



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 4, 2026 – 10:19 PM EDT

PDB ID : 2PPS / pdb_00002pps
Title : PHOTOSYNTHETIC REACTION CENTER AND CORE ANTENNA SYSTEM (TRIMERIC), ALPHA CARBON ONLY
Authors : Krauss, N.; Schubert, W.-D.; Klukas, O.; Fromme, P.; Witt, H.T.; Saenger, W.
Deposited on : 1997-05-27
Resolution : 4.00 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

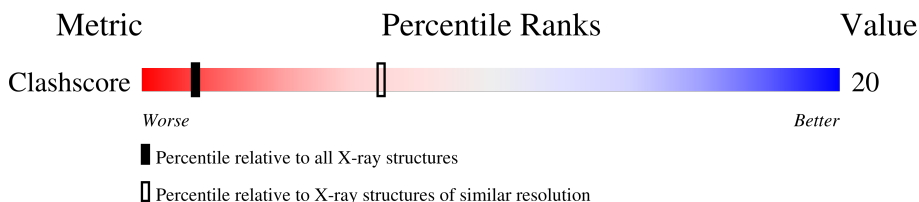
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.00 Å.

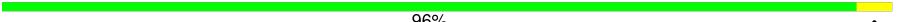
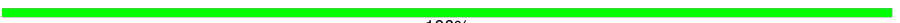
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1129 (4.20-3.80)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	478	 96% .
2	B	503	 96% .
3	L	111	 100%
4	K	64	 95% 5%
5	F	130	 99% .
6	C	80	 92% 8%

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
9	SF4	B	2008	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 3616 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 PHOTOSYSTEM I.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
1	A	478	Total C 478 478	0	0	478

- Molecule 2 is a protein called PHOTOSYSTEM I.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	B	503	Total C 503 503	0	0	503

- Molecule 3 is a protein called PHOTOSYSTEM I.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
3	L	111	Total C 111 111	0	0	111

- Molecule 4 is a protein called PHOTOSYSTEM I.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
4	K	64	Total C 64 64	0	0	64

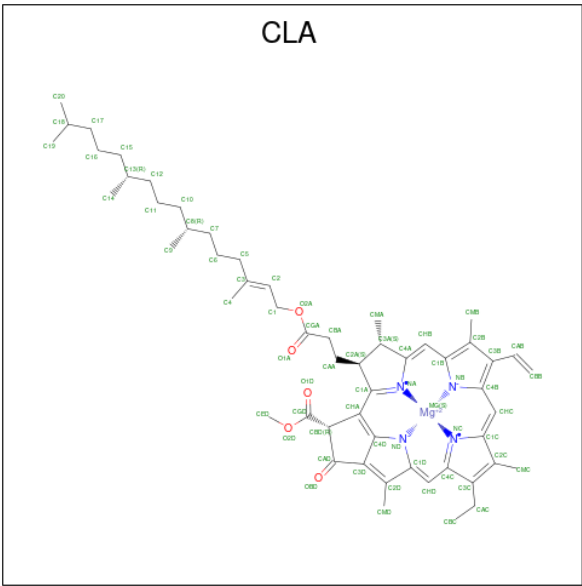
- Molecule 5 is a protein called PHOTOSYSTEM I.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
5	F	130	Total C 130 130	0	0	130

- Molecule 6 is a protein called PHOTOSYSTEM I.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
6	C	80	Total C 80 80	0	0	80

- Molecule 7 is CHLOROPHYLL A (CCD ID: CLA) (formula: C₅₅H₇₂MgN₄O₅).



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

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

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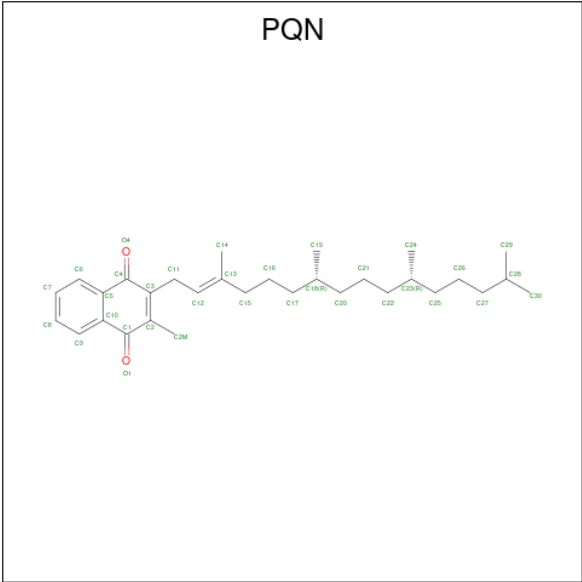
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	B	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	B	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	B	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	B	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	B	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	B	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	B	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	B	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	B	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	B	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	B	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	B	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	B	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	B	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	L	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	L	1	Total	C	Mg	N	0	0
			25	20	1	4		

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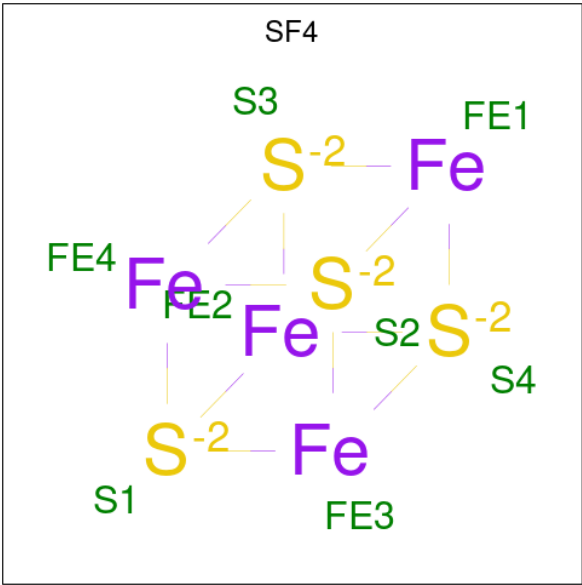
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	L	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	L	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	K	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	K	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	F	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	F	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	F	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	F	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	F	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	F	1	Total	C	Mg	N	0	0
			25	20	1	4		
7	F	1	Total	C	Mg	N	0	0
			25	20	1	4		

- Molecule 8 is PHYLLOQUINONE (CCD ID: PQN) (formula: C₃₁H₄₆O₂).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total	C	0	0
			1	1		

- Molecule 9 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



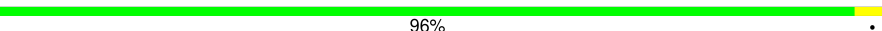
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	Fe	S	0	0
			8	4	4		
9	C	1	Total	Fe	S	0	0
			8	4	4		
9	C	1	Total	Fe	S	0	0
			8	4	4		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

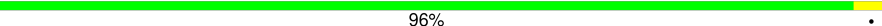
Note EDS was not executed.

- Molecule 1: PHOTOSYSTEM I

Chain A:  96%

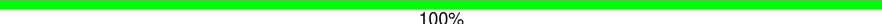


- Molecule 2: PHOTOSYSTEM I

Chain B:  96%

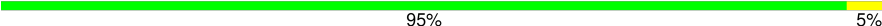


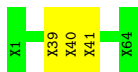
- Molecule 3: PHOTOSYSTEM I

Chain L:  100%

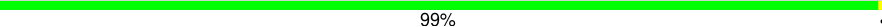
There are no outlier residues recorded for this chain.

- Molecule 4: PHOTOSYSTEM I

Chain K:  95% 5%



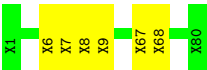
- Molecule 5: PHOTOSYSTEM I

Chain F:  99%



- Molecule 6: PHOTOSYSTEM I

Chain C:  92% 8%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	286.00Å 286.00Å 167.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) – 4.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-4.00)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	0.10	Depositor
Refinement program		Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3616	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

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: CLA, SF4, PQN

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

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	478	0	0	16	0
2	B	503	0	0	16	0
3	L	111	0	0	0	0
4	K	64	0	0	2	0
5	F	130	0	0	1	0
6	C	80	0	0	4	0
7	A	1000	0	120	41	0
7	B	850	0	102	12	0
7	F	225	0	27	8	0
7	K	50	0	6	0	0
7	L	100	0	12	0	0
8	B	1	0	0	0	0
9	B	8	0	0	3	0
9	C	16	0	0	0	0
All	All	3616	0	267	78	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 20.

The worst 5 of 78 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)
7:A:3014:CLA:HHC	7:A:3029:CLA:C3D	1.61	1.31
1:A:94:UNK:CA	1:A:107:UNK:CA	2.11	1.29
2:B:470:UNK:CA	2:B:474:UNK:CA	2.12	1.27
1:A:295:UNK:CA	7:A:3016:CLA:C3C	2.19	1.20
2:B:428:UNK:CA	7:B:2005:CLA:C3A	2.20	1.20

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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 [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 93 ligands modelled in this entry, 1 is modelled with single atom - leaving 92 for Mogul analysis.

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
7	CLA	A	2502	-	24,32,73	2.88	7 (29%)	31,54,113	2.34	8 (25%)
7	CLA	B	3063	-	24,32,73	2.89	8 (33%)	31,54,113	2.34	8 (25%)
7	CLA	B	3020	-	24,32,73	2.89	7 (29%)	31,54,113	2.35	8 (25%)
7	CLA	A	3009	-	24,32,73	2.87	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	B	3081	-	24,32,73	2.88	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	L	3064	-	24,32,73	3.07	9 (37%)	31,54,113	2.38	8 (25%)
7	CLA	B	3042	-	24,32,73	2.87	7 (29%)	31,54,113	2.33	8 (25%)
7	CLA	B	3003	-	24,32,73	2.89	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	A	3052	-	24,32,73	2.88	8 (33%)	31,54,113	2.34	8 (25%)
7	CLA	L	3036	-	24,32,73	2.89	8 (33%)	31,54,113	2.34	8 (25%)
7	CLA	A	3067	-	24,32,73	2.87	7 (29%)	31,54,113	2.33	8 (25%)
7	CLA	B	3069	-	24,32,73	2.88	7 (29%)	31,54,113	2.35	8 (25%)
7	CLA	A	3018	-	24,32,73	2.87	8 (33%)	31,54,113	2.34	8 (25%)
7	CLA	A	3014	-	24,32,73	3.08	9 (37%)	31,54,113	2.38	8 (25%)
7	CLA	A	3026	-	24,32,73	2.89	8 (33%)	31,54,113	2.36	8 (25%)
7	CLA	F	3061	-	24,32,73	2.90	7 (29%)	31,54,113	2.36	8 (25%)
7	CLA	A	3071	-	24,32,73	2.88	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	B	2501	-	24,32,73	2.90	8 (33%)	31,54,113	2.36	8 (25%)
7	CLA	B	2003	-	24,32,73	3.02	7 (29%)	31,54,113	2.35	8 (25%)
7	CLA	B	3011	-	24,32,73	2.89	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	A	3065	-	24,32,73	2.88	8 (33%)	31,54,113	2.34	8 (25%)
7	CLA	B	3066	-	24,32,73	2.88	7 (29%)	31,54,113	2.35	8 (25%)
7	CLA	F	3031	-	24,32,73	2.86	7 (29%)	31,54,113	2.32	8 (25%)
7	CLA	A	3017	-	24,32,73	2.88	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	B	3074	-	24,32,73	2.89	7 (29%)	31,54,113	2.36	8 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	CLA	A	3062	-	24,32,73	2.89	8 (33%)	31,54,113	2.33	8 (25%)
7	CLA	A	3047	-	24,32,73	2.89	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	F	3002	-	24,32,73	2.89	8 (33%)	31,54,113	2.36	8 (25%)
7	CLA	A	3029	-	24,32,73	2.89	8 (33%)	31,54,113	2.36	8 (25%)
7	CLA	F	3033	-	24,32,73	2.87	8 (33%)	31,54,113	2.33	8 (25%)
7	CLA	B	3008	-	24,32,73	2.87	7 (29%)	31,54,113	2.34	8 (25%)
7	CLA	A	3032	-	24,32,73	2.88	8 (33%)	31,54,113	2.34	8 (25%)
7	CLA	B	3076	-	24,32,73	2.87	8 (33%)	31,54,113	2.34	8 (25%)
7	CLA	A	3013	-	24,32,73	2.88	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	A	3016	-	24,32,73	2.88	7 (29%)	31,54,113	2.36	8 (25%)
7	CLA	B	3035	-	24,32,73	2.87	7 (29%)	31,54,113	2.34	8 (25%)
7	CLA	L	3038	-	24,32,73	2.86	7 (29%)	31,54,113	2.33	8 (25%)
7	CLA	A	3005	-	24,32,73	2.88	8 (33%)	31,54,113	2.34	8 (25%)
7	CLA	B	3025	-	24,32,73	2.87	8 (33%)	31,54,113	2.34	8 (25%)
7	CLA	A	3027	-	24,32,73	2.88	8 (33%)	31,54,113	2.36	8 (25%)
7	CLA	B	2002	-	24,32,73	2.90	8 (33%)	31,54,113	2.33	8 (25%)
7	CLA	F	3012	-	24,32,73	2.88	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	B	3001	-	24,32,73	2.89	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	A	3053	-	24,32,73	2.89	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	A	3021	-	24,32,73	2.88	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	K	3050	-	24,32,73	2.87	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	B	3006	-	24,32,73	2.88	8 (33%)	31,54,113	2.36	8 (25%)
7	CLA	A	3072	-	24,32,73	2.89	8 (33%)	31,54,113	2.36	8 (25%)
7	CLA	A	3057	-	24,32,73	2.88	7 (29%)	31,54,113	2.34	8 (25%)
7	CLA	B	3055	-	24,32,73	2.88	8 (33%)	31,54,113	2.33	8 (25%)
7	CLA	B	3034	-	24,32,73	2.87	7 (29%)	31,54,113	2.35	8 (25%)
7	CLA	F	3022	-	24,32,73	2.89	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	A	3077	-	24,32,73	2.88	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	B	3015	-	24,32,73	2.88	8 (33%)	31,54,113	2.36	8 (25%)
7	CLA	F	3059	-	24,32,73	2.88	8 (33%)	31,54,113	2.34	8 (25%)
7	CLA	F	3054	-	24,32,73	2.89	7 (29%)	31,54,113	2.36	8 (25%)
7	CLA	B	3046	-	24,32,73	2.88	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	A	3030	-	24,32,73	2.88	8 (33%)	31,54,113	2.34	8 (25%)
7	CLA	A	3073	-	24,32,73	2.88	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	A	2001	-	24,32,73	3.02	7 (29%)	31,54,113	2.35	8 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	CLA	K	3051	-	24,32,73	2.88	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	B	3075	-	24,32,73	2.87	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	A	3045	-	24,32,73	2.88	7 (29%)	31,54,113	2.35	8 (25%)
7	CLA	A	3058	-	24,32,73	2.90	8 (33%)	31,54,113	2.36	8 (25%)
7	CLA	B	3019	-	24,32,73	2.88	8 (33%)	31,54,113	2.34	8 (25%)
7	CLA	B	3037	-	24,32,73	2.88	8 (33%)	31,54,113	2.36	8 (25%)
7	CLA	B	3080	-	24,32,73	2.88	7 (29%)	31,54,113	2.36	8 (25%)
7	CLA	B	3044	-	24,32,73	2.88	7 (29%)	31,54,113	2.35	8 (25%)
7	CLA	A	3024	-	24,32,73	2.88	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	A	3056	-	24,32,73	2.89	8 (33%)	31,54,113	2.36	8 (25%)
7	CLA	A	3040	-	24,32,73	2.88	8 (33%)	31,54,113	2.34	8 (25%)
7	CLA	A	3007	-	24,32,73	2.89	8 (33%)	31,54,113	2.36	8 (25%)
9	SF4	B	2008	-	0,12,12	-	-	-	-	-
7	CLA	B	3023	-	24,32,73	2.88	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	B	2004	-	24,32,73	2.95	8 (33%)	31,54,113	2.34	8 (25%)
7	CLA	B	3028	-	24,32,73	2.89	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	A	3048	-	24,32,73	2.90	7 (29%)	31,54,113	2.36	8 (25%)
7	CLA	B	3060	-	24,32,73	2.88	7 (29%)	31,54,113	2.36	8 (25%)
7	CLA	A	3039	-	24,32,73	2.89	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	A	3041	-	24,32,73	2.89	8 (33%)	31,54,113	2.36	8 (25%)
7	CLA	A	3068	-	24,32,73	2.88	7 (29%)	31,54,113	2.35	8 (25%)
7	CLA	B	2005	-	24,32,73	2.88	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	L	3049	-	24,32,73	2.87	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	A	3079	-	24,32,73	2.88	8 (33%)	31,54,113	2.34	8 (25%)
7	CLA	B	3010	-	24,32,73	2.90	8 (33%)	31,54,113	2.36	8 (25%)
7	CLA	B	3070	-	24,32,73	2.89	7 (29%)	31,54,113	2.35	8 (25%)
7	CLA	F	3004	-	24,32,73	2.88	8 (33%)	31,54,113	2.35	8 (25%)
7	CLA	A	3043	-	24,32,73	2.88	7 (29%)	31,54,113	2.35	8 (25%)
7	CLA	A	2006	-	24,32,73	2.87	8 (33%)	31,54,113	2.34	8 (25%)
9	SF4	C	2009	-	0,12,12	-	-	-	-	-
9	SF4	C	2010	-	0,12,12	-	-	-	-	-
7	CLA	A	3078	-	24,32,73	2.86	7 (29%)	31,54,113	2.32	8 (25%)

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
9	SF4	C	2010	-	-	-	0/6/5/5
9	SF4	B	2008	-	-	-	0/6/5/5
9	SF4	C	2009	-	-	-	0/6/5/5

The worst 5 of 687 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	3014	CLA	C3D-C2D	8.93	1.55	1.35
7	L	3064	CLA	C3D-C2D	8.87	1.55	1.35
7	B	2003	CLA	MG-NB	7.08	2.19	2.05
7	A	2001	CLA	MG-NB	6.85	2.19	2.05
7	B	2501	CLA	C3A-C2A	-6.76	1.35	1.52

The worst 5 of 712 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	F	3061	CLA	C1B-NB-C4B	6.81	111.09	106.31
7	B	3003	CLA	C1B-NB-C4B	6.81	111.09	106.31
7	F	3054	CLA	C1B-NB-C4B	6.80	111.08	106.31
7	B	3060	CLA	C1B-NB-C4B	6.77	111.06	106.31
7	A	3068	CLA	C1B-NB-C4B	6.77	111.06	106.31

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

28 monomers are involved in 57 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	3020	CLA	1	0
7	B	3003	CLA	2	0
7	B	3069	CLA	1	0
7	A	3018	CLA	1	0
7	A	3014	CLA	8	0
7	A	3026	CLA	1	0
7	A	3071	CLA	4	0
7	B	3011	CLA	2	0
7	F	3031	CLA	1	0
7	A	3017	CLA	1	0
7	F	3002	CLA	5	0
7	A	3029	CLA	10	0

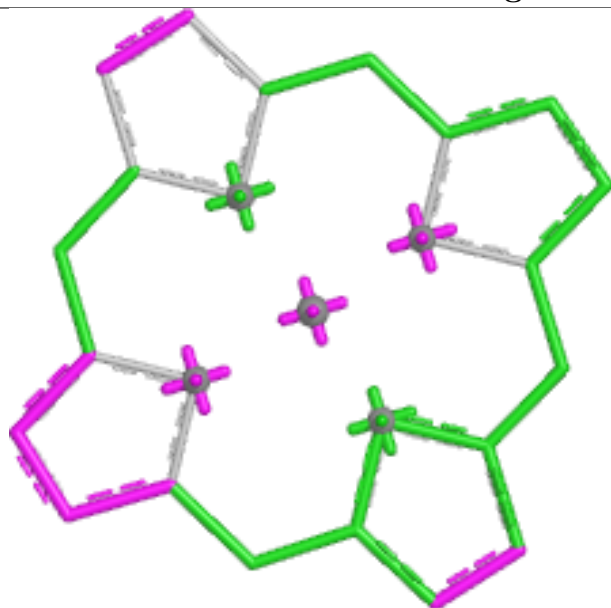
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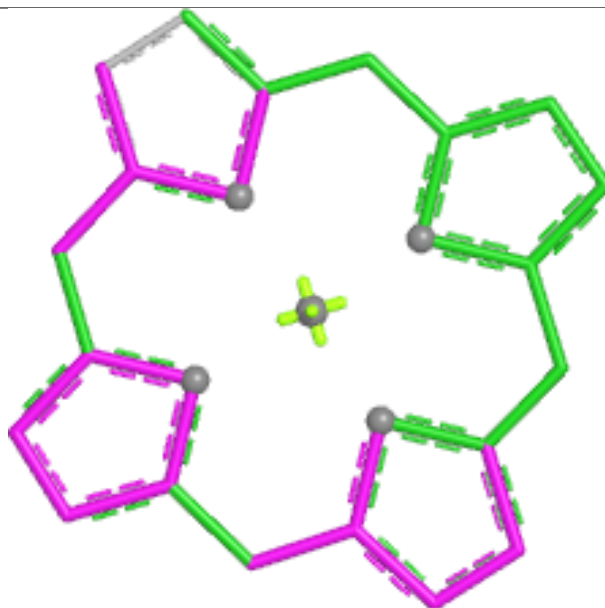
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	3016	CLA	6	0
7	A	3005	CLA	3	0
7	A	3027	CLA	10	0
7	F	3012	CLA	2	0
7	B	3001	CLA	2	0
7	B	3006	CLA	2	0
7	A	3057	CLA	3	0
7	B	3034	CLA	2	0
7	A	3030	CLA	1	0
7	A	3024	CLA	9	0
7	A	3056	CLA	3	0
7	A	3007	CLA	5	0
9	B	2008	SF4	3	0
7	A	3039	CLA	3	0
7	B	2005	CLA	4	0
7	A	3079	CLA	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.

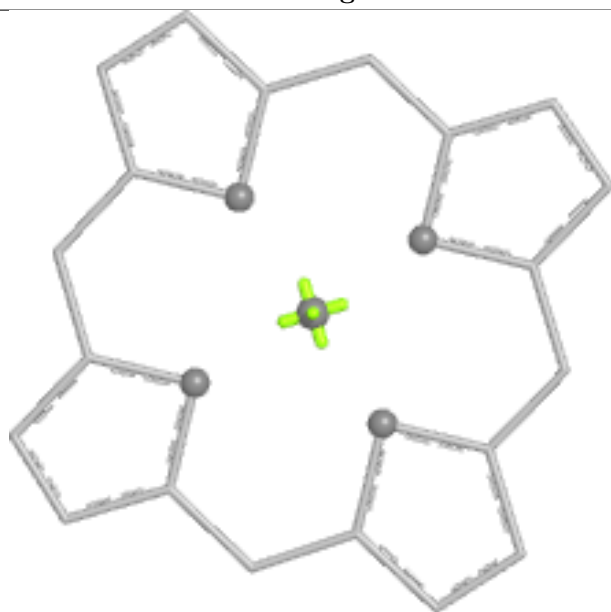
Ligand CLA A 2502



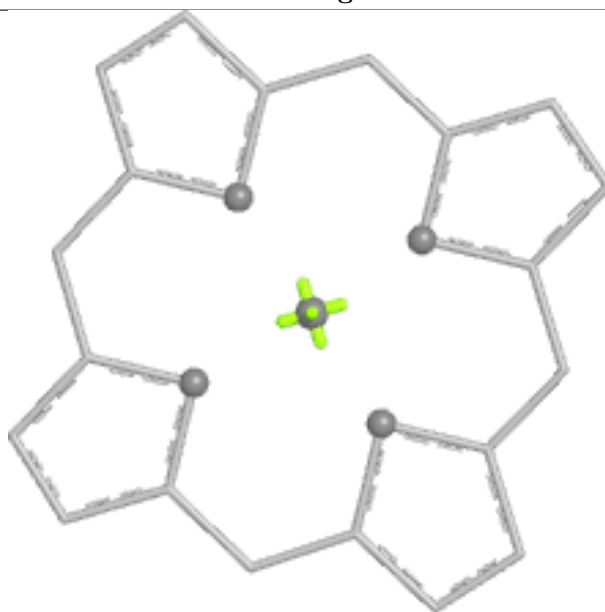
Bond lengths



Bond angles

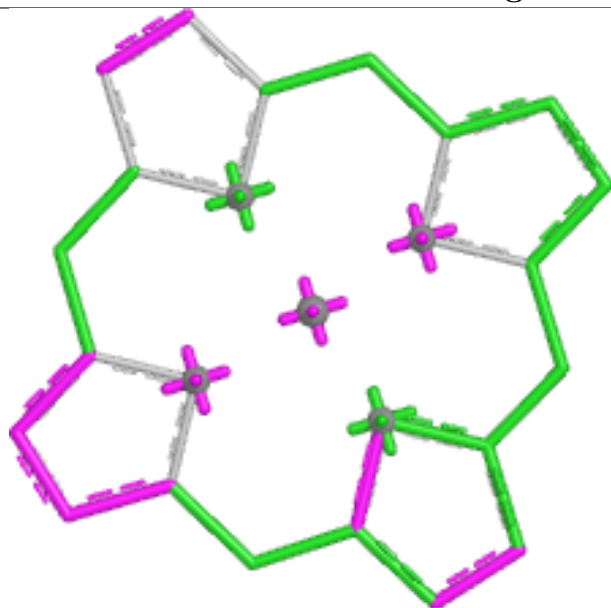


Torsions

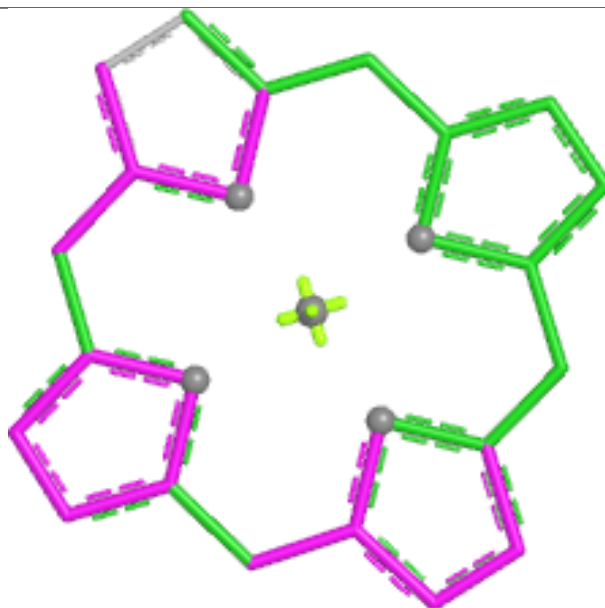


Rings

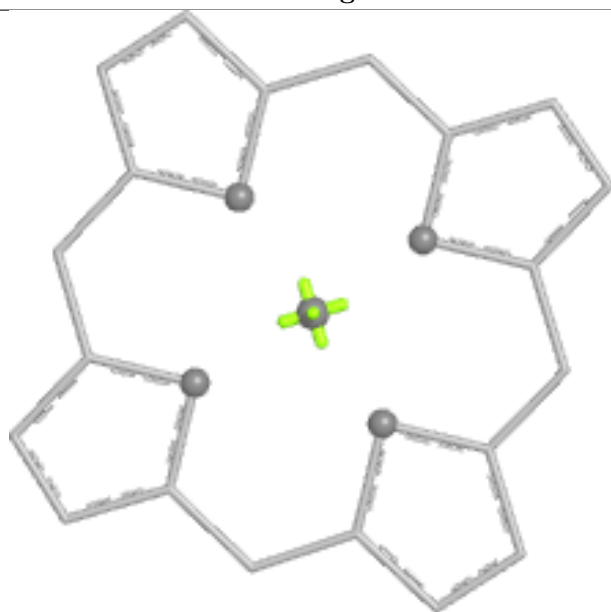
Ligand CLA B 3063



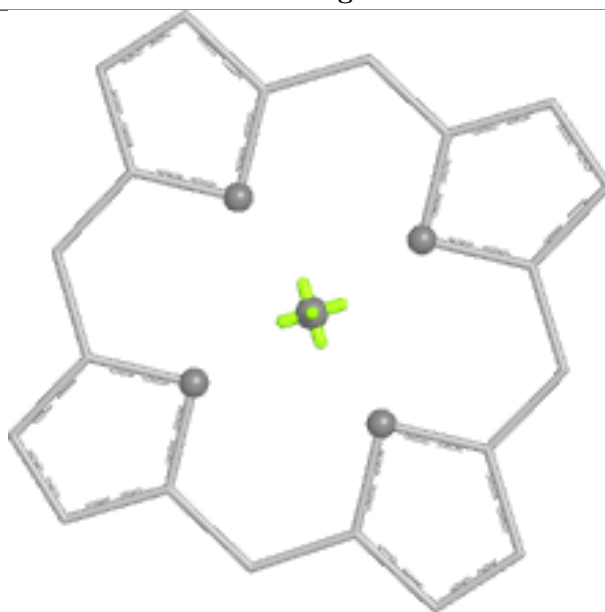
Bond lengths



Bond angles

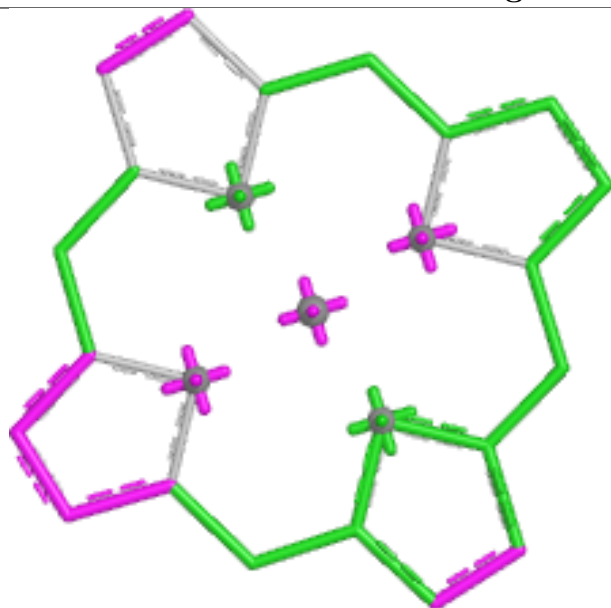


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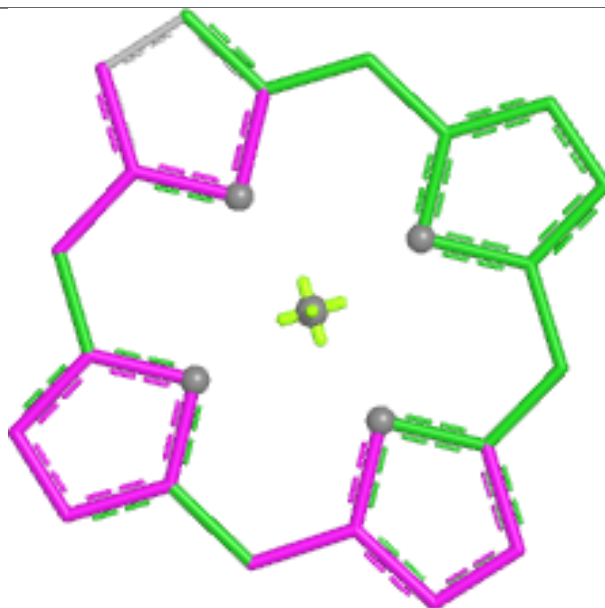


Rings

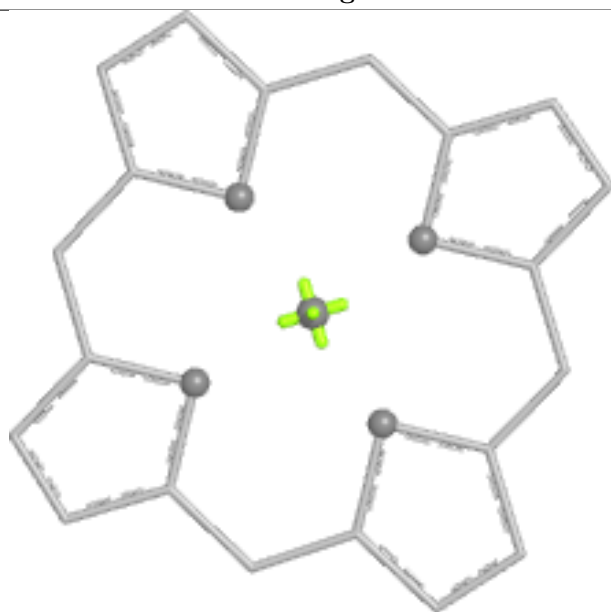
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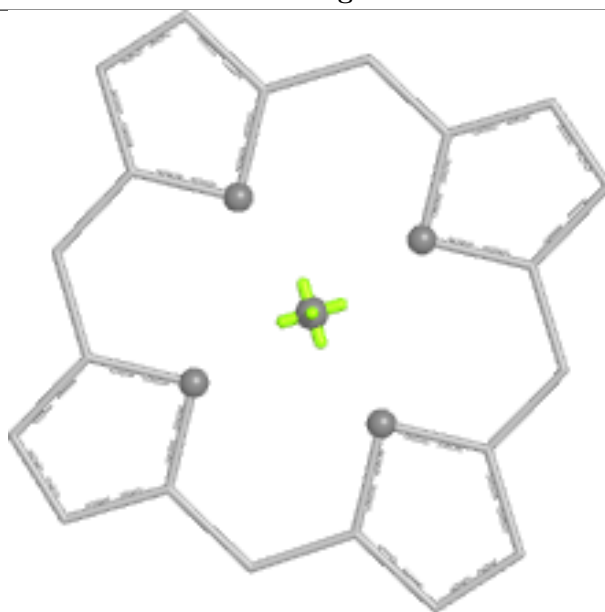
Bond lengths



Bond angles

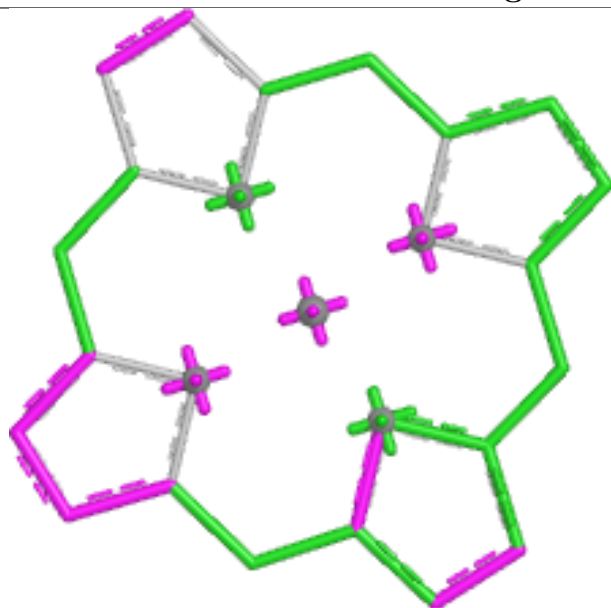


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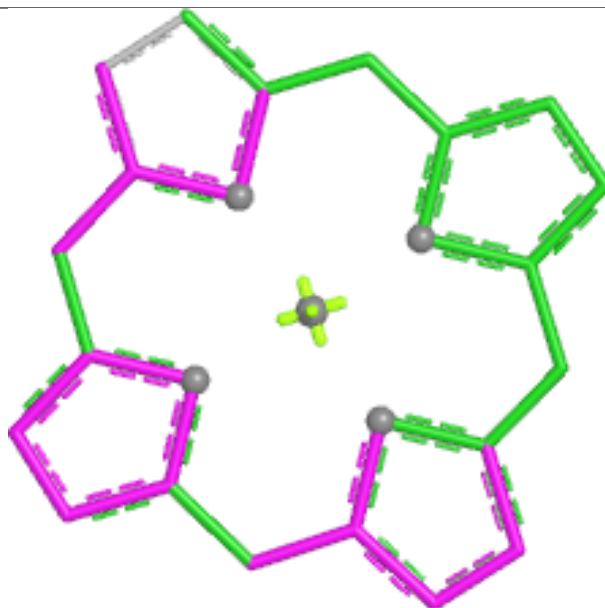


Rings

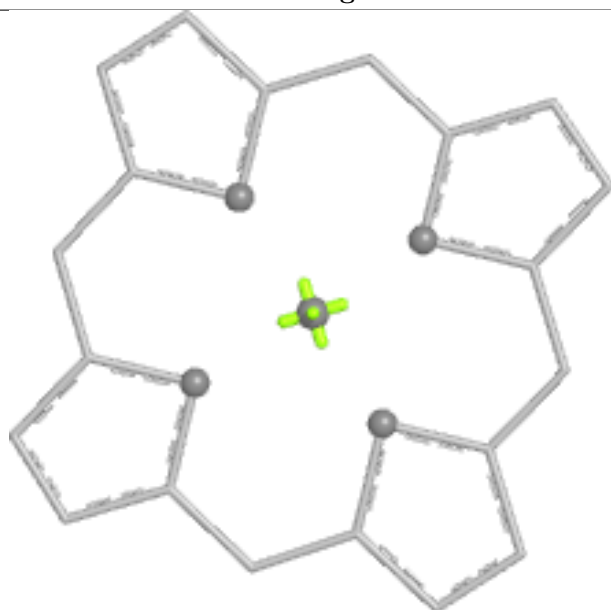
Ligand CLA A 3009



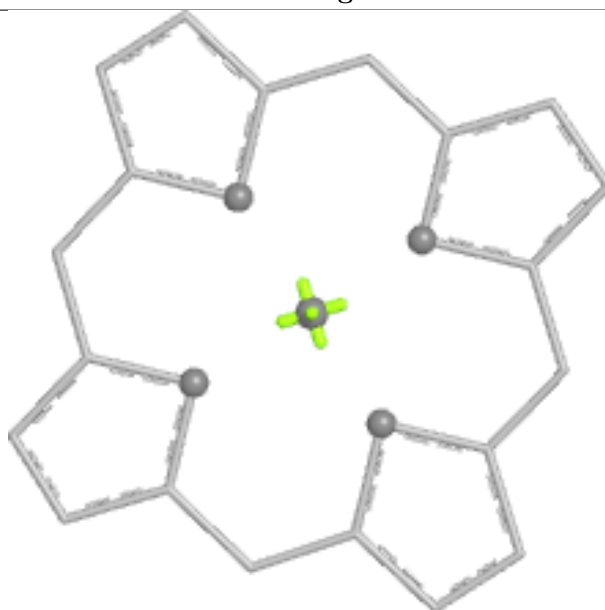
Bond lengths



Bond angles

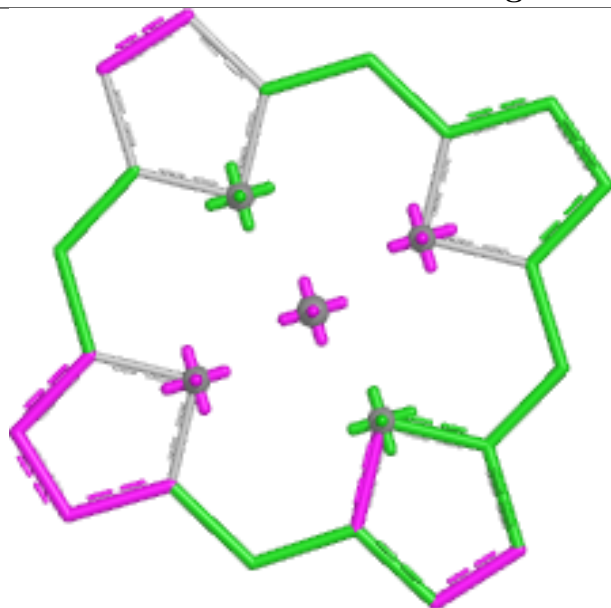


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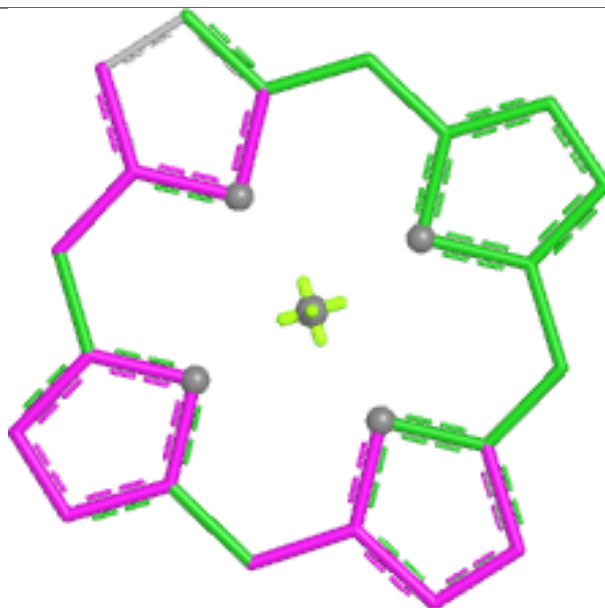


Rings

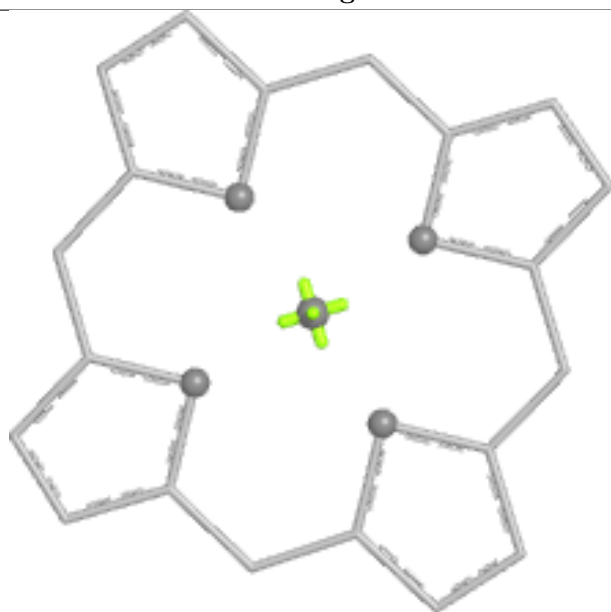
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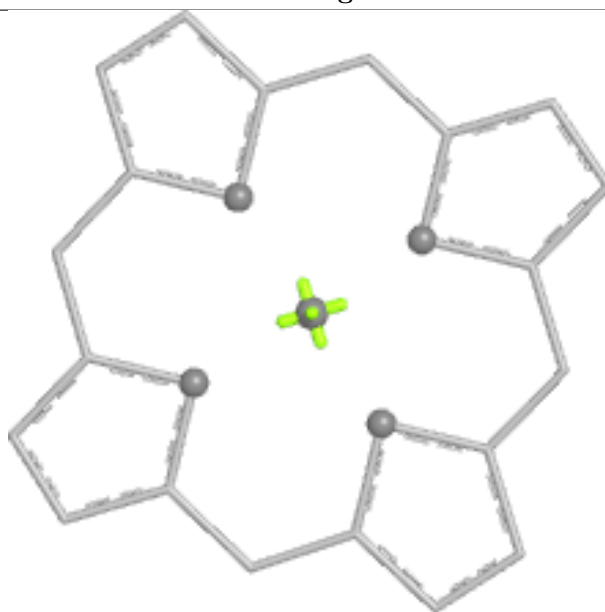
Bond lengths



Bond angles

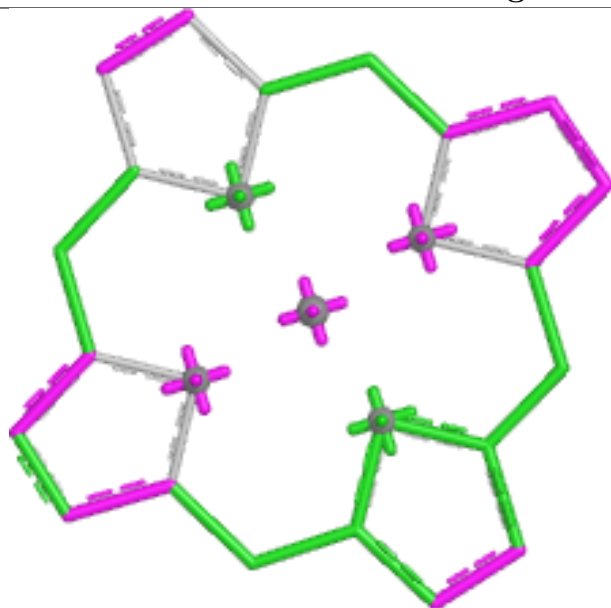


Torsions

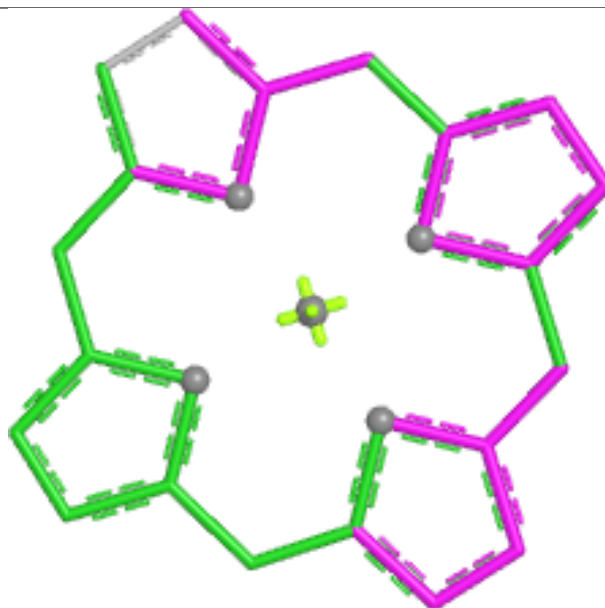


Rings

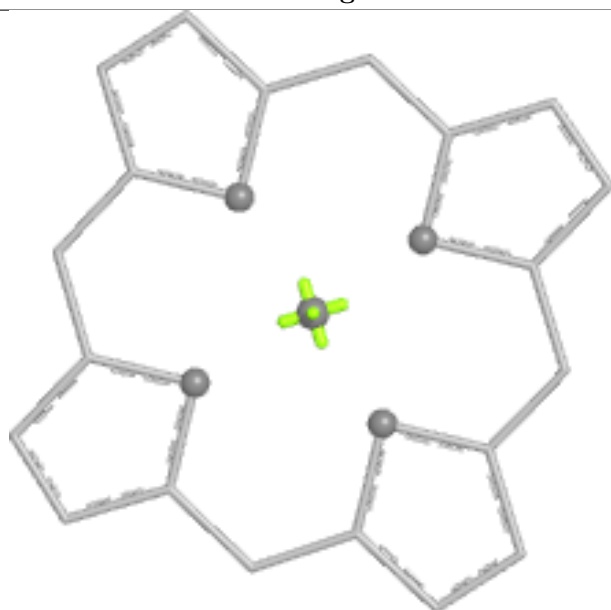
Ligand CLA L 3064



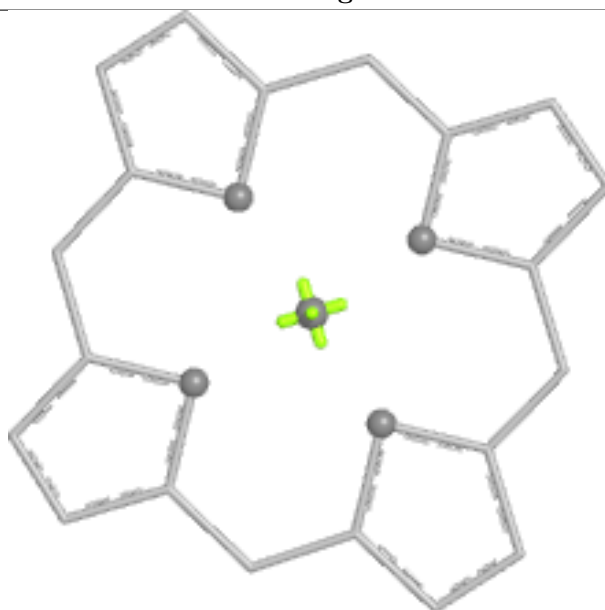
Bond lengths



Bond angles

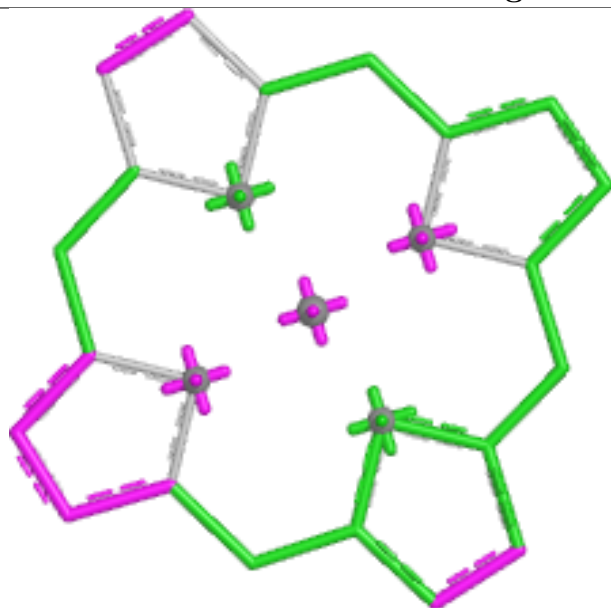


Torsions

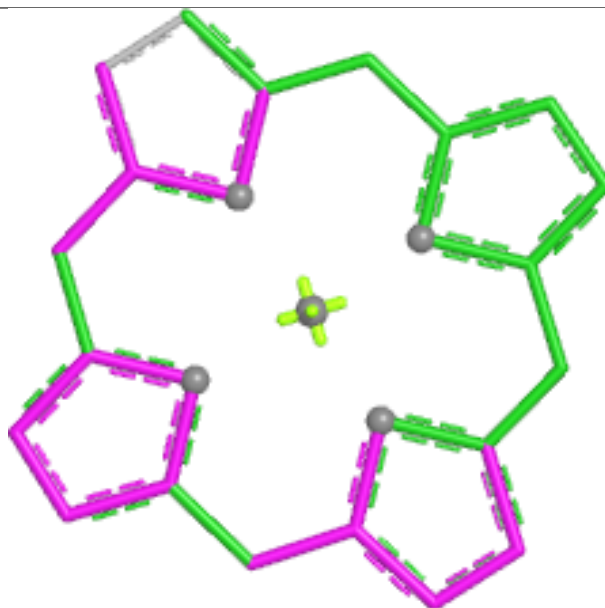


Rings

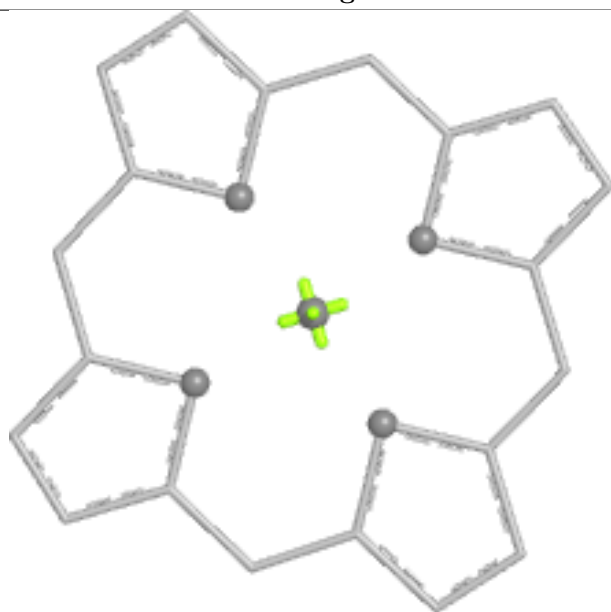
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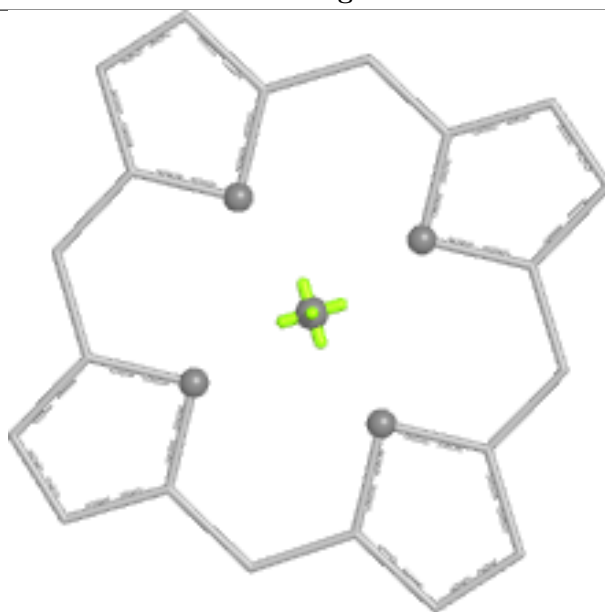
Bond lengths



Bond angles

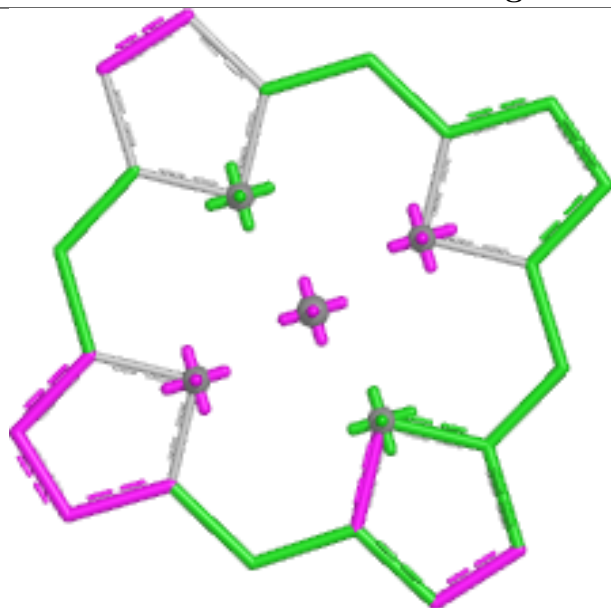


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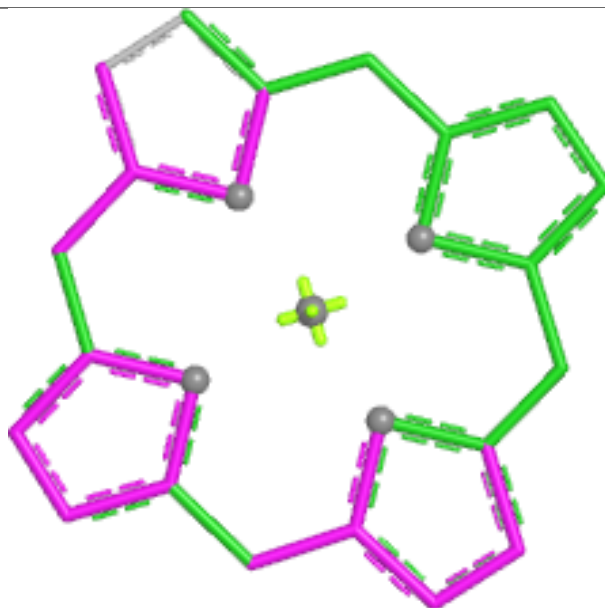


Rings

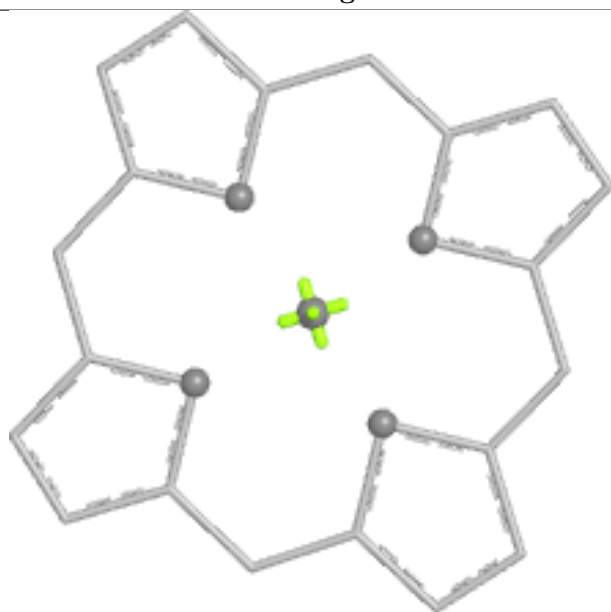
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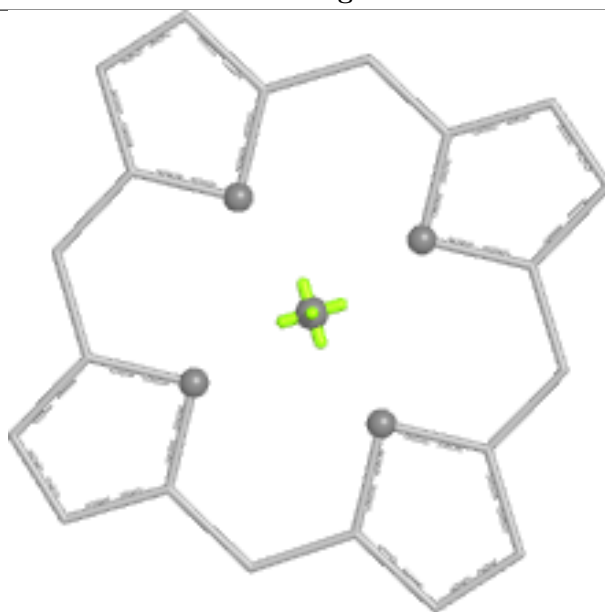
Bond lengths



Bond angles

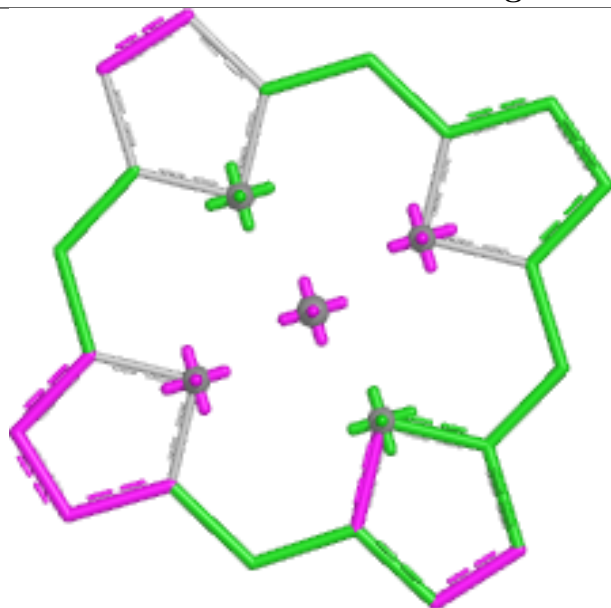


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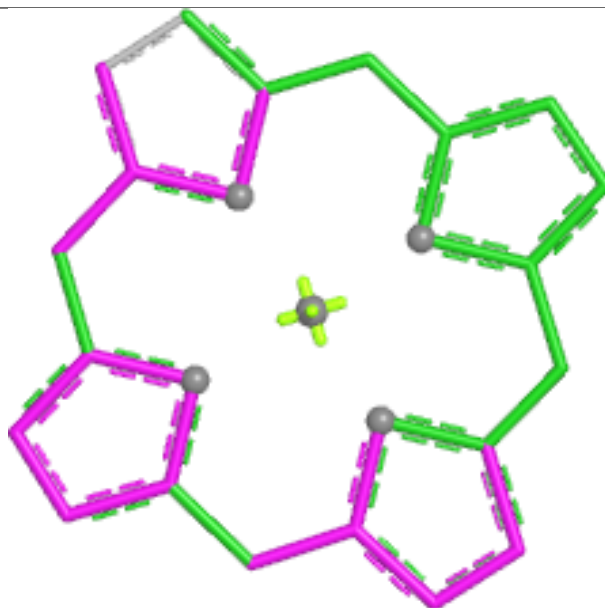


Rings

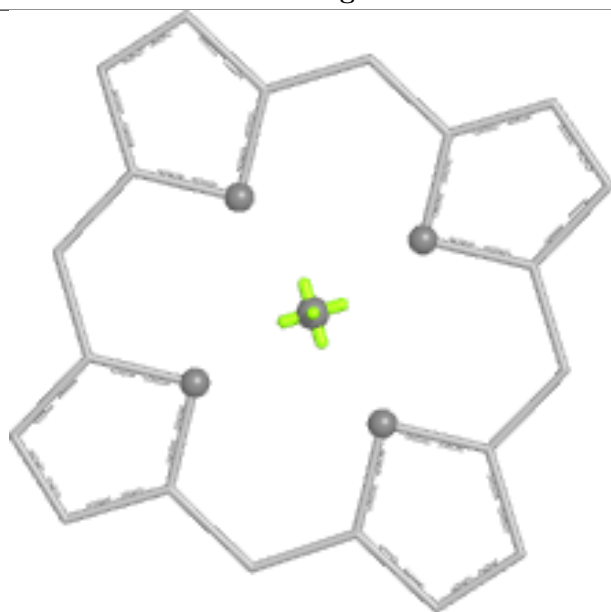
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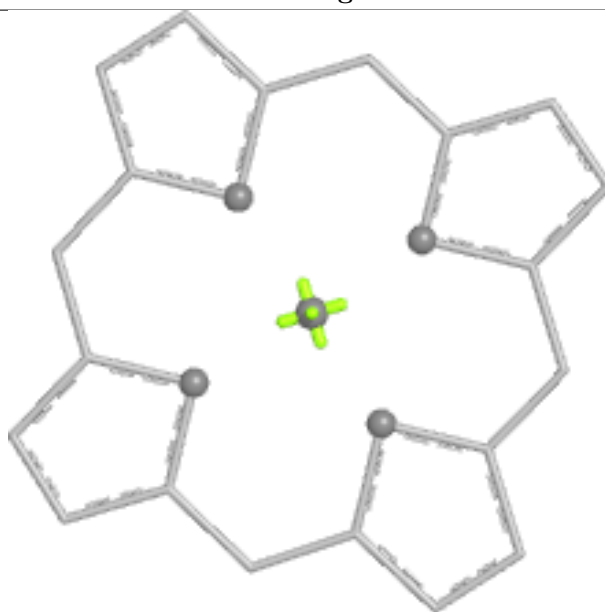
Bond lengths



Bond angles

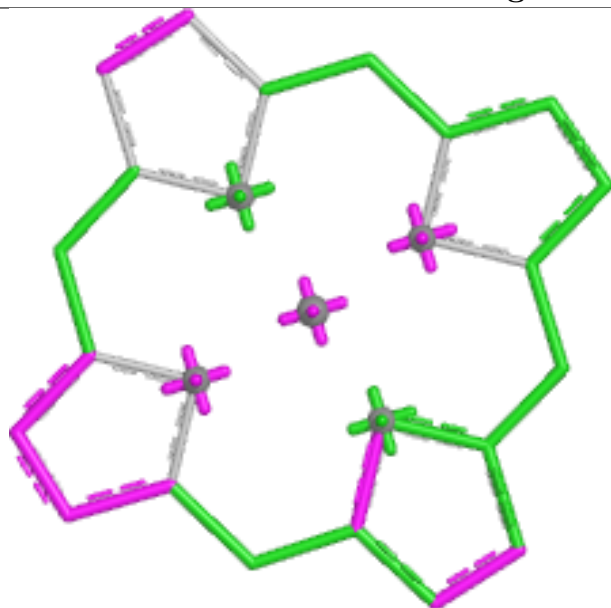


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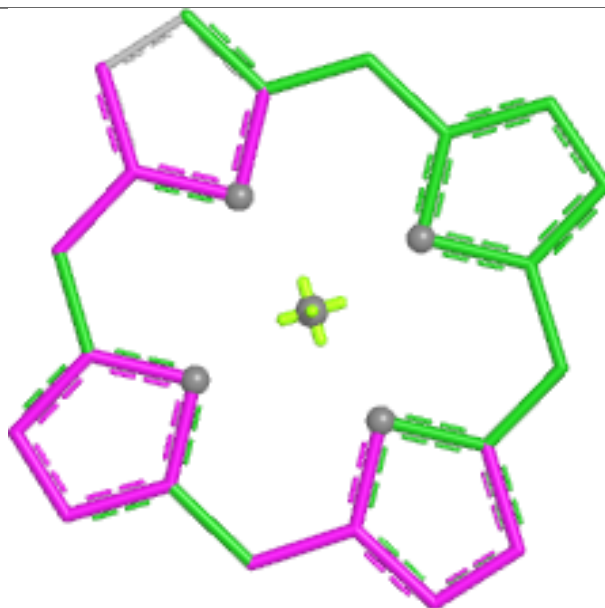


Rings

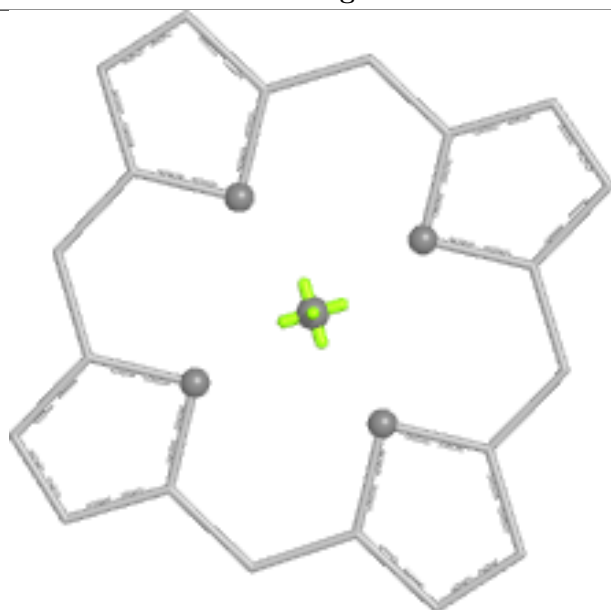
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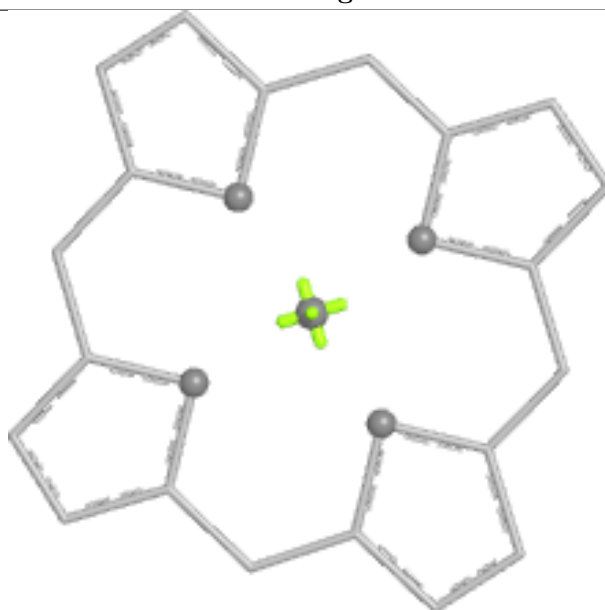
Bond lengths



Bond angles

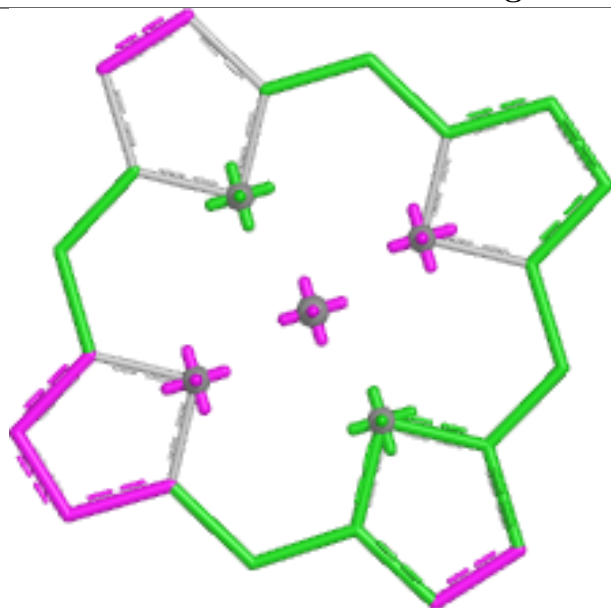


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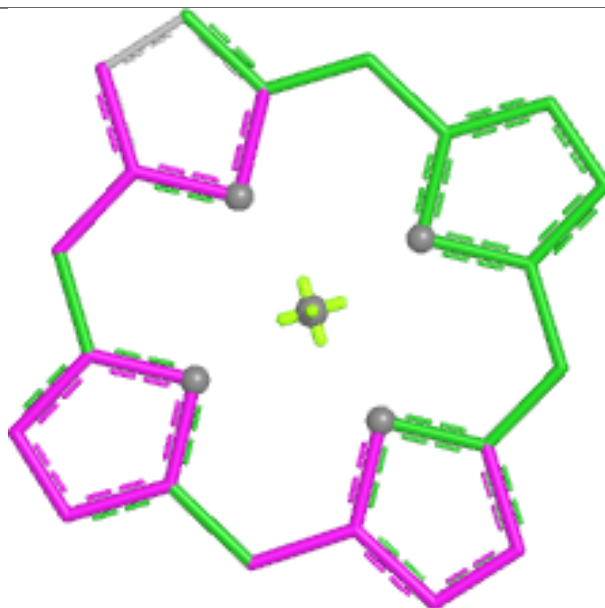


Rings

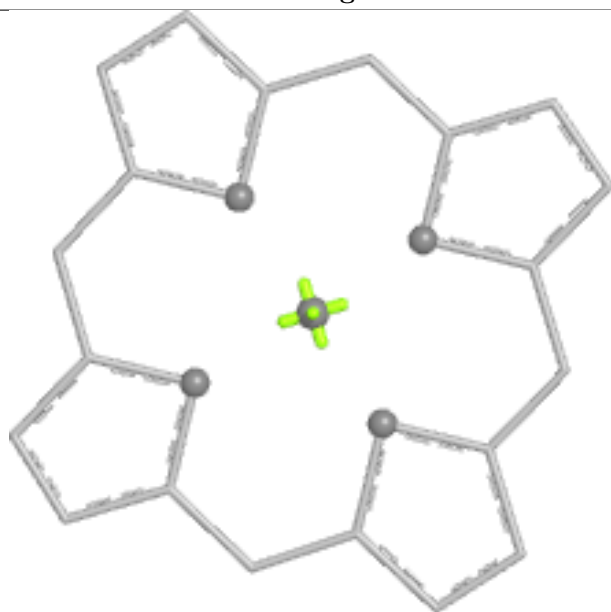
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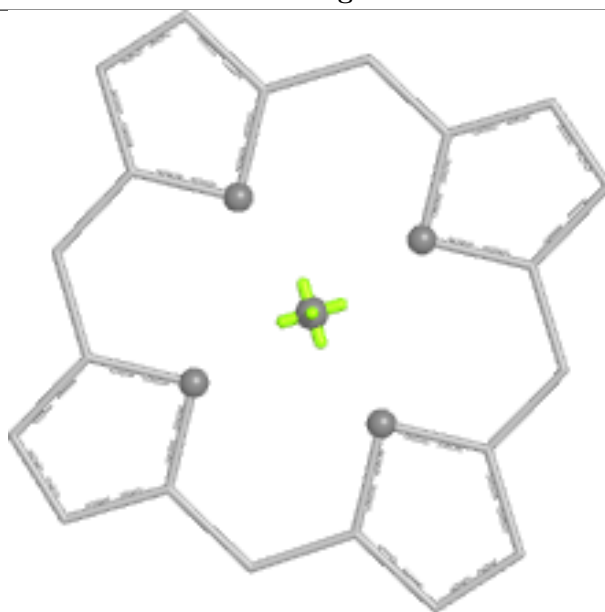
Bond lengths



Bond angles

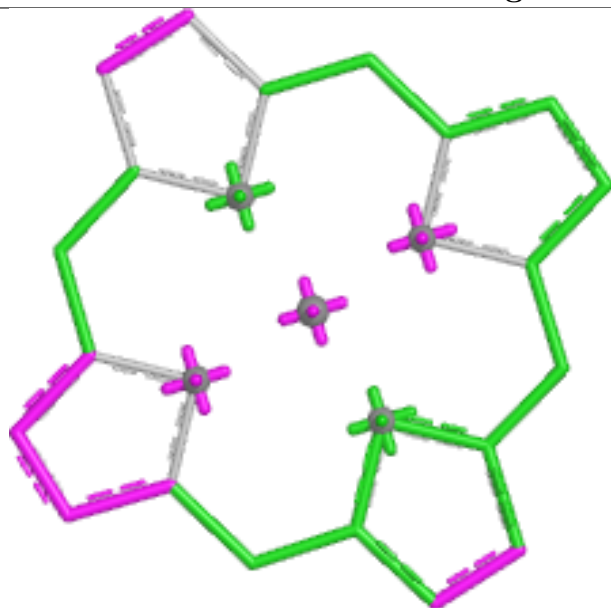


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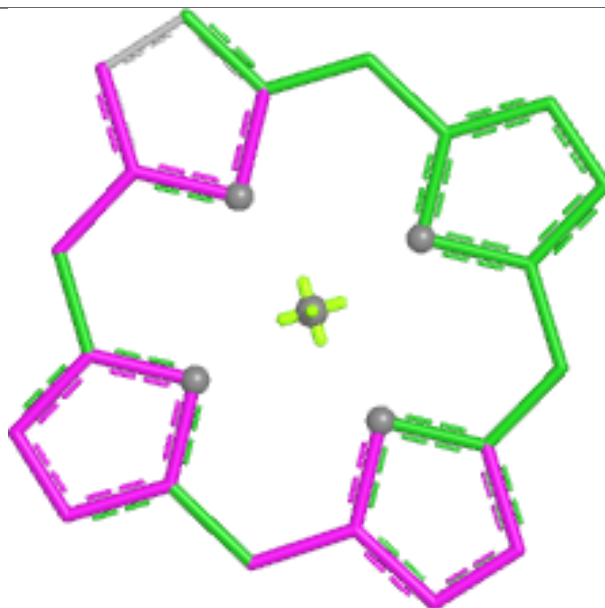


Rings

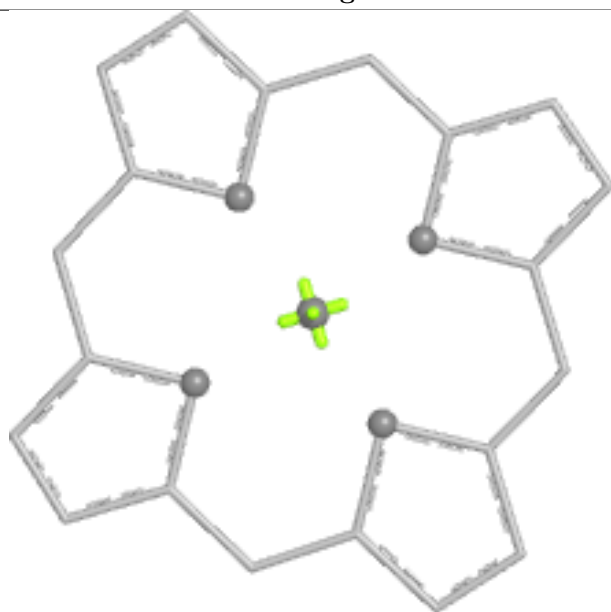
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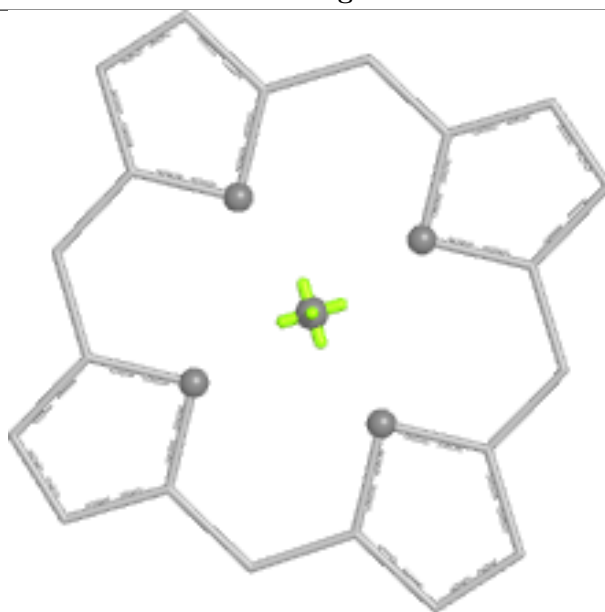
Bond lengths



Bond angles

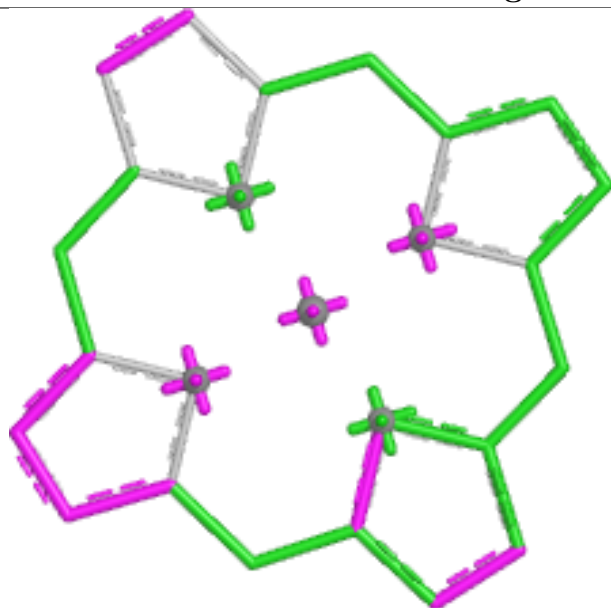


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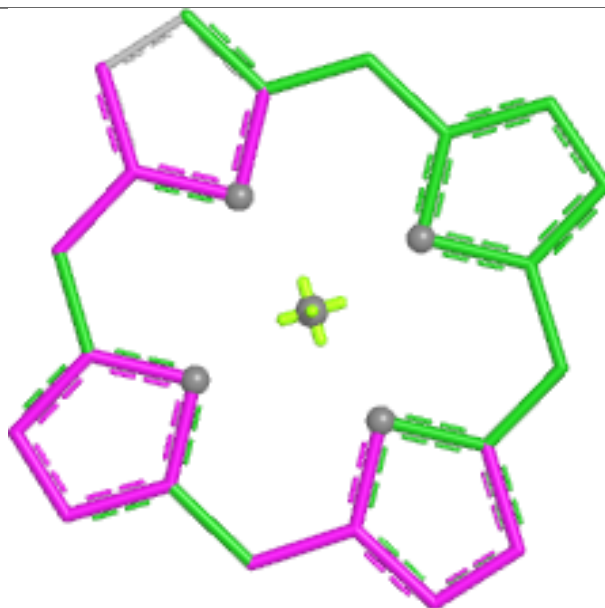


Rings

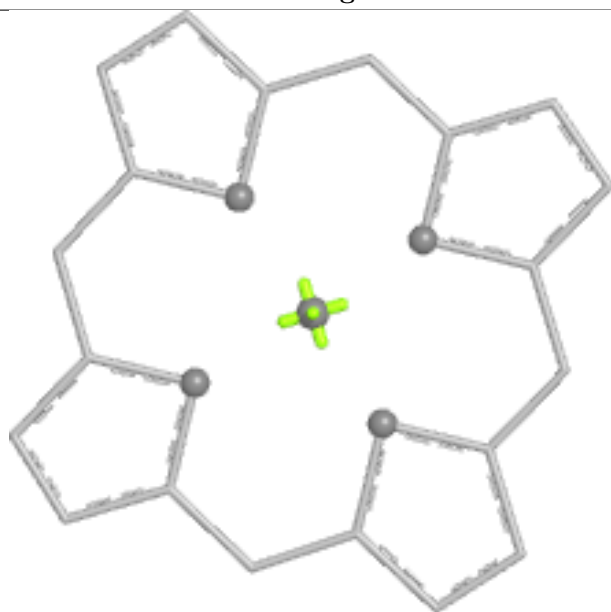
Ligand CLA A 3018



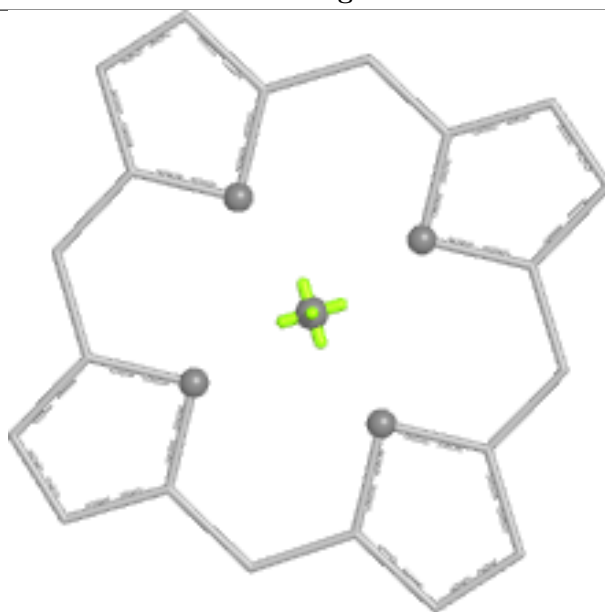
Bond lengths



Bond angles

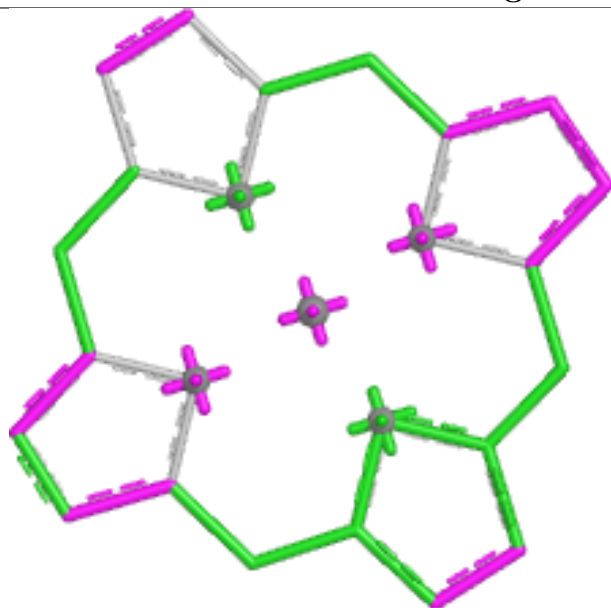


Torsions

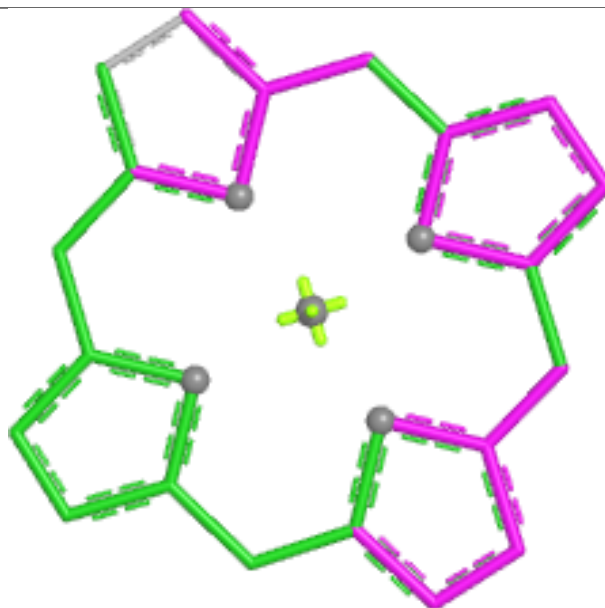


Rings

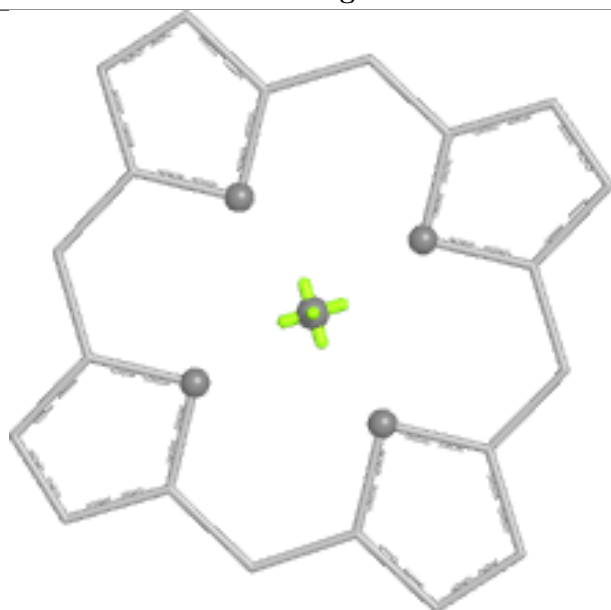
Ligand CLA A 3014



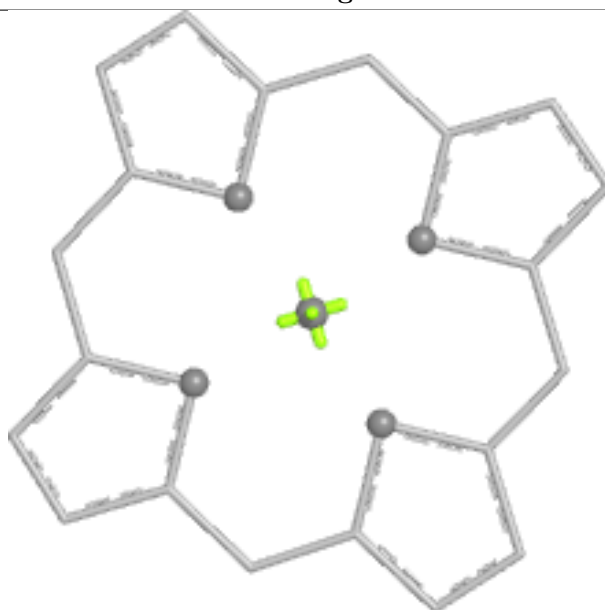
Bond lengths



Bond angles

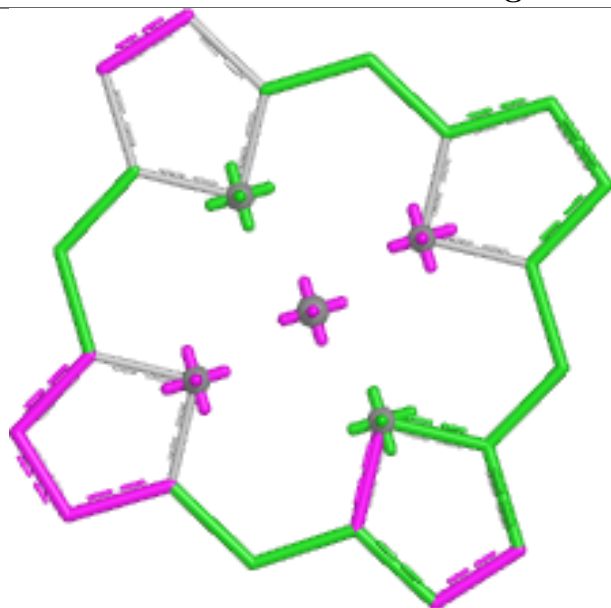


Torsions

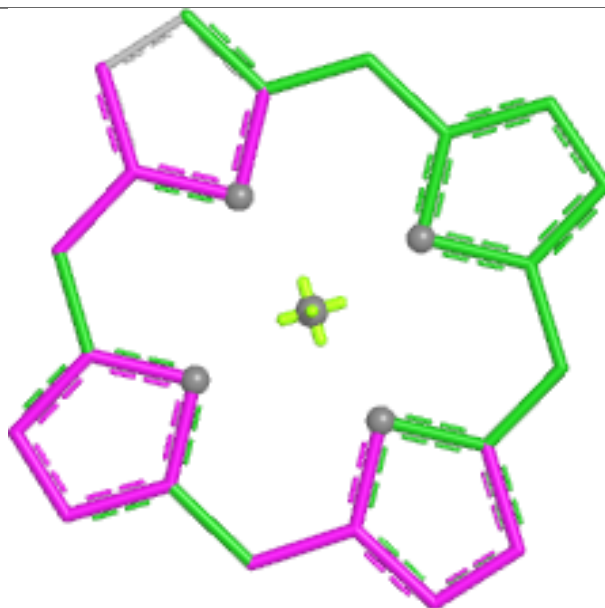


Rings

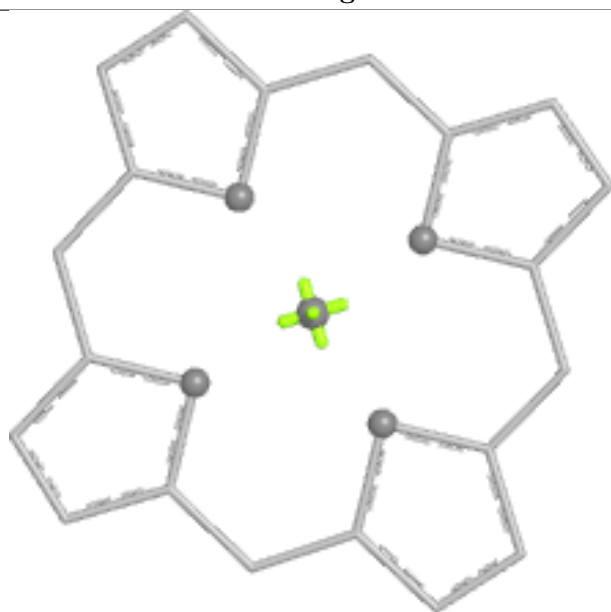
Ligand CLA A 3026



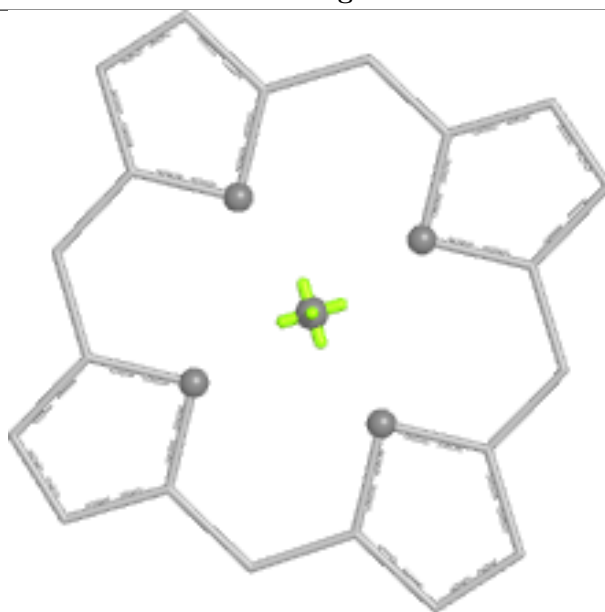
Bond lengths



Bond angles

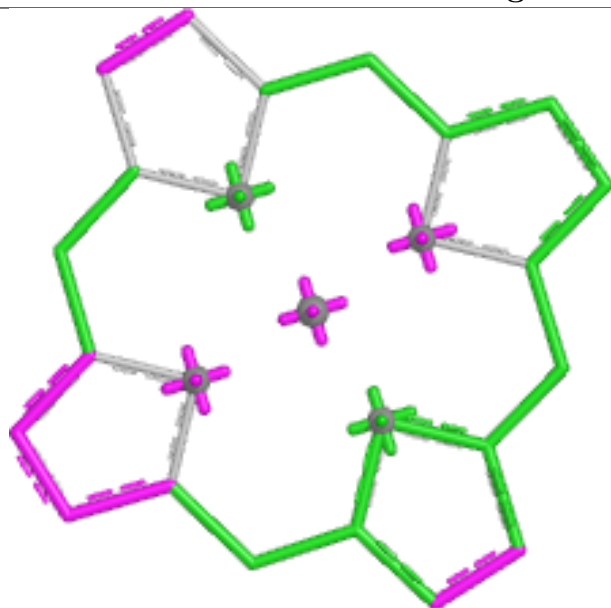


Torsions

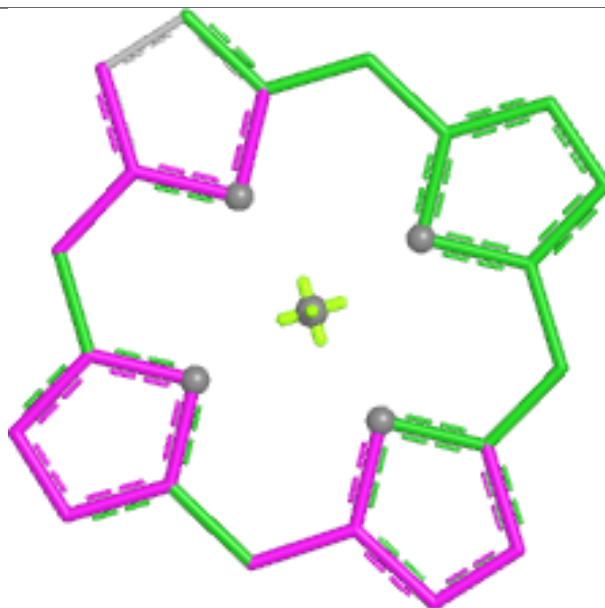


Rings

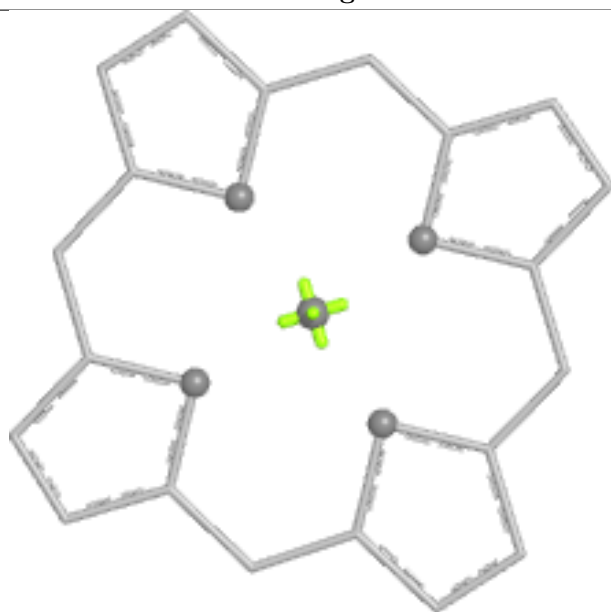
Ligand CLA F 3061



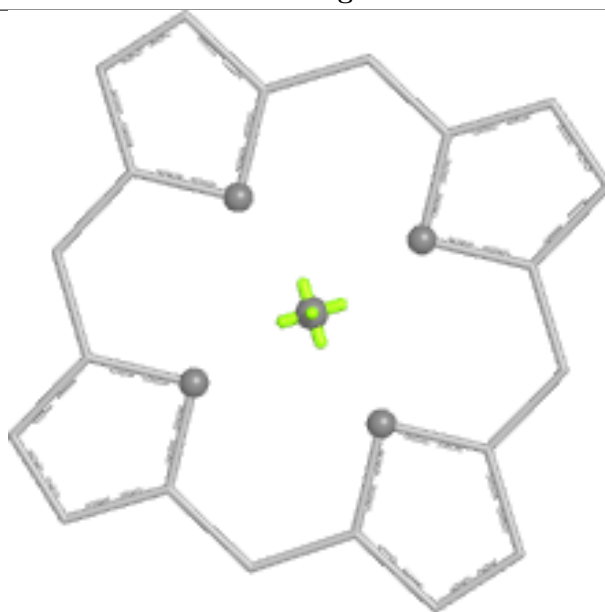
Bond lengths



Bond angles

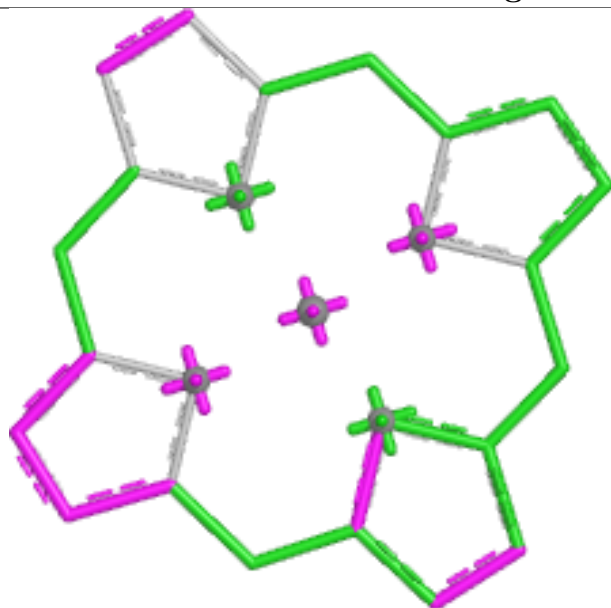


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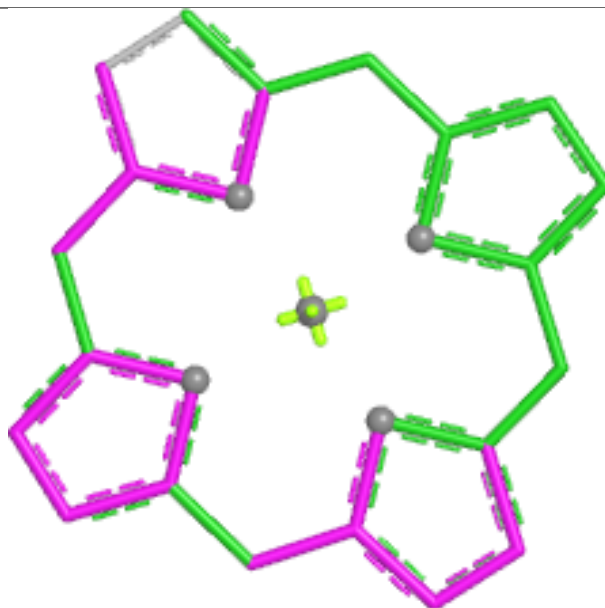


Rings

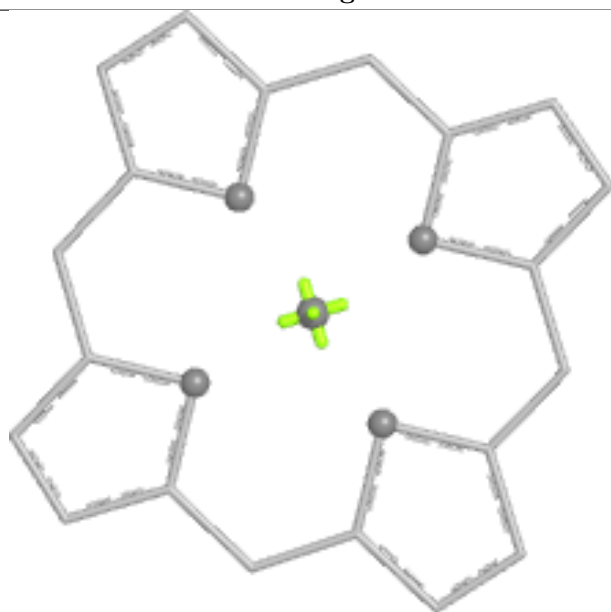
Ligand CLA A 3071



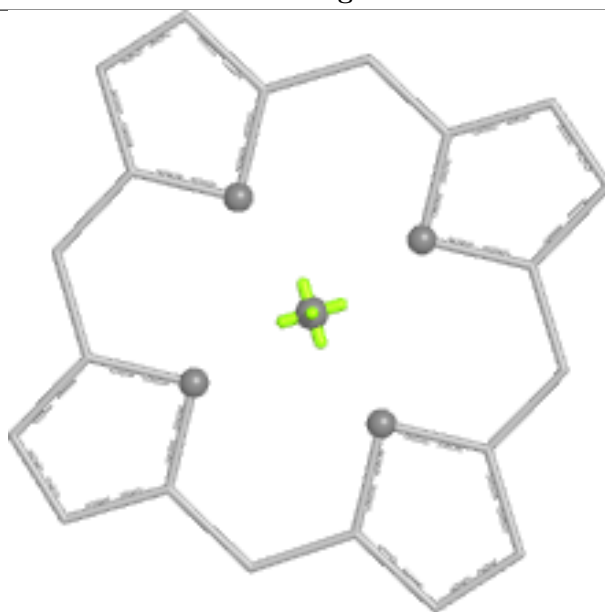
Bond lengths



Bond angles

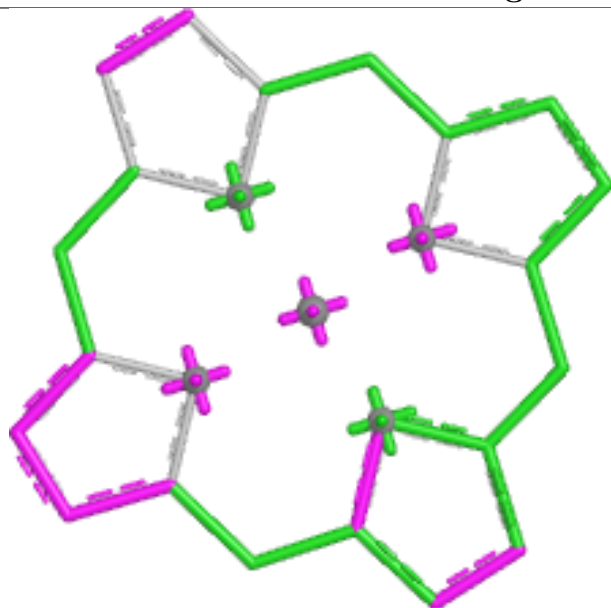


Torsions

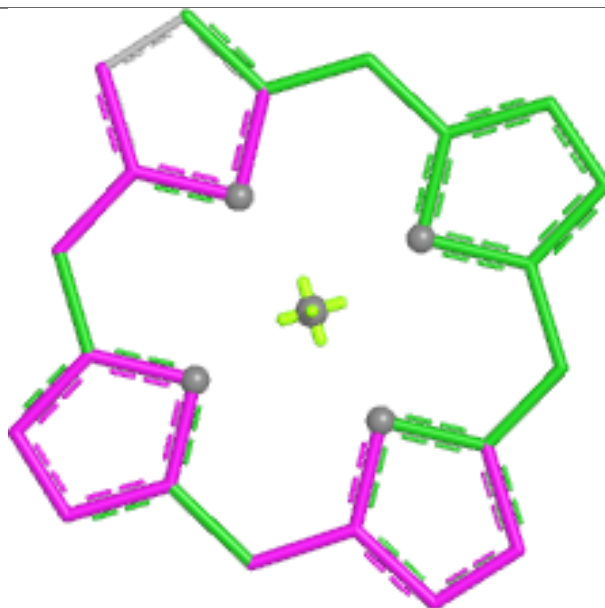


Rings

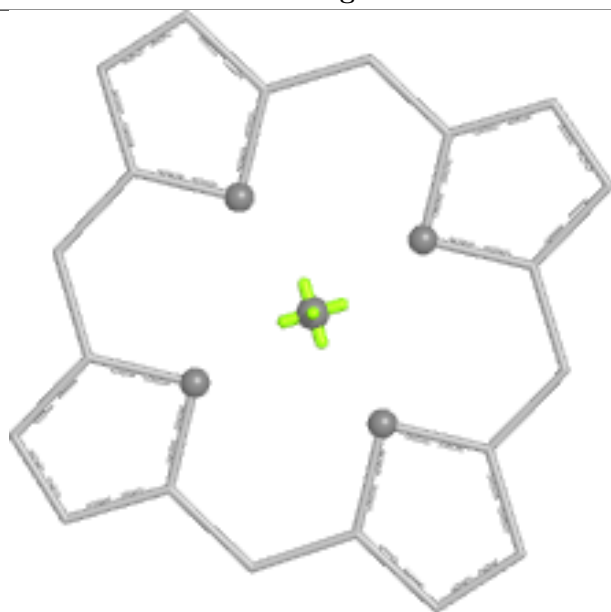
Ligand CLA B 2501



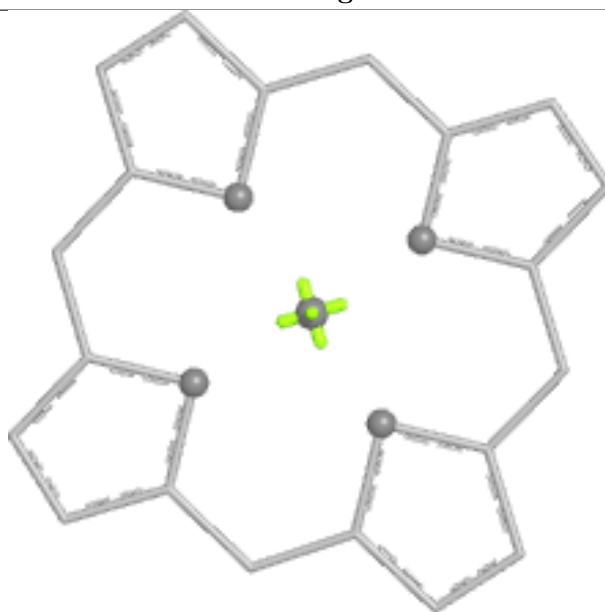
Bond lengths



Bond angles

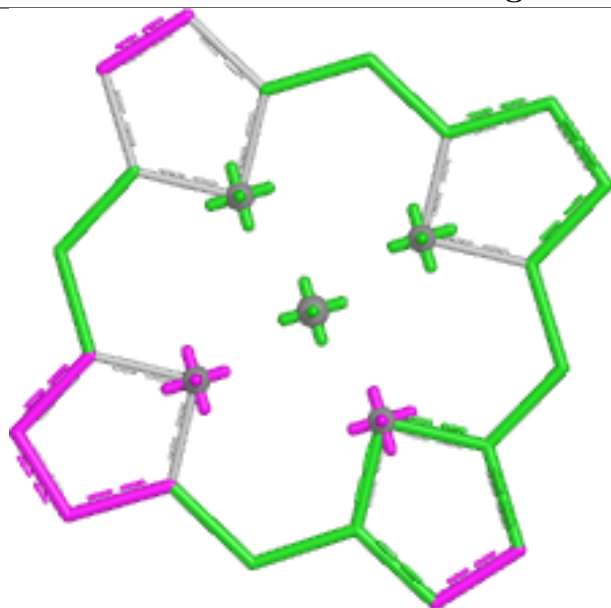


Torsions

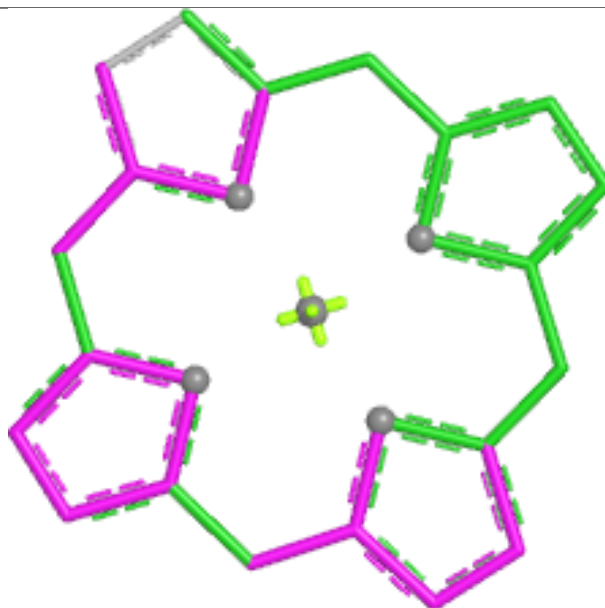


Rings

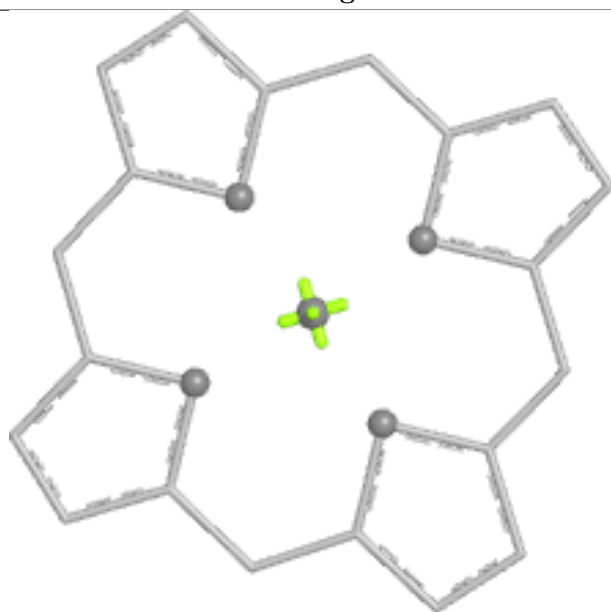
Ligand CLA B 2003



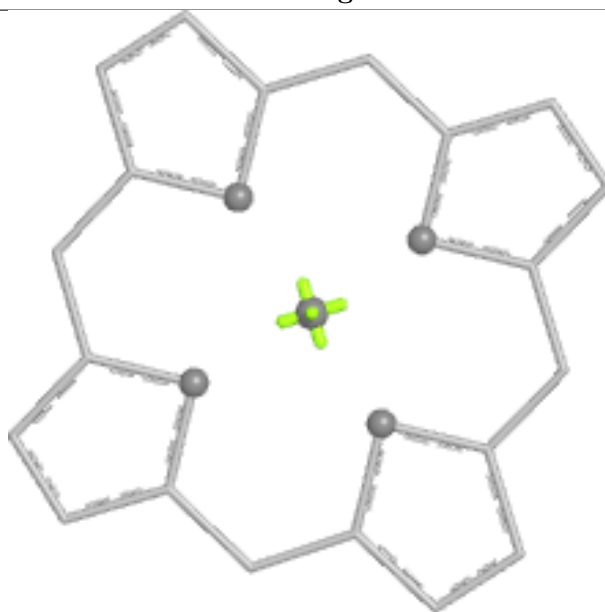
Bond lengths



Bond angles

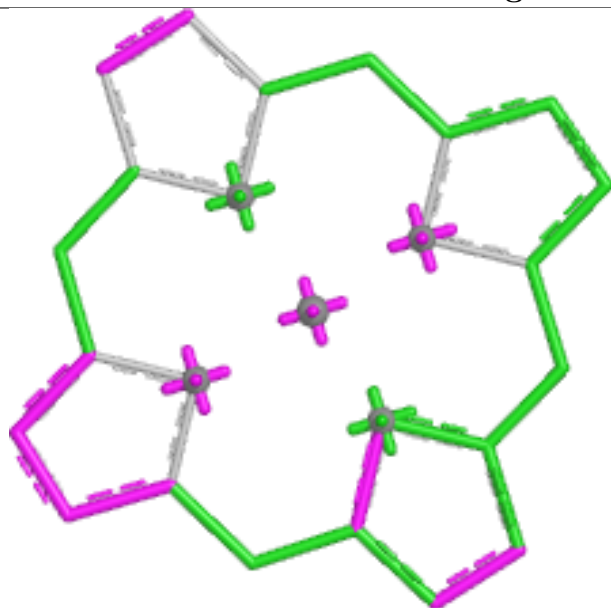


Torsions

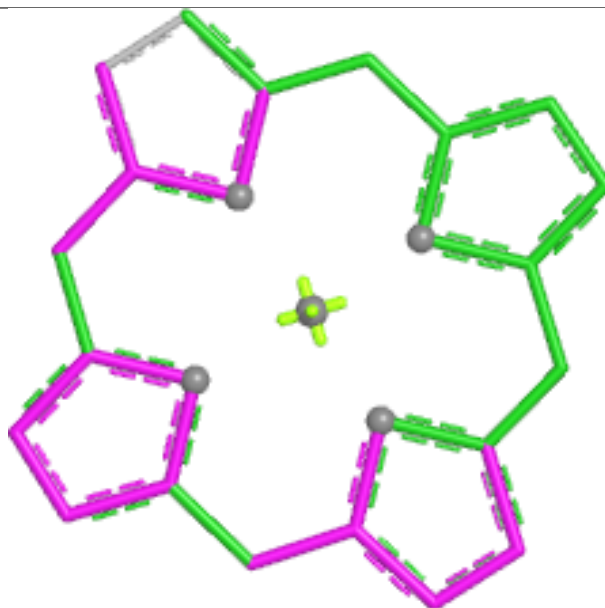


Rings

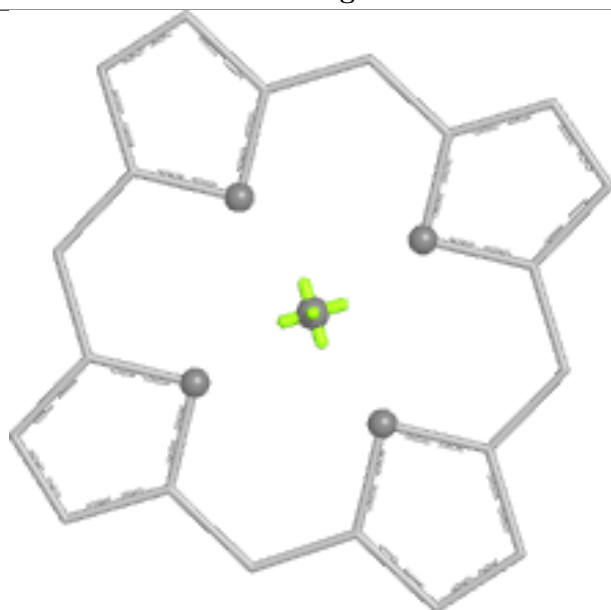
Ligand CLA B 3011



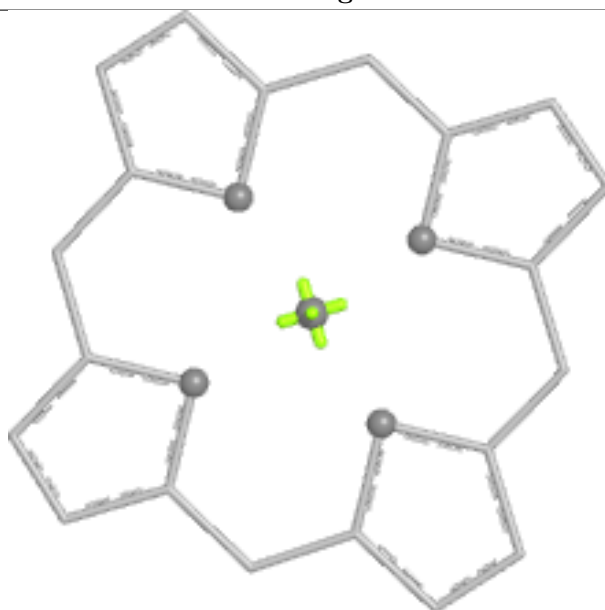
Bond lengths



Bond angles

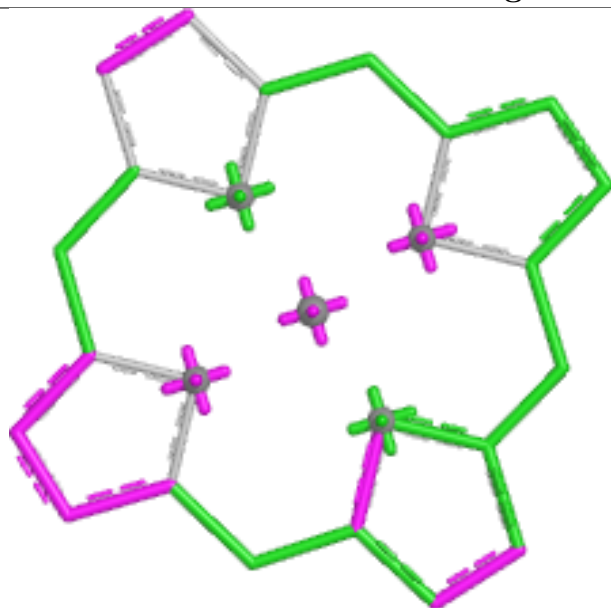


Torsions

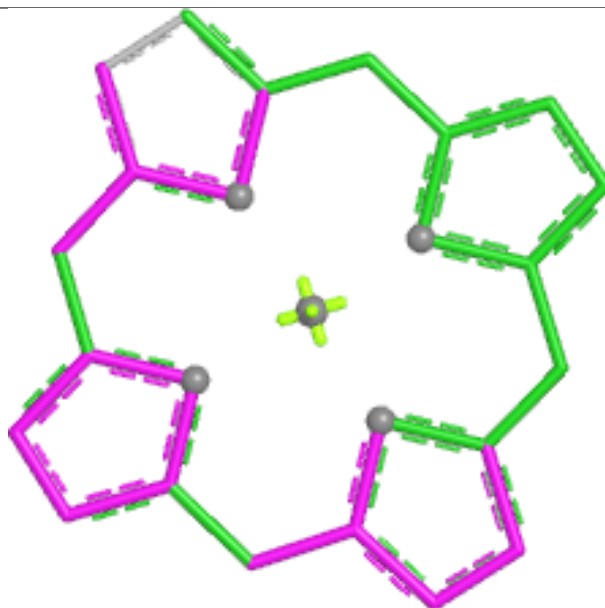


Rings

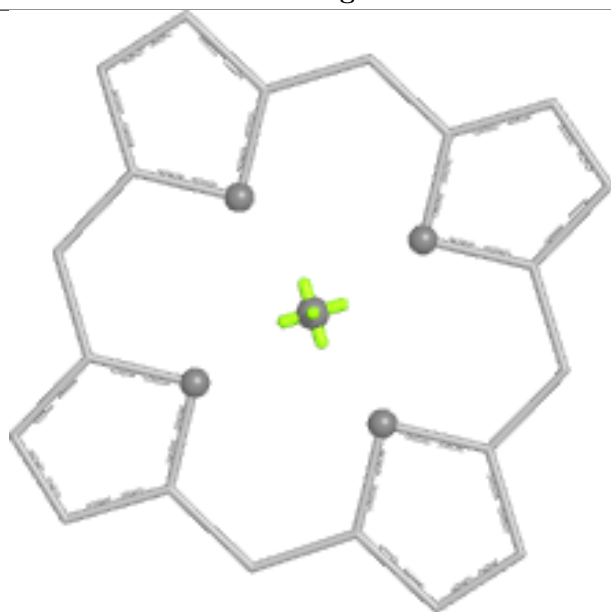
Ligand CLA A 3065



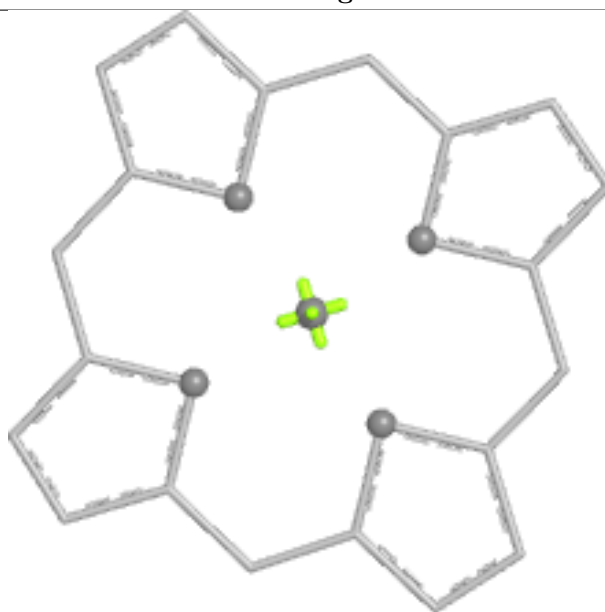
Bond lengths



Bond angles

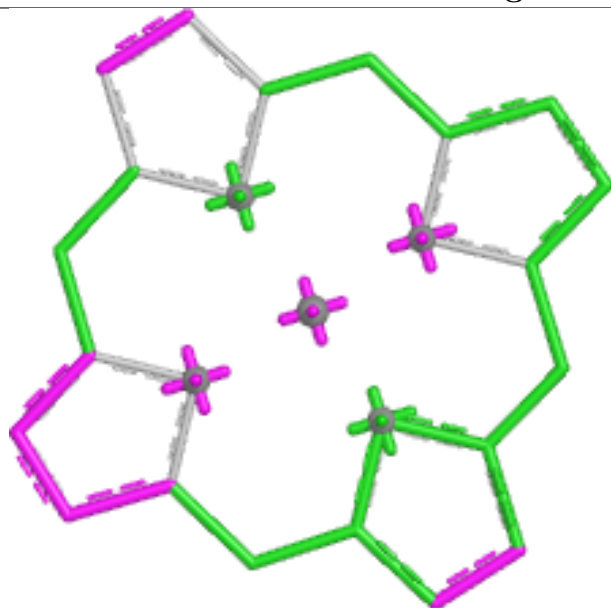


Torsions

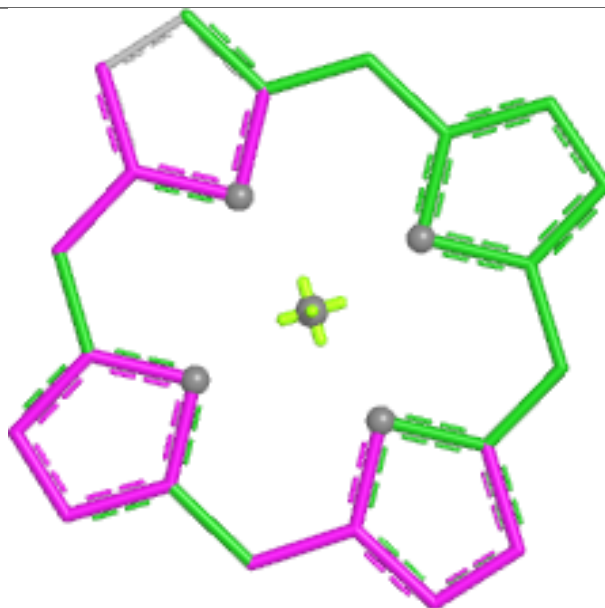


Rings

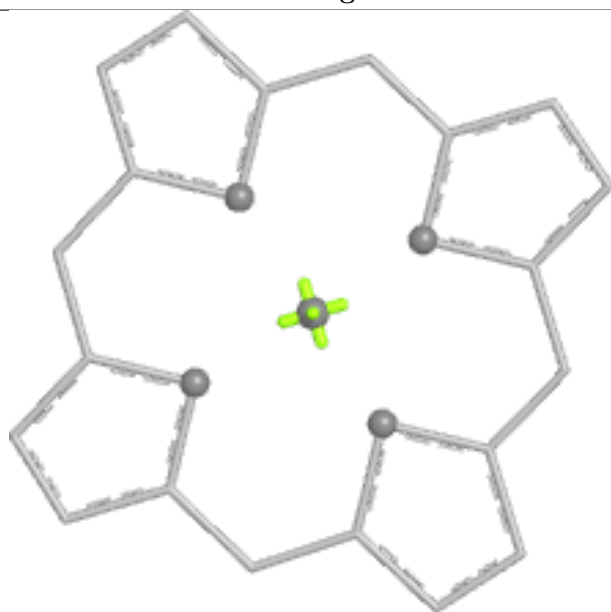
Ligand CLA B 3066



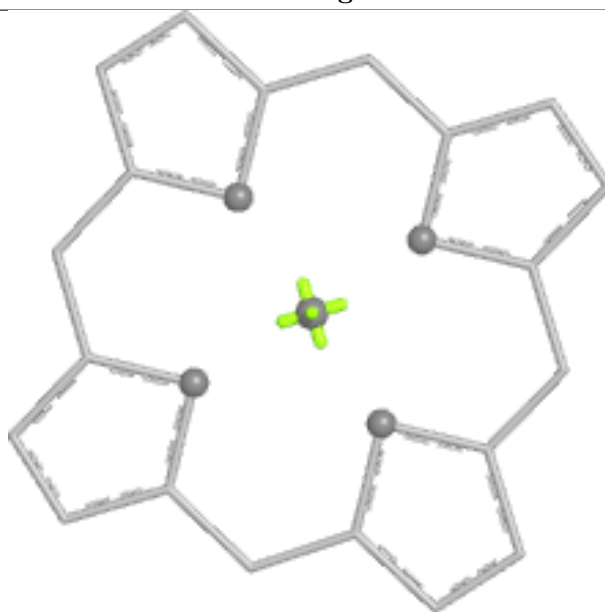
Bond lengths



Bond angles

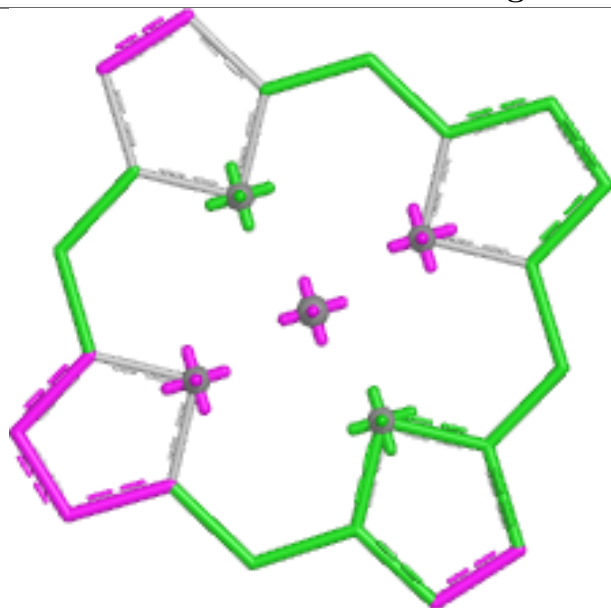


Torsions

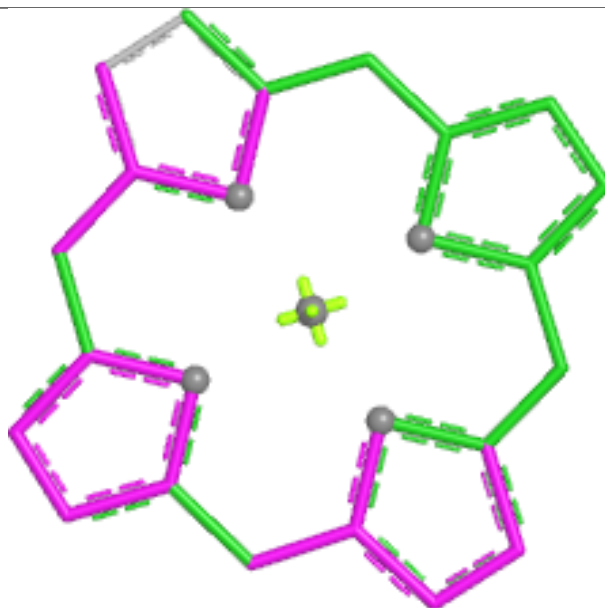


Rings

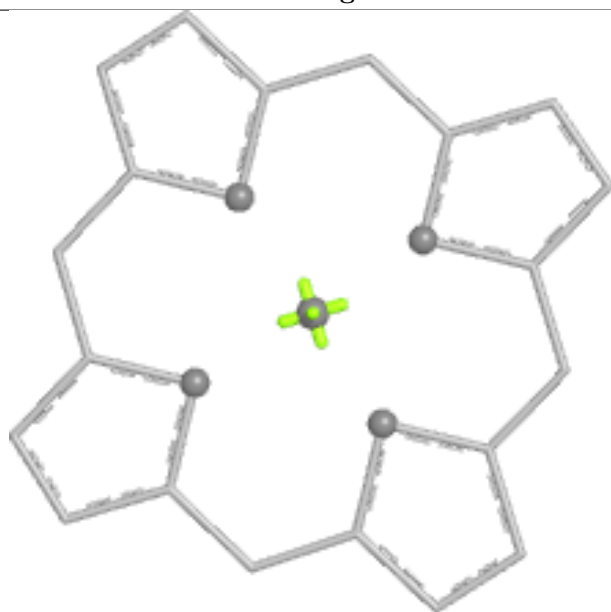
Ligand CLA F 3031



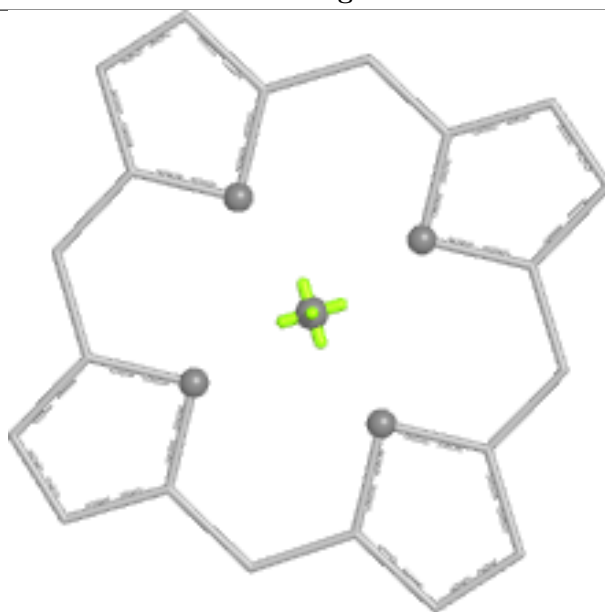
Bond lengths



Bond angles

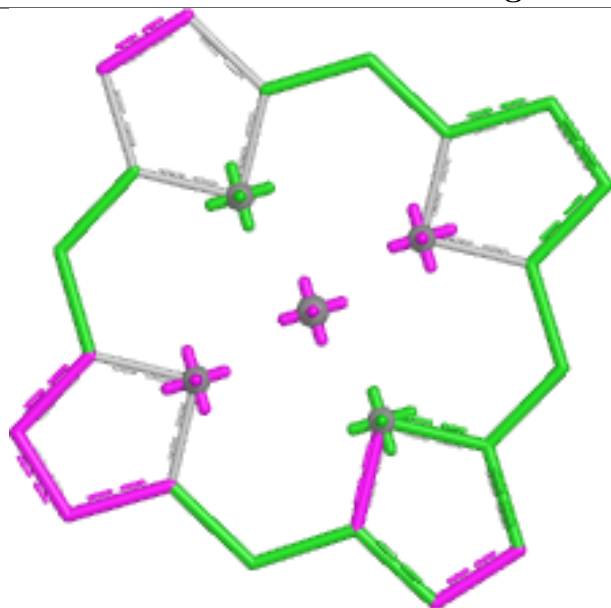


Torsions

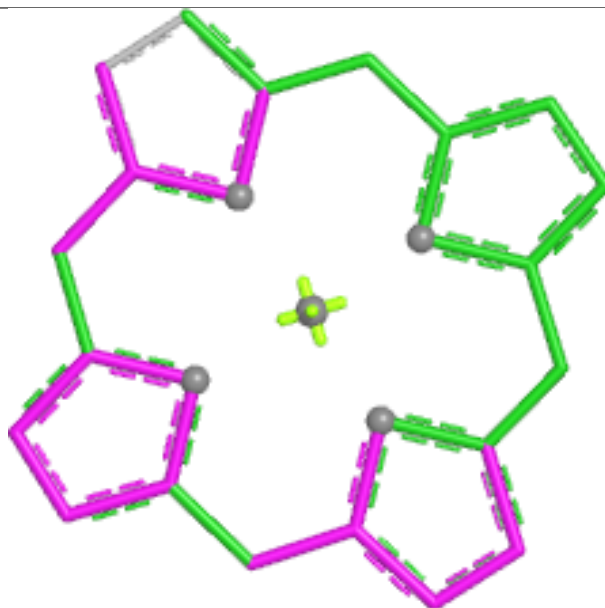


Rings

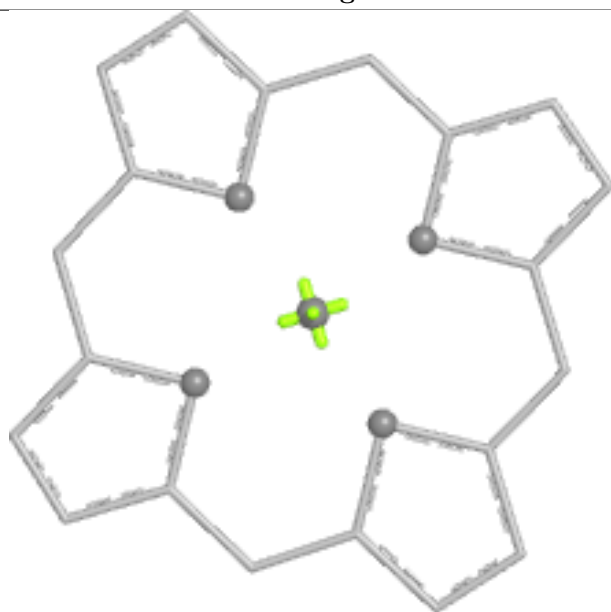
Ligand CLA A 3017



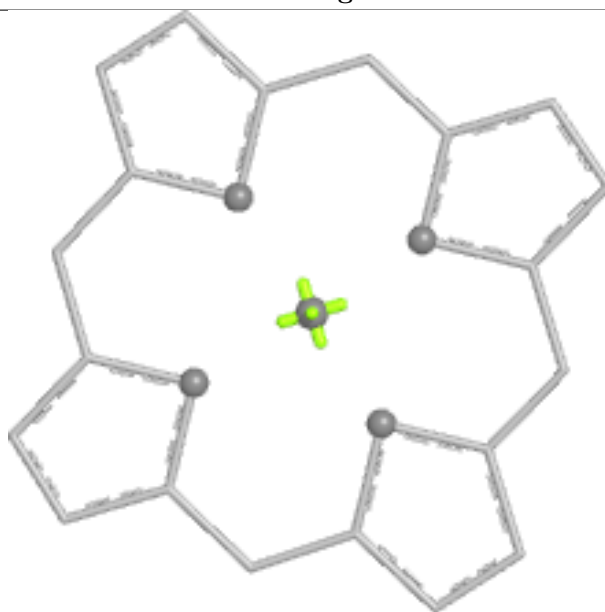
Bond lengths



Bond angles

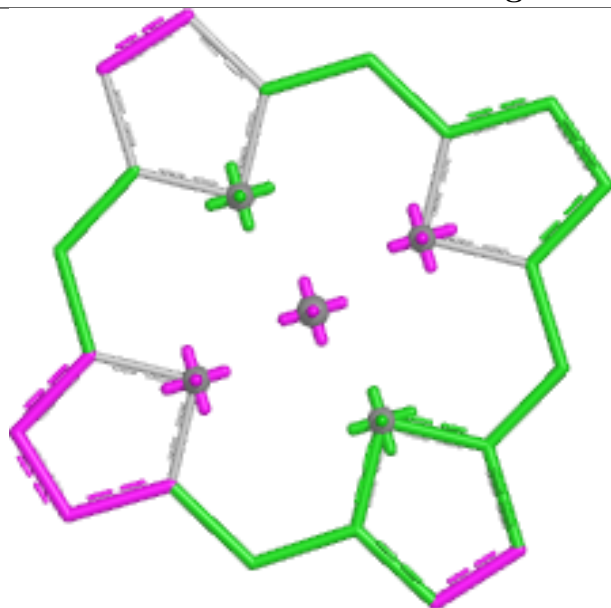


Torsions

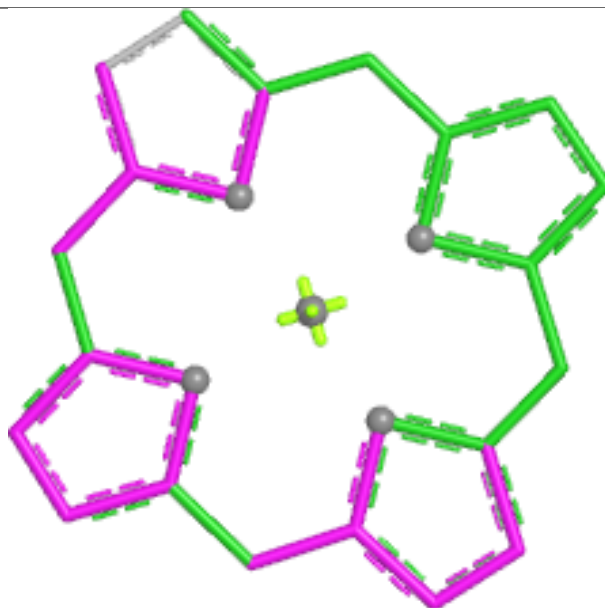


Rings

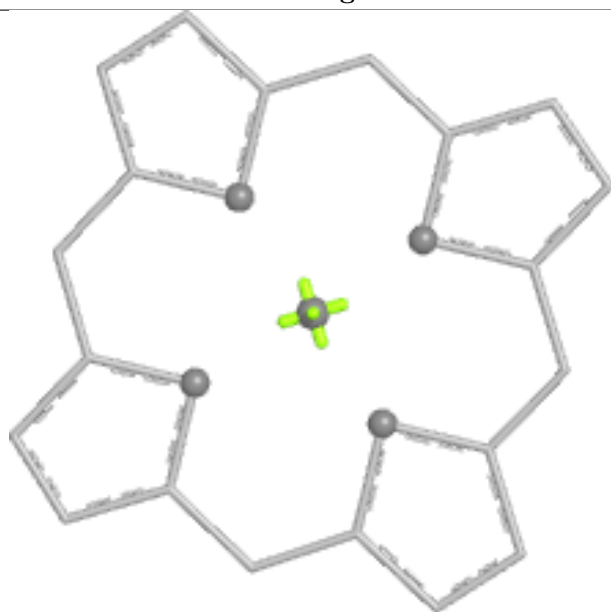
Ligand CLA B 3074



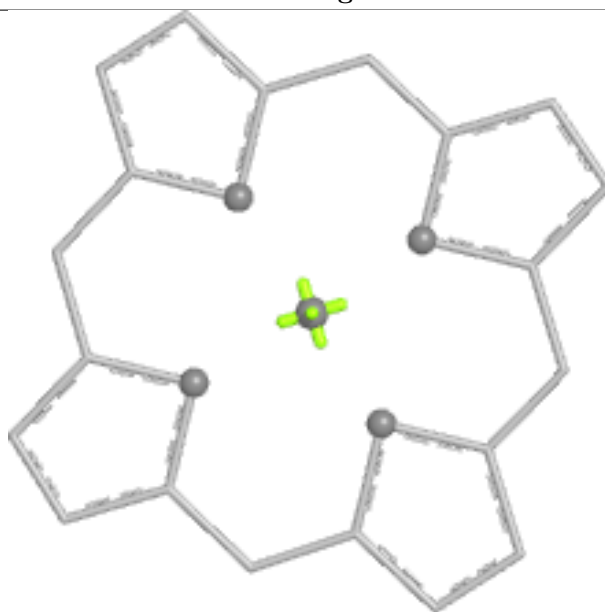
Bond lengths



Bond angles

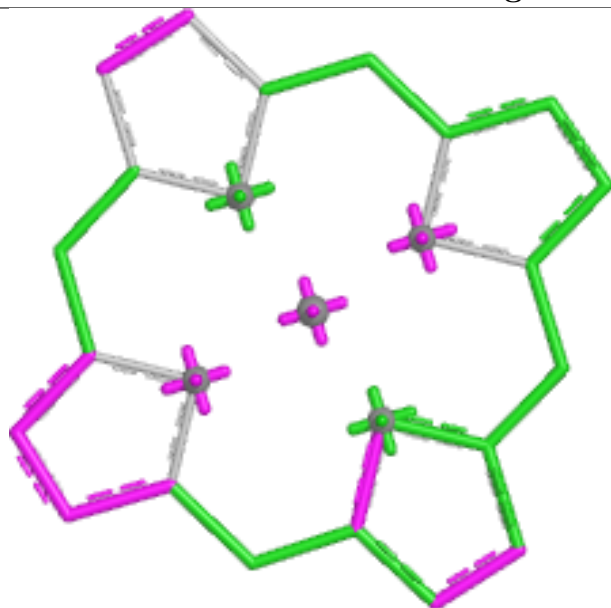


Torsions

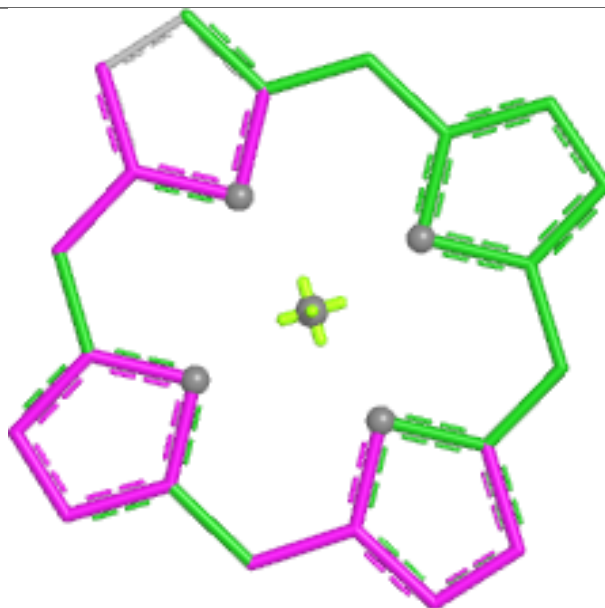


Rings

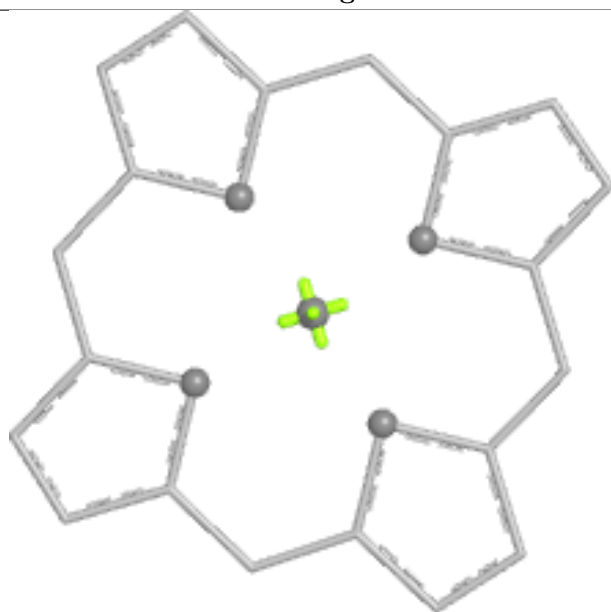
Ligand CLA A 3062



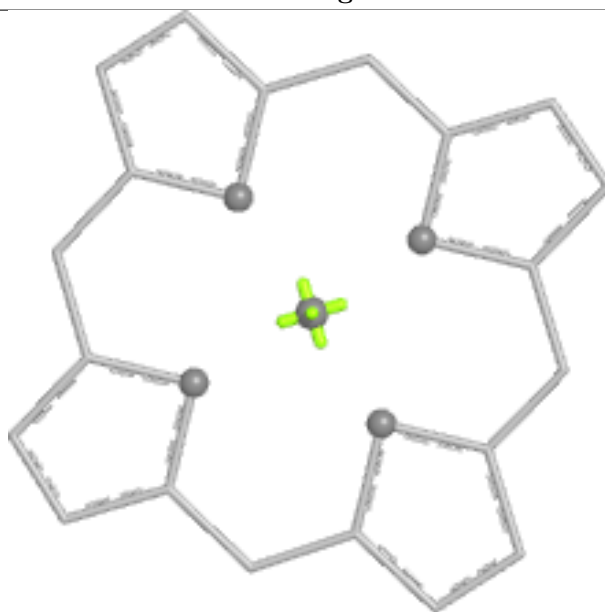
Bond lengths



Bond angles

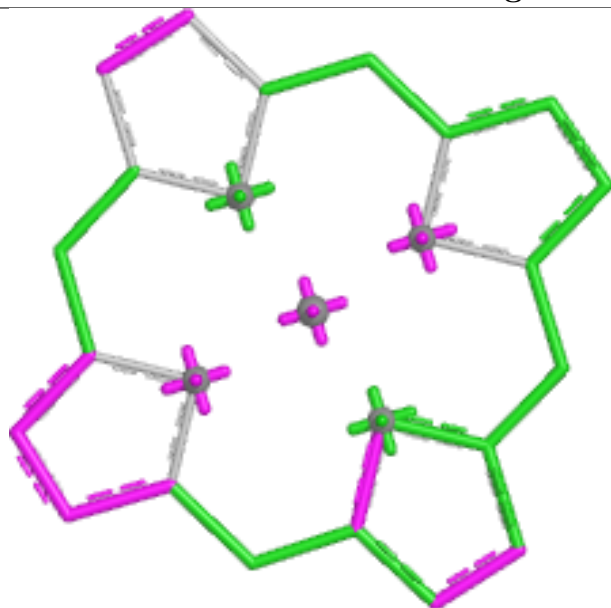


Torsions

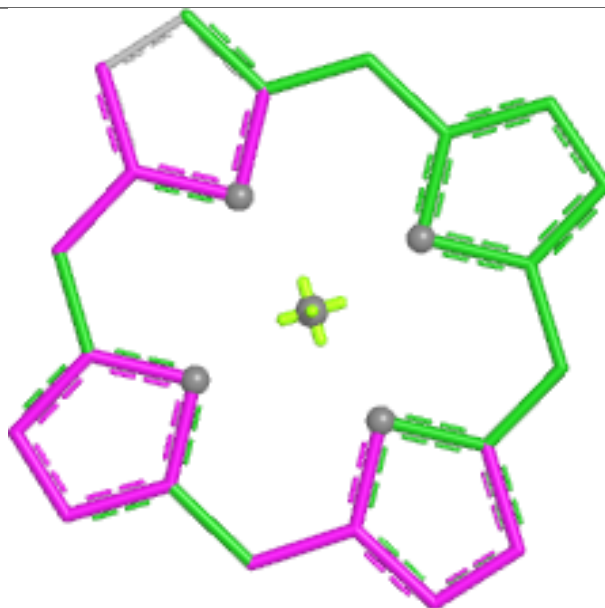


Rings

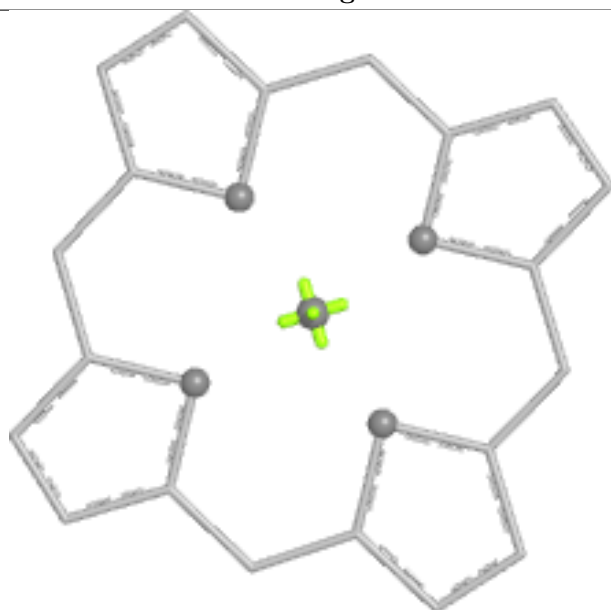
Ligand CLA A 3047



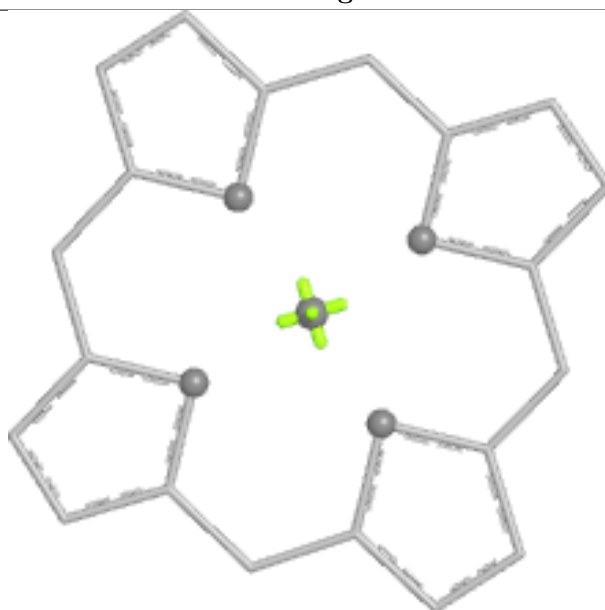
Bond lengths



Bond angles

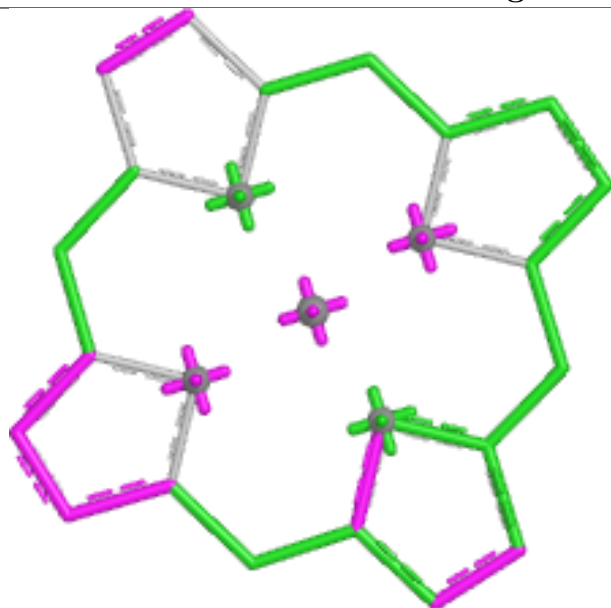


Torsions

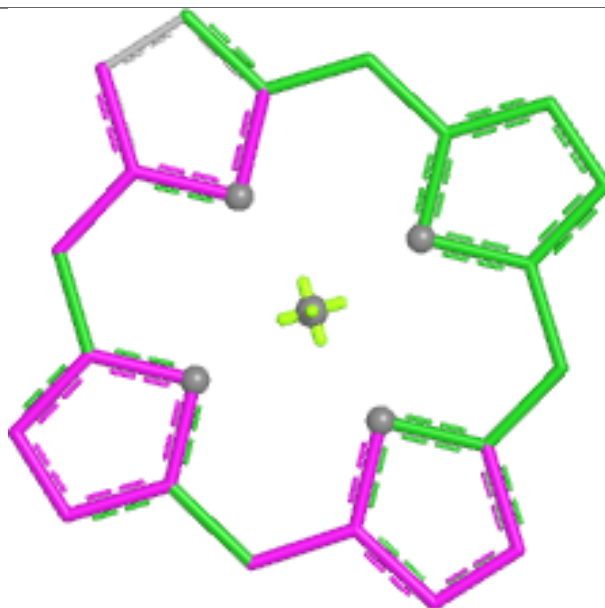


Rings

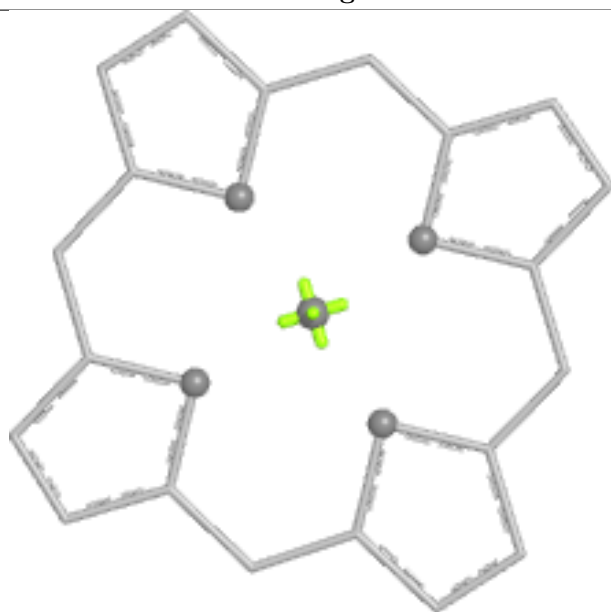
Ligand CLA F 3002



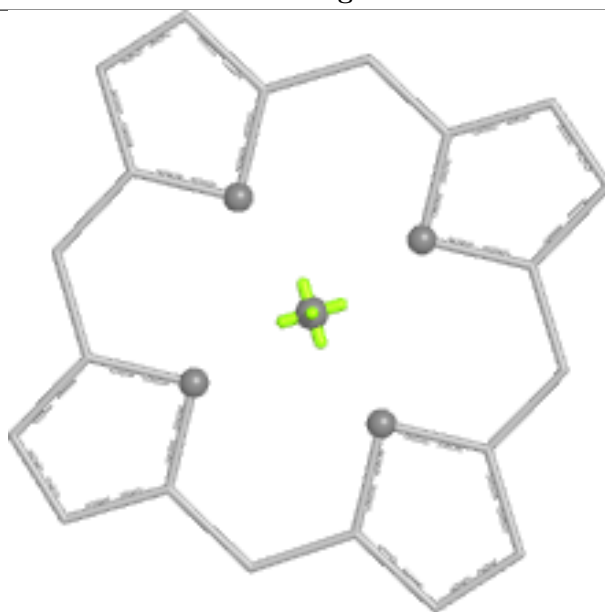
Bond lengths



Bond angles

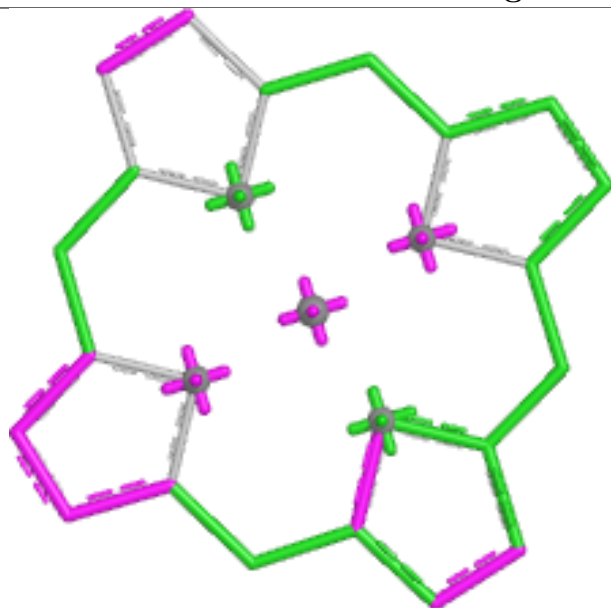


Torsions

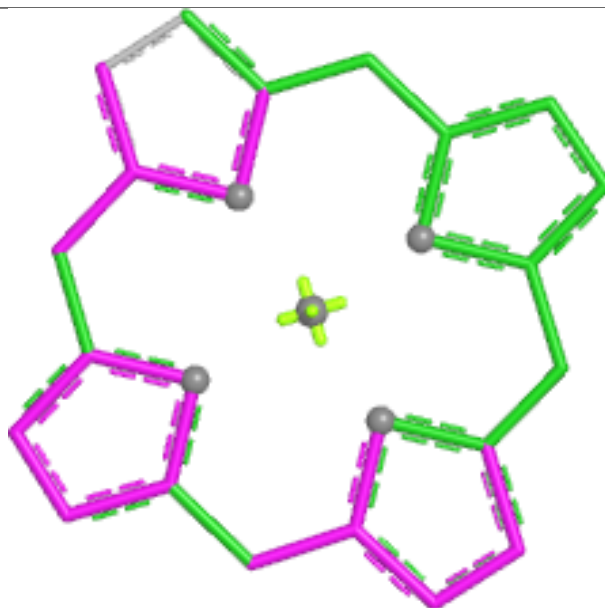


Rings

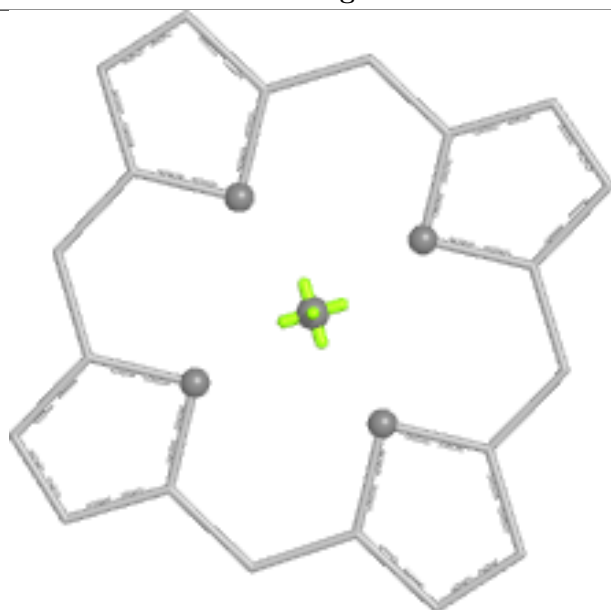
Ligand CLA A 3029



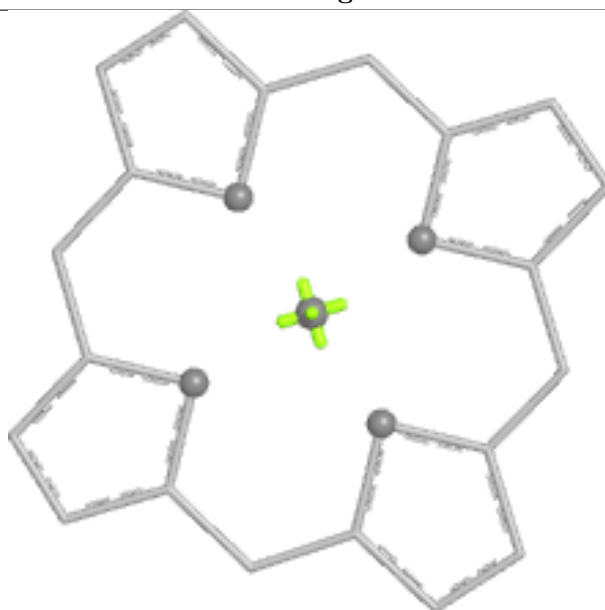
Bond lengths



Bond angles

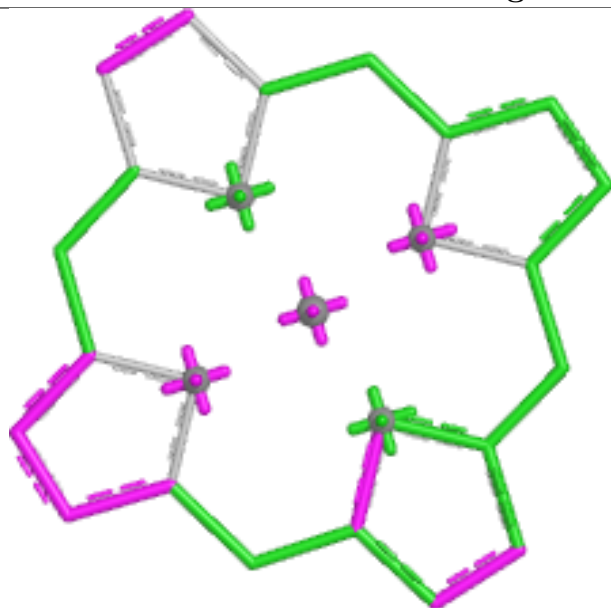


Torsions

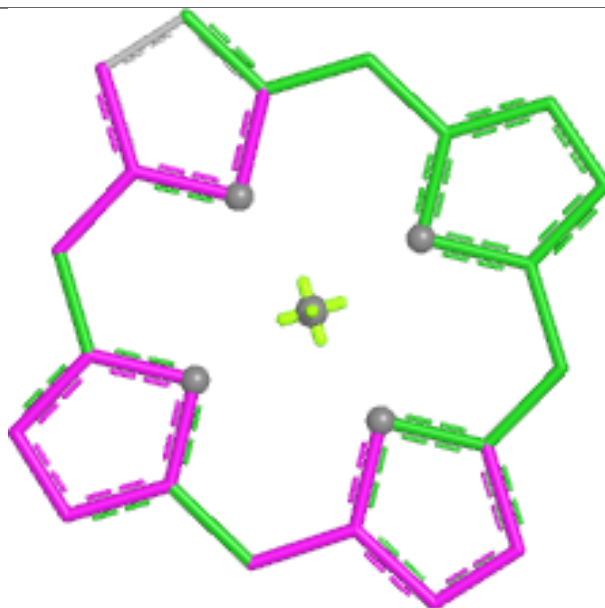


Rings

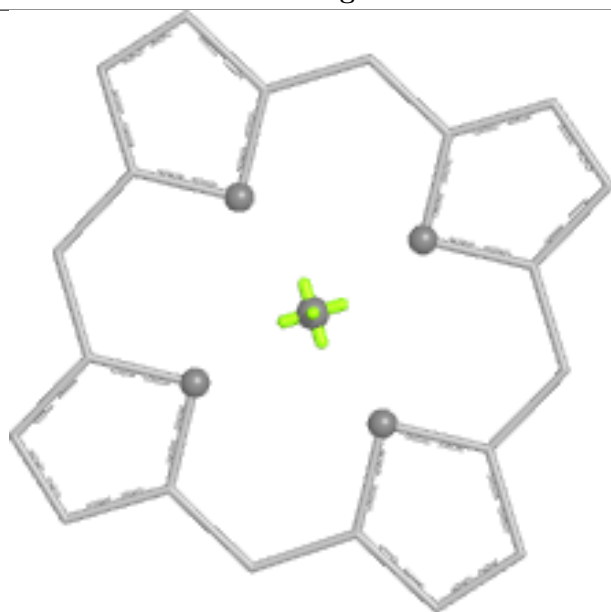
Ligand CLA F 3033



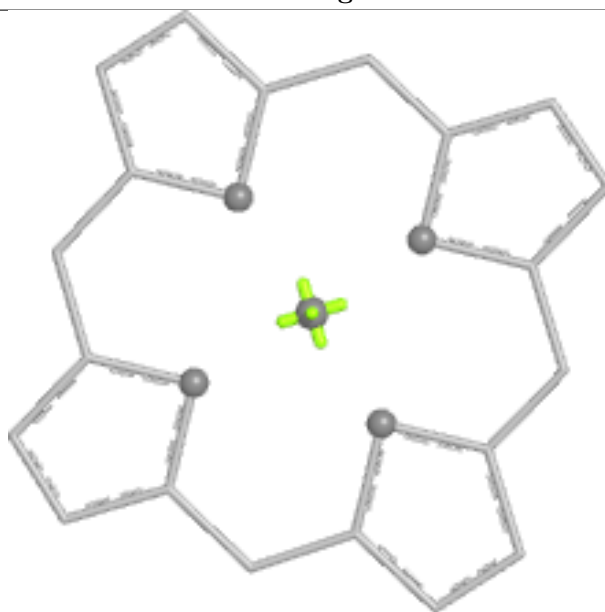
Bond lengths



Bond angles

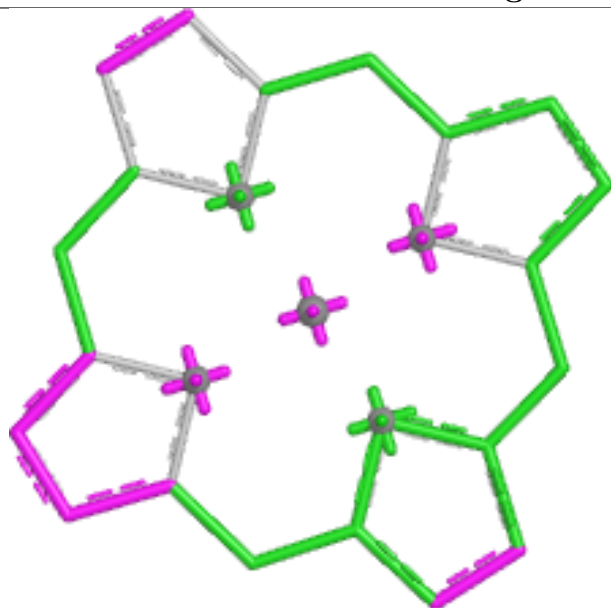


Torsions

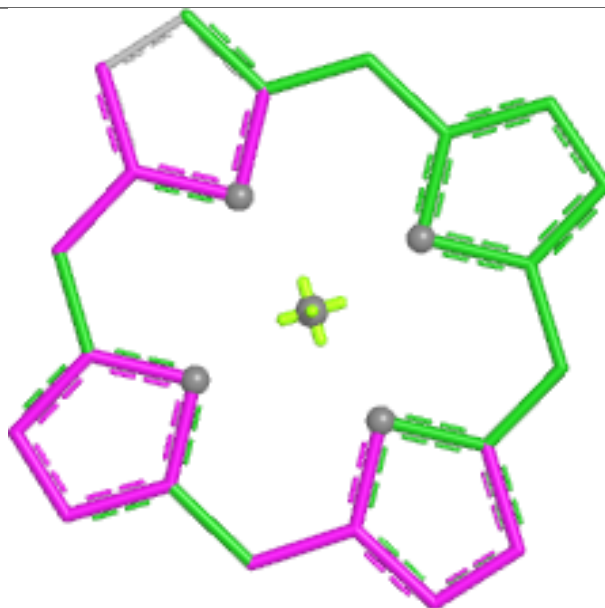


Rings

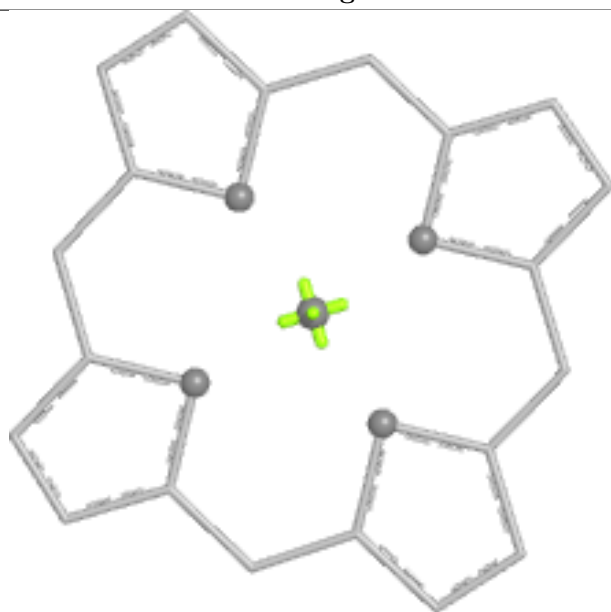
Ligand CLA B 3008



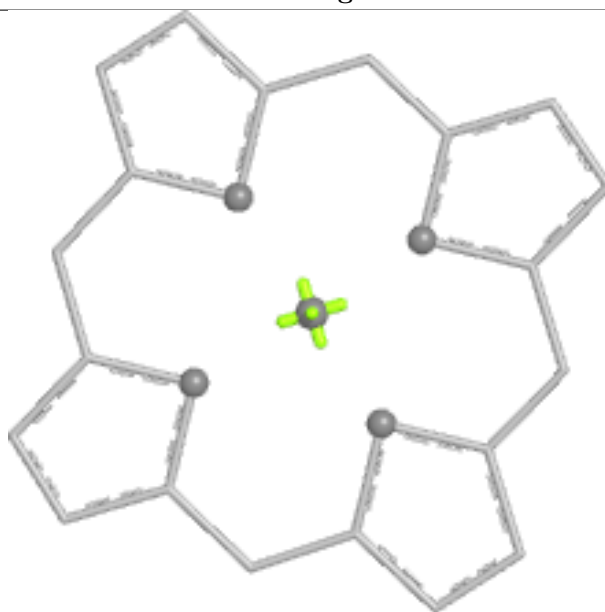
Bond lengths



Bond angles

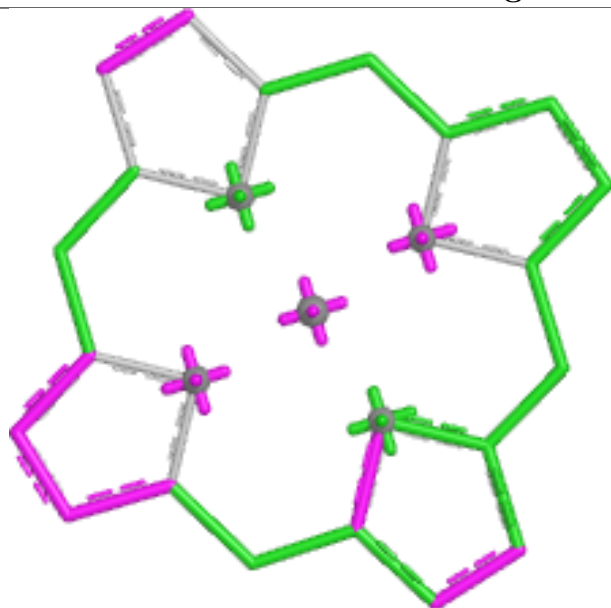


Torsions

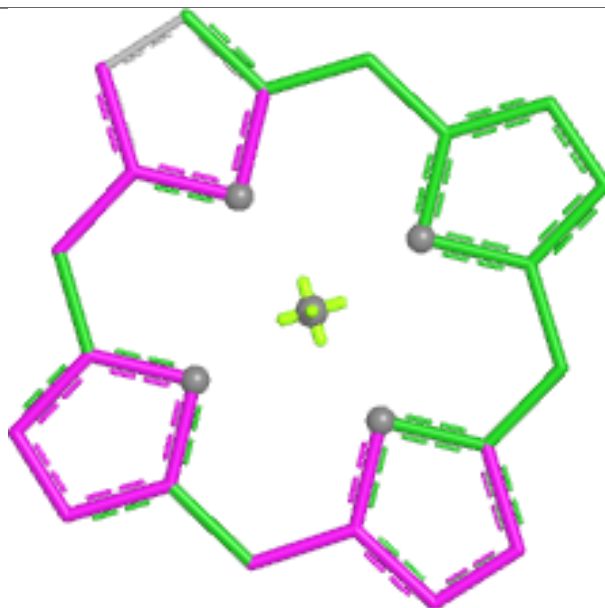


Rings

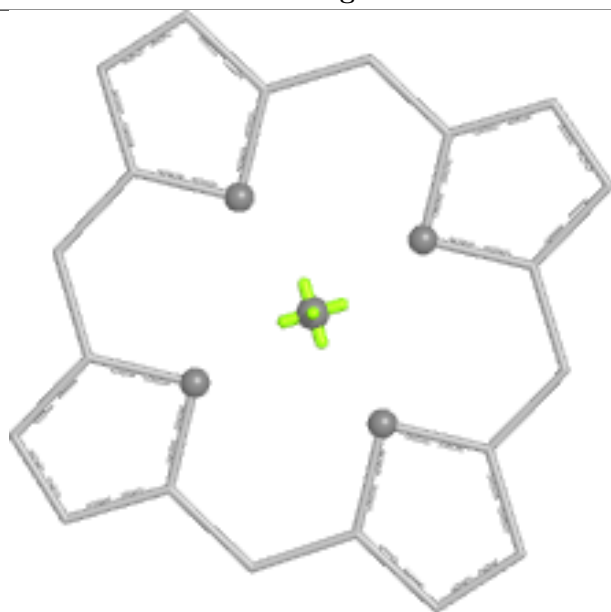
Ligand CLA A 3032



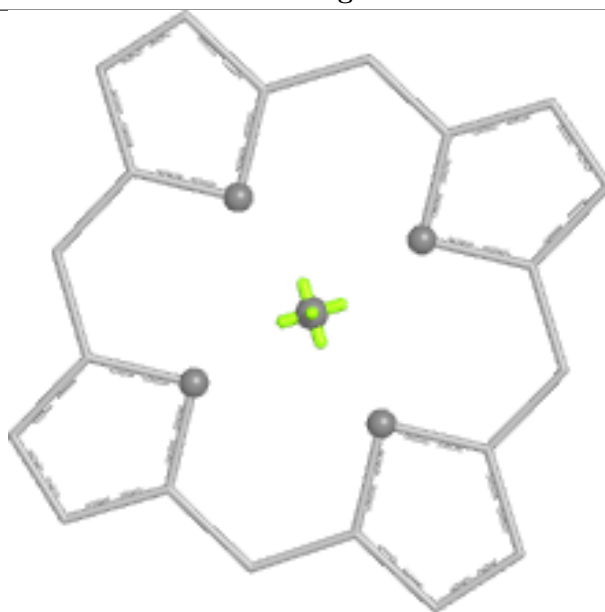
Bond lengths



Bond angles

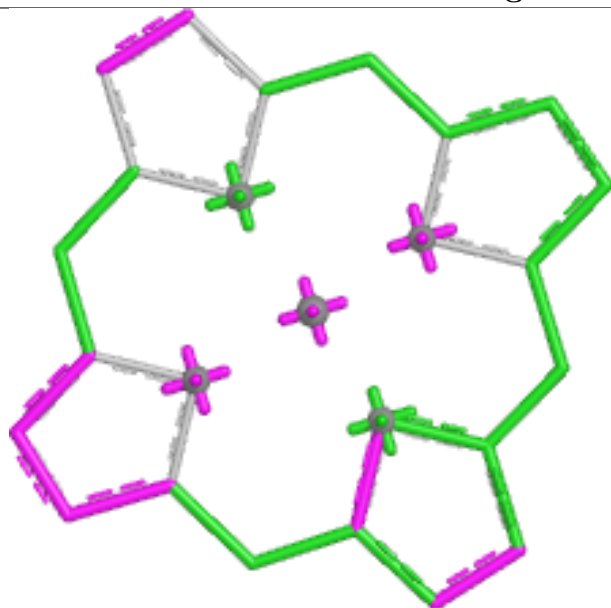


Torsions

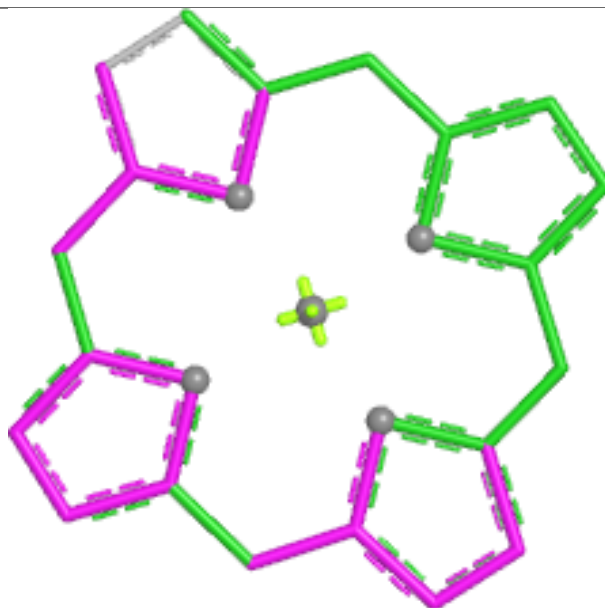


Rings

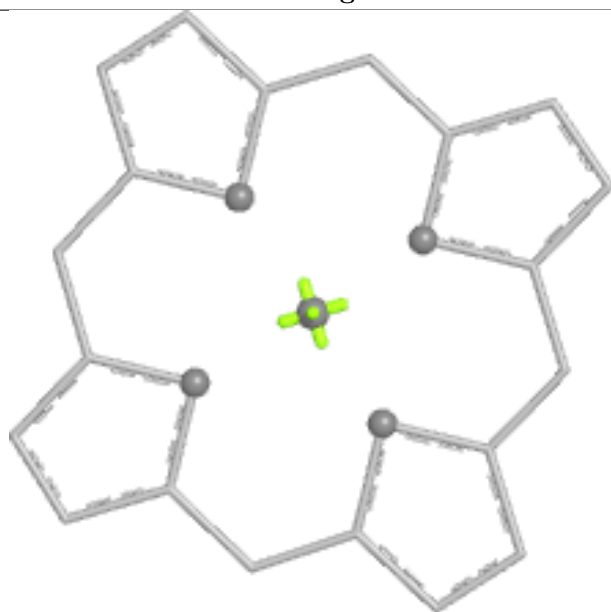
Ligand CLA B 3076



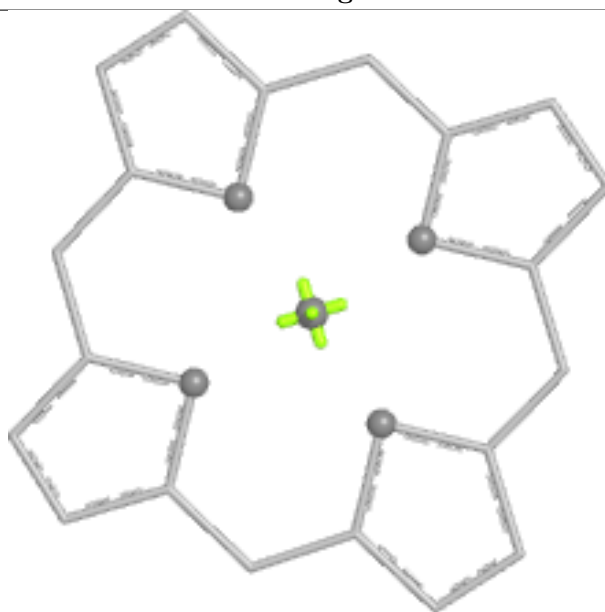
Bond lengths



Bond angles

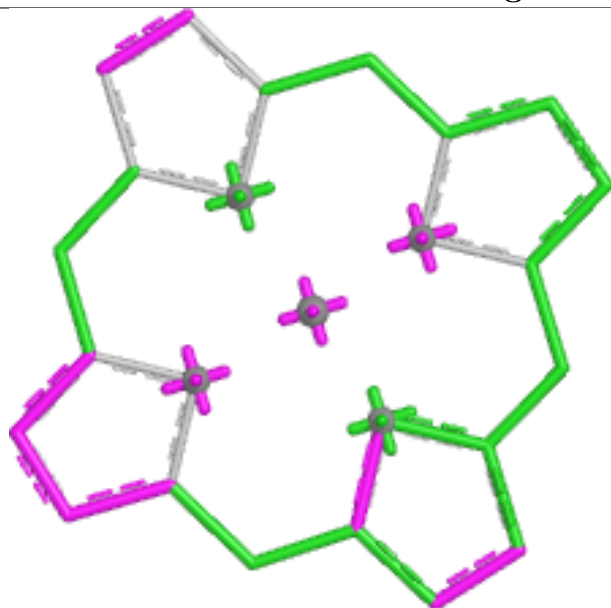


Torsions

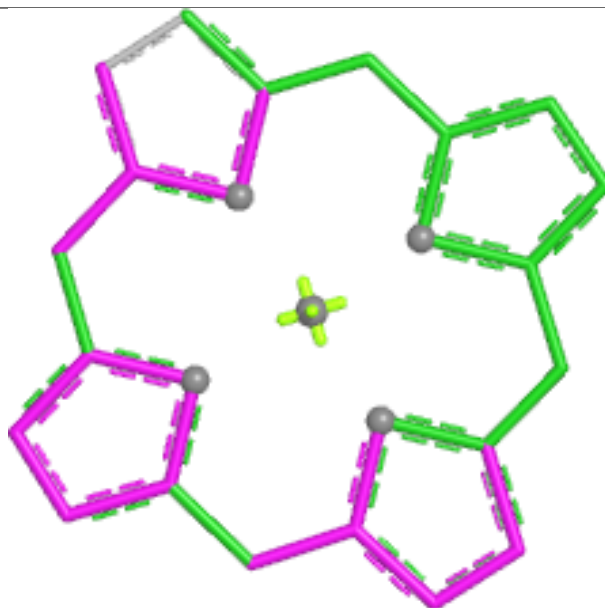


Rings

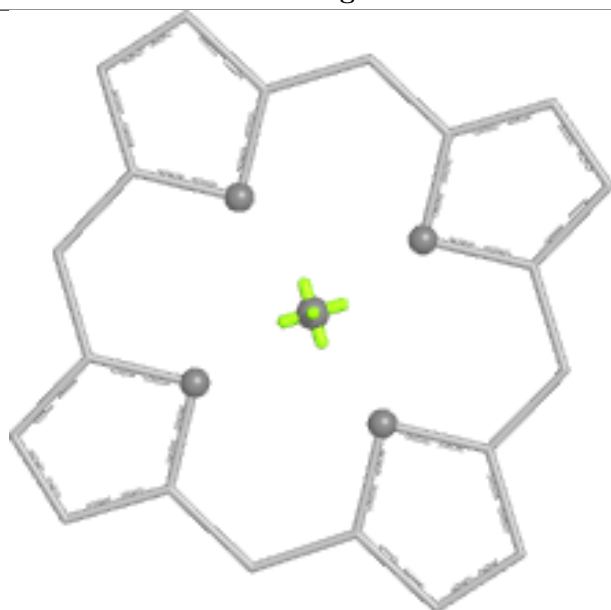
Ligand CLA A 3013



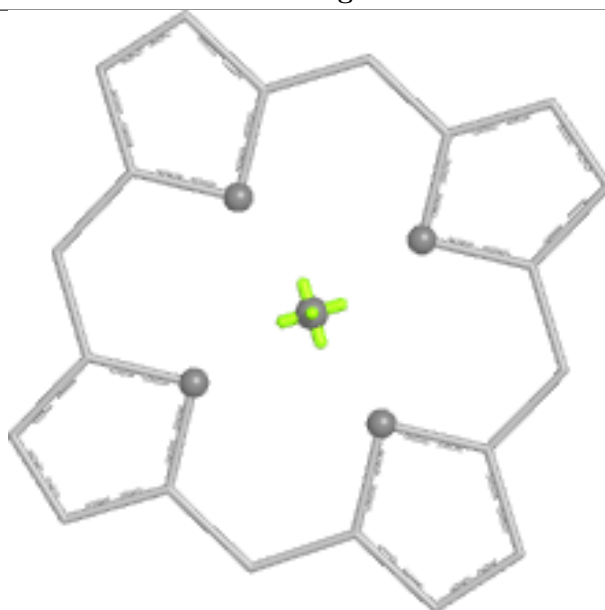
Bond lengths



Bond angles

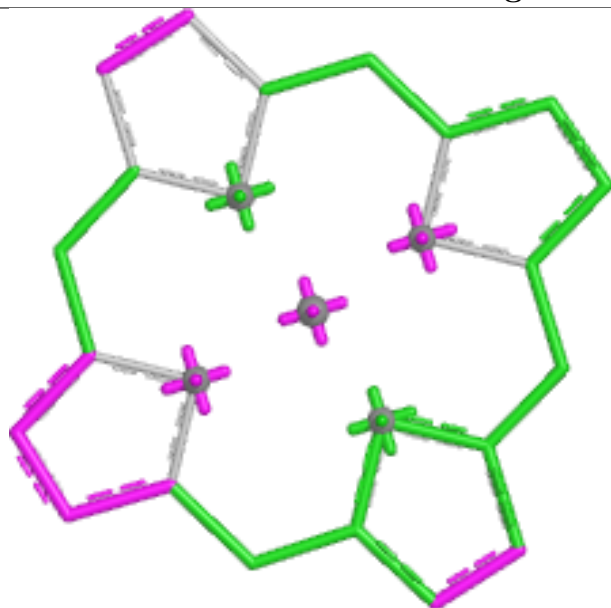


Torsions

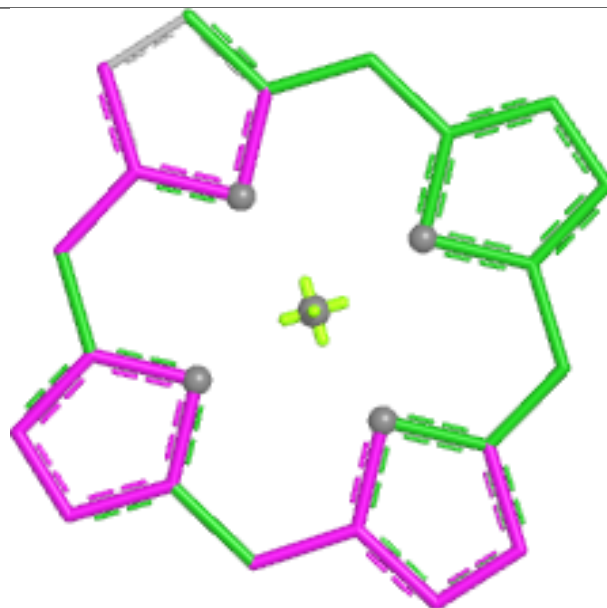


Rings

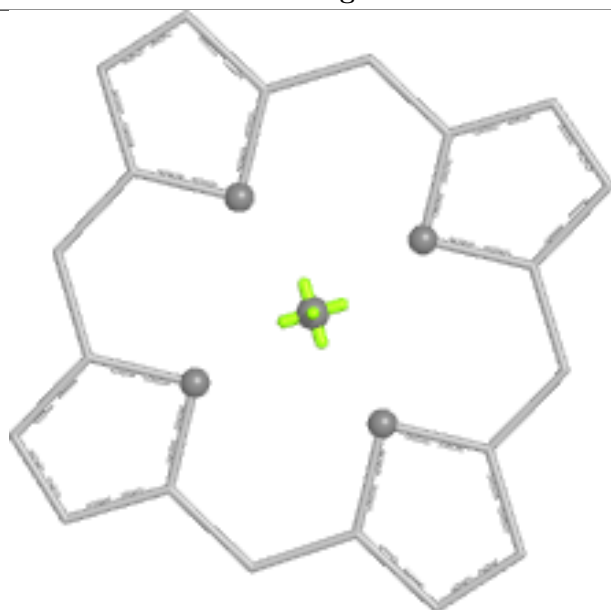
Ligand CLA A 3016



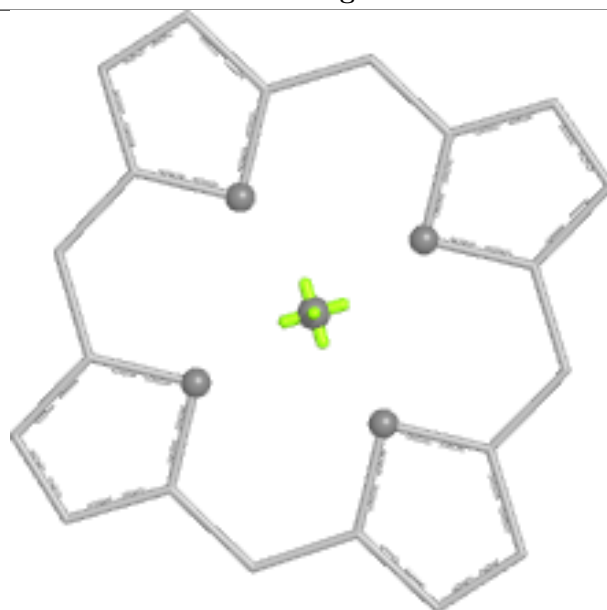
Bond lengths



Bond angles

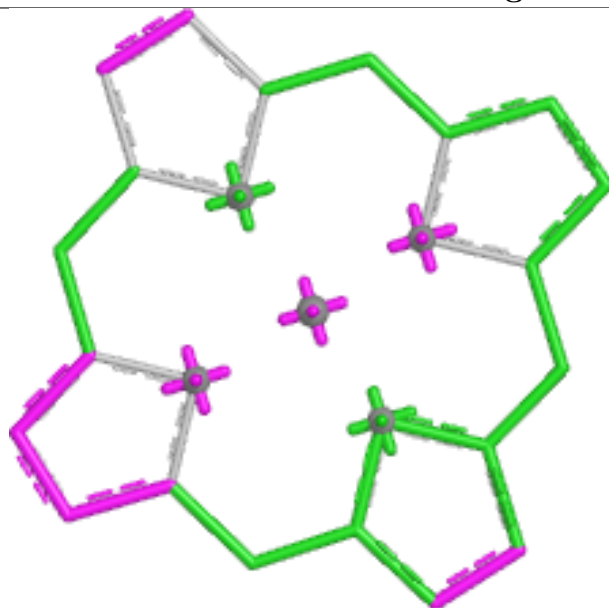


Torsions

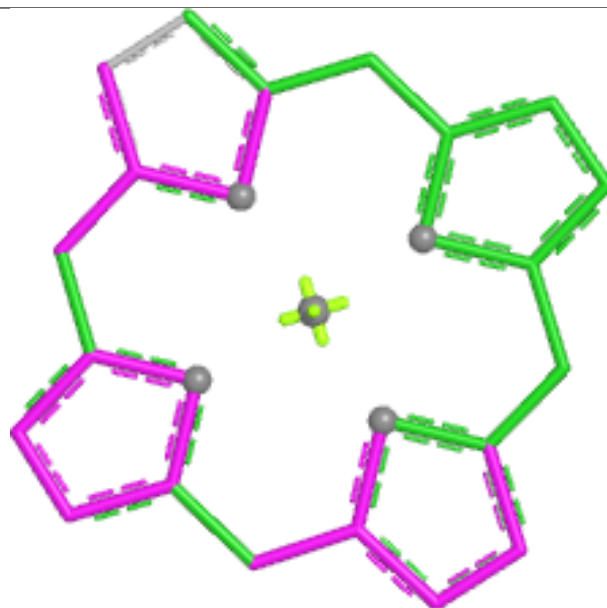


Rings

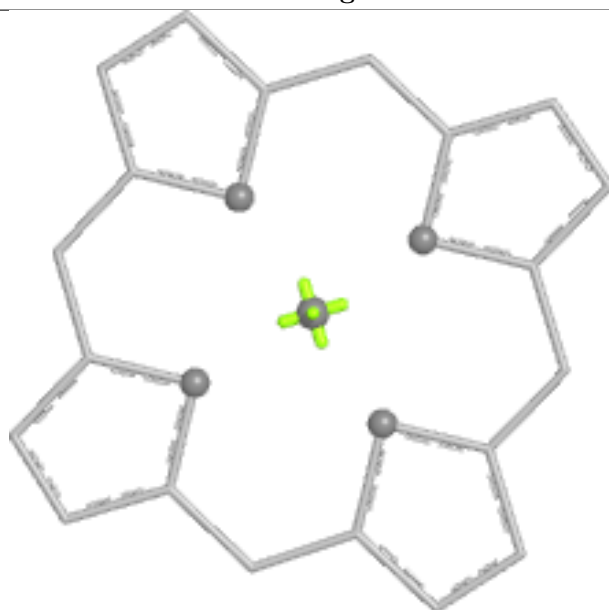
Ligand CLA B 3035



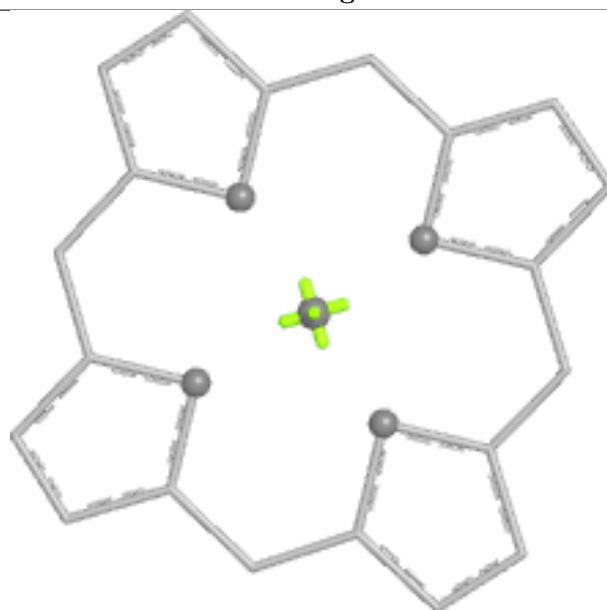
Bond lengths



Bond angles

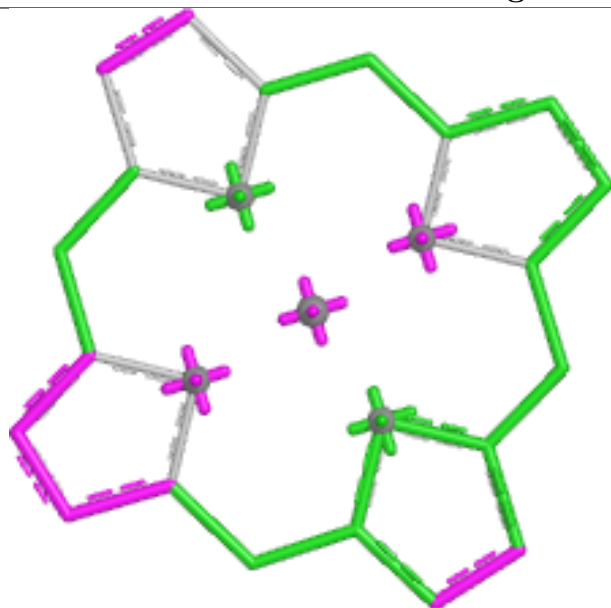


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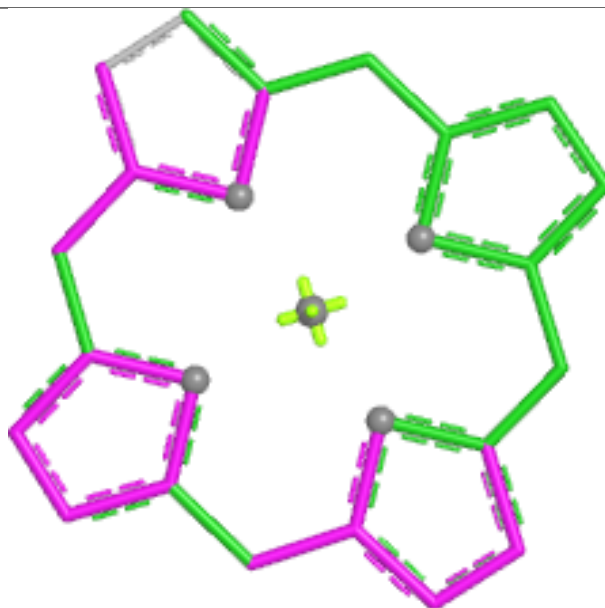


Rings

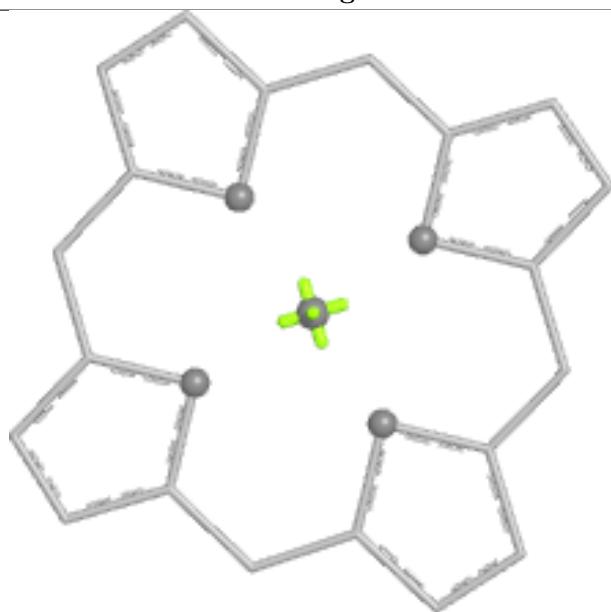
Ligand CLA L 3038



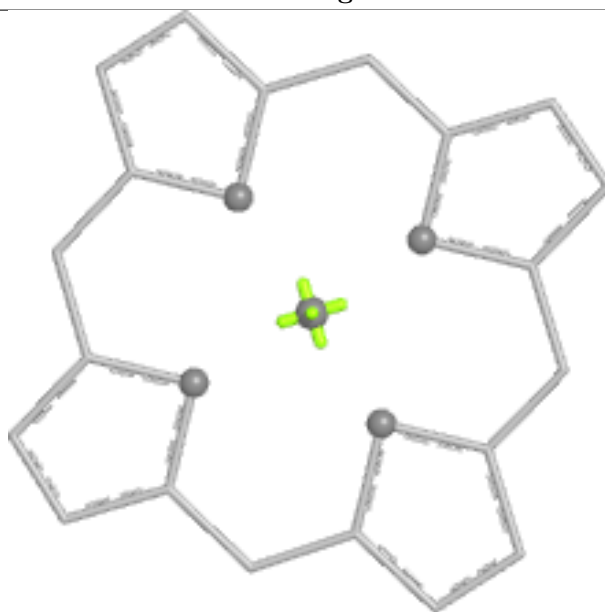
Bond lengths



Bond angles

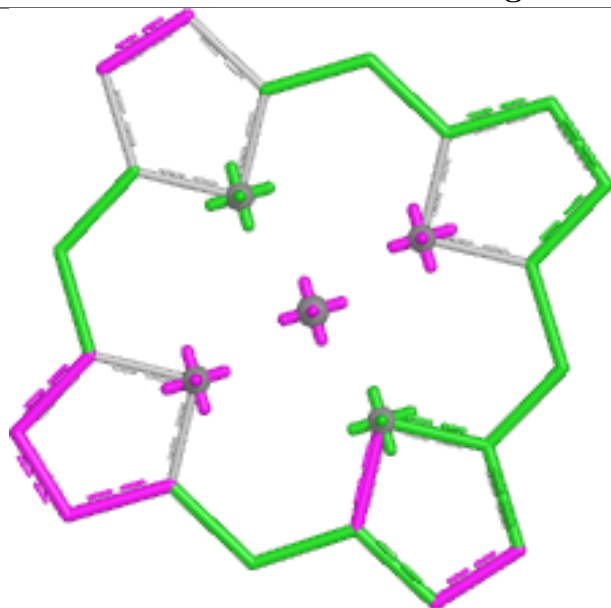


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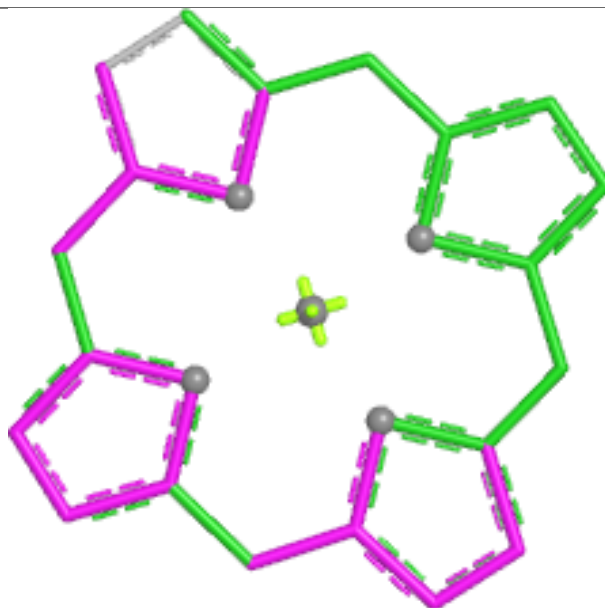


Rings

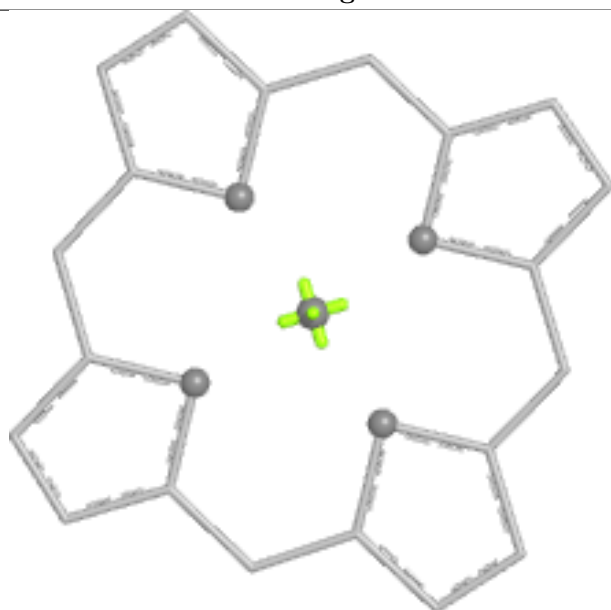
Ligand CLA A 3005



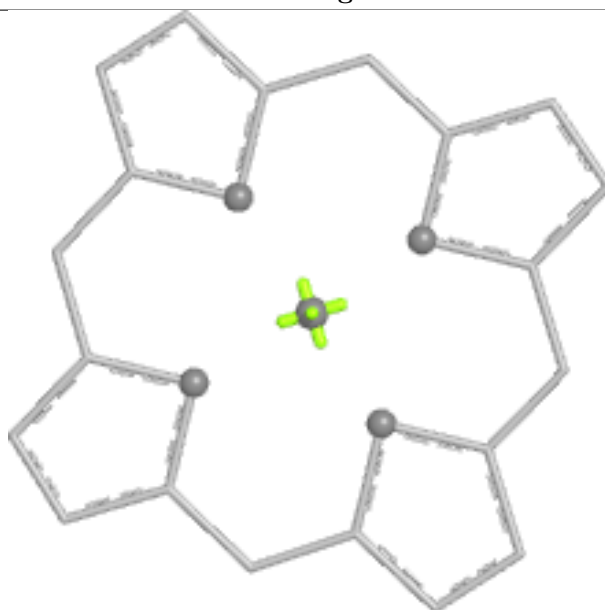
Bond lengths



Bond angles

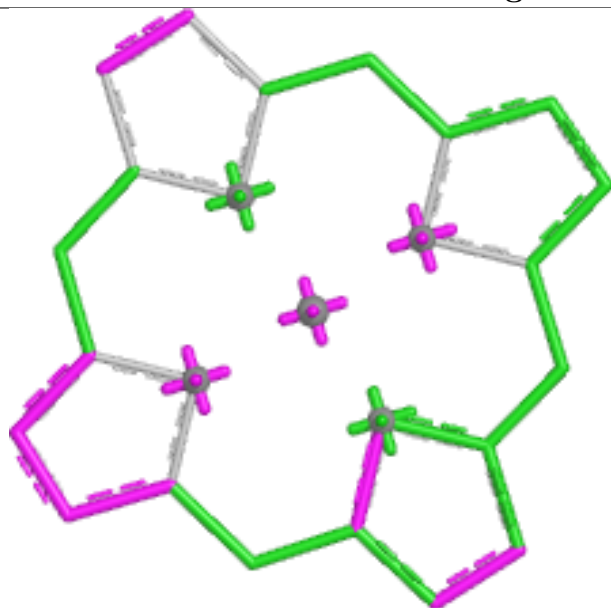


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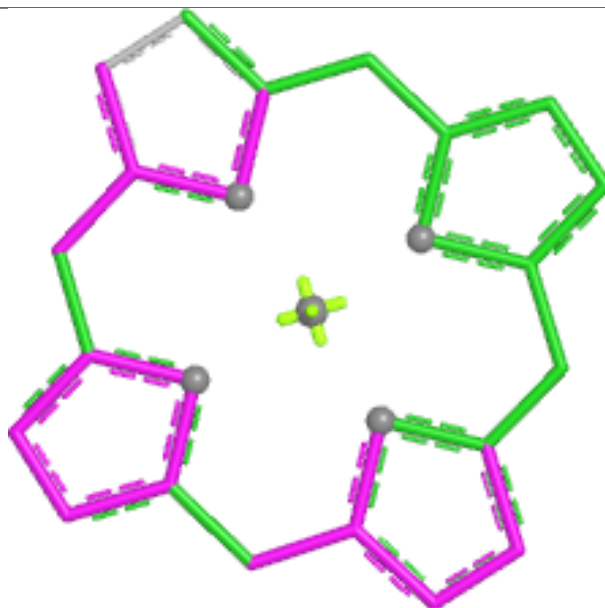


Rings

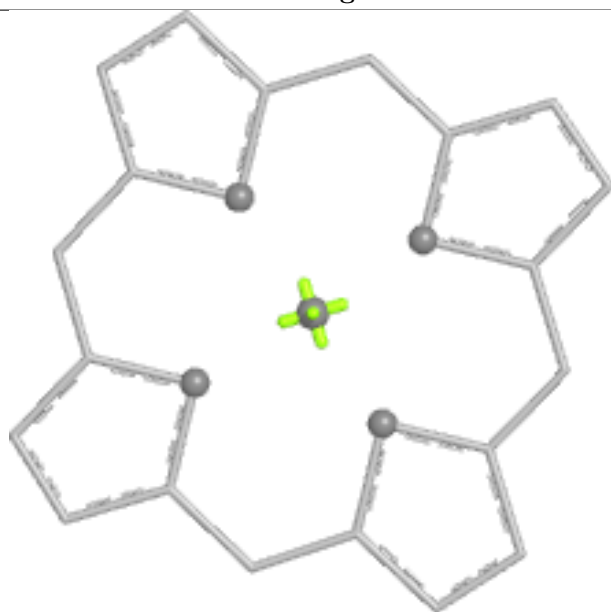
Ligand CLA B 3025



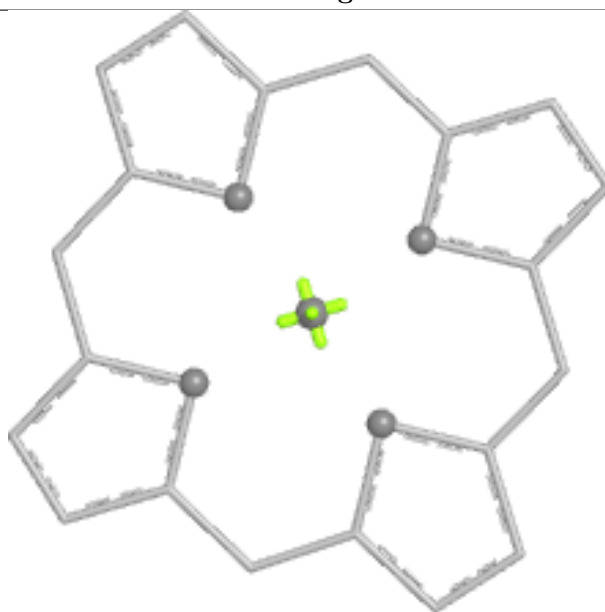
Bond lengths



Bond angles

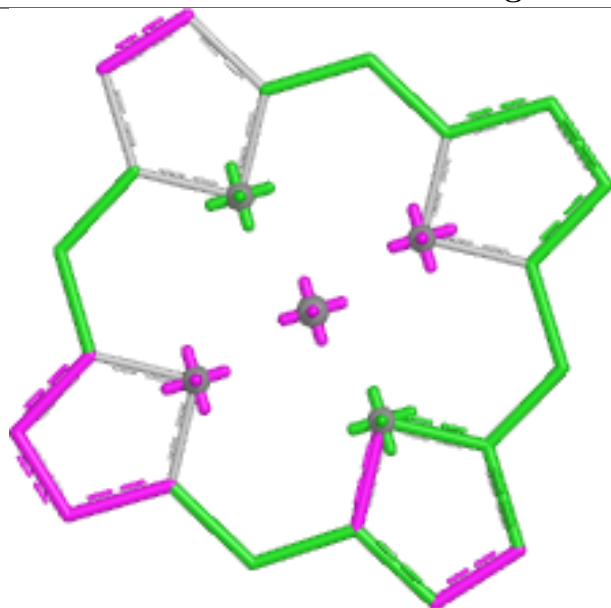


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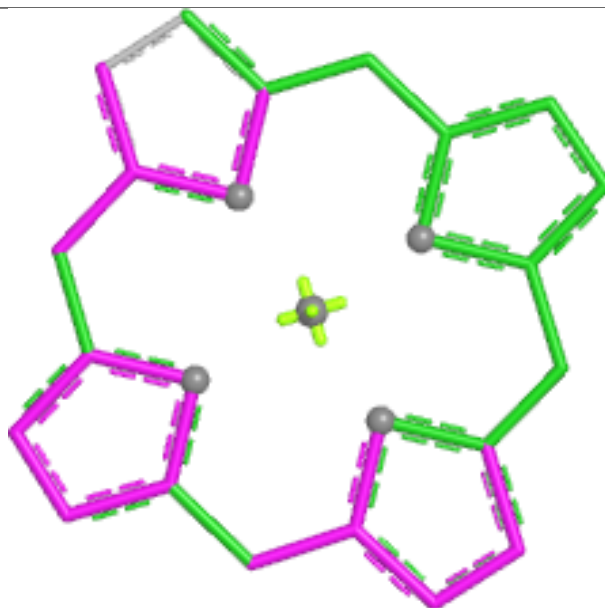


Rings

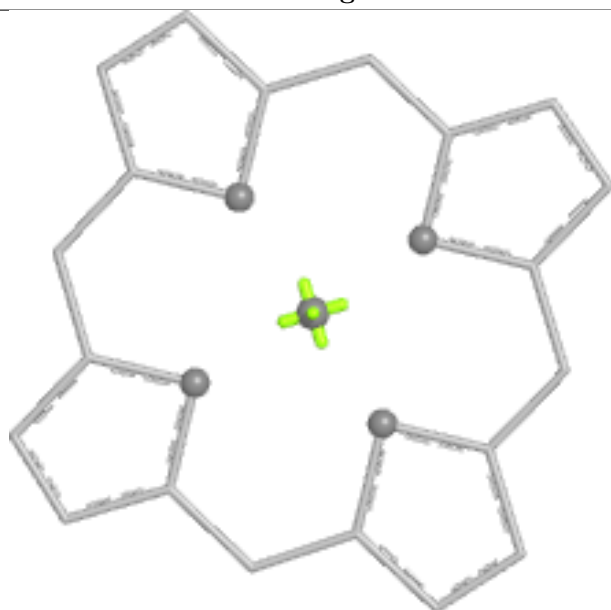
Ligand CLA A 3027



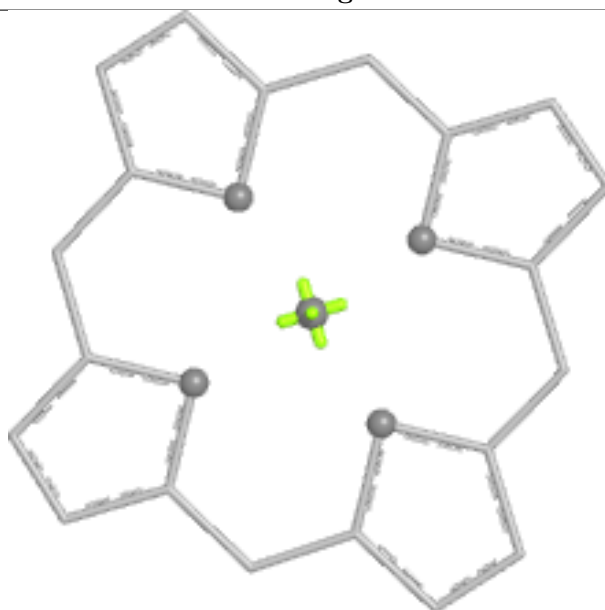
Bond lengths



Bond angles

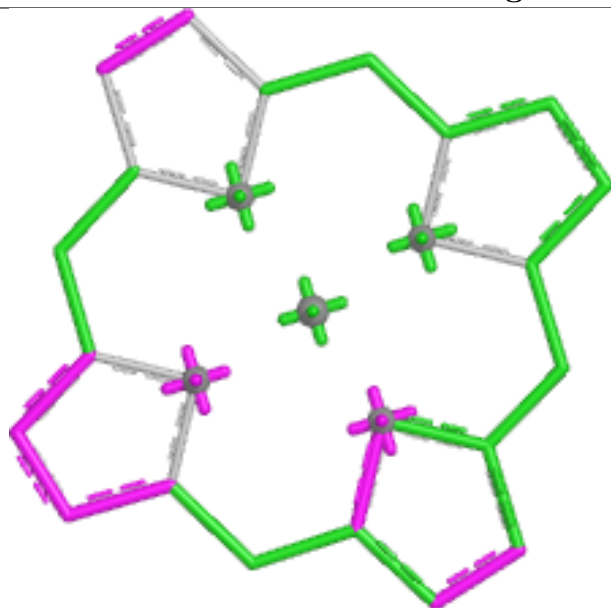


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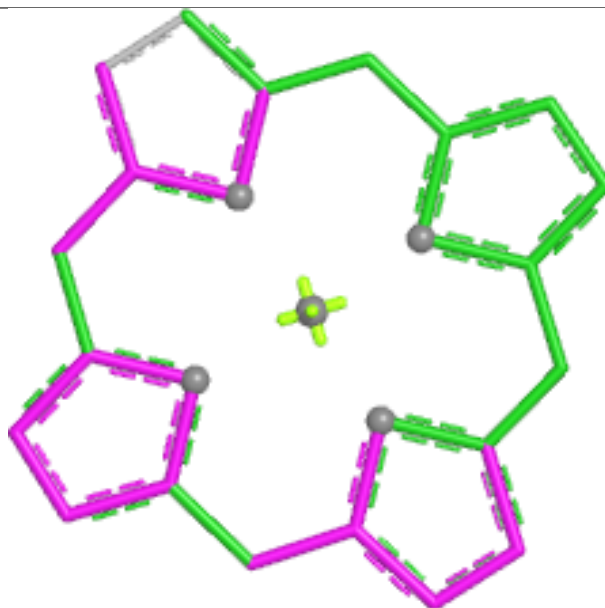


Rings

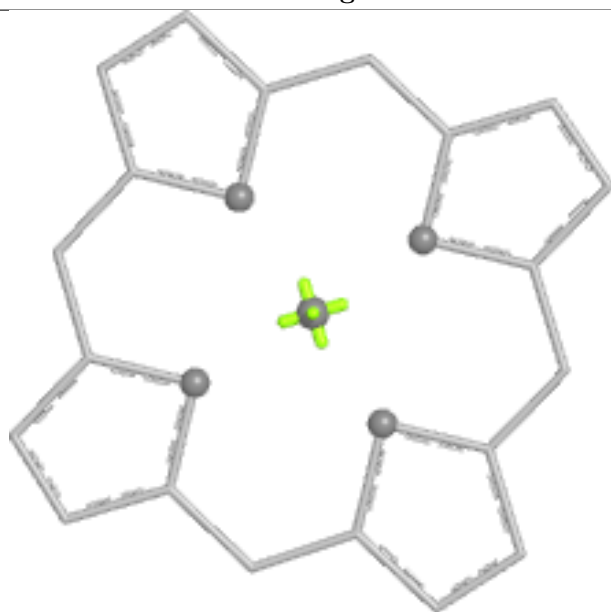
Ligand CLA B 2002



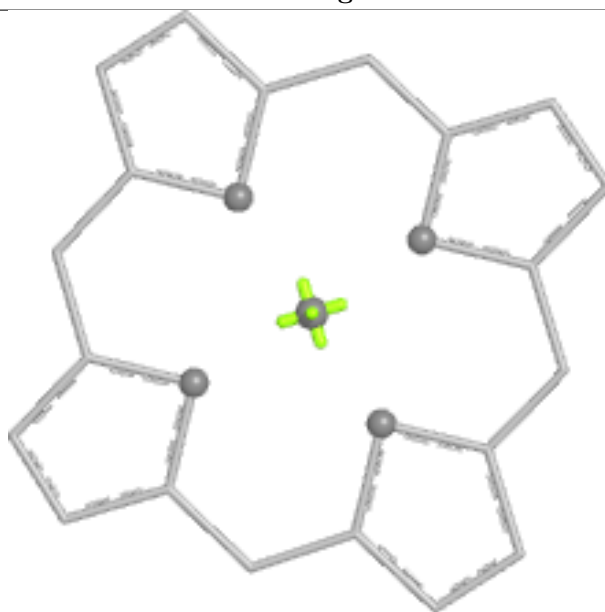
Bond lengths



Bond angles

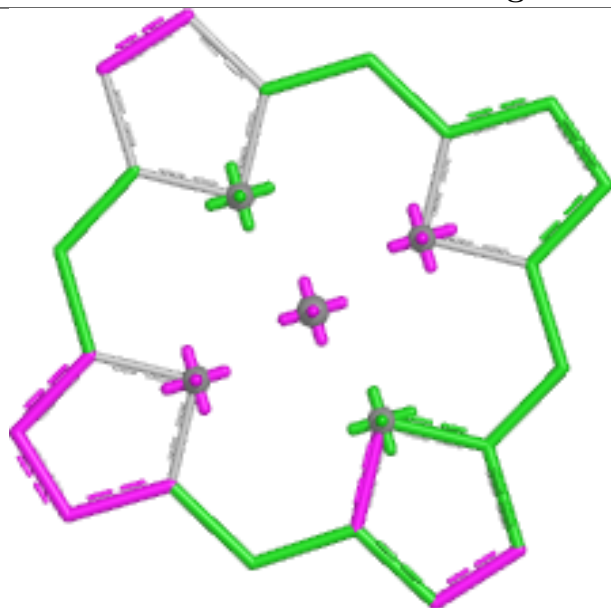


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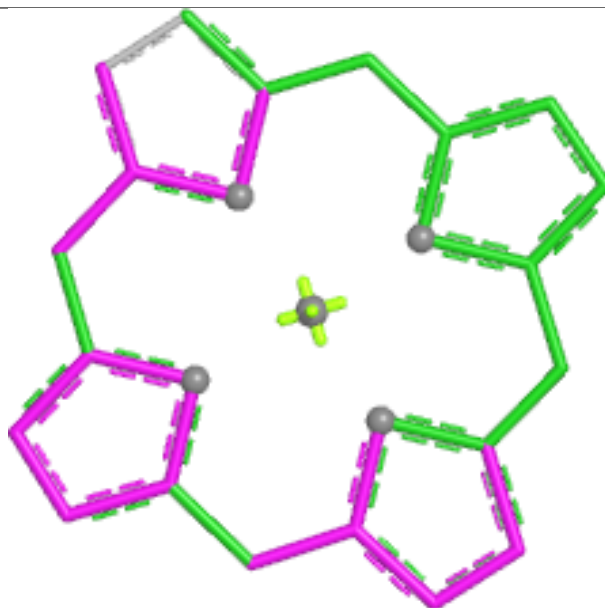


Rings

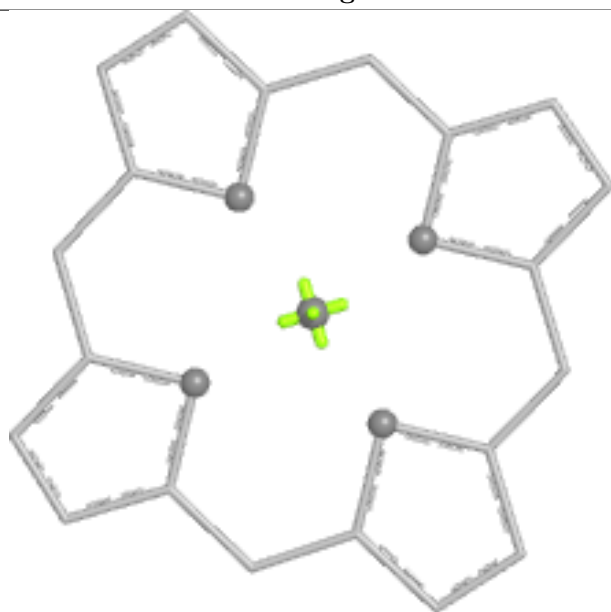
Ligand CLA F 3012



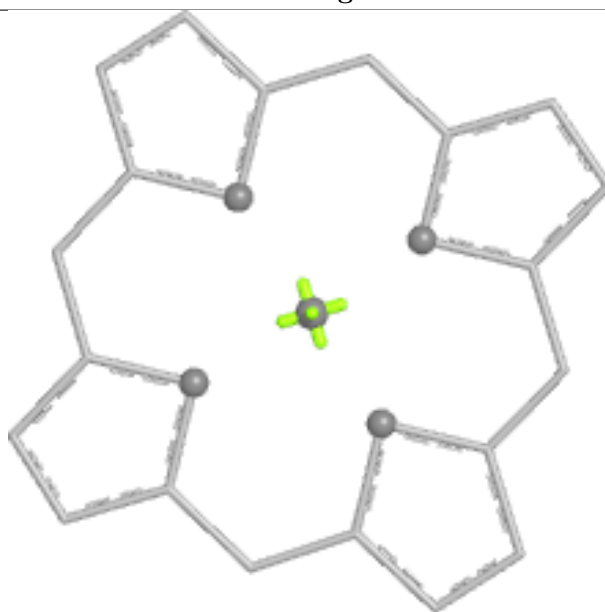
Bond lengths



Bond angles

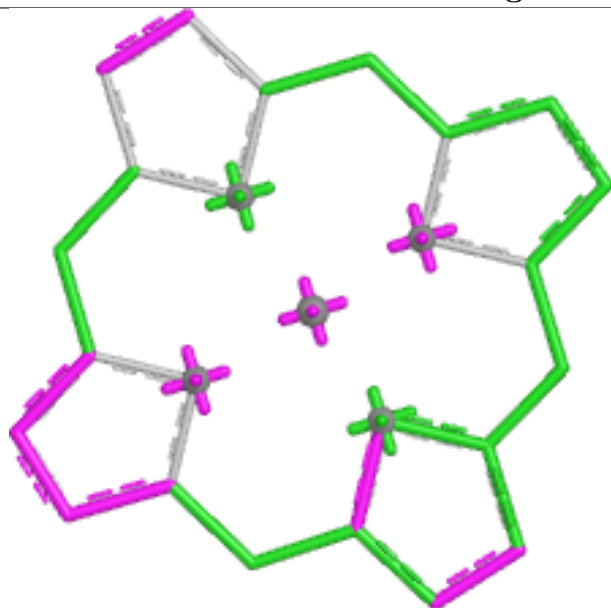


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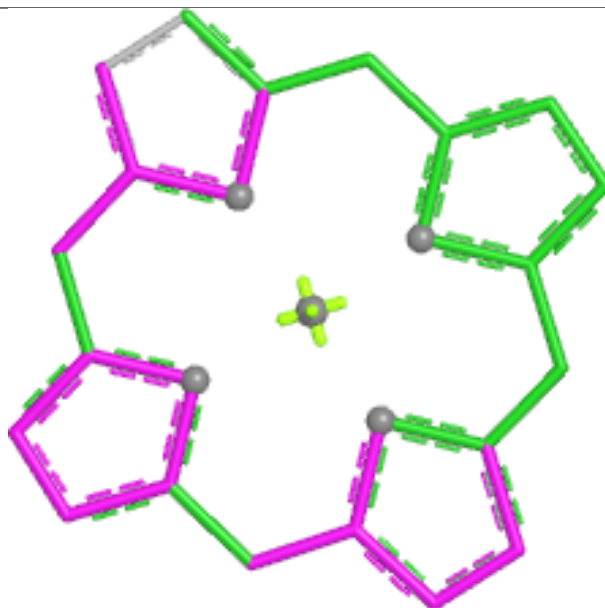


Rings

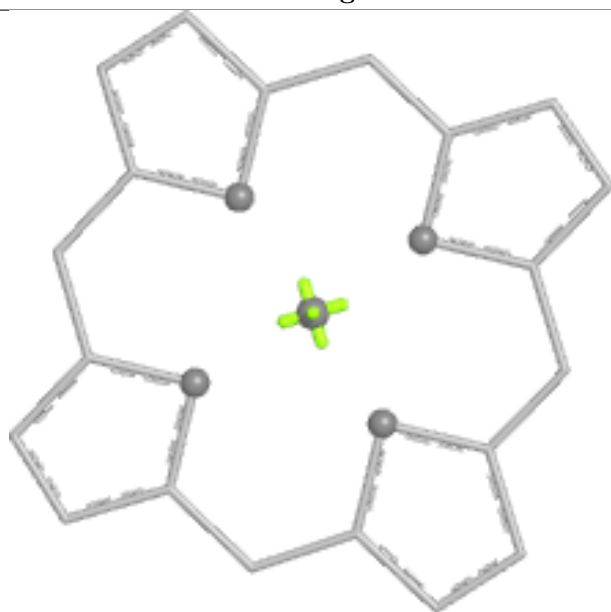
Ligand CLA B 3001



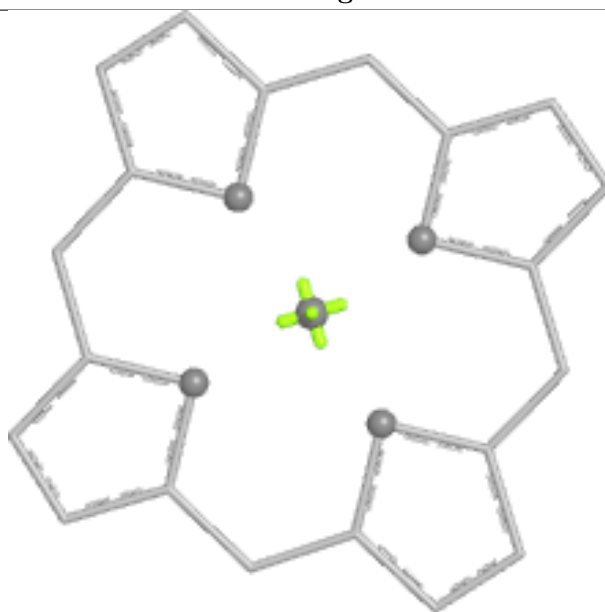
Bond lengths



Bond angles

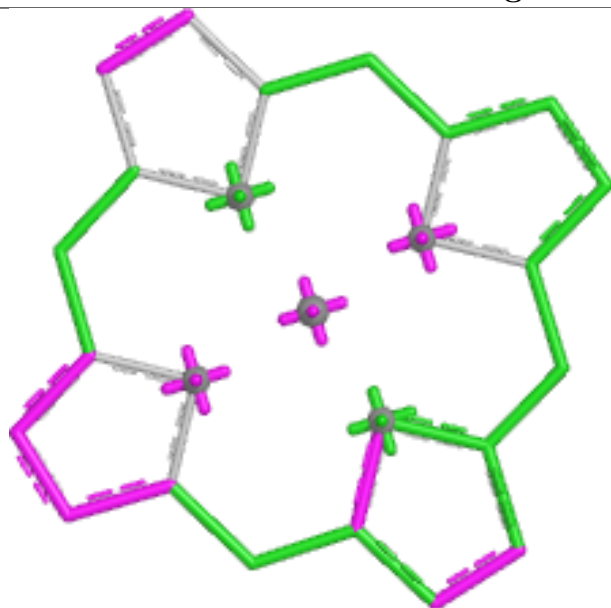


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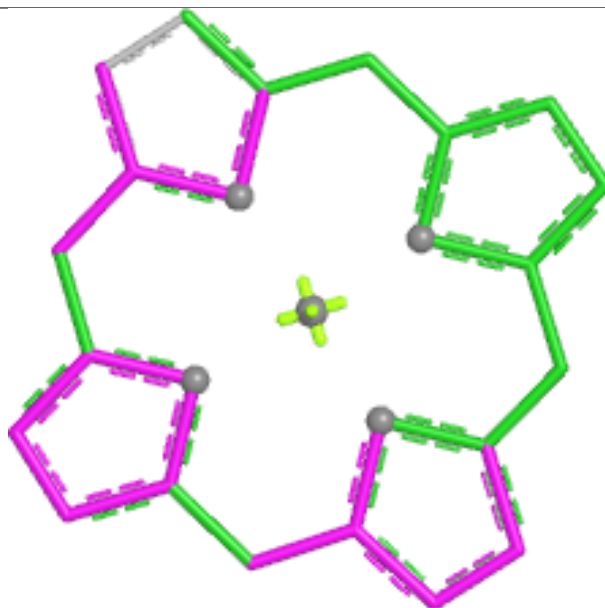


Rings

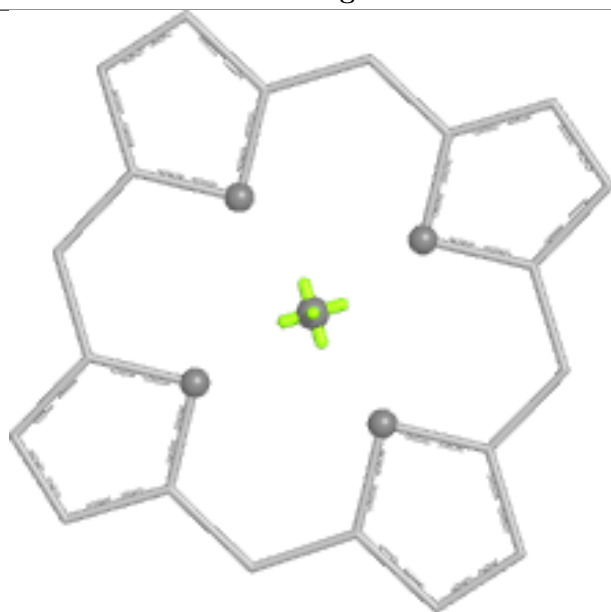
Ligand CLA A 3053



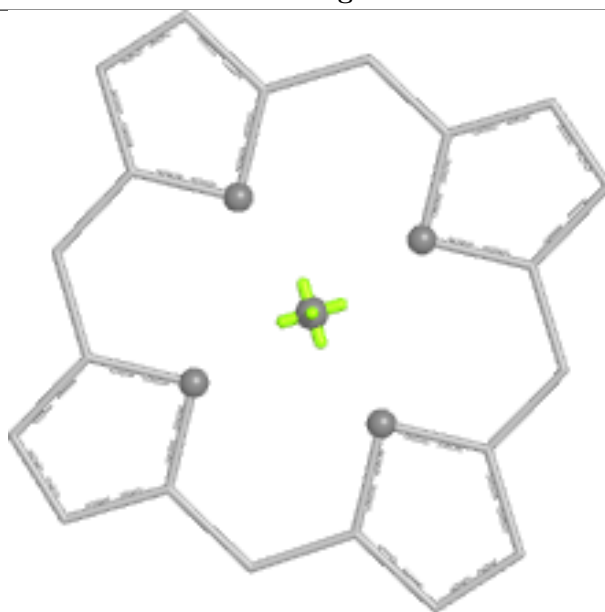
Bond lengths



Bond angles

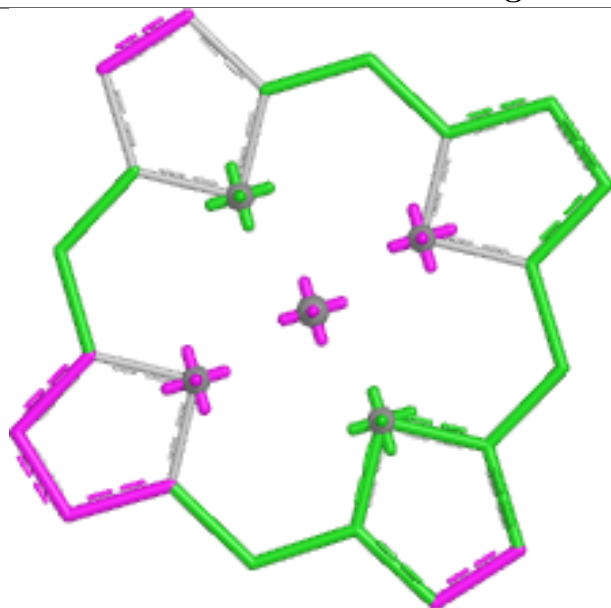


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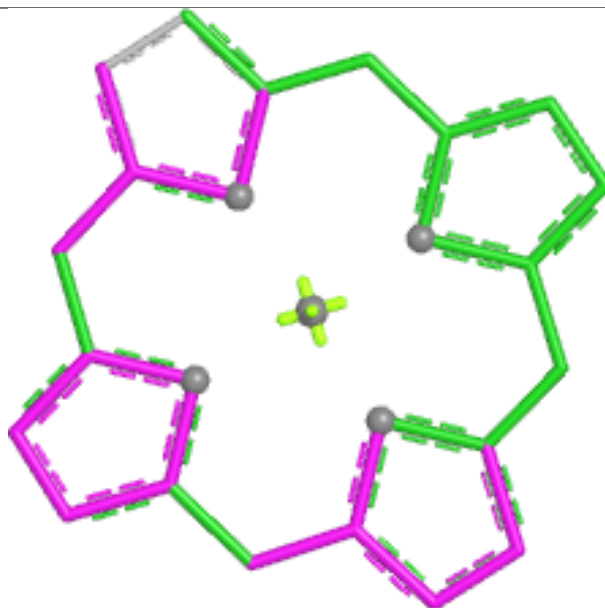


Rings

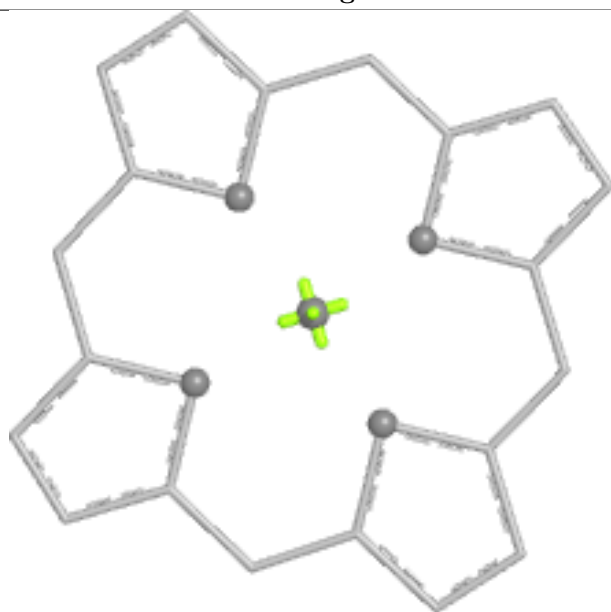
Ligand CLA A 3021



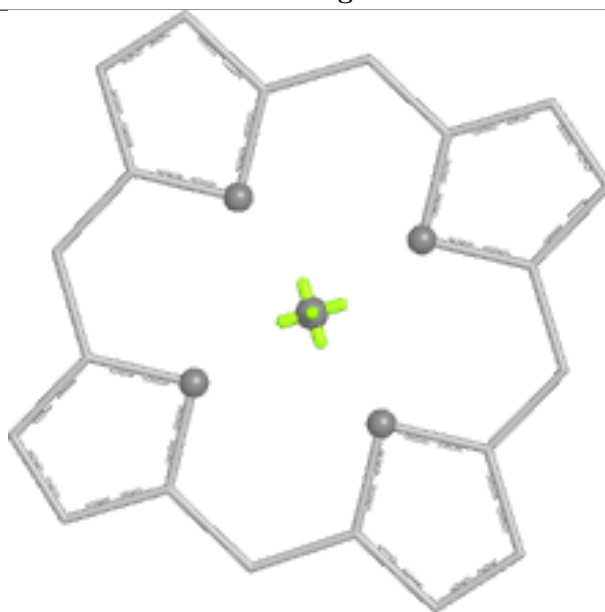
Bond lengths



Bond angles

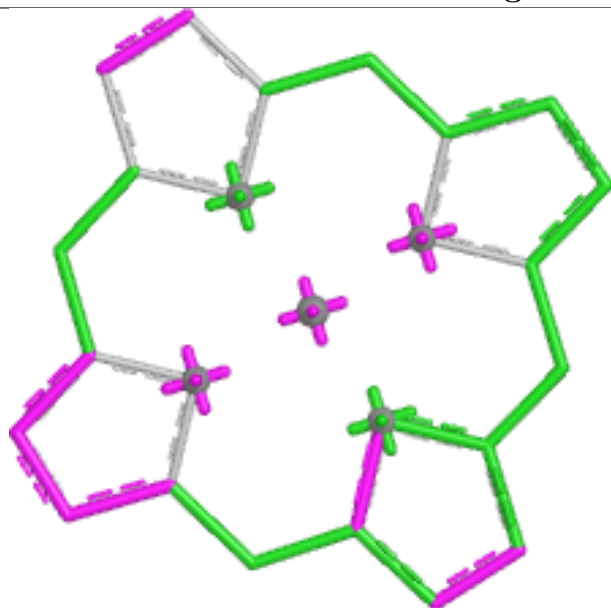


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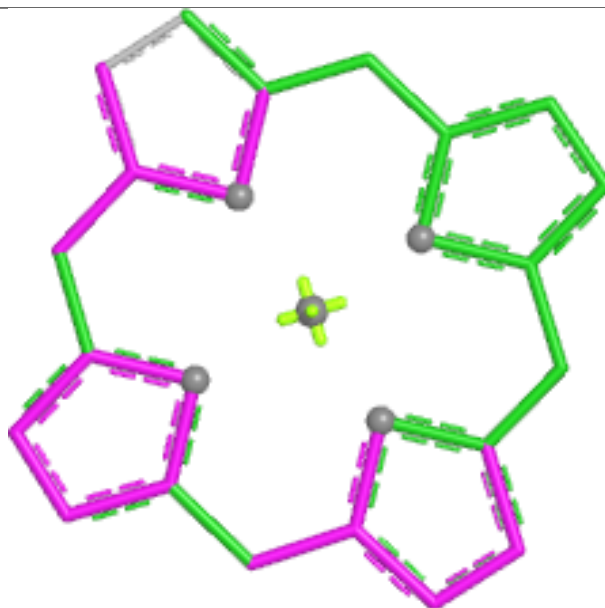


Rings

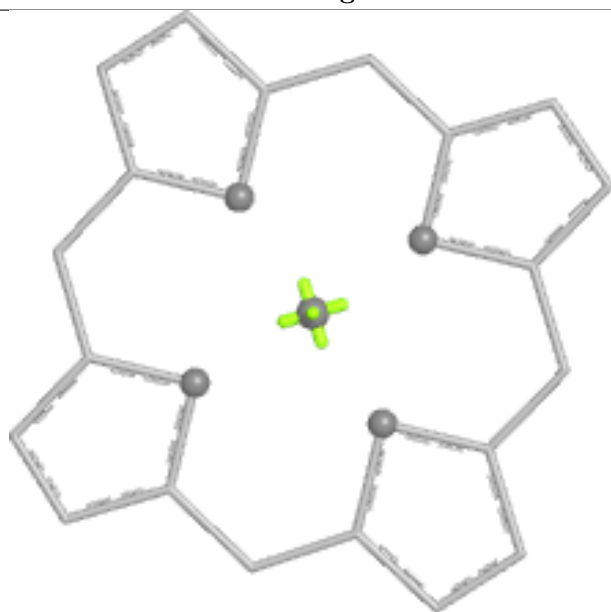
Ligand CLA K 3050



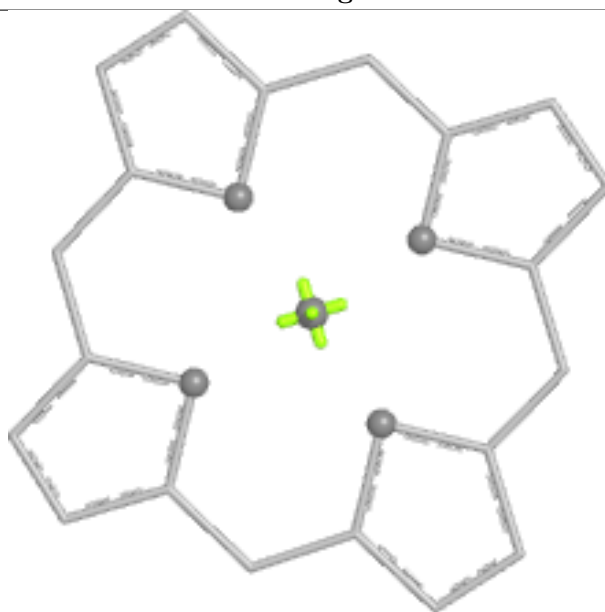
Bond lengths



Bond angles

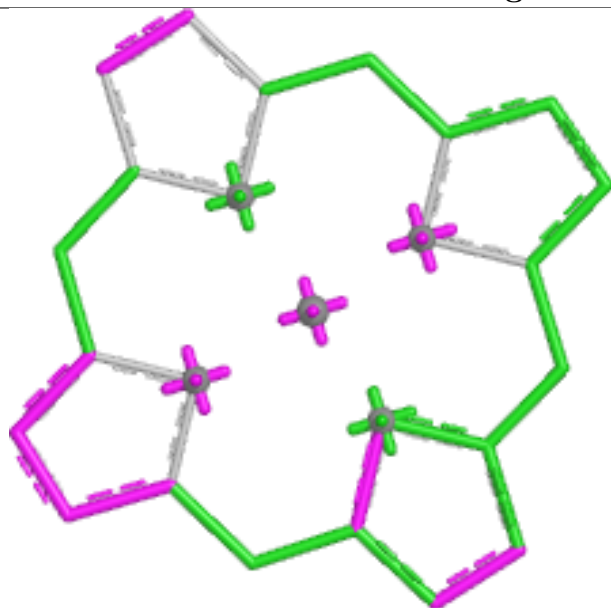


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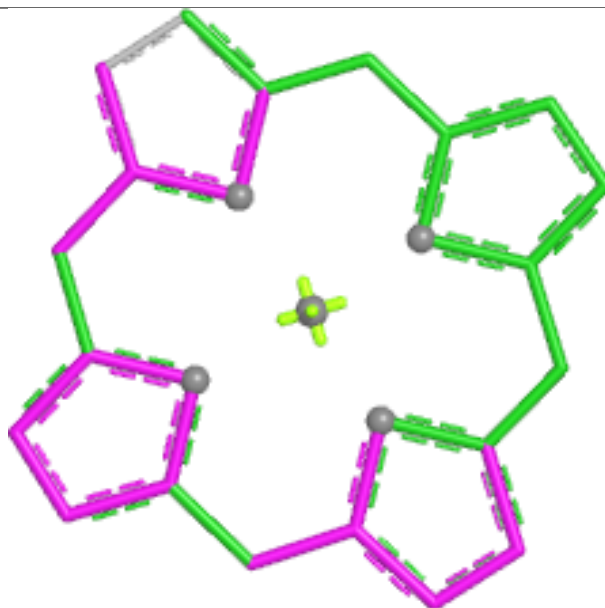


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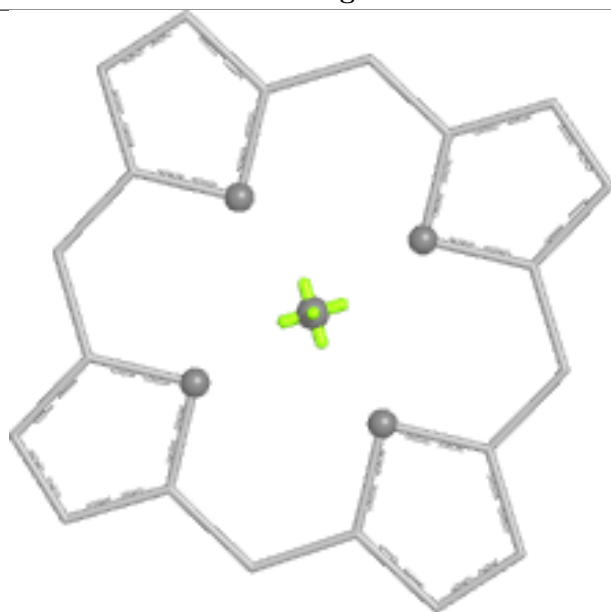
Ligand CLA B 3006



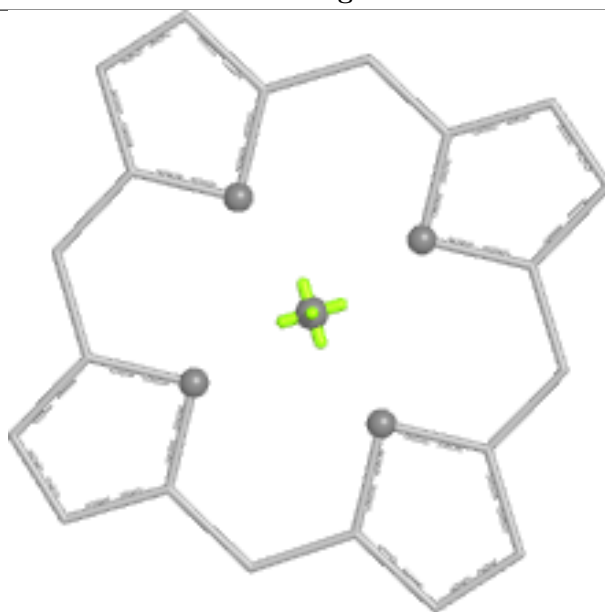
Bond lengths



Bond angles

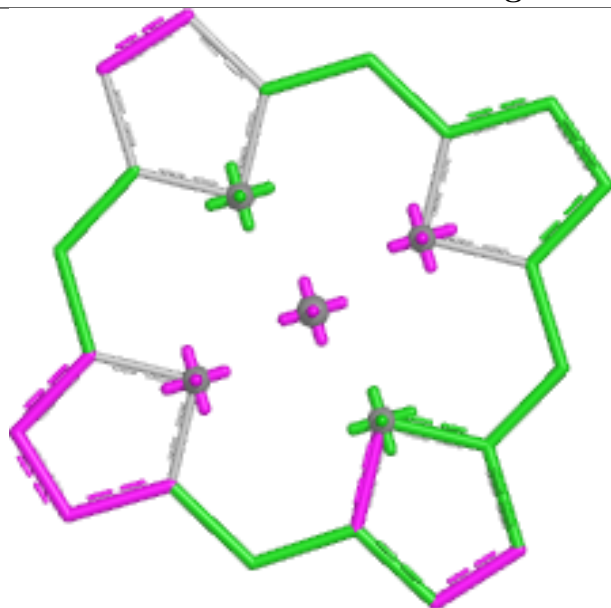


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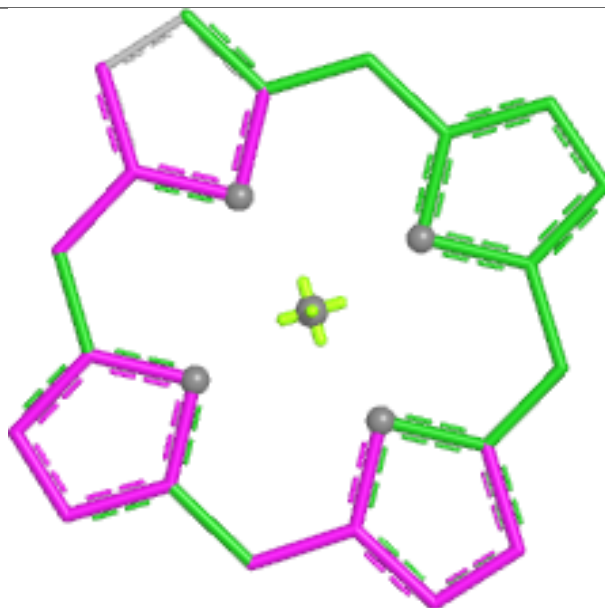


Rings

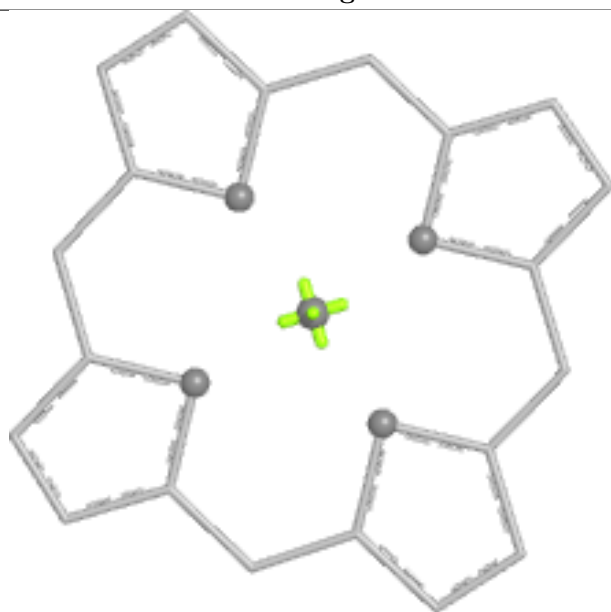
Ligand CLA A 3072



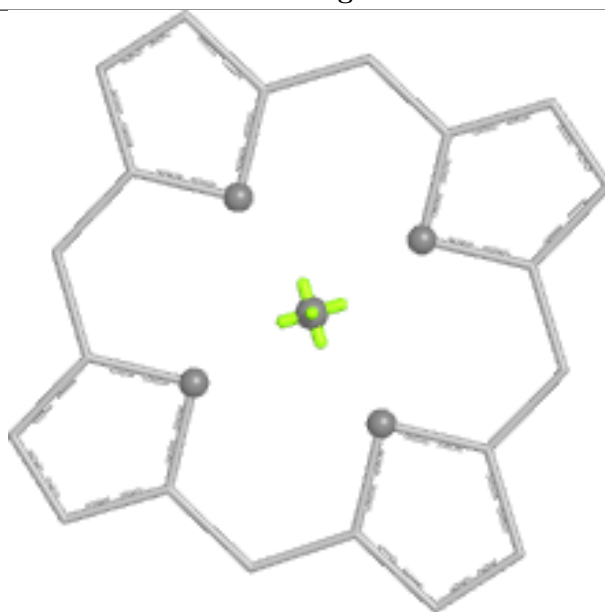
Bond lengths



Bond angles

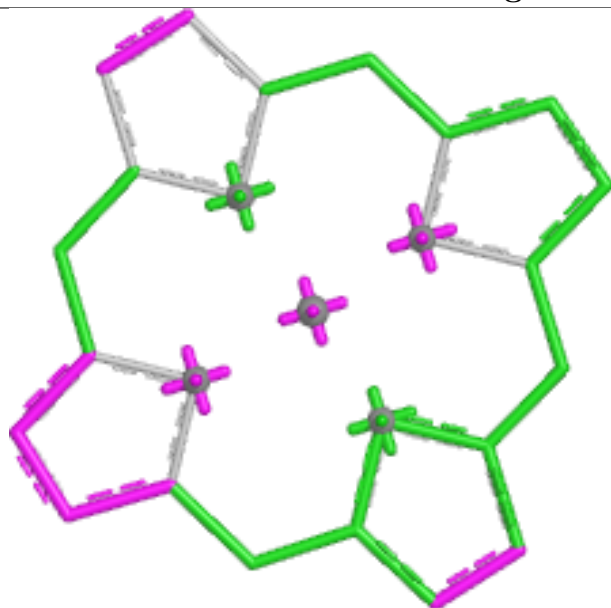


Torsions

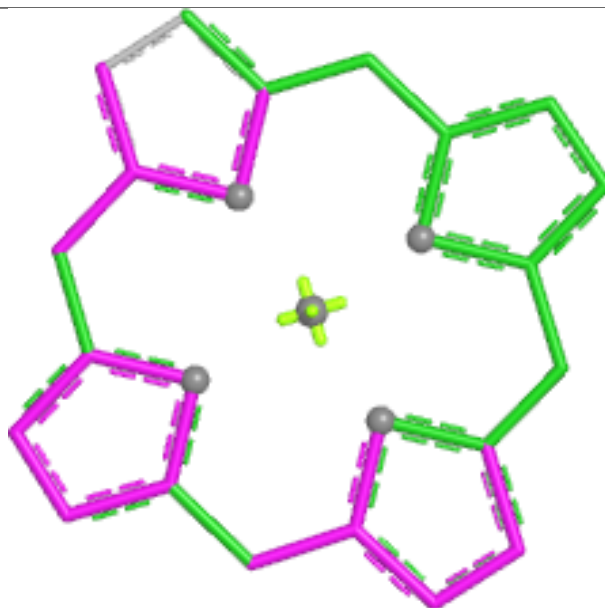


Rings

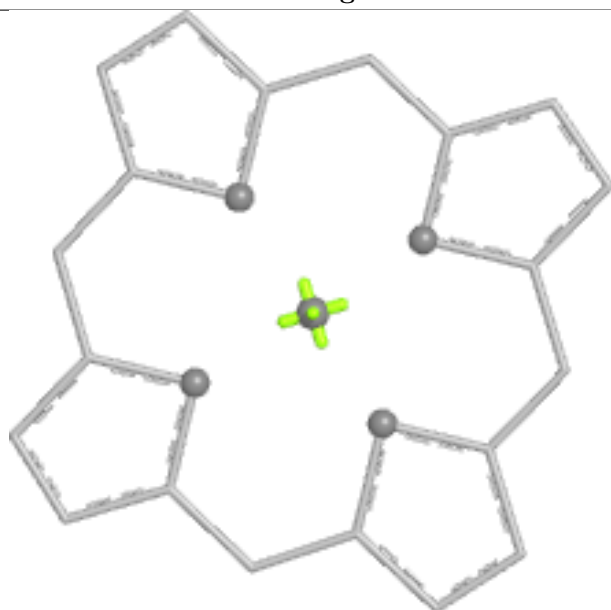
Ligand CLA A 3057



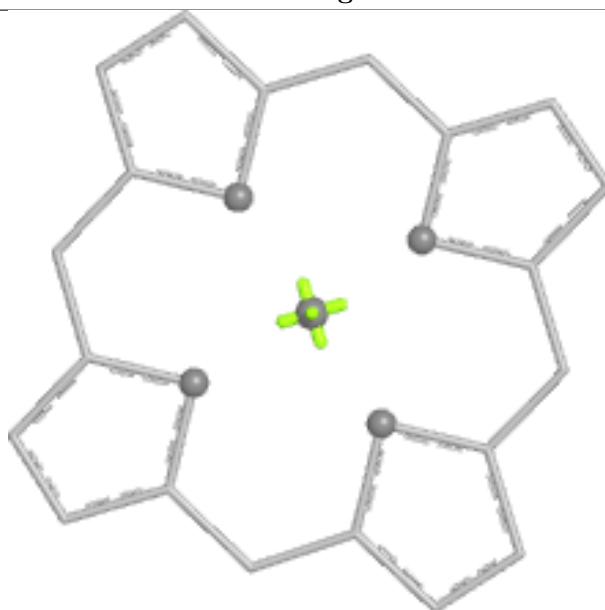
Bond lengths



Bond angles

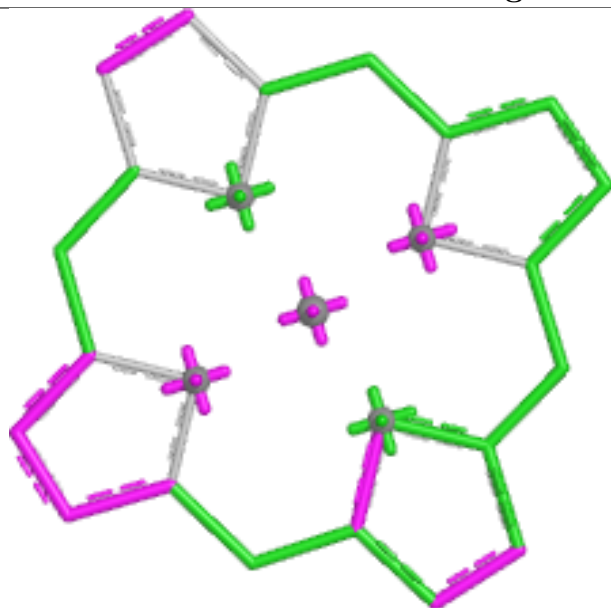


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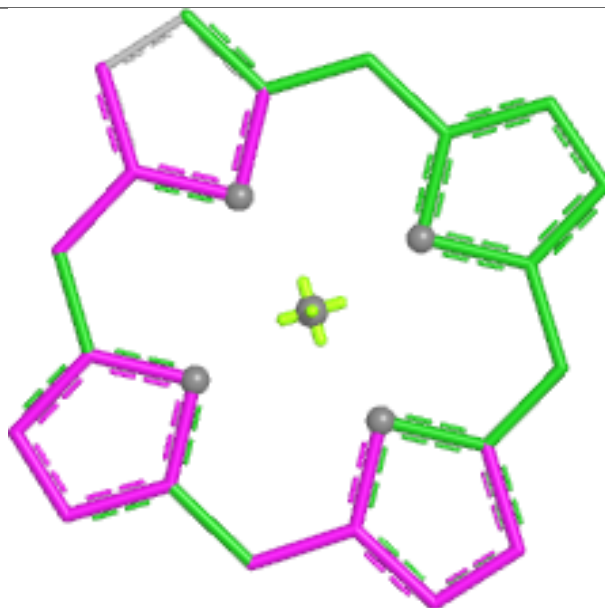


Rings

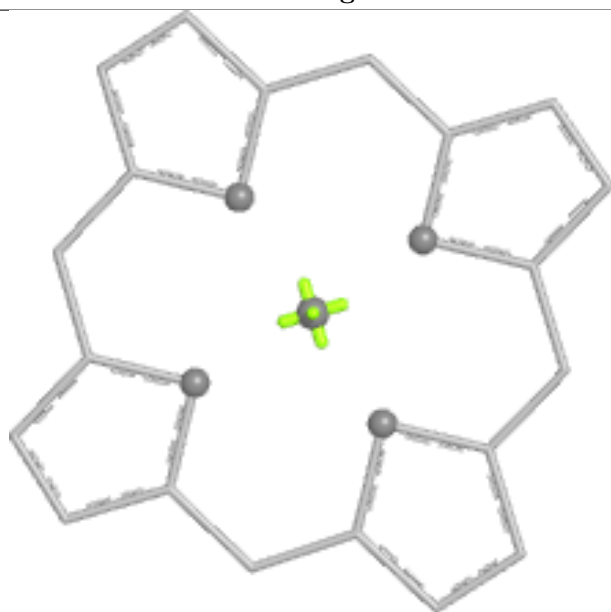
Ligand CLA B 3055



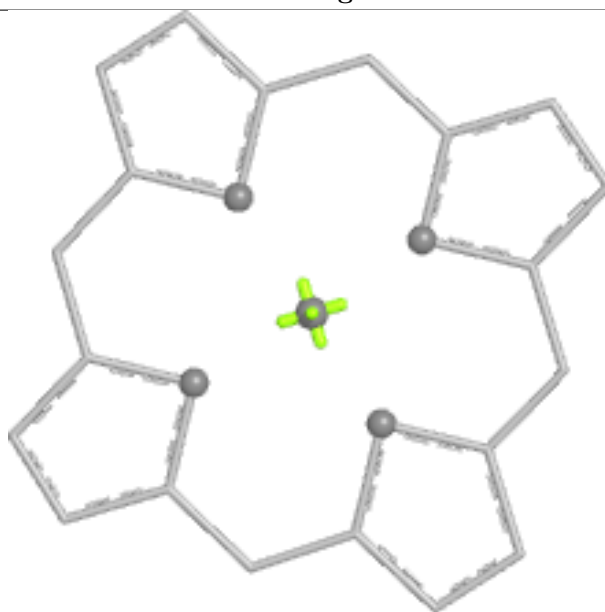
Bond lengths



Bond angles

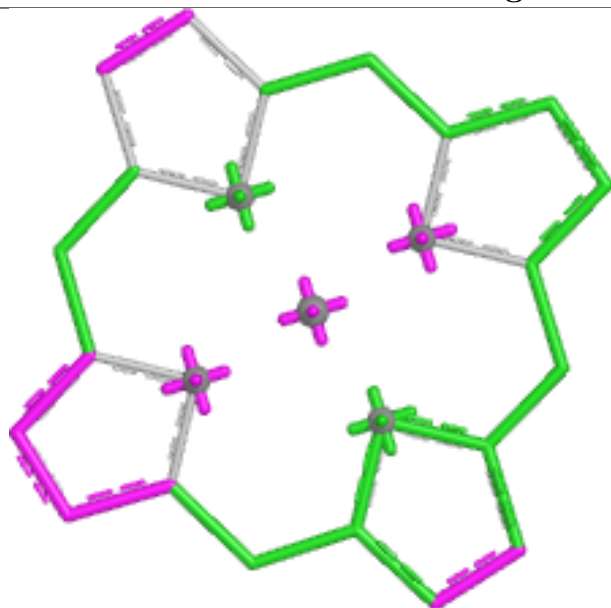


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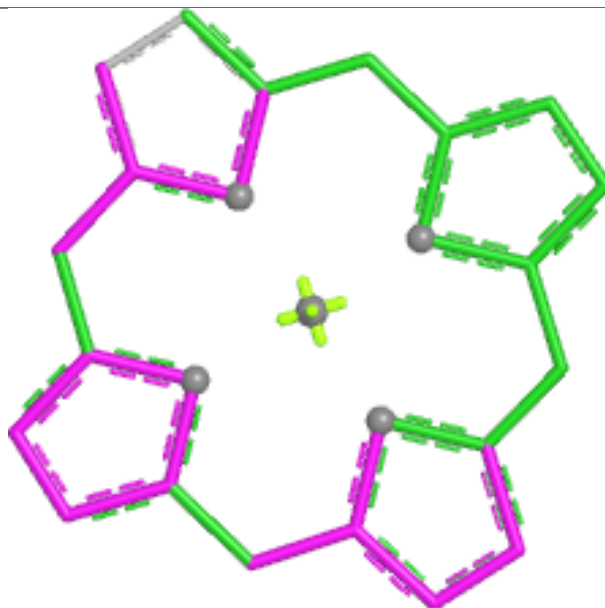


Rings

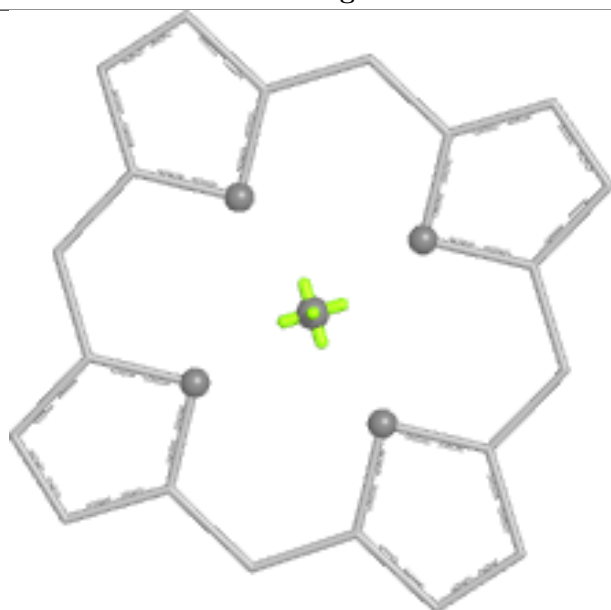
Ligand CLA B 3034



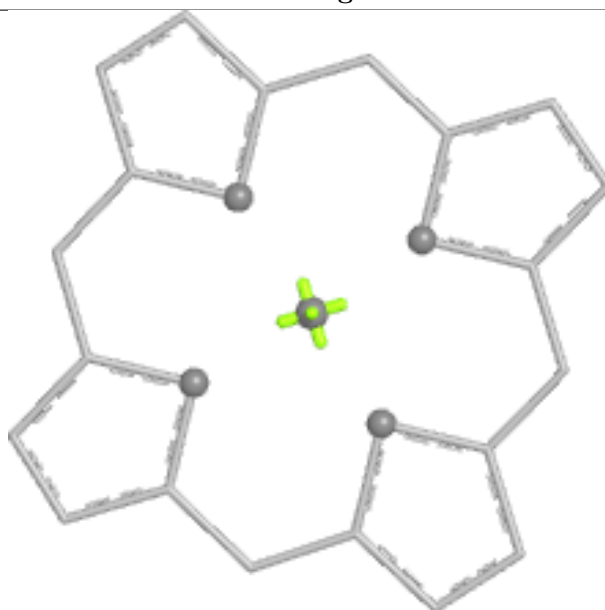
Bond lengths



Bond angles

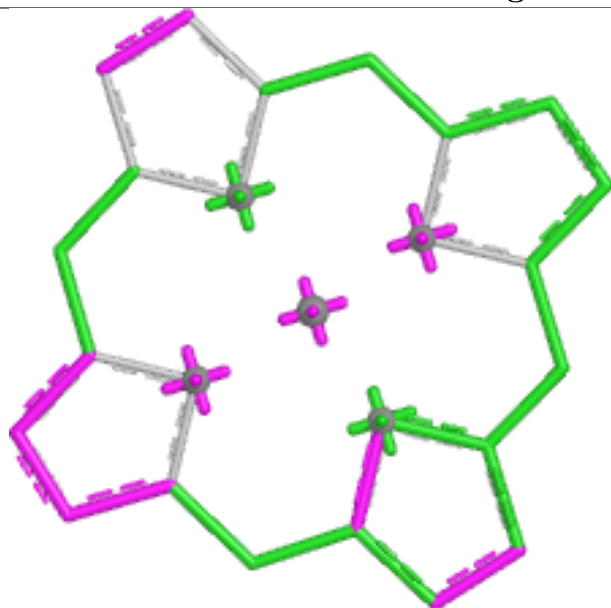


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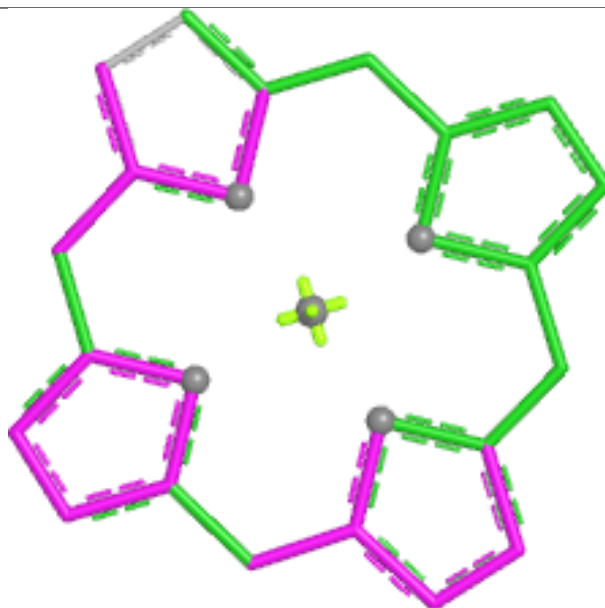


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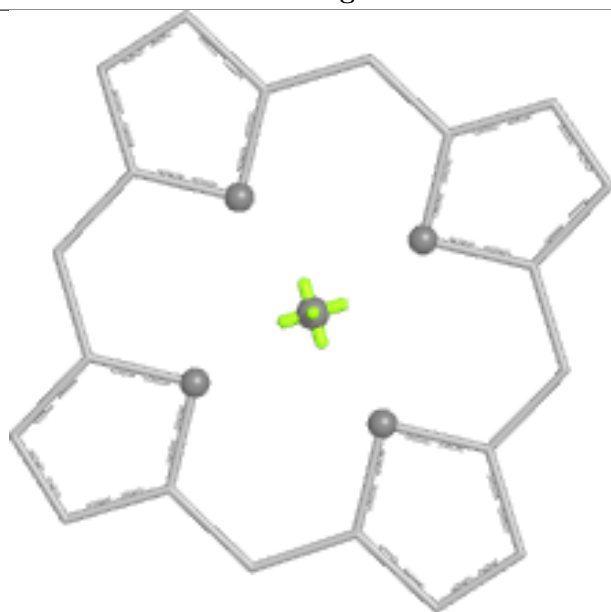
Ligand CLA F 3022



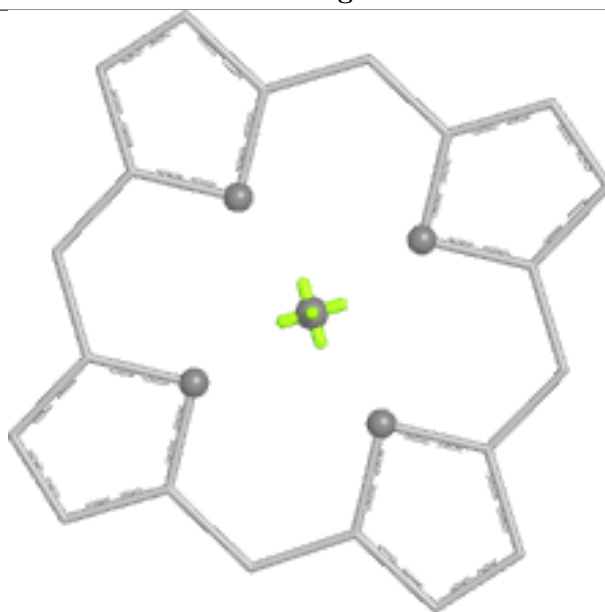
Bond lengths



Bond angles

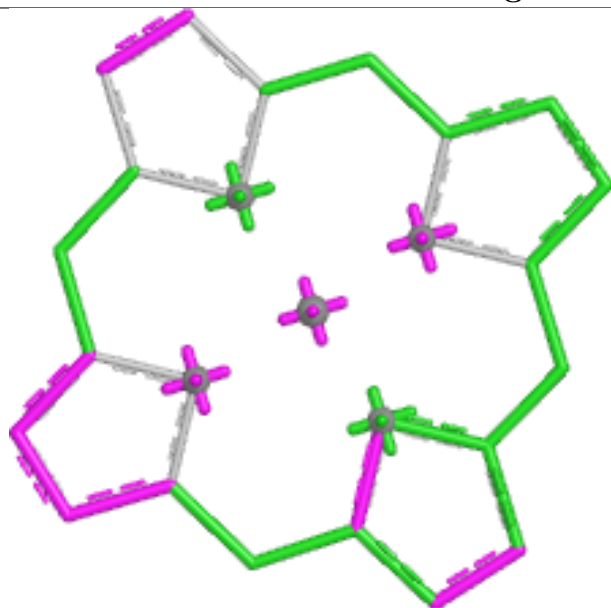


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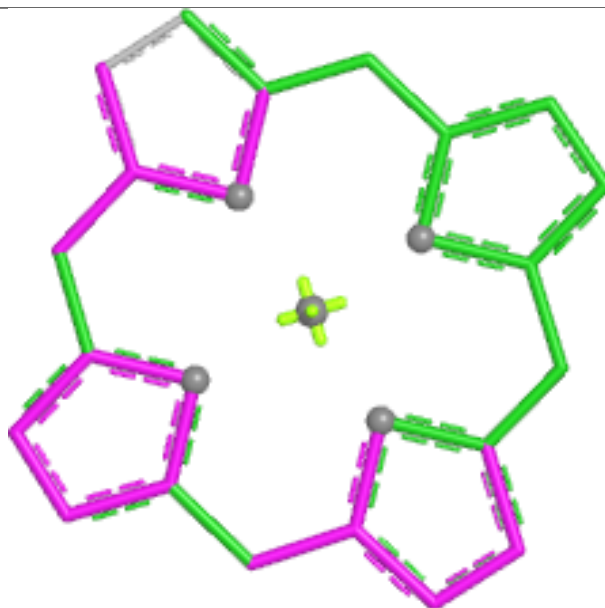


Rings

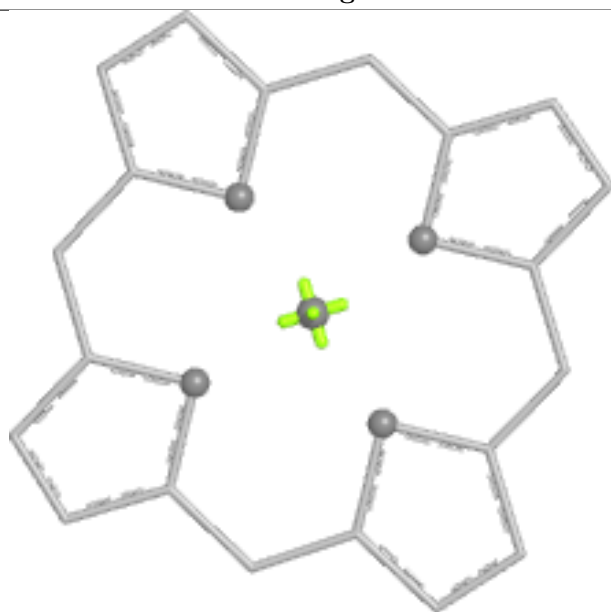
Ligand CLA A 3077



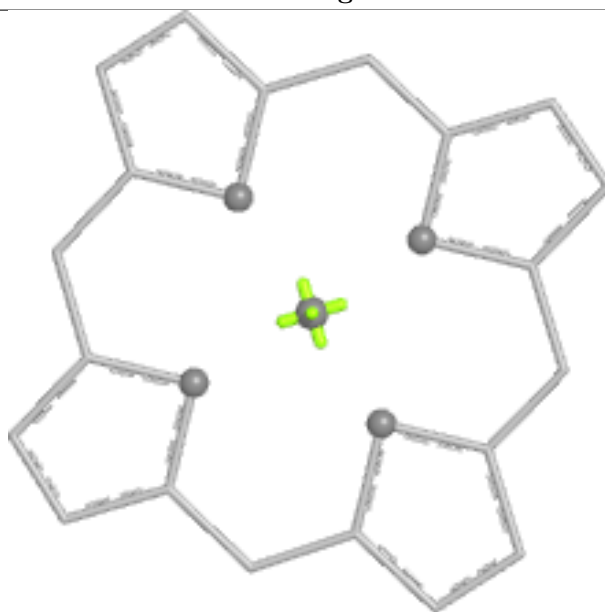
Bond lengths



Bond angles

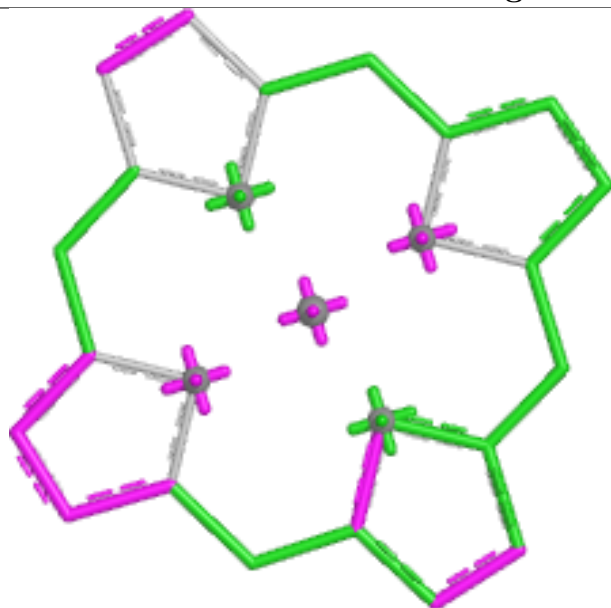


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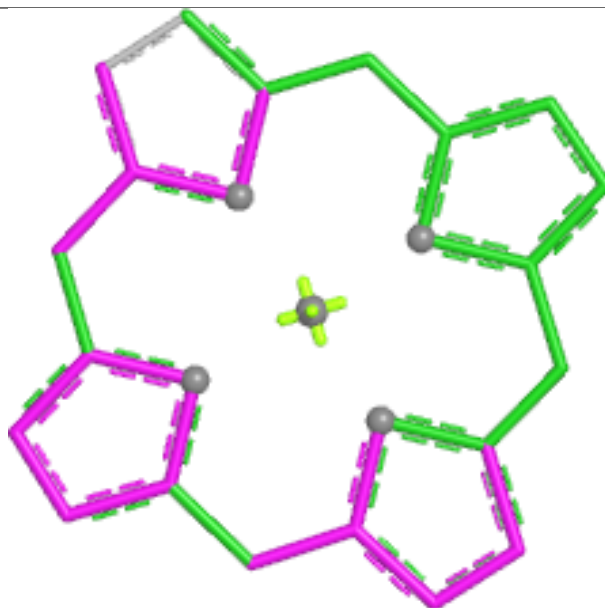


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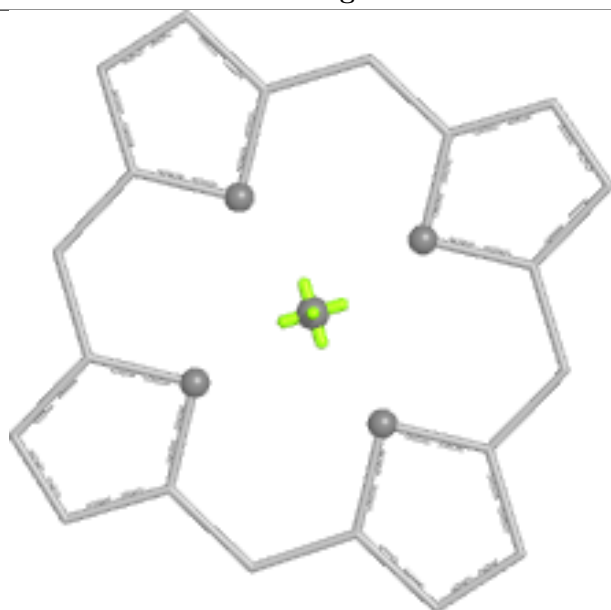
Ligand CLA B 3015



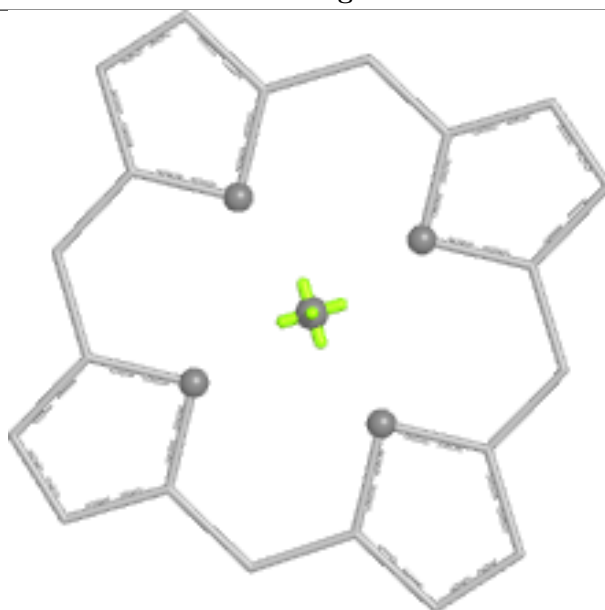
Bond lengths



Bond angles

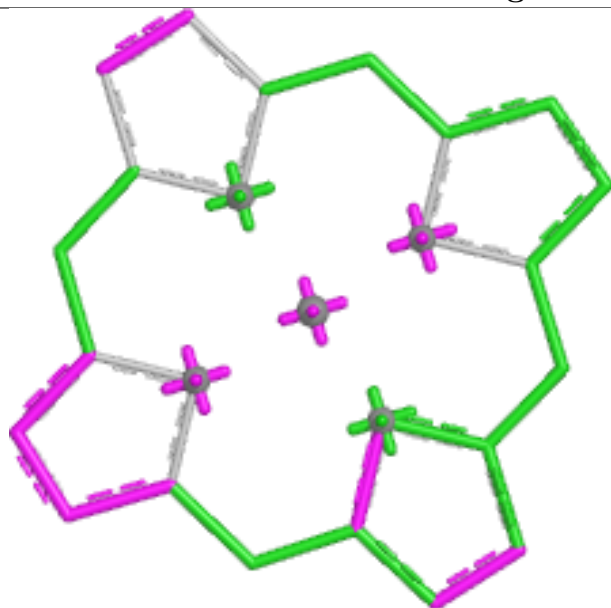


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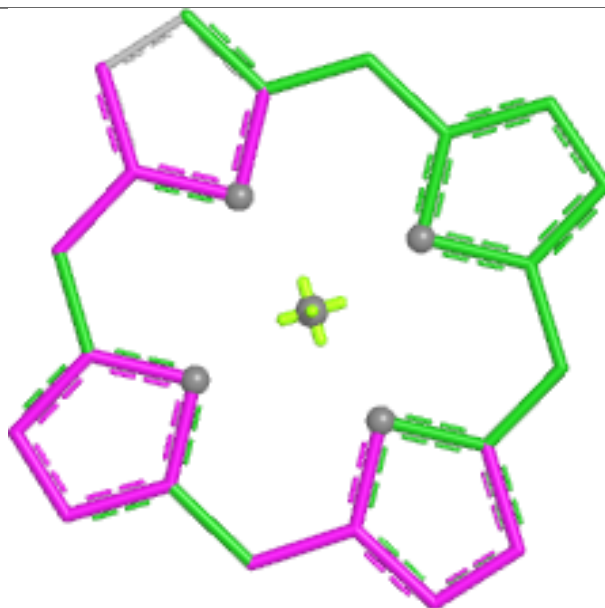


Rings

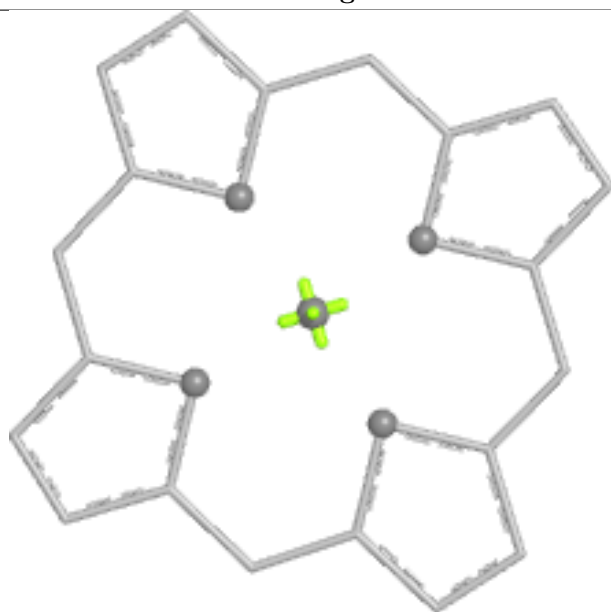
Ligand CLA F 3059



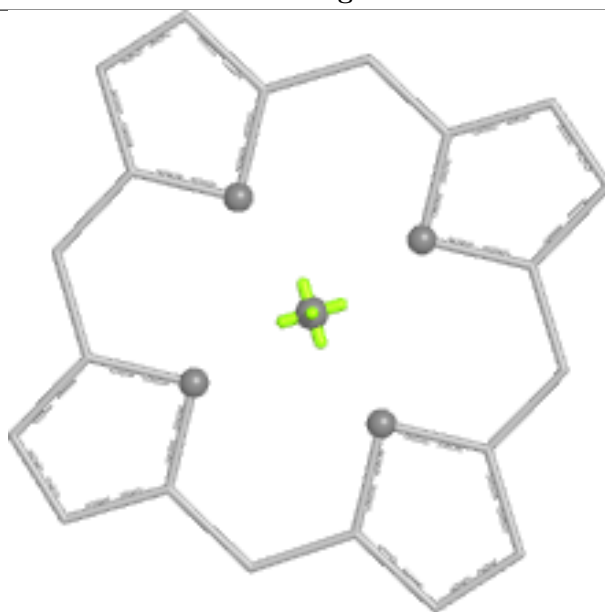
Bond lengths



Bond angles

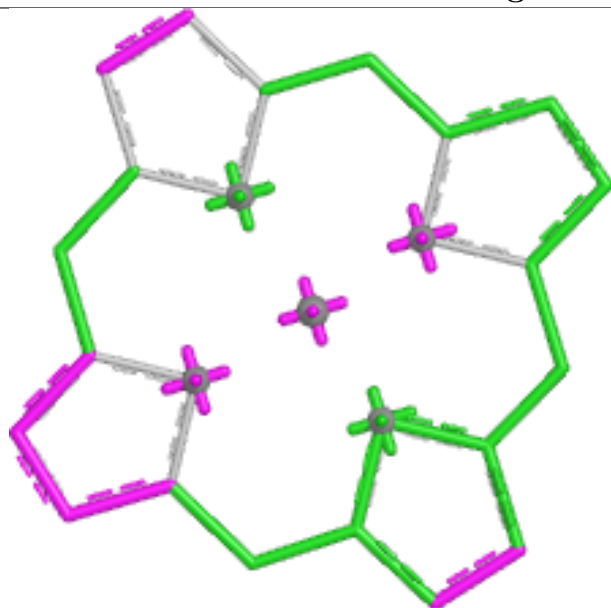


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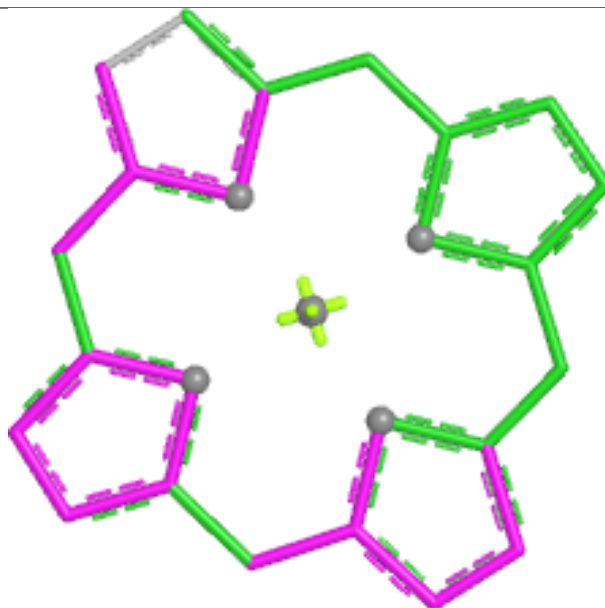


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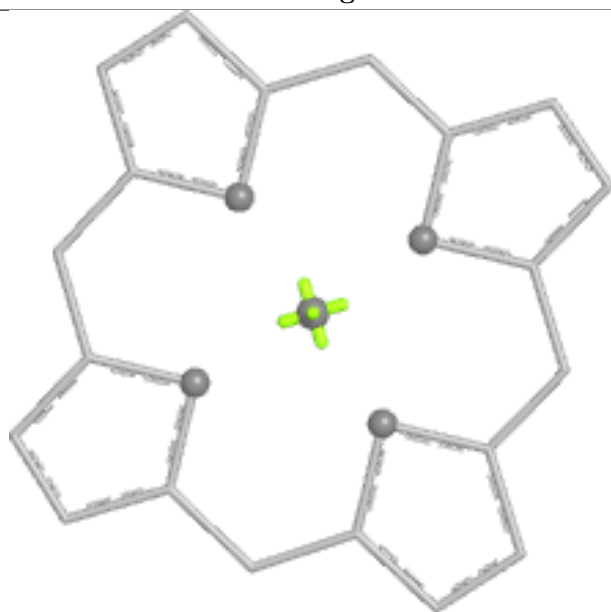
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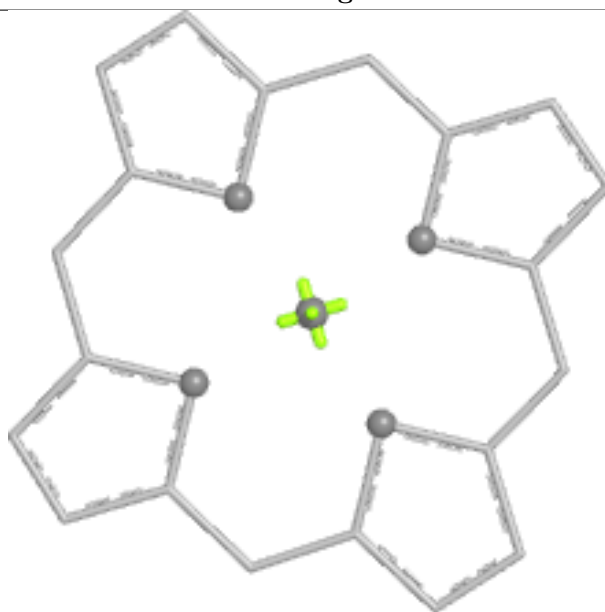
Bond lengths



Bond angles

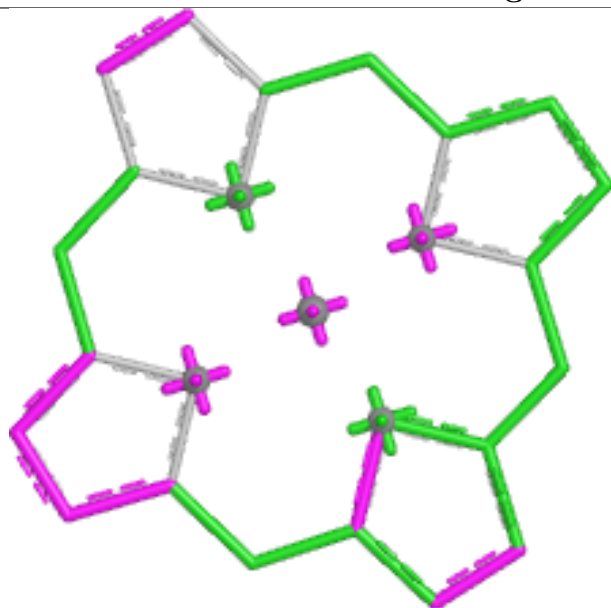


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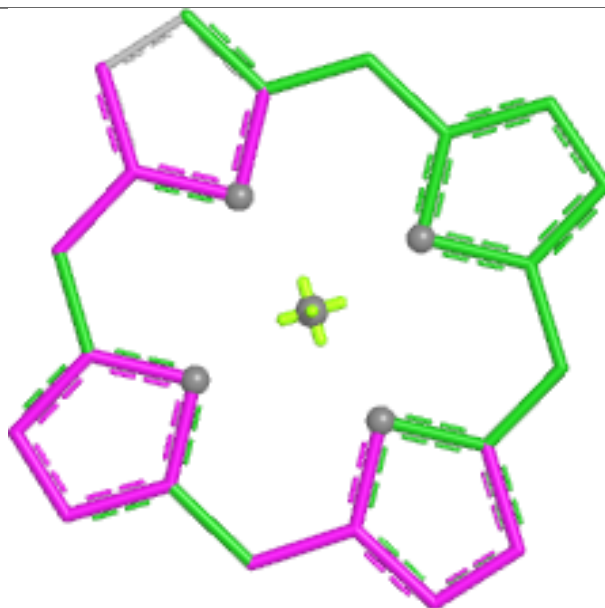


Rings

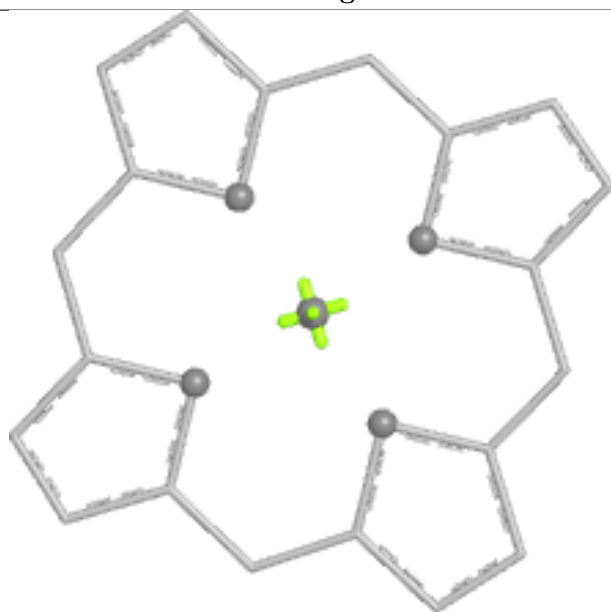
Ligand CLA B 3046



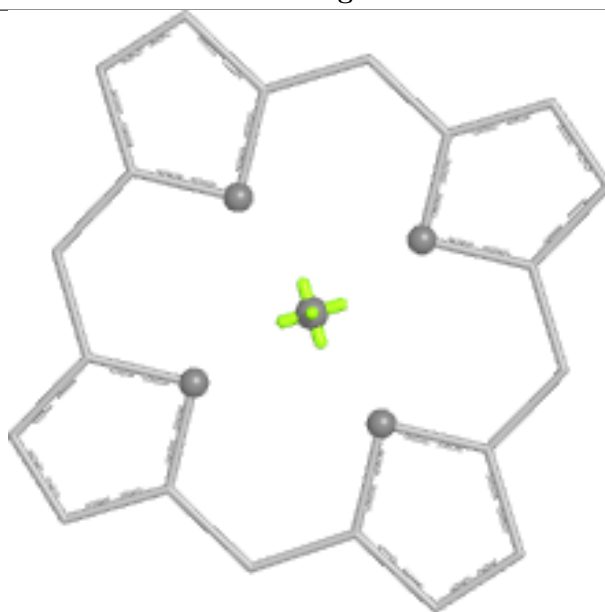
Bond lengths



Bond angles

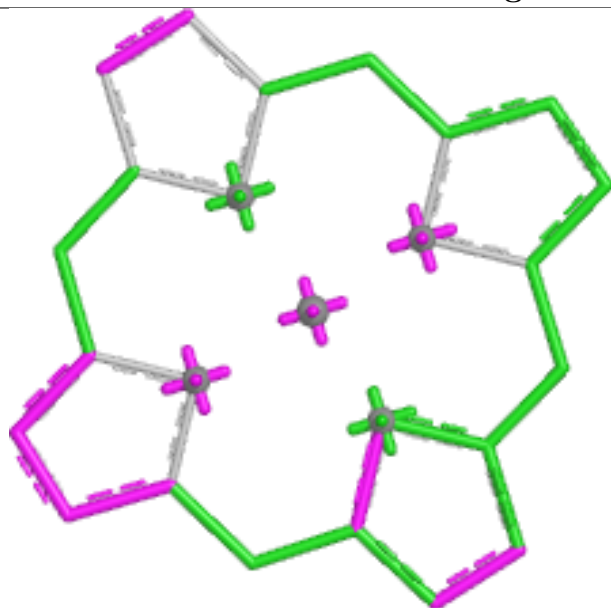


Torsions

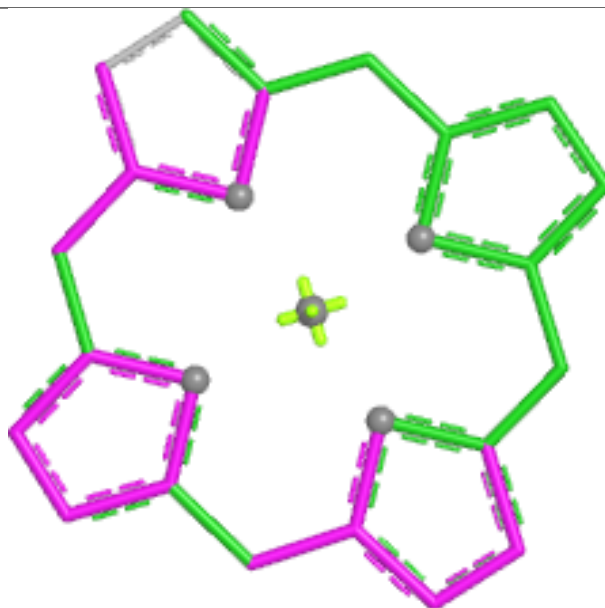


Rings

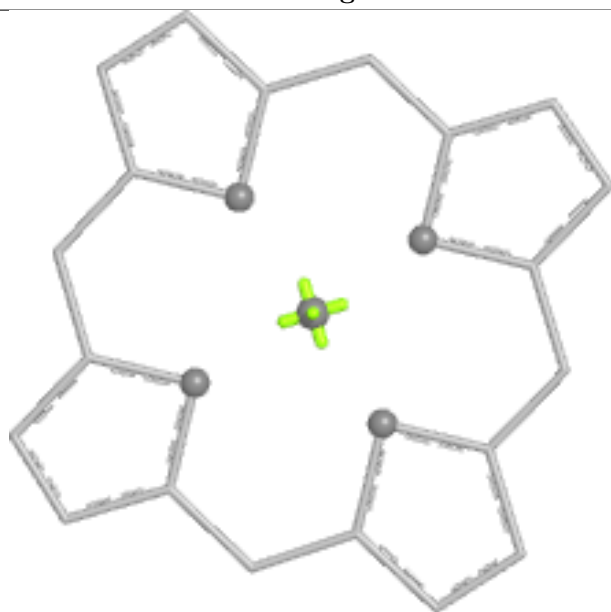
Ligand CLA A 3030



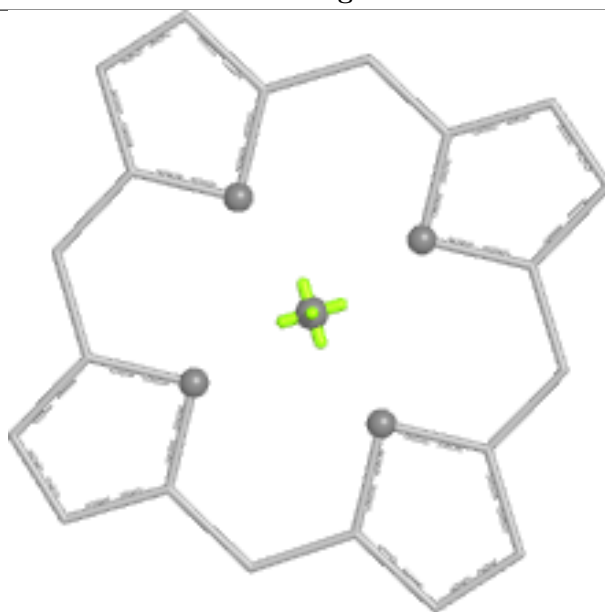
Bond lengths



Bond angles

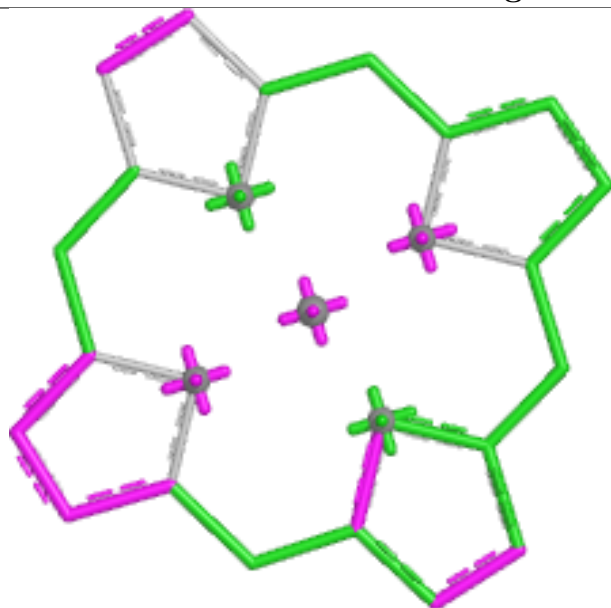


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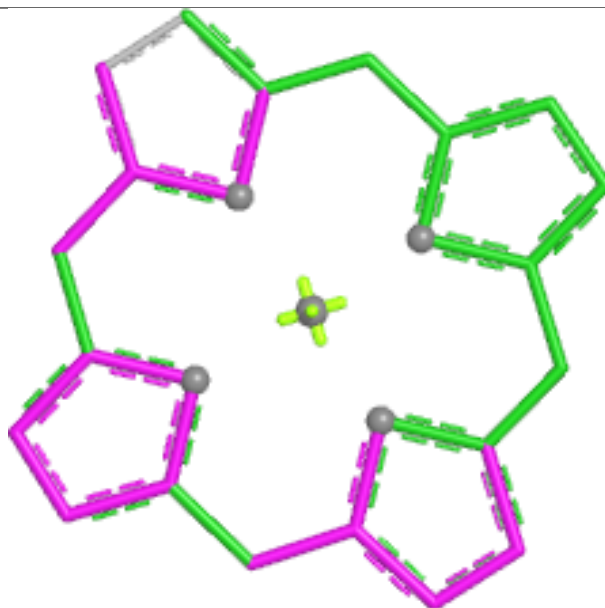


Rings

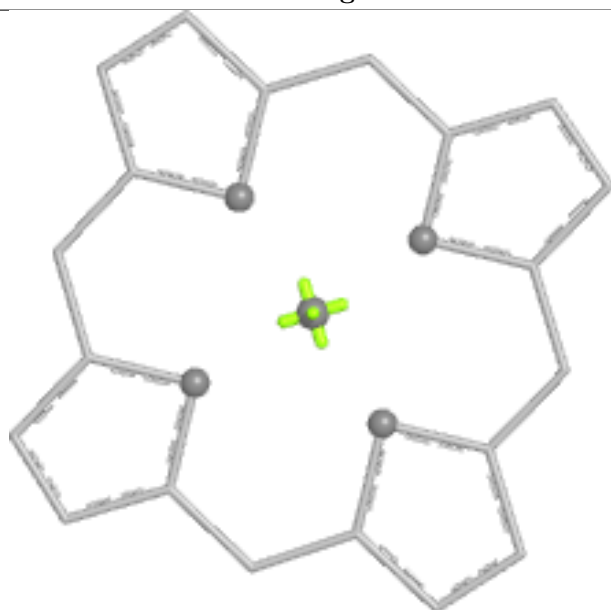
Ligand CLA A 3073



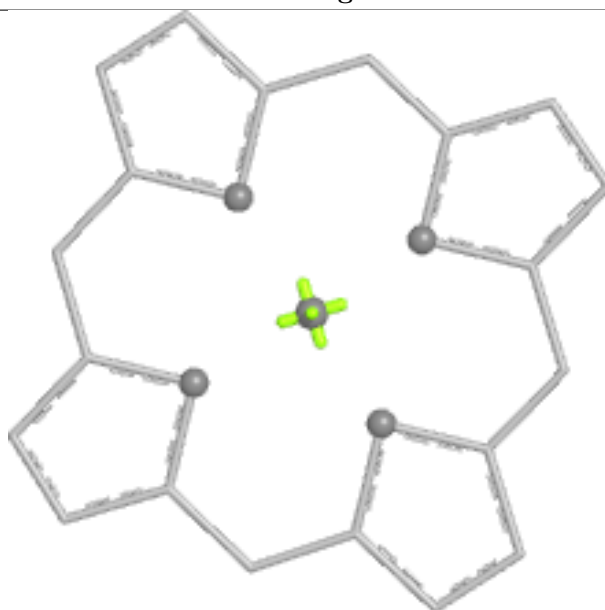
Bond lengths



Bond angles

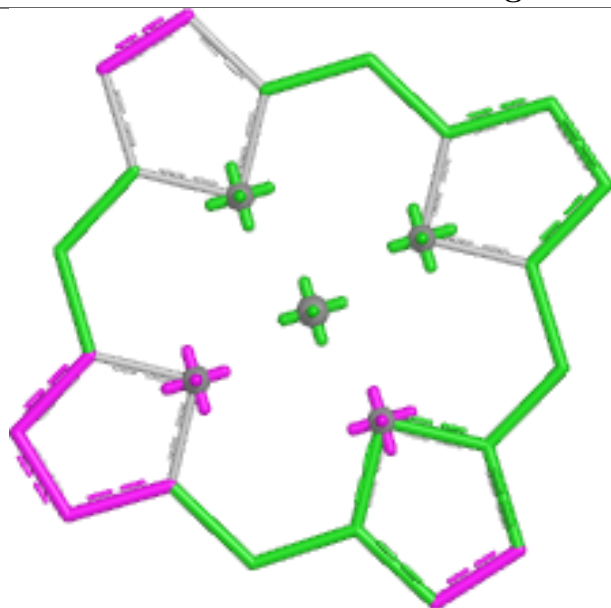


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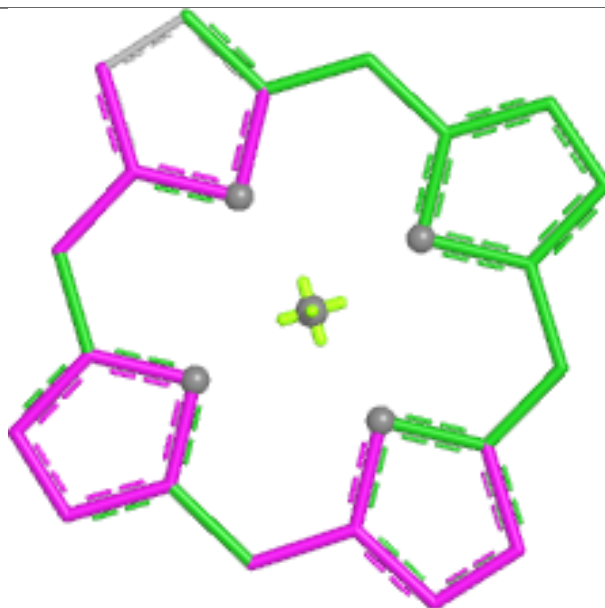


Rings

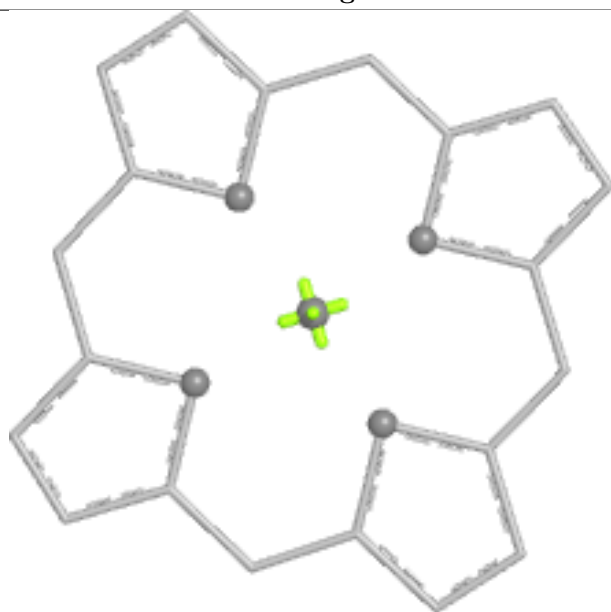
Ligand CLA A 2001



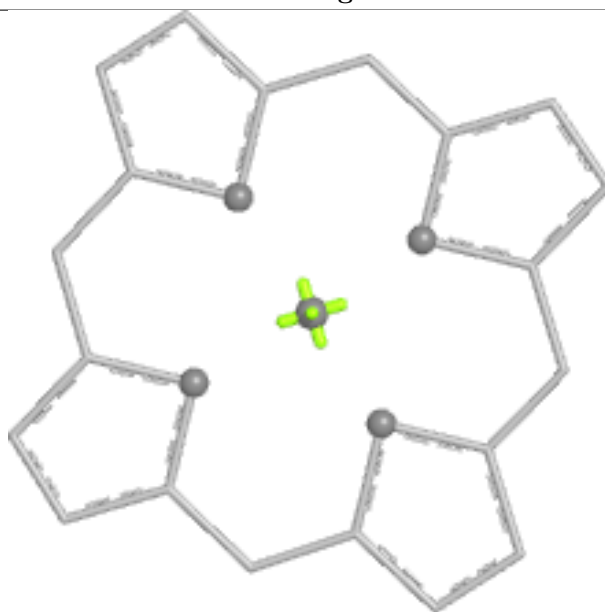
Bond lengths



Bond angles

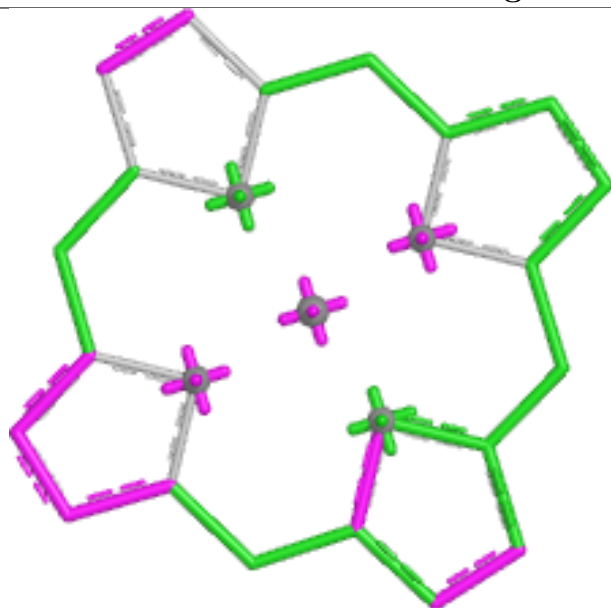


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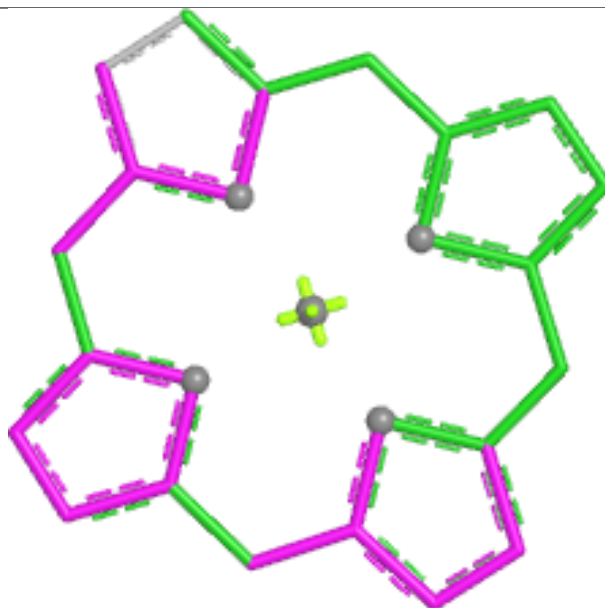


Rings

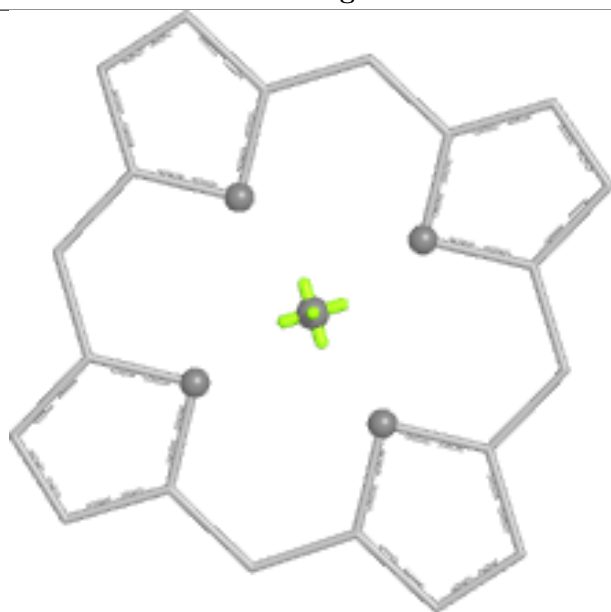
Ligand CLA K 3051



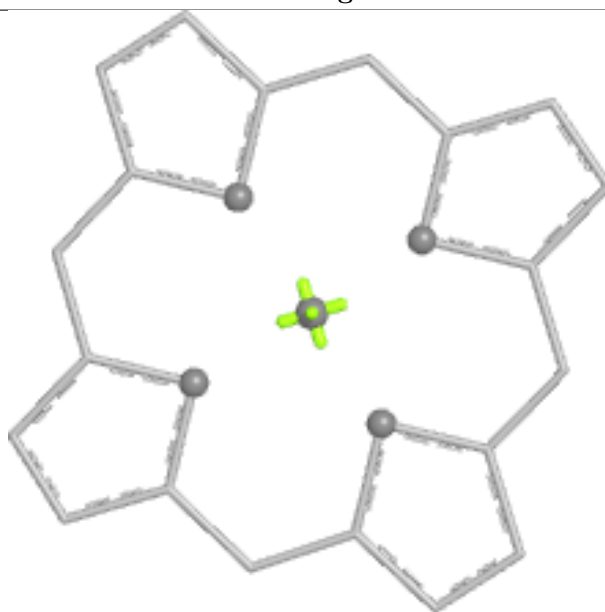
Bond lengths



Bond angles

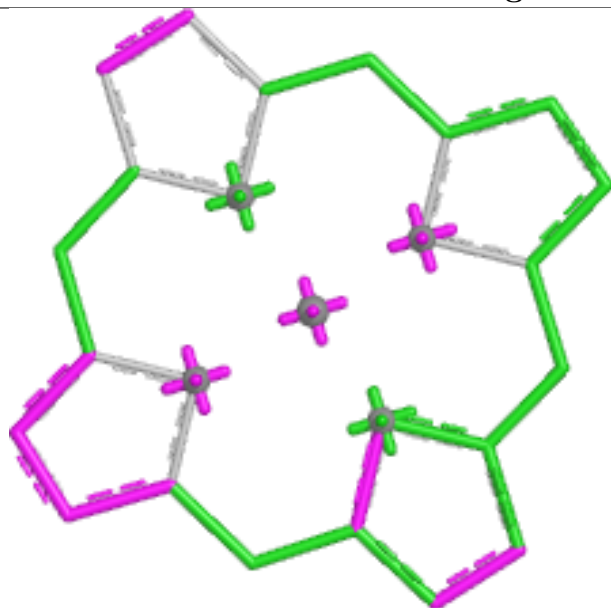


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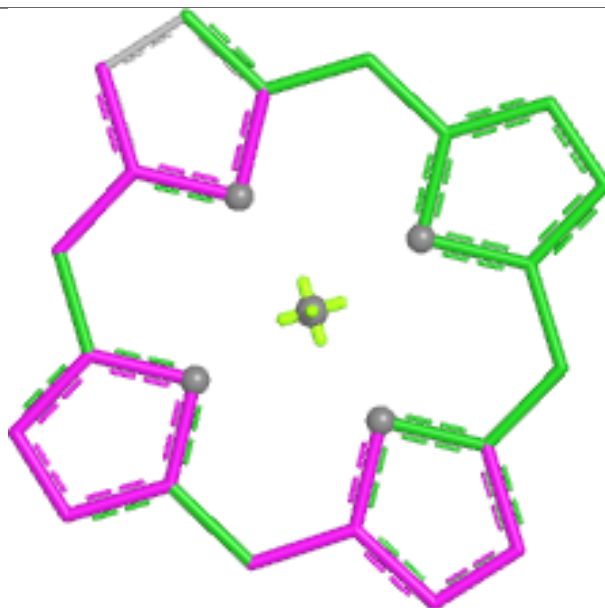


Rings

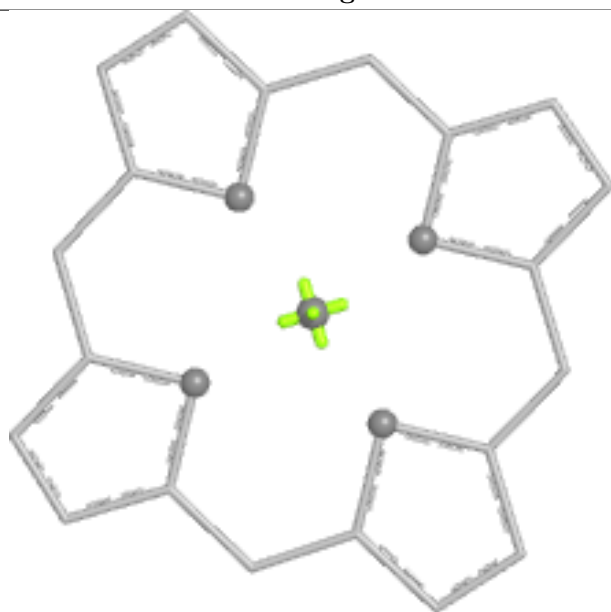
Ligand CLA B 3075



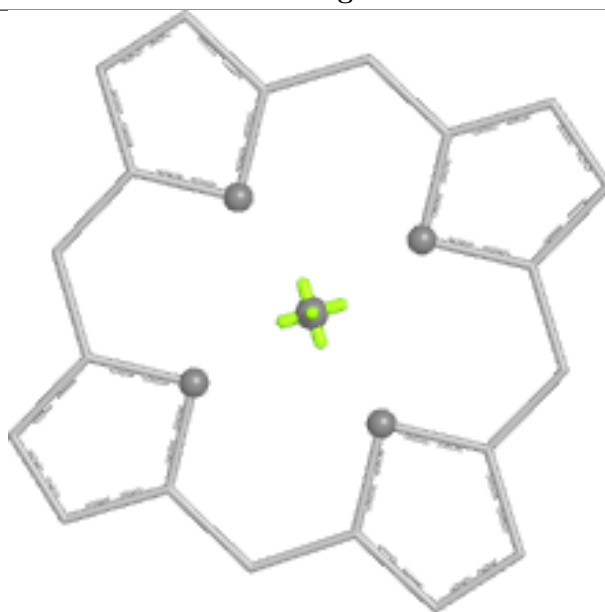
Bond lengths



Bond angles

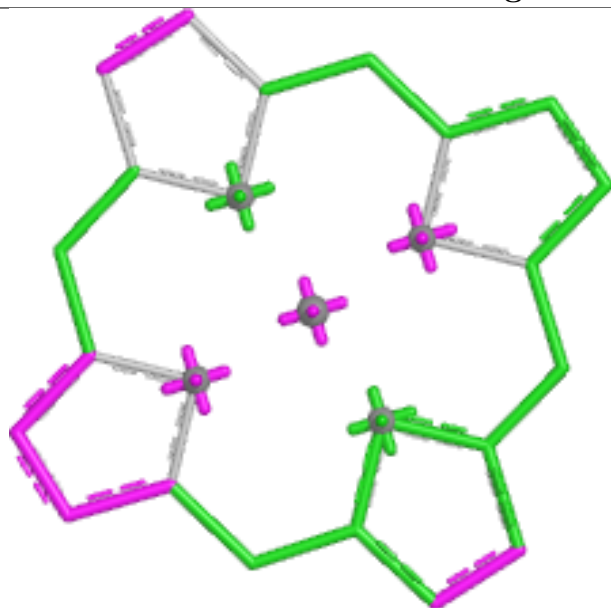


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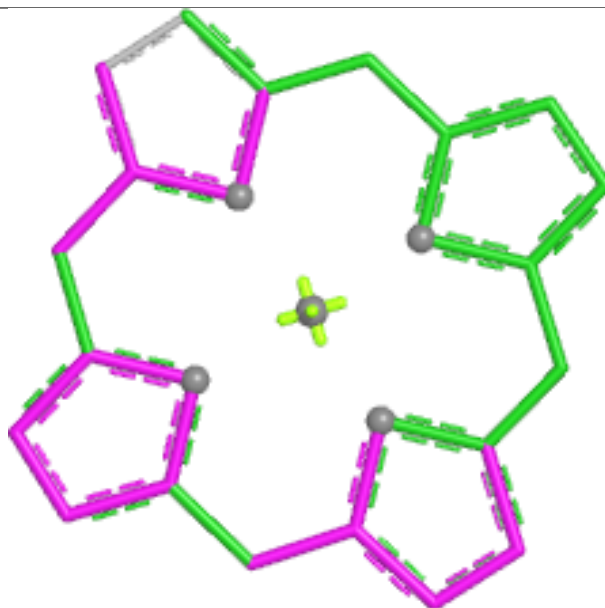


Rings

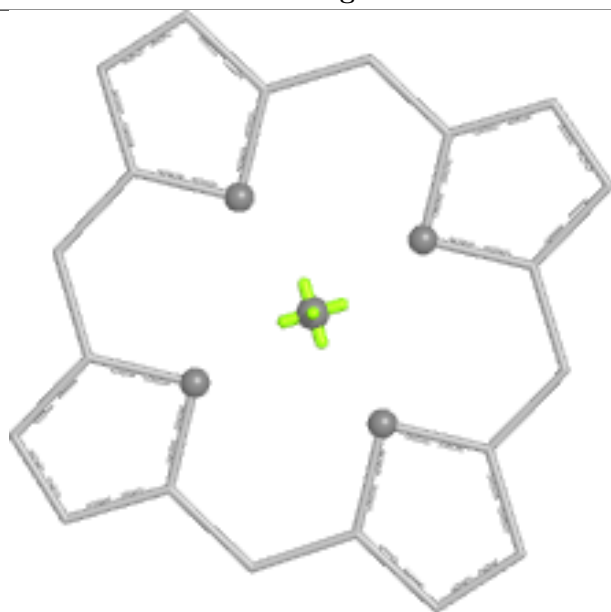
Ligand CLA A 3045



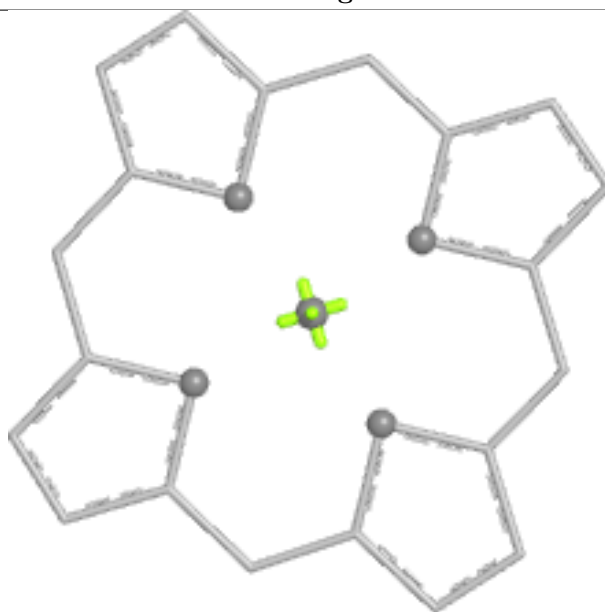
Bond lengths



Bond angles

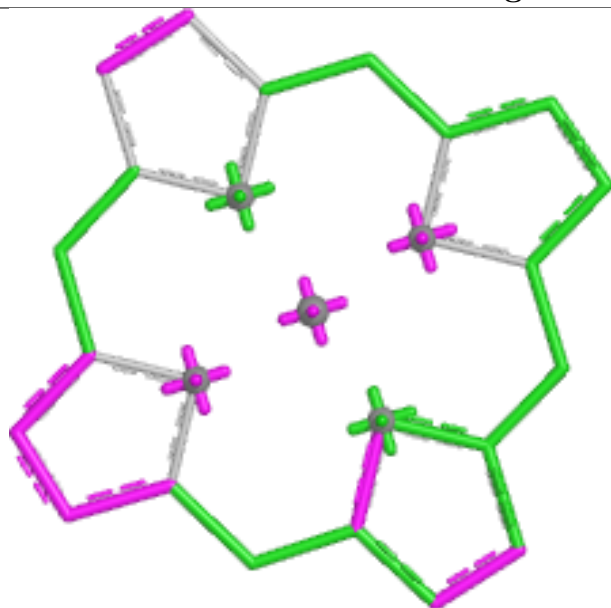


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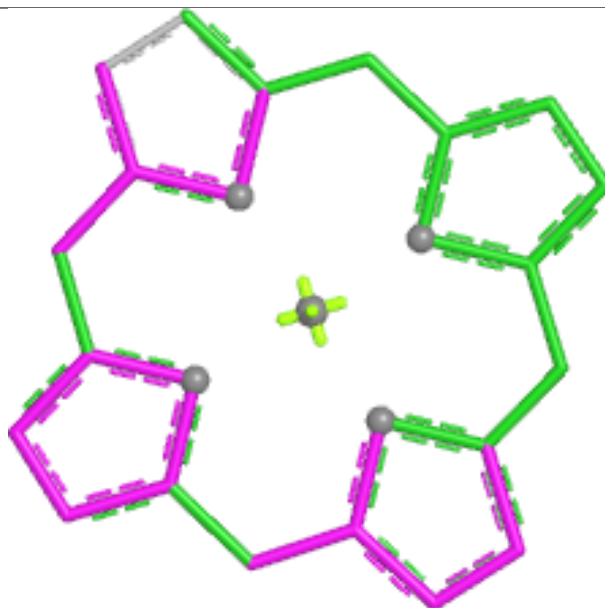


Rings

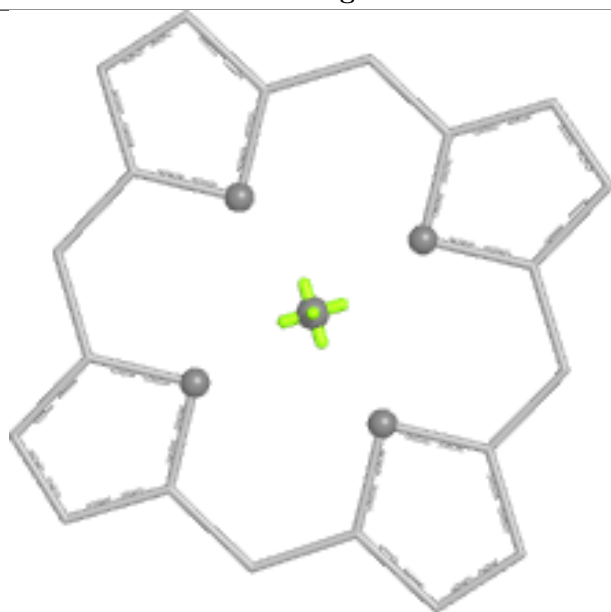
Ligand CLA A 3058



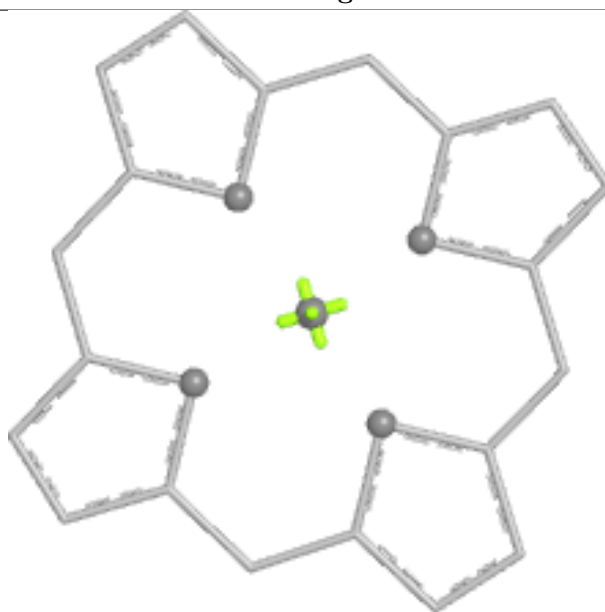
Bond lengths



Bond angles

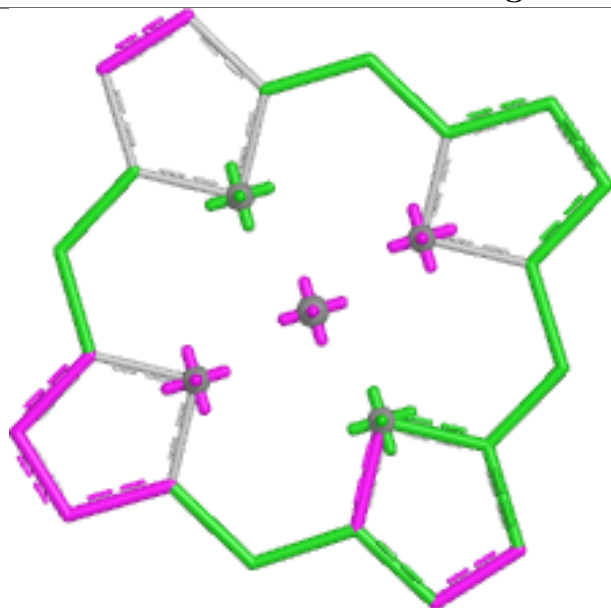


Torsions

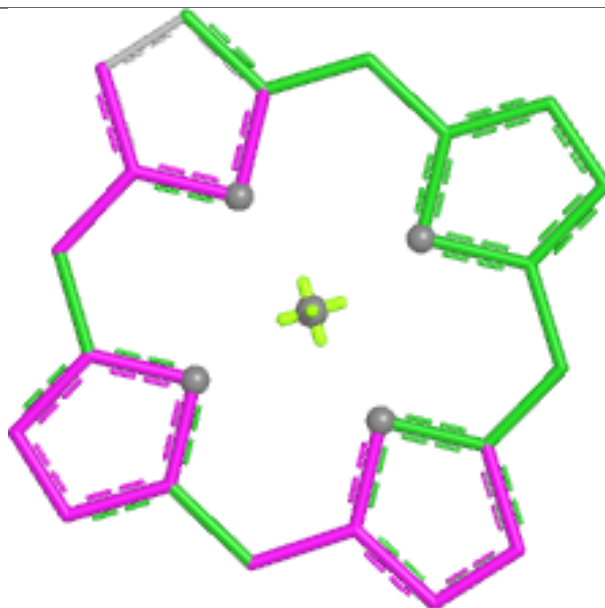


Rings

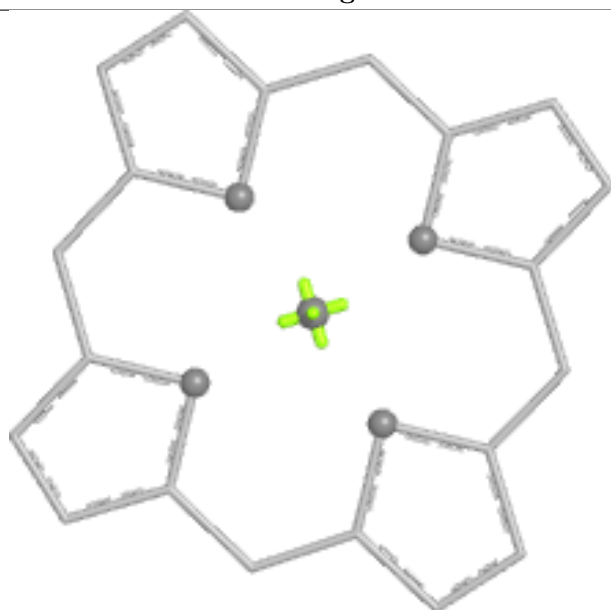
Ligand CLA B 3019



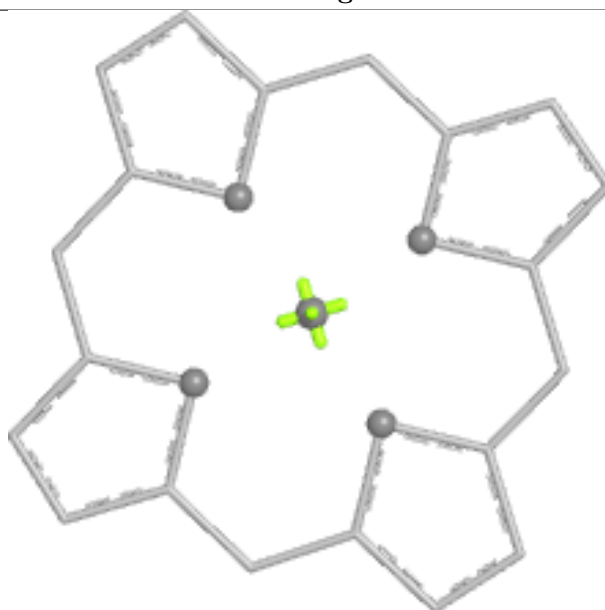
Bond lengths



Bond angles

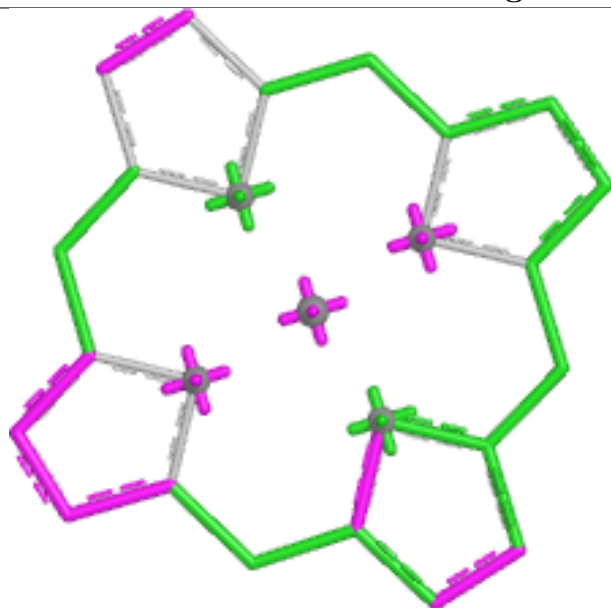


Torsions

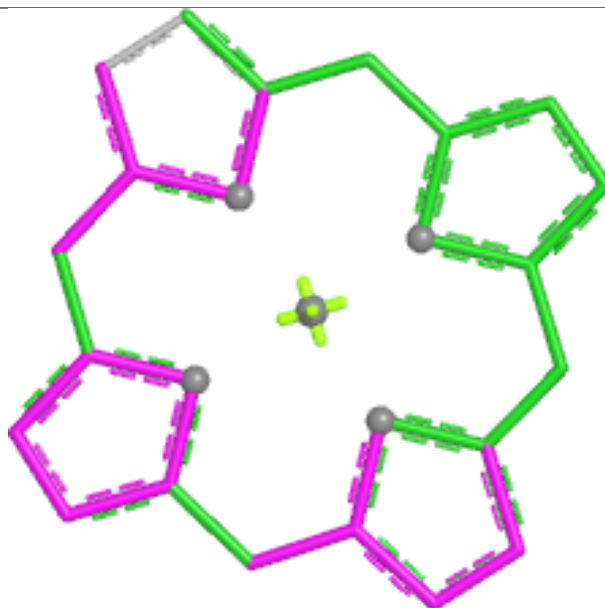


Rings

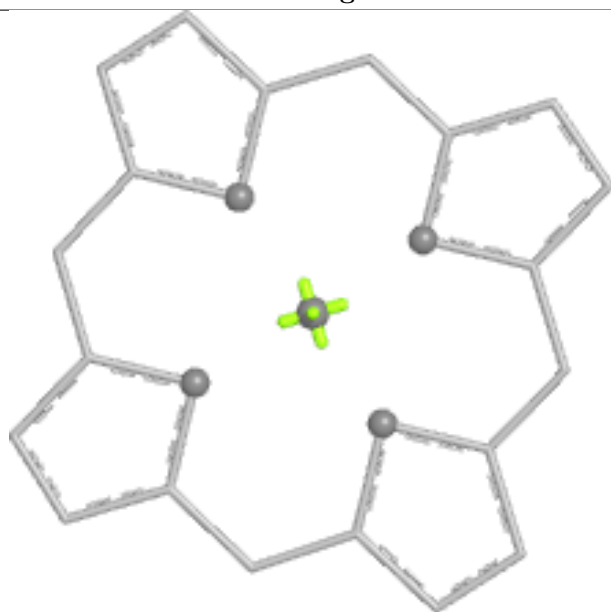
Ligand CLA B 3037



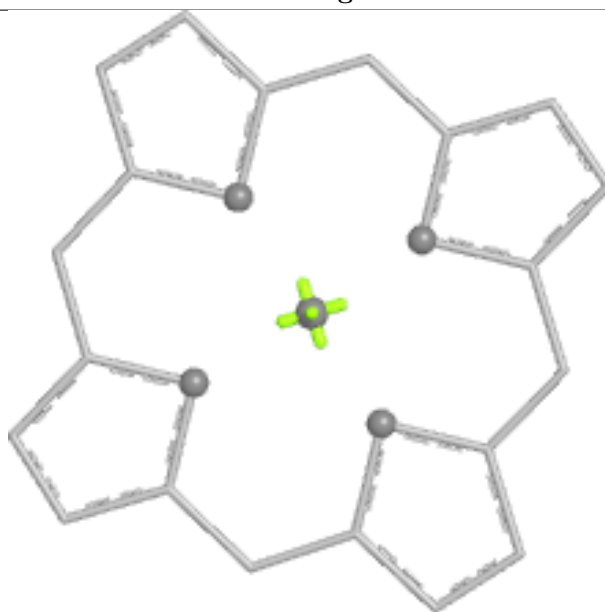
Bond lengths



Bond angles

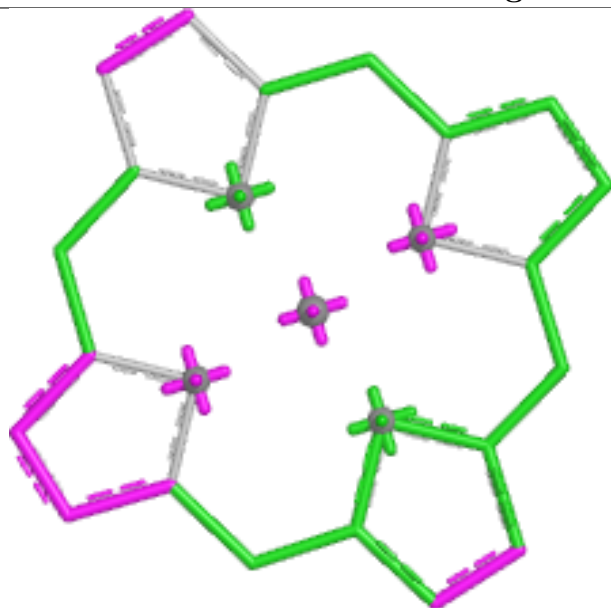


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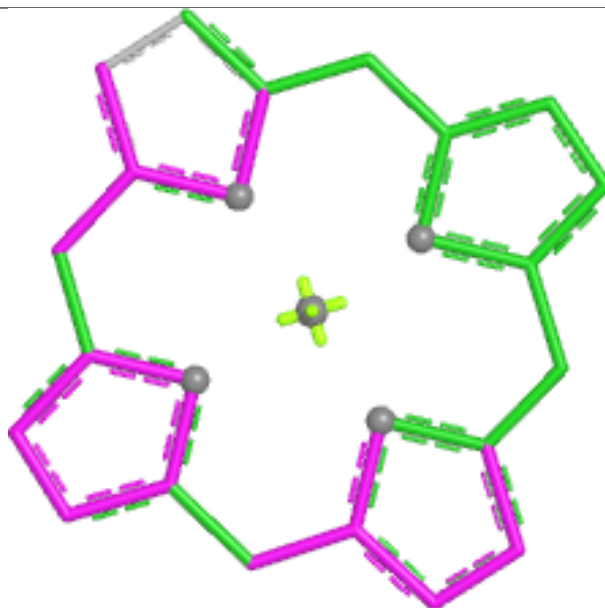


Rings

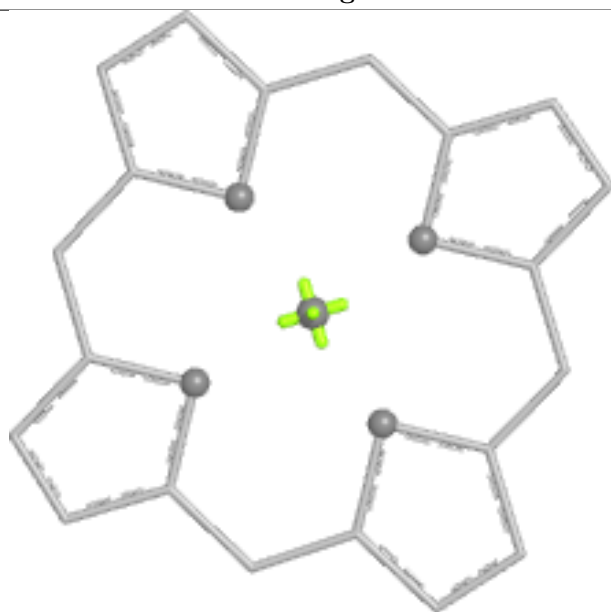
Ligand CLA B 3080



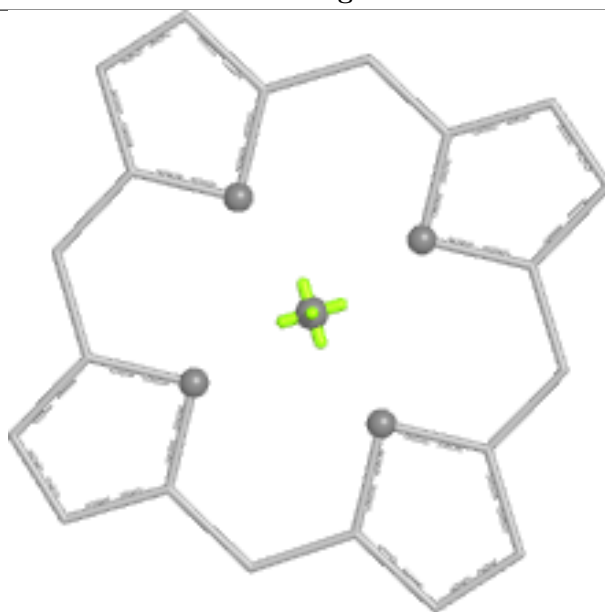
Bond lengths



Bond angles

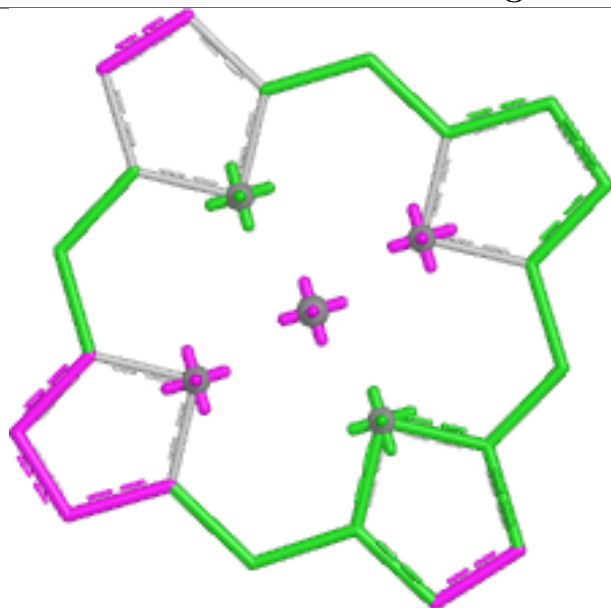


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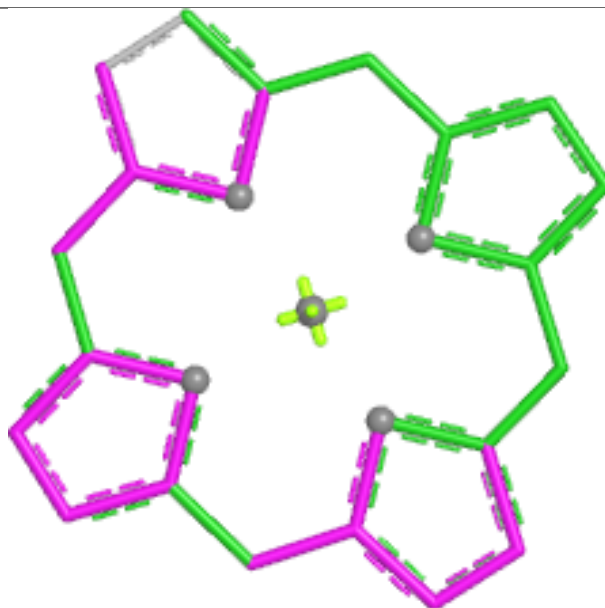


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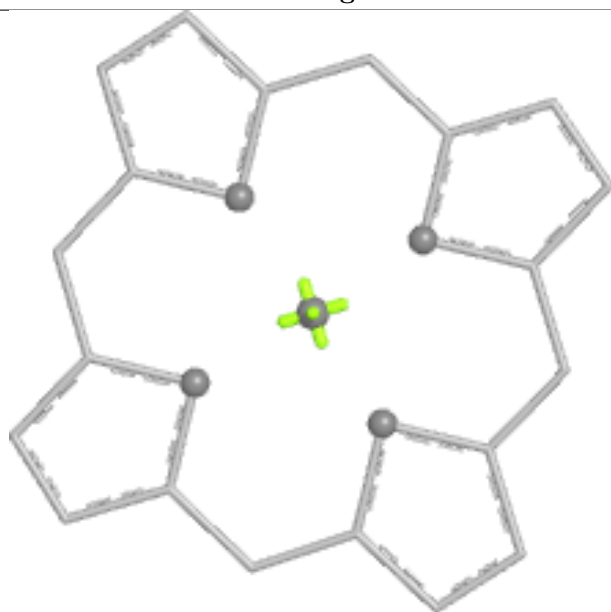
Ligand CLA B 3044



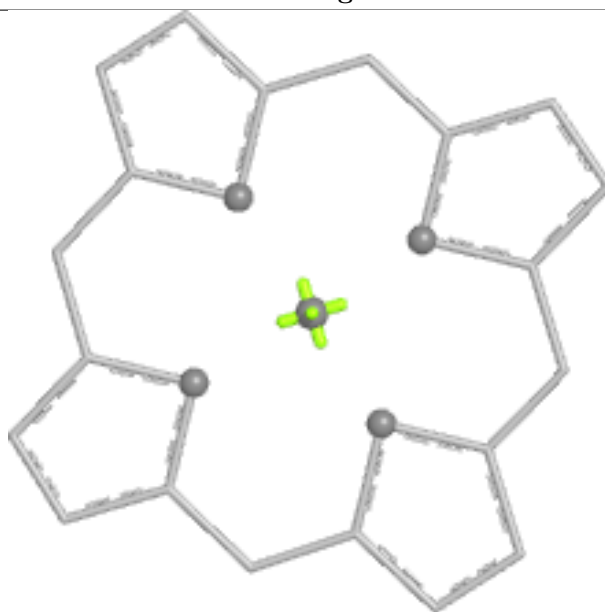
Bond lengths



Bond angles

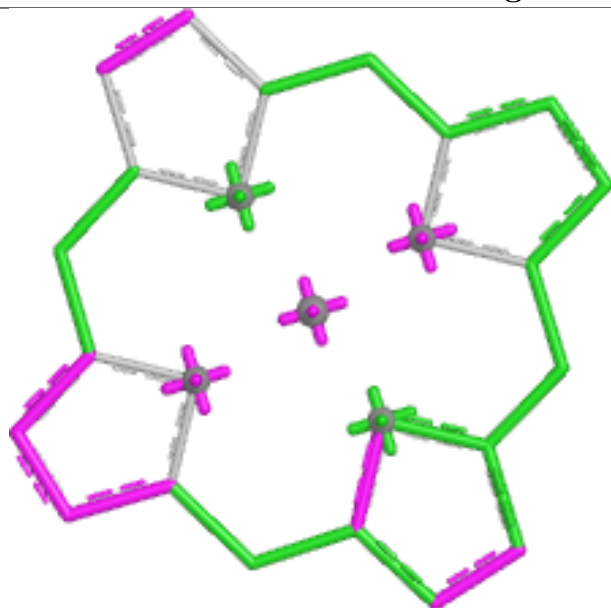


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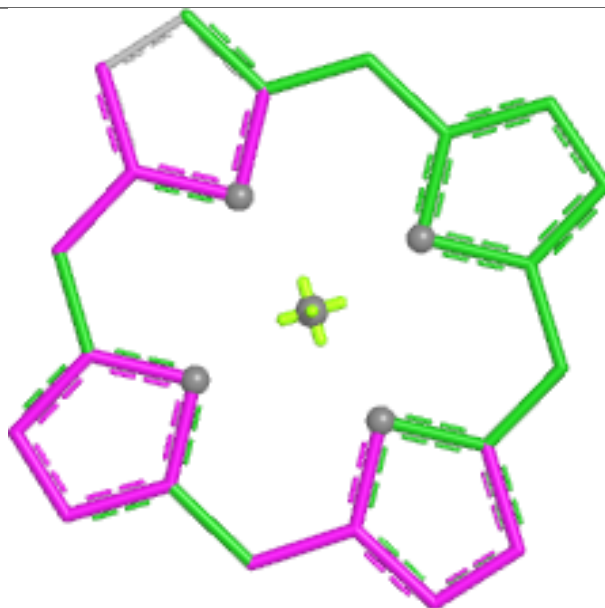


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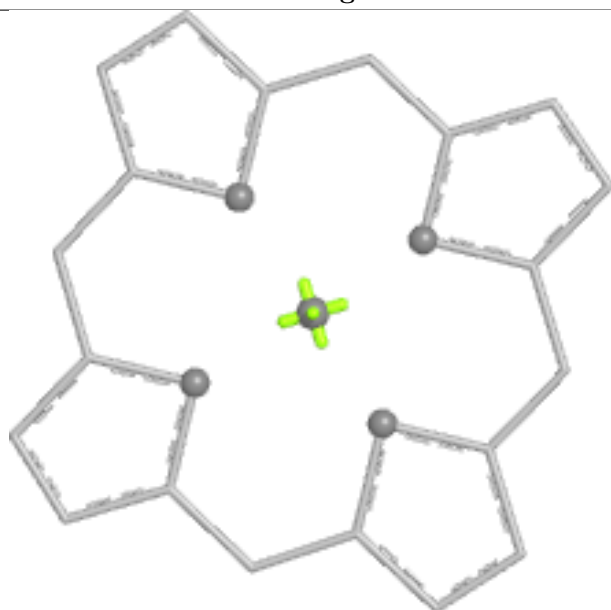
Ligand CLA A 3024



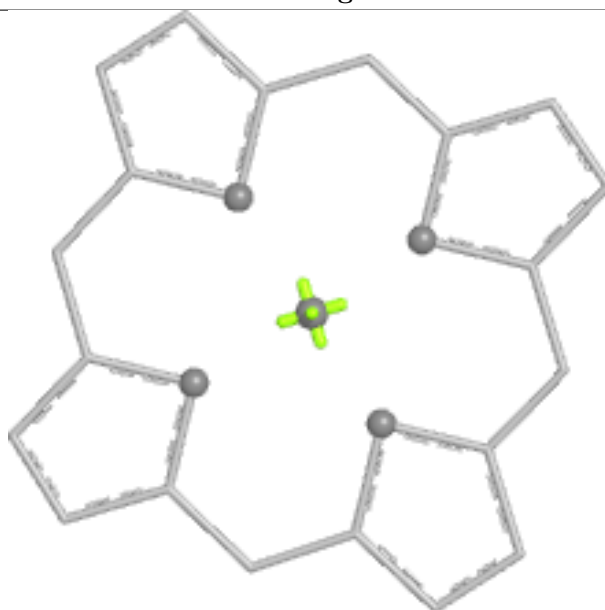
Bond lengths



Bond angles

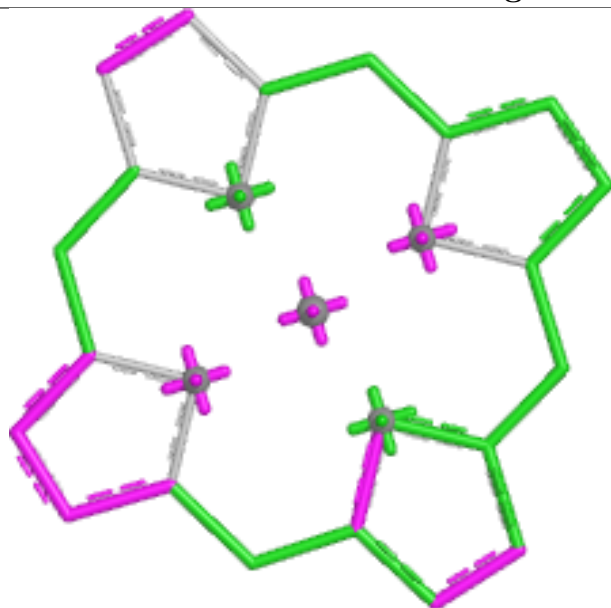


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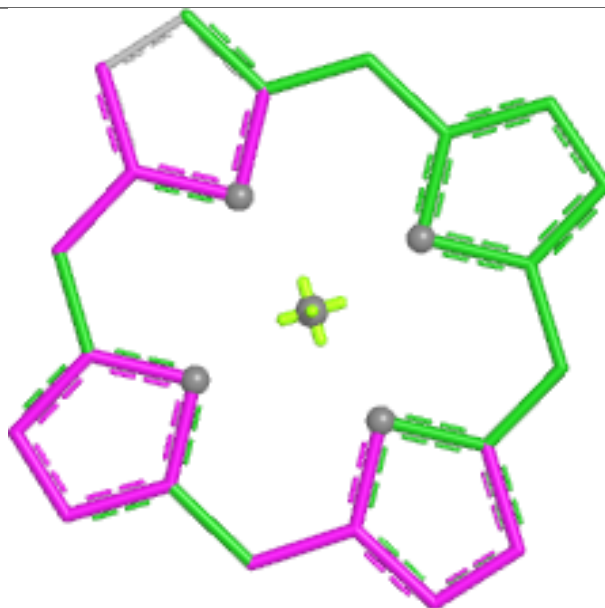


Rings

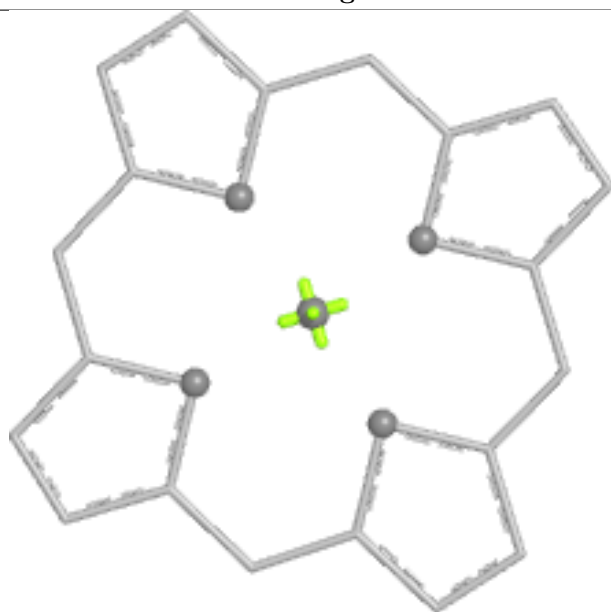
Ligand CLA A 3056



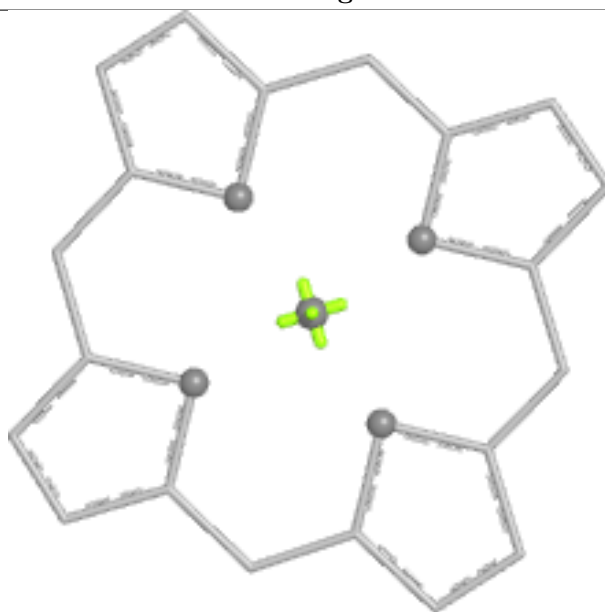
Bond lengths



Bond angles

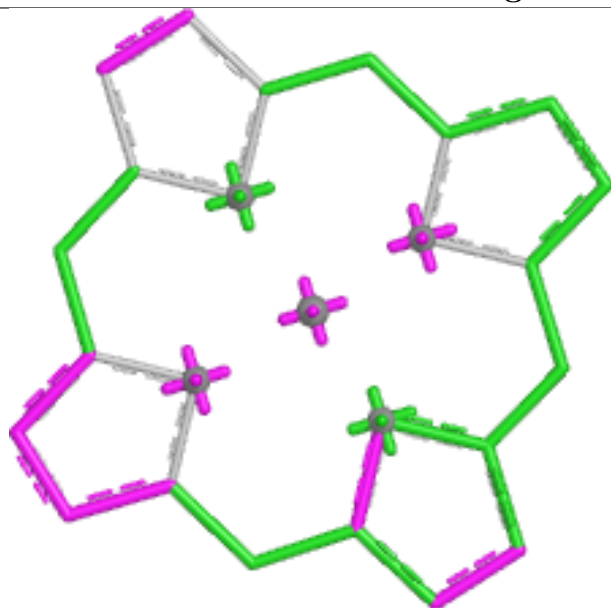


Torsions

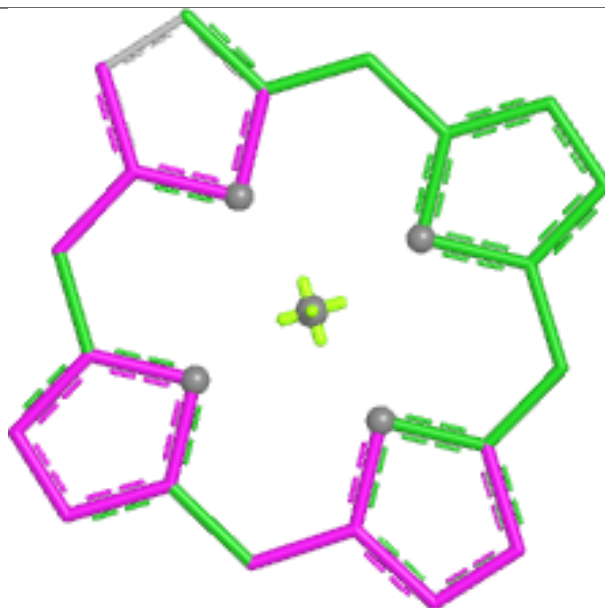


Rings

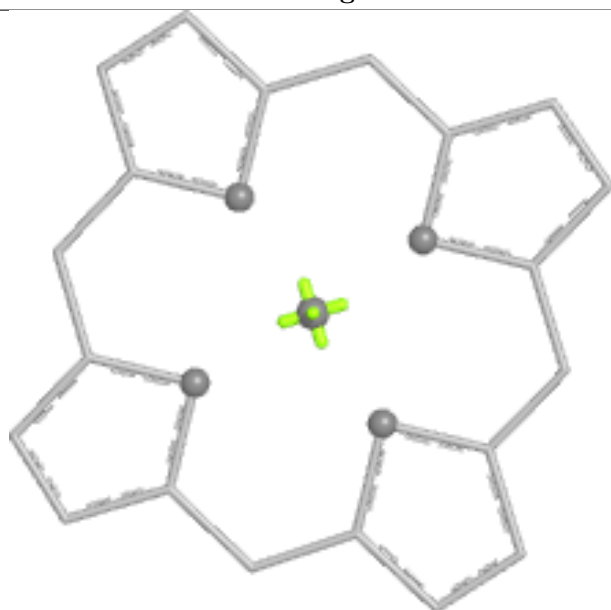
Ligand CLA A 3040



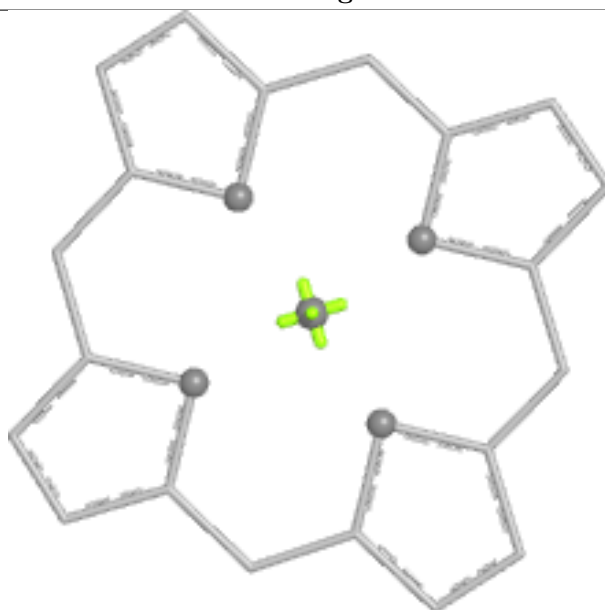
Bond lengths



Bond angles

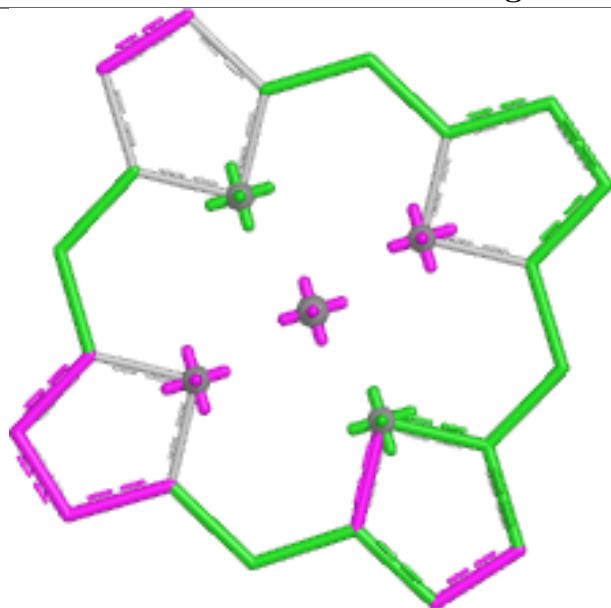


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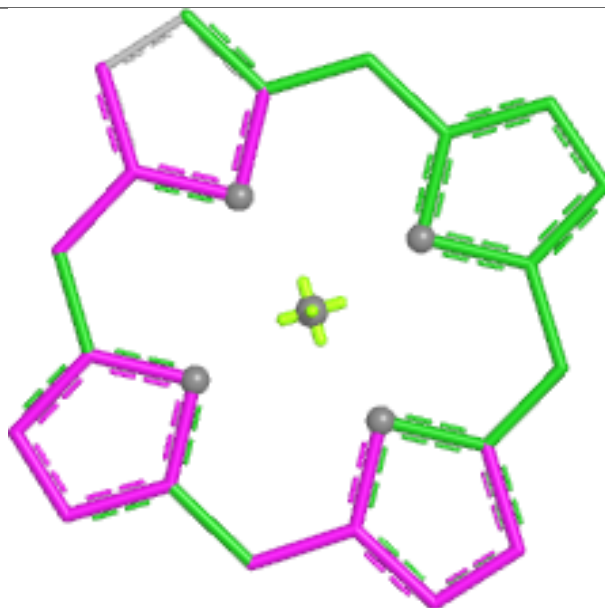


Rings

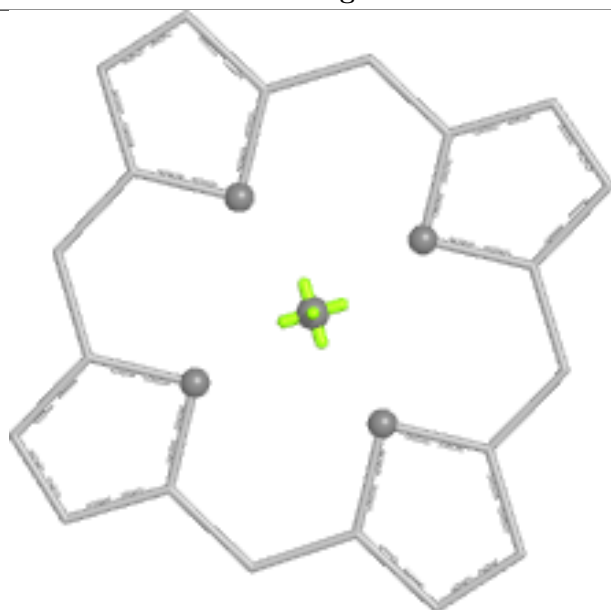
Ligand CLA A 3007



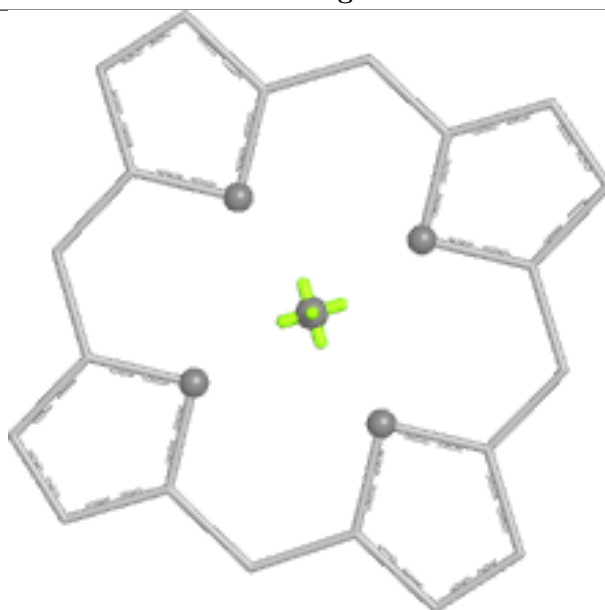
Bond lengths



Bond angles

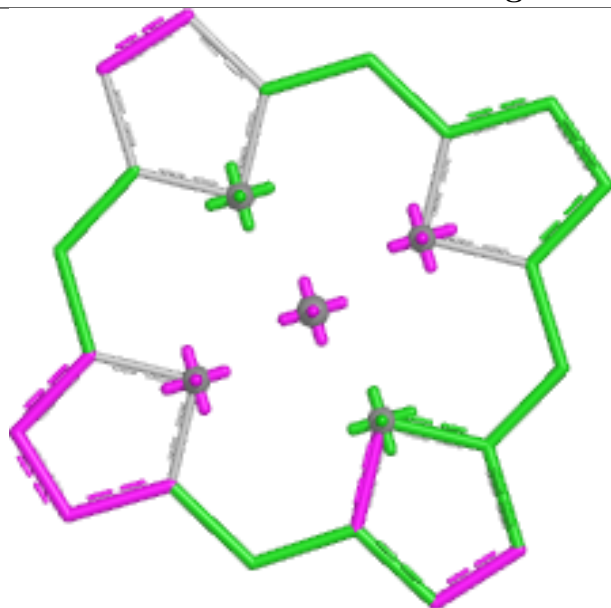


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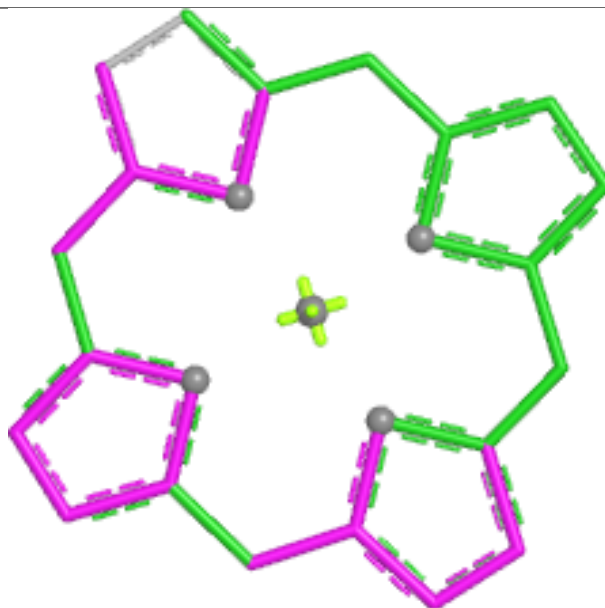


Rings

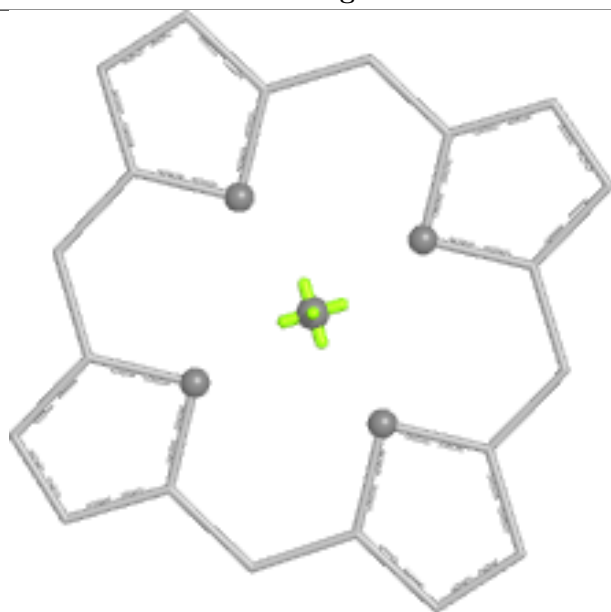
Ligand CLA B 3023



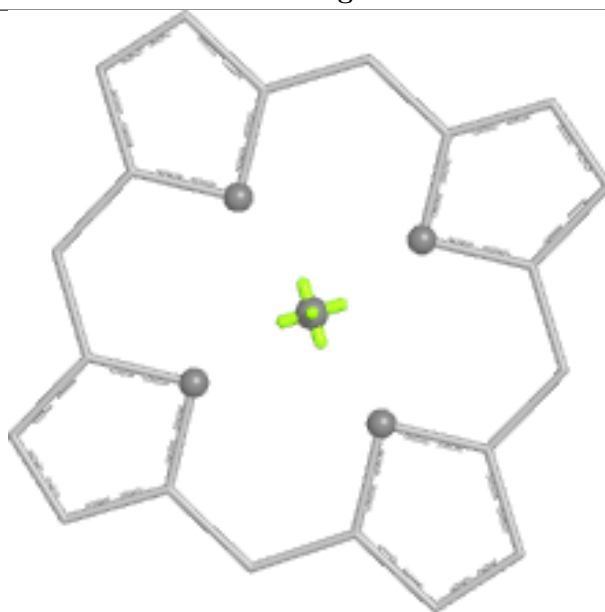
Bond lengths



Bond angles

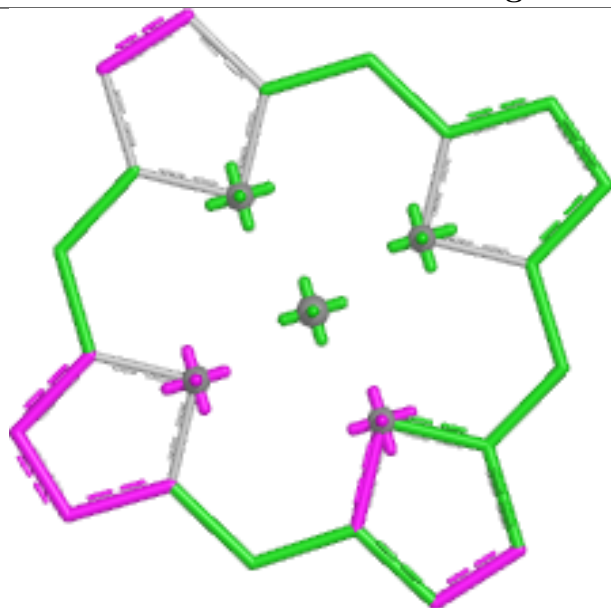


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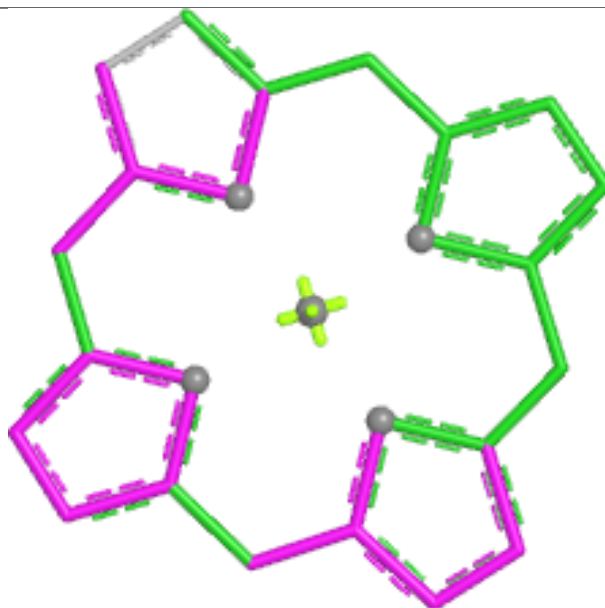


Rings

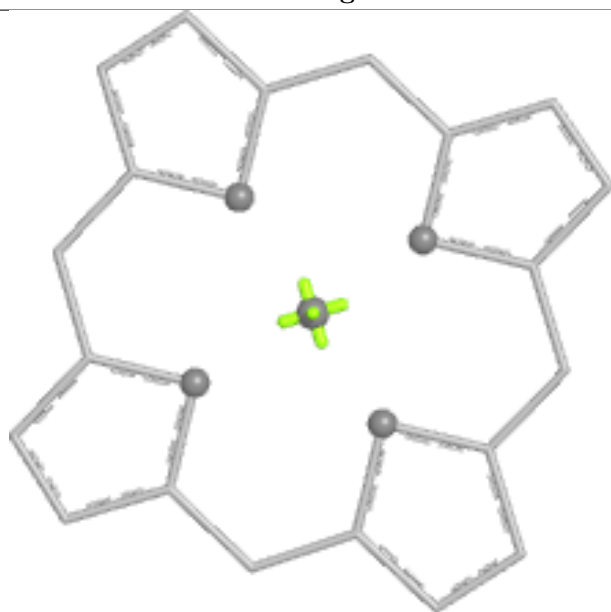
Ligand CLA B 2004



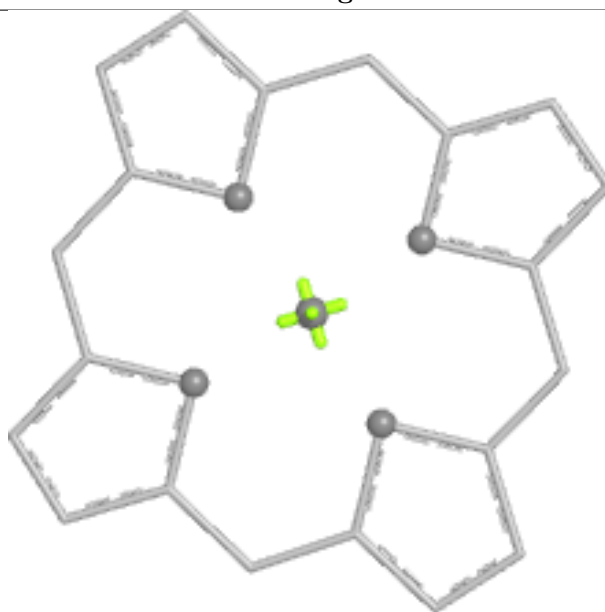
Bond lengths



Bond angles

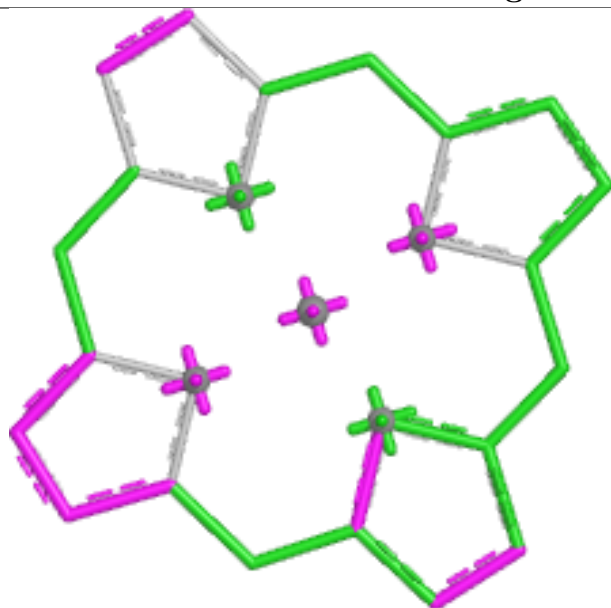


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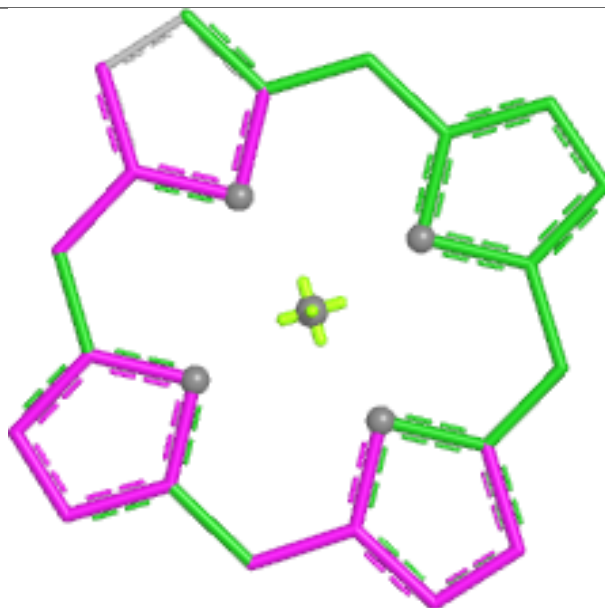


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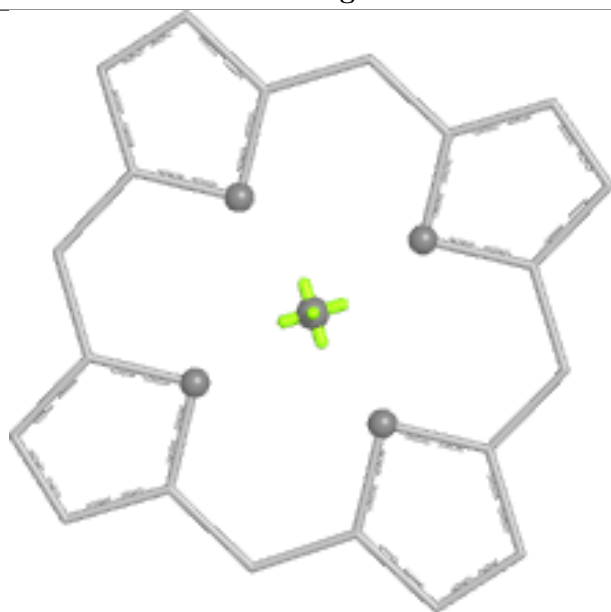
Ligand CLA B 3028



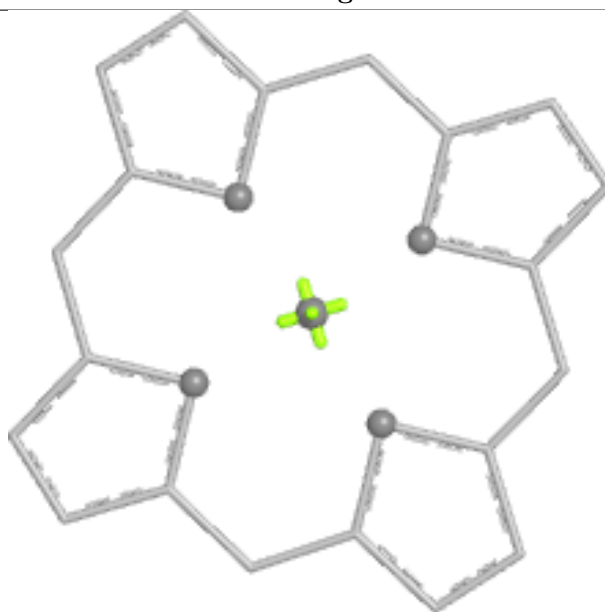
Bond lengths



Bond angles

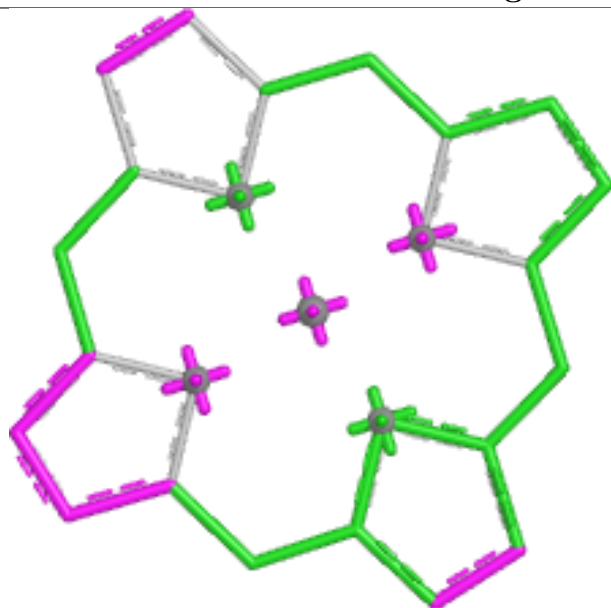


Torsions

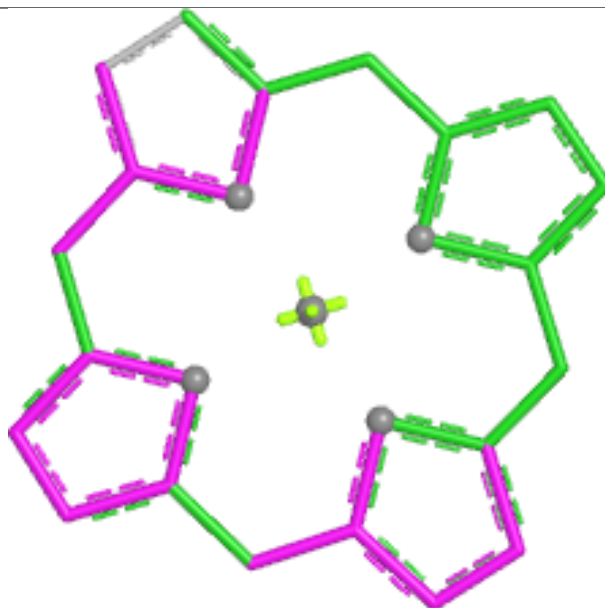


Rings

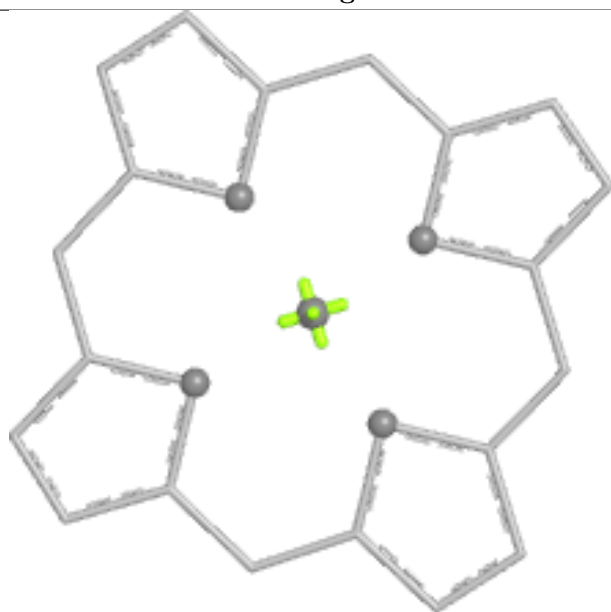
Ligand CLA A 3048



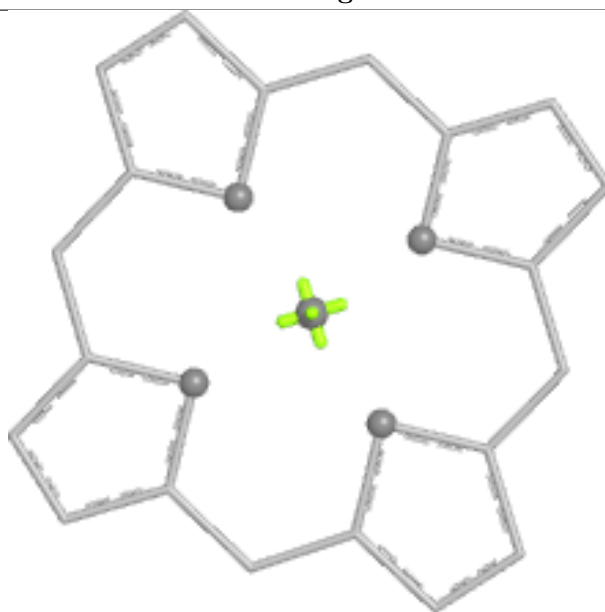
Bond lengths



Bond angles

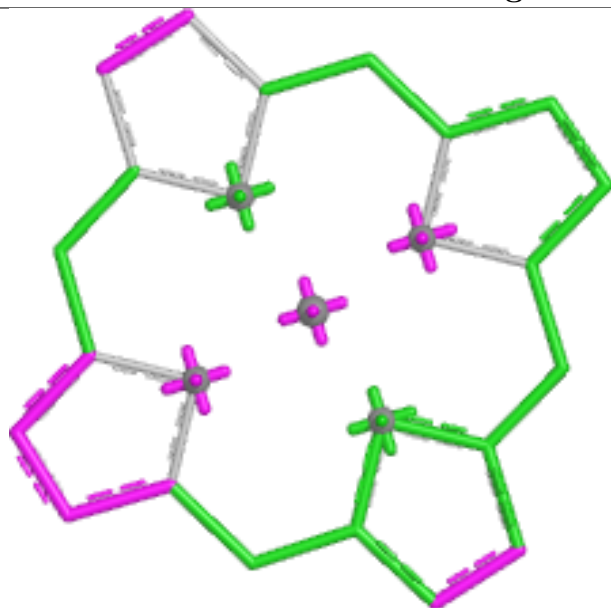


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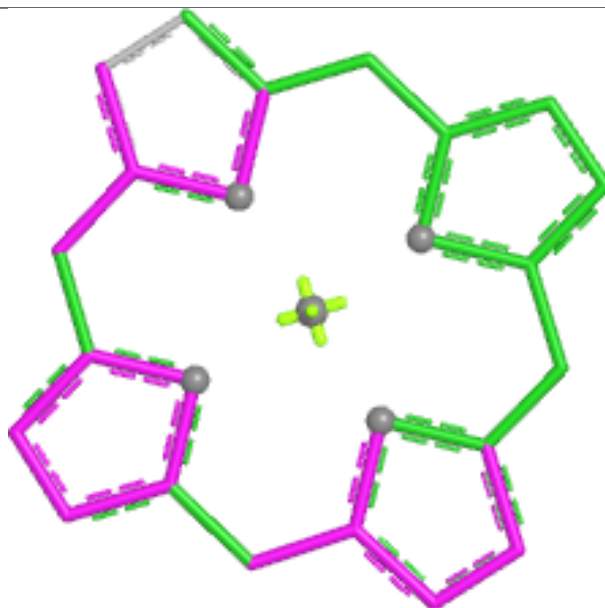


Rings

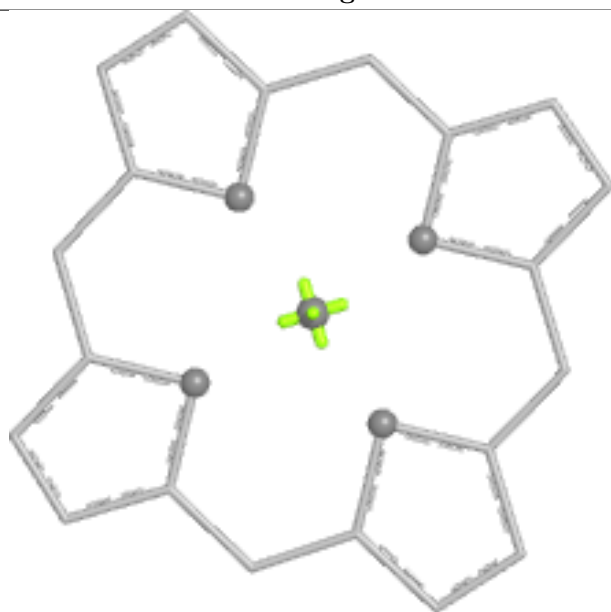
Ligand CLA B 3060



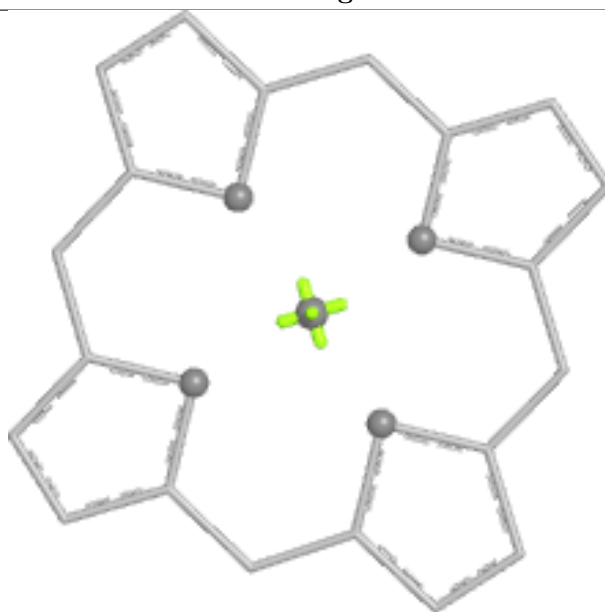
Bond lengths



Bond angles

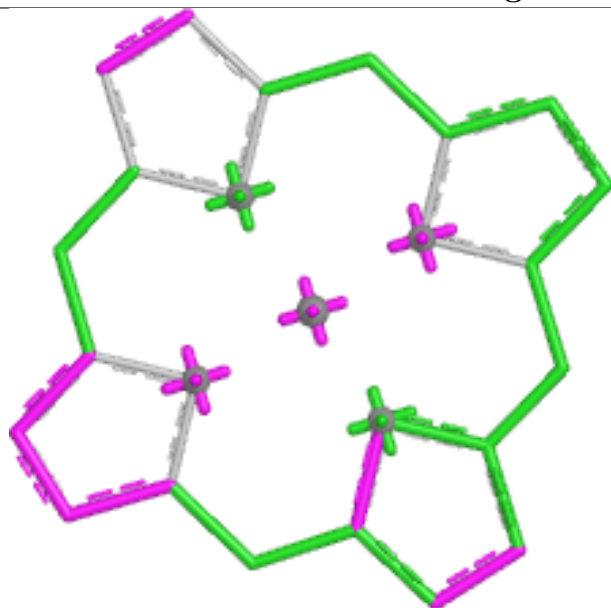


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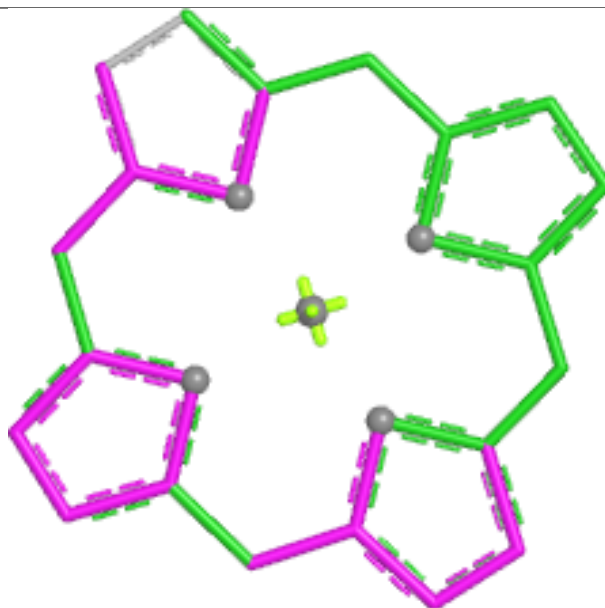


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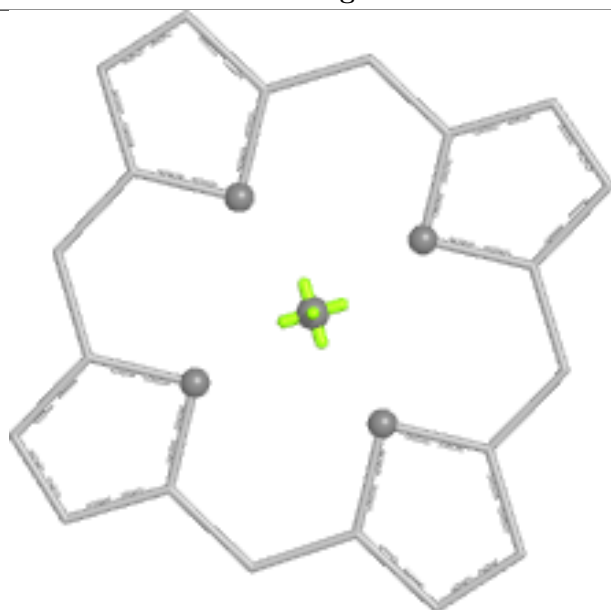
Ligand CLA A 3039



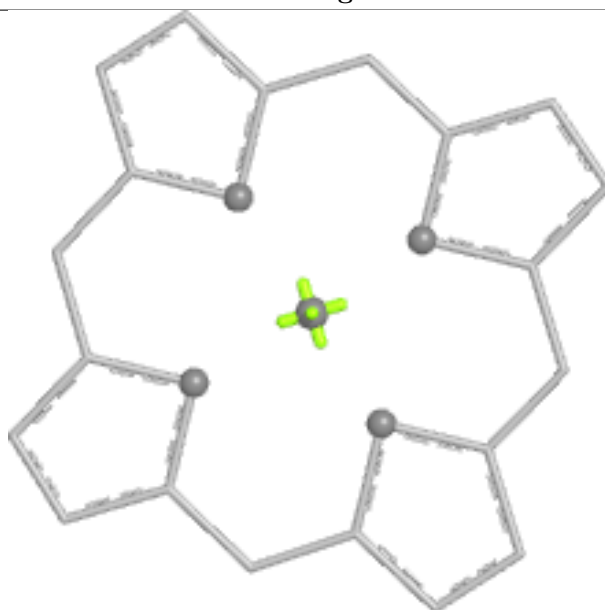
Bond lengths



Bond angles

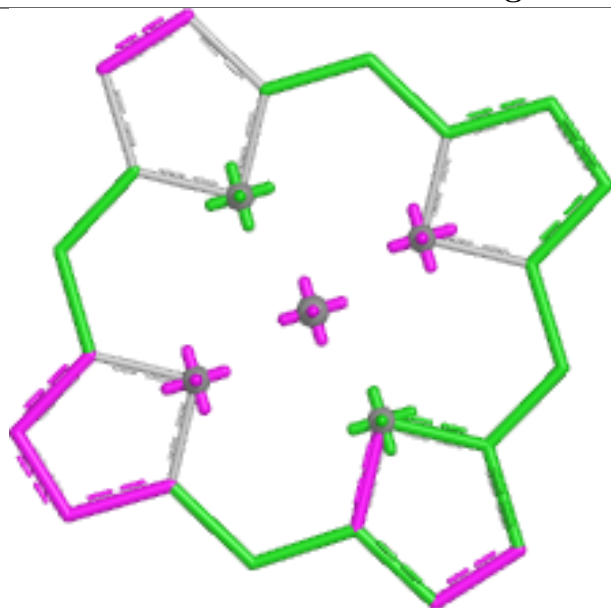


Torsions

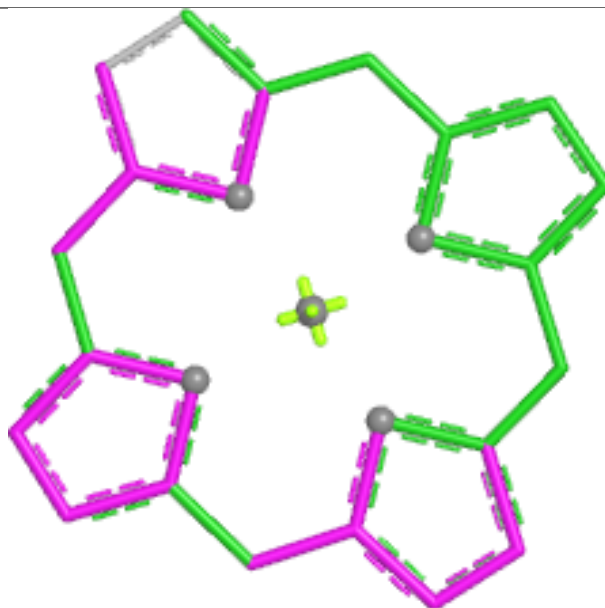


Rings

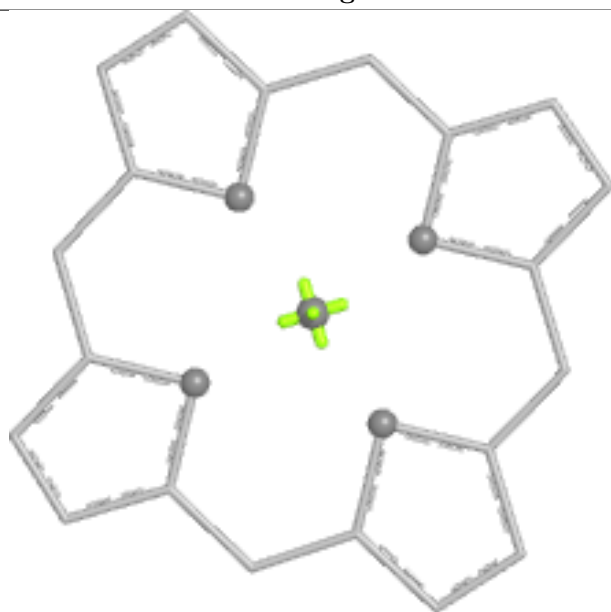
Ligand CLA A 3041



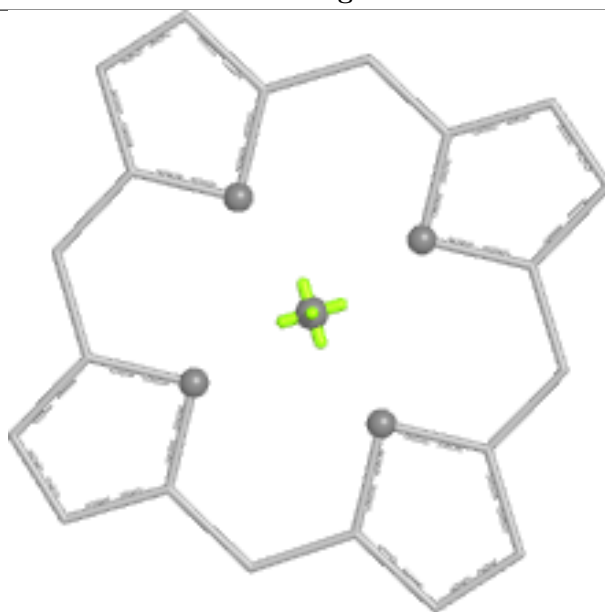
Bond lengths



Bond angles

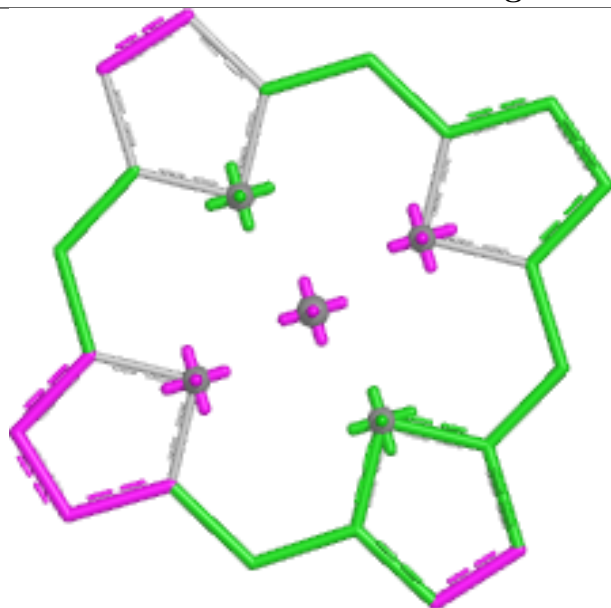


Torsions

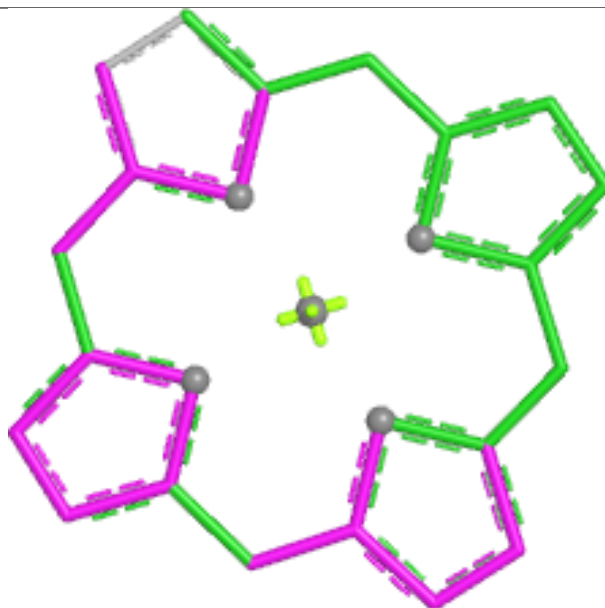


Rings

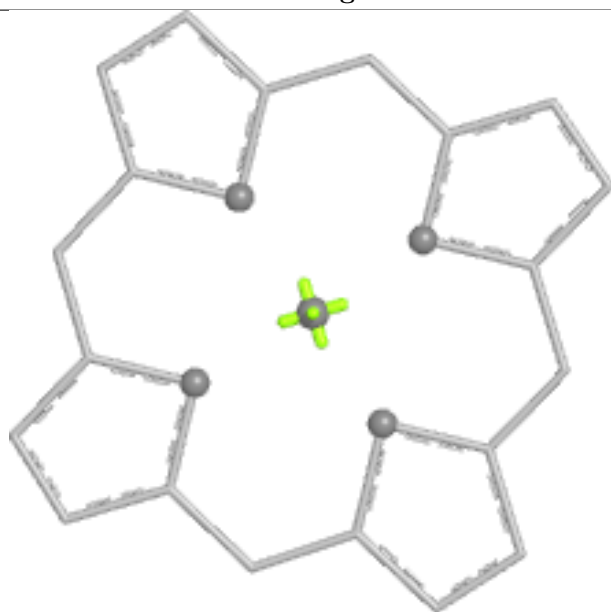
Ligand CLA A 3068



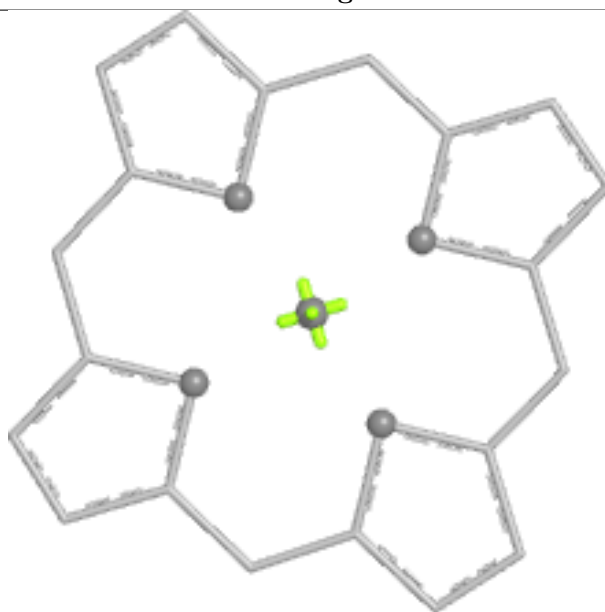
Bond lengths



Bond angles

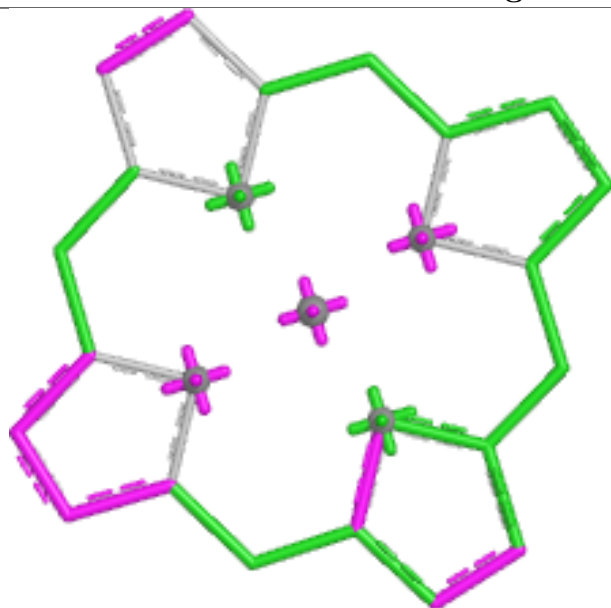


Torsions

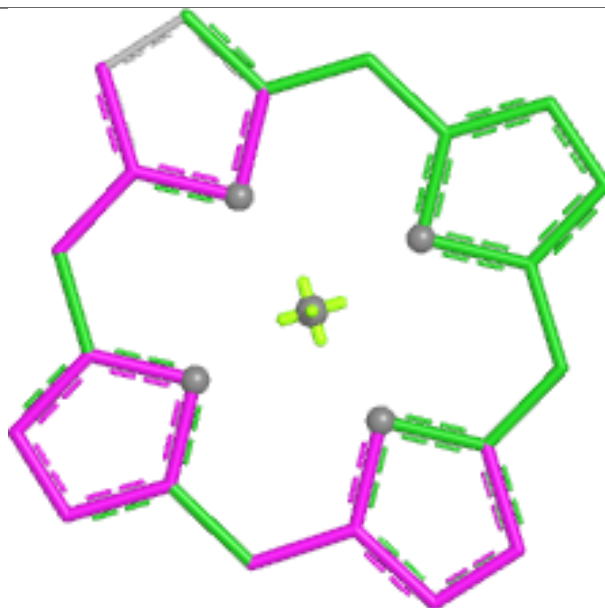


Rings

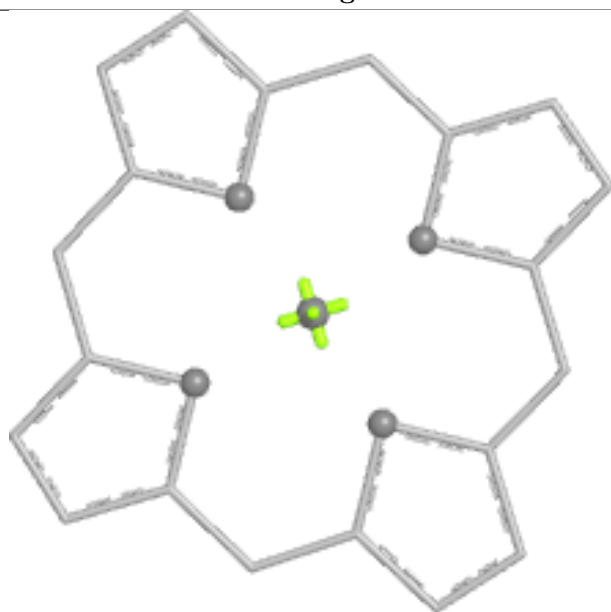
Ligand CLA B 2005



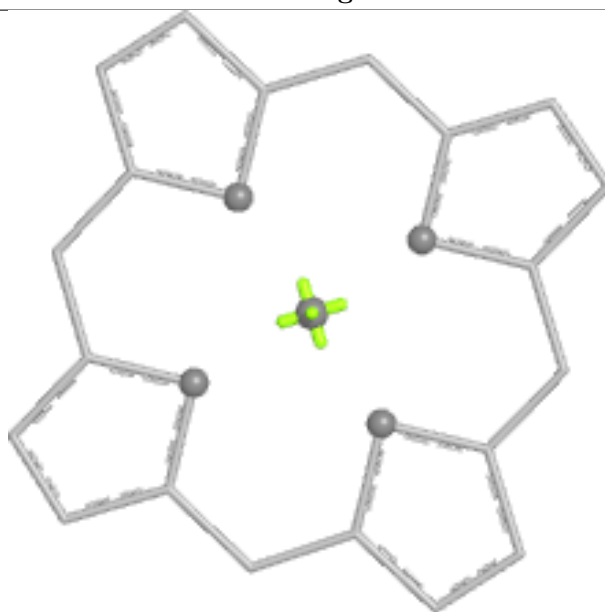
Bond lengths



Bond angles

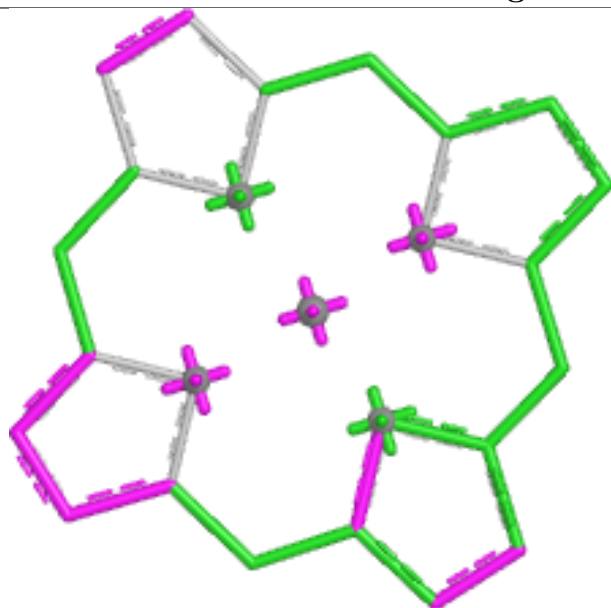


Torsions

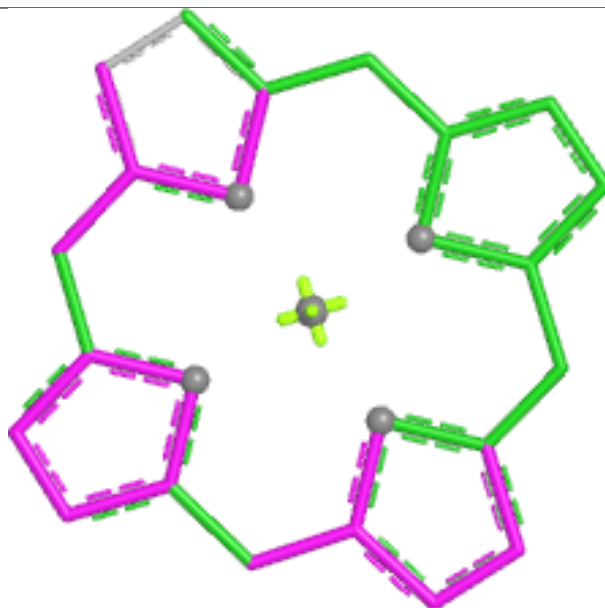


Rings

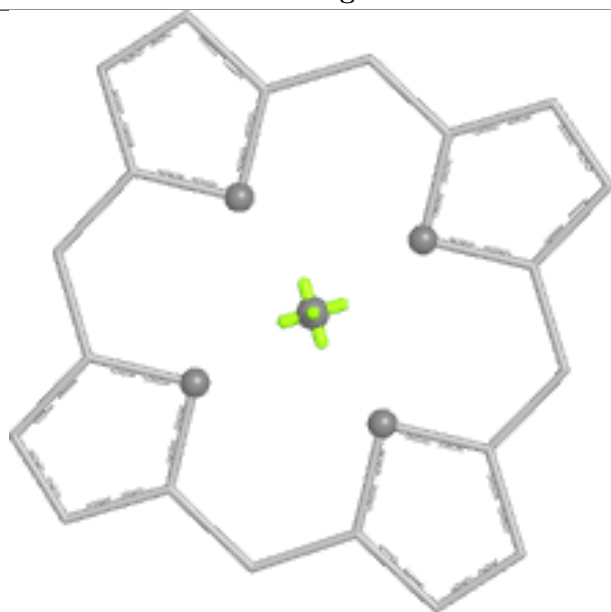
Ligand CLA L 3049



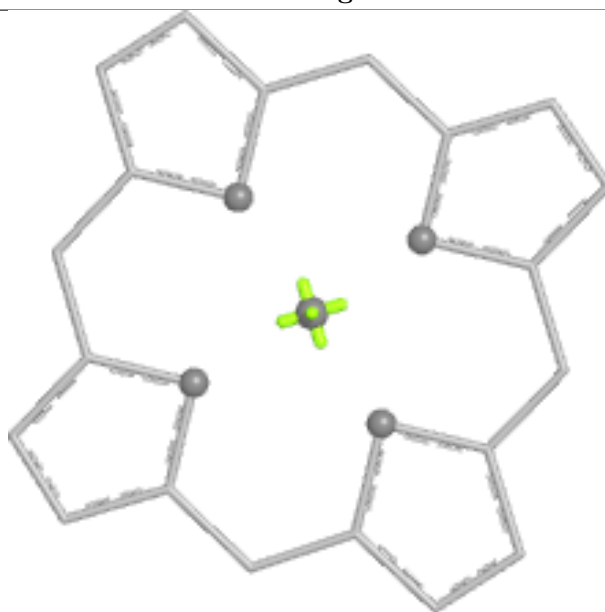
Bond lengths



Bond angles

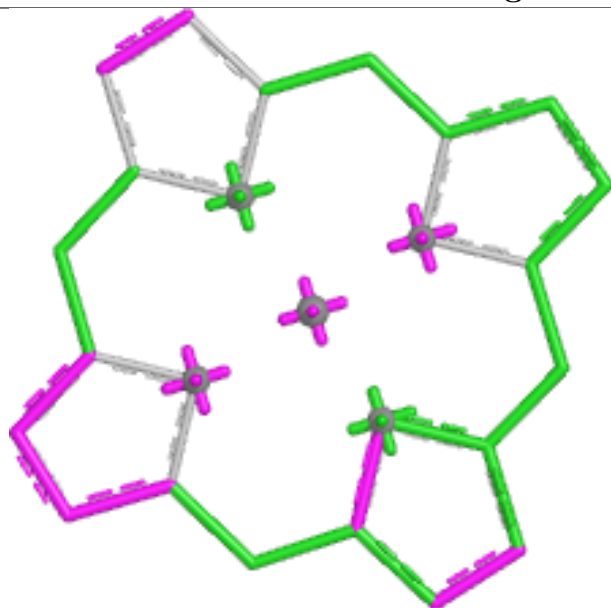


Torsions

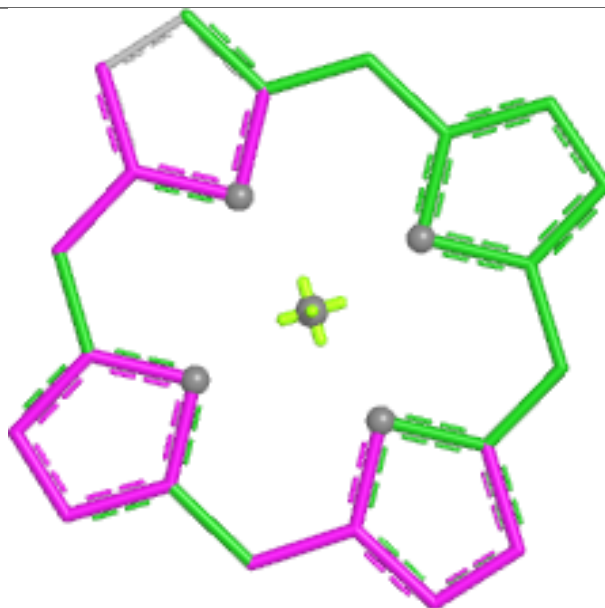


Rings

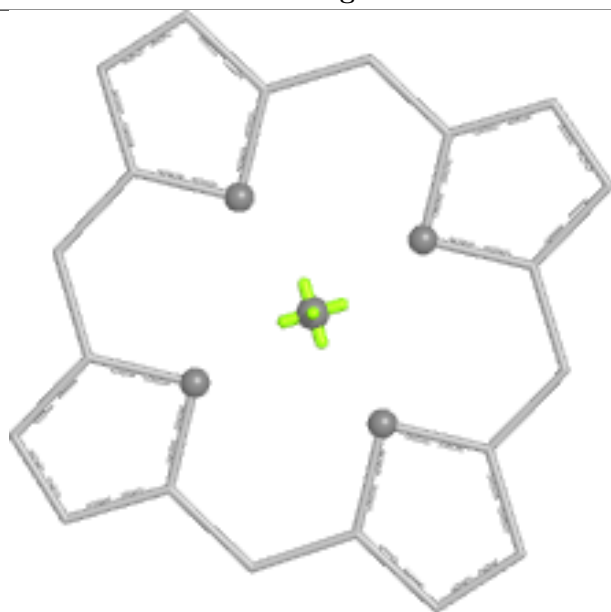
Ligand CLA A 3079



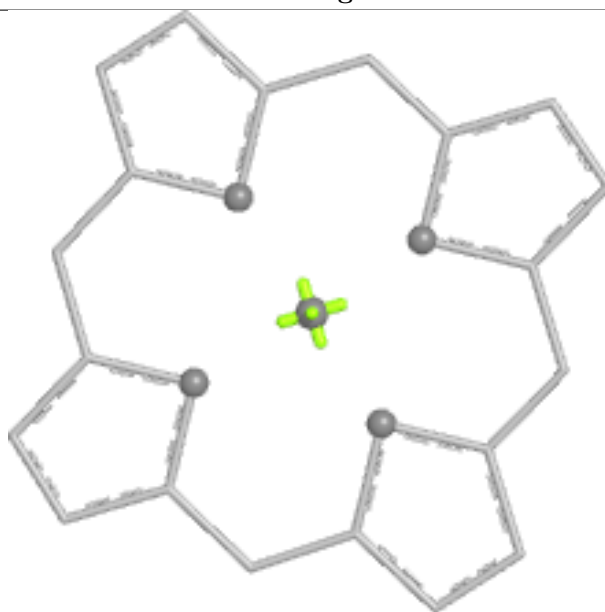
Bond lengths



Bond angles

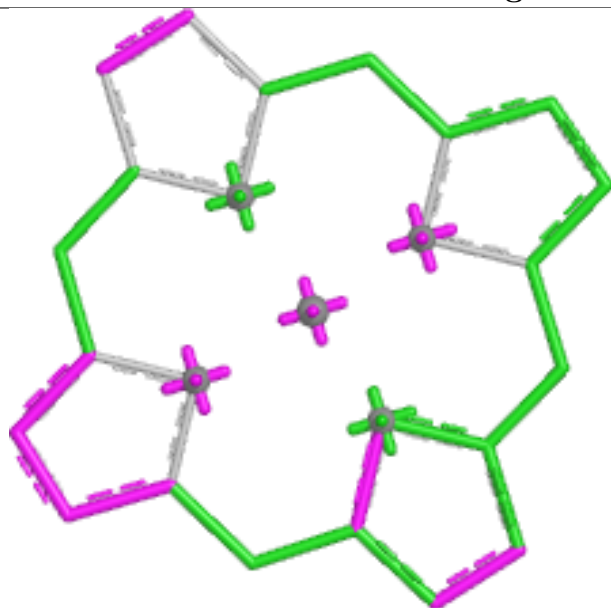


Torsions

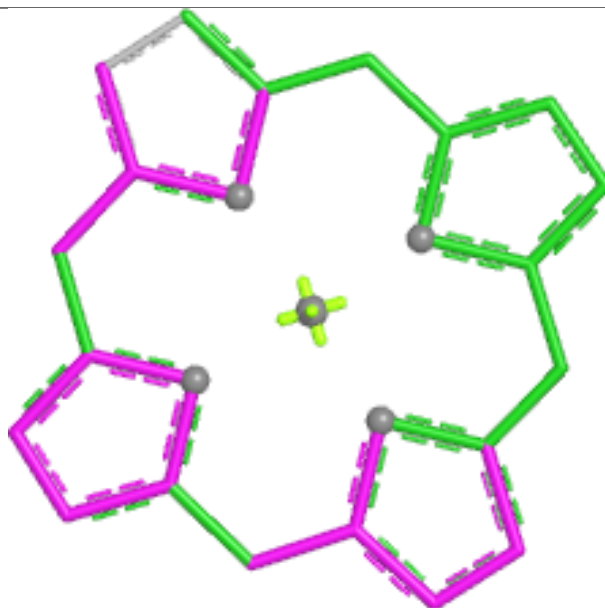


Rings

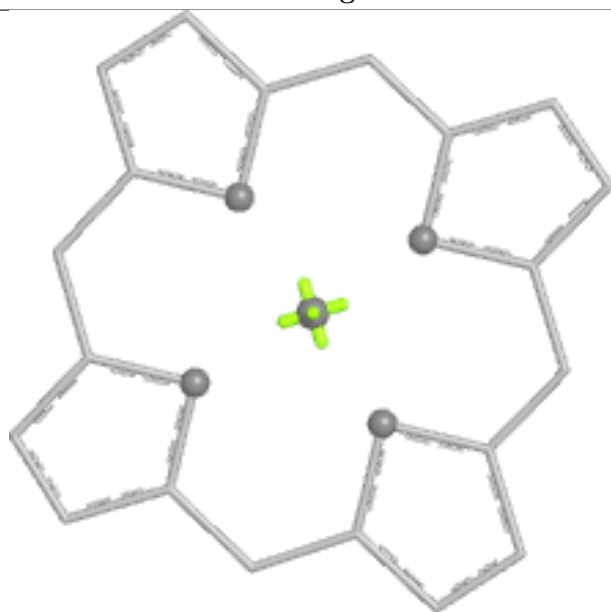
Ligand CLA B 3010



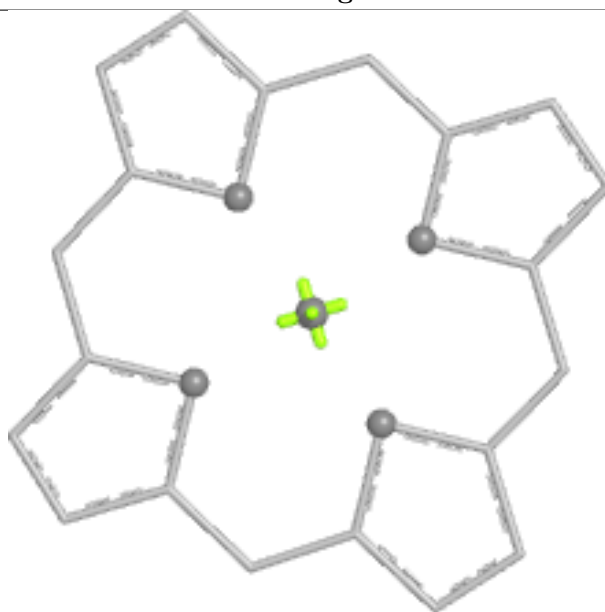
Bond lengths



Bond angles

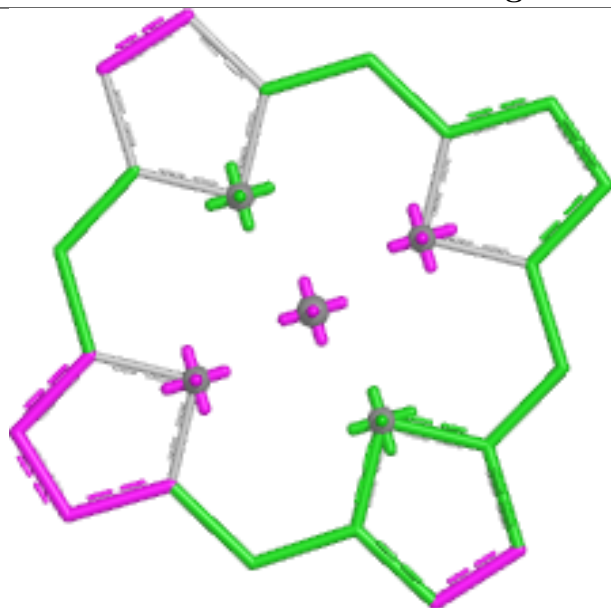


Torsions

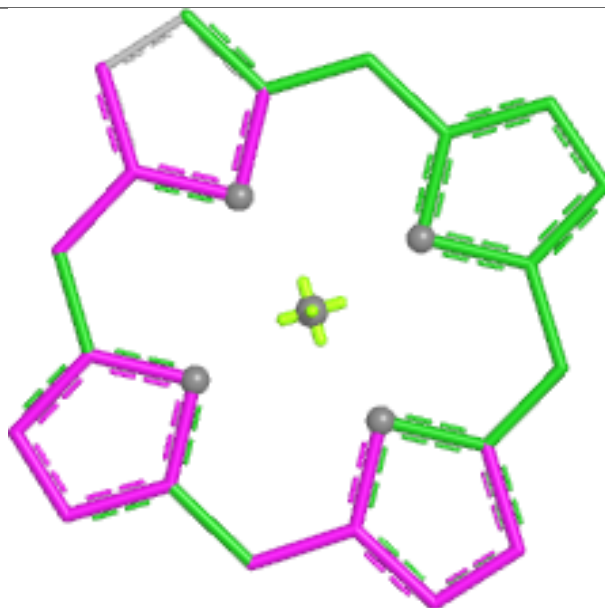


Rings

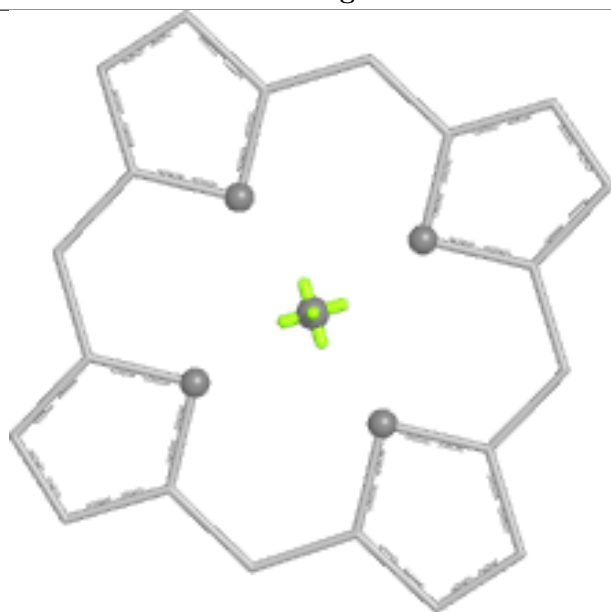
Ligand CLA B 3070



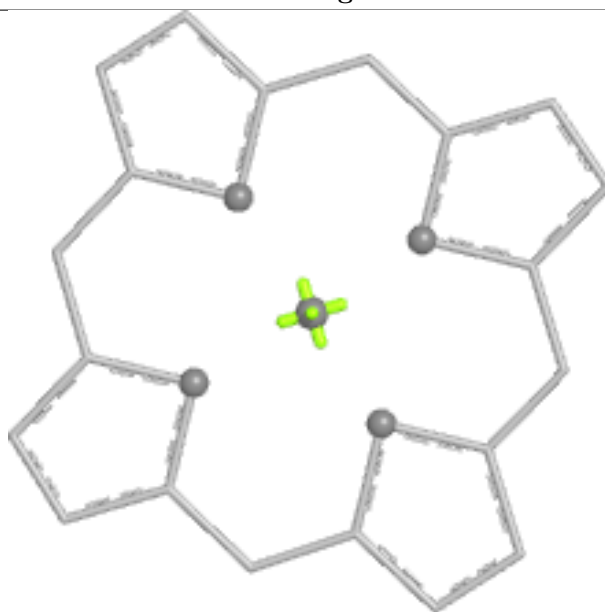
Bond lengths



Bond angles

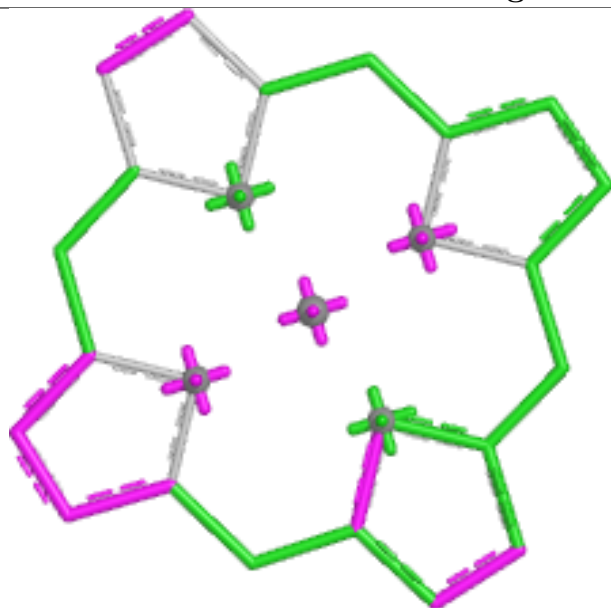


Torsions

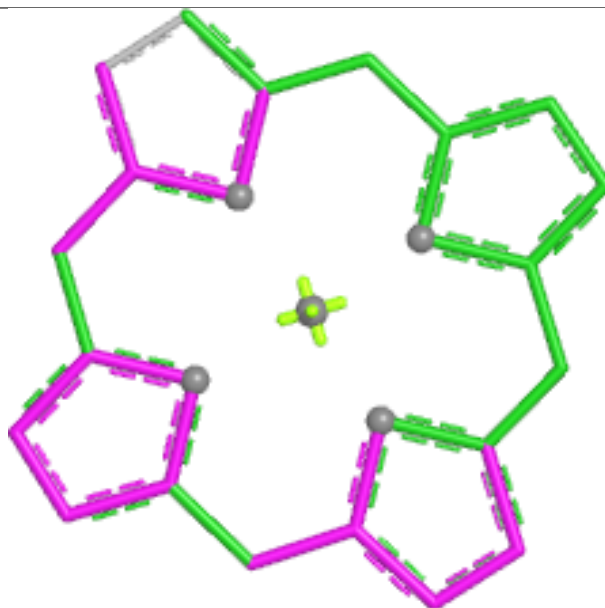


Rings

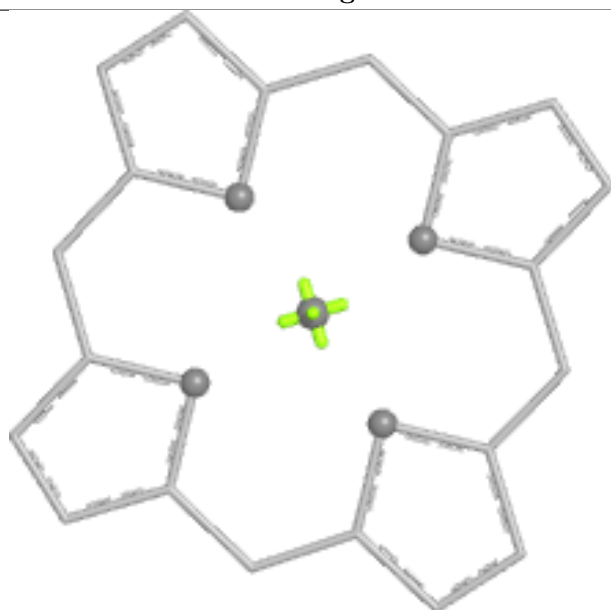
Ligand CLA F 3004



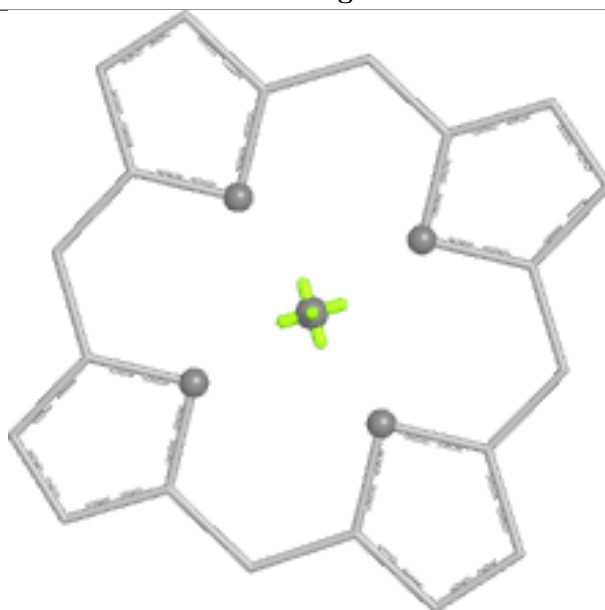
Bond lengths



Bond angles

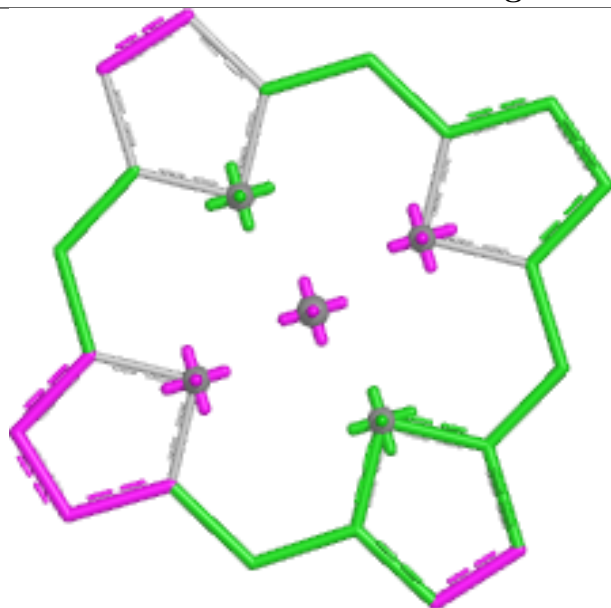


Torsions

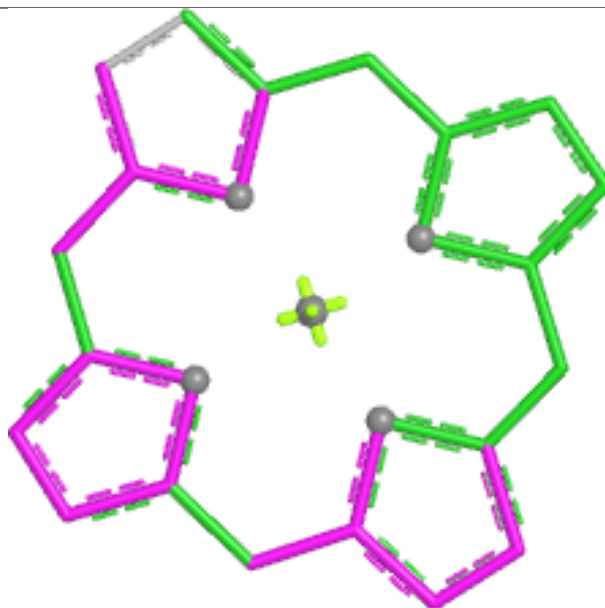


Rings

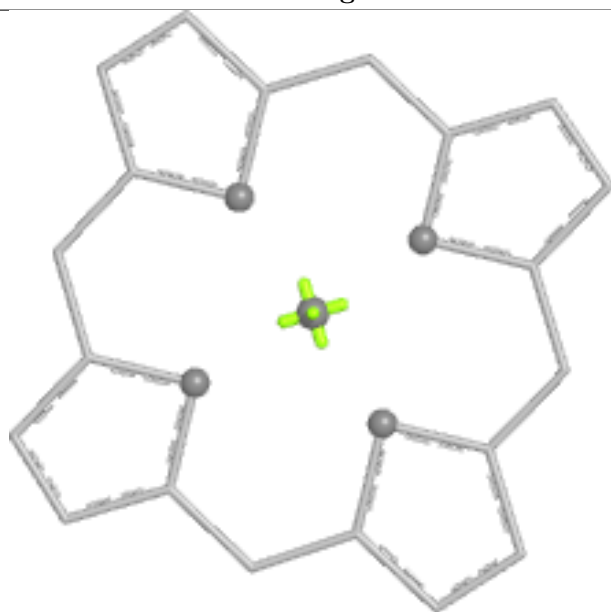
Ligand CLA A 3043



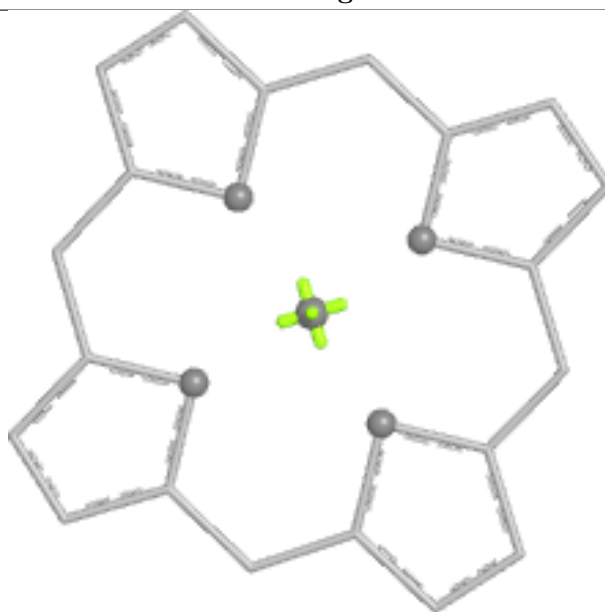
Bond lengths



Bond angles

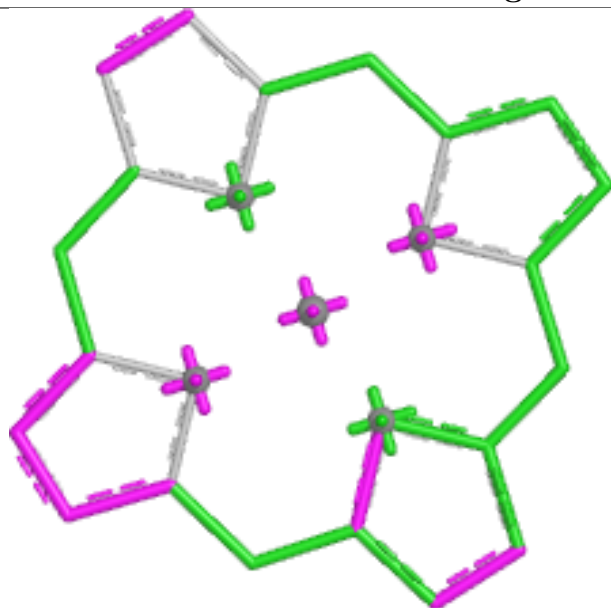


Torsions

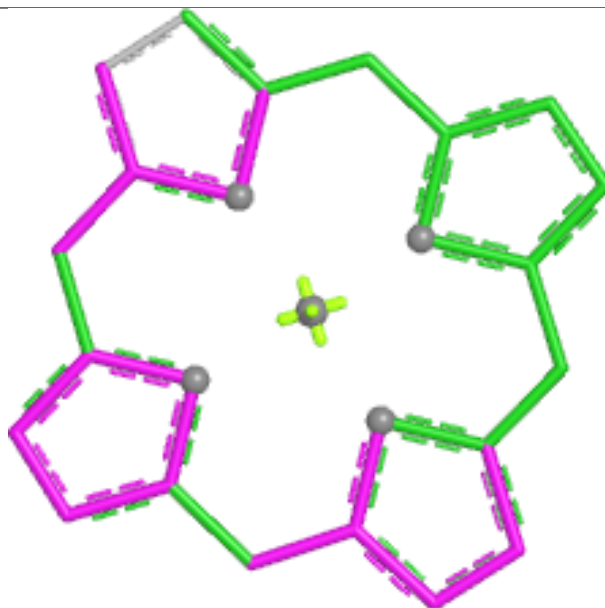


Rings

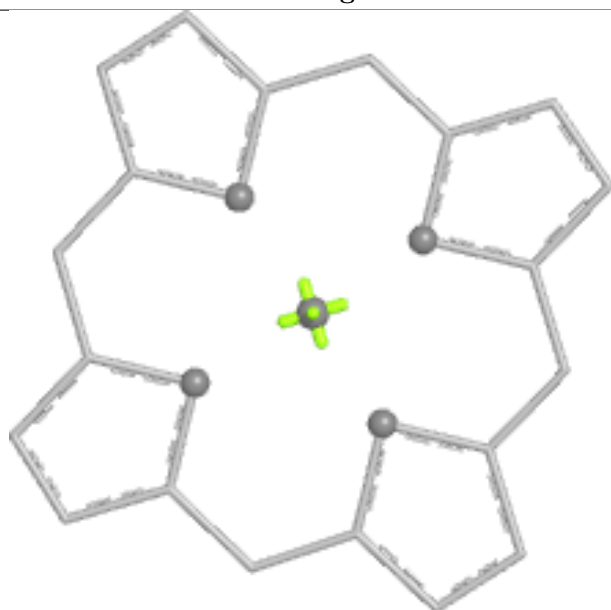
Ligand CLA A 2006



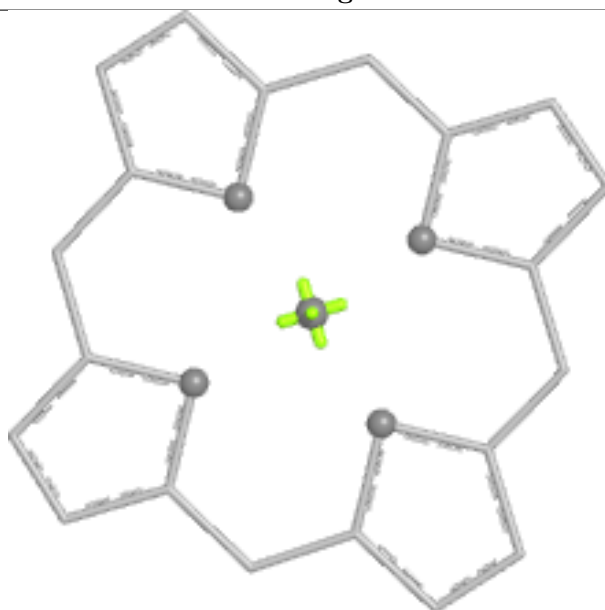
Bond lengths



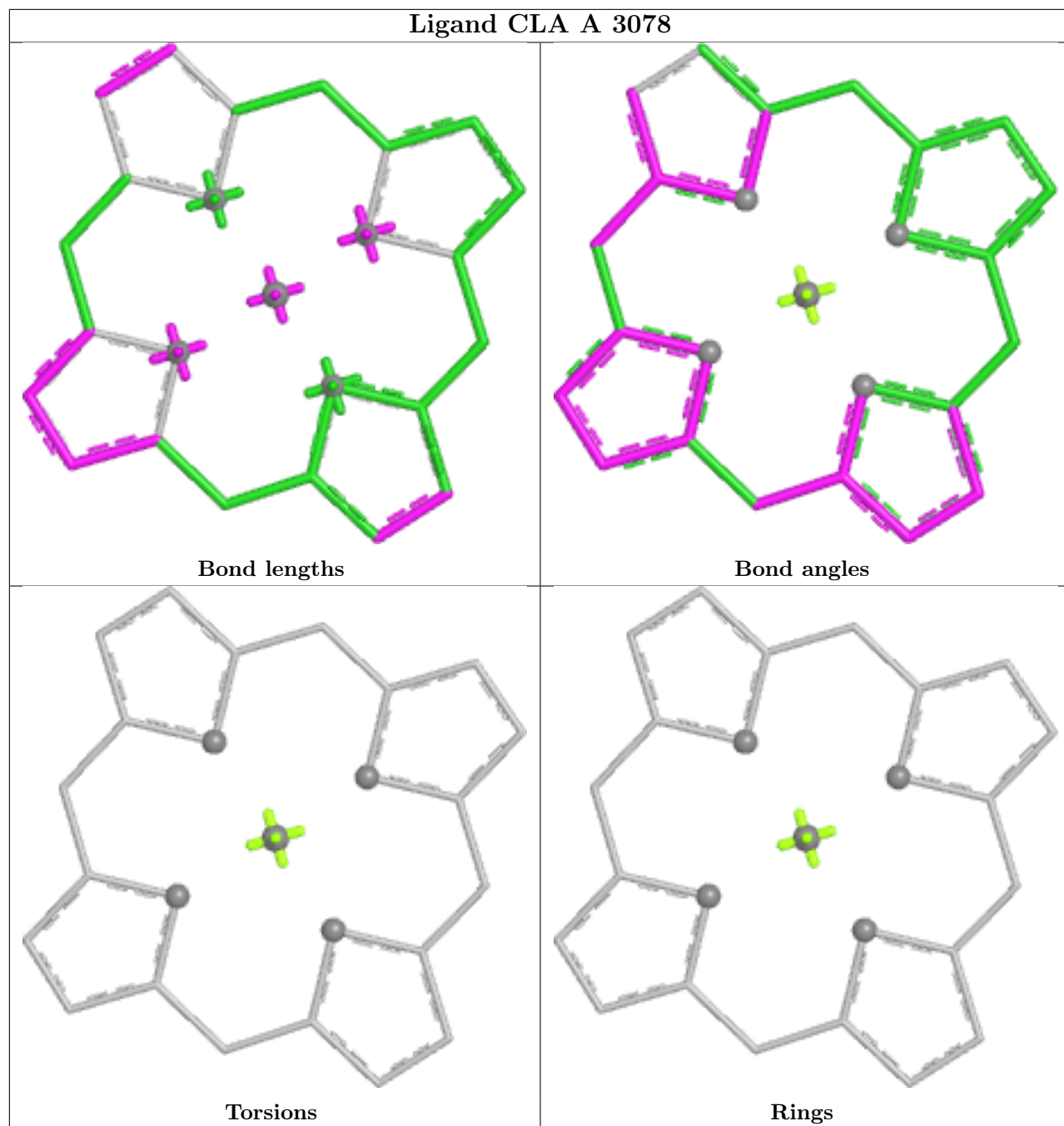
Bond angles



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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.