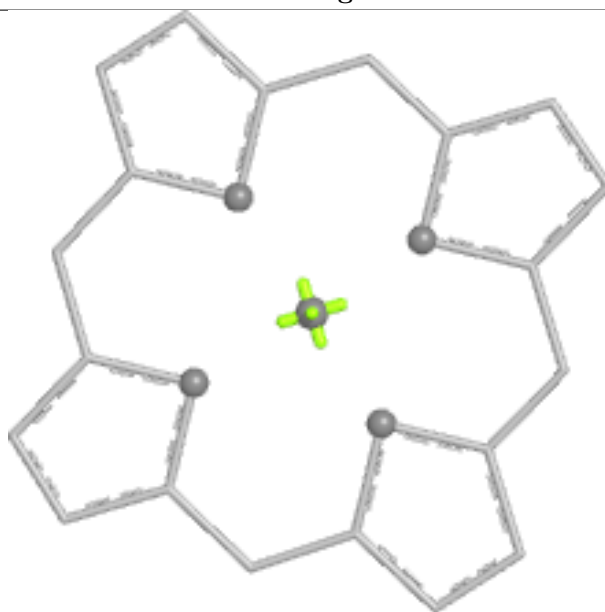
Bond lengths



Bond angles

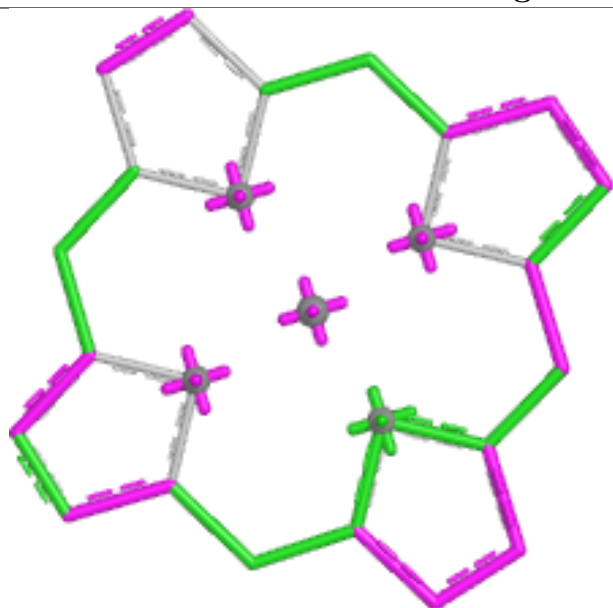


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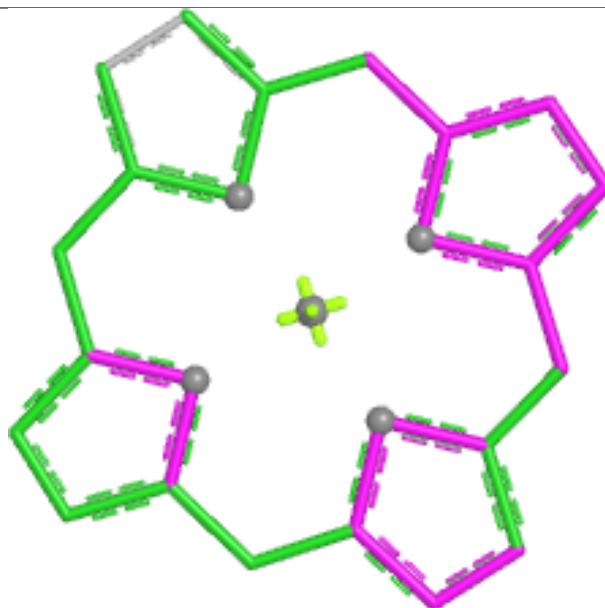


Rings

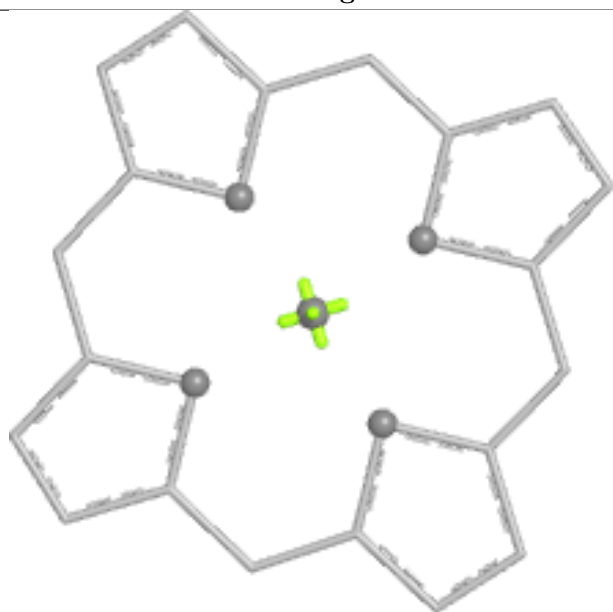
Ligand CLA A 254



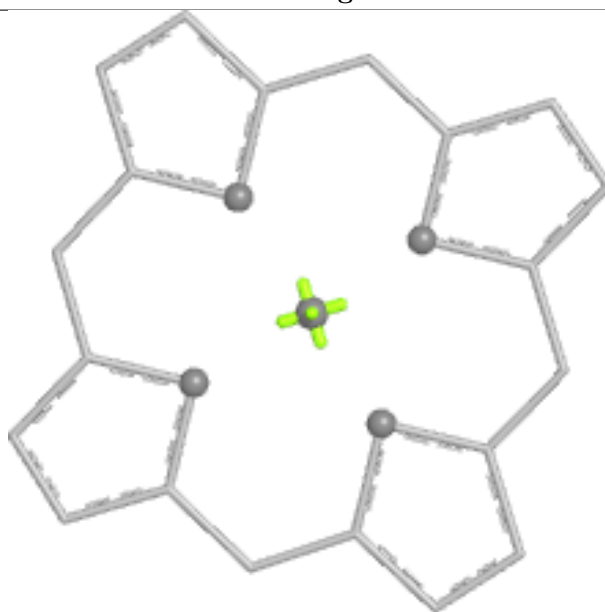
Bond lengths



Bond angles

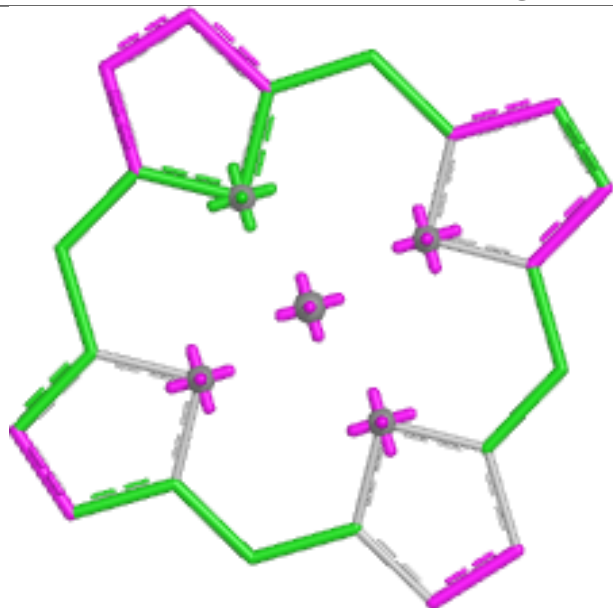


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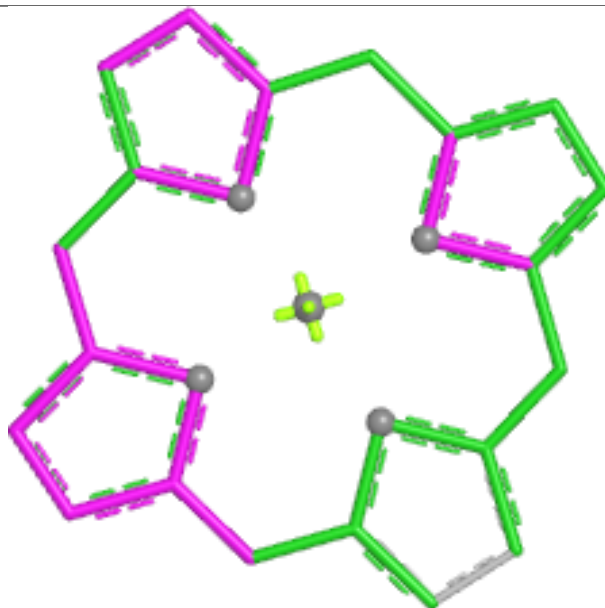


Rings

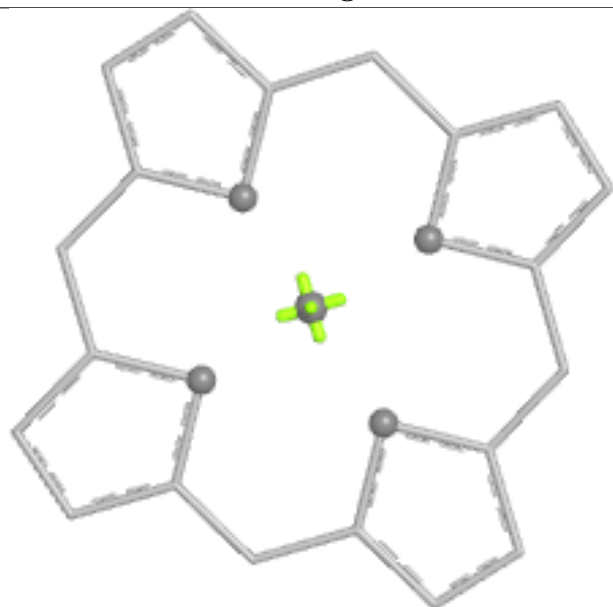
Ligand CHL A 262



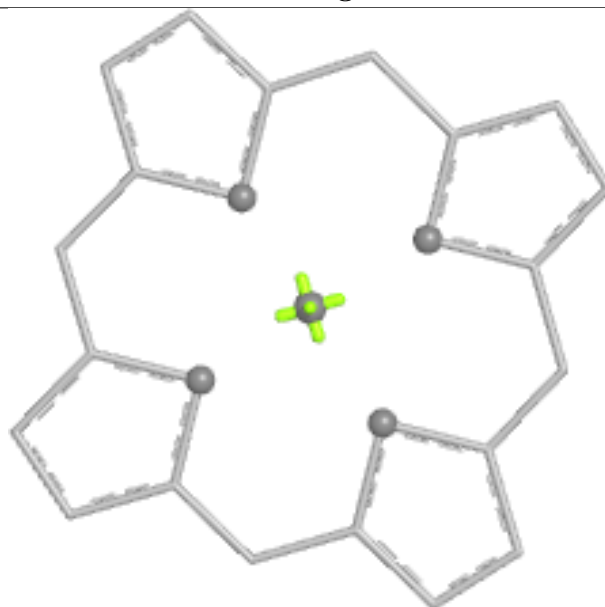
Bond lengths



Bond angles

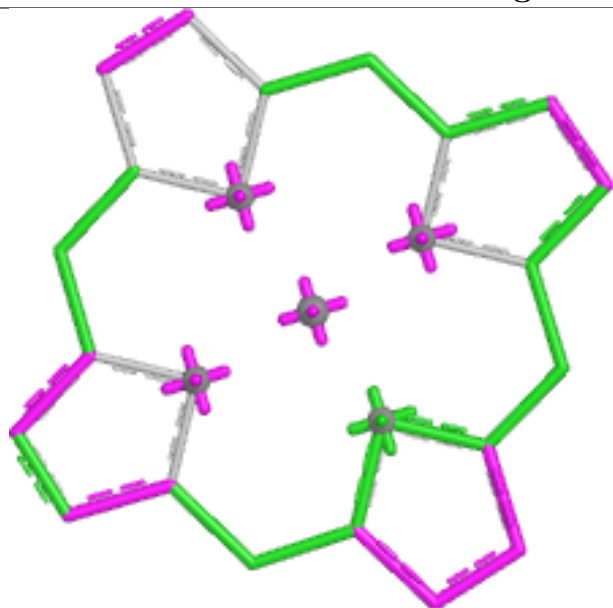


Torsions

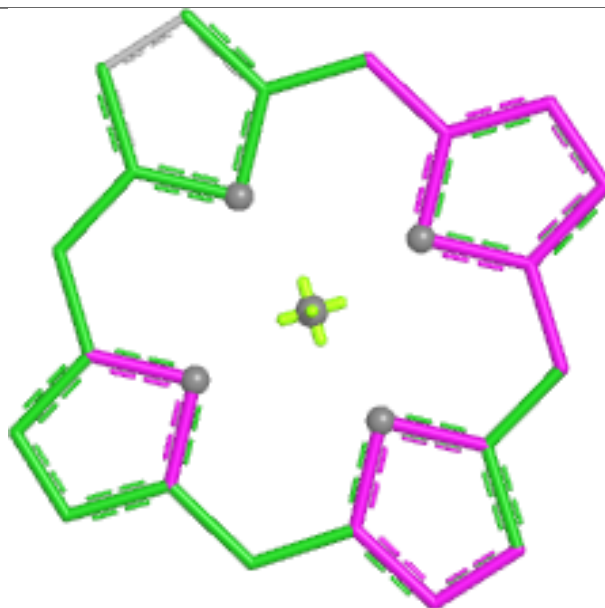


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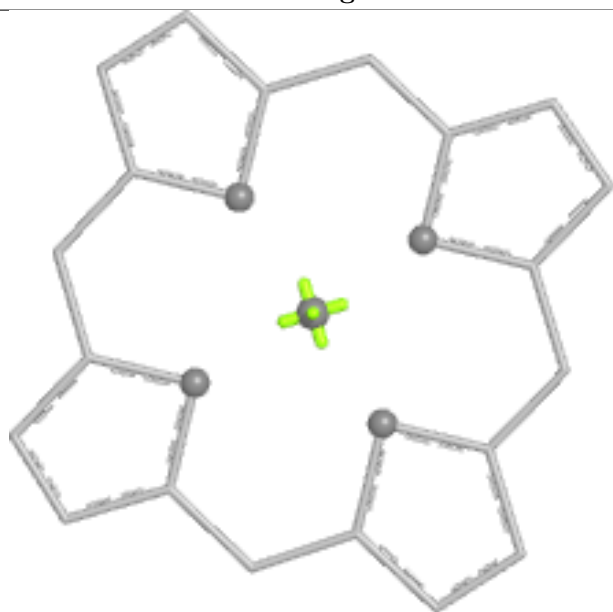
Ligand CLA A 255



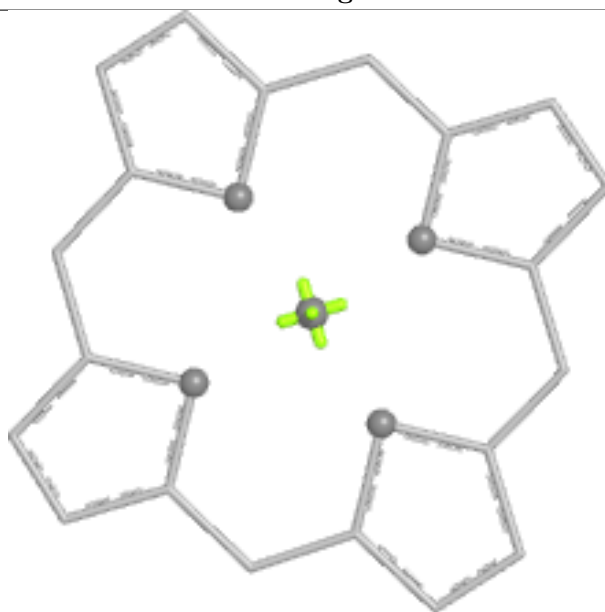
Bond lengths



Bond angles

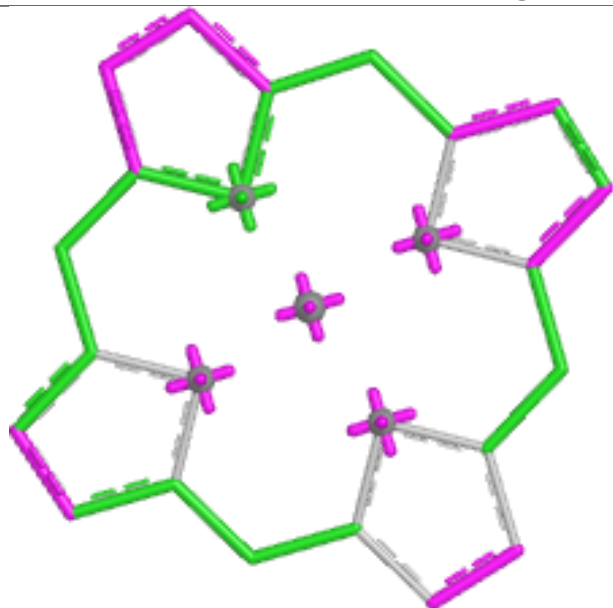


Torsions

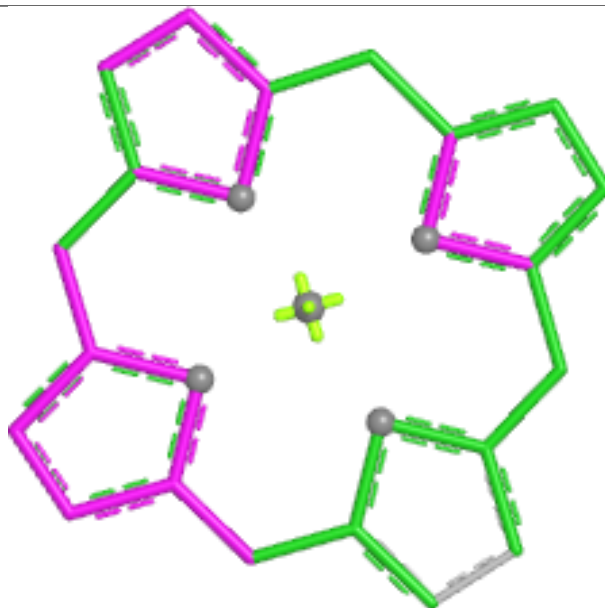


Rings

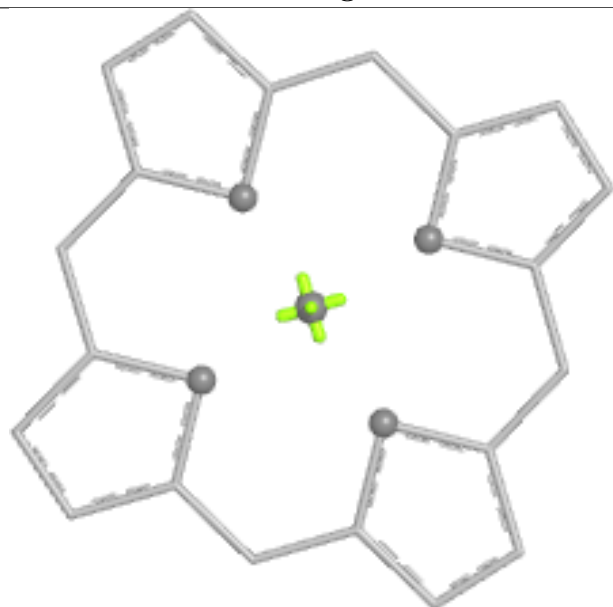
Ligand CHL A 266



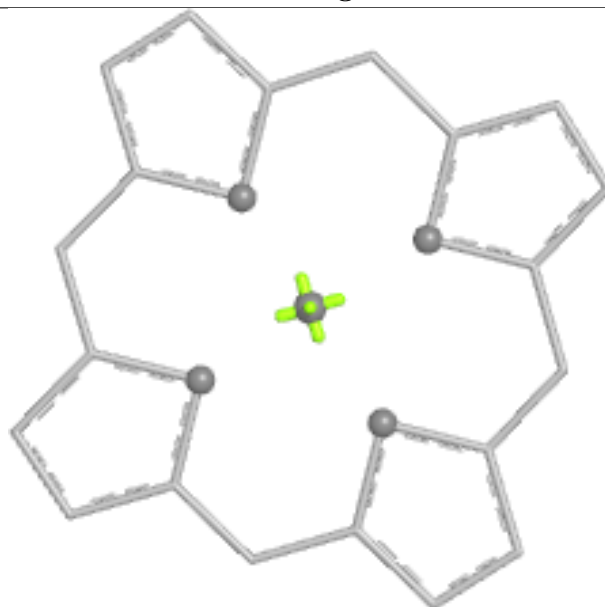
Bond lengths



Bond angles

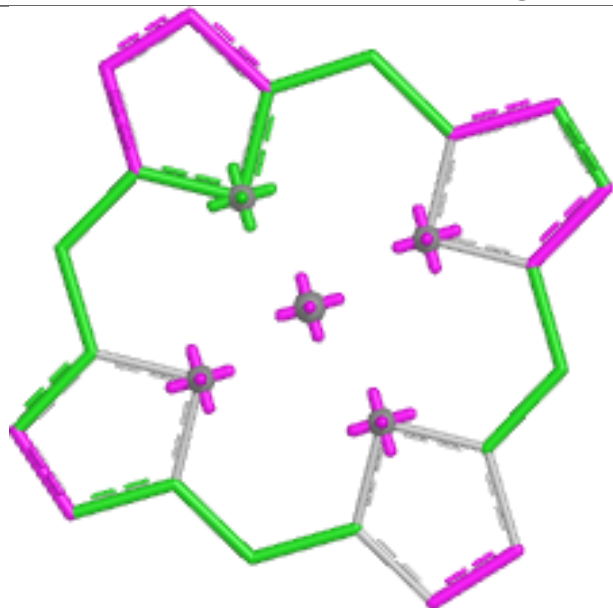


Torsions

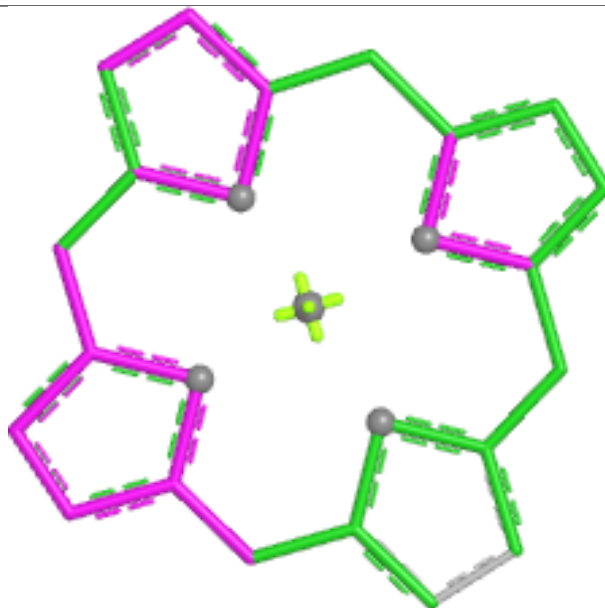


Rings

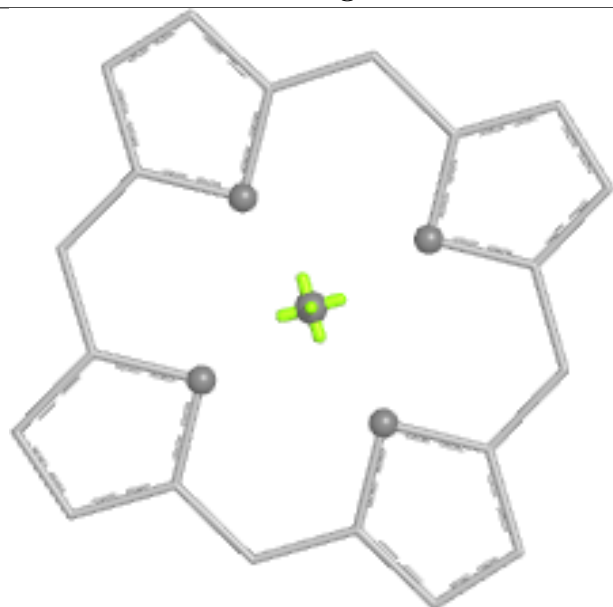
Ligand CHL A 263



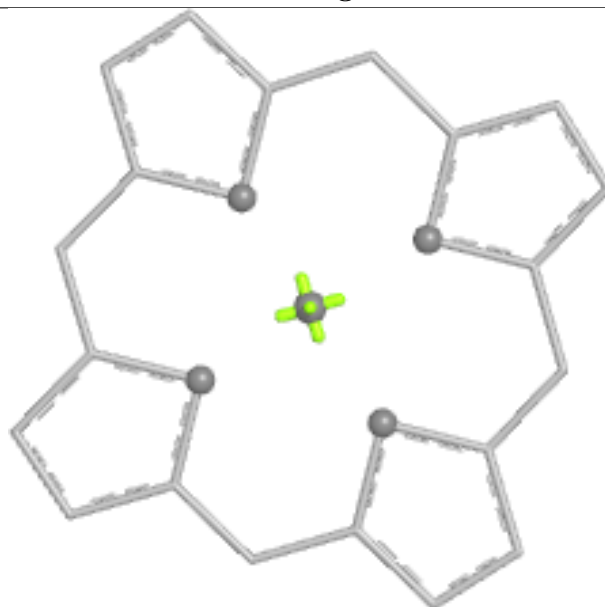
Bond lengths



Bond angles

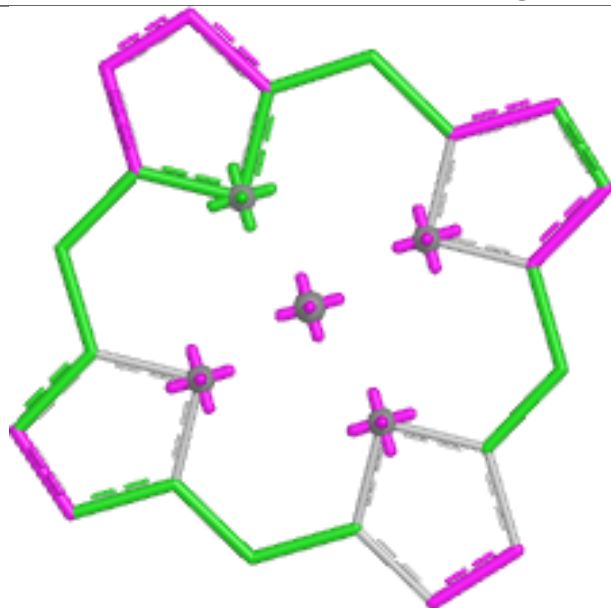


Torsions

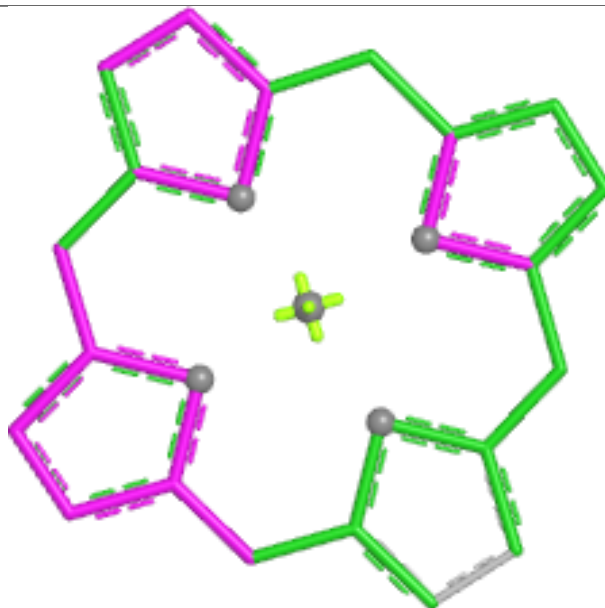


Rings

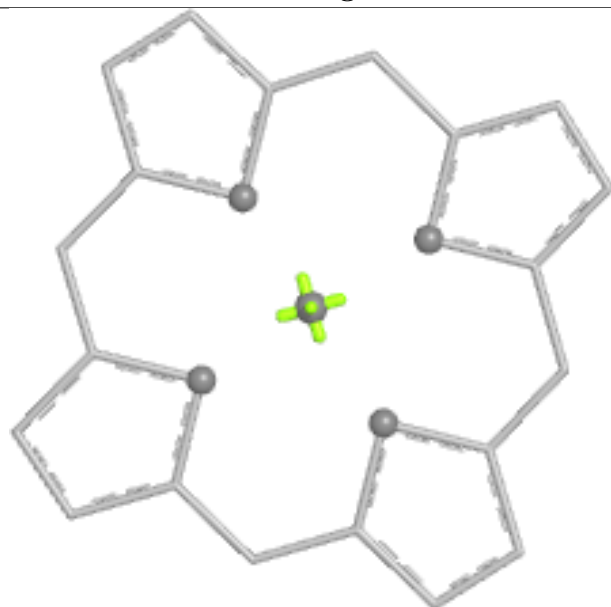
Ligand CHL A 261



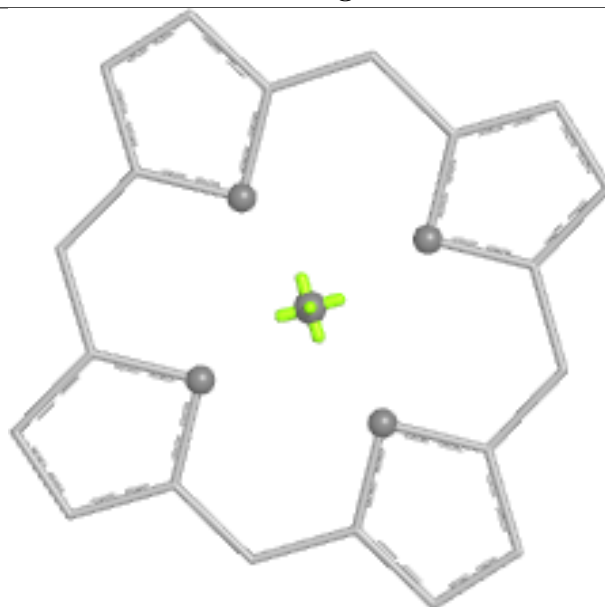
Bond lengths



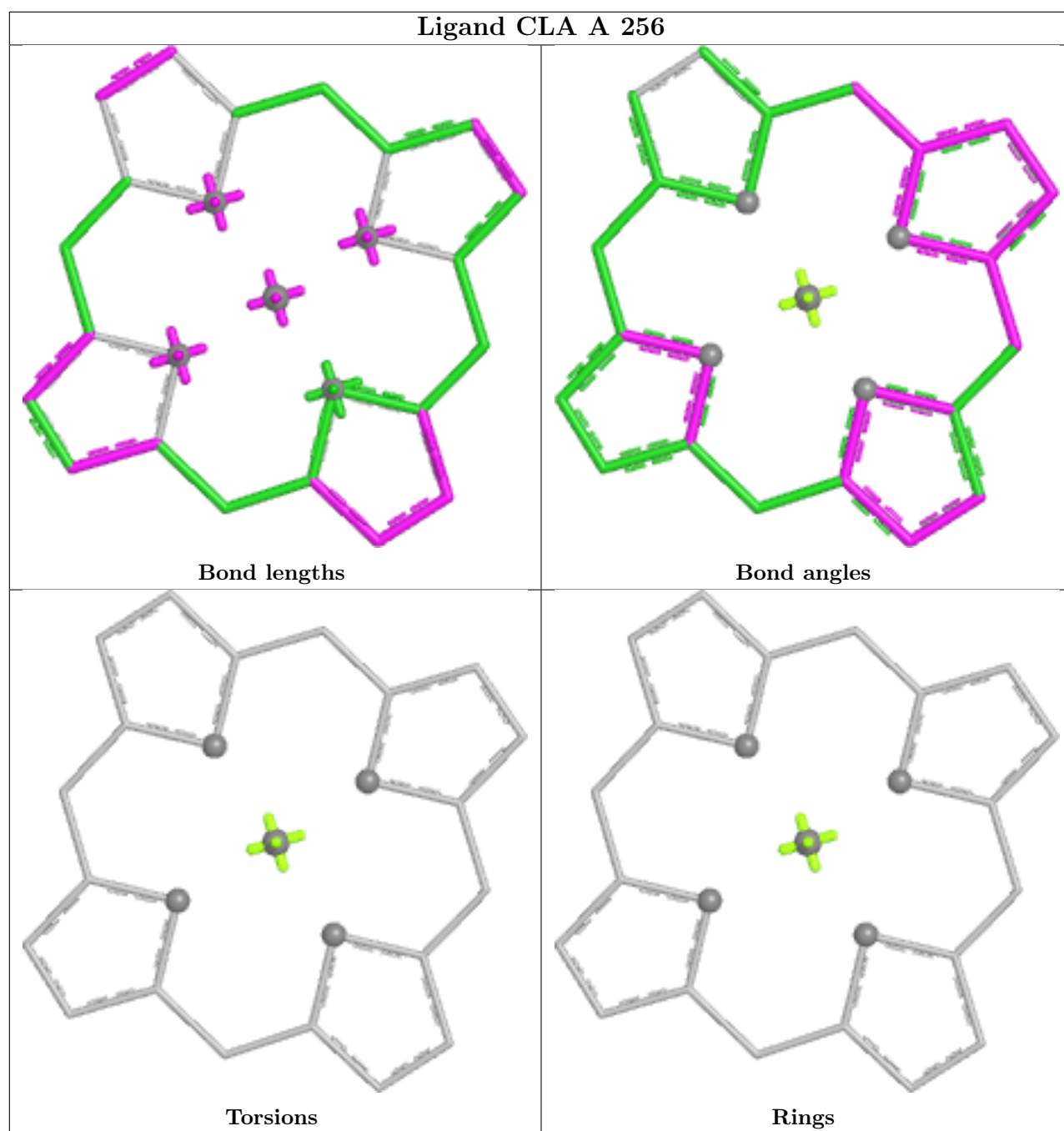
Bond angles



Torsions



Rings



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	101/232 (43%)	-0.36	7 (6%) 23 28	295, 297, 297, 297	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	56	GLU	4.6
1	A	85	LEU	4.0
1	A	89	GLY	4.0
1	A	213	LEU	2.5
1	A	84	LEU	2.5

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

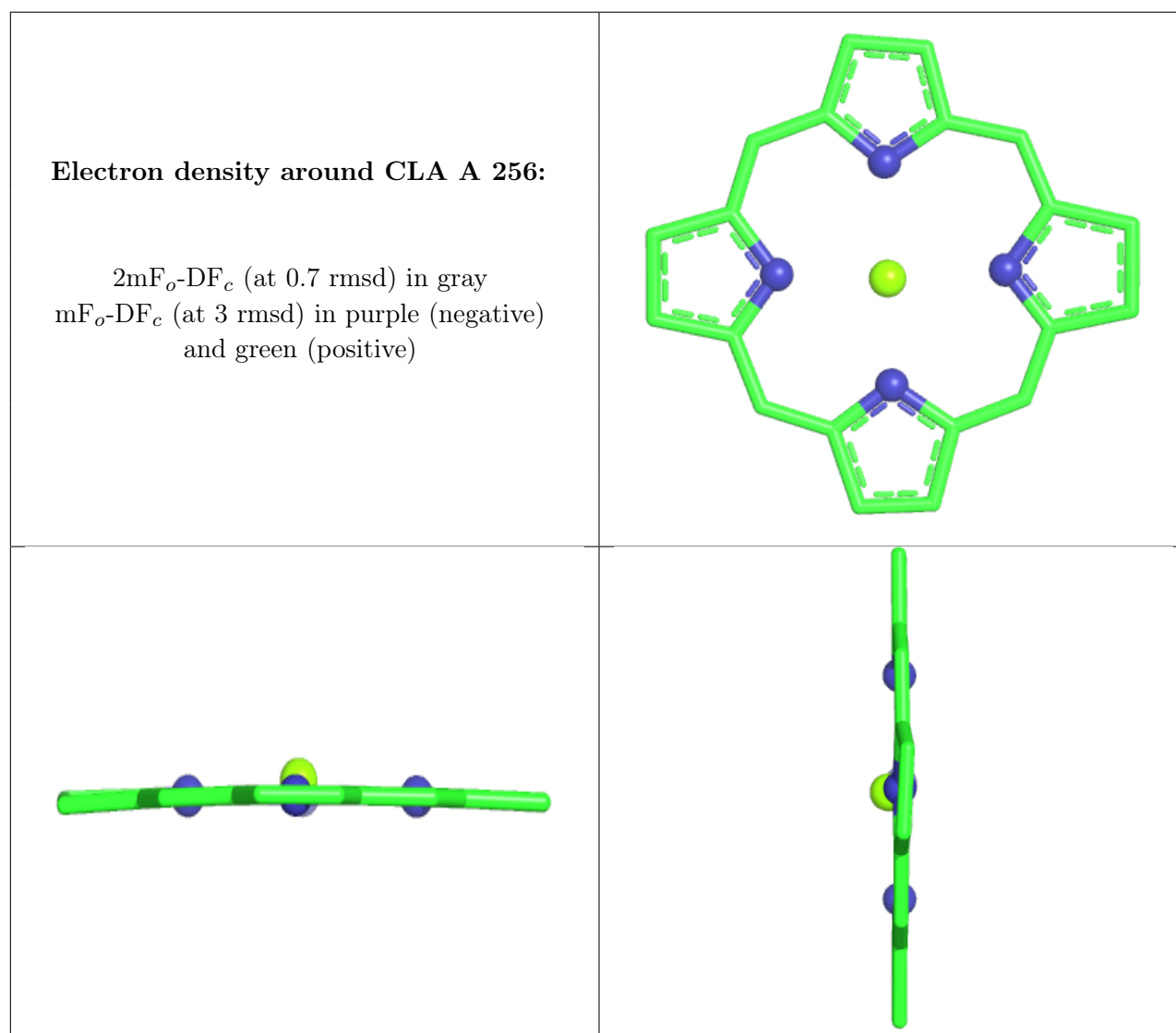
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	CLA	A	256	25/65	0.94	0.12	294,296,296,296	0
2	CLA	A	255	25/65	0.97	0.09	296,296,296,296	0

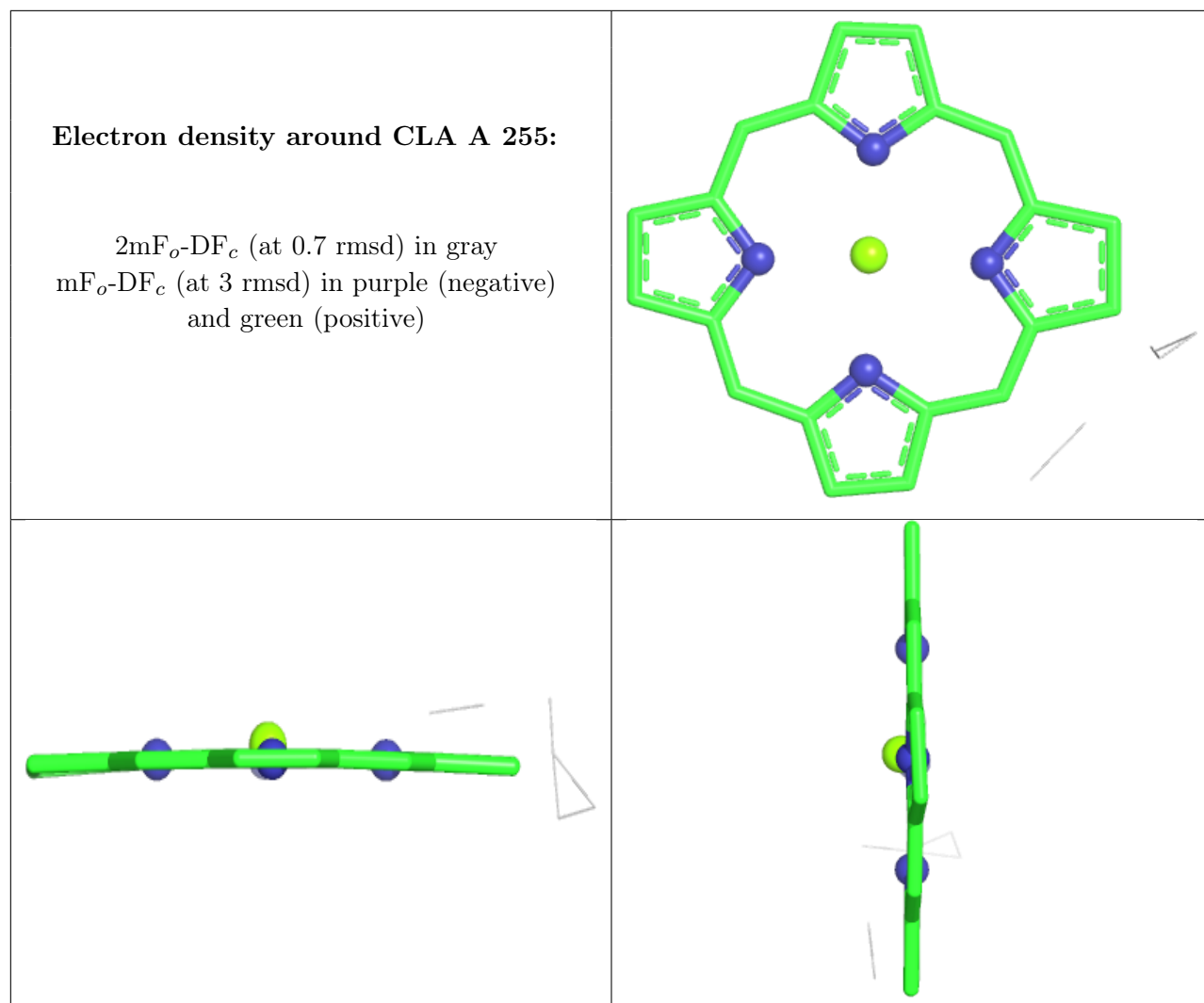
Continued on next page...

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	CHL	A	262	25/66	0.97	0.09	295,296,296,296	0
3	CHL	A	265	25/66	0.97	0.07	296,296,296,296	0
3	CHL	A	266	25/66	0.97	0.11	295,296,296,296	0
3	CHL	A	263	25/66	0.98	0.07	294,296,296,296	0
3	CHL	A	261	25/66	0.98	0.07	295,296,296,296	0
2	CLA	A	251	25/65	0.98	0.11	293,296,296,296	0
2	CLA	A	257	25/65	0.99	0.08	296,296,296,296	0
2	CLA	A	252	25/65	0.99	0.06	295,296,296,296	0
2	CLA	A	254	25/65	0.99	0.07	294,296,296,296	0
2	CLA	A	253	25/65	1.00	0.03	295,296,296,296	0

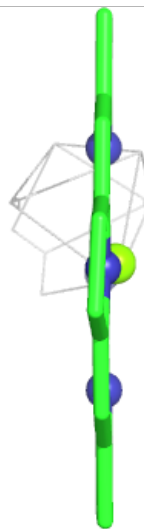
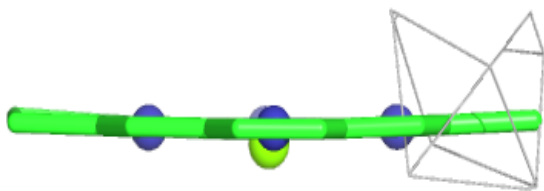
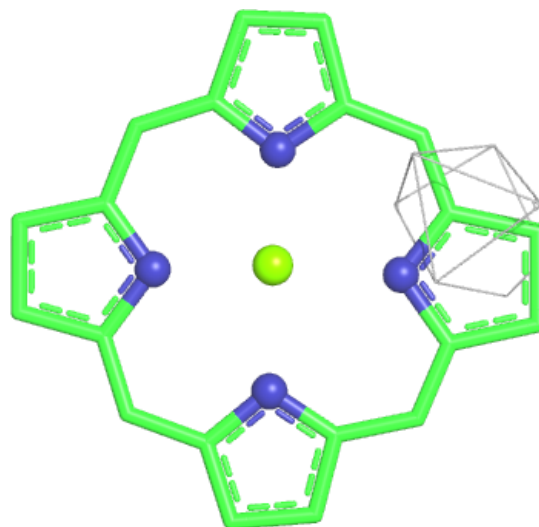
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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





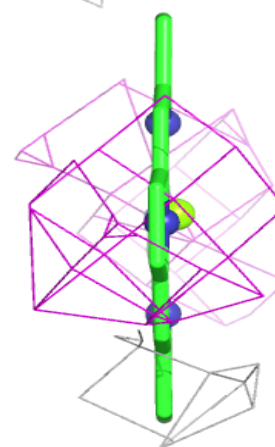
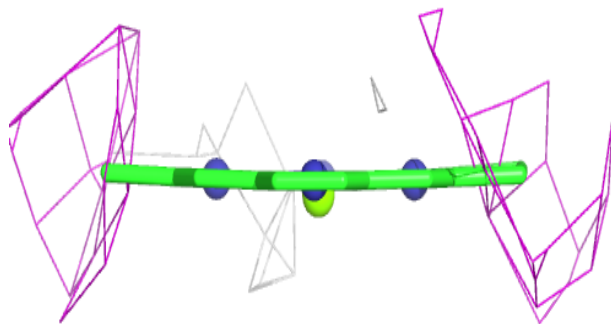
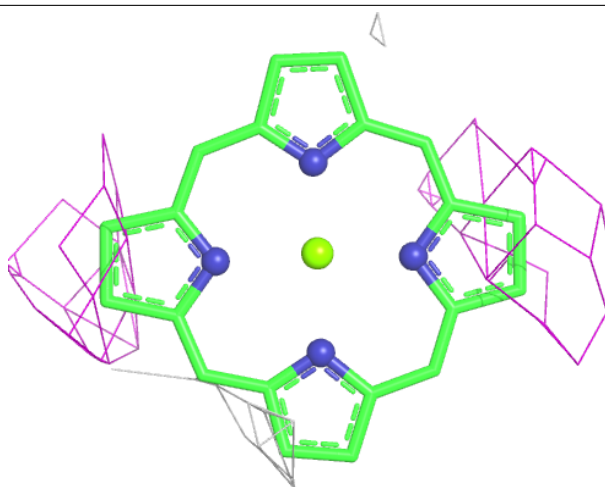
Electron density around CHL A 262:

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



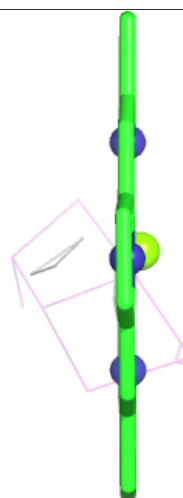
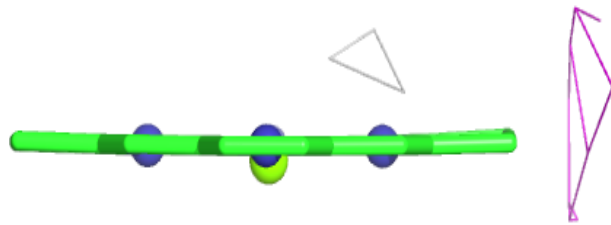
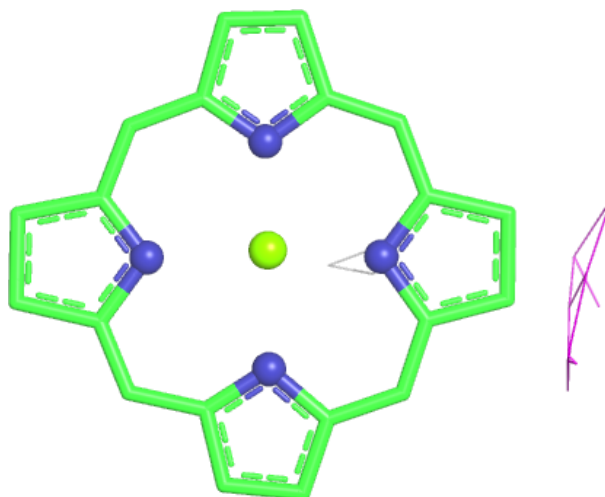
Electron density around CHL A 265:

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



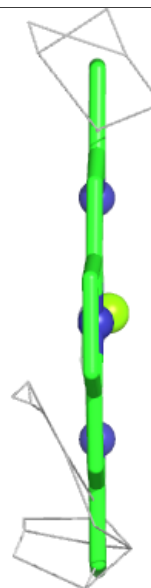
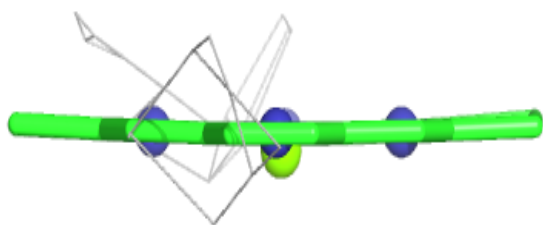
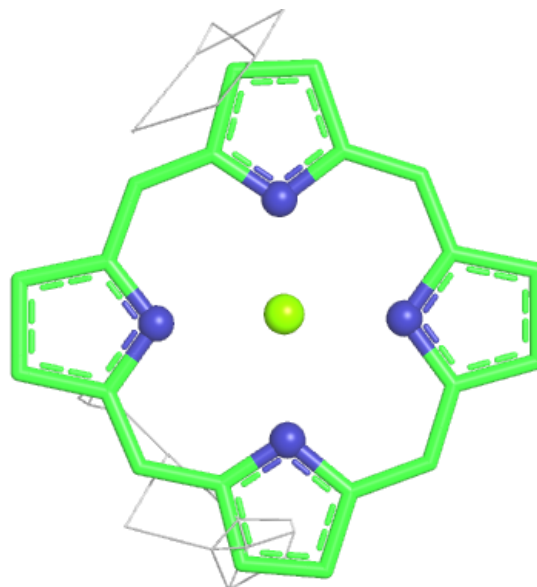
Electron density around CHL A 266:

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



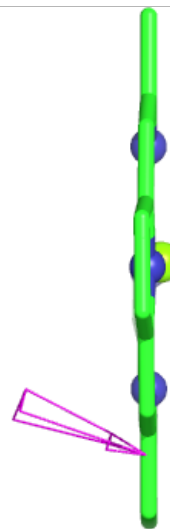
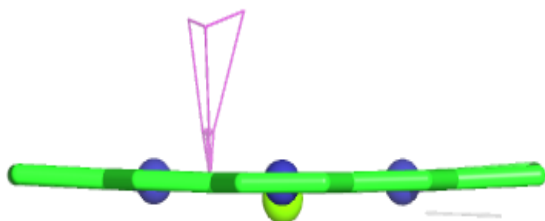
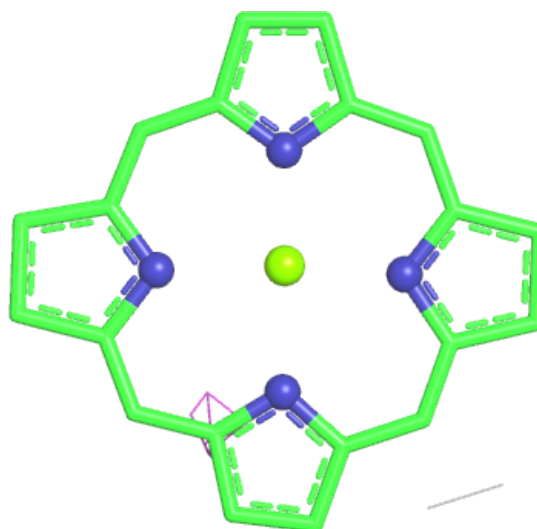
Electron density around CHL A 263:

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



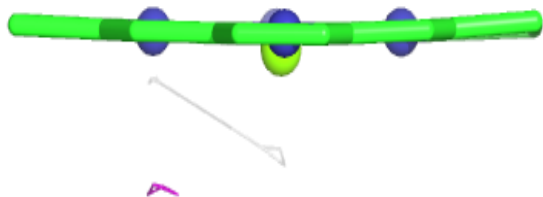
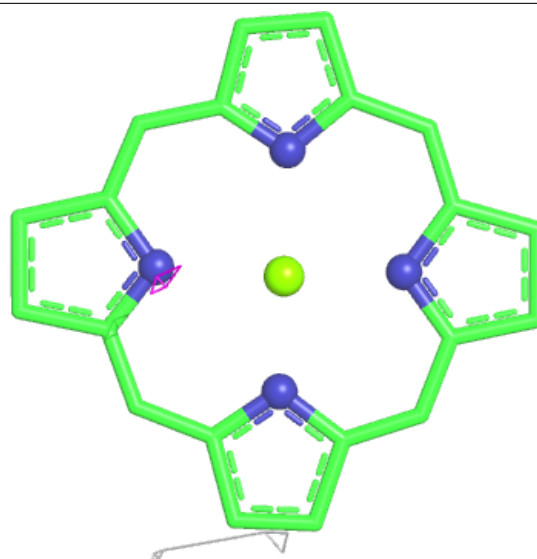
Electron density around CHL A 261:

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



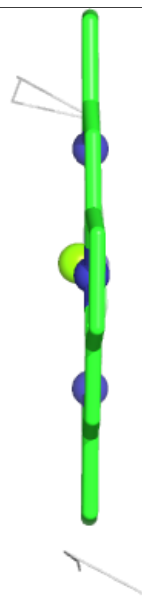
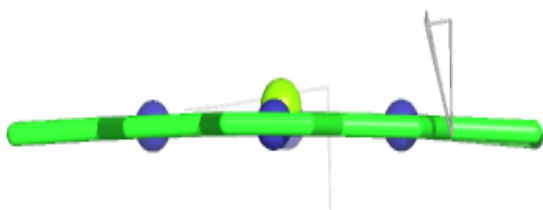
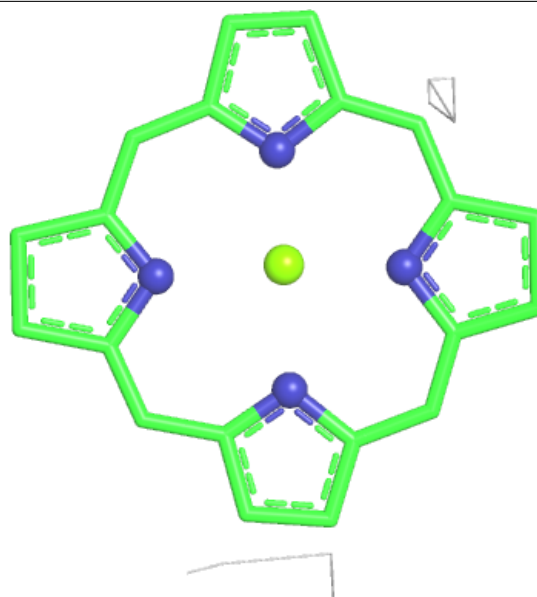
Electron density around CLA A 251:

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



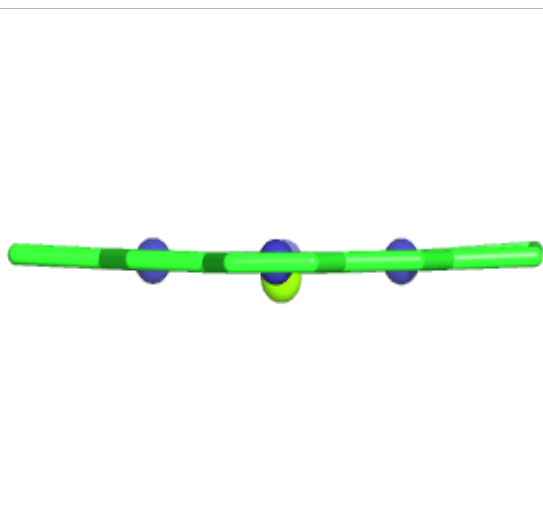
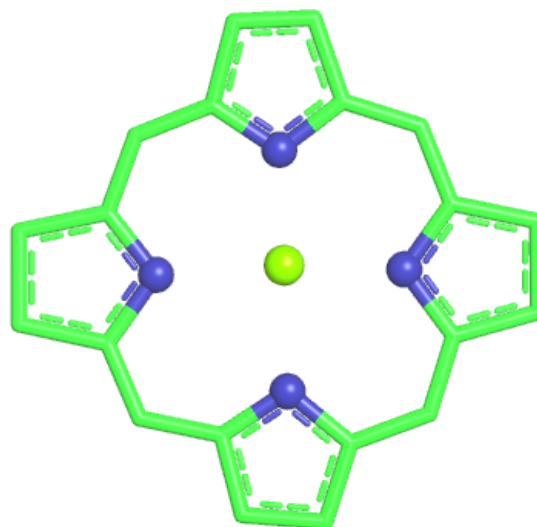
Electron density around CLA A 257:

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



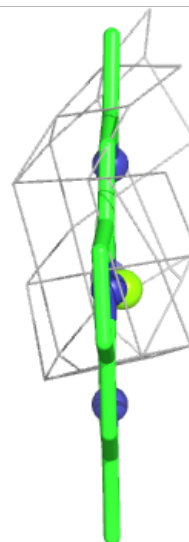
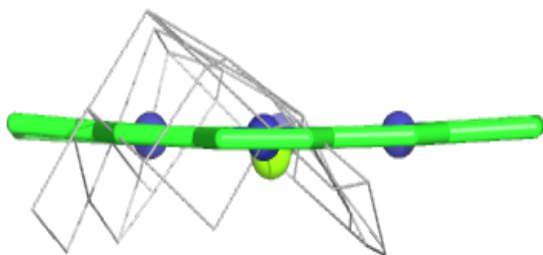
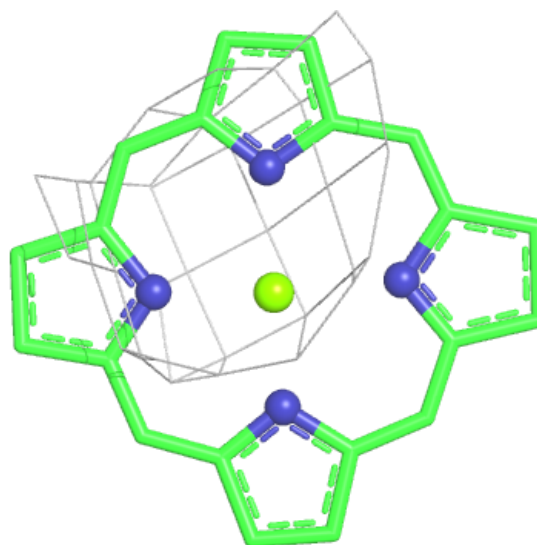
Electron density around CLA A 252:

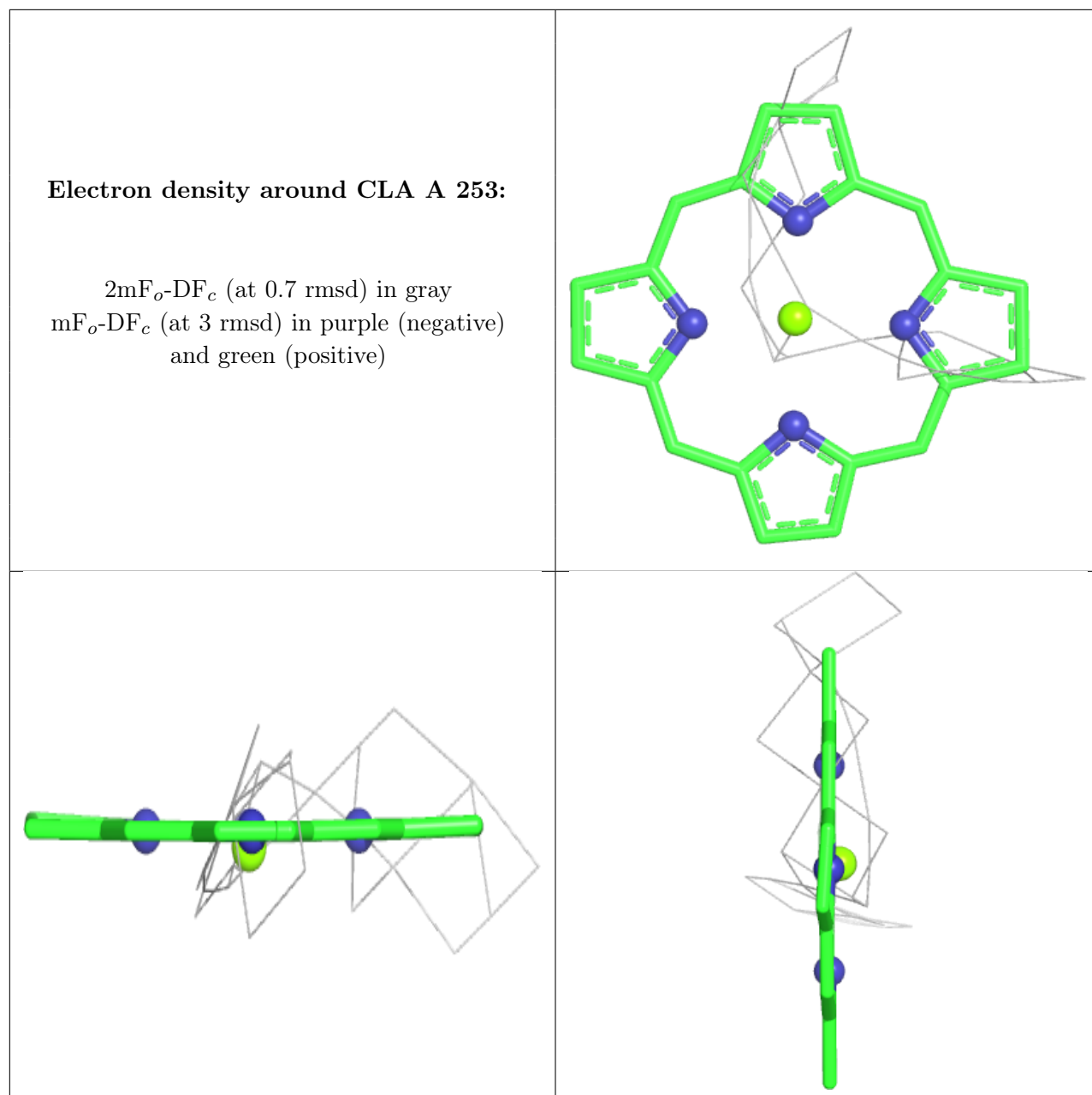
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around CLA A 254:

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





6.5 Other polymers ⓘ

There are no such residues in this entry.