



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 2, 2026 – 01:21 pm BST

PDB ID : 9S39 / pdb_00009s39
Title : Serial crystallography structure of a photosynthetic reaction center using a goniometer-compatible 96-well chip-based platform
Authors : Ghosh, S.; Banacore, A.
Deposited on : 2025-07-24
Resolution : 3.30 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	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

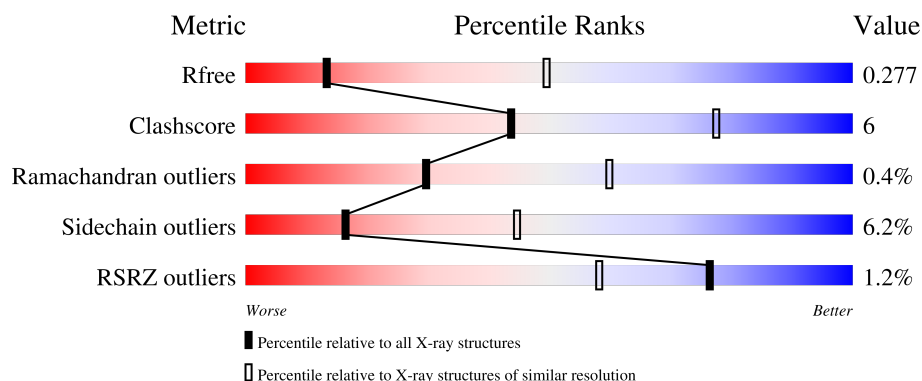
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	C	332	<div> <div>%</div> <div> <div></div> <div>83%</div> <div>14%</div> <div>.</div> </div> </div>
2	H	242	<div> <div>3%</div> <div> <div></div> <div>74%</div> <div>21%</div> <div>..</div> </div> </div>
3	L	273	<div> <div>%</div> <div> <div></div> <div>82%</div> <div>16%</div> <div>.</div> </div> </div>
4	M	323	<div> <div>%</div> <div> <div></div> <div>83%</div> <div>15%</div> <div>.</div> </div> </div>
5	D	8	<div> <div></div> <div> <div>62%</div> <div>38%</div> </div> </div>

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
7	SO4	H	303	-	-	X	-
8	BCB	L	400	X	-	-	-
8	BCB	L	401	X	-	-	-
8	BCB	M	403	X	-	-	-
8	BCB	M	404	X	-	-	-
9	BPB	L	402	X	-	-	-
9	BPB	M	405	X	-	-	-

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 19384 atoms, of which 9349 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 Photosynthetic reaction center cytochrome c subunit.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	C	332	Total	C	H	N	O	S	0	2	0
			5112	1640	2509	466	479	18			

- Molecule 2 is a protein called Reaction center protein H chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	H	242	Total	C	H	N	O	S	0	2	0
			3753	1213	1854	324	361	1			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	?	-	LEU	deletion	UNP P06008
H	?	-	GLY	deletion	UNP P06008
H	?	-	LEU	deletion	UNP P06008
H	?	-	VAL	deletion	UNP P06008
H	?	-	LYS	deletion	UNP P06008
H	?	-	LEU	deletion	UNP P06008
H	?	-	ALA	deletion	UNP P06008
H	?	-	PRO	deletion	UNP P06008

- Molecule 3 is a protein called Reaction center protein L chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	L	273	Total	C	H	N	O	S	0	1	0
			4223	1459	2052	350	355	7			

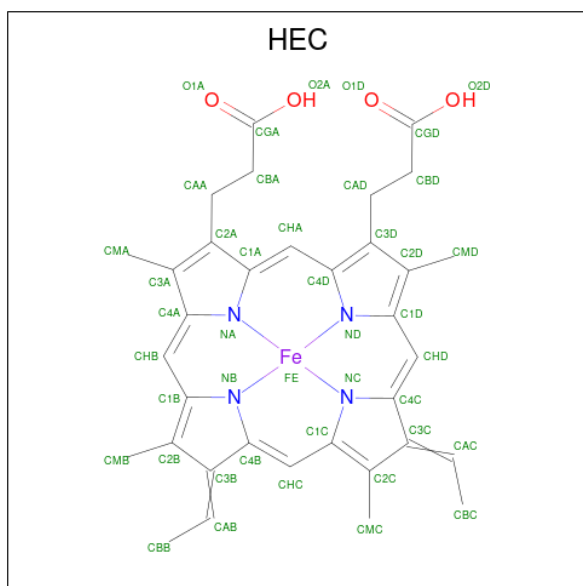
- Molecule 4 is a protein called Reaction center protein M chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	M	323	Total	C	H	N	O	S	0	2	0
			4945	1702	2390	419	423	11			

- Molecule 5 is a protein called FME-TYR-HIS-GLY-ALA-LEU-ALA-GLN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	D	8	Total	C	H	N	O	S	0	0
			118	40	55	11	11	1		

- Molecule 6 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{34}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).



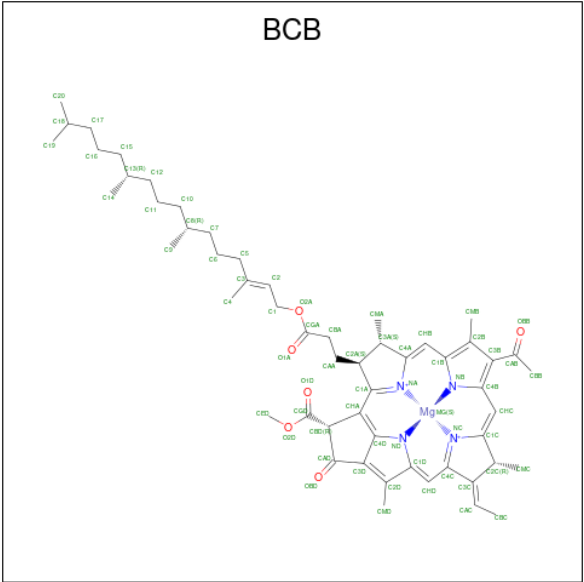
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	C	1	Total	C	Fe	H	N	O	0
			61	34	1	18	4	4	
6	C	1	Total	C	Fe	H	N	O	0
			61	34	1	18	4	4	
6	C	1	Total	C	Fe	H	N	O	0
			61	34	1	18	4	4	
6	C	1	Total	C	Fe	H	N	O	0
			61	34	1	18	4	4	

- Molecule 7 is SULFATE ION (CCD ID: SO4) (formula: O_4S) (labeled as "Ligand of Interest" by depositor).



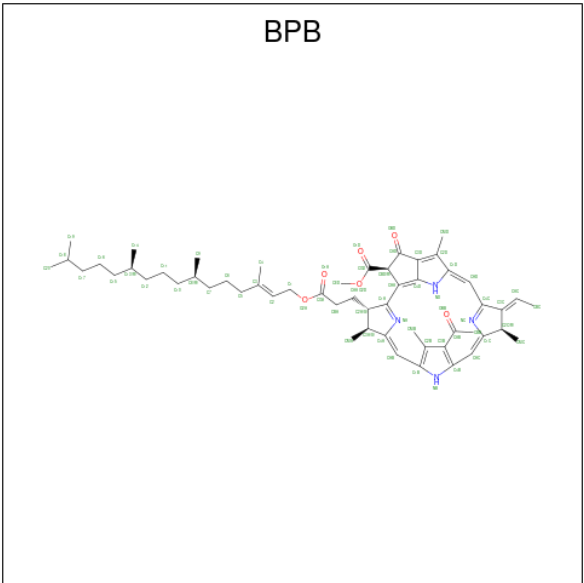
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	O	S	0	0
			5	4	1		
7	C	1	Total	O	S	0	0
			5	4	1		
7	H	1	Total	O	S	0	0
			5	4	1		
7	H	1	Total	O	S	0	0
			5	4	1		
7	H	1	Total	O	S	0	0
			5	4	1		
7	M	1	Total	O	S	0	0
			5	4	1		
7	M	1	Total	O	S	0	0
			5	4	1		
7	M	1	Total	O	S	0	0
			5	4	1		

- Molecule 8 is BACTERIOCHLOROPHYLL B (CCD ID: BCB) (formula: $C_{55}H_{72}MgN_4O_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
8	L	1	Total	C	H	Mg	N	O	0	0
			123	55	57	1	4	6		
8	L	1	Total	C	H	Mg	N	O	0	0
			123	55	57	1	4	6		
8	M	1	Total	C	H	Mg	N	O	0	0
			123	55	57	1	4	6		
8	M	1	Total	C	H	Mg	N	O	0	0
			123	55	57	1	4	6		

- Molecule 9 is BACTERIOPHEOPHYTIN B (CCD ID: BPB) (formula: $C_{55}H_{74}N_4O_6$) (labeled as "Ligand of Interest" by depositor).

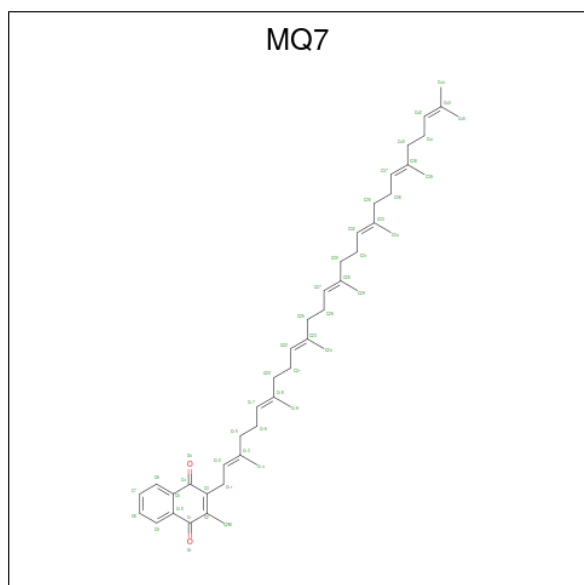


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	L	1	Total	C	H	N	O	0	0
			123	55	58	4	6		
9	M	1	Total	C	H	N	O	0	0
			123	55	58	4	6		

- Molecule 10 is FE (II) ION (CCD ID: FE2) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

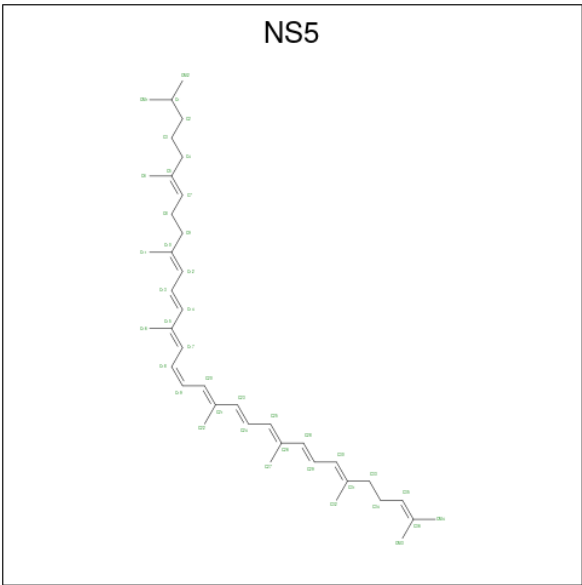
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	M	1	Total	Fe	0	0
			1	1		

- Molecule 11 is MENAQUINONE-7 (CCD ID: MQ7) (formula: C₄₆H₆₄O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	M	1	Total	C	H	O	0	0
			85	46	37	2		

- Molecule 12 is 15-cis-1,2-dihydroneurosporene (CCD ID: NS5) (formula: C₄₀H₆₀) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	M	1	Total	C	H	0	0
			76	40	36		

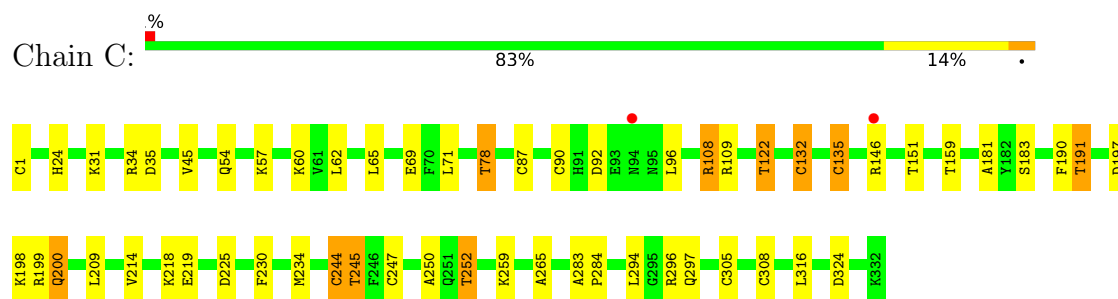
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	C	19	Total	O	0	0
			19	19		
13	H	10	Total	O	0	0
			10	10		
13	L	10	Total	O	0	0
			10	10		
13	M	10	Total	O	0	0
			10	10		

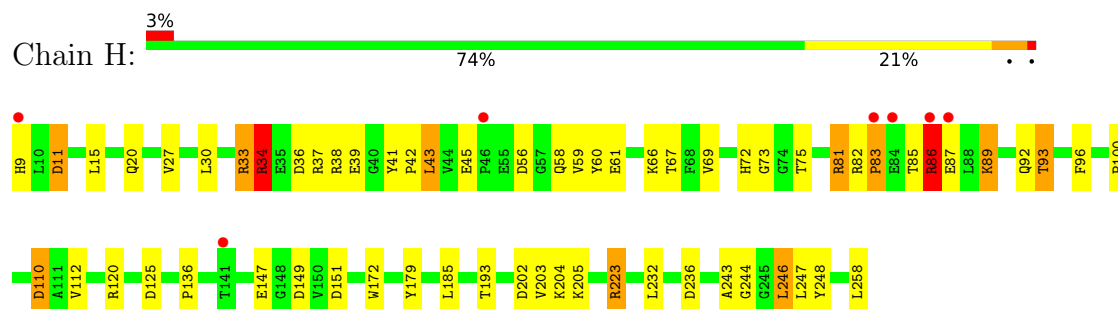
3 Residue-property plots

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

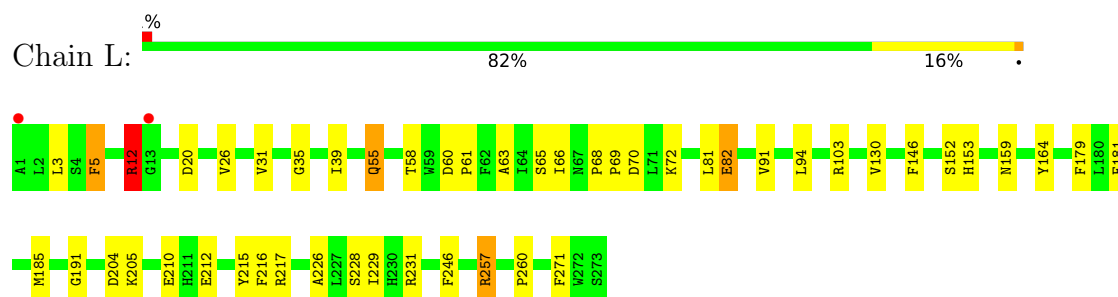
- Molecule 1: Photosynthetic reaction center cytochrome c subunit



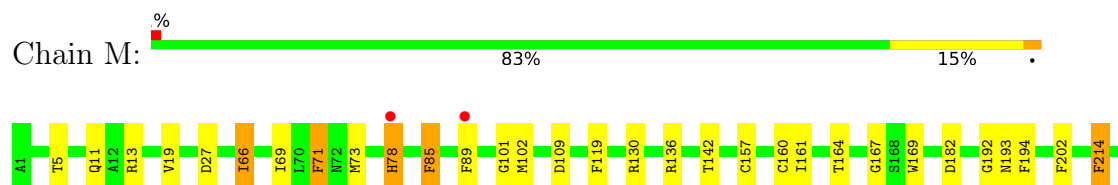
- Molecule 2: Reaction center protein H chain

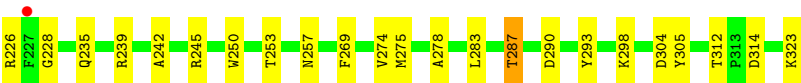


- Molecule 3: Reaction center protein L chain



- Molecule 4: Reaction center protein M chain





● Molecule 5: FME-TYR-HIS-GLY-ALA-LEU-ALA-GLN



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	226.50Å 226.50Å 113.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	60.00 – 3.30 60.00 – 3.30	Depositor EDS
% Data completeness (in resolution range)	98.9 (60.00-3.30) 99.0 (60.00-3.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.98 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0430 (refmacat 0.4.100)	Depositor
R, R_{free}	0.246 , 0.296 0.225 , 0.277	Depositor DCC
R_{free} test set	8510 reflections (4.30%)	wwPDB-VP
Wilson B-factor (Å ²)	21.0	Xtriage
Anisotropy	0.014	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 79.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	19384	wwPDB-VP
Average B, all atoms (Å ²)	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.90% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BCB, BPB, NS5, SO4, FE2, FME, HEC, MQ7

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	C	0.69	0/2670	1.42	13/3637 (0.4%)
2	H	0.78	3/1942 (0.2%)	1.56	25/2651 (0.9%)
3	L	0.69	0/2259	1.49	25/3084 (0.8%)
4	M	0.72	0/2659	1.46	20/3637 (0.5%)
5	D	0.68	0/54	1.17	1/72 (1.4%)
All	All	0.72	3/9584 (0.0%)	1.48	84/13081 (0.6%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	5
2	H	0	9
3	L	0	3
4	M	0	4
All	All	0	21

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	58	GLN	C-N	-7.12	1.25	1.33
2	H	59	VAL	N-CA	-6.16	1.38	1.46
2	H	58	GLN	CA-C	-5.96	1.45	1.52

The worst 5 of 84 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	122	THR	CA-CB-OG1	-13.29	89.67	109.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	58	GLN	CA-C-N	-12.92	98.06	120.29
2	H	58	GLN	C-N-CA	-12.92	98.06	120.29
2	H	58	GLN	CA-C-O	11.64	132.76	120.42
2	H	151	ASP	CB-CA-C	9.38	118.88	110.44

There are no chirality outliers.

5 of 21 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	108	ARG	Sidechain
1	C	109	ARG	Sidechain
1	C	199	ARG	Sidechain
1	C	296	ARG	Sidechain
1	C	34	ARG	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2603	2509	2587	45	0
2	H	1899	1854	1884	33	0
3	L	2171	2052	2092	16	0
4	M	2555	2390	2443	24	0
5	D	63	55	58	1	0
6	C	172	72	128	35	0
7	C	10	0	0	0	0
7	H	15	0	0	3	0
7	M	15	0	0	0	0
8	L	132	114	144	3	0
8	M	132	114	144	5	0
9	L	65	58	74	1	0
9	M	65	58	74	9	0
10	M	1	0	0	0	0
11	M	48	37	64	2	0
12	M	40	36	60	2	0
13	C	19	0	0	0	0
13	H	10	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	L	10	0	0	1	0
13	M	10	0	0	0	0
All	All	10035	9349	9752	120	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 6.

The worst 5 of 120 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:56:ASP:O	2:H:60:TYR:CD1	1.65	1.46
1:C:135:CYS:SG	6:C:402:HEC:CAC	2.27	1.21
1:C:90:CYS:SG	6:C:401:HEC:CAC	2.30	1.20
2:H:86[A]:ARG:HG2	2:H:86[A]:ARG:HH21	1.05	1.18
1:C:87:CYS:SG	6:C:401:HEC:CAB	2.34	1.15

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	330/332 (99%)	312 (94%)	18 (6%)	0	100	100
2	H	238/242 (98%)	224 (94%)	12 (5%)	2 (1%)	16	45
3	L	271/273 (99%)	259 (96%)	11 (4%)	1 (0%)	30	60
4	M	321/323 (99%)	309 (96%)	10 (3%)	2 (1%)	21	52
5	D	6/8 (75%)	6 (100%)	0	0	100	100
All	All	1166/1178 (99%)	1110 (95%)	51 (4%)	5 (0%)	30	60

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	L	66[A]	ILE
2	H	73	GLY
4	M	192	GLY
4	M	193	ASN
2	H	83	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	281/281 (100%)	259 (92%)	22 (8%)	11	36
2	H	202/202 (100%)	183 (91%)	19 (9%)	8	30
3	L	218/218 (100%)	207 (95%)	11 (5%)	22	50
4	M	249/249 (100%)	242 (97%)	7 (3%)	38	62
5	D	4/4 (100%)	4 (100%)	0	100	100
All	All	954/954 (100%)	895 (94%)	59 (6%)	16	45

5 of 59 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	72	HIS
4	M	194	PHE
2	H	185	LEU
4	M	85	PHE
3	L	185	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
3	L	183	ASN
4	M	4	GLN
4	M	87	GLN
4	M	11	GLN
1	C	302	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	FME	D	1	5	8,9,10	0.52	0	7,9,11	1.48	1 (14%)

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
5	FME	D	1	5	-	2/7/9/11	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	1	FME	O-C-CA	-3.56	115.44	124.78

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	1	FME	CA-CB-CG-SD
5	D	1	FME	C-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 21 ligands modelled in this entry, 1 is monoatomic - leaving 20 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	$\# Z > 2$
6	HEC	C	401	1	46,50,50	2.25	11 (23%)	60,82,82	1.81	17 (28%)
12	NS5	M	406	-	39,39,39	1.72	5 (12%)	44,46,46	1.79	9 (20%)
7	SO4	C	406	-	4,4,4	0.35	0	6,6,6	0.30	0
7	SO4	M	408	-	4,4,4	0.31	0	6,6,6	0.32	0
7	SO4	H	302	-	4,4,4	0.26	0	6,6,6	0.43	0
11	MQ7	M	402	-	49,49,49	0.67	1 (2%)	60,63,63	0.80	1 (1%)
9	BPB	L	402	-	57,70,70	1.03	5 (8%)	56,101,101	1.38	5 (8%)
7	SO4	H	303	-	4,4,4	0.30	0	6,6,6	0.12	0
7	SO4	H	301	-	4,4,4	0.34	0	6,6,6	0.20	0
7	SO4	M	409	-	4,4,4	0.36	0	6,6,6	0.19	0
8	BCB	L	401	3	63,74,74	1.92	11 (17%)	60,115,115	2.76	12 (20%)
6	HEC	C	402	1	46,50,50	2.39	12 (26%)	60,82,82	1.67	14 (23%)
7	SO4	C	405	-	4,4,4	0.28	0	6,6,6	0.20	0
8	BCB	L	400	3	63,74,74	1.69	10 (15%)	60,115,115	3.06	11 (18%)
9	BPB	M	405	-	57,70,70	1.32	5 (8%)	56,101,101	1.58	9 (16%)
7	SO4	M	407	-	4,4,4	0.34	0	6,6,6	0.22	0
8	BCB	M	403	4	63,74,74	1.74	10 (15%)	60,115,115	2.87	12 (20%)
8	BCB	M	404	4	63,74,74	2.04	8 (12%)	60,115,115	2.45	13 (21%)
6	HEC	C	404	1	46,50,50	2.59	5 (10%)	60,82,82	1.70	18 (30%)
6	HEC	C	403	1	46,50,50	2.86	13 (28%)	60,82,82	1.78	12 (20%)

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
8	BCB	L	401	3	2/2/26/26	11/37/137/137	-
8	BCB	L	400	3	2/2/26/26	8/37/137/137	-
9	BPB	M	405	-	1/1/23/23	18/37/105/105	0/5/6/6
11	MQ7	M	402	-	-	3/41/61/61	0/2/2/2
8	BCB	M	403	4	3/3/26/26	19/37/137/137	-
8	BCB	M	404	4	2/2/26/26	11/37/137/137	-
9	BPB	L	402	-	1/1/23/23	6/37/105/105	0/5/6/6
6	HEC	C	401	1	-	3/14/54/54	-
6	HEC	C	402	1	-	8/14/54/54	-
6	HEC	C	404	1	-	7/14/54/54	-
6	HEC	C	403	1	-	3/14/54/54	-
12	NS5	M	406	-	-	7/43/43/43	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	404	HEC	CAB-C3B	11.87	1.49	1.34
6	C	403	HEC	CAC-C3C	11.25	1.49	1.34
6	C	403	HEC	CAB-C3B	11.00	1.48	1.34
6	C	402	HEC	CAC-C3C	10.14	1.47	1.34
6	C	404	HEC	CAC-C3C	9.71	1.47	1.34

The worst 5 of 133 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	L	400	BCB	C4B-CHC-C1C	16.26	131.35	121.39
8	L	401	BCB	C1B-CHB-C4A	14.57	130.32	121.39
8	M	403	BCB	C4B-CHC-C1C	13.55	129.69	121.39
8	L	400	BCB	C1B-CHB-C4A	12.35	128.96	121.39
8	M	403	BCB	C1B-CHB-C4A	11.40	128.38	121.39

5 of 11 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
8	L	400	BCB	NC

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Mol	Chain	Res	Type	Atom
8	L	400	BCB	NA
8	L	401	BCB	NC
8	L	401	BCB	NA
8	M	403	BCB	NC

5 of 104 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	C	402	HEC	C2B-C3B-CAB-CBB
6	C	402	HEC	C2C-C3C-CAC-CBC
6	C	403	HEC	C2B-C3B-CAB-CBB
6	C	403	HEC	C4B-C3B-CAB-CBB
6	C	404	HEC	C2C-C3C-CAC-CBC

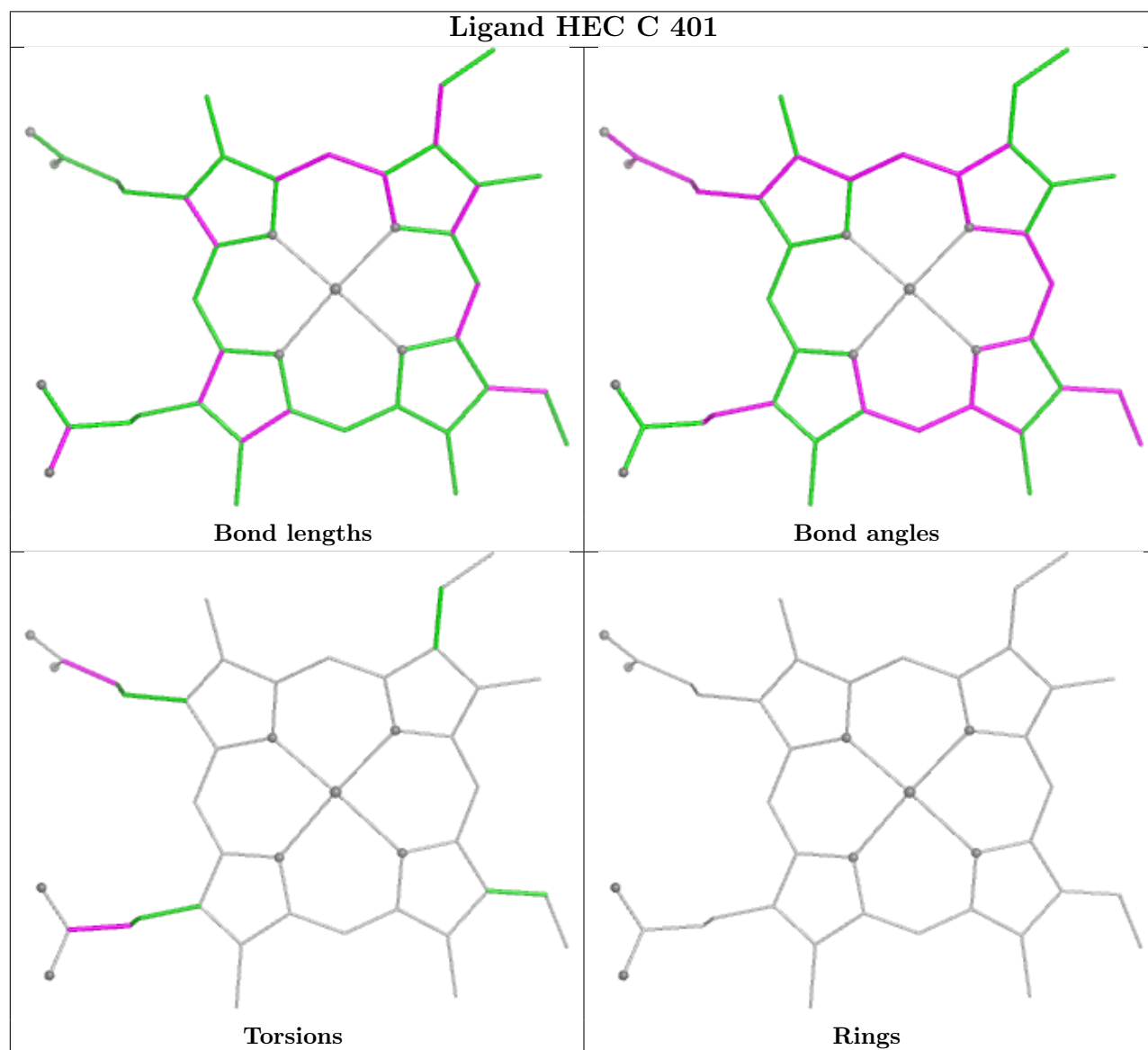
There are no ring outliers.

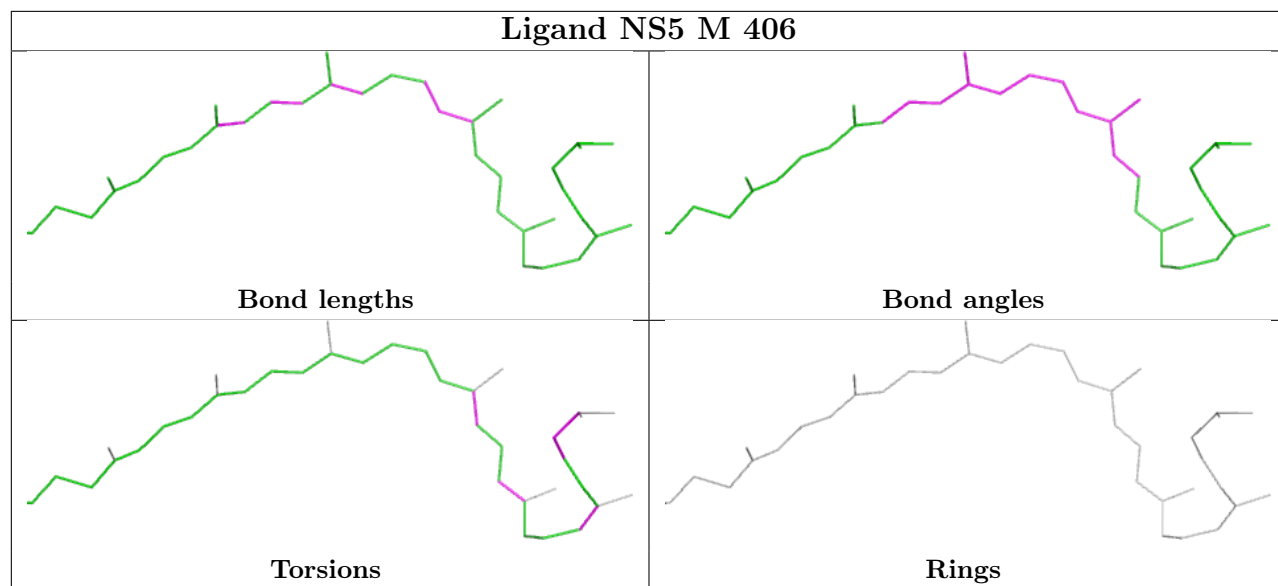
13 monomers are involved in 57 short contacts:

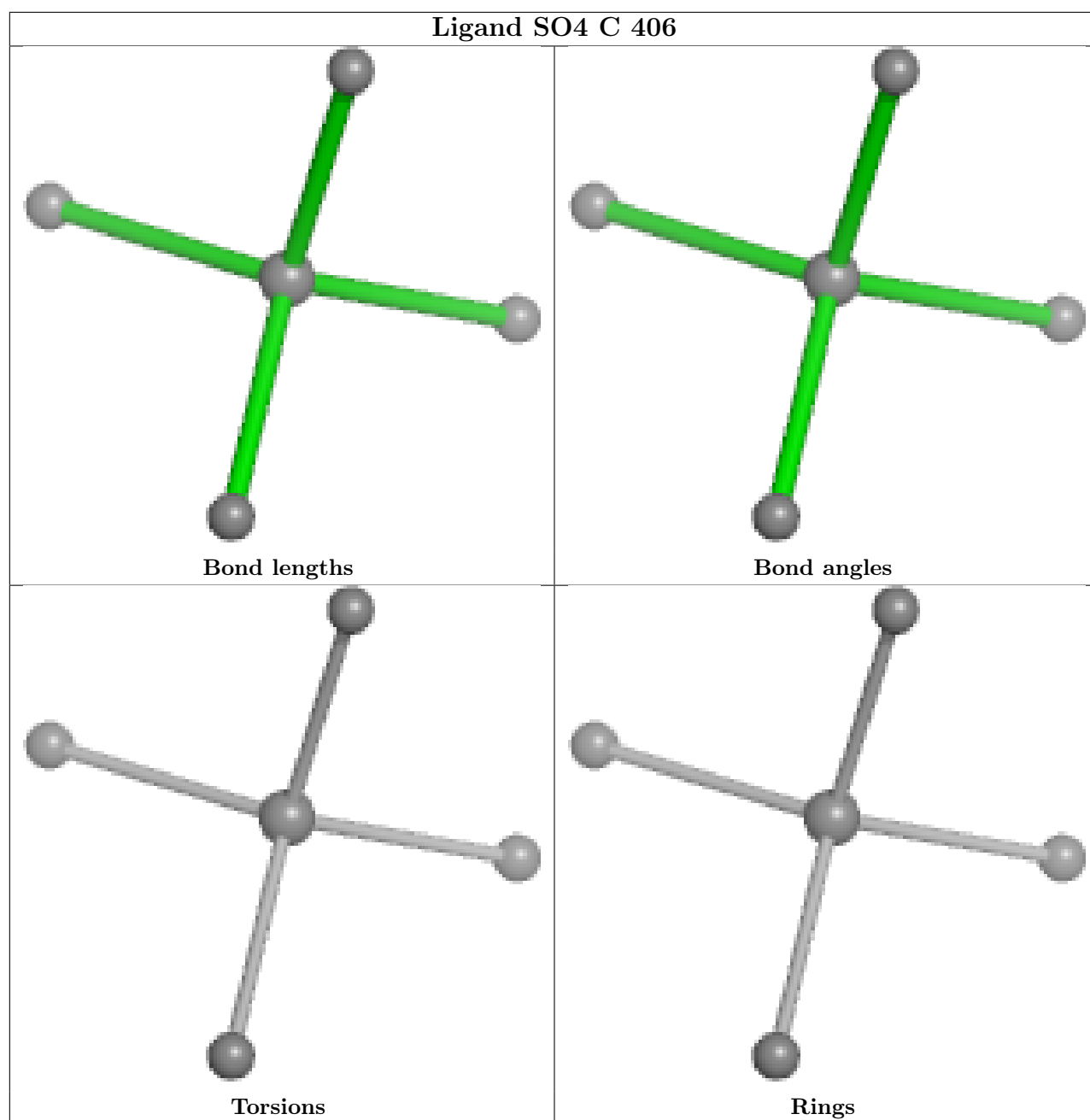
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	401	HEC	12	0
12	M	406	NS5	2	0
11	M	402	MQ7	2	0
9	L	402	BPB	1	0
7	H	303	SO4	3	0
8	L	401	BCB	2	0
6	C	402	HEC	7	0
8	L	400	BCB	1	0
9	M	405	BPB	9	0
8	M	403	BCB	1	0
8	M	404	BCB	4	0
6	C	404	HEC	8	0
6	C	403	HEC	8	0

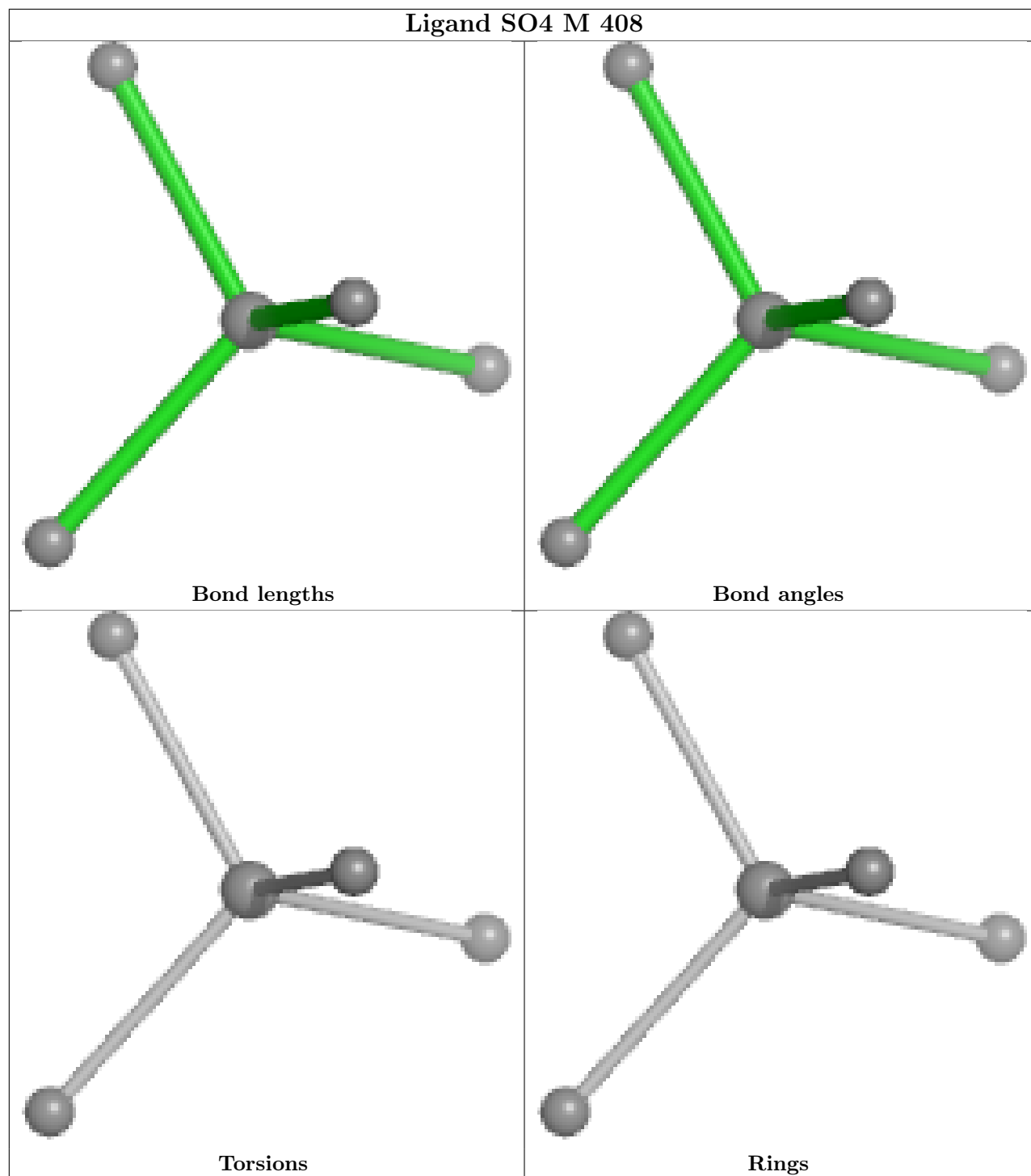
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

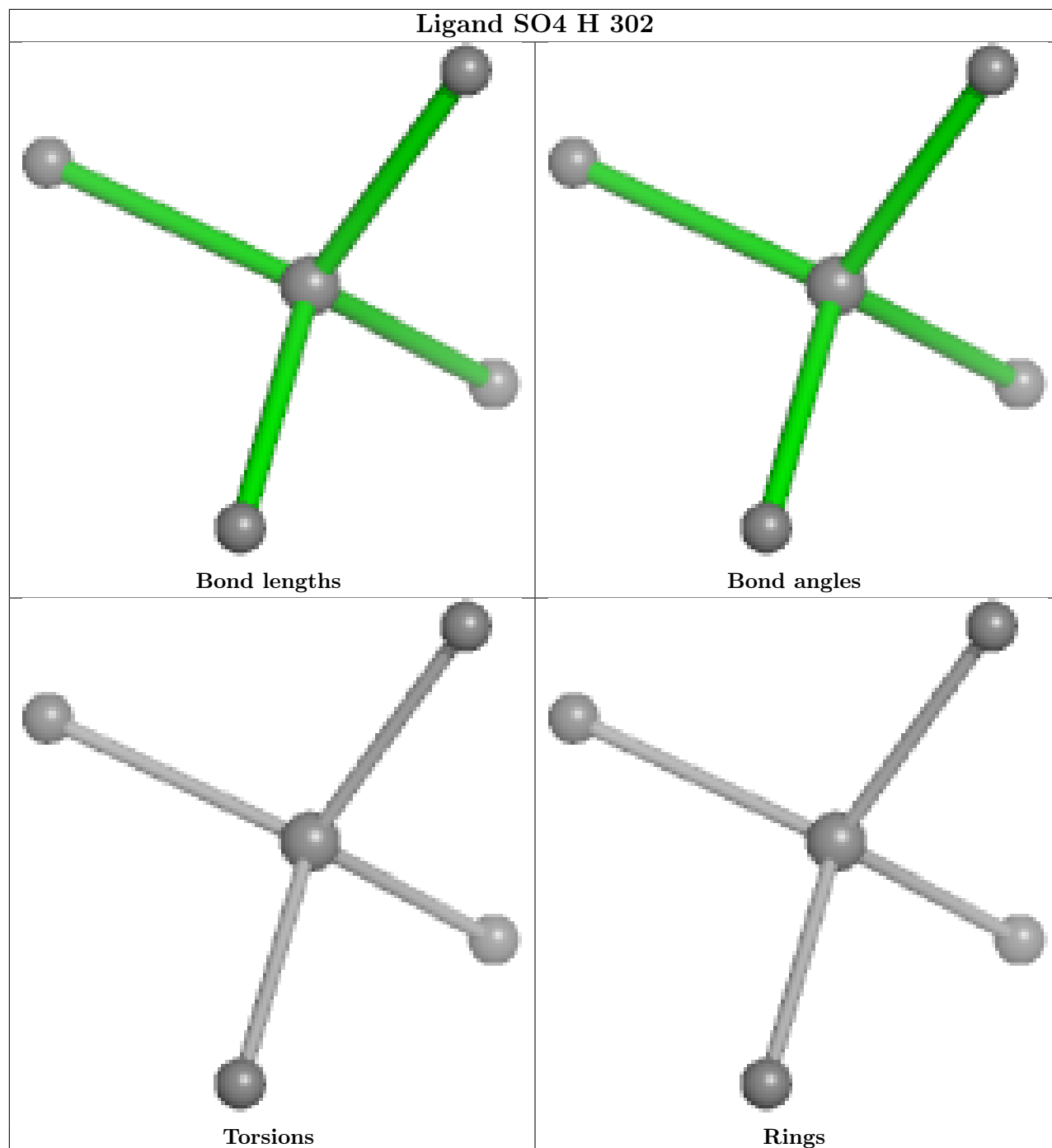
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

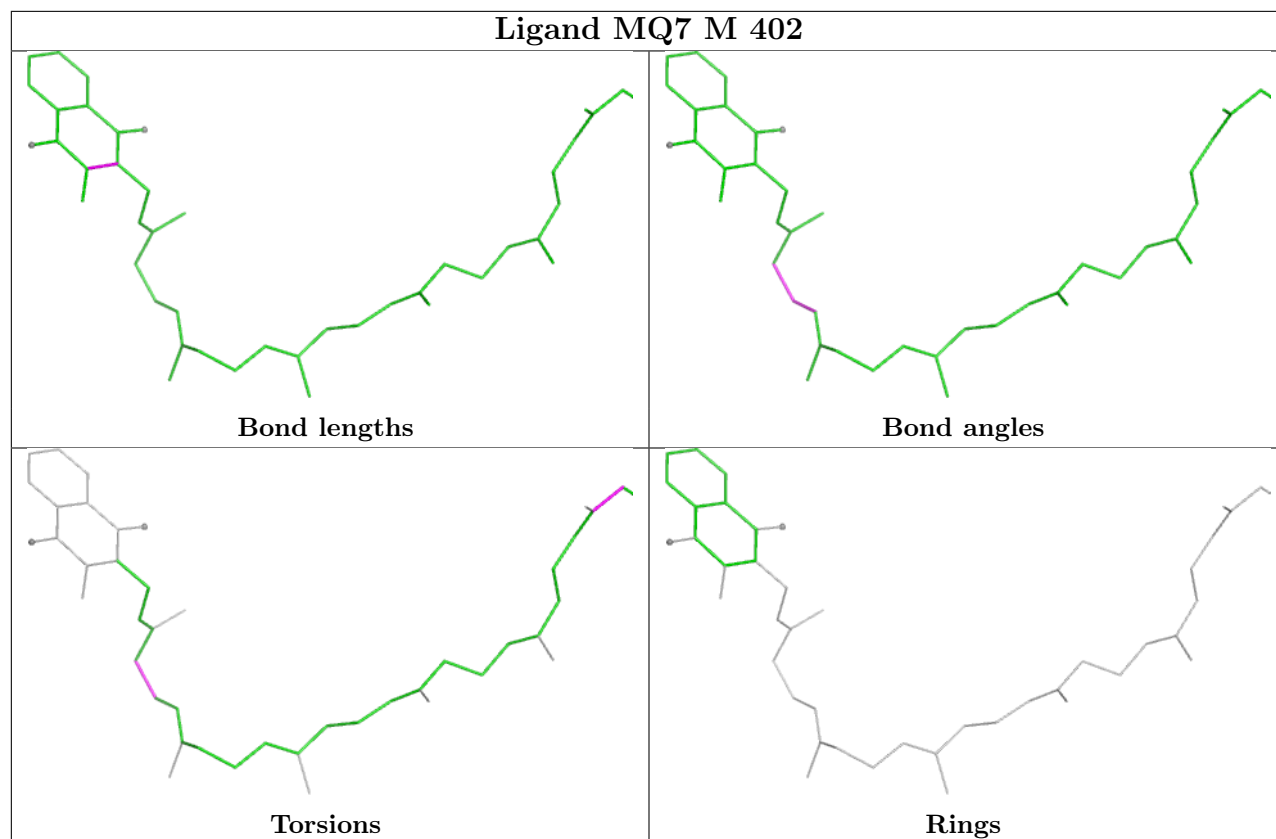


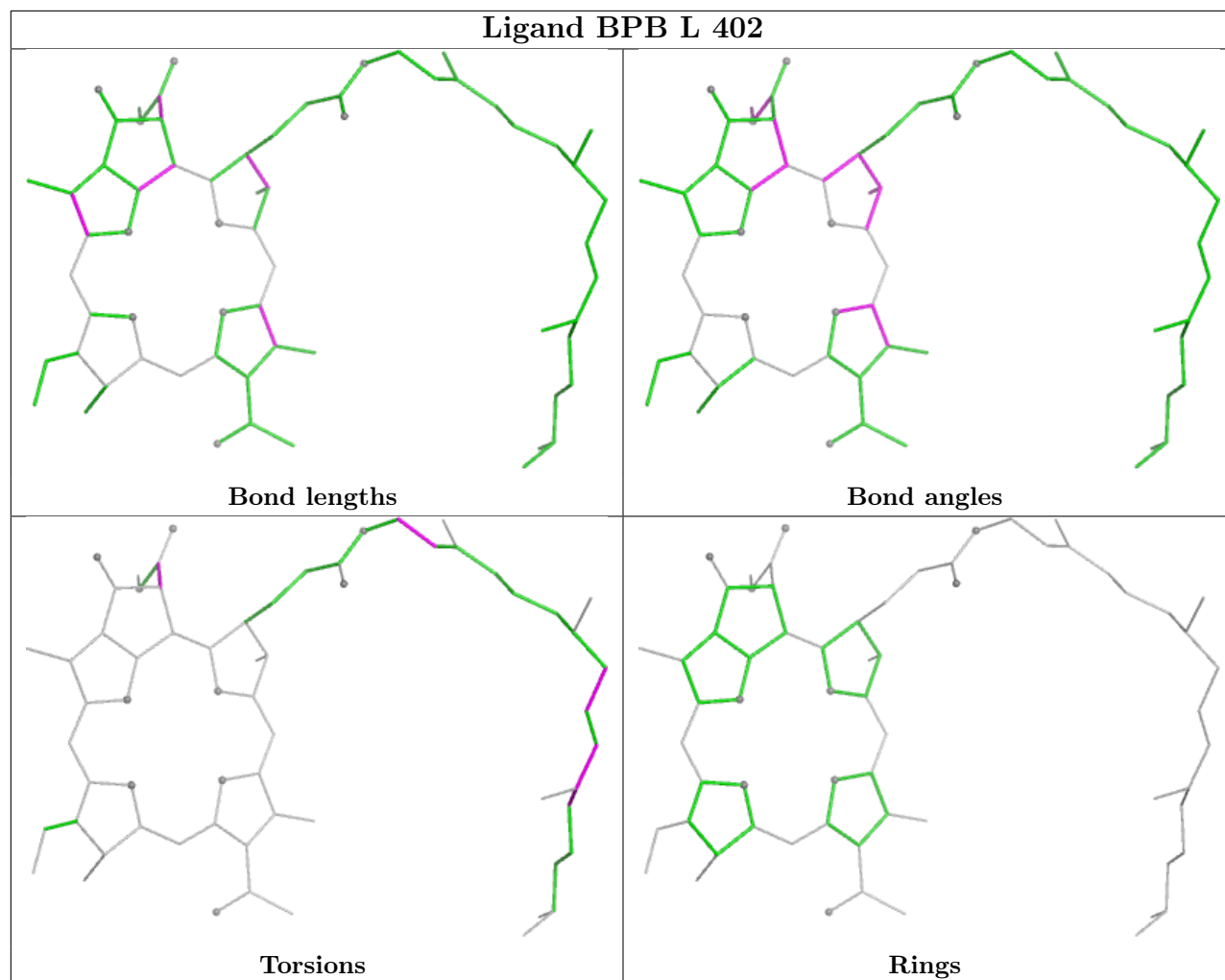


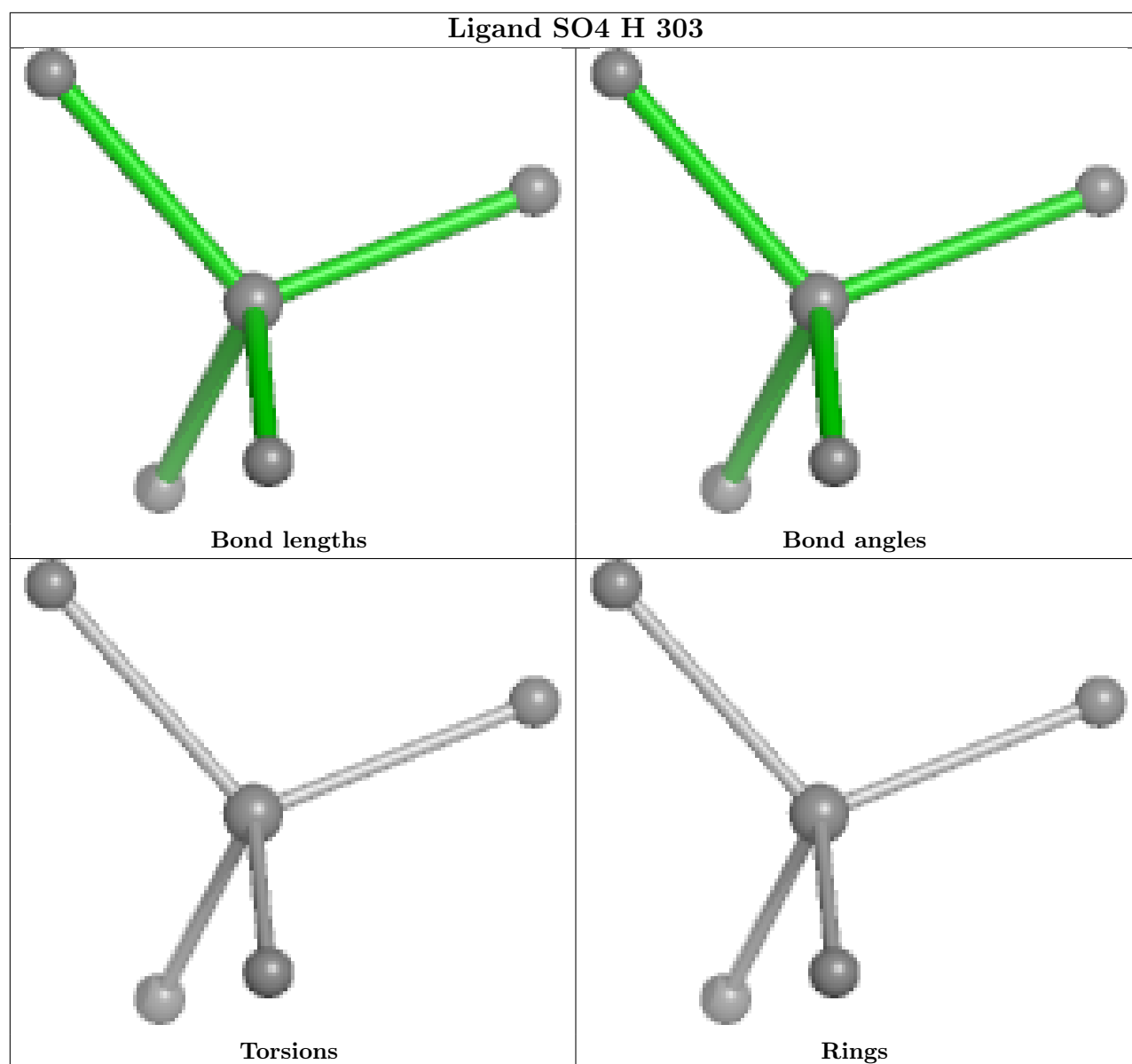


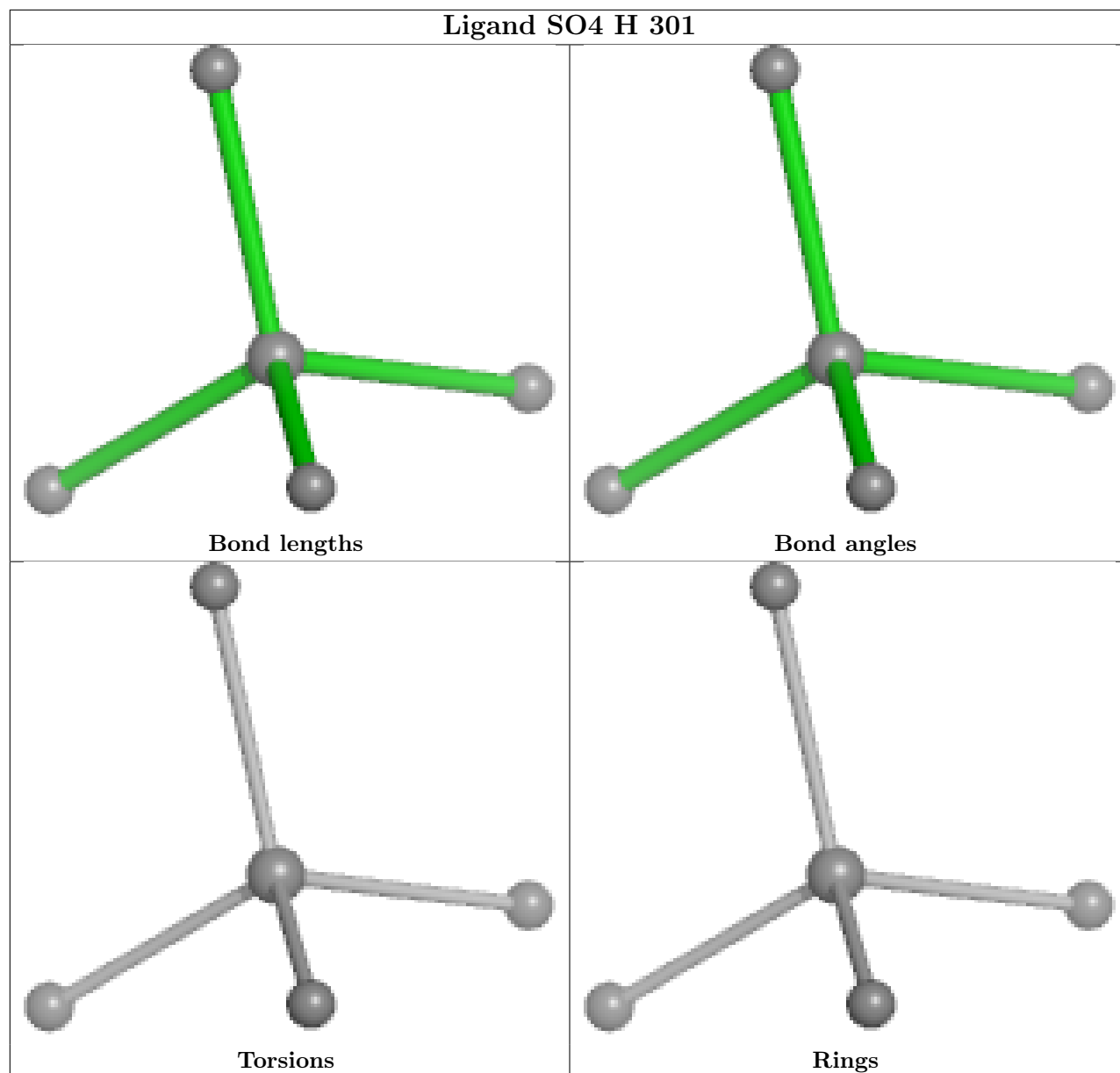


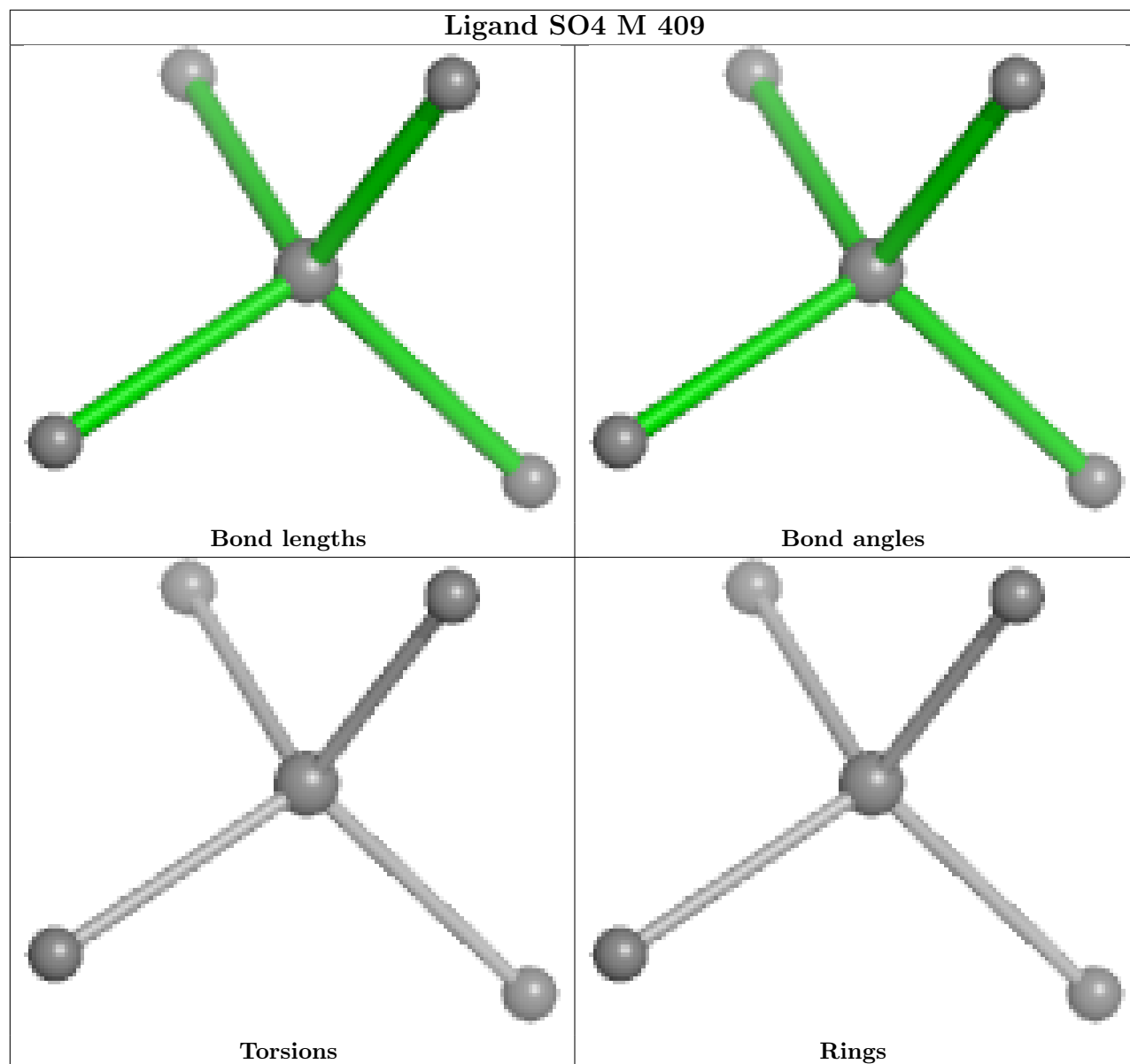


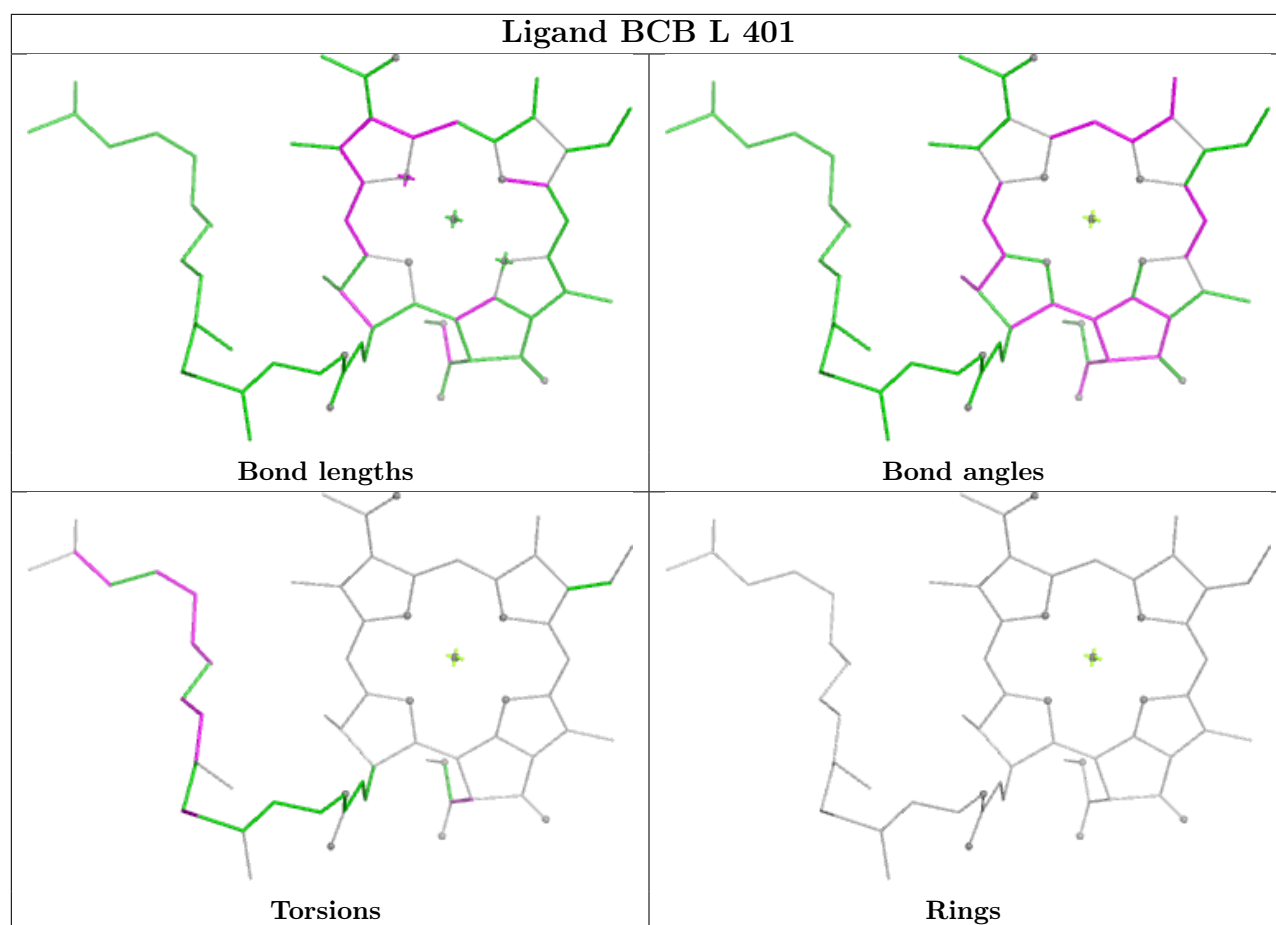


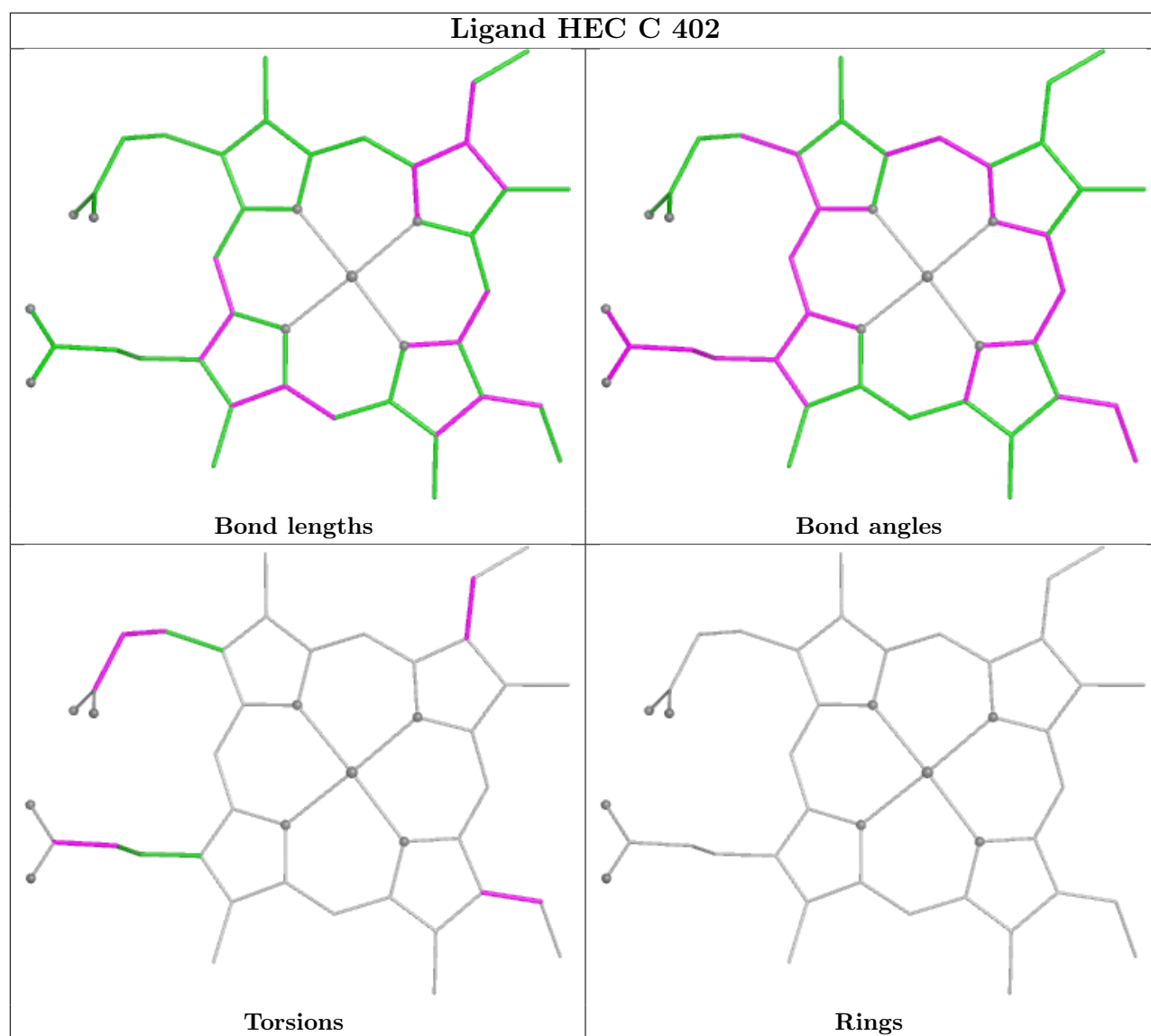


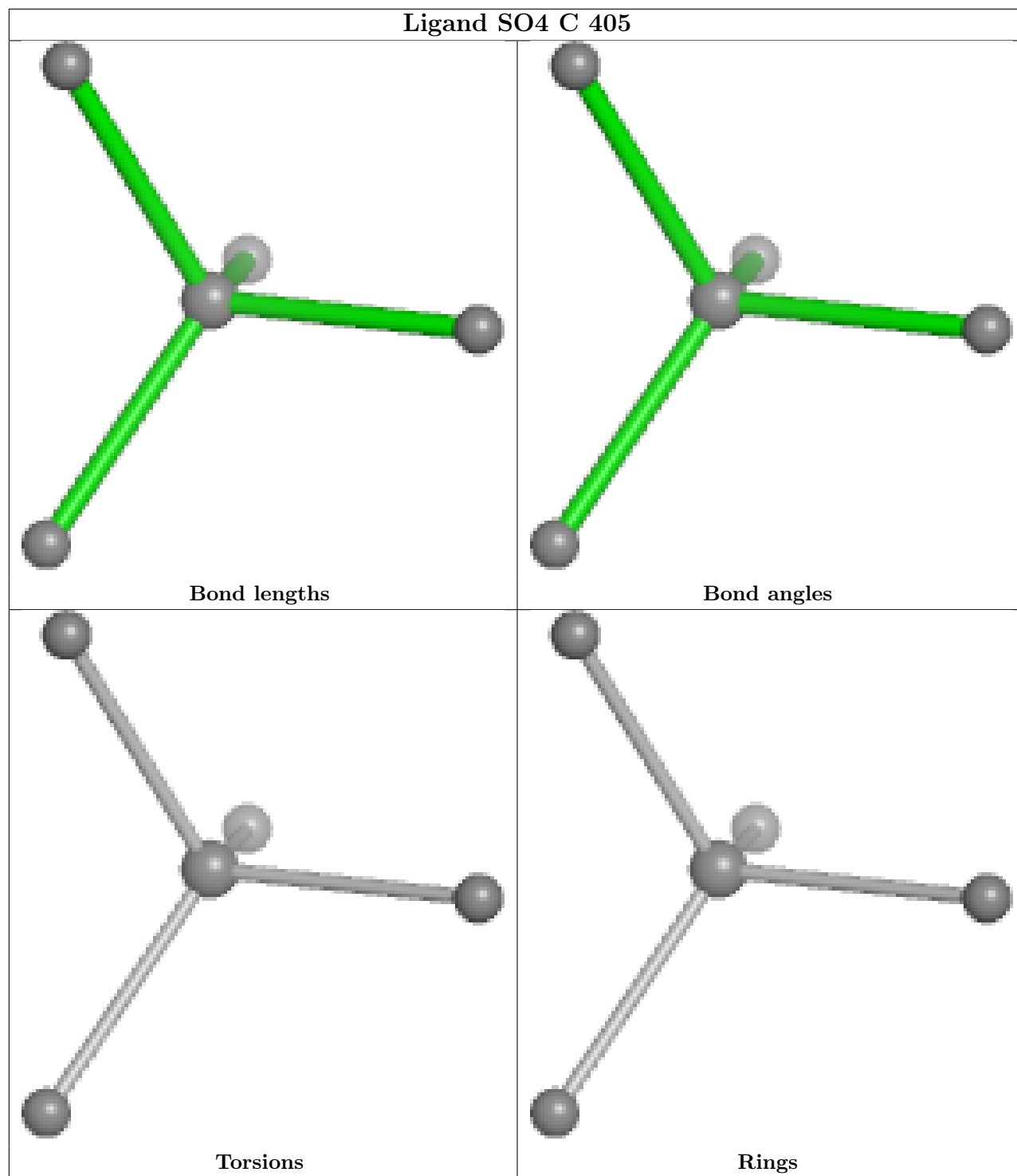


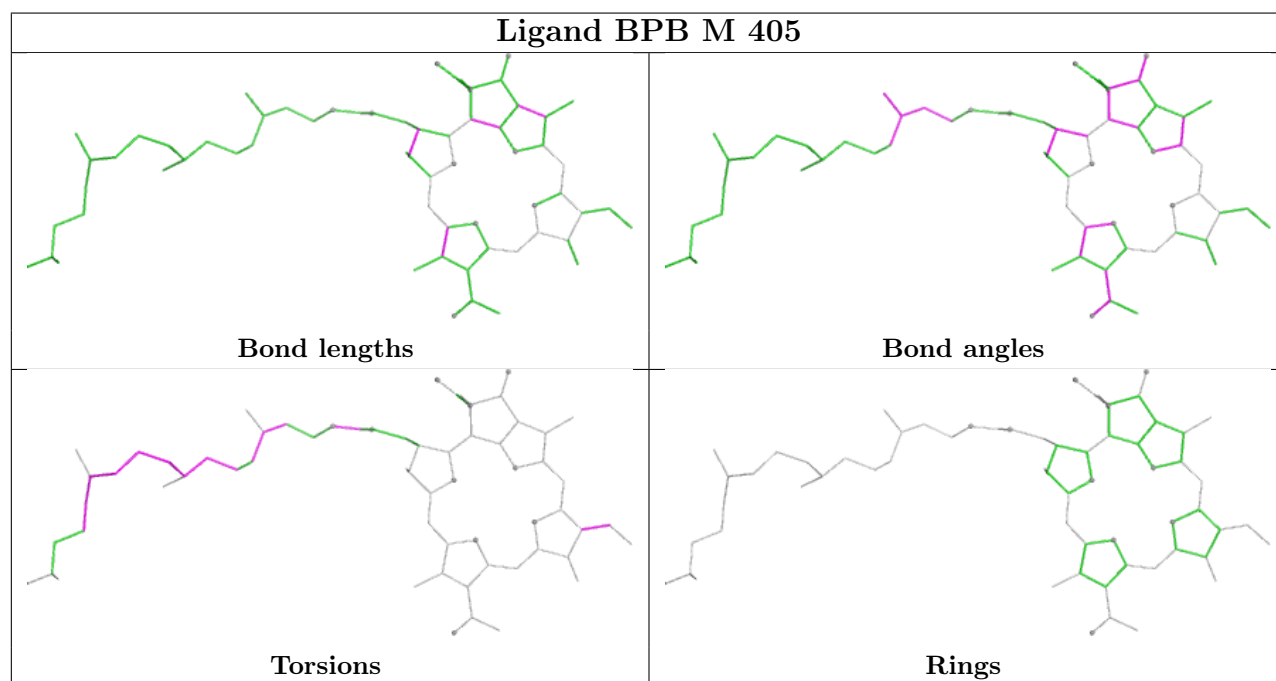
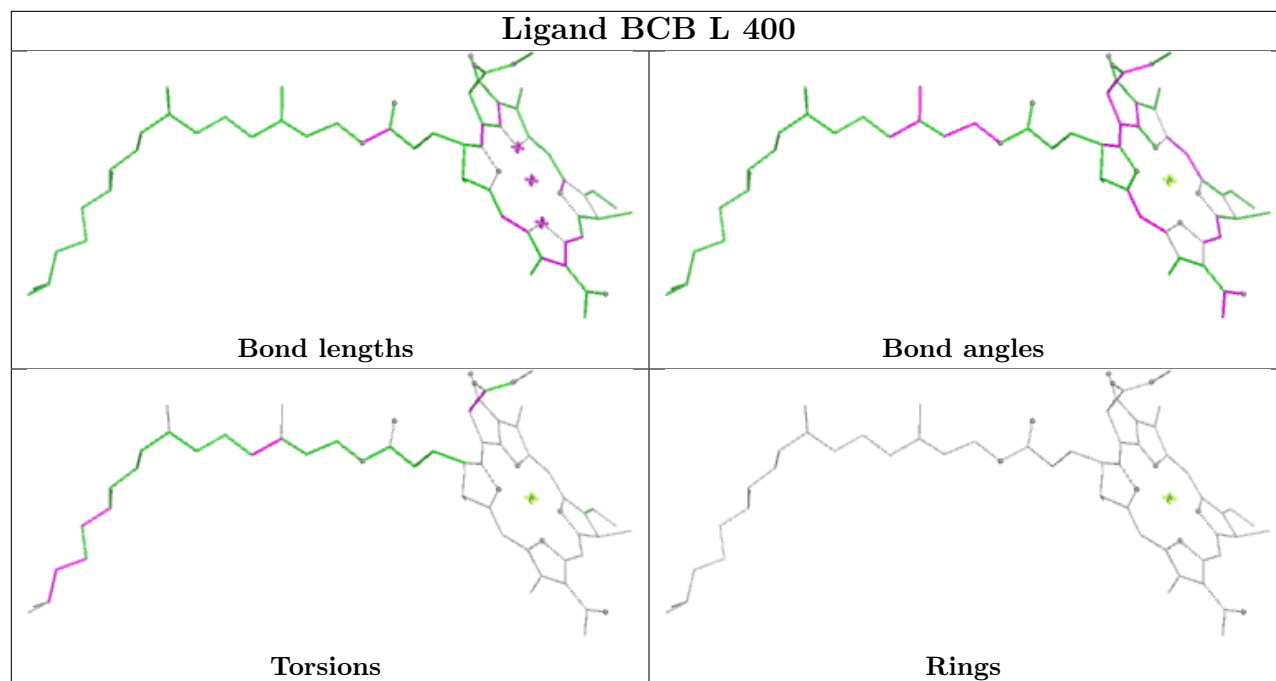




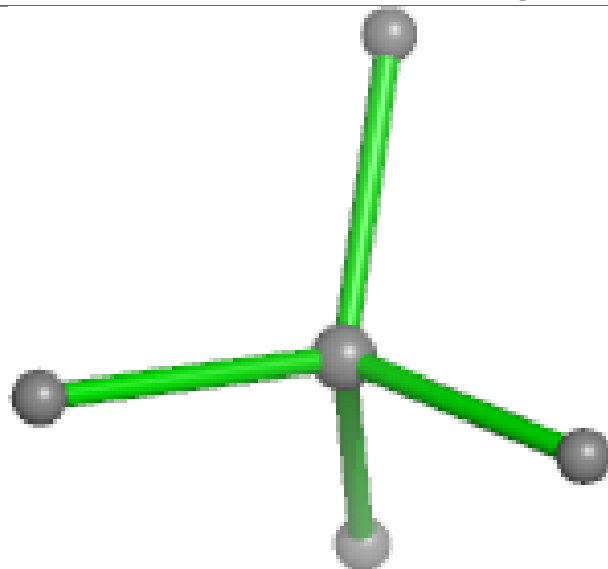




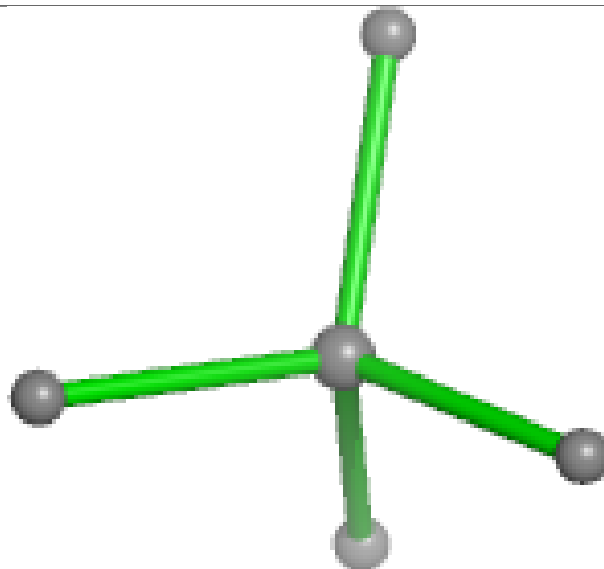




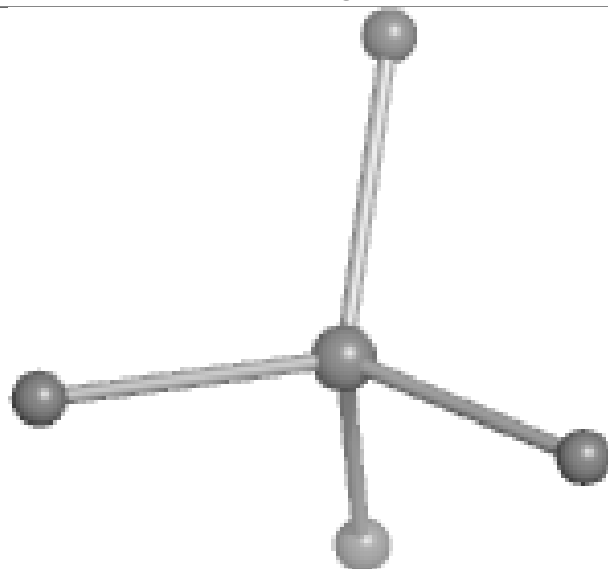
Ligand SO4 M 407



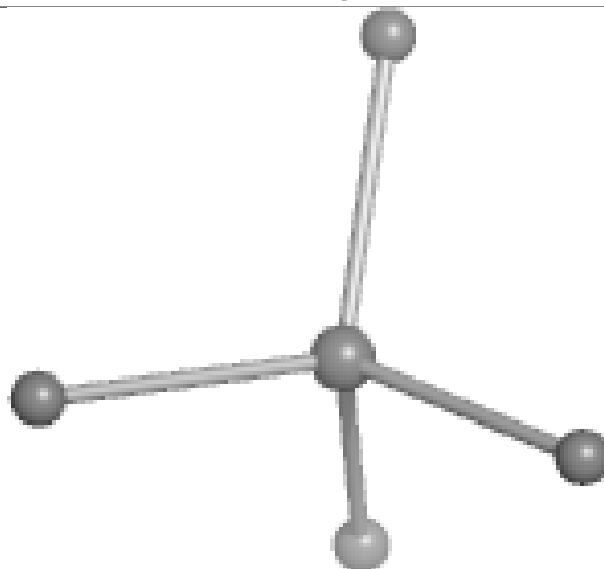
Bond lengths



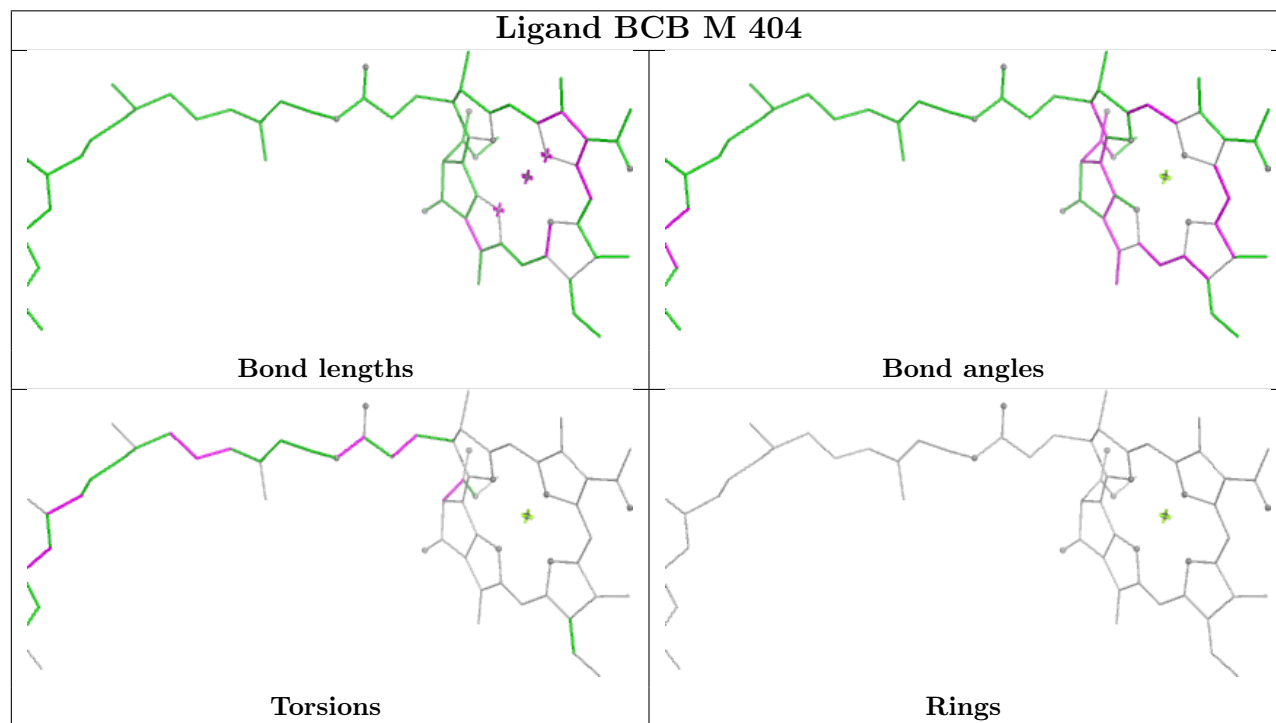
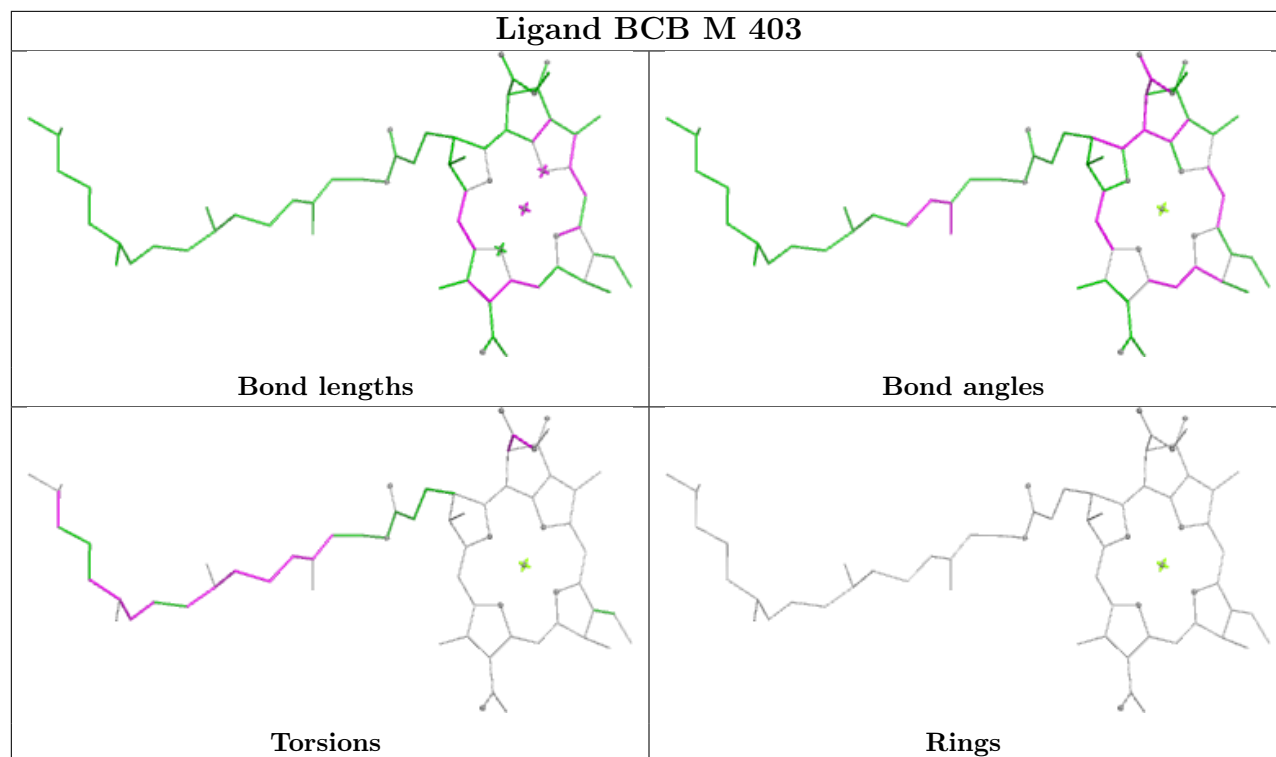
Bond angles

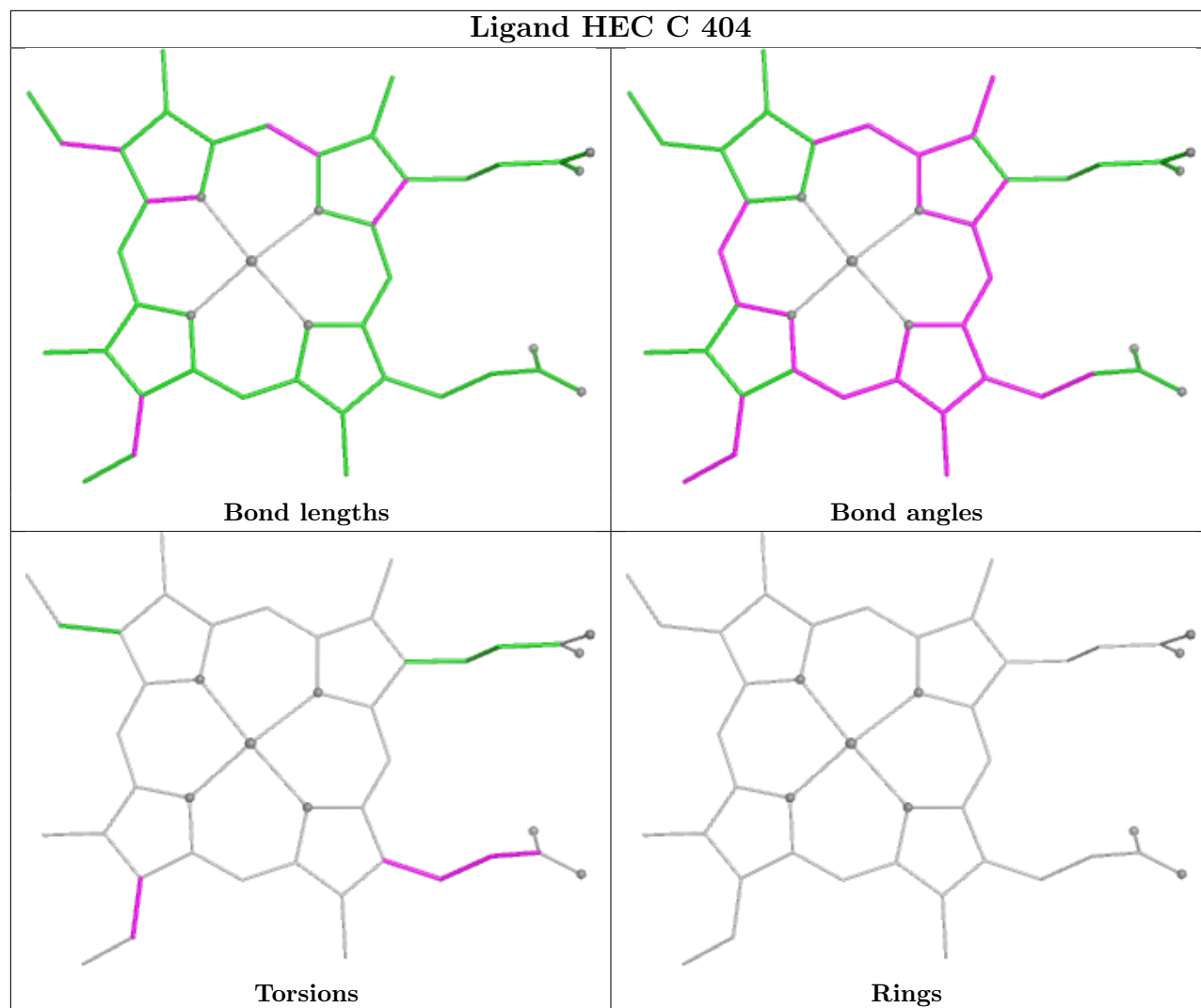


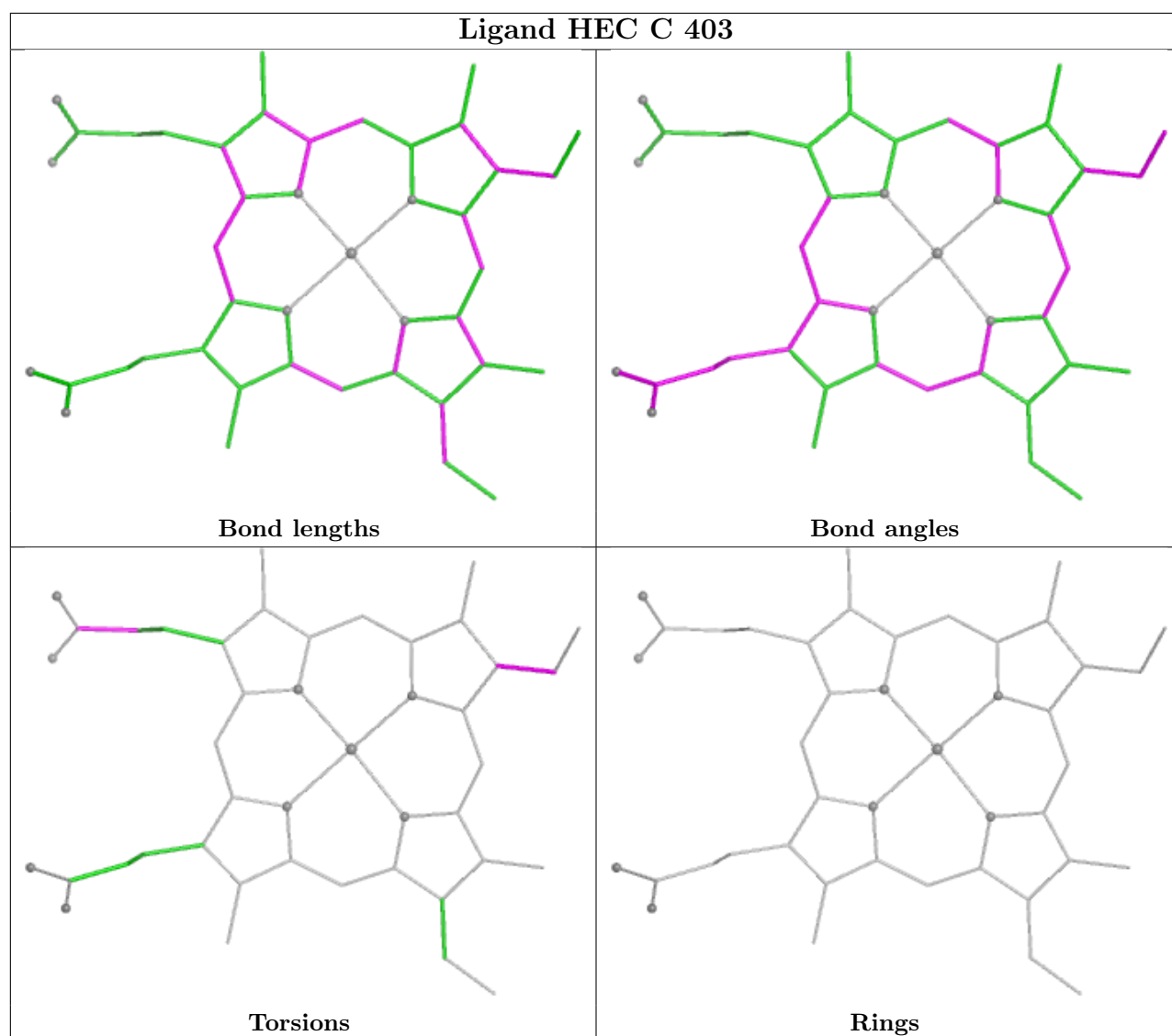
Torsions



Rings







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	H	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	H	46:PRO	C	55:GLU	N	13.88

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	C	332/332 (100%)	-0.41	2 (0%) 85 73	33, 96, 132, 174	2 (0%)
2	H	242/242 (100%)	-0.04	7 (2%) 53 35	55, 108, 157, 254	1 (0%)
3	L	273/273 (100%)	-0.36	2 (0%) 84 70	61, 90, 127, 140	0
4	M	323/323 (100%)	-0.36	3 (0%) 81 65	44, 92, 125, 167	1 (0%)
5	D	7/8 (87%)	0.08	0 100 100	104, 111, 171, 182	0
All	All	1177/1178 (99%)	-0.31	14 (1%) 76 58	33, 95, 136, 254	4 (0%)

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	86[A]	ARG	6.7
1	C	94[A]	ASN	5.7
4	M	78[A]	HIS	5.5
4	M	89	PHE	4.3
2	H	9	HIS	3.9

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	FME	D	1	10/11	0.94	0.18	105,117,126,127	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

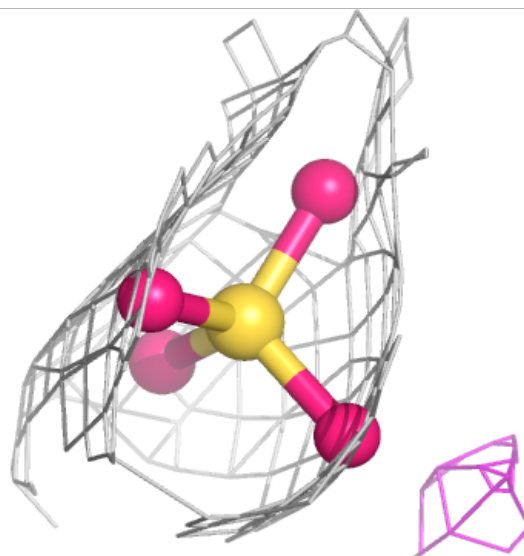
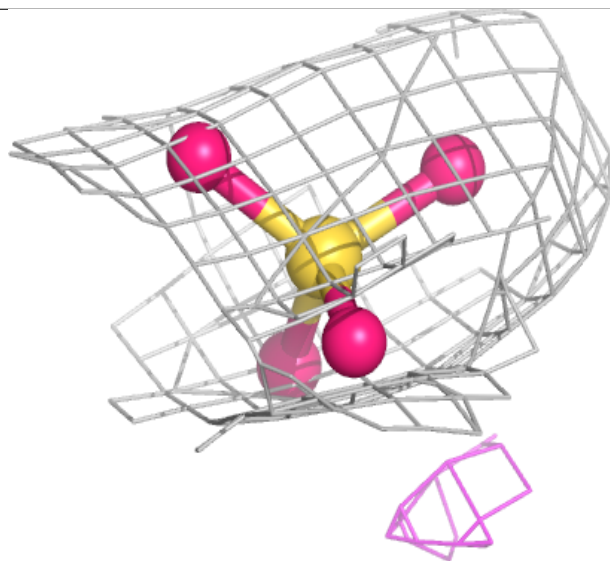
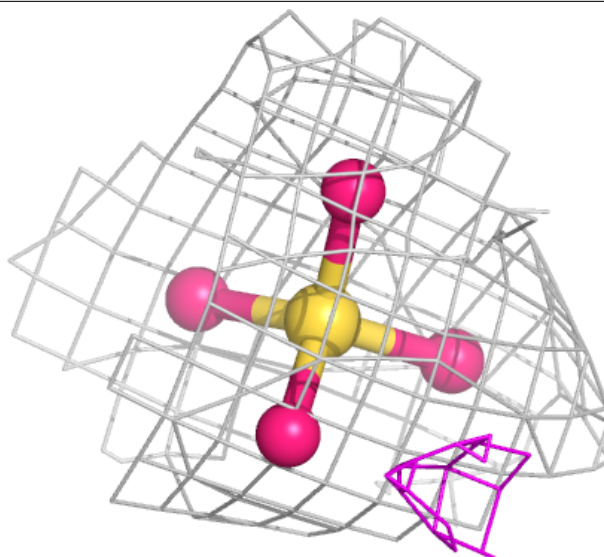
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	SO4	C	406	5/5	0.63	0.13	121,172,217,276	0
7	SO4	M	409	5/5	0.65	0.12	112,189,214,237	0
7	SO4	C	405	5/5	0.71	0.11	130,159,198,258	0
7	SO4	H	302	5/5	0.82	0.16	112,125,150,180	0
7	SO4	H	301	5/5	0.88	0.17	106,113,143,145	0
7	SO4	H	303	5/5	0.93	0.10	76,190,221,256	0
12	NS5	M	406	40/40	0.95	0.22	68,115,174,176	0
9	BPB	M	405	65/65	0.96	0.13	69,103,170,184	0
11	MQ7	M	402	48/48	0.96	0.14	63,83,124,140	0
8	BCB	M	403	66/66	0.96	0.13	56,104,168,173	0
9	BPB	L	402	65/65	0.97	0.10	59,87,97,102	0
7	SO4	M	407	5/5	0.97	0.06	106,112,138,182	0
8	BCB	L	401	66/66	0.97	0.10	61,83,105,118	0
7	SO4	M	408	5/5	0.97	0.07	83,102,121,133	0
8	BCB	L	400	66/66	0.98	0.08	58,79,101,111	0
8	BCB	M	404	66/66	0.98	0.09	44,79,126,143	0
6	HEC	C	401	43/43	0.98	0.08	69,97,132,148	0
6	HEC	C	403	43/43	0.99	0.07	58,71,88,95	0
6	HEC	C	404	43/43	0.99	0.06	52,74,104,116	0
6	HEC	C	402	43/43	0.99	0.06	44,88,109,117	0
10	FE2	M	401	1/1	1.00	0.02	72,72,72,72	0

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

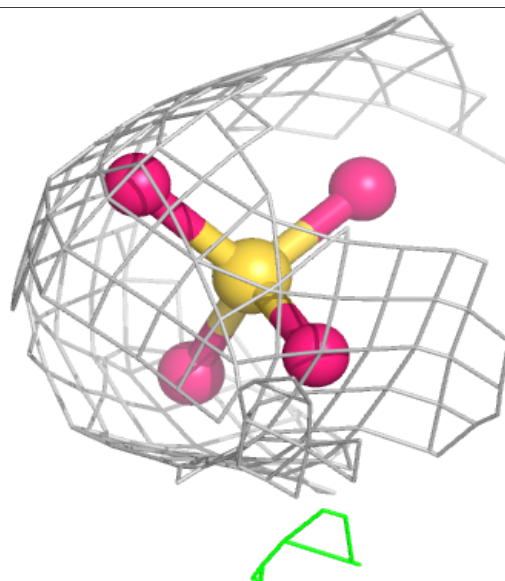
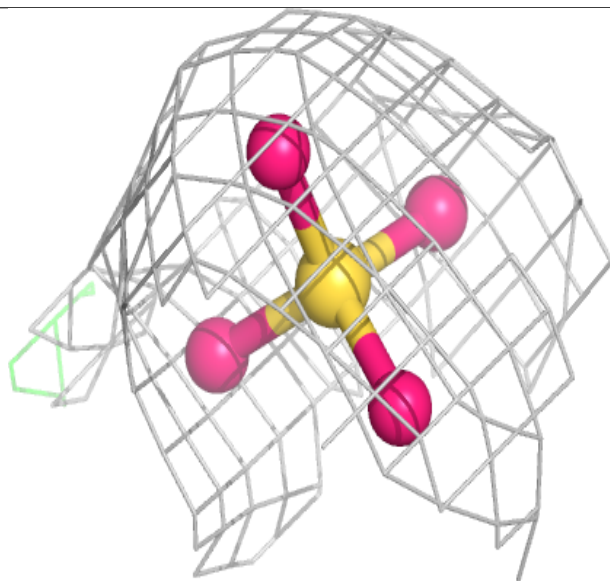
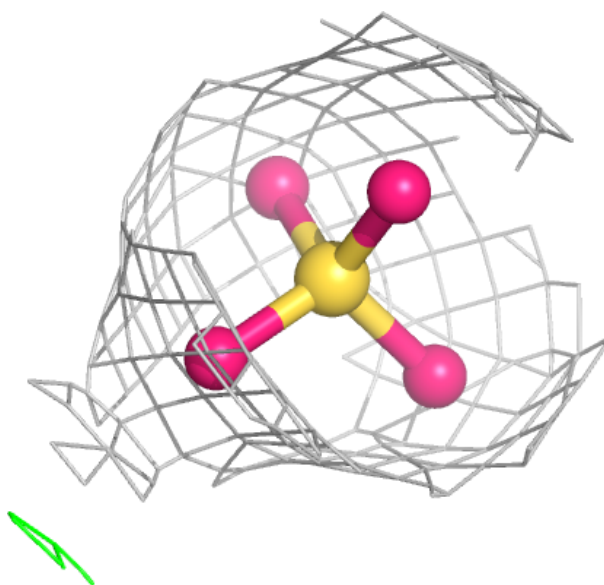
Electron density around SO4 C 406:

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



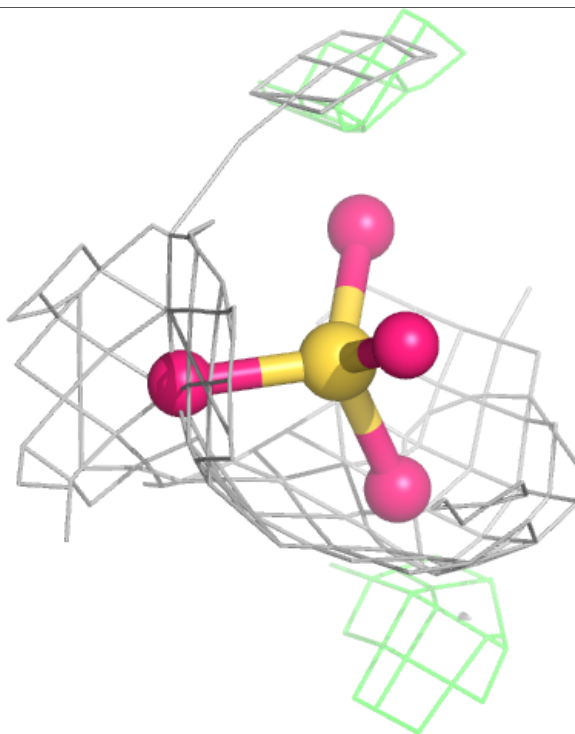
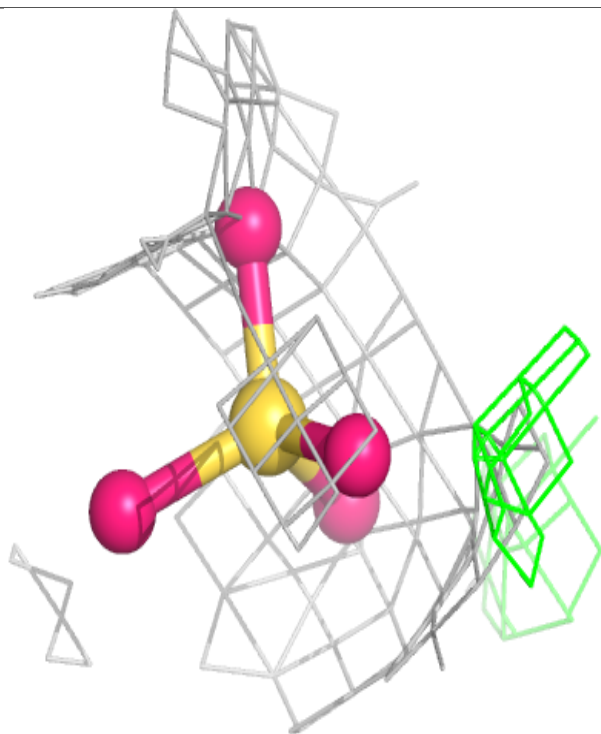
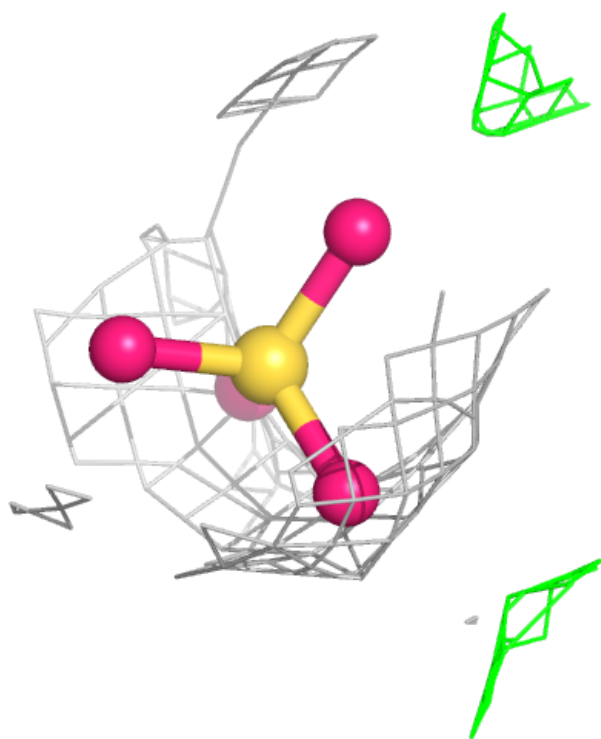
Electron density around SO4 M 409:

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



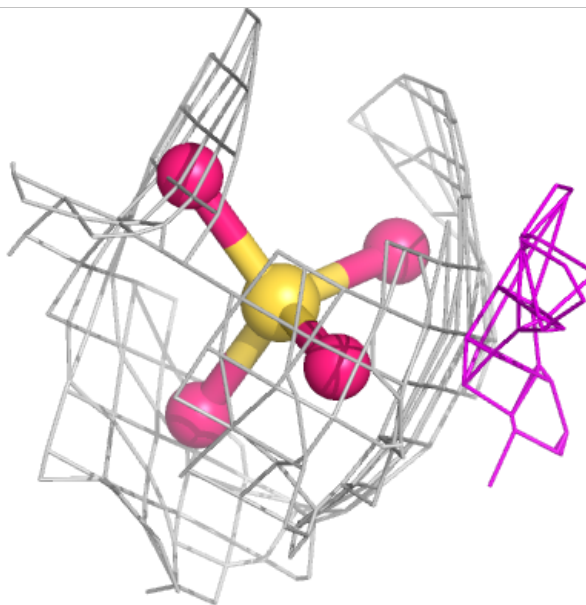
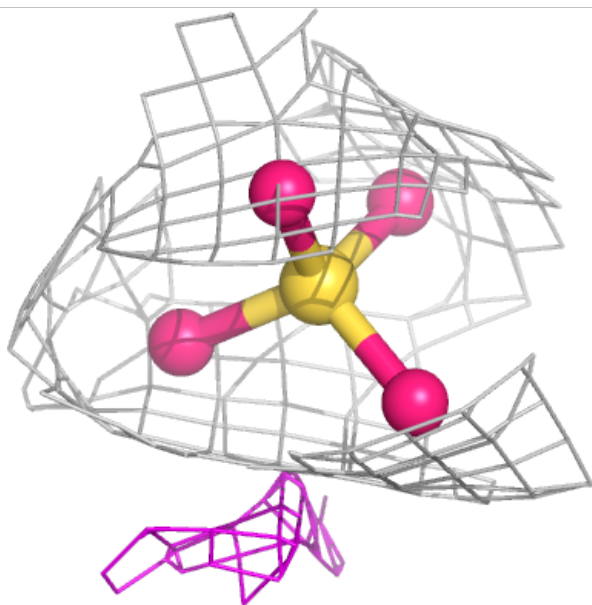
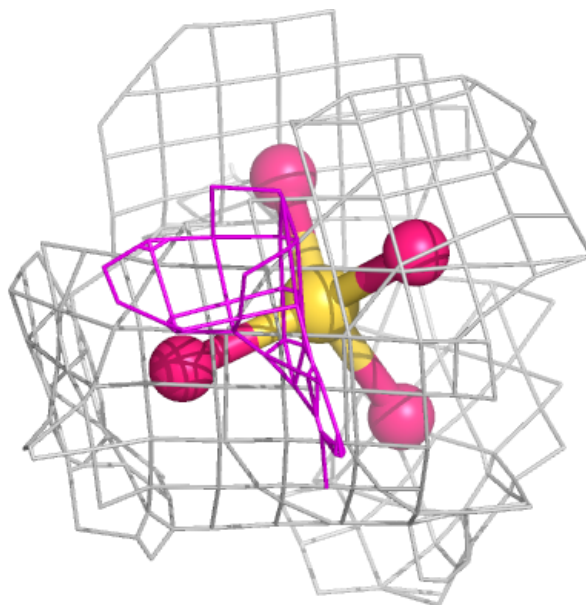
Electron density around SO4 C 405:

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and green (positive)



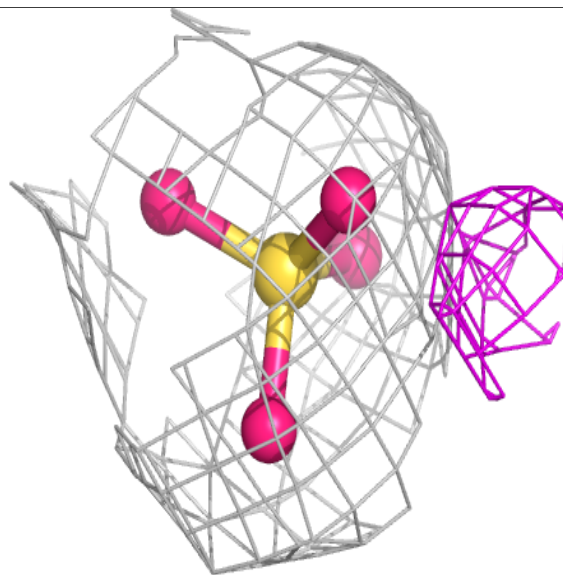
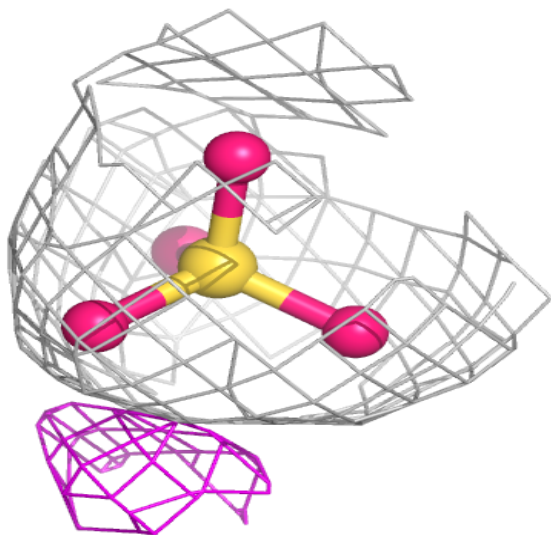
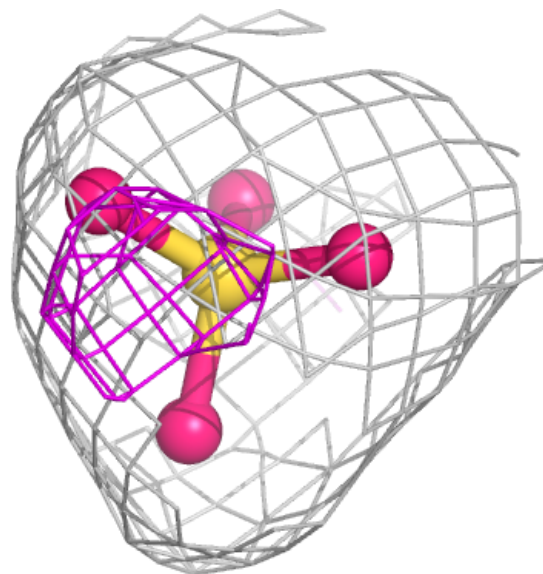
Electron density around SO4 H 302:

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



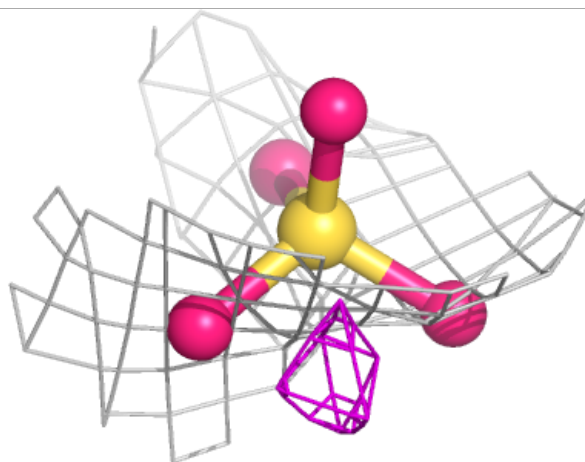
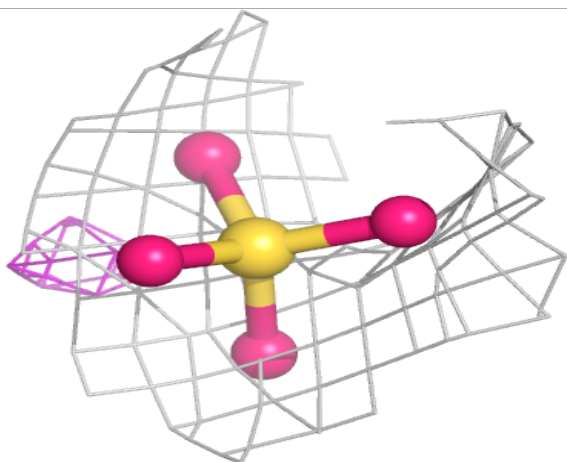
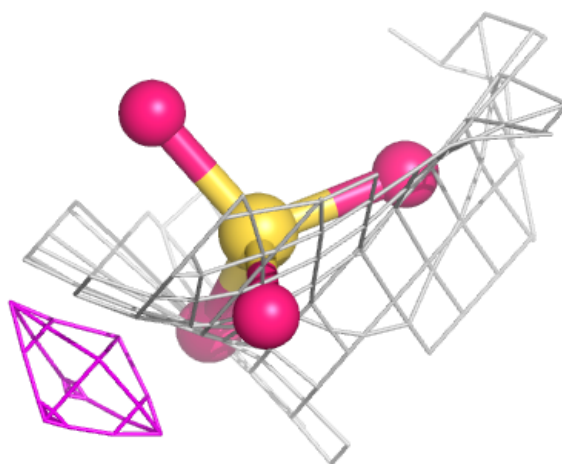
Electron density around SO4 H 301:

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



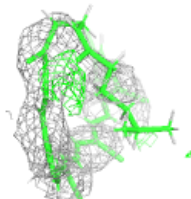
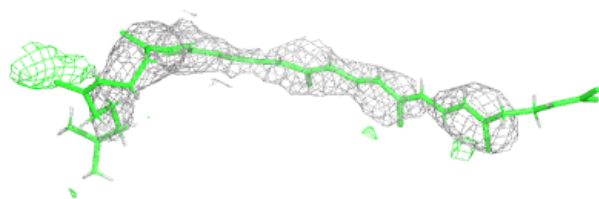
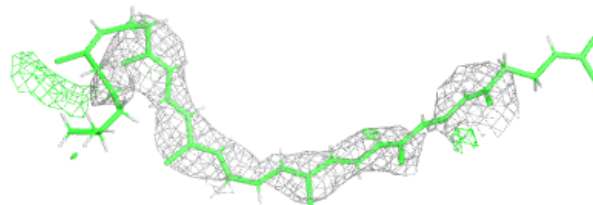
Electron density around SO4 H 303:

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

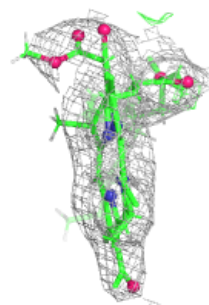
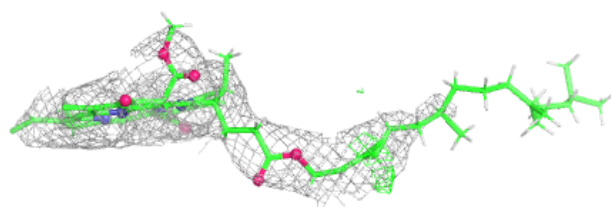
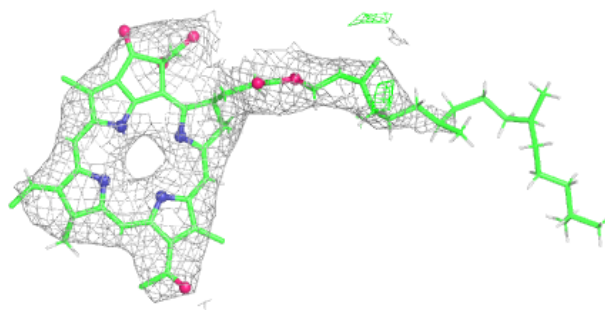


Electron density around NS5 M 406:

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

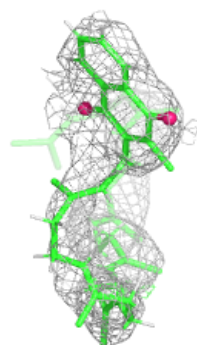
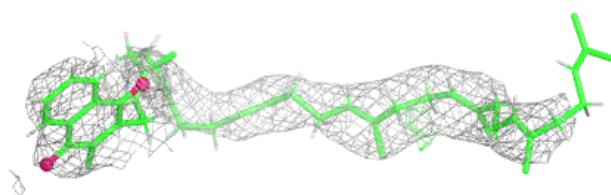
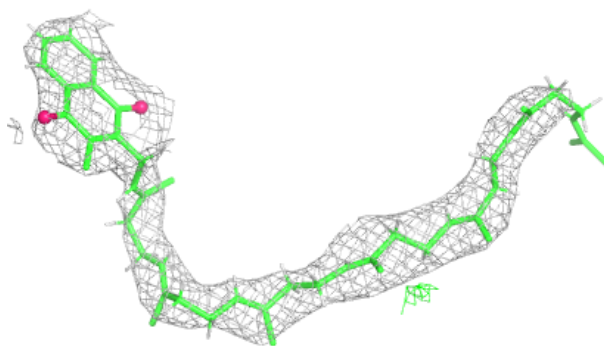
**Electron density around BPB M 405:**

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

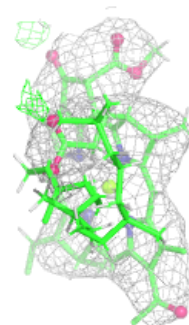
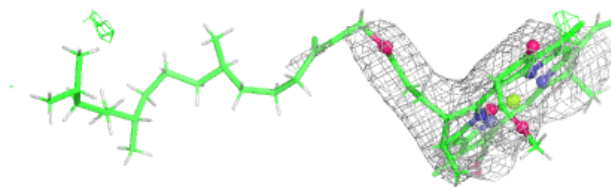
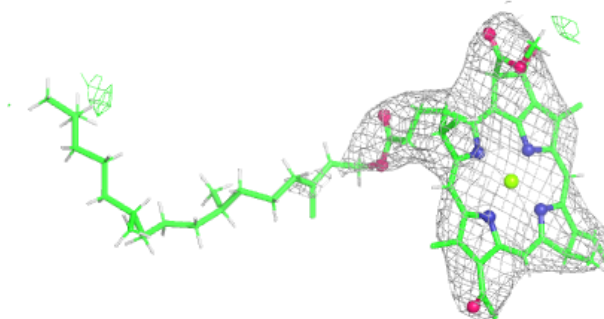


Electron density around MQ7 M 402:

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

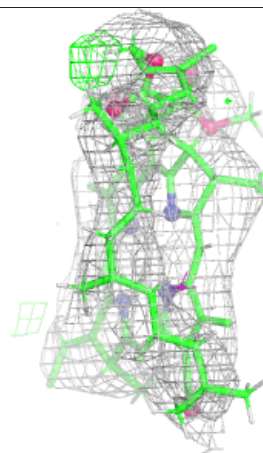
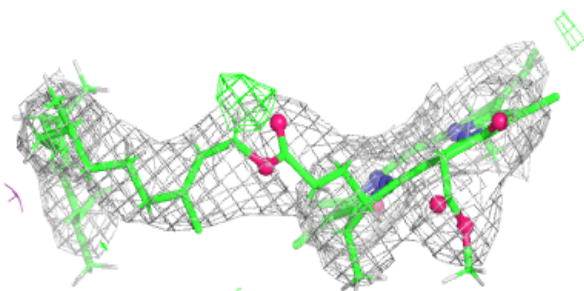
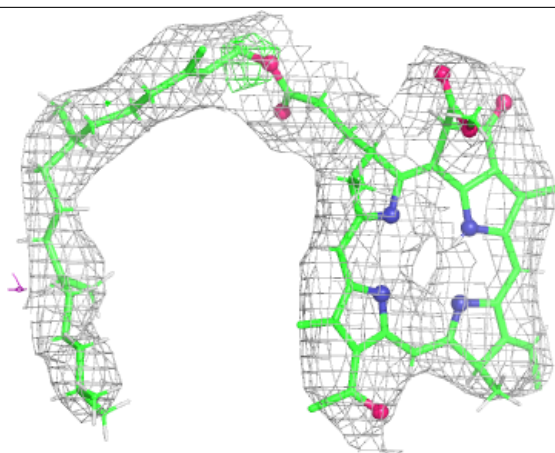
**Electron density around BCB M 403:**

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



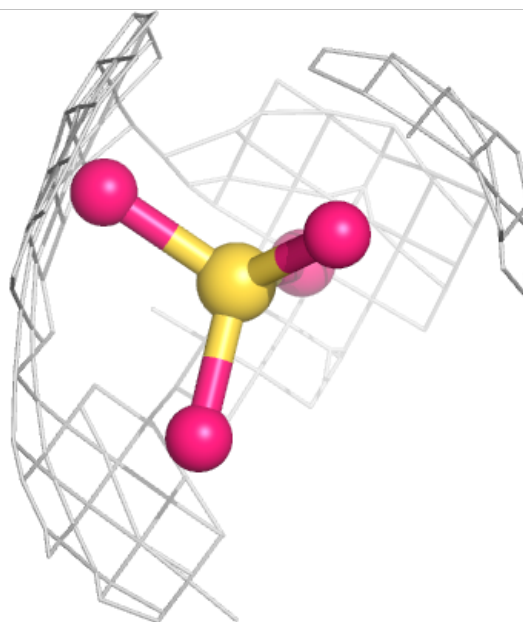
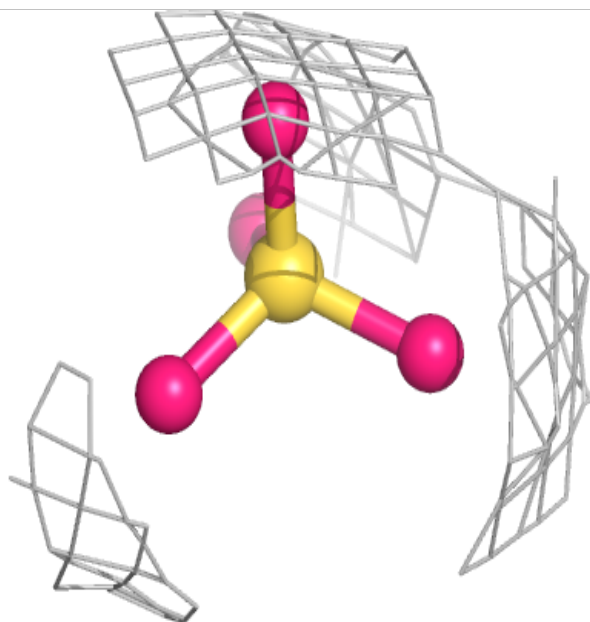
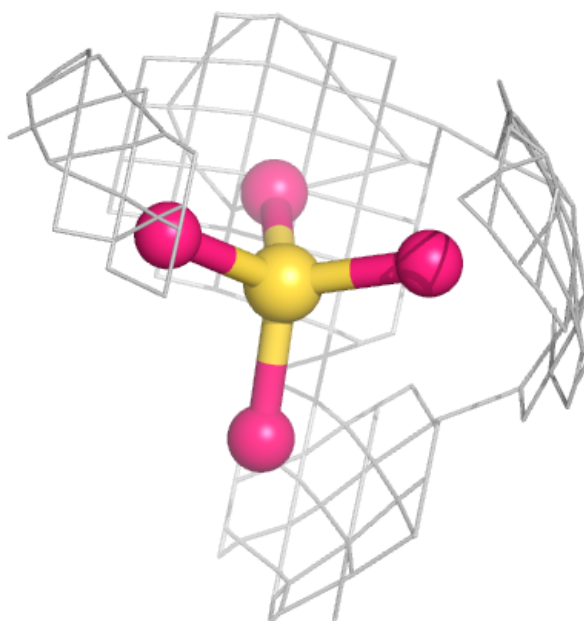
Electron density around BPB L 402:

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



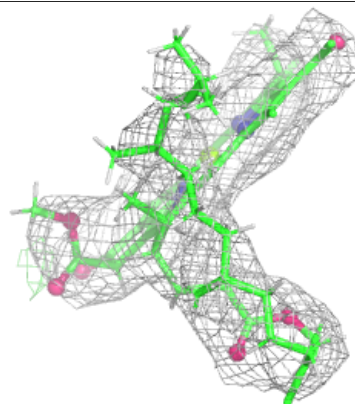
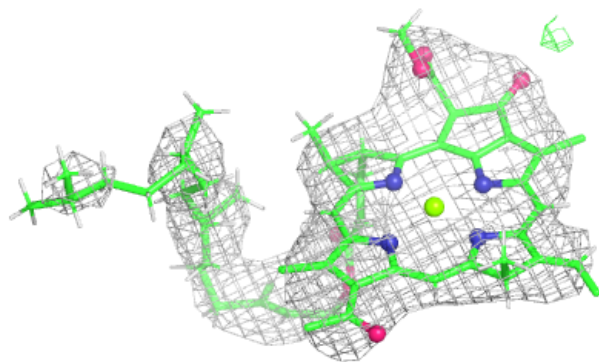
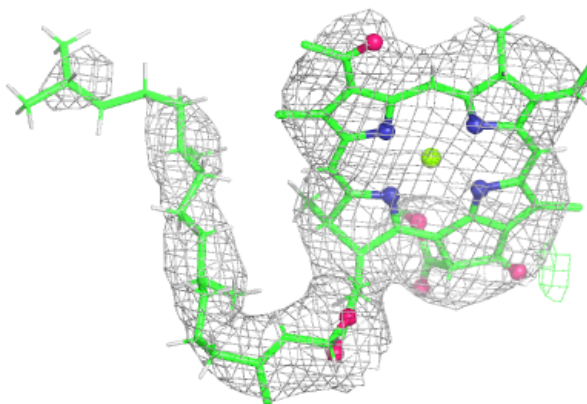
Electron density around SO4 M 407:

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



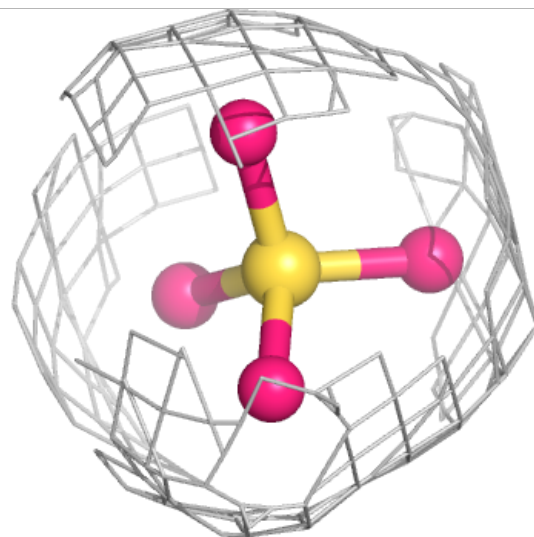
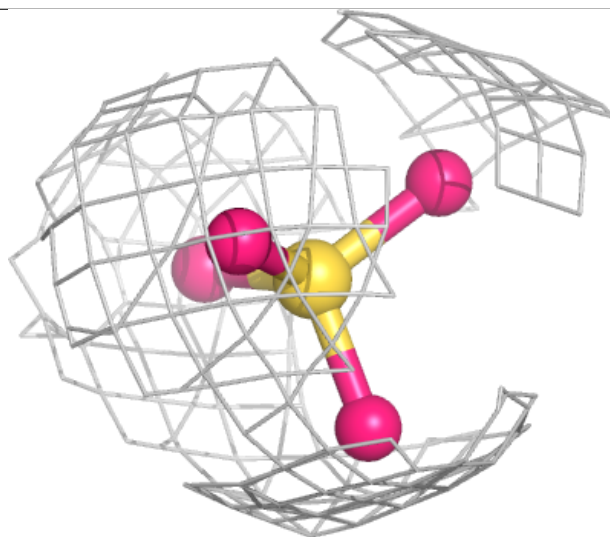
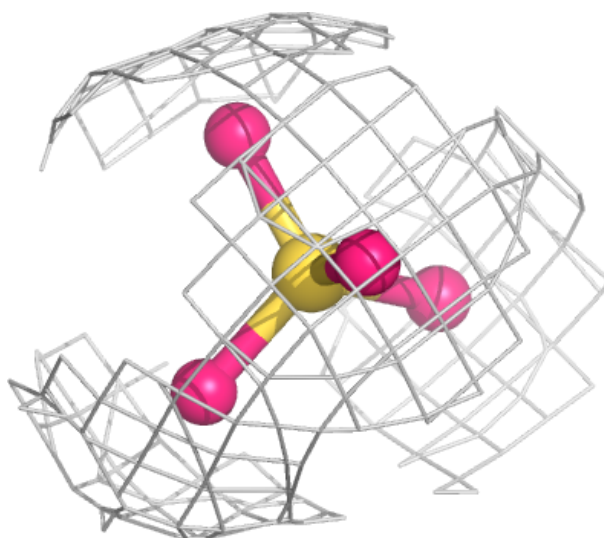
Electron density around BCB L 401:

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



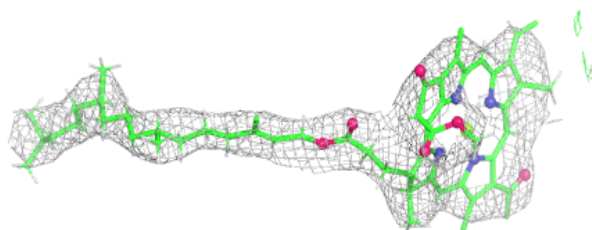
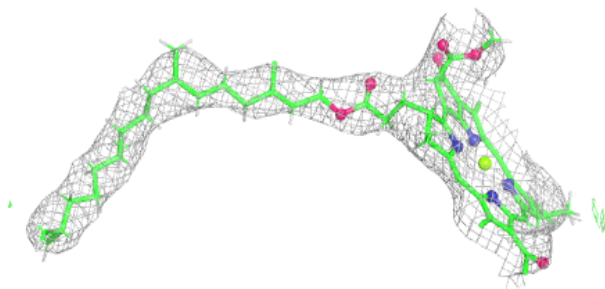
Electron density around SO4 M 408:

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

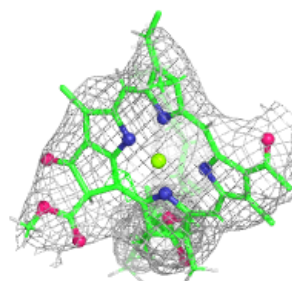
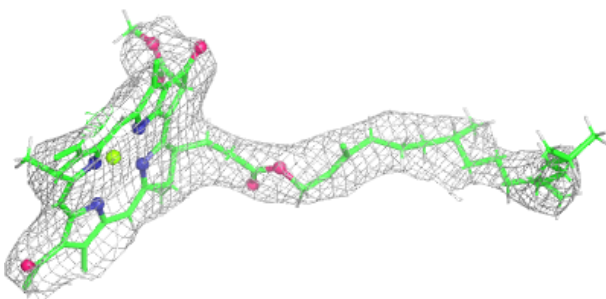
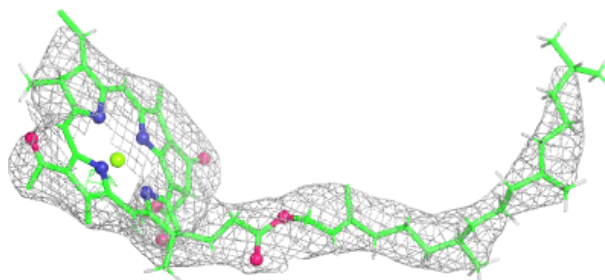


Electron density around BCB L 400:

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

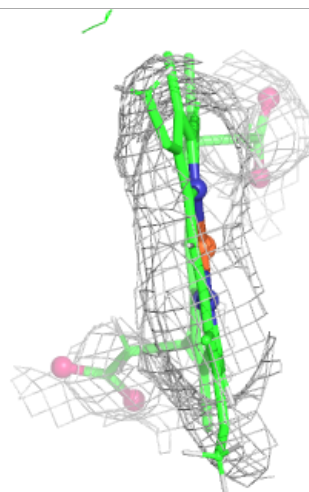
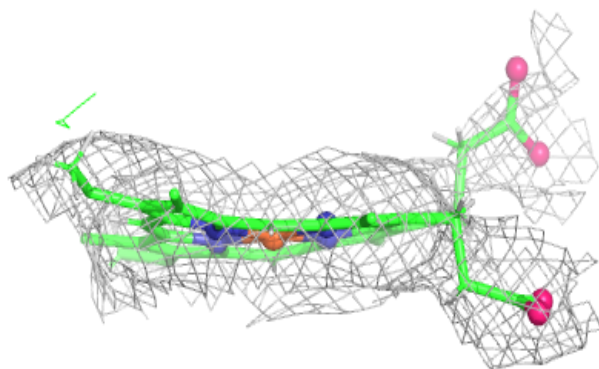
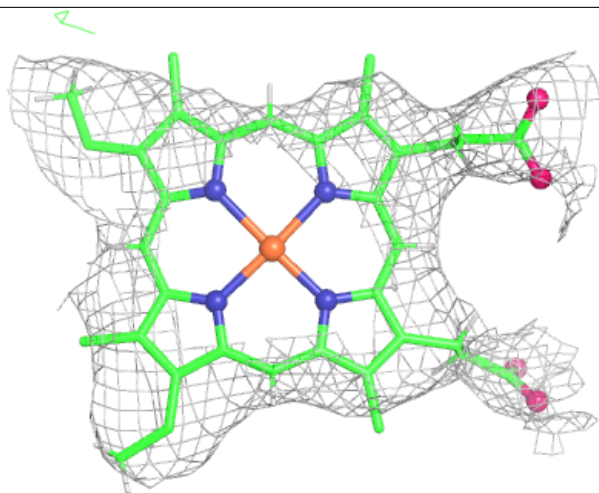
**Electron density around BCB M 404:**

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



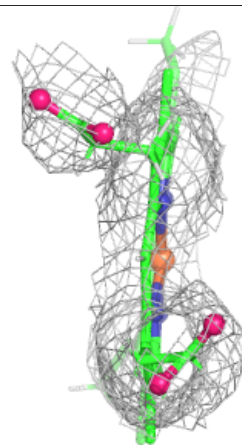
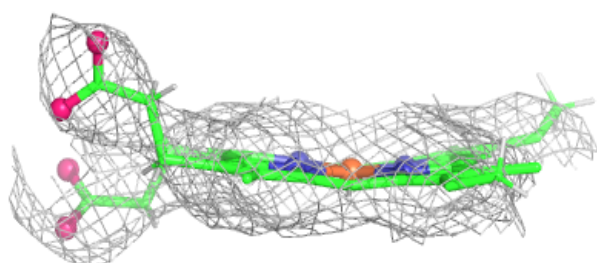
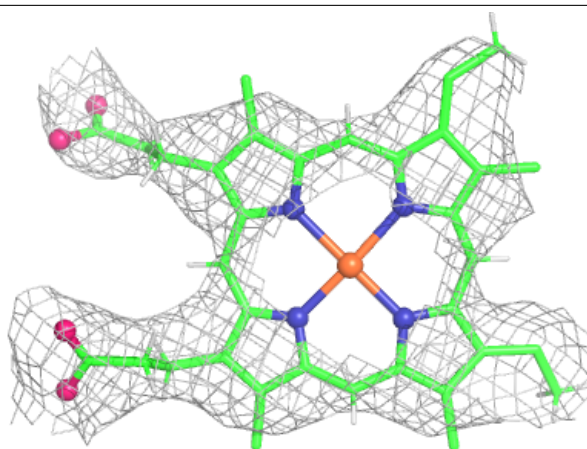
Electron density around HEC C 401:

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



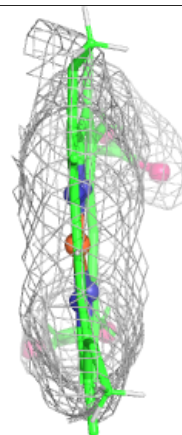
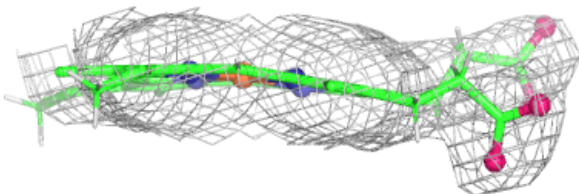
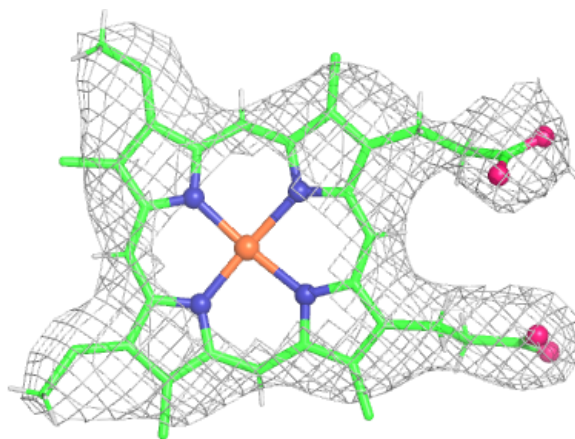
Electron density around HEC C 403:

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



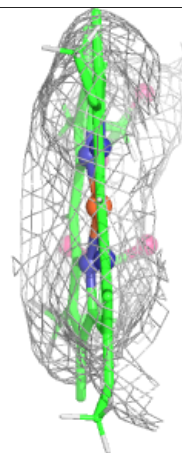
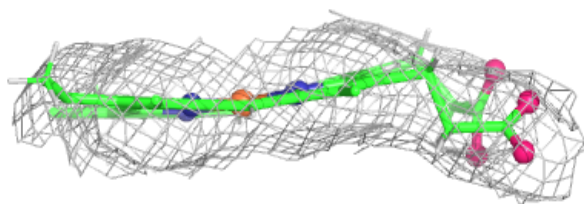
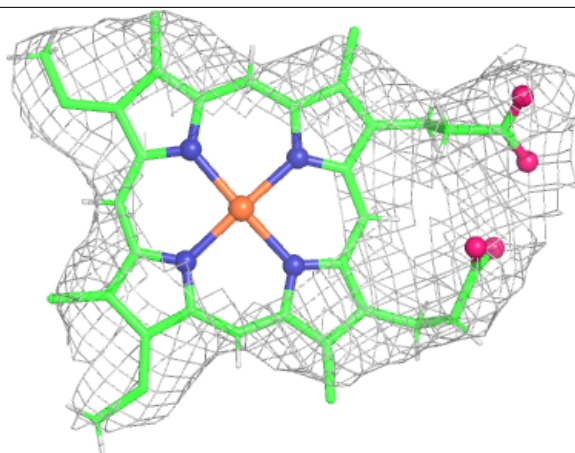
Electron density around HEC C 404:

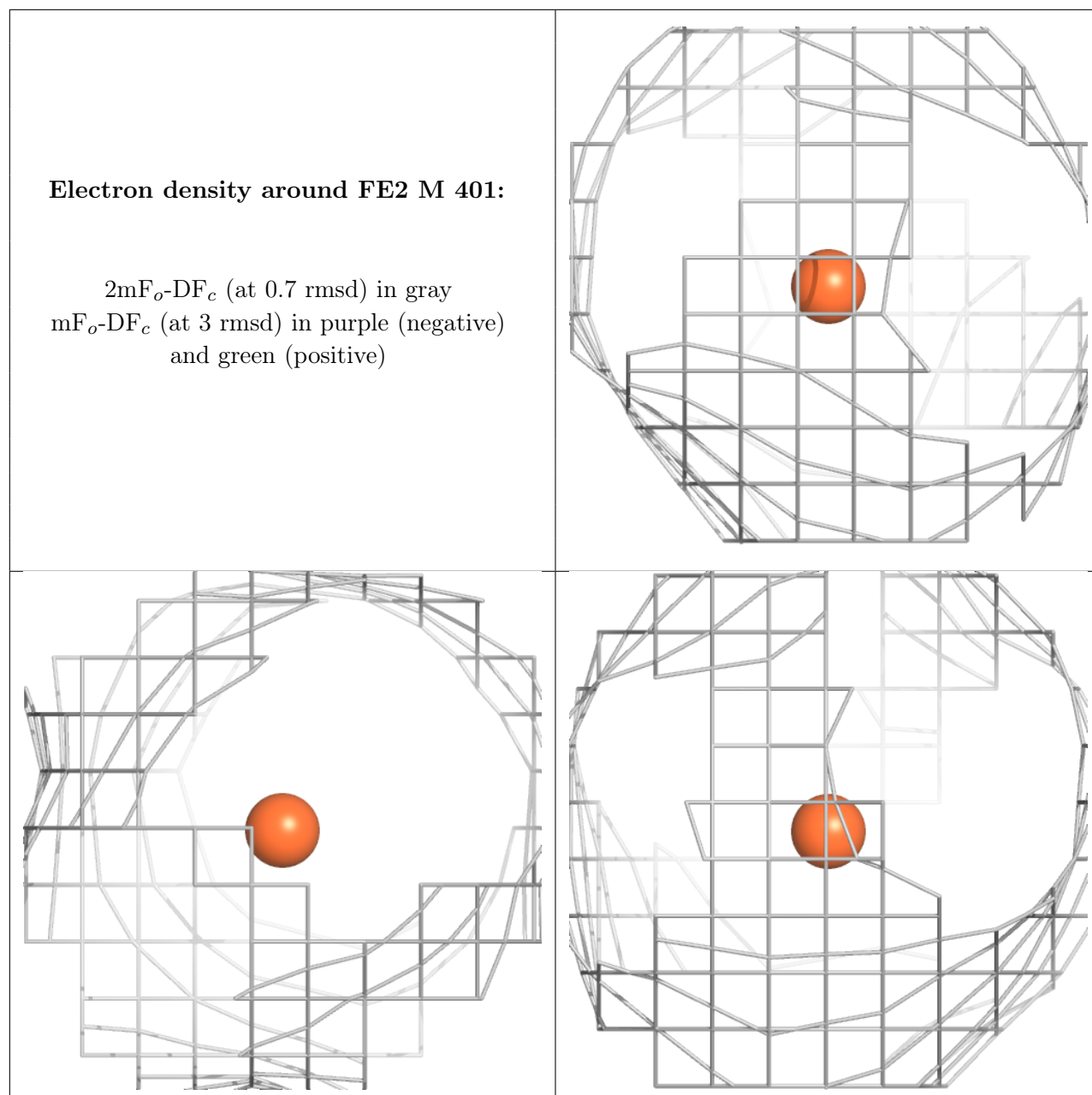
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEC C 402:

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





6.5 Other polymers ⓘ

There are no such residues in this entry.