



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 12:08 AM UTC

PDB ID : 6QPA / pdb_00006qpa
Title : Halothiobacillus neapolitanus sulfur oxygenase reductase
Authors : Frazao, C.; Klezin, A.; Poell, U.; Veith, A.; Ruehl, P.; Coelho, R.
Deposited on : 2019-02-13
Resolution : 2.10 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

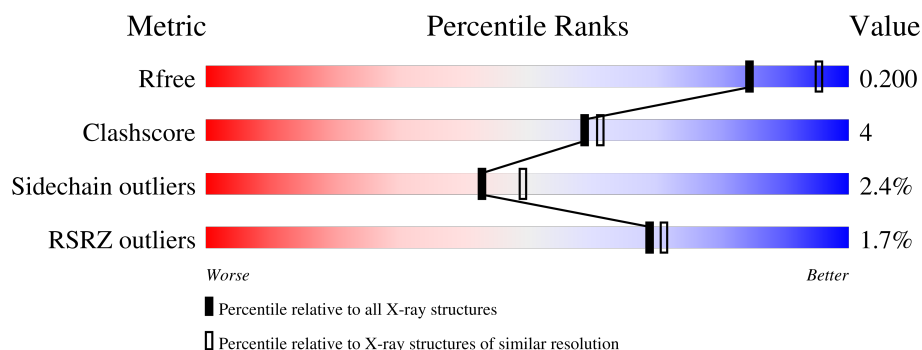
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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.



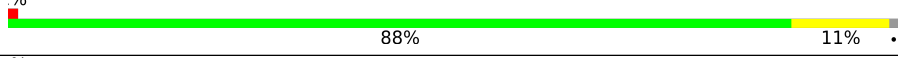
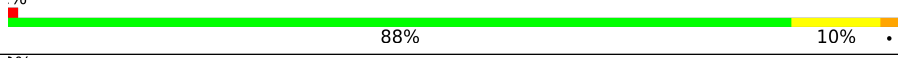
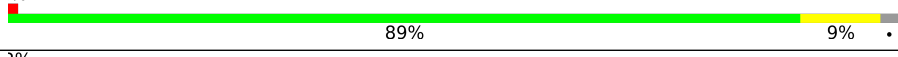
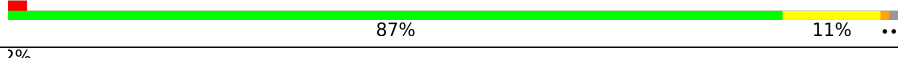
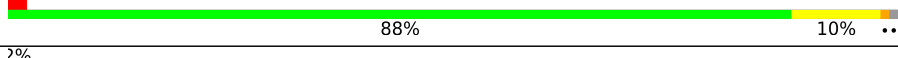
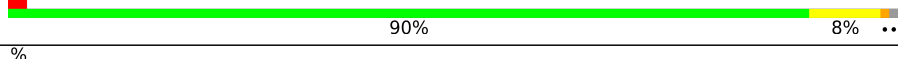
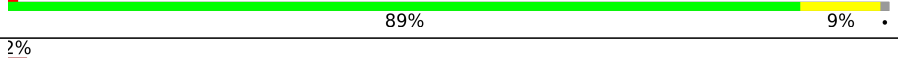
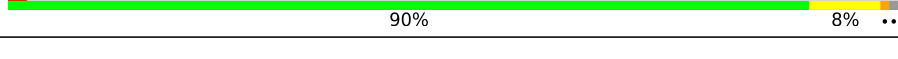
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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

Mol	Chain	Length	Quality of chain
1	A	314	% 87% 10% ..
1	B	314	% 87% 11% ..
1	C	314	2% 90% 8% ..
1	D	314	2% 86% 12% ..
1	E	314	3% 85% 14% .
1	F	314	2% 83% 15% ..

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Mol	Chain	Length	Quality of chain	
1	G	314		..
1	H	314		.
1	I	314		..
1	J	314		..
1	K	314		..
1	L	314		.
1	M	314		..
1	N	314		..
1	O	314		.
1	P	314		..
1	Q	314		..
1	R	314		..
1	T	314		..
1	U	314		..
1	V	314		.
1	W	314		.
1	Y	314		.
1	Z	314		..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 63067 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 Sulfur oxygenase/reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	310	Total	C	N	O	S	0	1	0
			2447	1561	412	447	27			
1	B	310	Total	C	N	O	S	0	1	0
			2447	1561	412	447	27			
1	C	310	Total	C	N	O	S	0	2	0
			2451	1563	413	448	27			
1	D	310	Total	C	N	O	S	0	3	0
			2456	1566	414	449	27			
1	E	310	Total	C	N	O	S	0	1	0
			2447	1561	412	447	27			
1	F	310	Total	C	N	O	S	0	2	0
			2452	1564	413	448	27			
1	G	310	Total	C	N	O	S	0	2	0
			2452	1564	413	448	27			
1	H	310	Total	C	N	O	S	0	2	0
			2452	1564	413	448	27			
1	I	310	Total	C	N	O	S	0	3	0
			2456	1566	414	449	27			
1	J	310	Total	C	N	O	S	0	2	0
			2451	1564	413	447	27			
1	K	310	Total	C	N	O	S	0	1	0
			2447	1561	412	447	27			
1	L	310	Total	C	N	O	S	0	3	0
			2456	1567	414	448	27			
1	M	310	Total	C	N	O	S	0	2	0
			2451	1564	413	447	27			
1	N	310	Total	C	N	O	S	0	2	0
			2452	1564	413	448	27			
1	O	309	Total	C	N	O	S	0	4	0
			2454	1565	415	447	27			
1	P	310	Total	C	N	O	S	0	4	0
			2460	1569	415	449	27			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	310	Total	C	N	O	S	0	3	0
			2456	1567	414	448	27			
1	R	310	Total	C	N	O	S	0	2	0
			2452	1564	413	448	27			
1	T	310	Total	C	N	O	S	0	2	0
			2452	1564	413	448	27			
1	U	310	Total	C	N	O	S	0	3	0
			2456	1566	414	449	27			
1	V	310	Total	C	N	O	S	0	1	0
			2447	1561	412	447	27			
1	W	310	Total	C	N	O	S	0	1	0
			2447	1561	412	447	27			
1	Y	310	Total	C	N	O	S	0	1	0
			2447	1561	412	447	27			
1	Z	310	Total	C	N	O	S	0	4	0
			2460	1569	415	449	27			

- Molecule 2 is FE (III) ION (CCD ID: FE) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

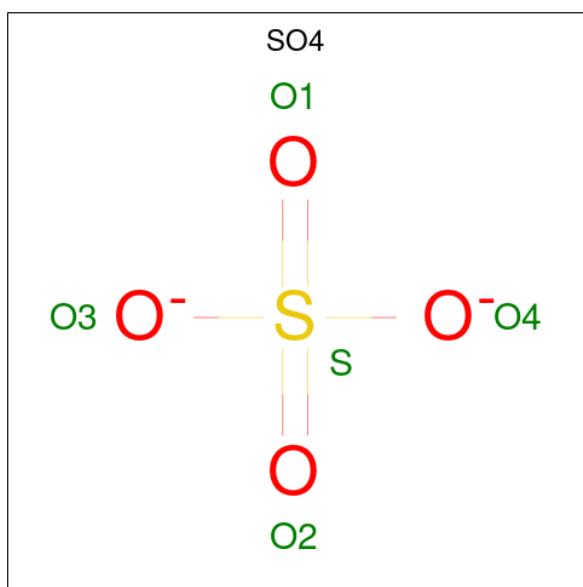
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Fe	0	0
			1	1		
2	B	1	Total	Fe	0	0
			1	1		
2	C	1	Total	Fe	0	0
			1	1		
2	D	1	Total	Fe	0	0
			1	1		
2	E	1	Total	Fe	0	0
			1	1		
2	F	1	Total	Fe	0	0
			1	1		
2	G	1	Total	Fe	0	0
			1	1		
2	H	1	Total	Fe	0	0
			1	1		
2	I	1	Total	Fe	0	0
			1	1		
2	J	1	Total	Fe	0	0
			1	1		
2	K	1	Total	Fe	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	L	1	Total 1	Fe 1	0	0
2	M	1	Total 1	Fe 1	0	0
2	N	1	Total 1	Fe 1	0	0
2	O	1	Total 1	Fe 1	0	0
2	P	1	Total 1	Fe 1	0	0
2	Q	1	Total 1	Fe 1	0	0
2	R	1	Total 1	Fe 1	0	0
2	T	1	Total 1	Fe 1	0	0
2	U	1	Total 1	Fe 1	0	0
2	V	1	Total 1	Fe 1	0	0
2	W	1	Total 1	Fe 1	0	0
2	Y	1	Total 1	Fe 1	0	0
2	Z	1	Total 1	Fe 1	0	0

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	F	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	I	1	Total	O	S	0	0
			5	4	1		
3	I	1	Total	O	S	0	0
			5	4	1		
3	J	1	Total	O	S	0	0
			5	4	1		
3	J	1	Total	O	S	0	0
			5	4	1		
3	K	1	Total	O	S	0	0
			5	4	1		
3	K	1	Total	O	S	0	0
			5	4	1		
3	L	1	Total	O	S	0	0
			5	4	1		
3	L	1	Total	O	S	0	0
			5	4	1		
3	M	1	Total	O	S	0	0
			5	4	1		
3	M	1	Total	O	S	0	0
			5	4	1		
3	N	1	Total	O	S	0	0
			5	4	1		
3	N	1	Total	O	S	0	0
			5	4	1		
3	O	1	Total	O	S	0	0
			5	4	1		
3	O	1	Total	O	S	0	0
			5	4	1		
3	P	1	Total	O	S	0	0
			5	4	1		
3	P	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	Q	1	Total	O	S	0	0
			5	4	1		
3	Q	1	Total	O	S	0	0
			5	4	1		
3	R	1	Total	O	S	0	0
			5	4	1		
3	T	1	Total	O	S	0	0
			5	4	1		
3	U	1	Total	O	S	0	0
			5	4	1		
3	U	1	Total	O	S	0	0
			5	4	1		
3	V	1	Total	O	S	0	0
			5	4	1		
3	V	1	Total	O	S	0	0
			5	4	1		
3	V	1	Total	O	S	0	0
			5	4	1		
3	W	1	Total	O	S	0	0
			5	4	1		
3	W	1	Total	O	S	0	0
			5	4	1		
3	Y	1	Total	O	S	0	0
			5	4	1		
3	Z	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	203	Total	O	0	0
			203	203		
4	B	191	Total	O	0	0
			191	191		
4	C	154	Total	O	0	0
			154	154		
4	D	118	Total	O	0	0
			118	118		
4	E	160	Total	O	0	0
			160	160		
4	F	122	Total	O	0	0
			122	122		

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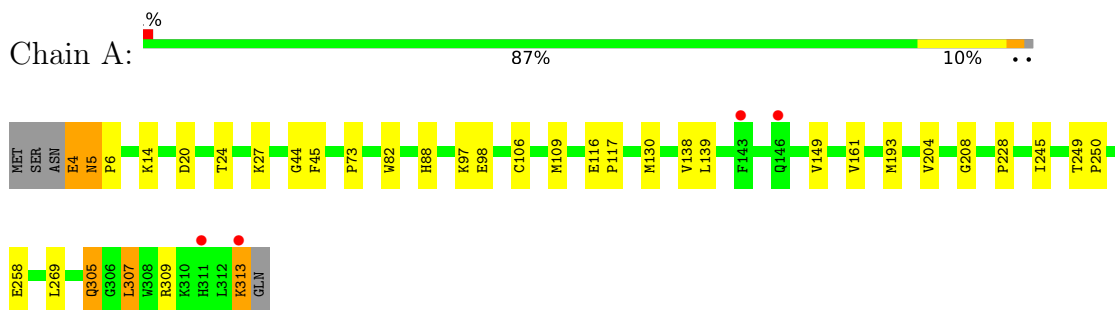
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	215	Total 215	O 215	0	0
4	H	186	Total 186	O 186	0	0
4	I	219	Total 219	O 219	0	0
4	J	204	Total 204	O 204	0	0
4	K	183	Total 183	O 183	0	0
4	L	101	Total 101	O 101	0	0
4	M	203	Total 203	O 203	0	0
4	N	219	Total 219	O 219	0	0
4	O	171	Total 171	O 171	0	0
4	P	153	Total 153	O 153	0	0
4	Q	221	Total 221	O 221	0	0
4	R	169	Total 169	O 169	0	0
4	T	174	Total 174	O 174	0	0
4	U	122	Total 122	O 122	0	0
4	V	116	Total 116	O 116	0	0
4	W	76	Total 76	O 76	0	0
4	Y	96	Total 96	O 96	0	0
4	Z	179	Total 179	O 179	0	0

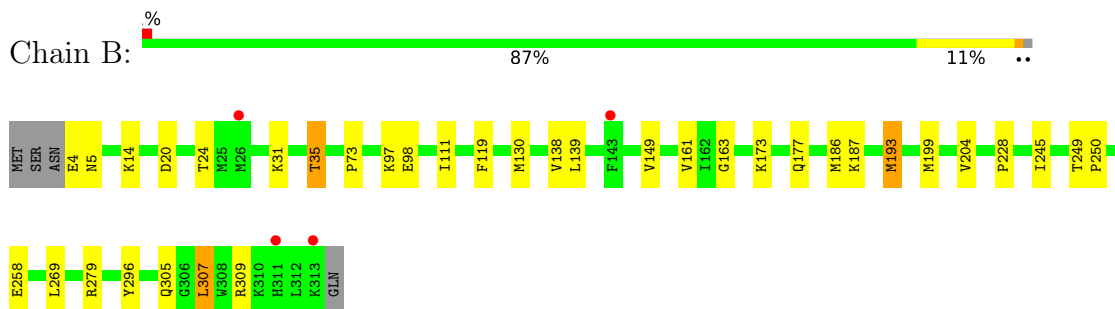
3 Residue-property plots [i](#)

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 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.

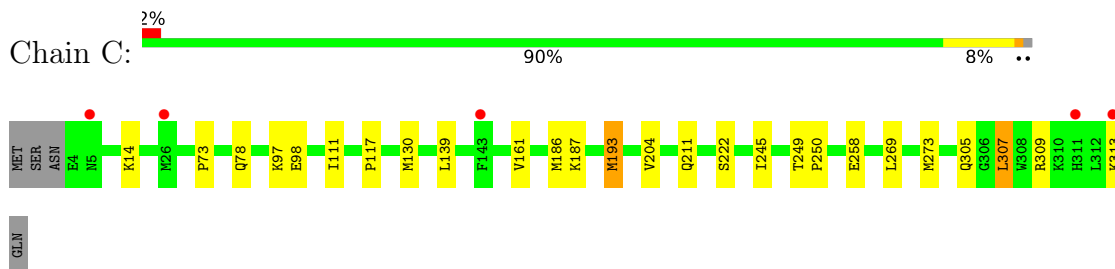
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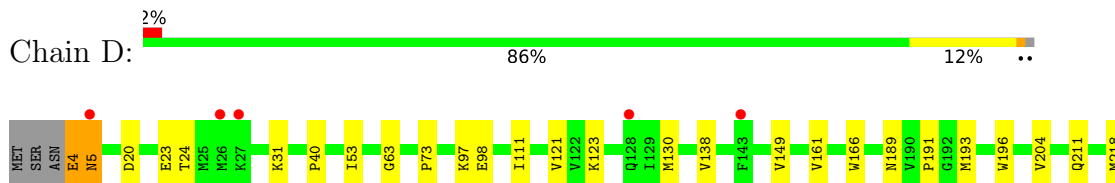
- Molecule 1: Sulfur oxygenase/reductase



- Molecule 1: Sulfur oxygenase/reductase

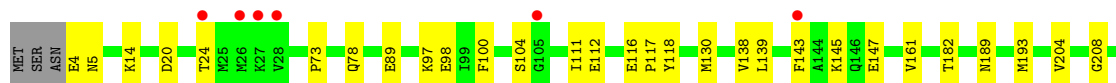
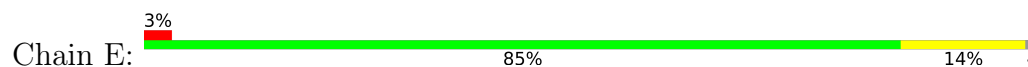


- Molecule 1: Sulfur oxygenase/reductase

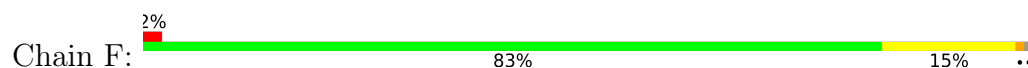




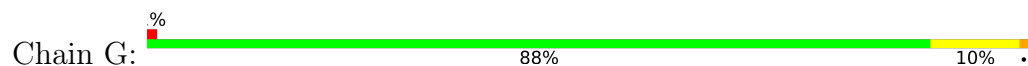
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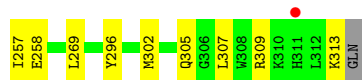
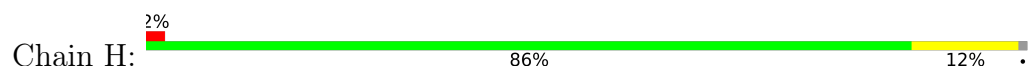
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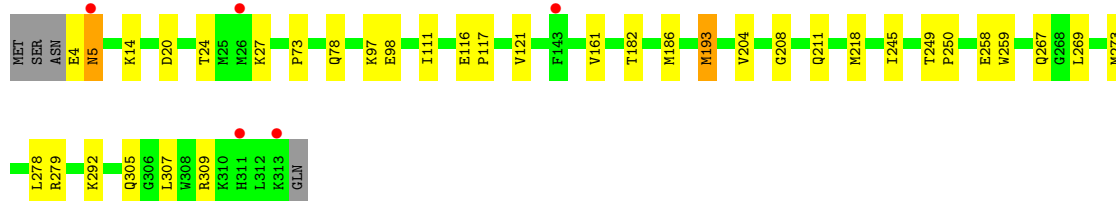
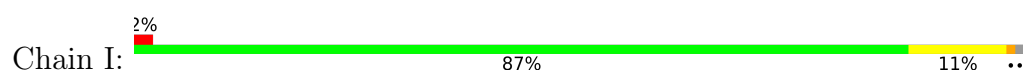
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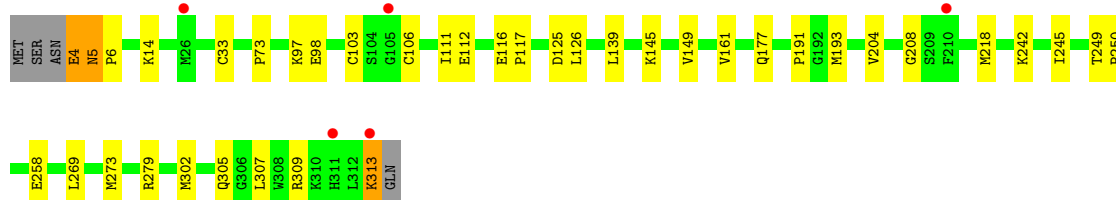
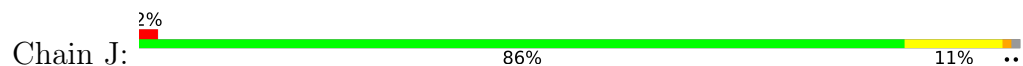
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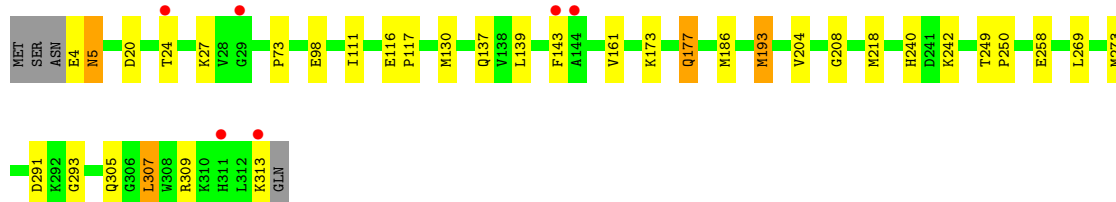
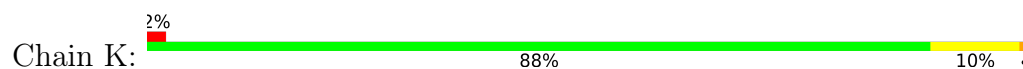
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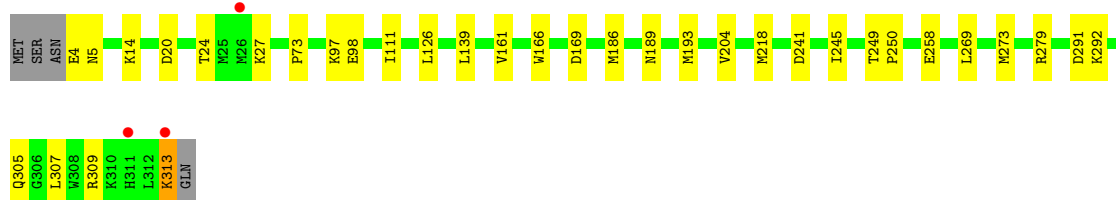
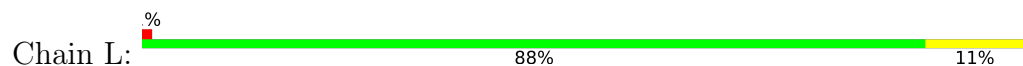
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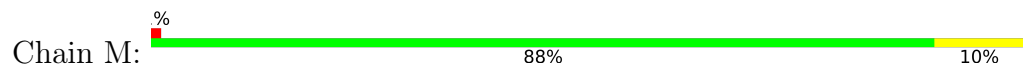
- Molecule 1: Sulfur oxygenase/reductase



- Molecule 1: Sulfur oxygenase/reductase

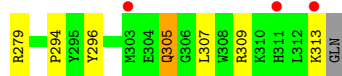
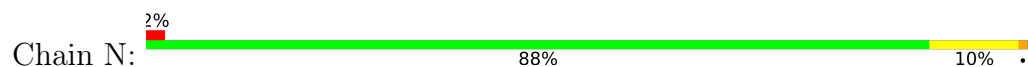


- Molecule 1: Sulfur oxygenase/reductase

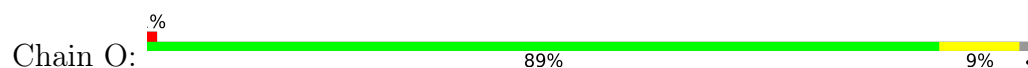




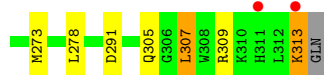
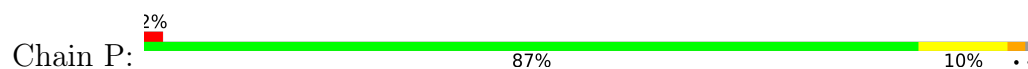
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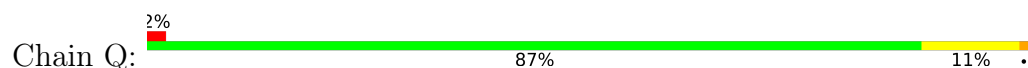
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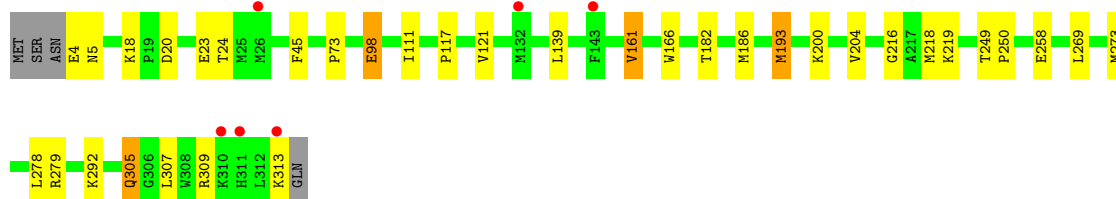
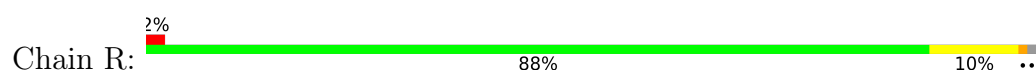
- Molecule 1: Sulfur oxygenase/reductase



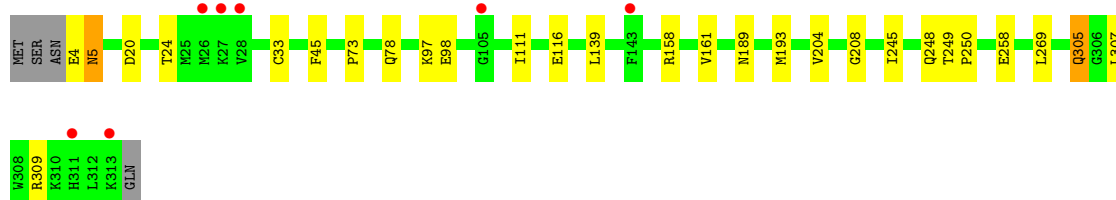
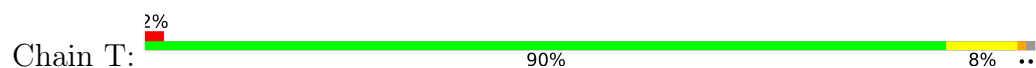
- Molecule 1: Sulfur oxygenase/reductase



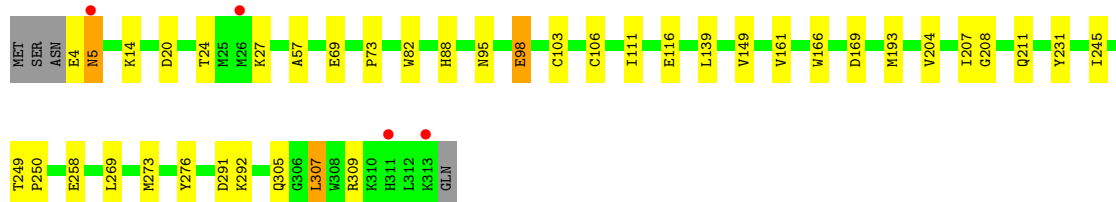
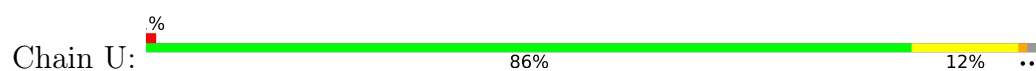
- Molecule 1: Sulfur oxygenase/reductase



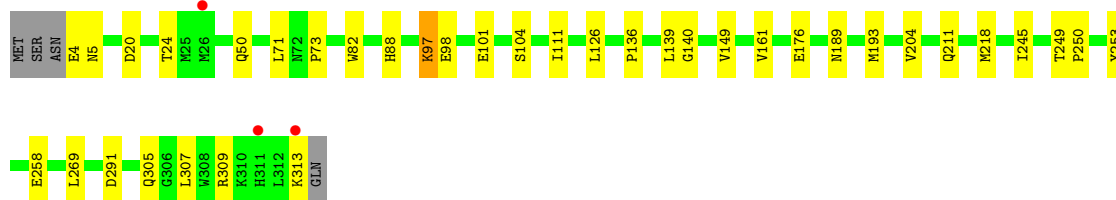
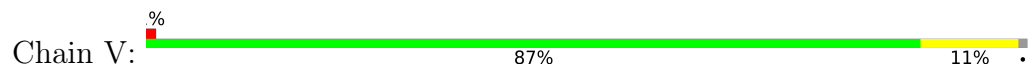
- Molecule 1: Sulfur oxygenase/reductase



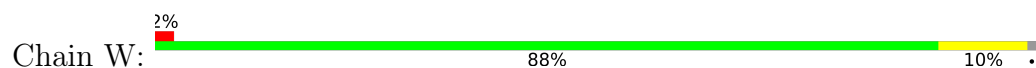
- Molecule 1: Sulfur oxygenase/reductase



- Molecule 1: Sulfur oxygenase/reductase

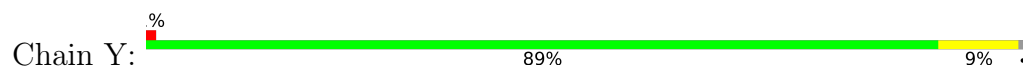


- Molecule 1: Sulfur oxygenase/reductase

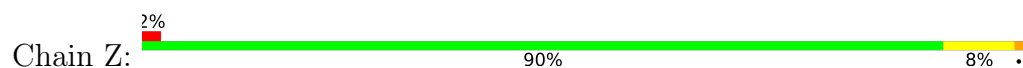




- Molecule 1: Sulfur oxygenase/reductase



- Molecule 1: Sulfur oxygenase/reductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	200.84Å 212.45Å 215.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	83.69 – 2.10 83.69 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (83.69-2.10) 96.1 (83.69-2.10)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.48 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.162 , 0.200 0.162 , 0.200	Depositor DCC
R_{free} test set	1998 reflections (0.38%)	wwPDB-VP
Wilson B-factor (Å ²)	33.5	Xtriage
Anisotropy	0.309	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 61.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.013 for -h,l,k	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	63067	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.80% 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: SO4, CSS, FE

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.37	0/2510	0.56	0/3399
1	B	0.37	0/2510	0.58	0/3399
1	C	0.32	0/2519	0.53	0/3411
1	D	0.29	0/2527	0.51	0/3423
1	E	0.34	0/2510	0.54	0/3399
1	F	0.29	0/2518	0.51	0/3411
1	G	0.41	0/2518	0.59	1/3411 (0.0%)
1	H	0.37	0/2518	0.57	0/3411
1	I	0.41	0/2527	0.59	1/3423 (0.0%)
1	J	0.38	0/2518	0.56	0/3407
1	K	0.37	0/2510	0.58	1/3399 (0.0%)
1	L	0.29	0/2526	0.50	0/3419
1	M	0.39	0/2518	0.58	1/3407 (0.0%)
1	N	0.41	0/2518	0.59	0/3411
1	O	0.35	0/2526	0.55	0/3419
1	P	0.33	0/2535	0.54	0/3431
1	Q	0.37	0/2526	0.58	1/3419 (0.0%)
1	R	0.36	0/2518	0.55	0/3411
1	T	0.35	0/2518	0.52	0/3411
1	U	0.31	0/2527	0.53	0/3423
1	V	0.30	0/2510	0.50	0/3399
1	W	0.27	0/2510	0.50	0/3399
1	Y	0.27	0/2510	0.48	0/3399
1	Z	0.40	0/2535	0.56	0/3431
All	All	0.35	0/60462	0.55	5/81872 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	193	MET	CA-CB-CG	-5.75	102.61	114.10
1	Q	193	MET	CA-CB-CG	5.74	125.58	114.10
1	M	193	MET	CA-CB-CG	-5.11	103.88	114.10
1	K	193	MET	CA-CB-CG	-5.03	104.03	114.10
1	G	193	MET	CA-CB-CG	-5.00	104.09	114.10

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	2447	0	2362	22	0
1	B	2447	0	2362	27	0
1	C	2451	0	2366	20	0
1	D	2456	0	2372	28	0
1	E	2447	0	2362	26	0
1	F	2452	0	2368	37	0
1	G	2452	0	2368	23	0
1	H	2452	0	2368	29	0
1	I	2456	0	2372	28	0
1	J	2451	0	2371	26	0
1	K	2447	0	2362	26	0
1	L	2456	0	2377	21	0
1	M	2451	0	2371	23	0
1	N	2452	0	2368	20	0
1	O	2454	0	2374	14	0
1	P	2460	0	2381	28	0
1	Q	2456	0	2377	25	0
1	R	2452	0	2368	24	0
1	T	2452	0	2368	18	0
1	U	2456	0	2372	27	0
1	V	2447	0	2362	25	0
1	W	2447	0	2362	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Y	2447	0	2362	18	0
1	Z	2460	0	2381	16	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
2	M	1	0	0	0	0
2	N	1	0	0	0	0
2	O	1	0	0	0	0
2	P	1	0	0	0	0
2	Q	1	0	0	0	0
2	R	1	0	0	0	0
2	T	1	0	0	0	0
2	U	1	0	0	0	0
2	V	1	0	0	0	0
2	W	1	0	0	0	0
2	Y	1	0	0	0	0
2	Z	1	0	0	0	0
3	A	15	0	0	0	0
3	B	10	0	0	0	0
3	C	15	0	0	0	0
3	D	10	0	0	0	0
3	E	10	0	0	0	0
3	F	15	0	0	0	0
3	G	10	0	0	1	0
3	H	10	0	0	0	0
3	I	10	0	0	0	0
3	J	10	0	0	1	0
3	K	10	0	0	0	0
3	L	10	0	0	1	0
3	M	10	0	0	0	0
3	N	10	0	0	0	0
3	O	10	0	0	0	0
3	P	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	Q	10	0	0	0	0
3	R	5	0	0	0	0
3	T	5	0	0	0	0
3	U	10	0	0	0	0
3	V	15	0	0	0	0
3	W	10	0	0	0	0
3	Y	5	0	0	0	0
3	Z	5	0	0	0	0
4	A	203	0	0	1	0
4	B	191	0	0	3	0
4	C	154	0	0	3	0
4	D	118	0	0	4	0
4	E	160	0	0	1	0
4	F	122	0	0	3	0
4	G	215	0	0	1	0
4	H	186	0	0	2	1
4	I	219	0	0	4	0
4	J	204	0	0	3	1
4	K	183	0	0	1	0
4	L	101	0	0	1	0
4	M	203	0	0	1	0
4	N	219	0	0	2	0
4	O	171	0	0	2	0
4	P	153	0	0	3	0
4	Q	221	0	0	4	0
4	R	169	0	0	1	0
4	T	174	0	0	1	0
4	U	122	0	0	3	0
4	V	116	0	0	1	0
4	W	76	0	0	0	0
4	Y	96	0	0	1	0
4	Z	179	0	0	0	0
All	All	63067	0	56856	514	1

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 4.

The worst 5 of 514 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:145:LYS:NZ	4:J:501:HOH:O	1.96	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:187:LYS:HA	1:B:193:MET:HG2	1.51	0.91
1:N:187:LYS:HA	1:N:193:MET:HG2	1.51	0.89
1:P:4:GLU:OE1	4:P:501:HOH:O	1.99	0.79
1:C:187:LYS:HA	1:C:193:MET:HG2	1.66	0.78

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:576:HOH:O	4:J:660:HOH:O[4_456]	1.93	0.27

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](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	263/266 (99%)	255 (97%)	8 (3%)	36	41
1	B	263/266 (99%)	257 (98%)	6 (2%)	44	51
1	C	264/266 (99%)	259 (98%)	5 (2%)	50	58
1	D	265/266 (100%)	258 (97%)	7 (3%)	40	46
1	E	263/266 (99%)	258 (98%)	5 (2%)	50	58
1	F	264/266 (99%)	258 (98%)	6 (2%)	44	51
1	G	264/266 (99%)	258 (98%)	6 (2%)	44	51
1	H	264/266 (99%)	259 (98%)	5 (2%)	50	58
1	I	265/266 (100%)	257 (97%)	8 (3%)	36	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J	264/266 (99%)	256 (97%)	8 (3%)	36	41
1	K	263/266 (99%)	255 (97%)	8 (3%)	36	41
1	L	265/266 (100%)	258 (97%)	7 (3%)	40	46
1	M	264/266 (99%)	256 (97%)	8 (3%)	36	41
1	N	264/266 (99%)	259 (98%)	5 (2%)	50	58
1	O	265/266 (100%)	256 (97%)	9 (3%)	32	35
1	P	266/266 (100%)	258 (97%)	8 (3%)	36	41
1	Q	265/266 (100%)	256 (97%)	9 (3%)	32	35
1	R	264/266 (99%)	257 (97%)	7 (3%)	39	45
1	T	264/266 (99%)	258 (98%)	6 (2%)	44	51
1	U	265/266 (100%)	256 (97%)	9 (3%)	32	35
1	V	257/266 (97%)	250 (97%)	7 (3%)	39	45
1	W	94/266 (35%)	93 (99%)	1 (1%)	65	74
1	Y	221/266 (83%)	217 (98%)	4 (2%)	51	60
1	Z	266/266 (100%)	258 (97%)	8 (3%)	36	41
All	All	6122/6384 (96%)	5962 (97%)	160 (3%)	43	46

5 of 160 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Q	307	LEU
1	V	104	SER
1	R	18	LYS
1	T	305	GLN
1	Y	305	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 110 such sidechains are listed below:

Mol	Chain	Res	Type
1	N	95	ASN
1	P	240	HIS
1	Z	177	GLN
1	W	78	GLN
1	N	201	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

48 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	CSS	F	103	1	4,6,7	1.44	0	2,6,8	1.41	0
1	CSS	Z	103	1	4,6,7	1.33	0	2,6,8	1.23	0
1	CSS	W	103	1	4,6,7	1.46	0	2,6,8	1.23	0
1	CSS	O	103	1	4,6,7	1.24	0	2,6,8	0.88	0
1	CSS	K	103	1	4,6,7	1.25	0	2,6,8	0.66	0
1	CSS	D	33	1	4,6,7	1.48	0	2,6,8	1.07	0
1	CSS	G	33	1	4,6,7	1.17	0	2,6,8	0.88	0
1	CSS	A	33	1	4,6,7	1.34	0	2,6,8	0.75	0
1	CSS	C	33	1	4,6,7	1.23	0	2,6,8	0.58	0
1	CSS	K	33	1	4,6,7	1.31	0	2,6,8	0.57	0
1	CSS	A	103	1	4,6,7	1.27	0	2,6,8	0.97	0
1	CSS	B	33	1	4,6,7	1.38	0	2,6,8	1.05	0
1	CSS	R	103	1	4,6,7	1.46	0	2,6,8	1.35	0
1	CSS	W	33	1	4,6,7	1.33	0	2,6,8	0.40	0
1	CSS	U	33	1	4,6,7	1.35	0	2,6,8	0.99	0
1	CSS	D	103	1	4,6,7	1.28	0	2,6,8	0.78	0
1	CSS	J	33	1	4,6,7	1.31	0	2,6,8	0.63	0
1	CSS	V	33	1	4,6,7	1.42	0	2,6,8	0.85	0
1	CSS	L	103	1	4,6,7	1.33	0	2,6,8	1.11	0
1	CSS	V	103	1	4,6,7	1.38	0	2,6,8	0.84	0
1	CSS	E	33	1	4,6,7	1.24	0	2,6,8	0.48	0
1	CSS	Y	33	1	4,6,7	1.35	0	2,6,8	0.61	0
1	CSS	I	103	1	4,6,7	1.28	0	2,6,8	0.82	0
1	CSS	Q	33	1	4,6,7	1.34	0	2,6,8	1.10	0
1	CSS	L	33	1	4,6,7	1.48	0	2,6,8	1.35	0
1	CSS	T	103	1	4,6,7	1.43	0	2,6,8	1.10	0
1	CSS	M	33	1	4,6,7	1.35	0	2,6,8	1.00	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	CSS	I	33	1	4,6,7	1.13	0	2,6,8	0.71	0
1	CSS	J	103	1	4,6,7	1.42	0	2,6,8	0.97	0
1	CSS	P	103	1	4,6,7	1.52	0	2,6,8	1.56	0
1	CSS	R	33	1	4,6,7	1.32	0	2,6,8	0.51	0
1	CSS	H	33	1	4,6,7	1.31	0	2,6,8	0.66	0
1	CSS	M	103	1	4,6,7	1.28	0	2,6,8	1.13	0
1	CSS	Y	103	1	4,6,7	1.44	0	2,6,8	1.30	0
1	CSS	O	33	1	4,6,7	1.46	0	2,6,8	1.08	0
1	CSS	P	33	1	4,6,7	1.28	0	2,6,8	0.77	0
1	CSS	H	103	1	4,6,7	1.27	0	2,6,8	1.16	0
1	CSS	G	103	1	4,6,7	1.37	0	2,6,8	1.19	0
1	CSS	Q	103	1	4,6,7	1.31	0	2,6,8	0.72	0
1	CSS	N	103	1	4,6,7	1.32	0	2,6,8	1.28	0
1	CSS	U	103	1	4,6,7	1.40	0	2,6,8	1.28	0
1	CSS	N	33	1	4,6,7	1.33	0	2,6,8	0.86	0
1	CSS	C	103	1	4,6,7	1.35	0	2,6,8	1.11	0
1	CSS	T	33	1	4,6,7	1.42	0	2,6,8	1.35	0
1	CSS	Z	33	1	4,6,7	1.33	0	2,6,8	0.92	0
1	CSS	B	103	1	4,6,7	1.41	0	2,6,8	1.12	0
1	CSS	F	33	1	4,6,7	1.42	0	2,6,8	0.75	0
1	CSS	E	103	1	4,6,7	1.42	0	2,6,8	0.73	0

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
1	CSS	F	103	1	-	0/1/5/7	-
1	CSS	Z	103	1	-	0/1/5/7	-
1	CSS	W	103	1	-	0/1/5/7	-
1	CSS	O	103	1	-	0/1/5/7	-
1	CSS	K	103	1	-	0/1/5/7	-
1	CSS	D	33	1	-	0/1/5/7	-
1	CSS	G	33	1	-	0/1/5/7	-
1	CSS	A	33	1	-	0/1/5/7	-
1	CSS	C	33	1	-	0/1/5/7	-
1	CSS	K	33	1	-	0/1/5/7	-
1	CSS	A	103	1	-	0/1/5/7	-
1	CSS	B	33	1	-	0/1/5/7	-
1	CSS	R	103	1	-	0/1/5/7	-
1	CSS	W	33	1	-	0/1/5/7	-
1	CSS	U	33	1	-	0/1/5/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CSS	D	103	1	-	0/1/5/7	-
1	CSS	J	33	1	-	0/1/5/7	-
1	CSS	V	33	1	-	0/1/5/7	-
1	CSS	L	103	1	-	0/1/5/7	-
1	CSS	V	103	1	-	0/1/5/7	-
1	CSS	E	33	1	-	0/1/5/7	-
1	CSS	Y	33	1	-	0/1/5/7	-
1	CSS	I	103	1	-	0/1/5/7	-
1	CSS	Q	33	1	-	0/1/5/7	-
1	CSS	L	33	1	-	0/1/5/7	-
1	CSS	T	103	1	-	0/1/5/7	-
1	CSS	M	33	1	-	0/1/5/7	-
1	CSS	I	33	1	-	0/1/5/7	-
1	CSS	J	103	1	-	0/1/5/7	-
1	CSS	P	103	1	-	0/1/5/7	-
1	CSS	R	33	1	-	0/1/5/7	-
1	CSS	H	33	1	-	0/1/5/7	-
1	CSS	M	103	1	-	0/1/5/7	-
1	CSS	Y	103	1	-	0/1/5/7	-
1	CSS	O	33	1	-	0/1/5/7	-
1	CSS	P	33	1	-	0/1/5/7	-
1	CSS	H	103	1	-	0/1/5/7	-
1	CSS	G	103	1	-	0/1/5/7	-
1	CSS	Q	103	1	-	0/1/5/7	-
1	CSS	N	103	1	-	0/1/5/7	-
1	CSS	U	103	1	-	0/1/5/7	-
1	CSS	N	33	1	-	0/1/5/7	-
1	CSS	C	103	1	-	0/1/5/7	-
1	CSS	T	33	1	-	0/1/5/7	-
1	CSS	Z	33	1	-	0/1/5/7	-
1	CSS	B	103	1	-	0/1/5/7	-
1	CSS	F	33	1	-	0/1/5/7	-
1	CSS	E	103	1	-	0/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	W	33	CSS	1	0
1	J	33	CSS	1	0
1	J	103	CSS	1	0
1	Y	103	CSS	1	0
1	U	103	CSS	2	0
1	T	33	CSS	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 72 ligands modelled in this entry, 24 are monoatomic - leaving 48 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	$\# Z > 2$
3	SO4	W	403	-	4,4,4	0.28	0	6,6,6	0.14	0
3	SO4	V	403	-	4,4,4	0.21	0	6,6,6	0.13	0
3	SO4	L	403	-	4,4,4	0.25	0	6,6,6	0.20	0
3	SO4	E	402	-	4,4,4	0.25	0	6,6,6	0.06	0
3	SO4	H	403	-	4,4,4	0.29	0	6,6,6	0.25	0
3	SO4	T	402	-	4,4,4	0.22	0	6,6,6	0.16	0
3	SO4	R	402	-	4,4,4	0.23	0	6,6,6	0.15	0
3	SO4	F	403	-	4,4,4	0.26	0	6,6,6	0.12	0
3	SO4	G	403	-	4,4,4	0.25	0	6,6,6	0.23	0
3	SO4	K	403	-	4,4,4	0.23	0	6,6,6	0.17	0
3	SO4	H	402	-	4,4,4	0.24	0	6,6,6	0.11	0
3	SO4	A	403	-	4,4,4	0.22	0	6,6,6	0.31	0
3	SO4	F	404	-	4,4,4	0.27	0	6,6,6	0.14	0
3	SO4	Q	403	-	4,4,4	0.32	0	6,6,6	0.24	0
3	SO4	Z	402	-	4,4,4	0.26	0	6,6,6	0.11	0
3	SO4	A	402	-	4,4,4	0.23	0	6,6,6	0.12	0
3	SO4	K	402	-	4,4,4	0.26	0	6,6,6	0.09	0
3	SO4	O	403	-	4,4,4	0.21	0	6,6,6	0.26	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	N	402	-	4,4,4	0.23	0	6,6,6	0.19	0
3	SO4	D	402	-	4,4,4	0.25	0	6,6,6	0.10	0
3	SO4	E	403	-	4,4,4	0.23	0	6,6,6	0.24	0
3	SO4	A	404	-	4,4,4	0.21	0	6,6,6	0.22	0
3	SO4	J	402	-	4,4,4	0.25	0	6,6,6	0.20	0
3	SO4	J	403	-	4,4,4	0.23	0	6,6,6	0.20	0
3	SO4	U	402	-	4,4,4	0.21	0	6,6,6	0.11	0
3	SO4	M	403	-	4,4,4	0.28	0	6,6,6	0.28	0
3	SO4	P	402	-	4,4,4	0.25	0	6,6,6	0.13	0
3	SO4	I	403	-	4,4,4	0.23	0	6,6,6	0.42	0
3	SO4	F	402	-	4,4,4	0.26	0	6,6,6	0.09	0
3	SO4	B	402	-	4,4,4	0.22	0	6,6,6	0.16	0
3	SO4	C	404	-	4,4,4	0.28	0	6,6,6	0.15	0
3	SO4	P	403	-	4,4,4	0.23	0	6,6,6	0.16	0
3	SO4	L	402	-	4,4,4	0.24	0	6,6,6	0.13	0
3	SO4	V	404	-	4,4,4	0.28	0	6,6,6	0.19	0
3	SO4	W	402	-	4,4,4	0.25	0	6,6,6	0.06	0
3	SO4	M	402	-	4,4,4	0.24	0	6,6,6	0.06	0
3	SO4	I	402	-	4,4,4	0.27	0	6,6,6	0.31	0
3	SO4	Y	402	-	4,4,4	0.23	0	6,6,6	0.09	0
3	SO4	D	403	-	4,4,4	0.23	0	6,6,6	0.18	0
3	SO4	G	402	-	4,4,4	0.25	0	6,6,6	0.20	0
3	SO4	C	402	-	4,4,4	0.24	0	6,6,6	0.15	0
3	SO4	N	403	-	4,4,4	0.27	0	6,6,6	0.27	0
3	SO4	Q	402	-	4,4,4	0.22	0	6,6,6	0.17	0
3	SO4	U	403	-	4,4,4	0.21	0	6,6,6	0.23	0
3	SO4	C	403	-	4,4,4	0.21	0	6,6,6	0.18	0
3	SO4	V	401	-	4,4,4	0.26	0	6,6,6	0.18	0
3	SO4	O	402	-	4,4,4	0.22	0	6,6,6	0.11	0
3	SO4	B	403	-	4,4,4	0.26	0	6,6,6	0.21	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

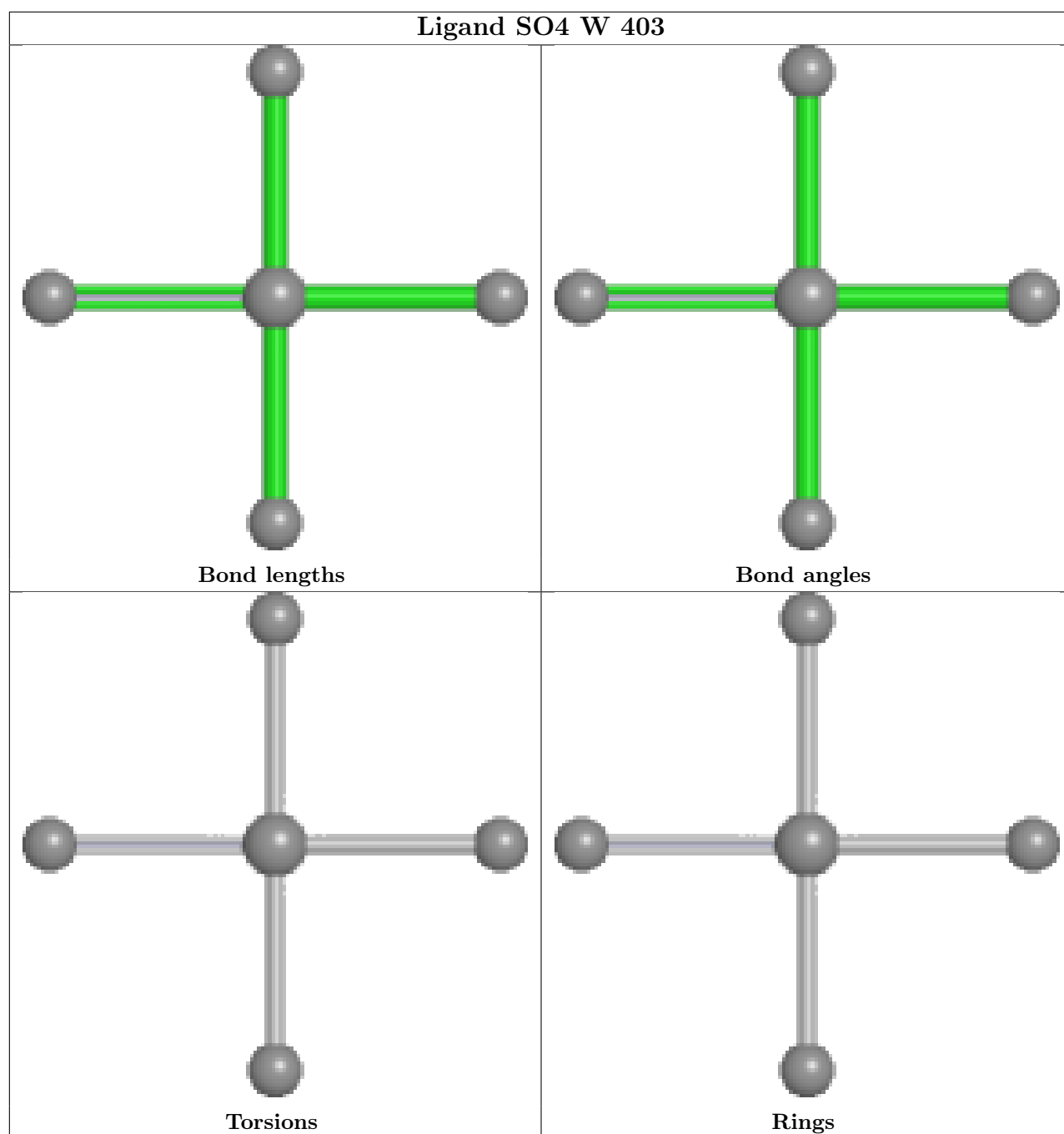
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	J	402	SO4	1	0

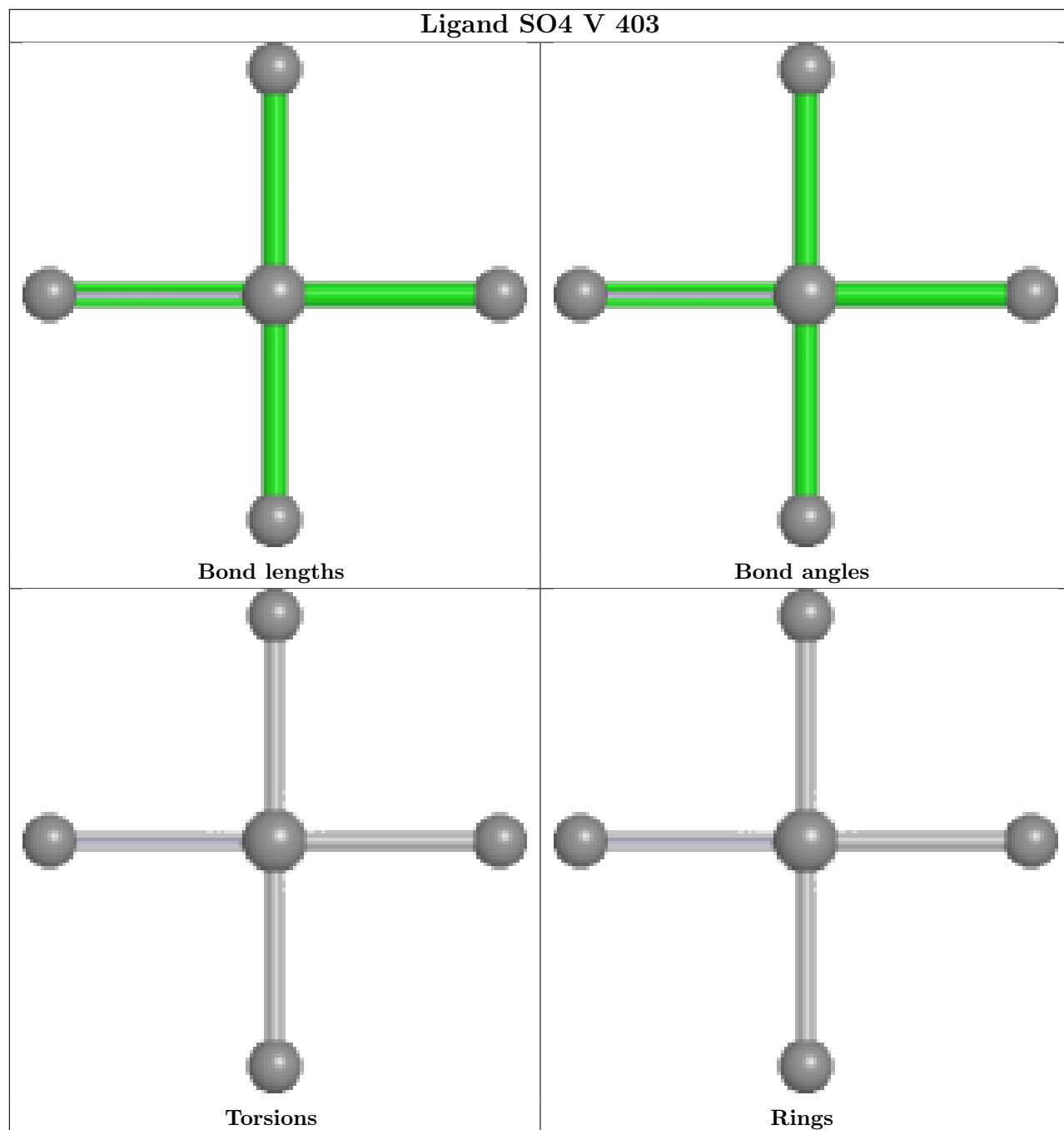
Continued on next page...

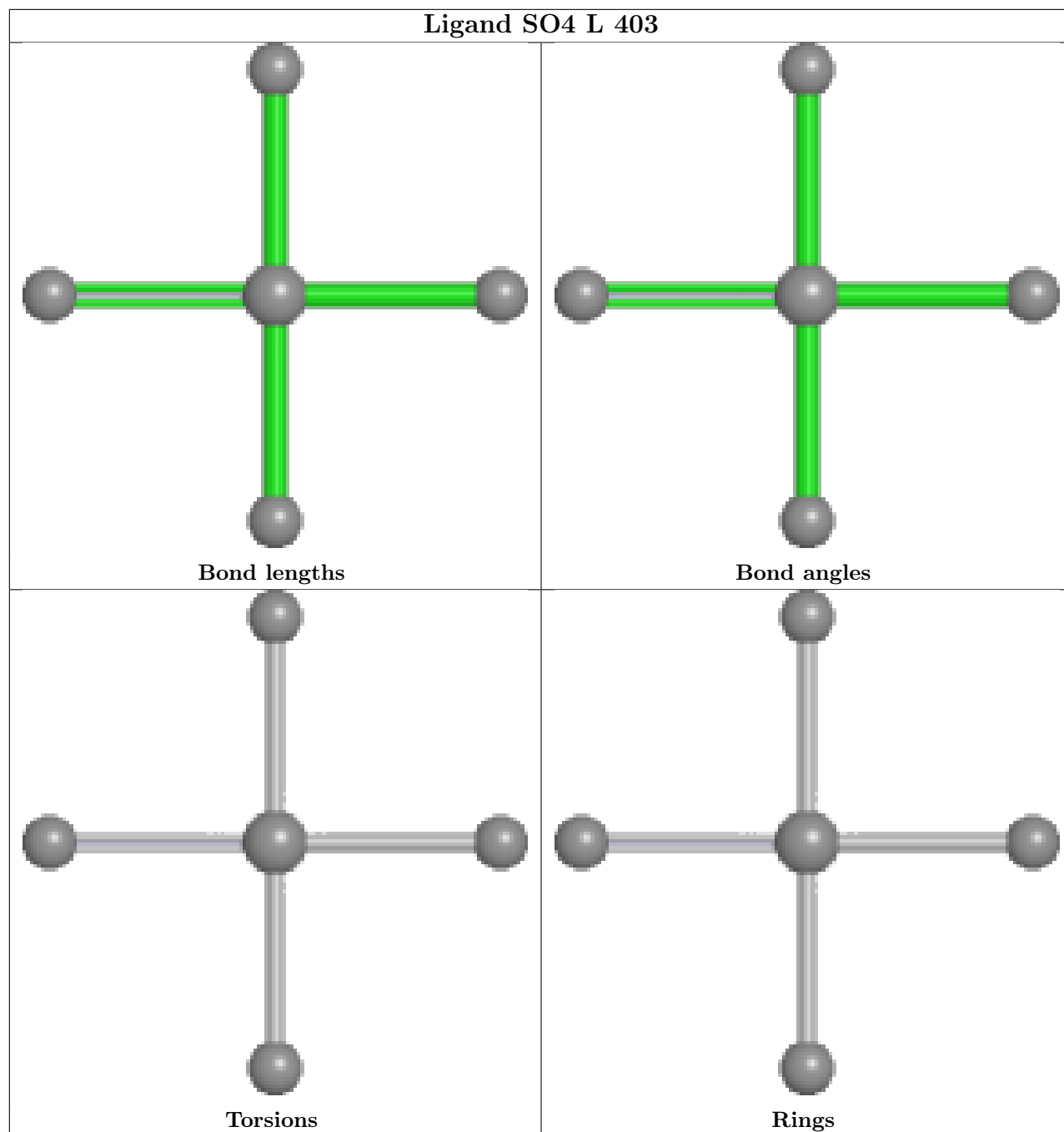
Continued from previous page...

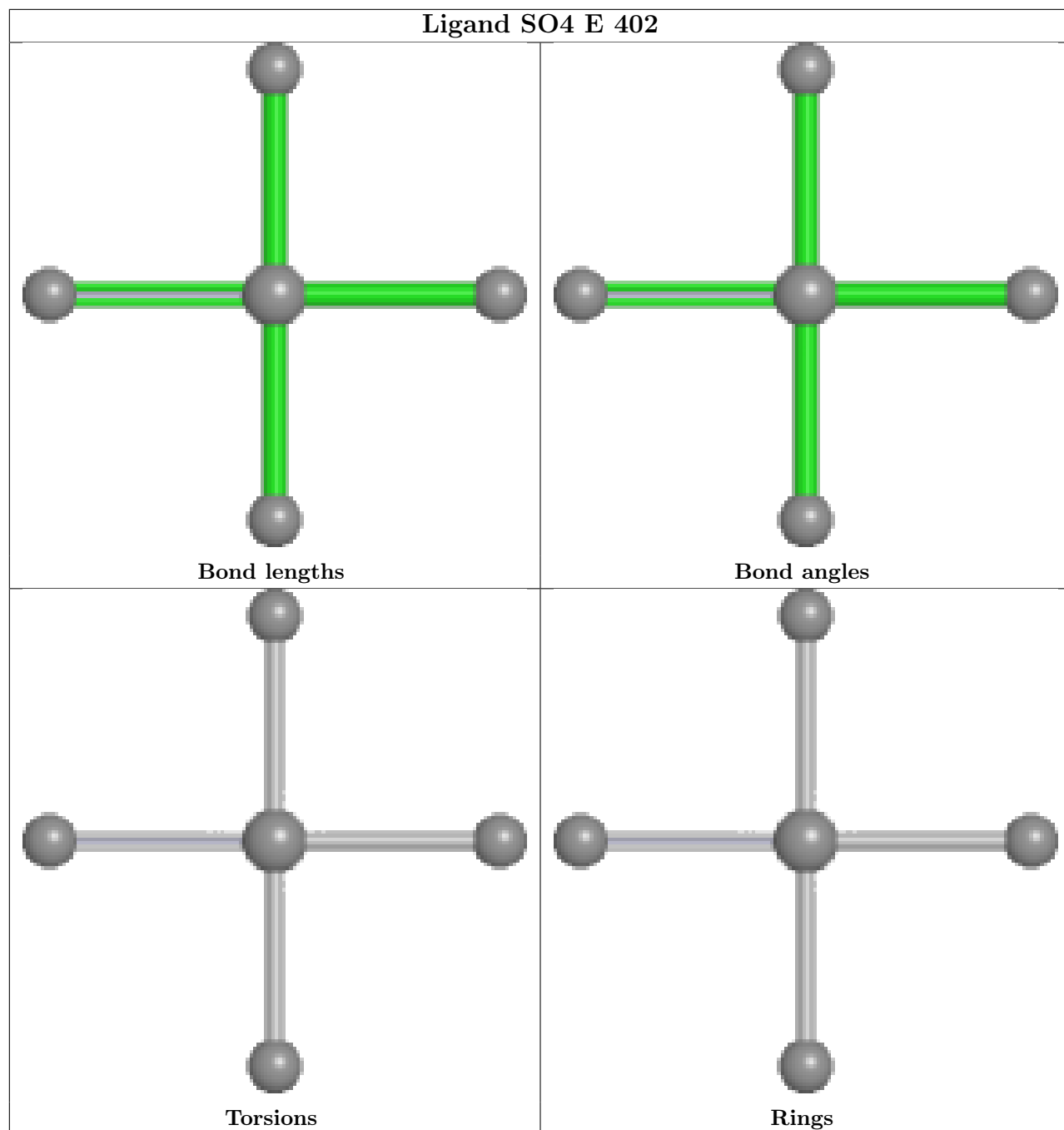
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L	402	SO4	1	0
3	G	402	SO4	1	0

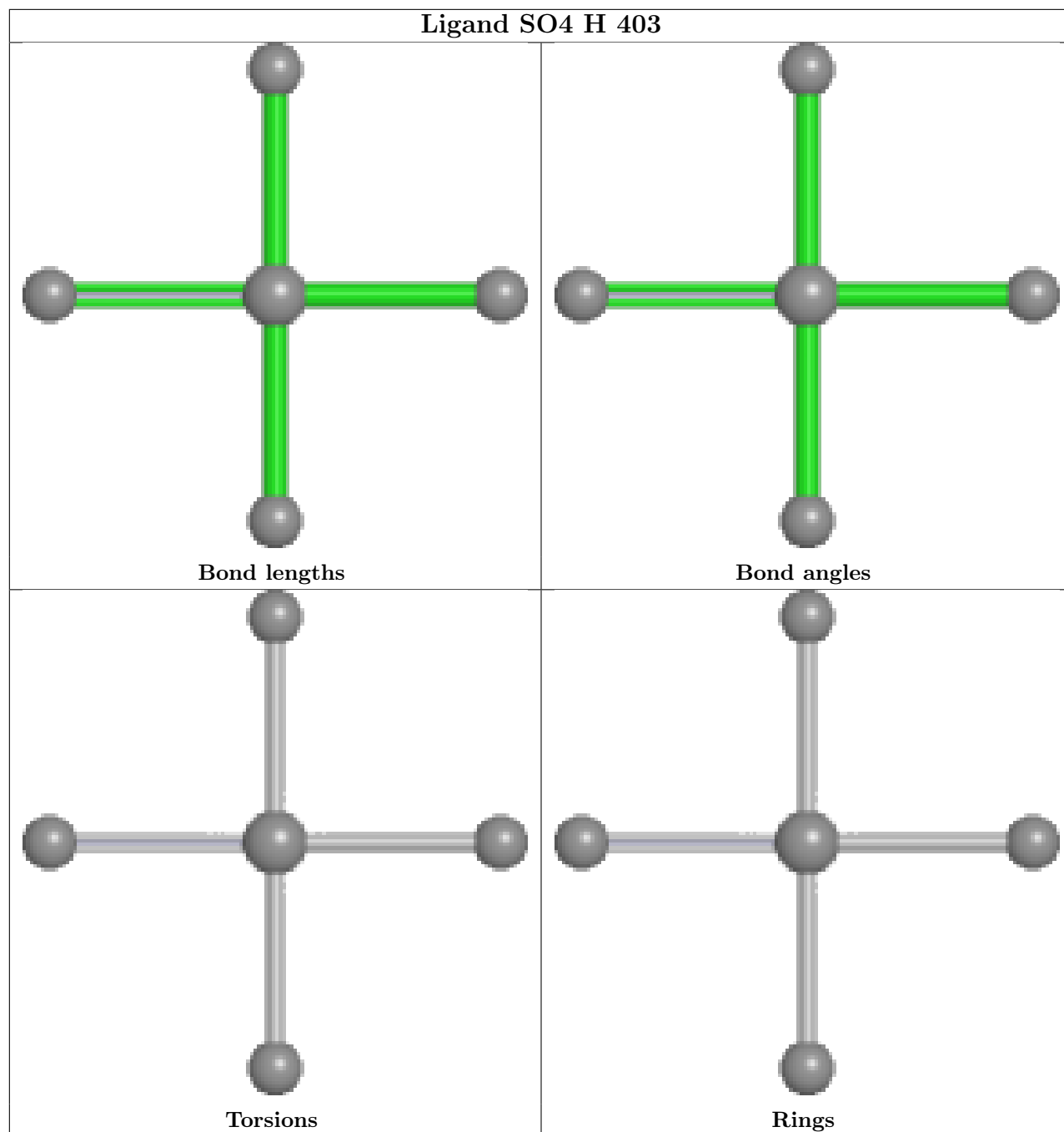
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

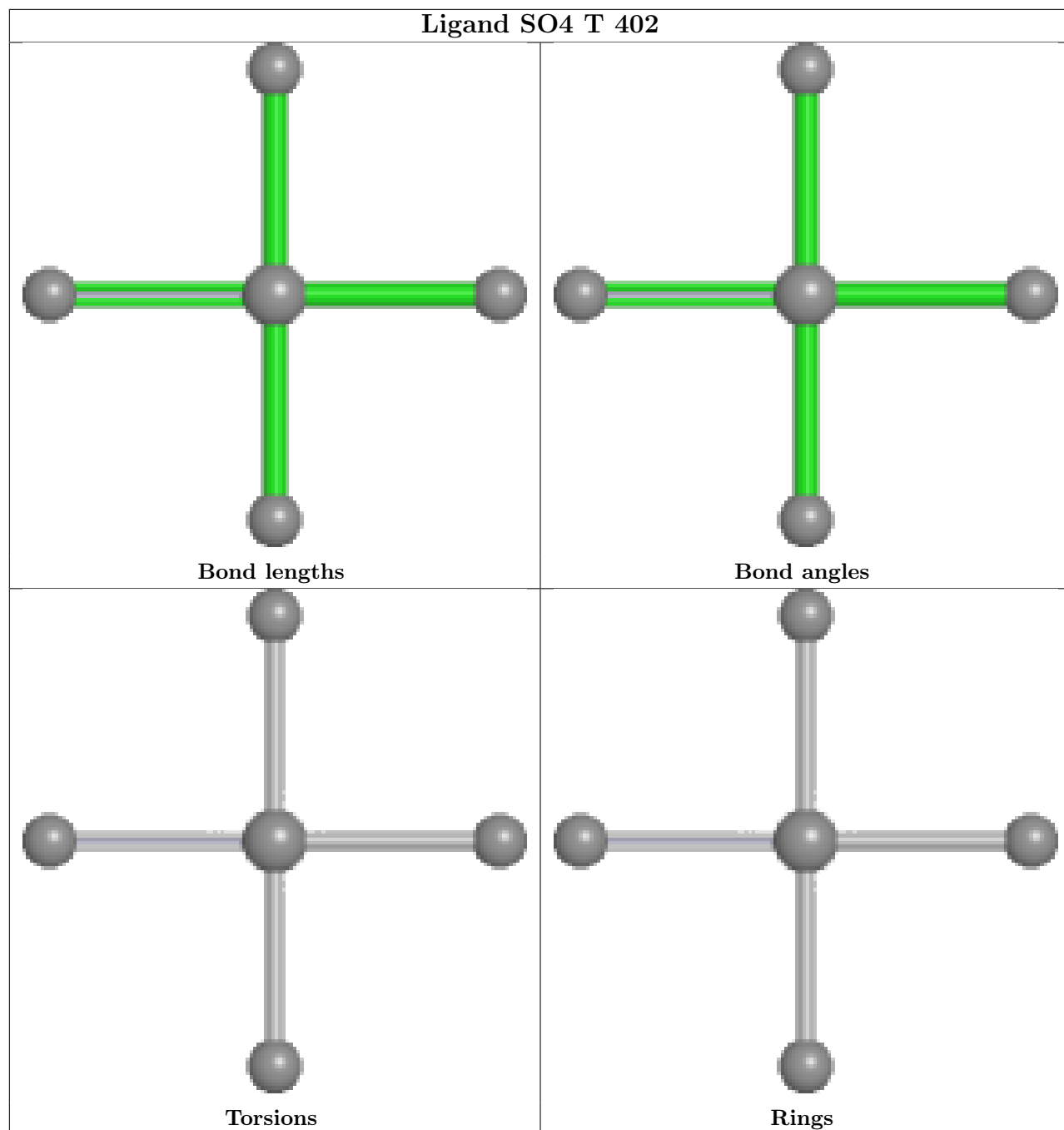


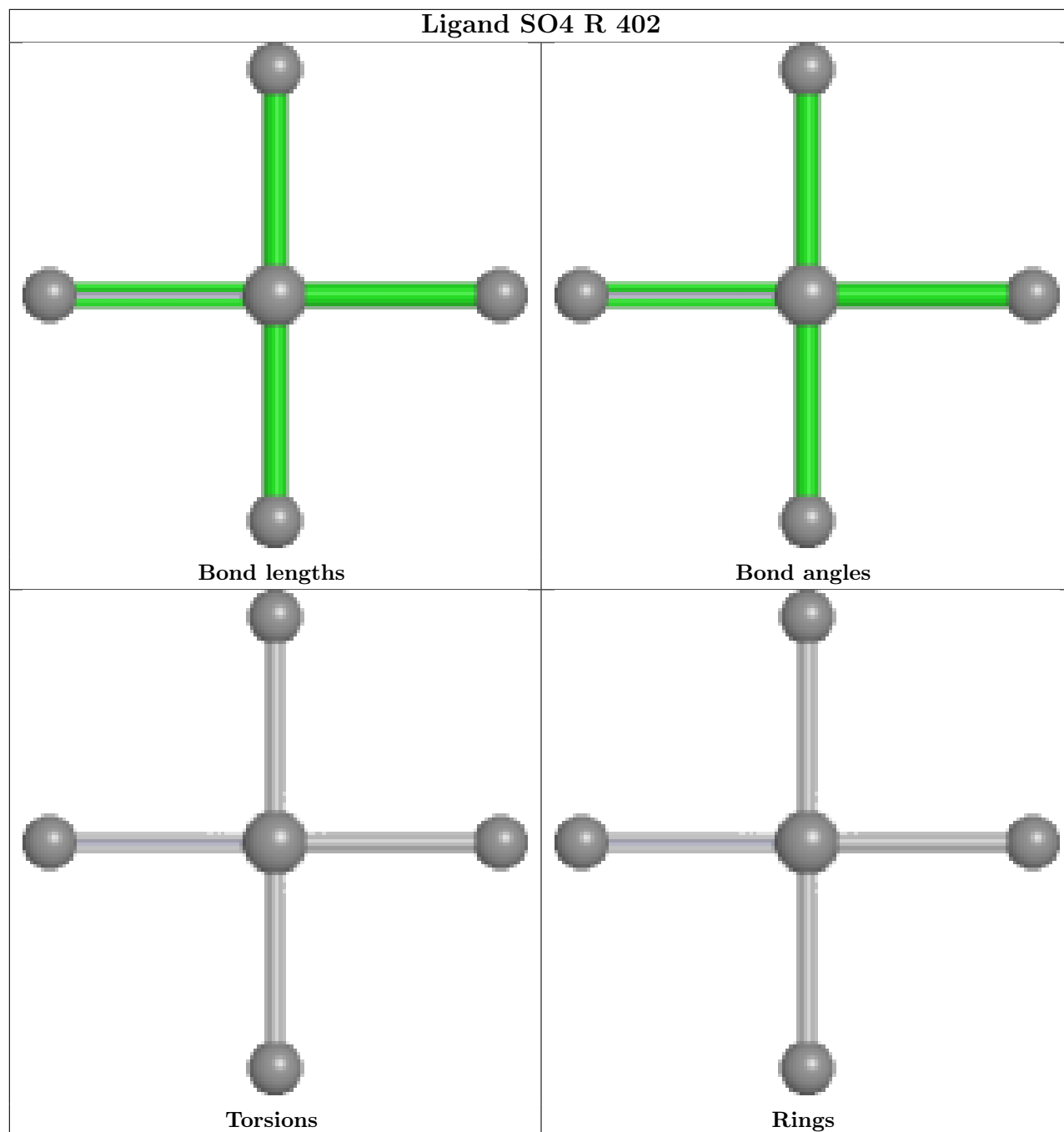


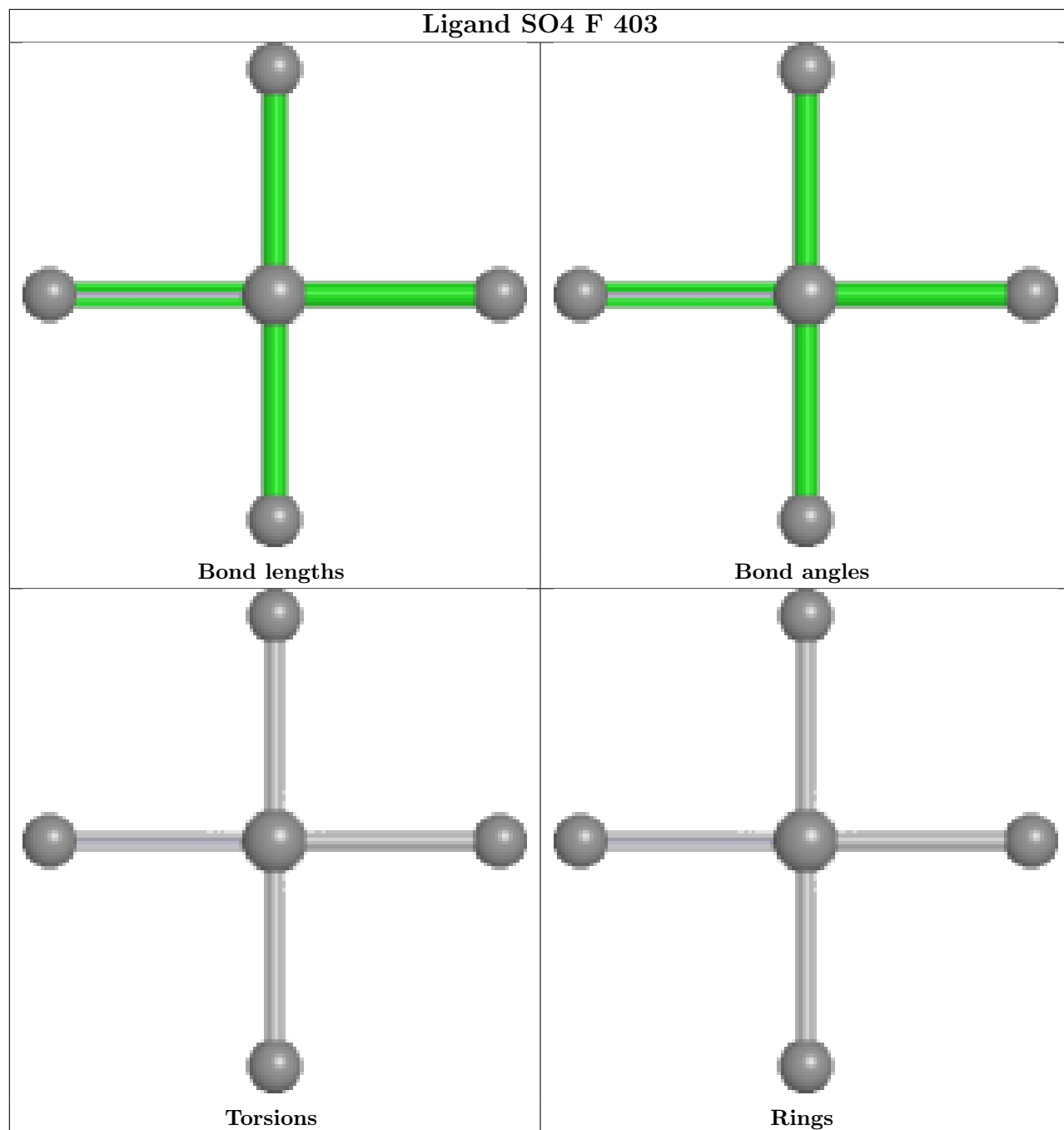


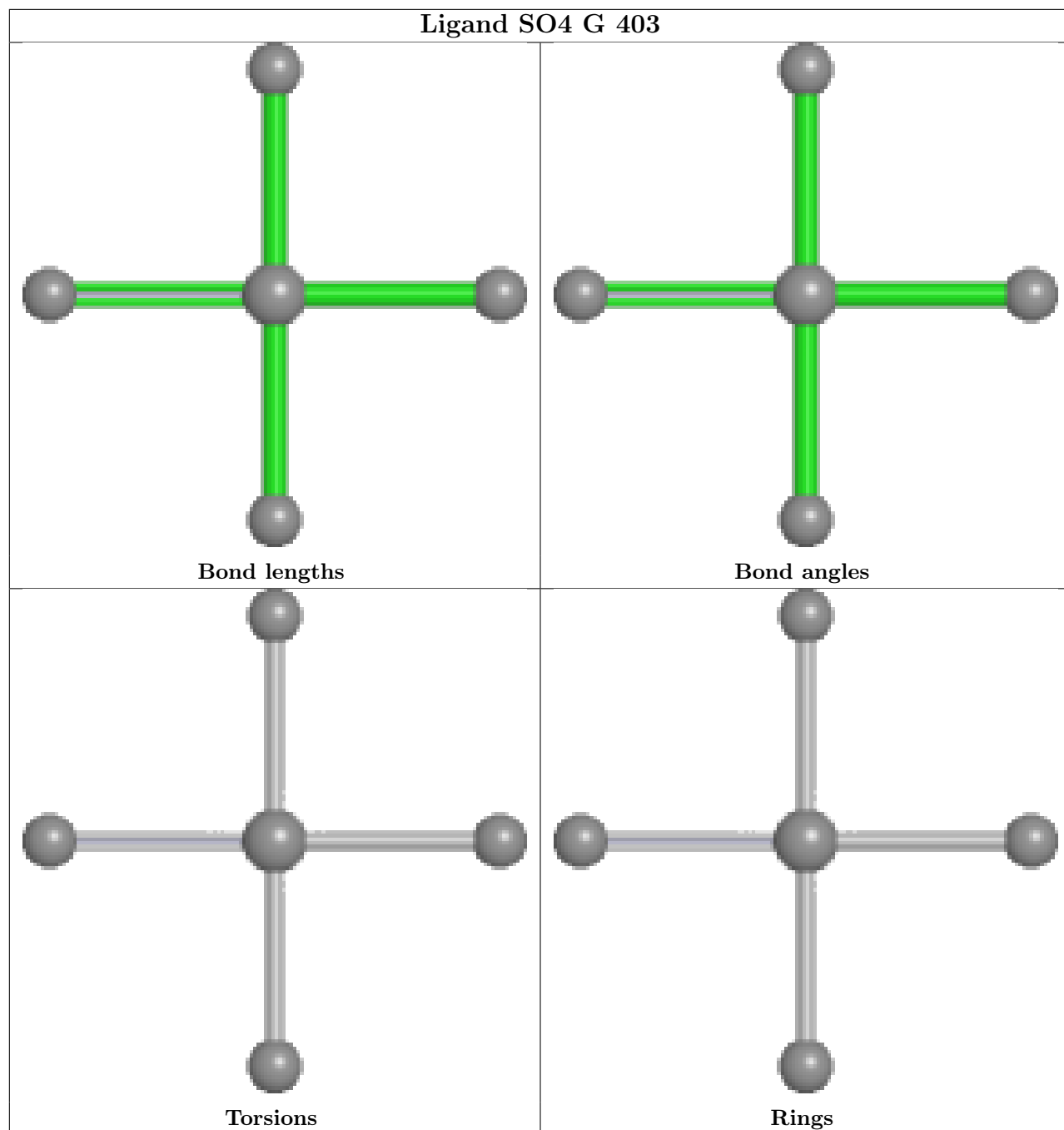


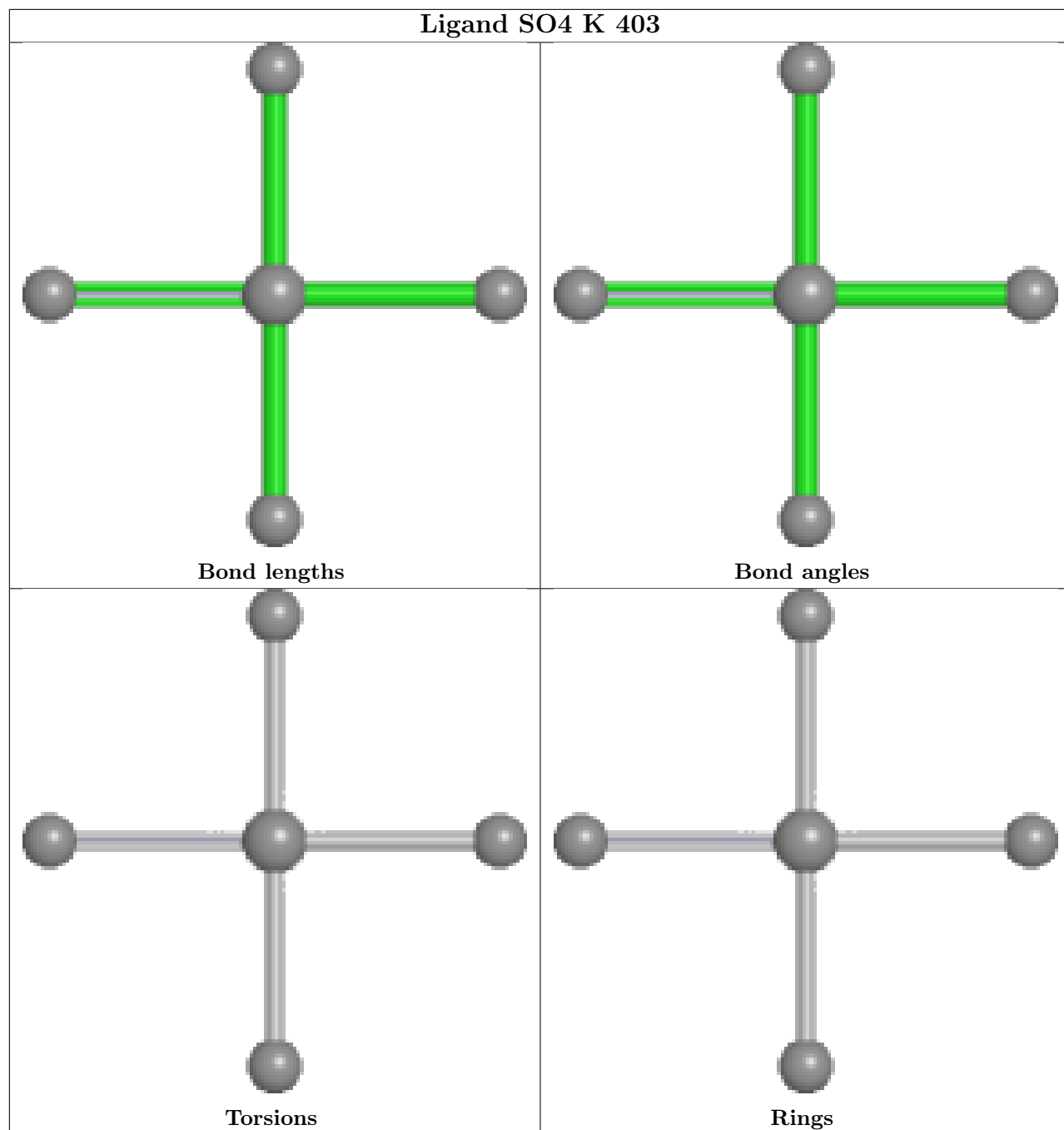


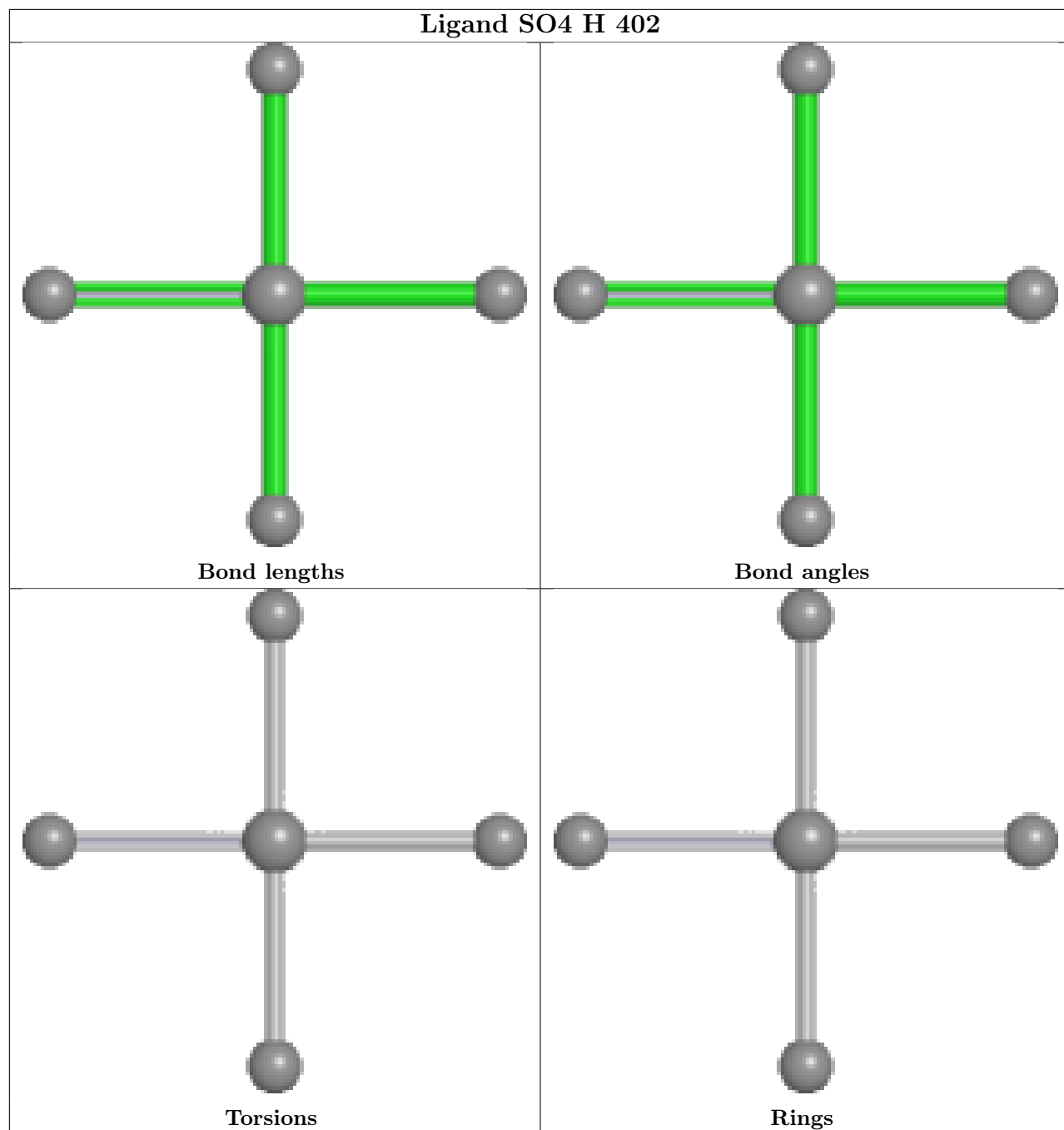


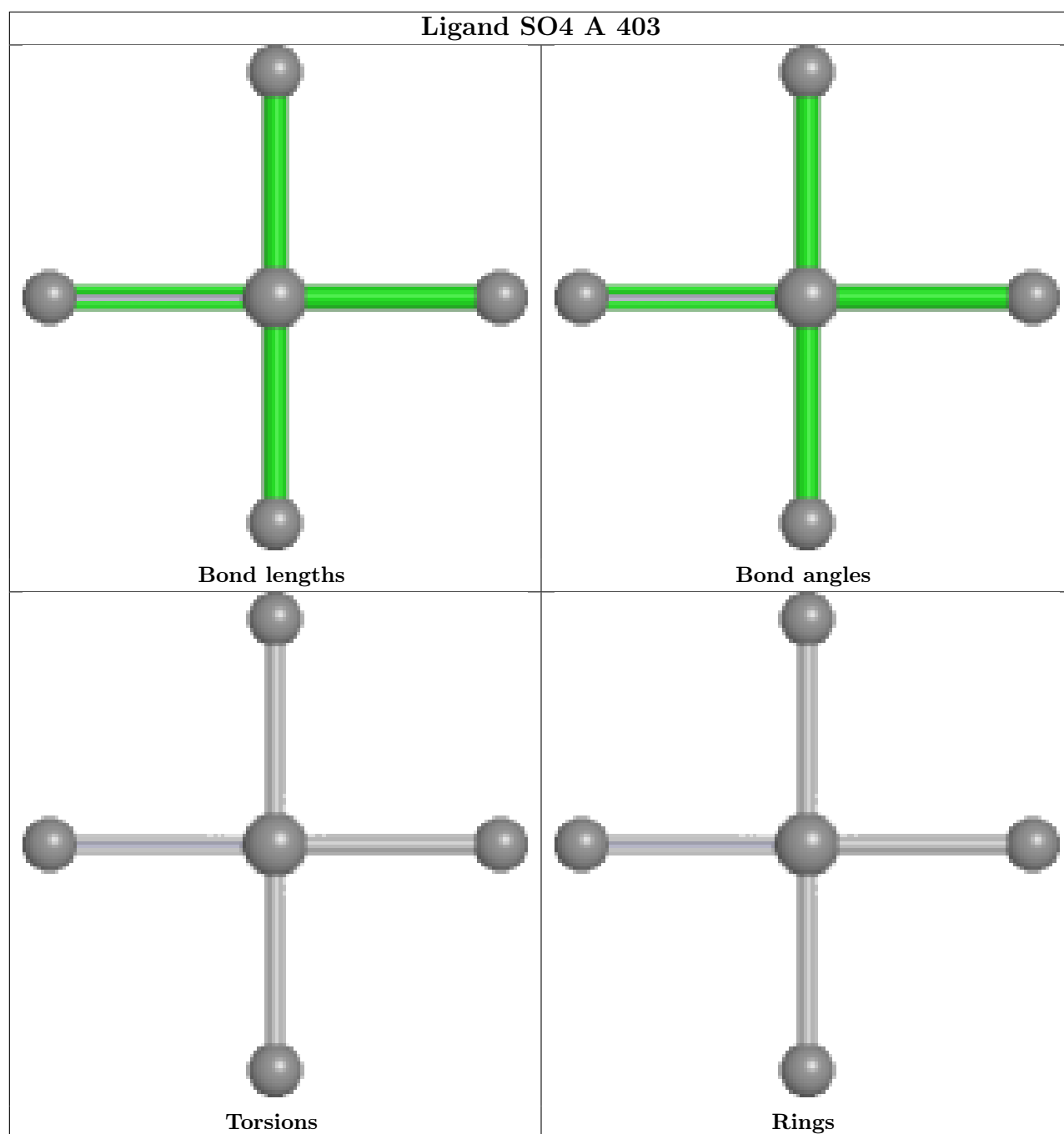


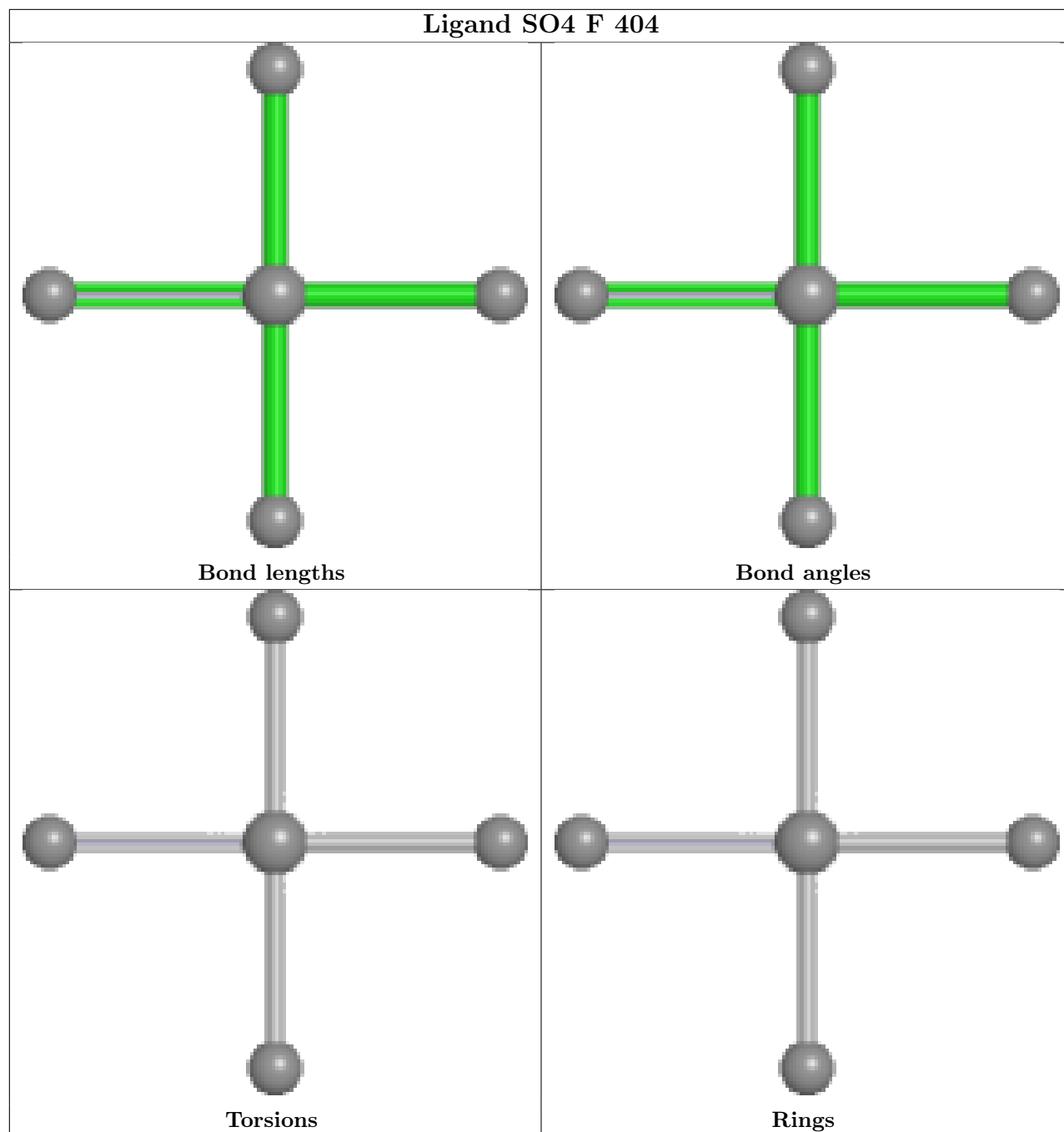


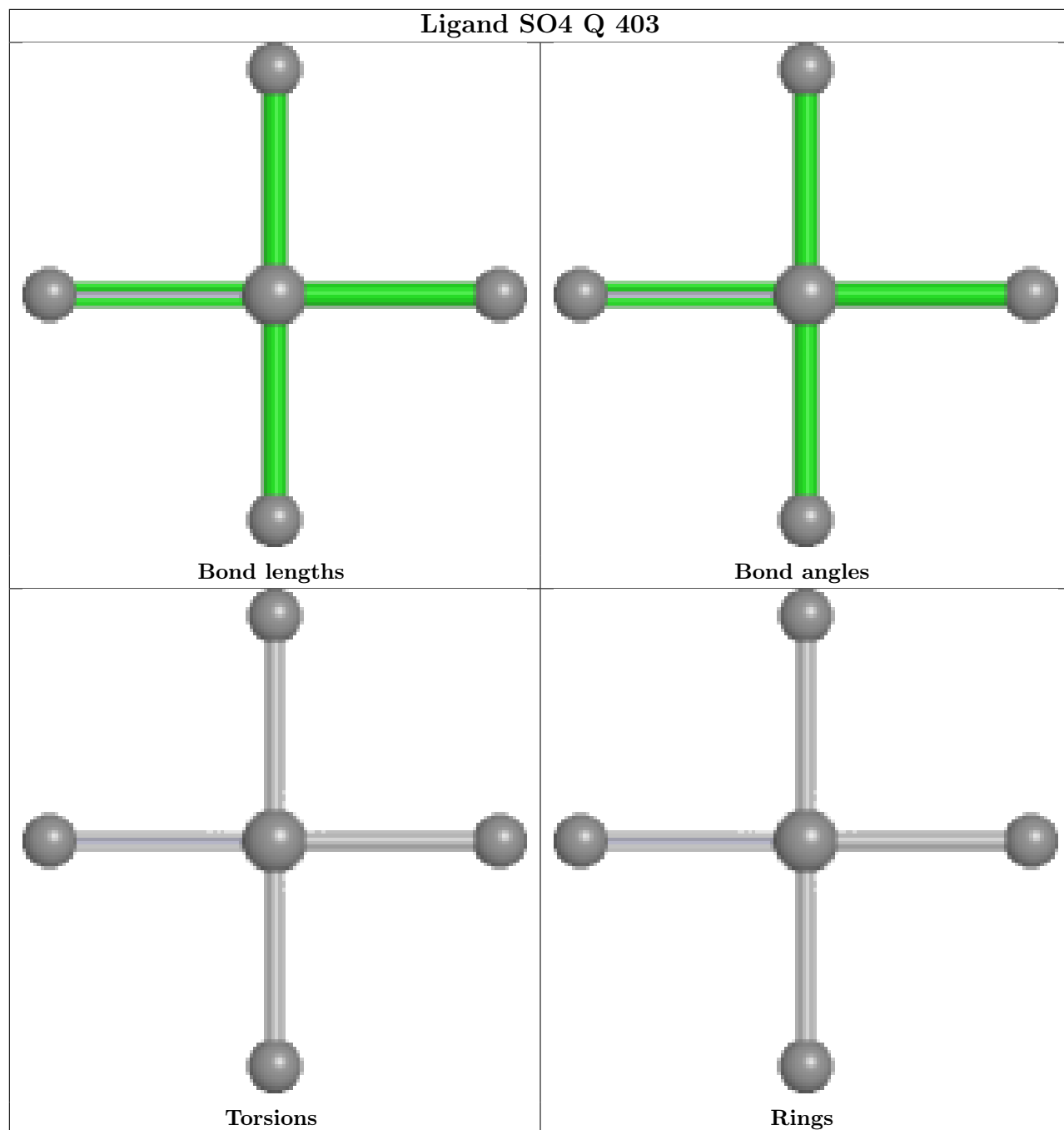


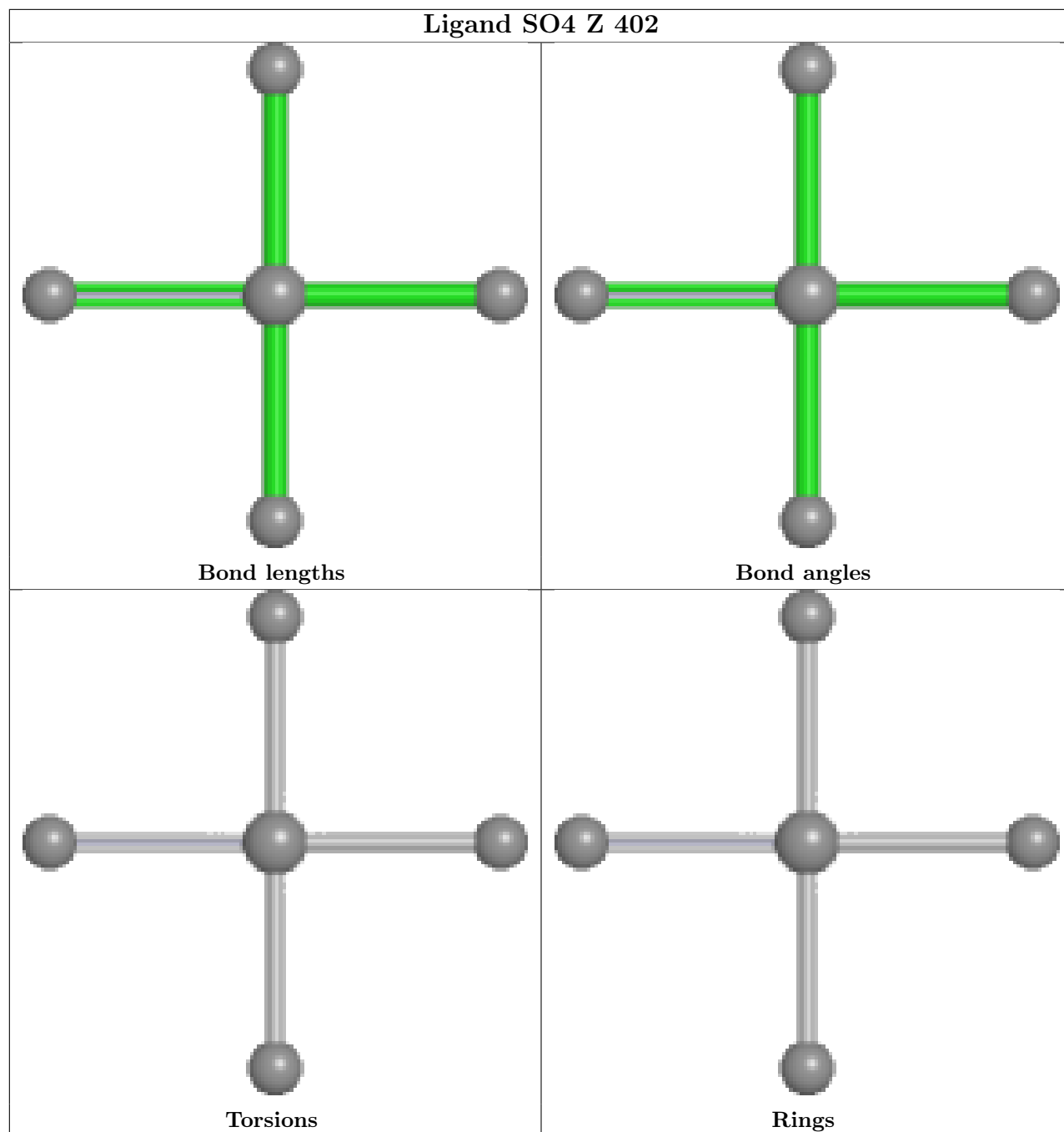


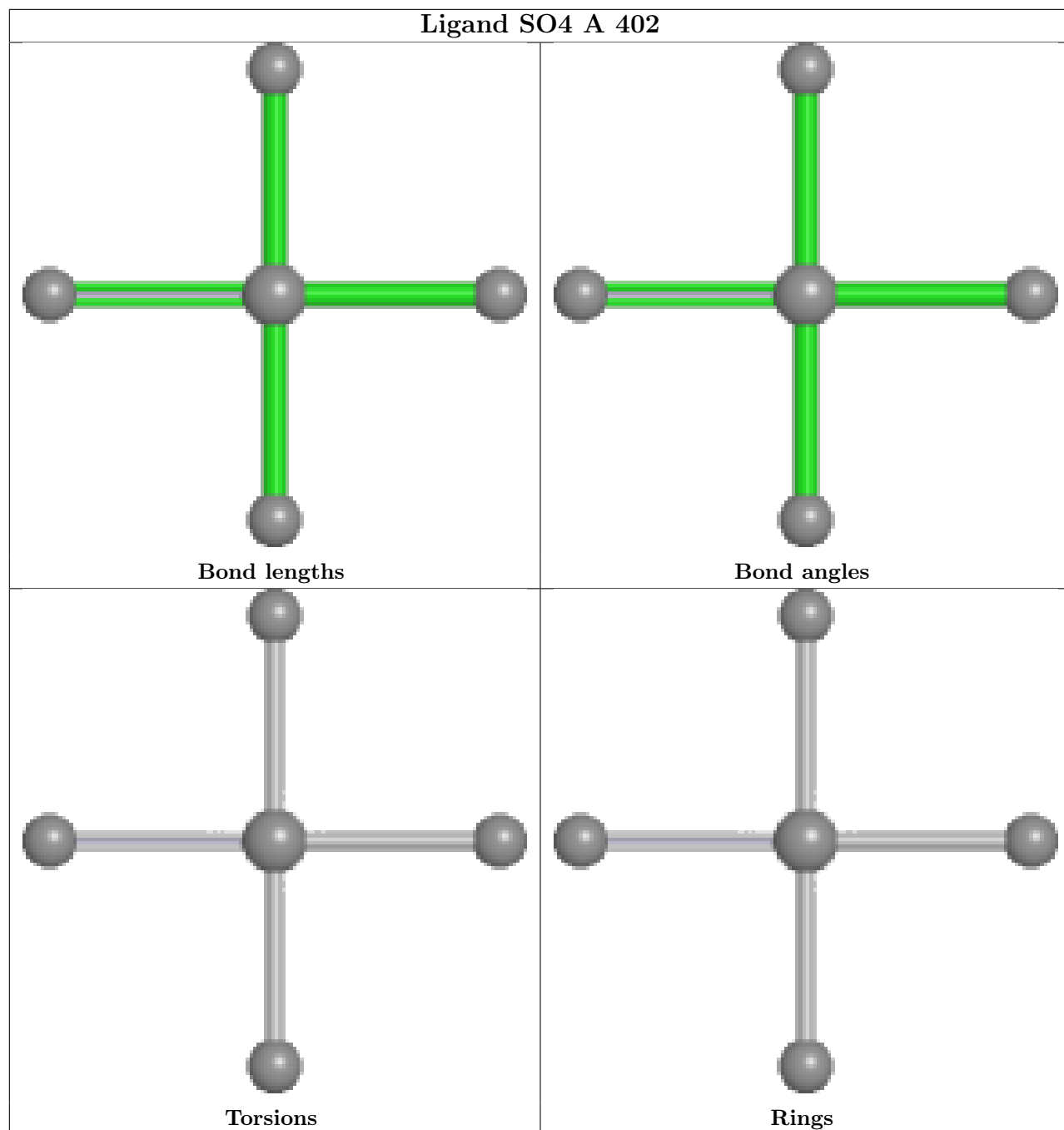


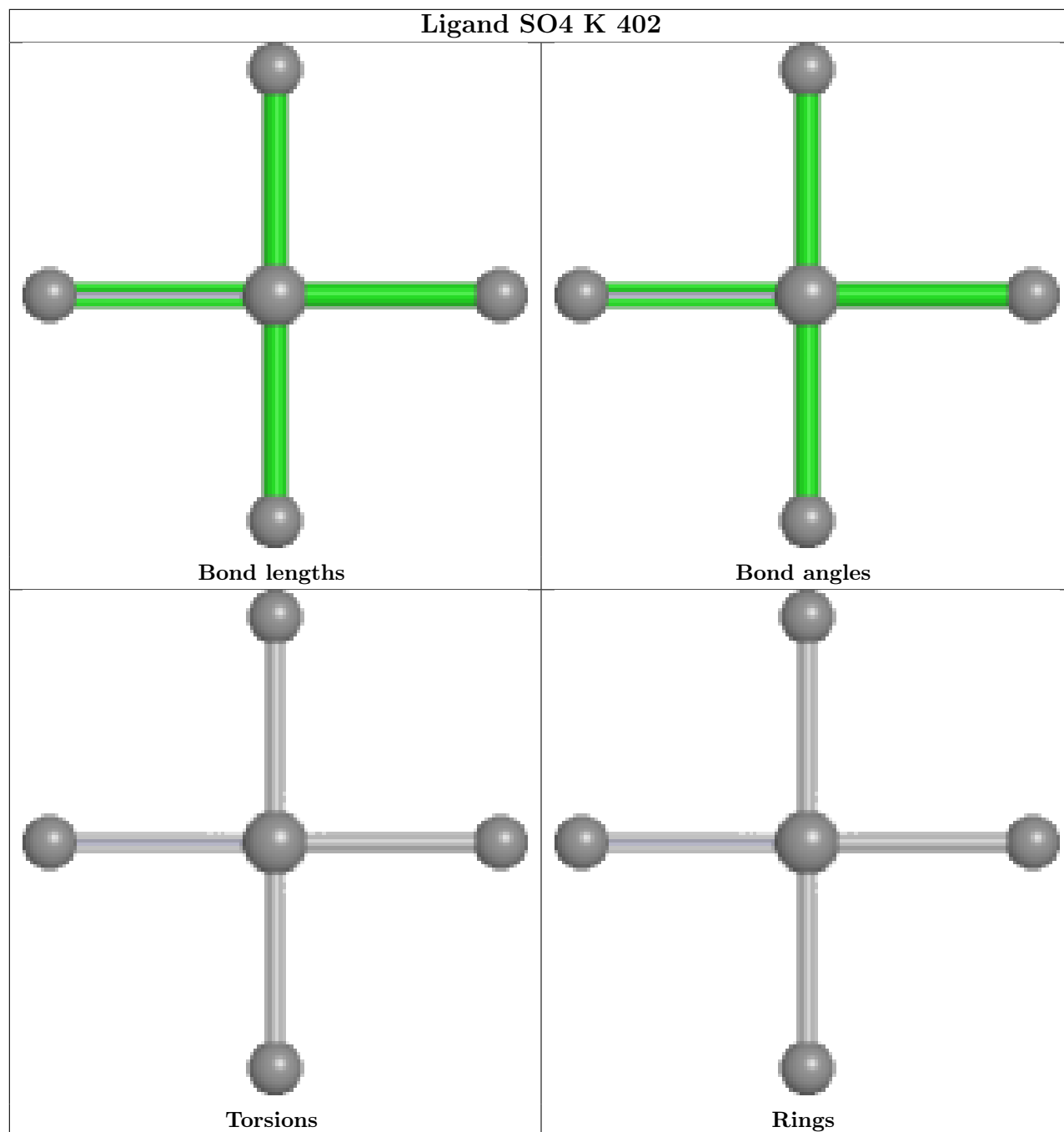


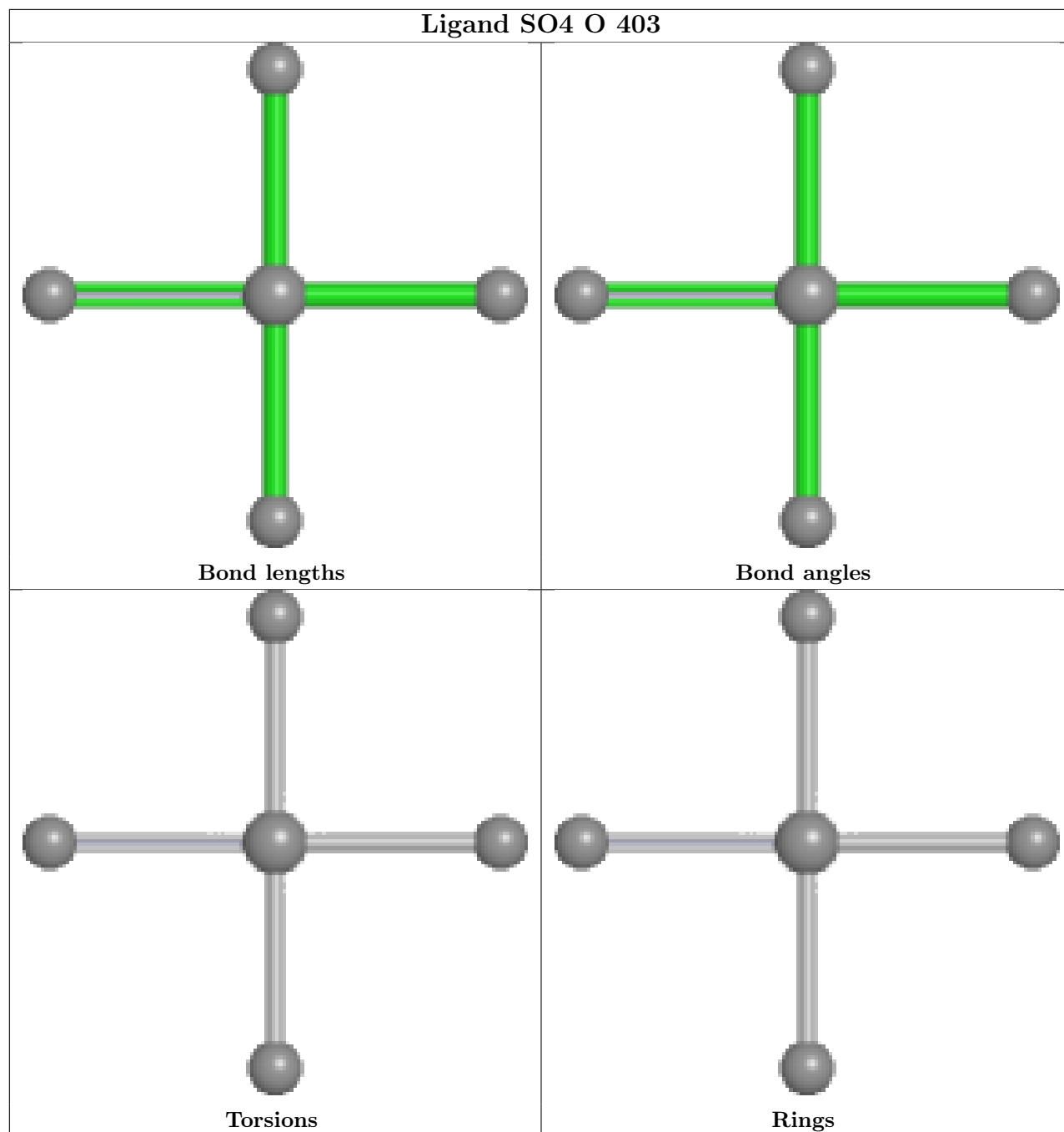


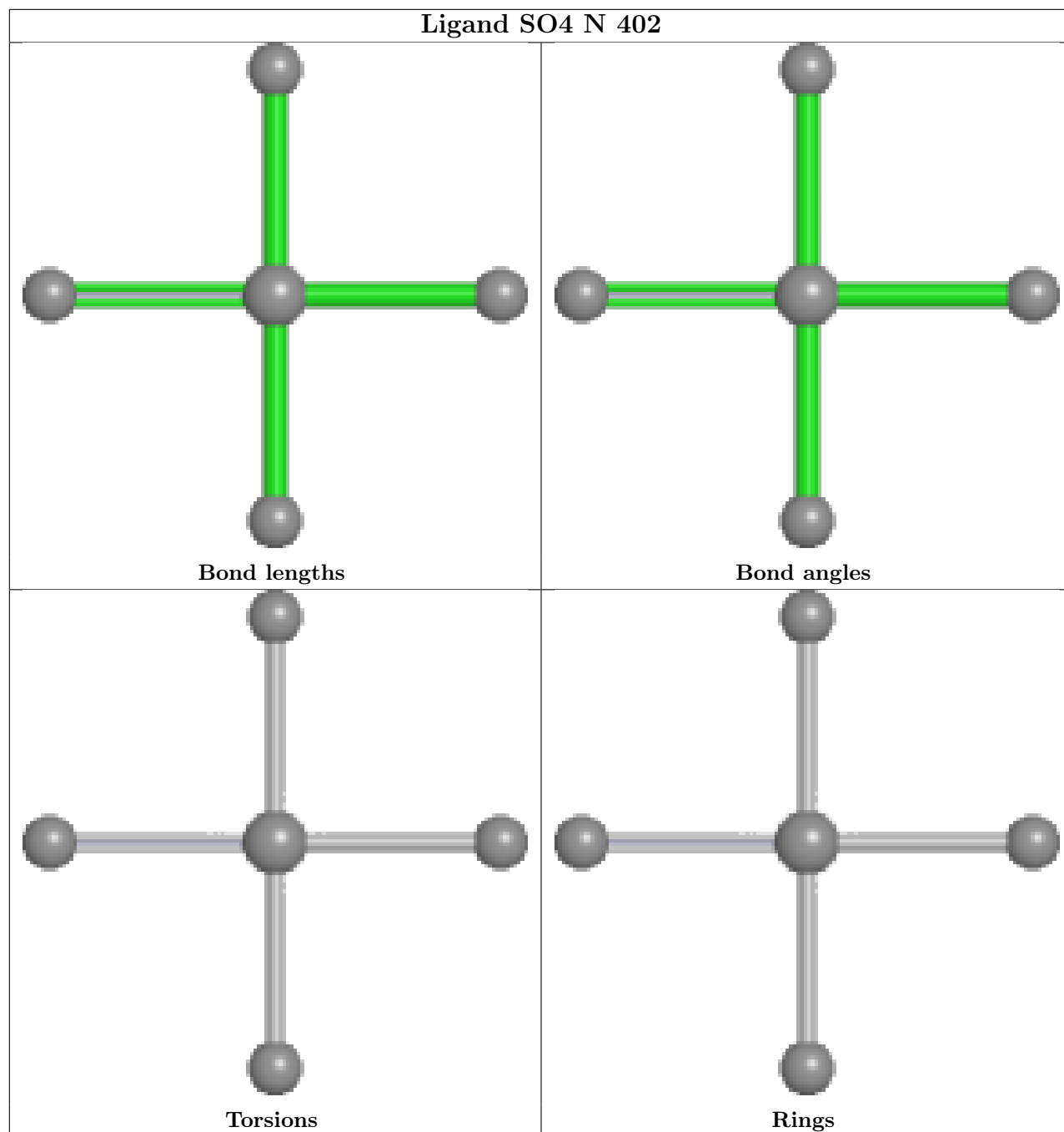


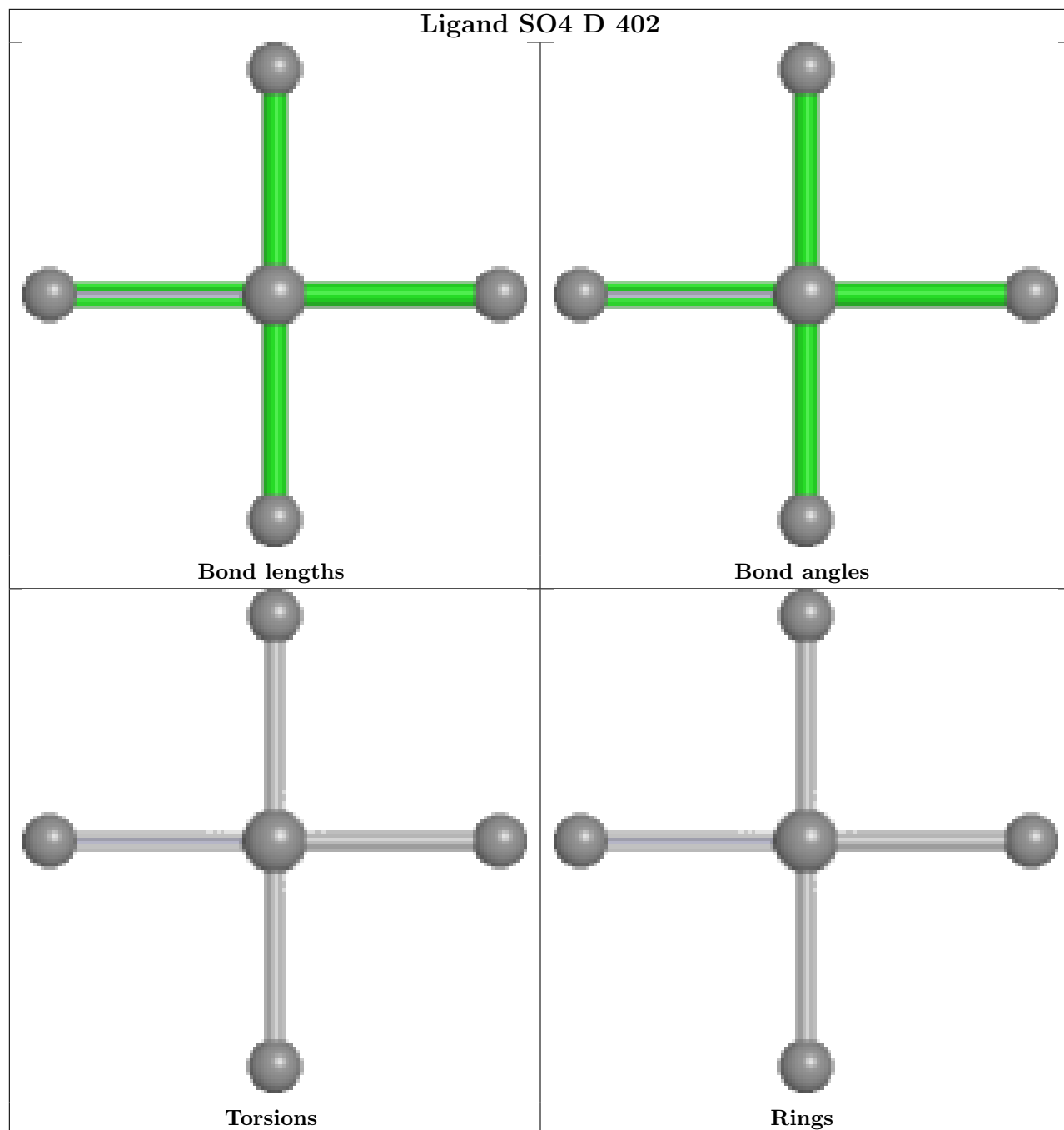


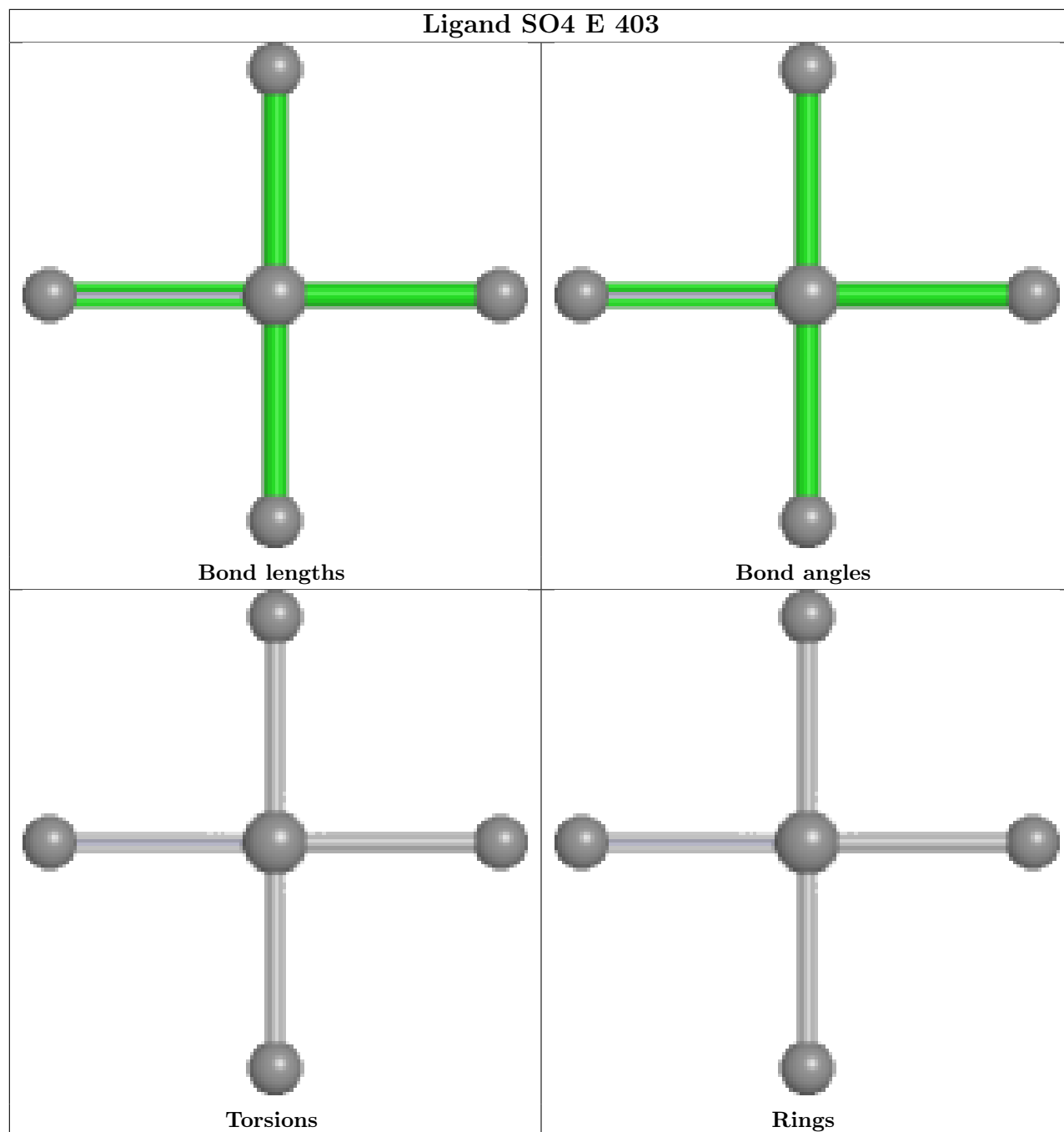


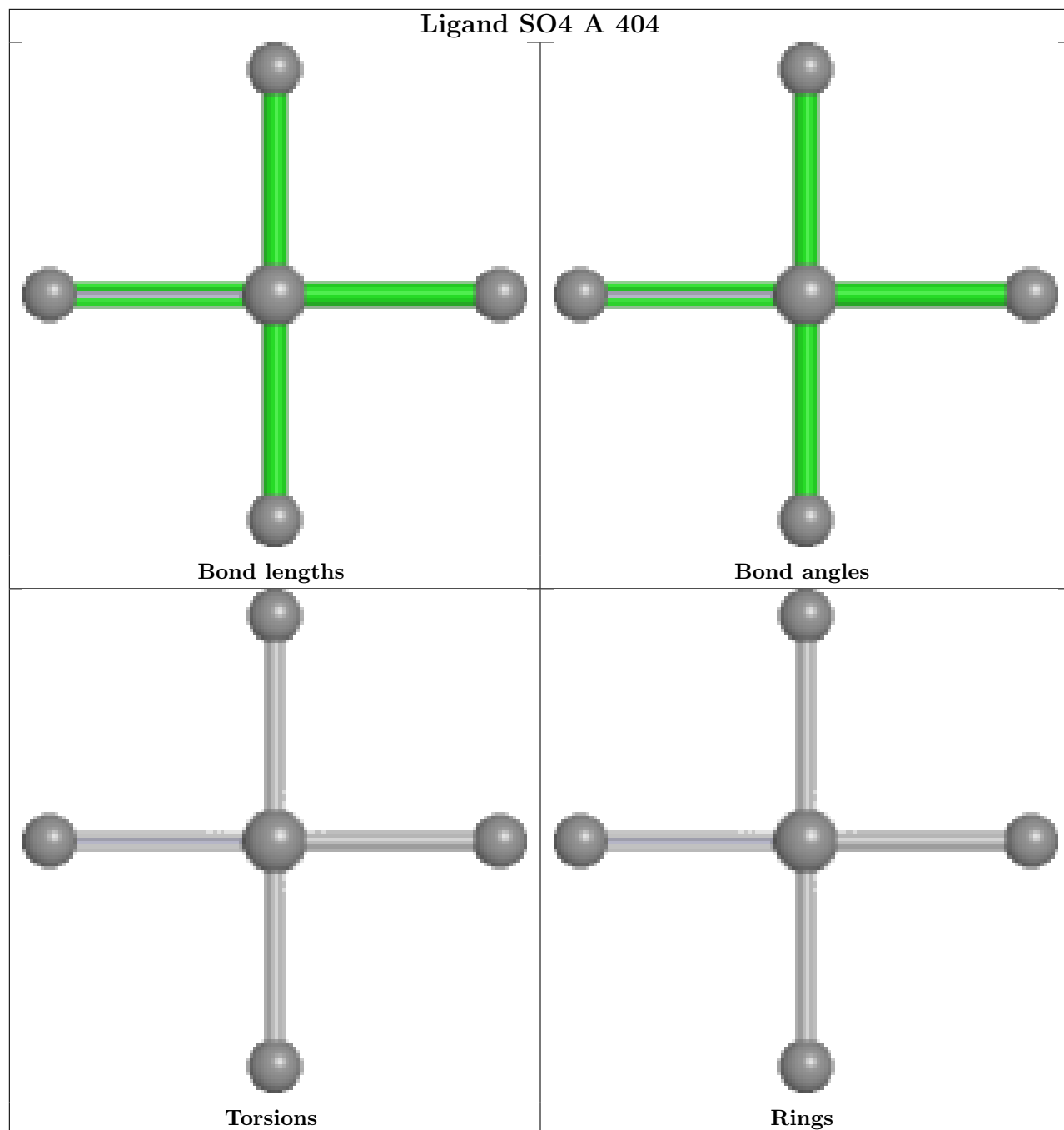


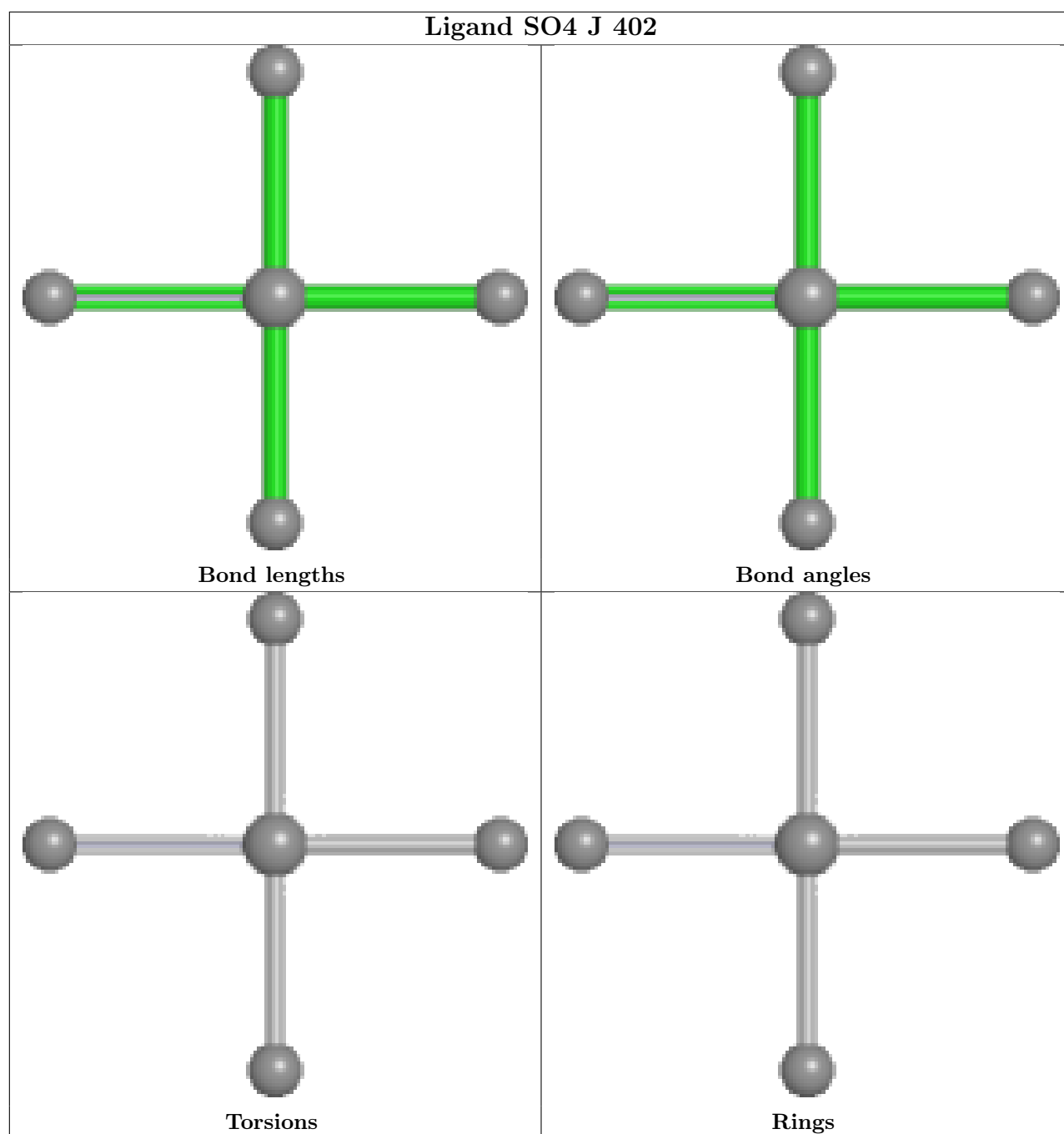


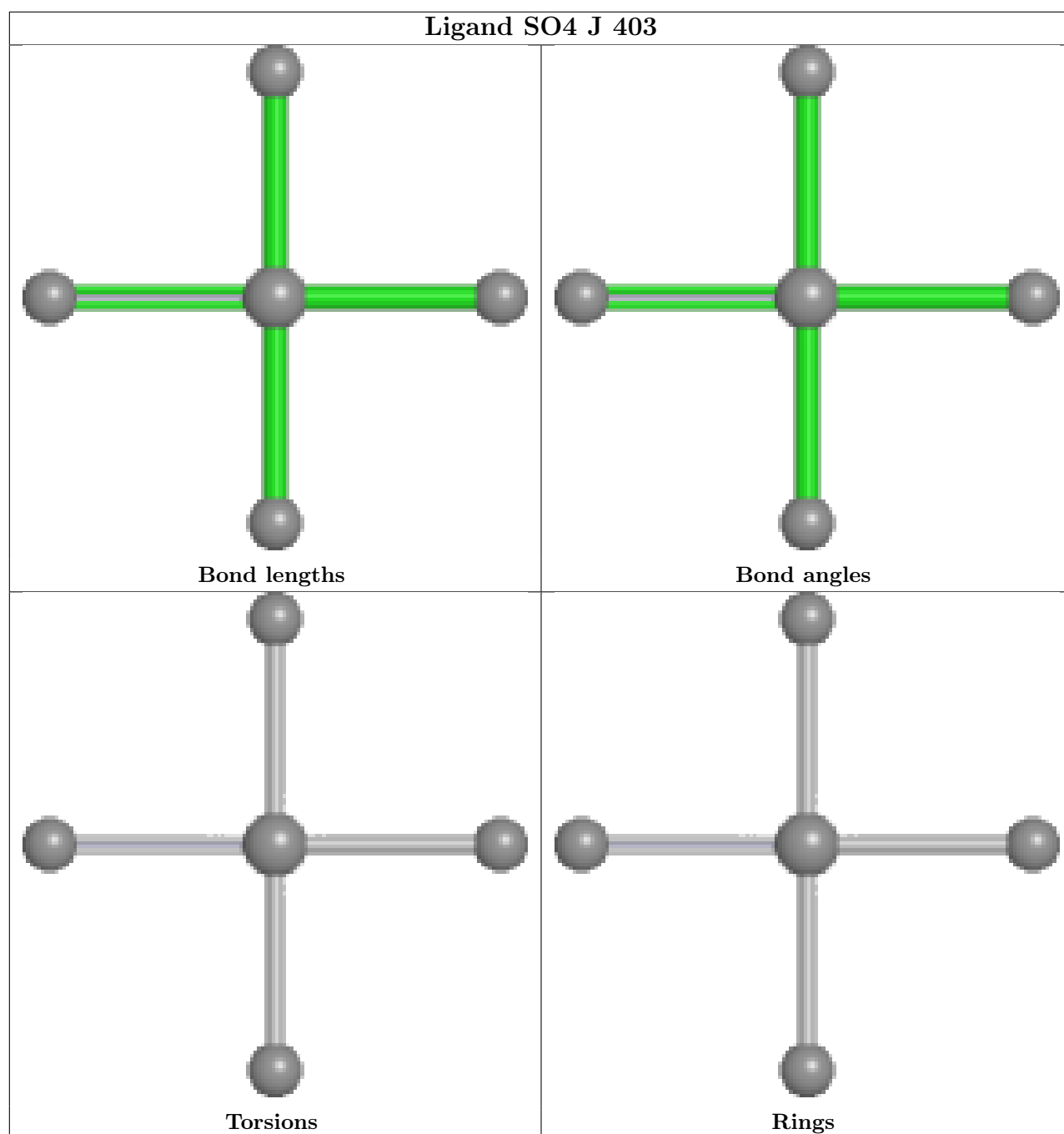


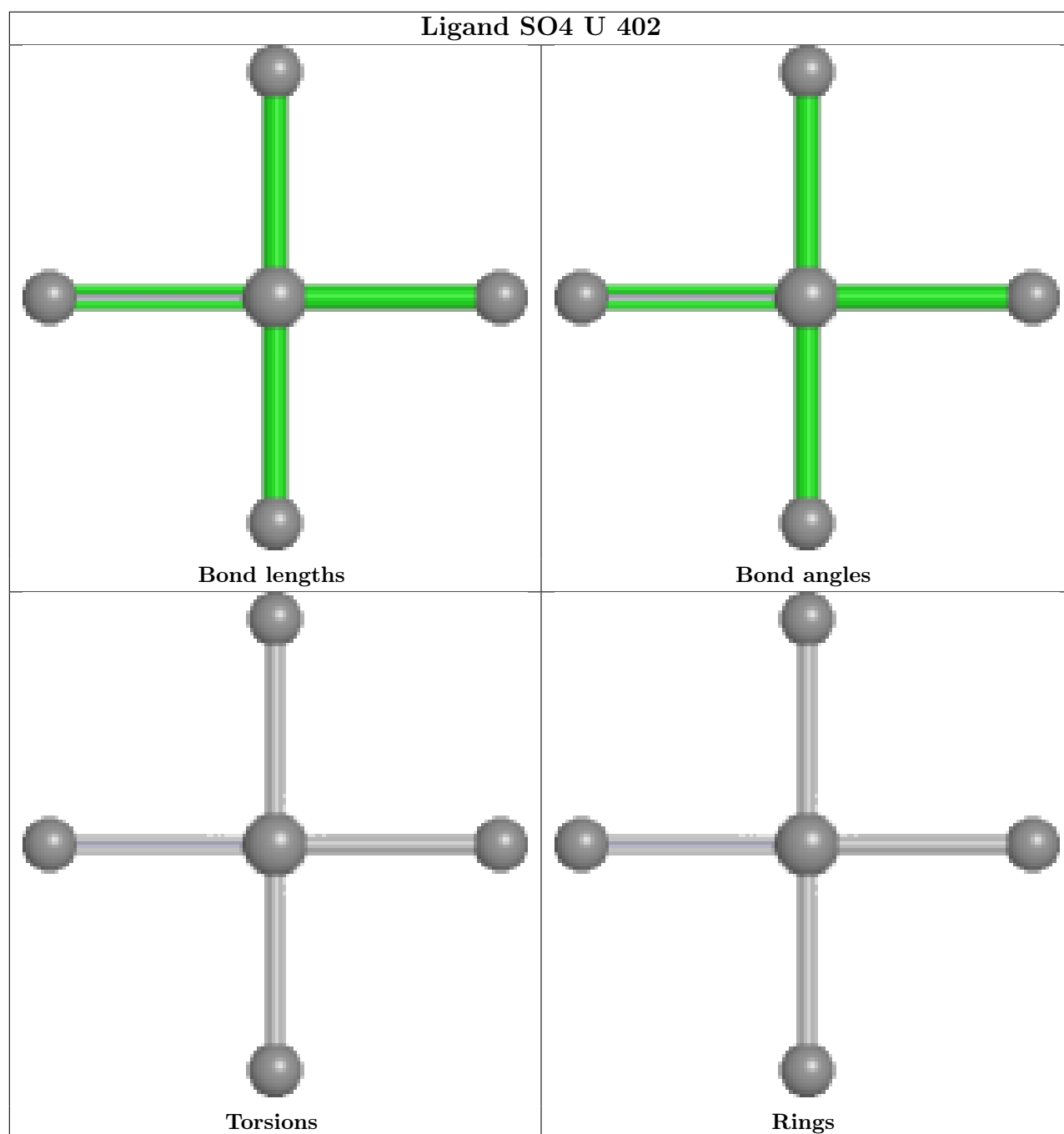


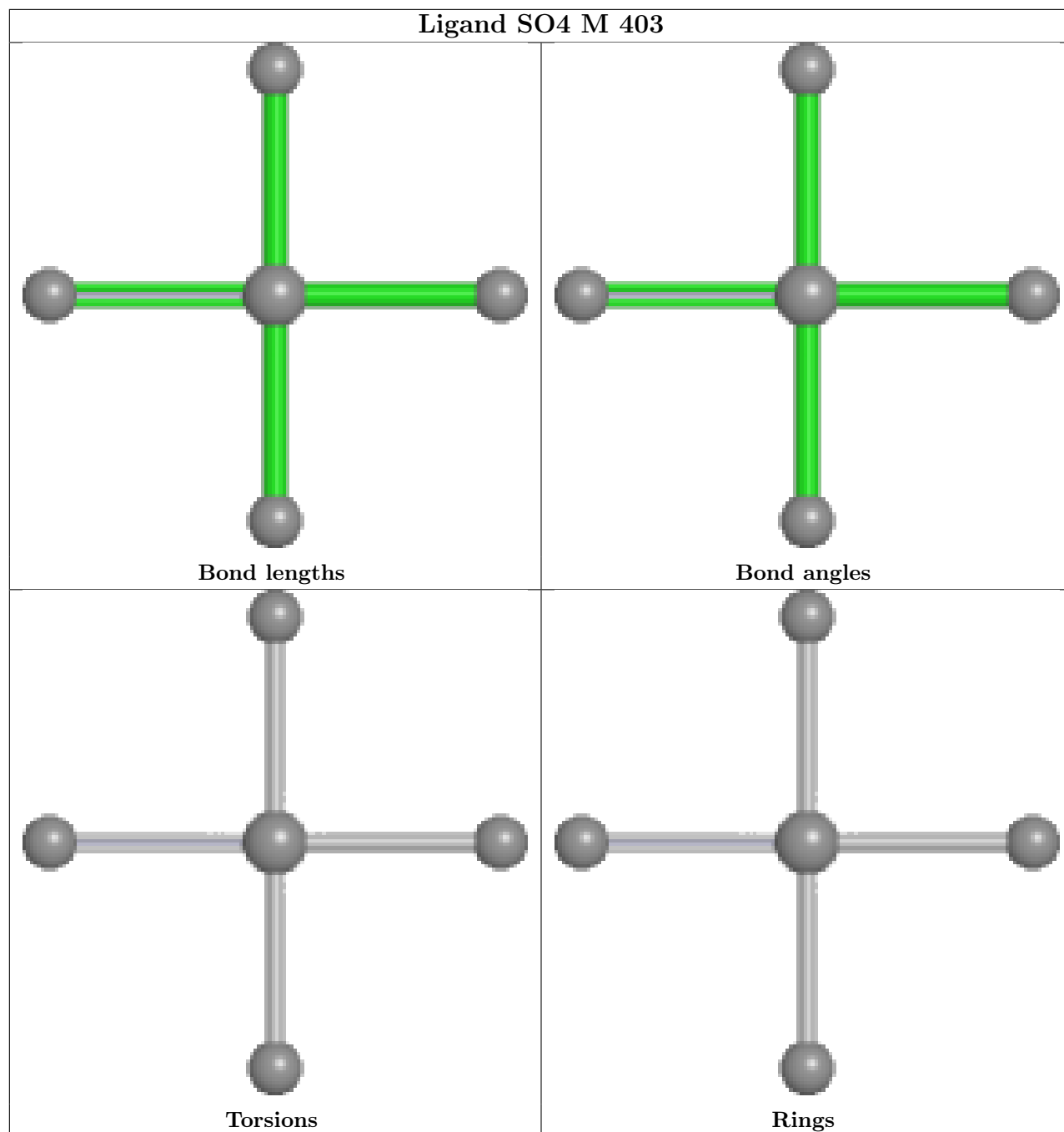


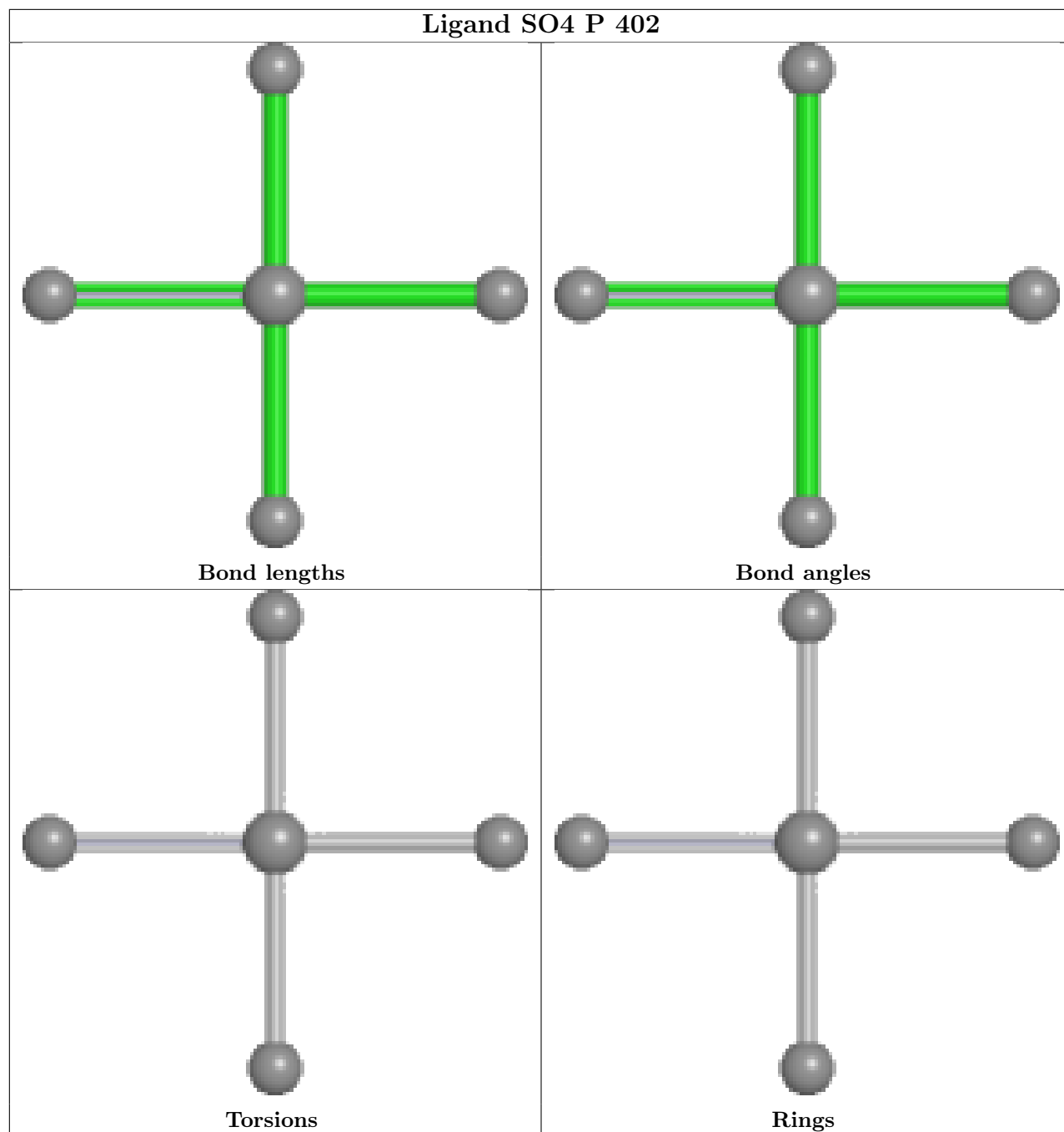


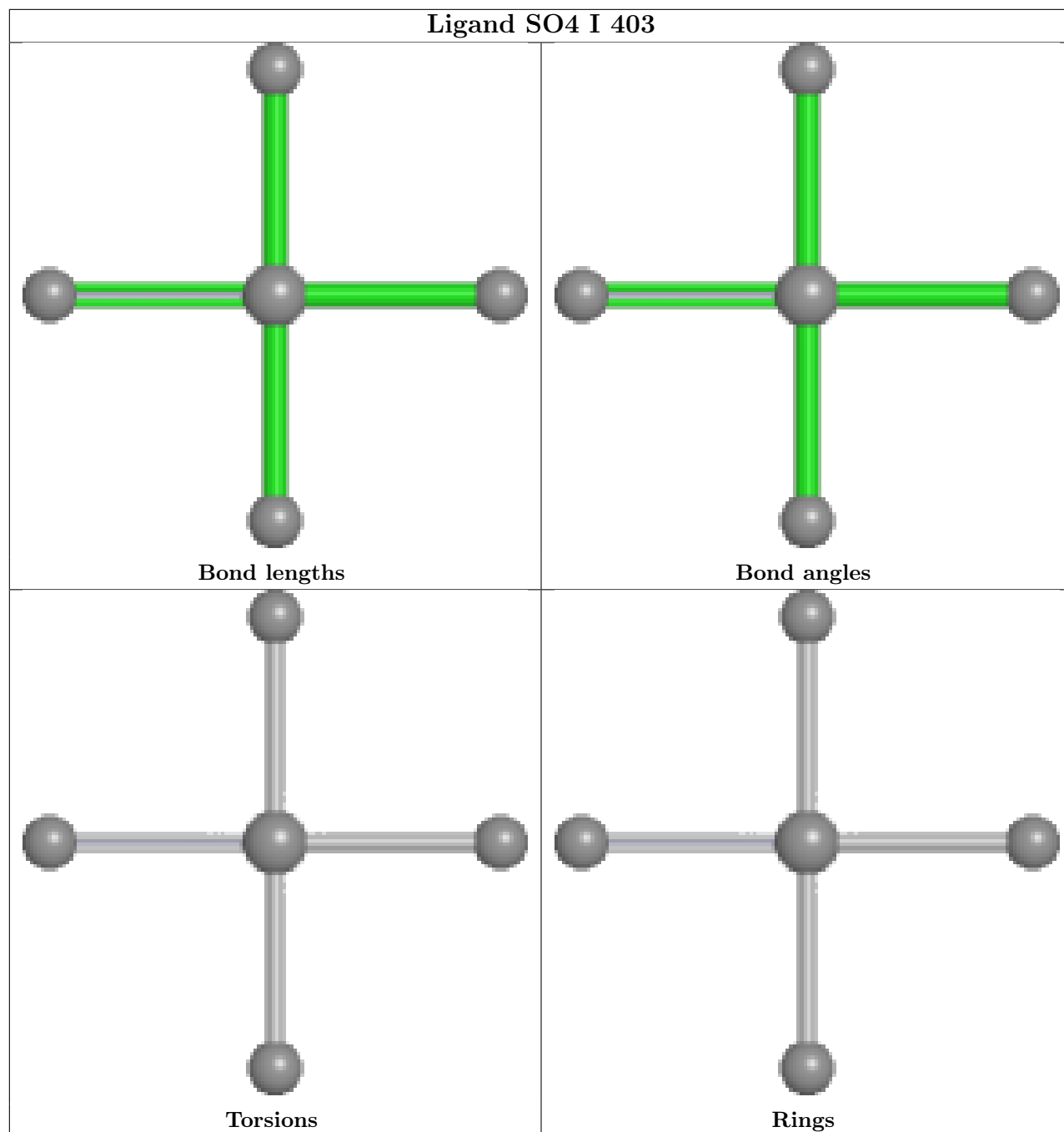


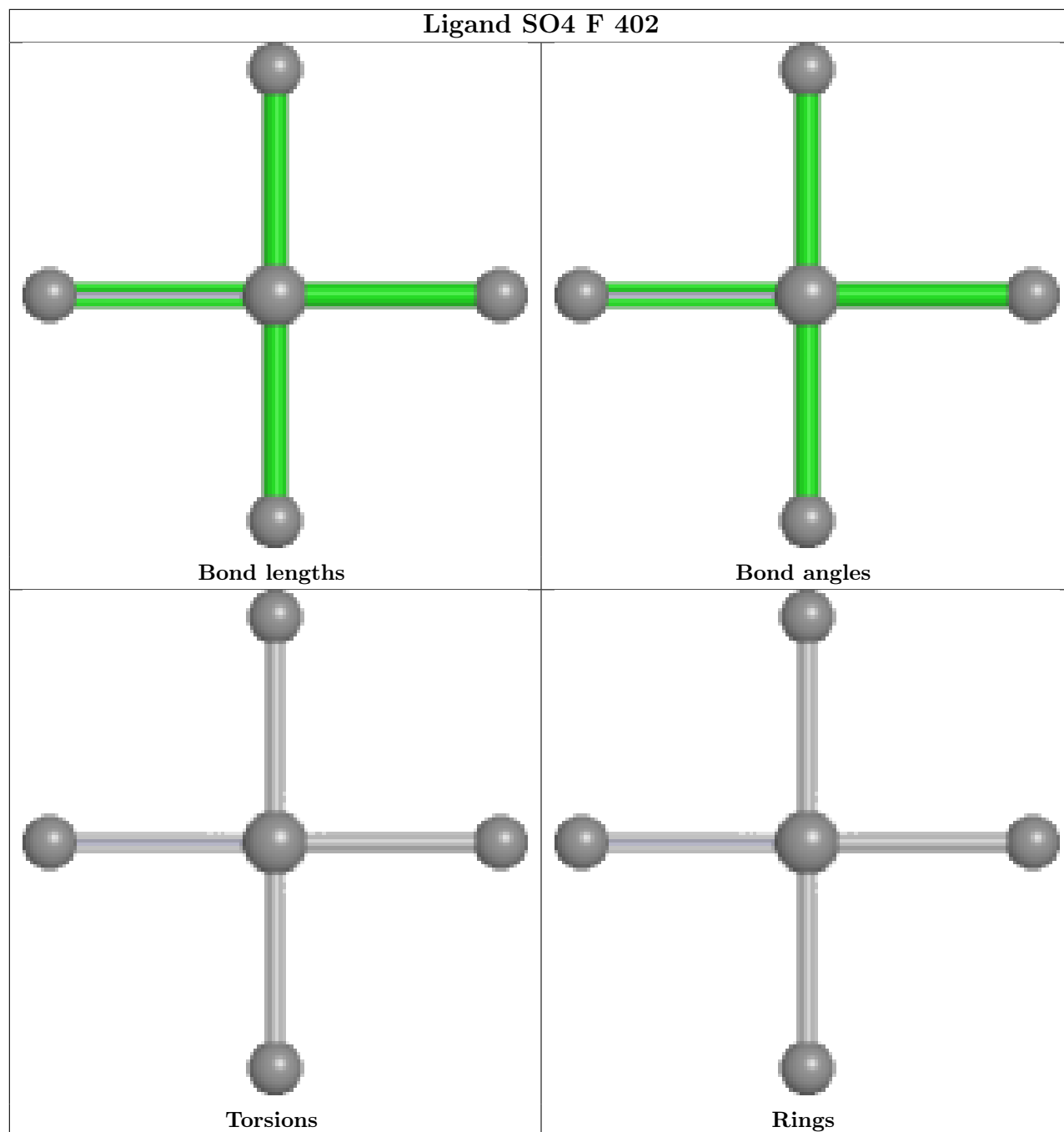


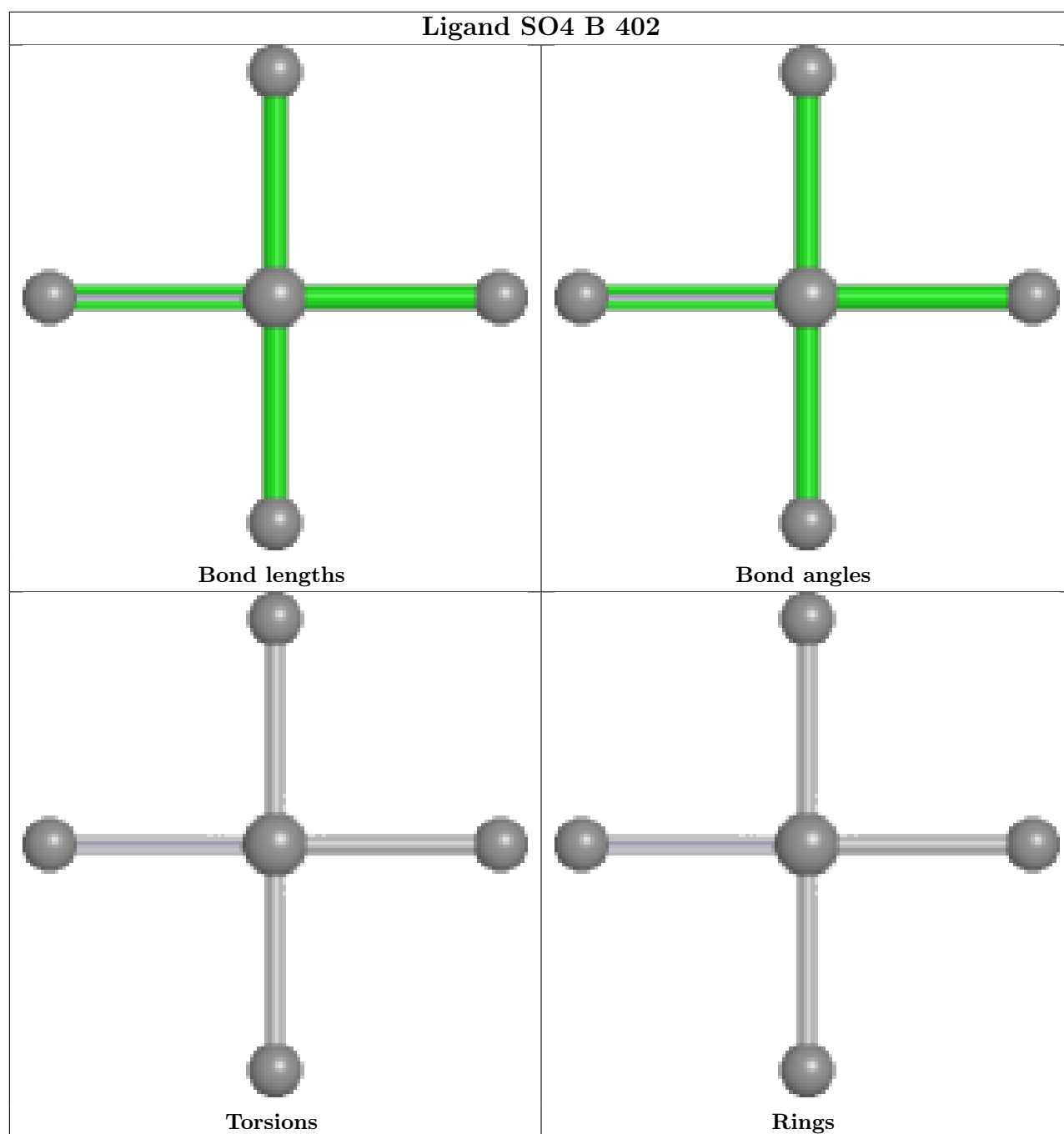


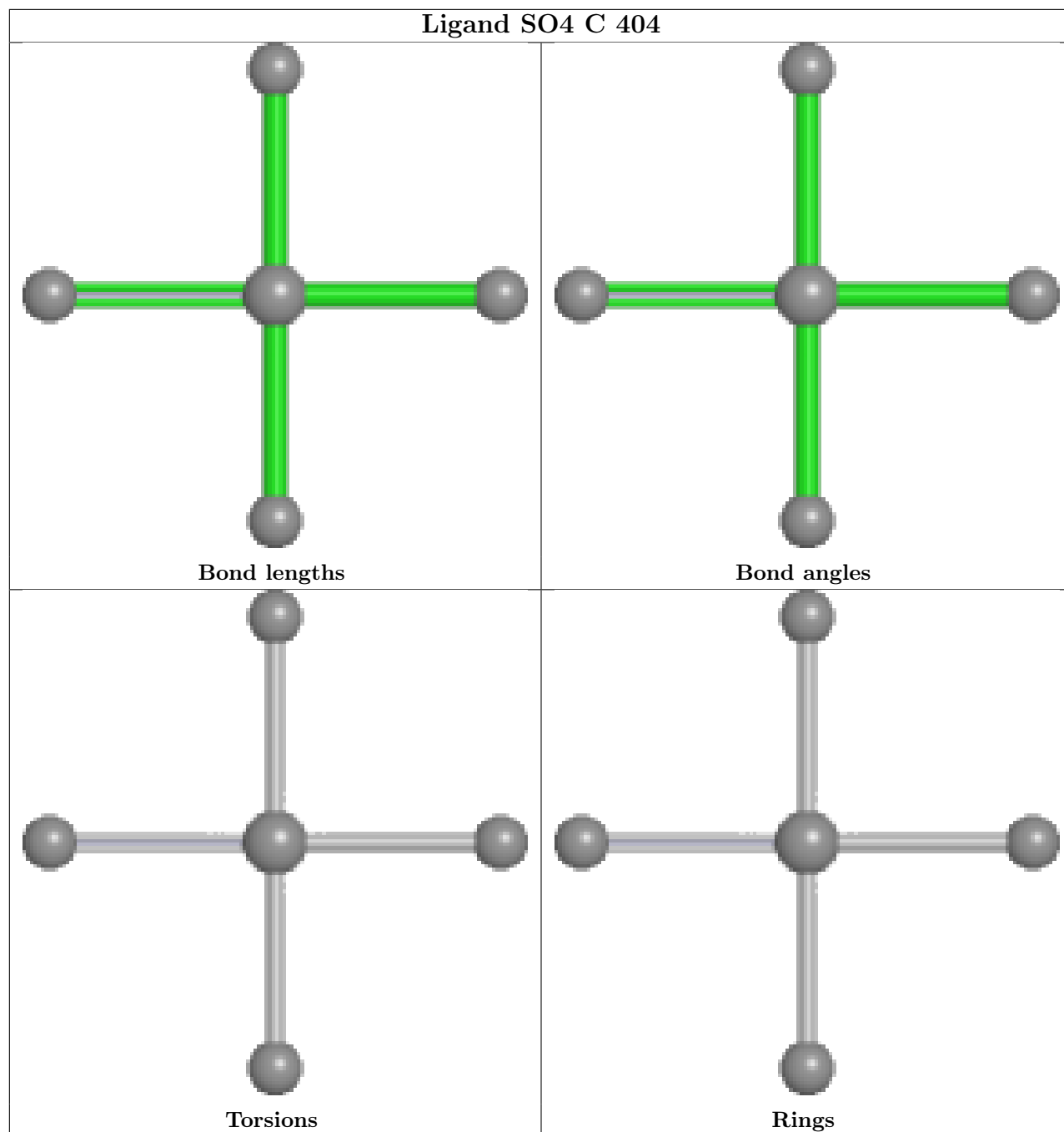


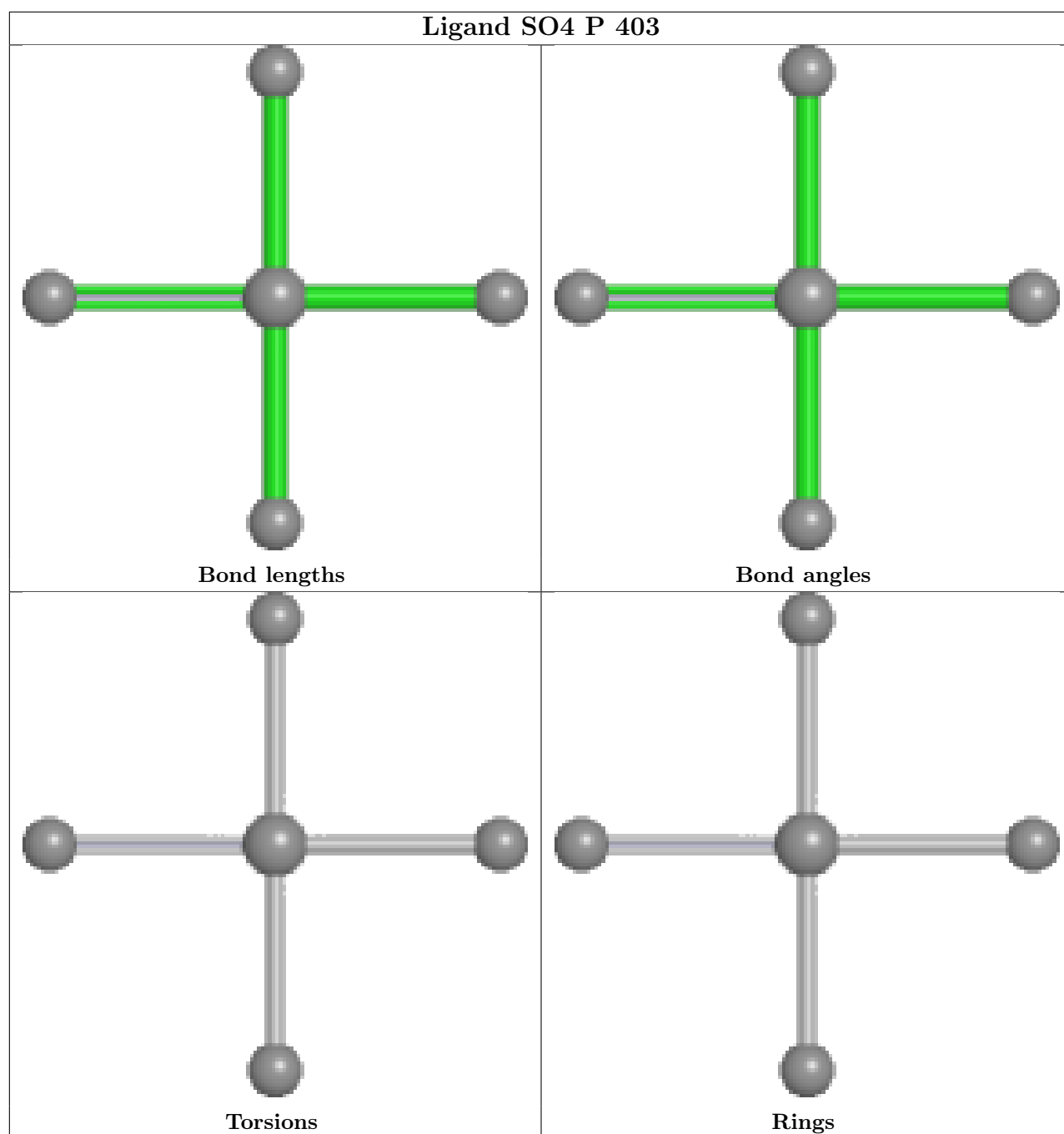


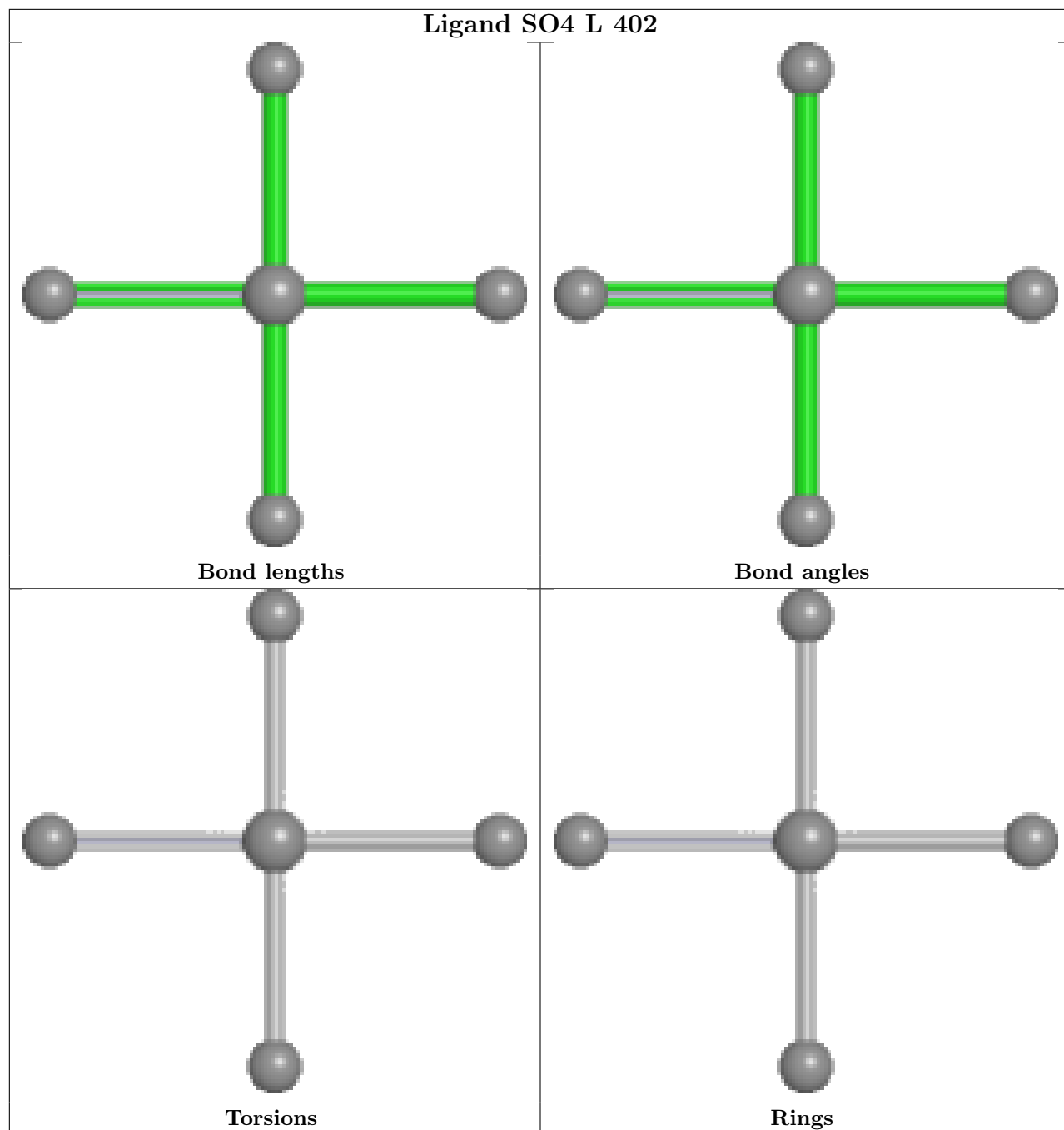


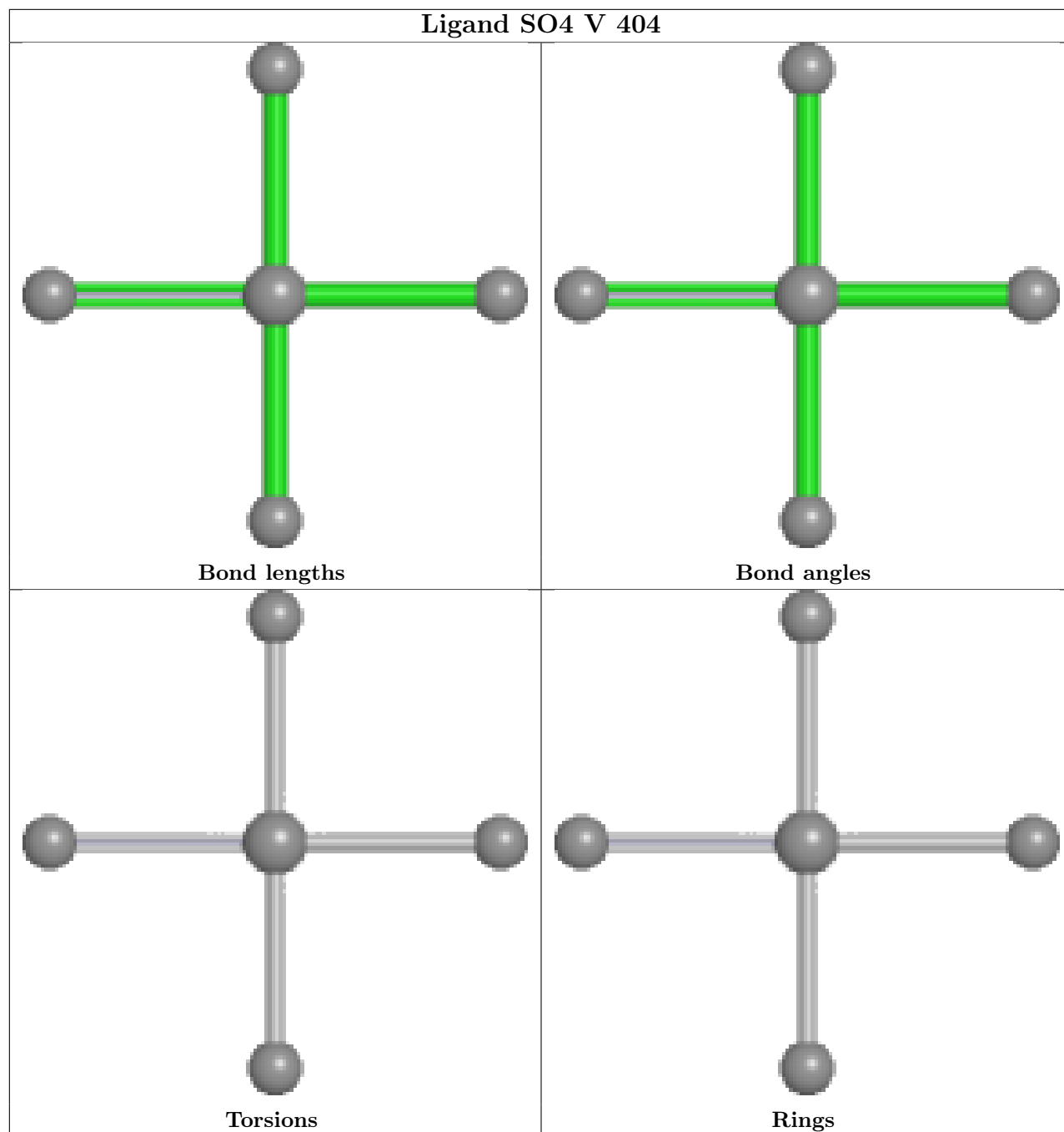


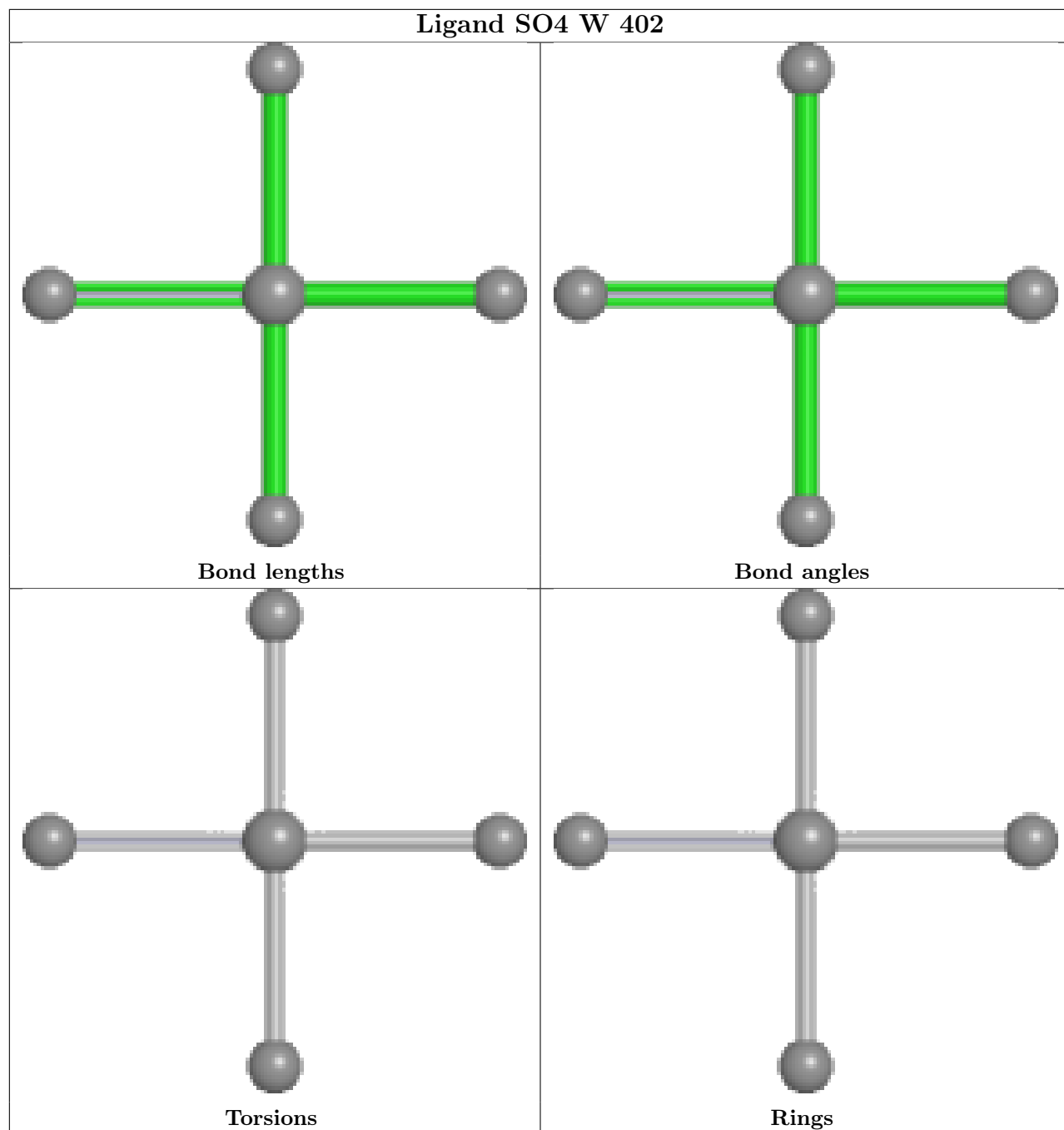


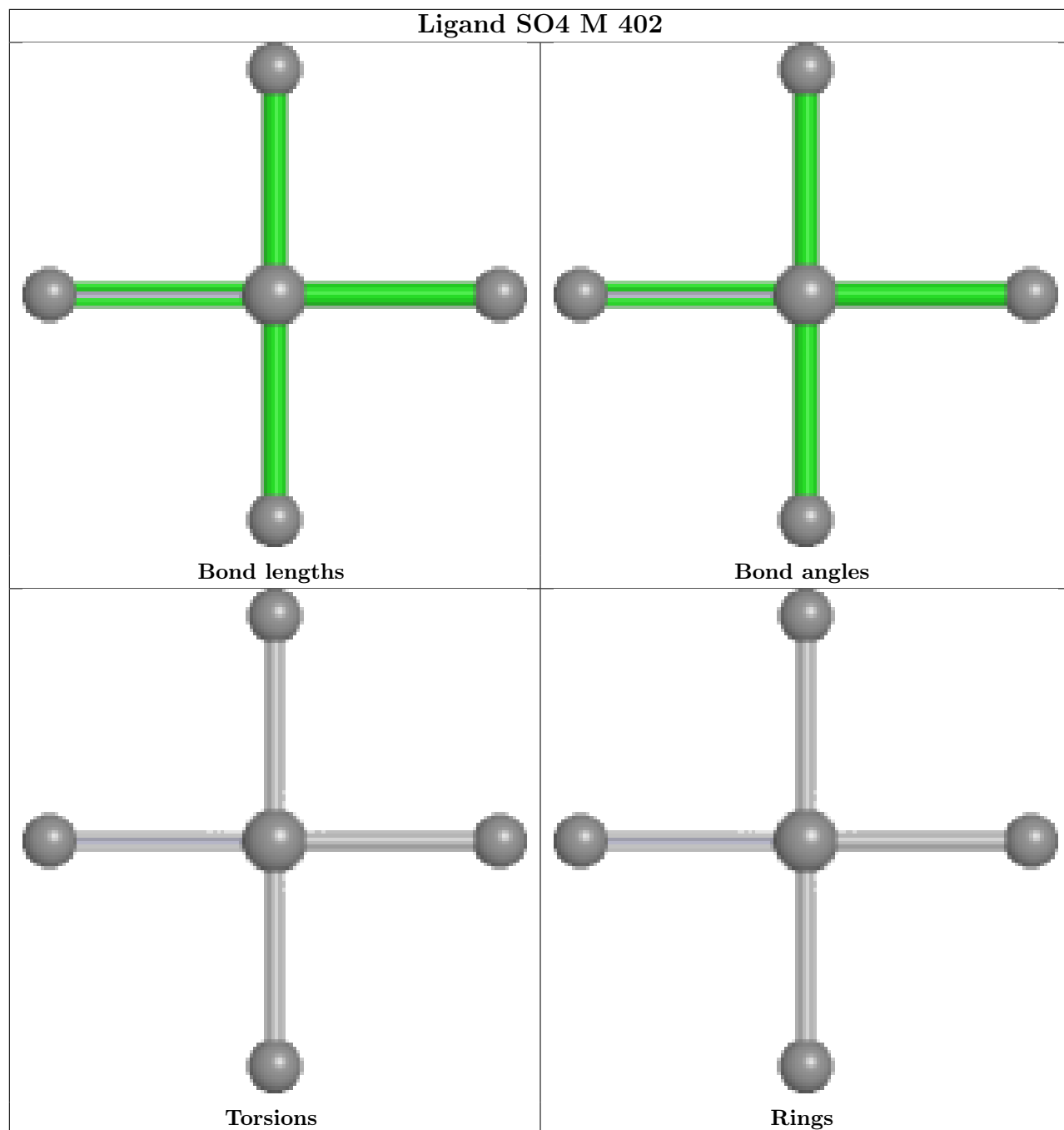


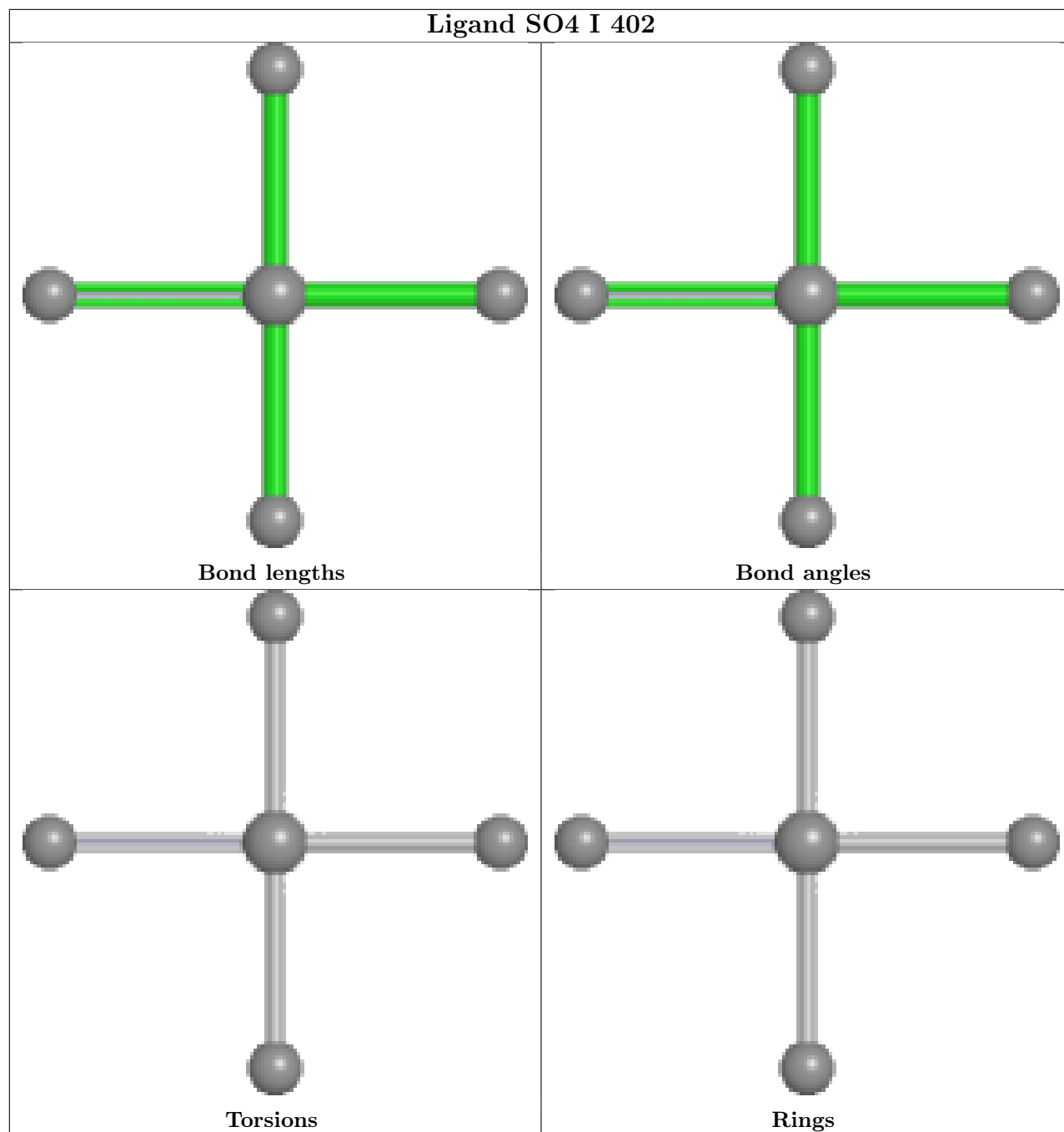


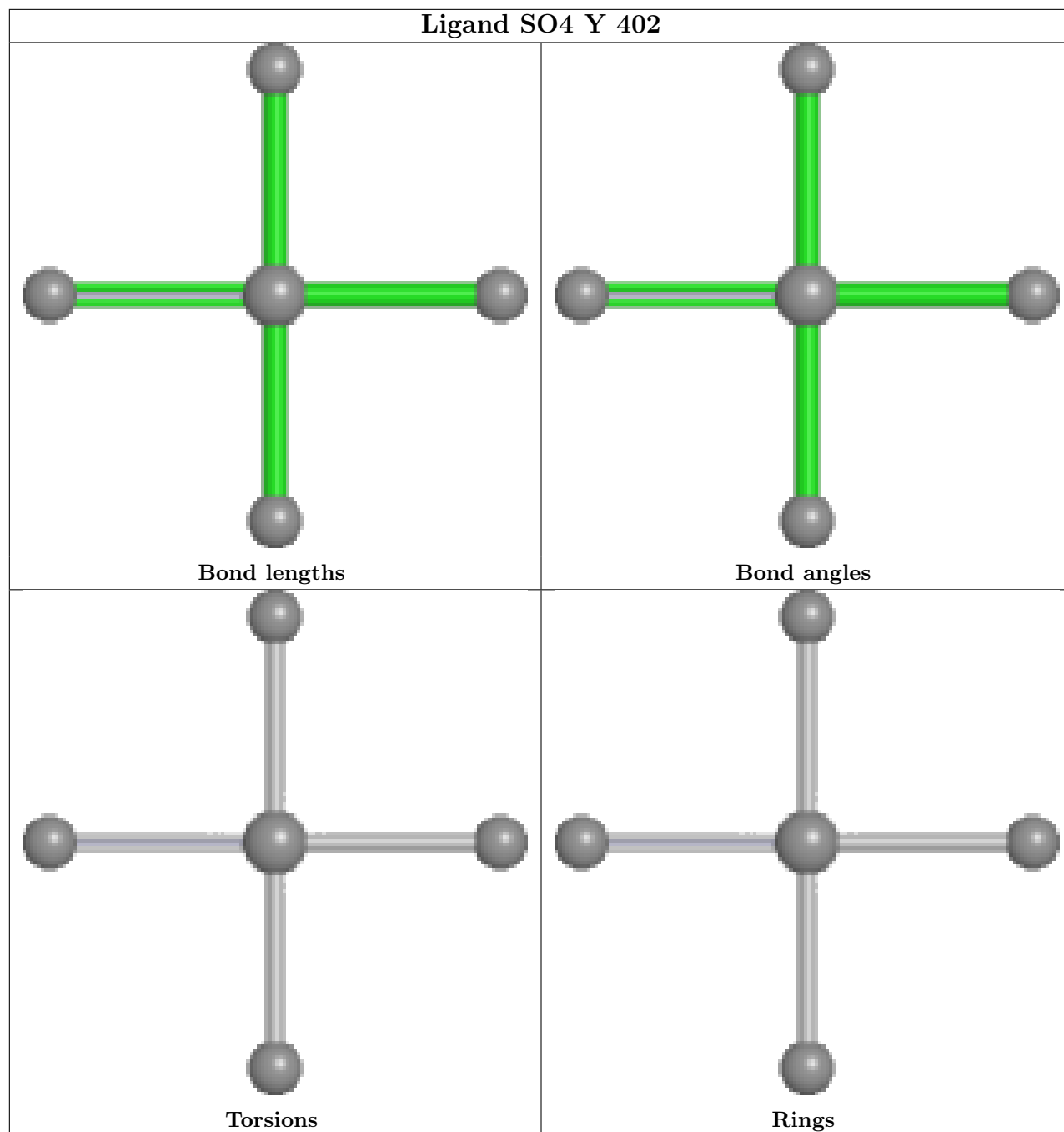


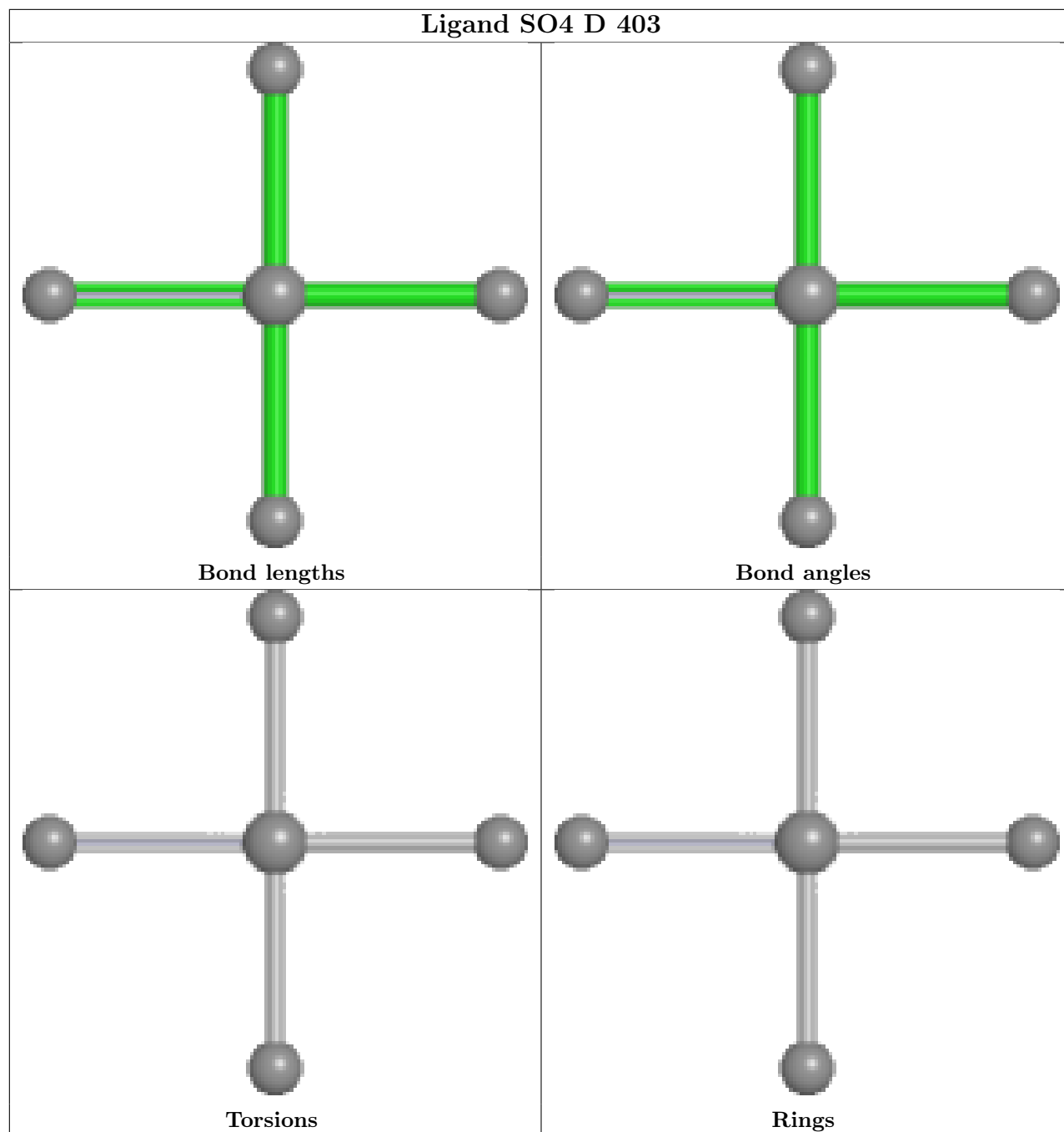


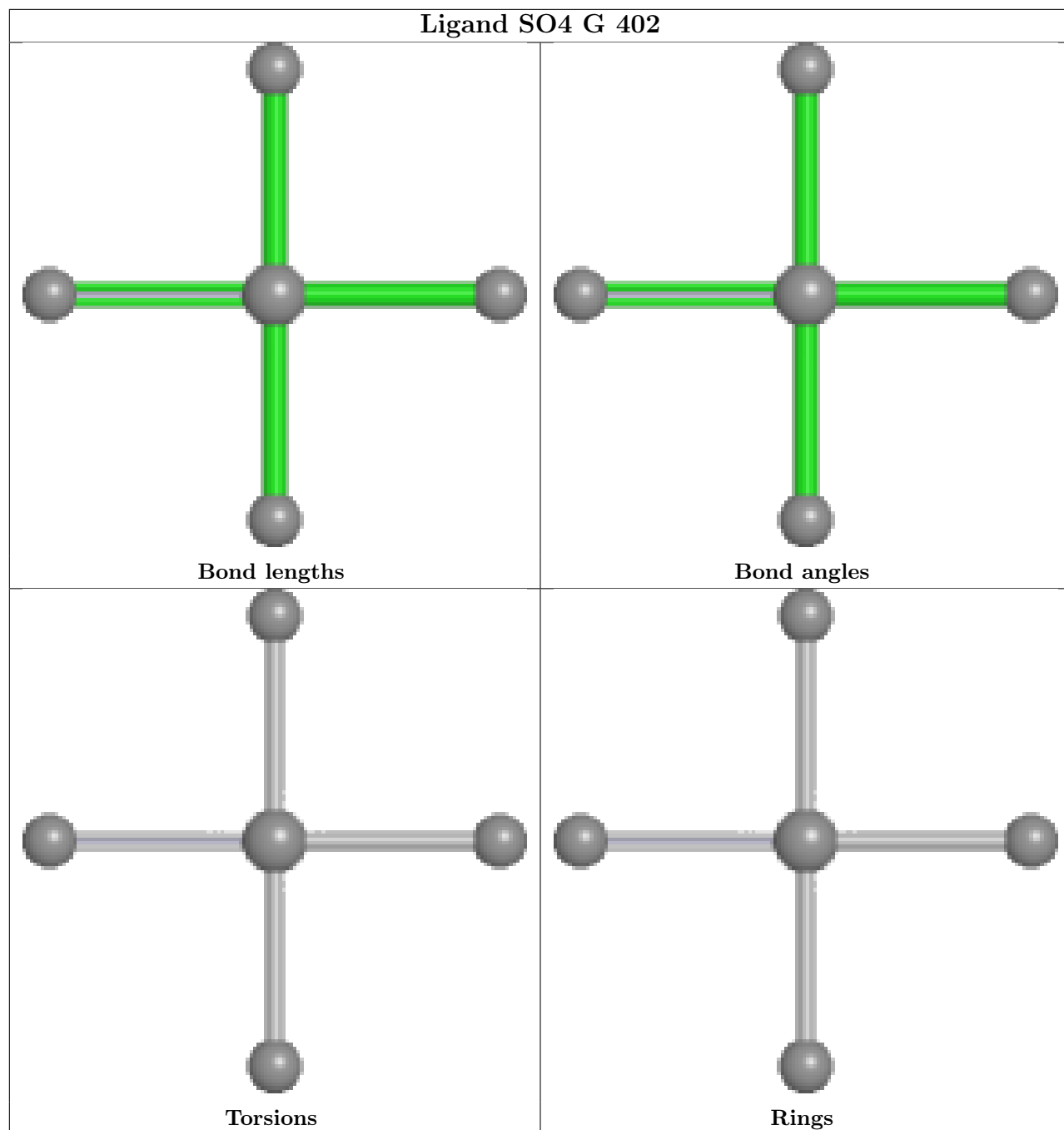


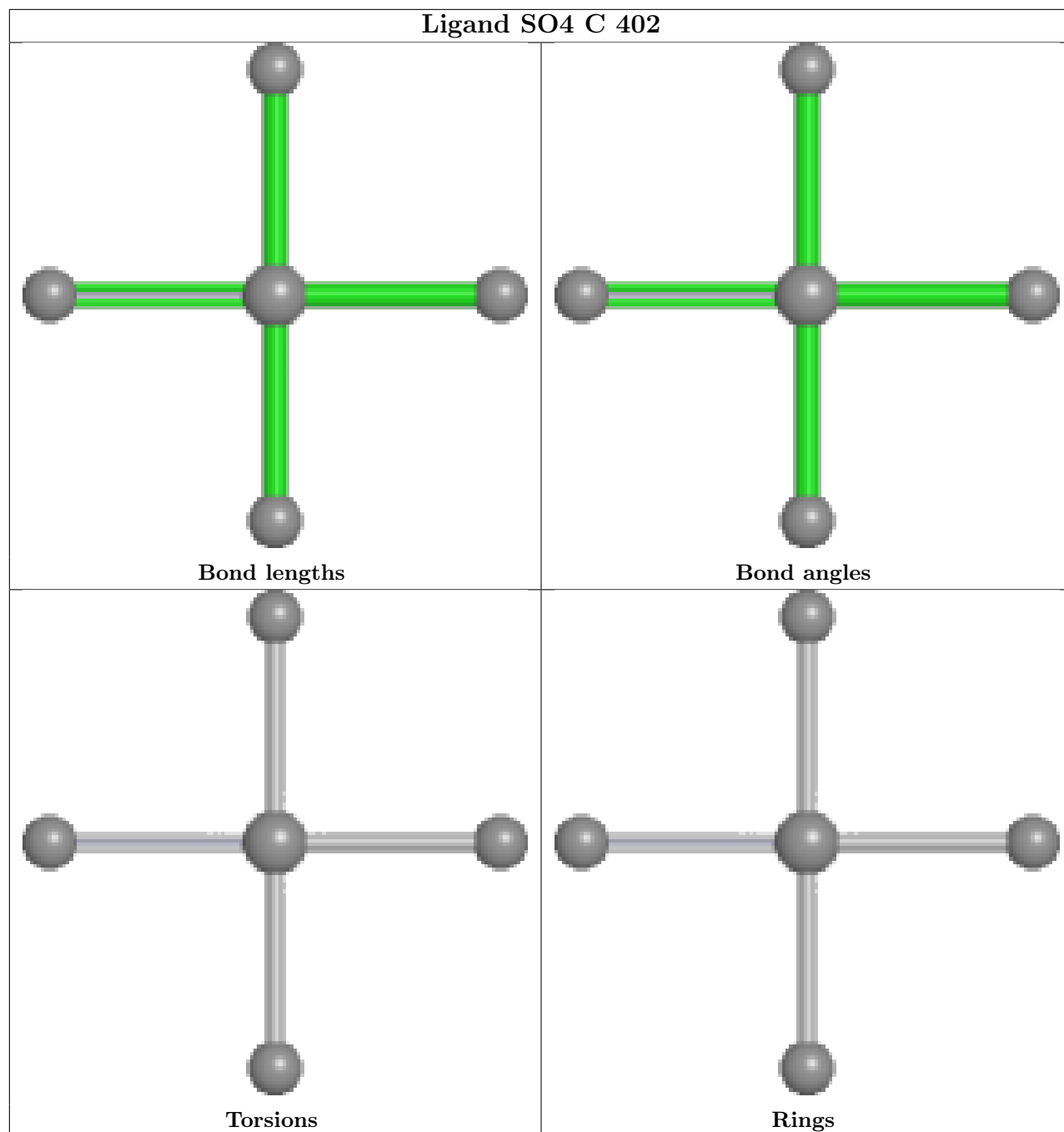


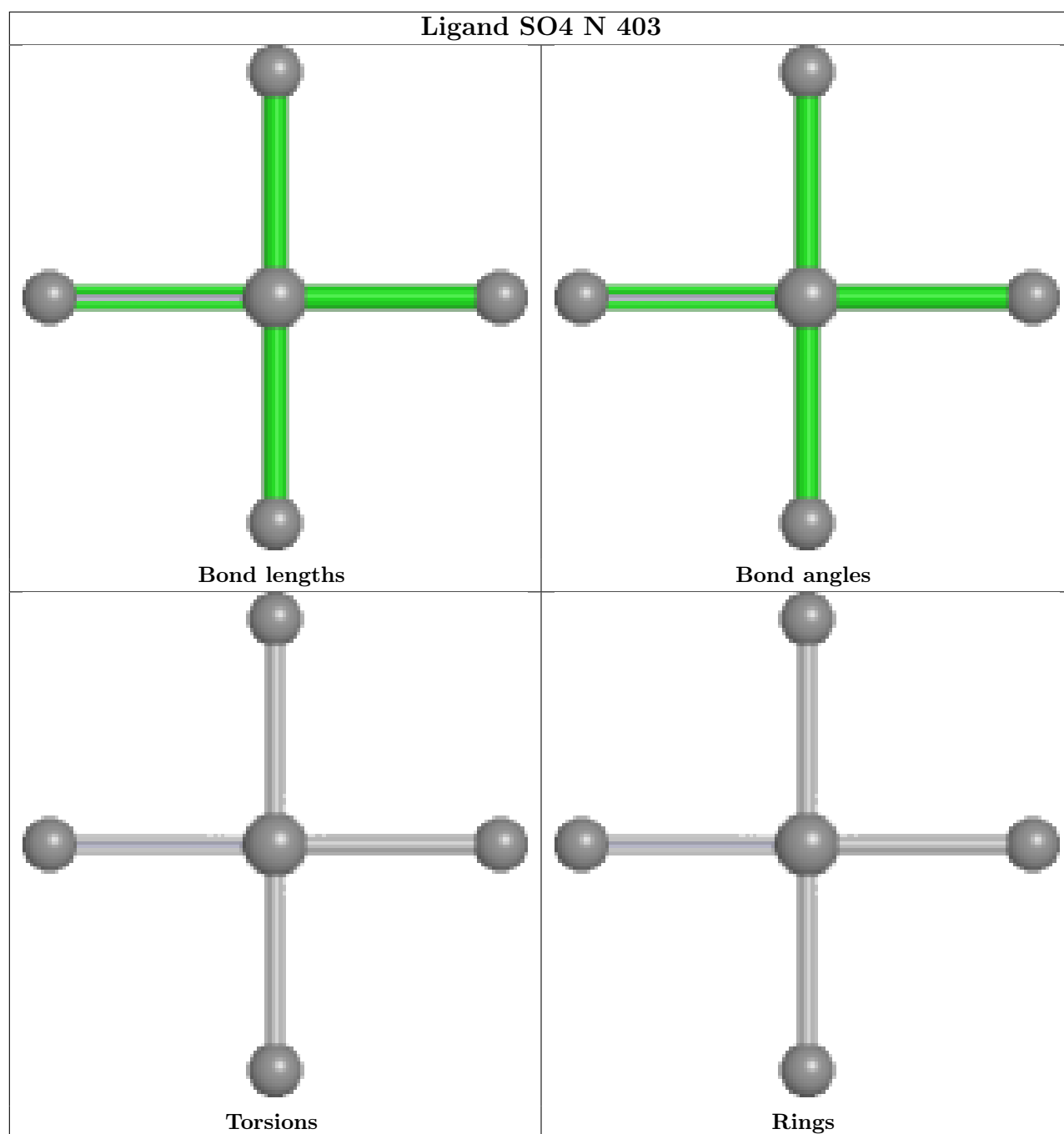


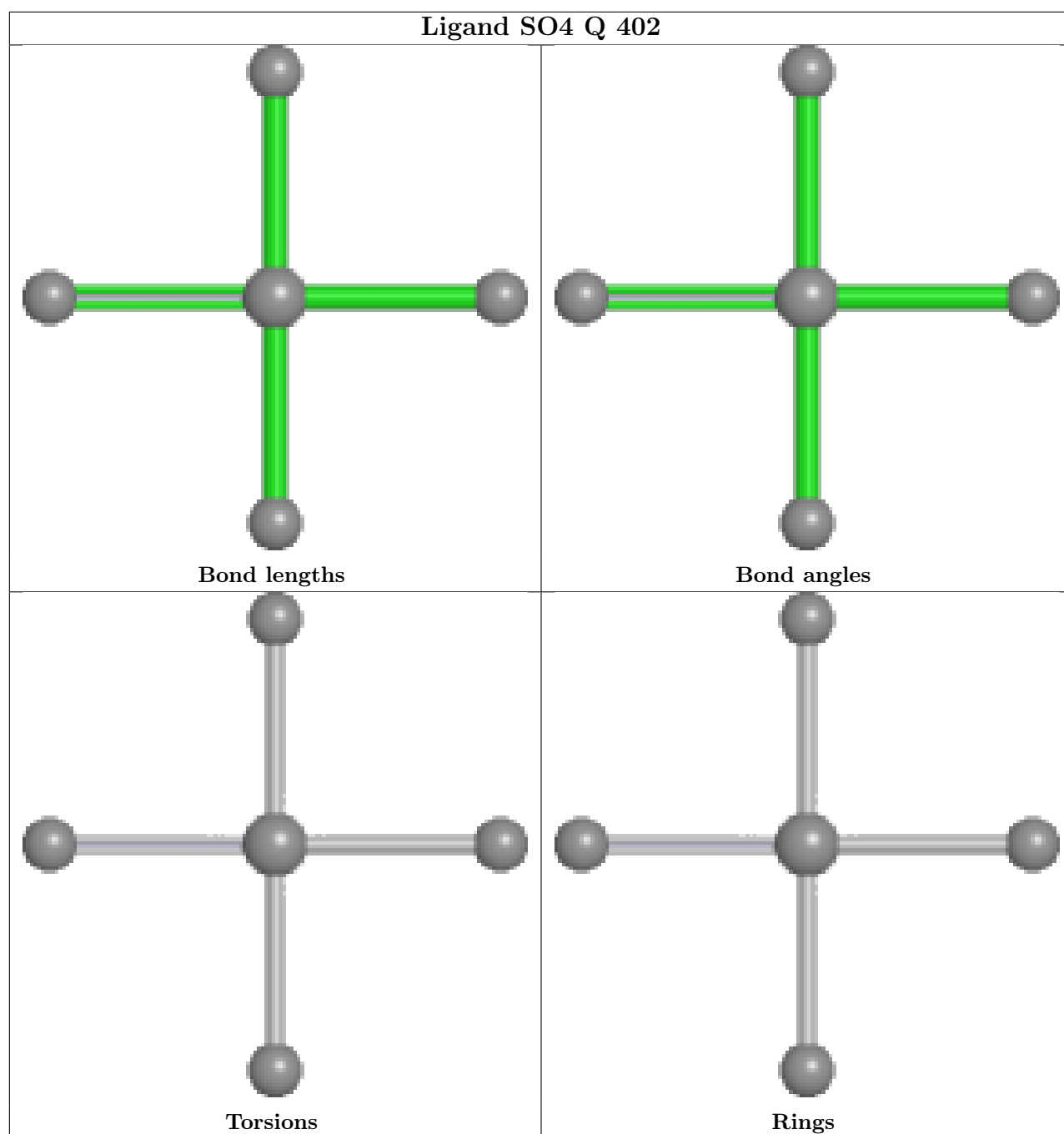


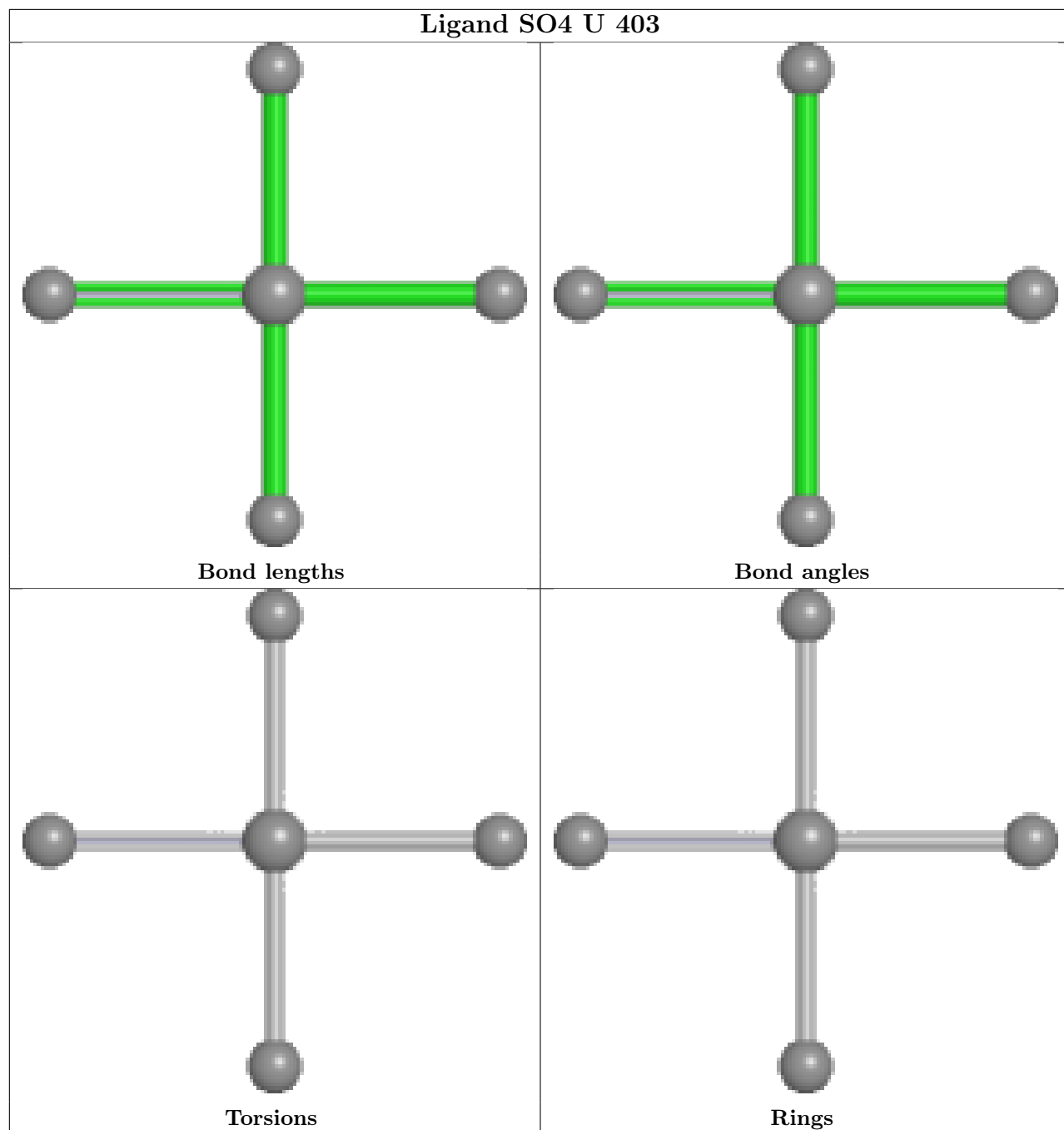


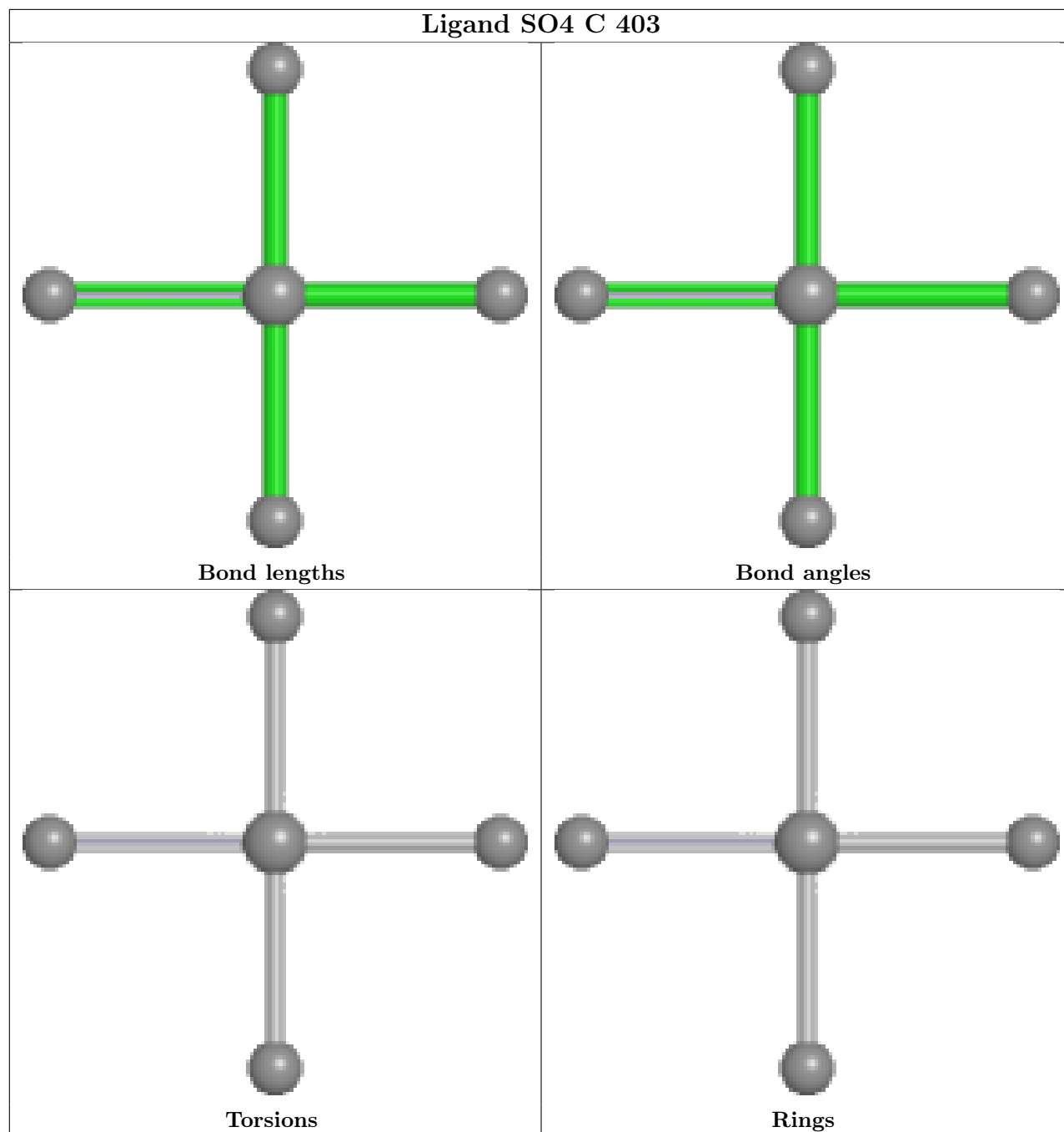


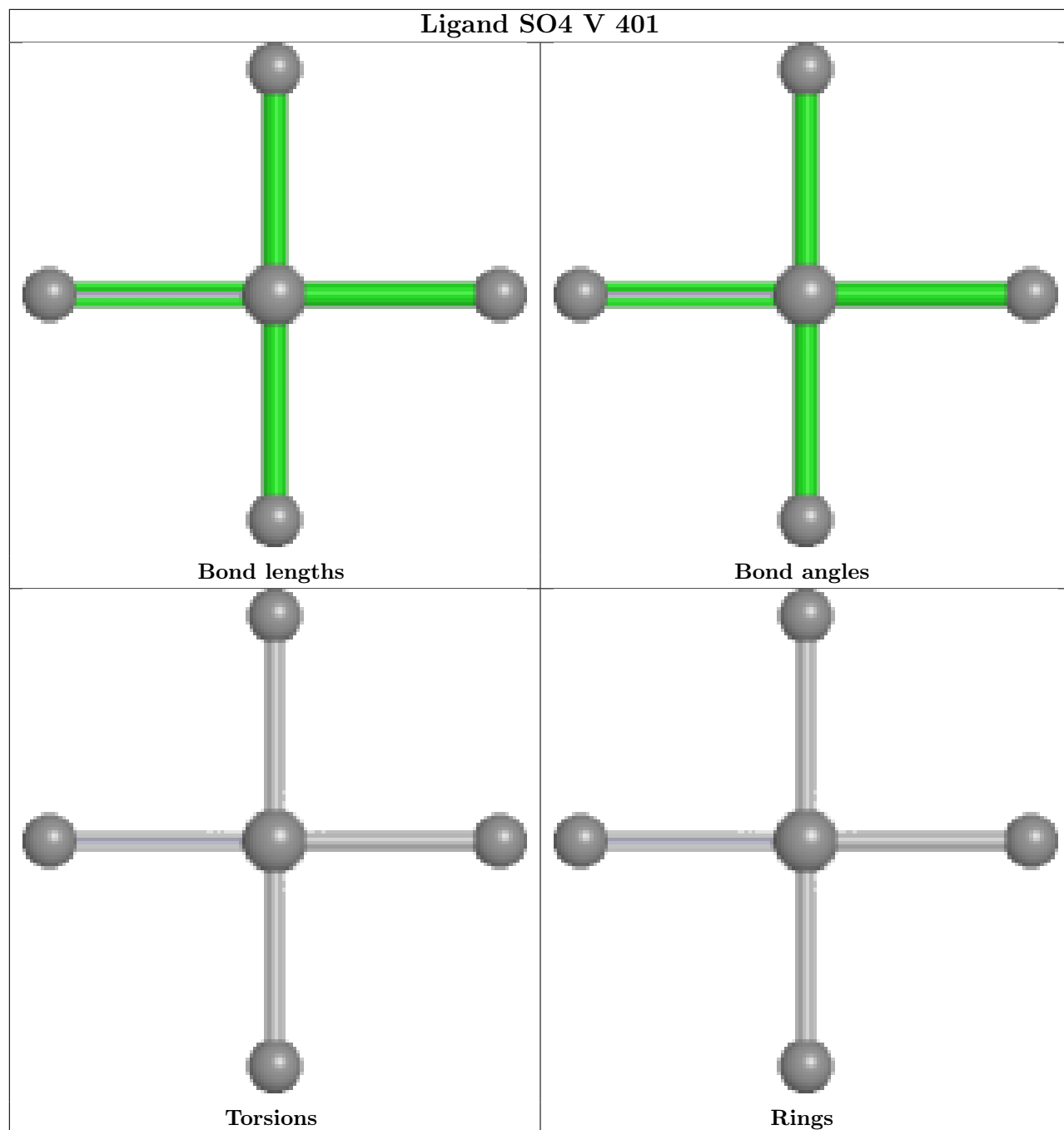


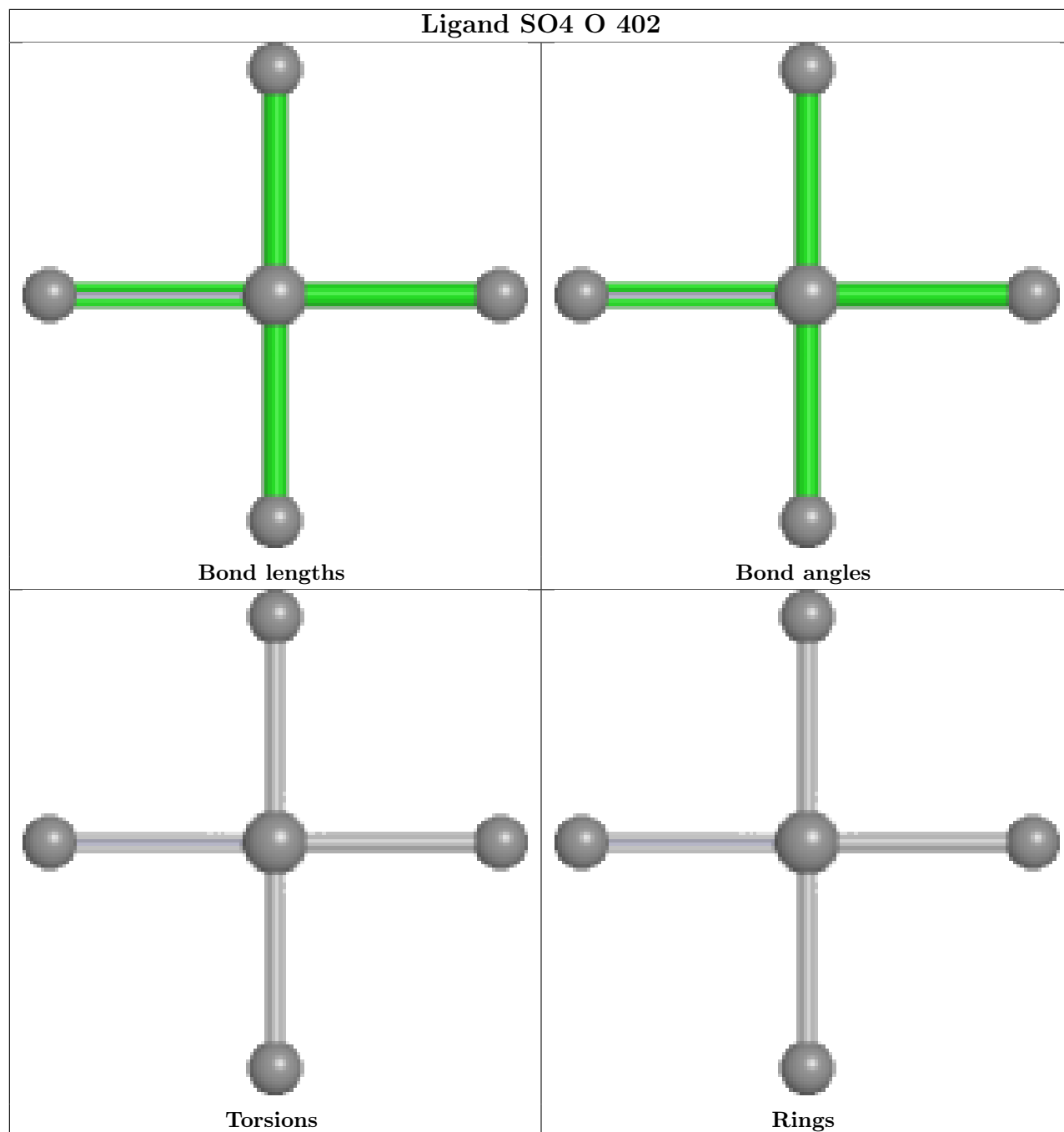


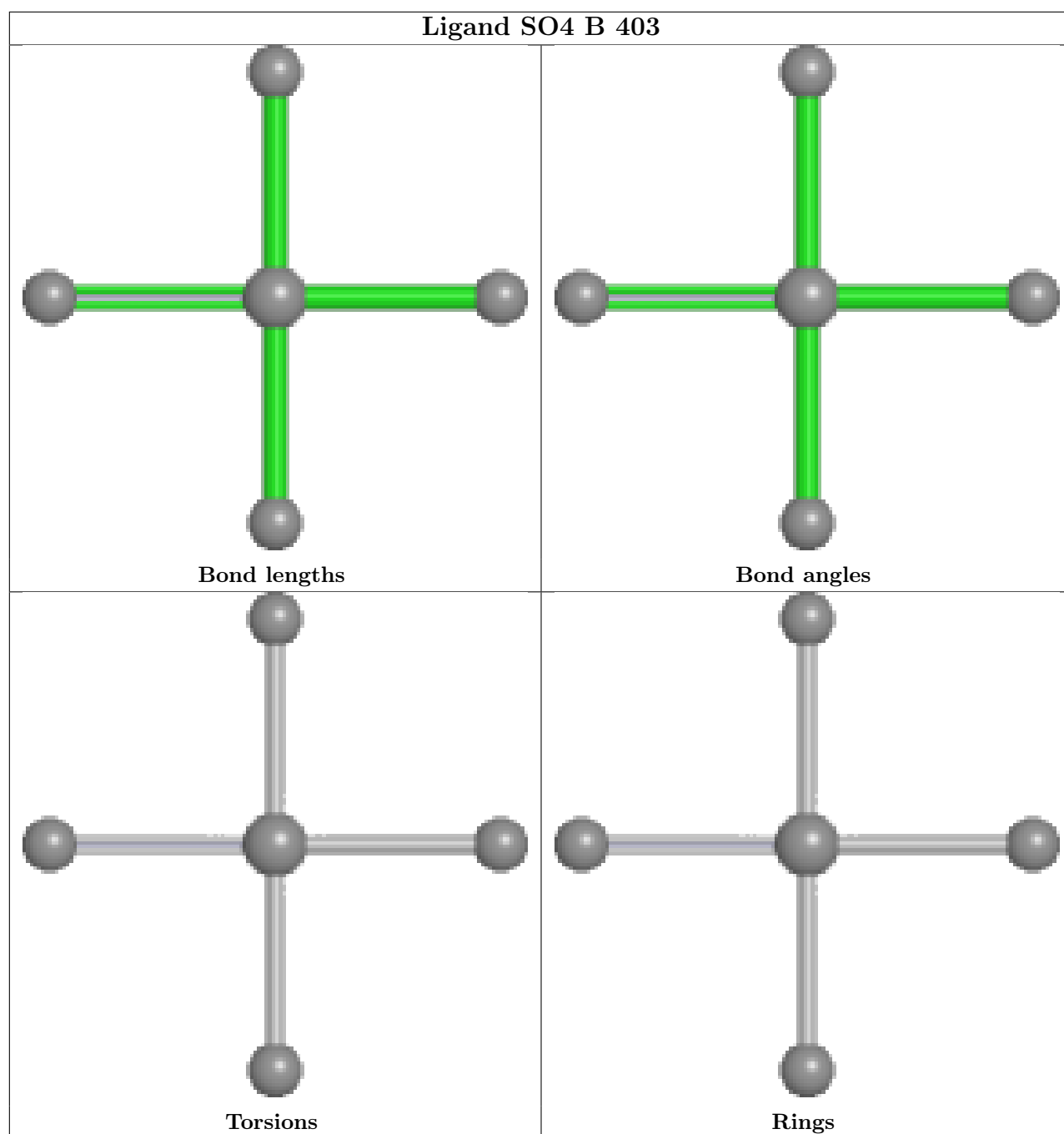












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	308/314 (98%)	-0.40	4 (1%) 75 77	27, 36, 66, 95	1 (0%)
1	B	308/314 (98%)	-0.39	4 (1%) 75 77	28, 36, 68, 94	1 (0%)
1	C	308/314 (98%)	-0.22	5 (1%) 70 73	26, 43, 70, 105	2 (0%)
1	D	308/314 (98%)	-0.17	7 (2%) 61 64	32, 48, 76, 112	3 (0%)
1	E	308/314 (98%)	-0.19	8 (2%) 57 60	29, 42, 74, 103	1 (0%)
1	F	308/314 (98%)	-0.02	7 (2%) 61 64	35, 48, 81, 116	2 (0%)
1	G	308/314 (98%)	-0.49	4 (1%) 75 77	24, 34, 60, 94	2 (0%)
1	H	308/314 (98%)	-0.36	5 (1%) 70 73	29, 38, 68, 99	2 (0%)
1	I	308/314 (98%)	-0.46	5 (1%) 70 73	22, 34, 61, 96	3 (0%)
1	J	308/314 (98%)	-0.35	5 (1%) 70 73	25, 37, 68, 94	2 (0%)
1	K	308/314 (98%)	-0.34	6 (1%) 66 69	27, 39, 70, 95	1 (0%)
1	L	308/314 (98%)	-0.15	3 (0%) 79 81	38, 48, 72, 105	3 (0%)
1	M	308/314 (98%)	-0.41	4 (1%) 75 77	25, 35, 65, 92	2 (0%)
1	N	308/314 (98%)	-0.46	7 (2%) 61 64	23, 33, 63, 102	2 (0%)
1	O	307/314 (97%)	-0.35	4 (1%) 75 77	20, 39, 67, 99	4 (1%)
1	P	308/314 (98%)	-0.24	5 (1%) 70 73	27, 44, 71, 103	4 (1%)
1	Q	308/314 (98%)	-0.38	7 (2%) 61 64	25, 37, 64, 94	3 (0%)
1	R	308/314 (98%)	-0.30	6 (1%) 66 69	30, 40, 71, 104	2 (0%)
1	T	308/314 (98%)	-0.28	7 (2%) 61 64	30, 40, 71, 99	2 (0%)
1	U	308/314 (98%)	-0.18	4 (1%) 75 77	30, 45, 74, 104	3 (0%)
1	V	308/314 (98%)	-0.13	3 (0%) 79 81	36, 48, 76, 104	1 (0%)
1	W	308/314 (98%)	0.04	5 (1%) 70 73	40, 54, 81, 122	1 (0%)
1	Y	308/314 (98%)	-0.05	4 (1%) 75 77	40, 51, 80, 103	1 (0%)
1	Z	308/314 (98%)	-0.39	5 (1%) 70 73	26, 36, 67, 98	4 (1%)

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	7391/7536 (98%)	-0.28	124 (1%) 69 71	20, 42, 72, 122	52 (0%)

The worst 5 of 124 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Q	313[A]	LYS	6.2
1	Z	313[A]	LYS	5.3
1	J	313[A]	LYS	4.8
1	P	313[A]	LYS	4.5
1	F	313	LYS	4.4

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

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
1	CSS	W	103	7/8	0.80	0.13	61,70,91,95	1
1	CSS	L	103	7/8	0.86	0.12	55,59,81,84	1
1	CSS	A	103	7/8	0.86	0.12	46,55,61,69	1
1	CSS	Q	103	7/8	0.87	0.12	43,56,72,80	1
1	CSS	Y	33	7/8	0.87	0.13	60,68,82,82	1
1	CSS	B	103	7/8	0.88	0.11	45,47,61,70	1
1	CSS	V	103	7/8	0.88	0.10	53,60,70,79	1
1	CSS	D	33	7/8	0.89	0.12	55,60,81,84	1
1	CSS	T	103	7/8	0.89	0.11	47,56,72,72	1
1	CSS	V	33	7/8	0.89	0.12	63,66,77,83	1
1	CSS	D	103	7/8	0.89	0.11	57,72,79,81	1
1	CSS	C	103	7/8	0.89	0.11	49,59,69,76	1
1	CSS	N	103	7/8	0.89	0.12	34,51,68,69	1
1	CSS	H	103	7/8	0.90	0.12	35,46,62,67	1
1	CSS	L	33	7/8	0.90	0.10	50,54,62,66	1
1	CSS	H	33	7/8	0.90	0.13	45,49,60,69	1
1	CSS	U	103	7/8	0.90	0.10	48,56,66,76	1
1	CSS	Y	103	7/8	0.90	0.10	56,67,75,80	1
1	CSS	Z	103	7/8	0.90	0.10	52,57,59,66	1
1	CSS	G	103	7/8	0.91	0.10	38,42,61,68	1
1	CSS	M	103	7/8	0.91	0.09	39,50,68,70	1
1	CSS	B	33	7/8	0.91	0.10	48,50,63,70	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	CSS	W	33	7/8	0.91	0.12	56,63,81,84	1
1	CSS	O	103	7/8	0.91	0.11	47,57,66,71	1
1	CSS	F	103	7/8	0.91	0.10	62,67,78,78	1
1	CSS	G	33	7/8	0.91	0.10	47,48,64,66	1
1	CSS	U	33	7/8	0.91	0.11	51,57,69,73	1
1	CSS	I	103	7/8	0.92	0.09	39,47,56,64	1
1	CSS	K	33	7/8	0.92	0.10	53,55,65,76	1
1	CSS	O	33	7/8	0.92	0.09	52,55,67,70	1
1	CSS	K	103	7/8	0.92	0.09	49,54,76,78	1
1	CSS	E	33	7/8	0.92	0.10	56,60,62,63	1
1	CSS	R	103	7/8	0.92	0.09	49,51,64,70	1
1	CSS	C	33	7/8	0.92	0.11	49,53,66,70	1
1	CSS	M	33	7/8	0.92	0.11	47,48,61,63	1
1	CSS	J	103	7/8	0.93	0.09	39,56,70,72	1
1	CSS	E	103	7/8	0.93	0.09	53,63,74,75	1
1	CSS	P	103	7/8	0.93	0.10	41,55,67,68	1
1	CSS	F	33	7/8	0.93	0.11	60,64,73,74	1
1	CSS	J	33	7/8	0.93	0.11	43,48,62,64	1
1	CSS	N	33	7/8	0.94	0.09	42,43,60,61	1
1	CSS	Q	33	7/8	0.94	0.09	52,53,60,63	1
1	CSS	A	33	7/8	0.94	0.09	41,44,59,65	1
1	CSS	P	33	7/8	0.94	0.10	50,54,70,71	1
1	CSS	Z	33	7/8	0.94	0.09	48,50,68,70	1
1	CSS	T	33	7/8	0.94	0.08	49,51,60,67	1
1	CSS	R	33	7/8	0.95	0.08	47,50,63,63	1
1	CSS	I	33	7/8	0.96	0.08	35,40,50,55	1

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	V	401	5/5	0.74	0.24	122,124,126,132	0
3	SO4	F	402	5/5	0.76	0.11	113,115,121,123	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	Y	402	5/5	0.77	0.11	133,133,134,136	0
3	SO4	E	402	5/5	0.78	0.12	138,140,141,142	0
3	SO4	G	402	5/5	0.79	0.13	112,112,115,117	0
3	SO4	H	402	5/5	0.79	0.12	109,115,119,119	0
3	SO4	U	402	5/5	0.79	0.11	119,120,120,121	0
3	SO4	D	402	5/5	0.79	0.11	121,124,124,126	0
3	SO4	W	402	5/5	0.79	0.11	119,120,121,124	0
3	SO4	F	404	5/5	0.79	0.19	115,116,120,126	0
3	SO4	L	402	5/5	0.80	0.10	114,114,117,118	0
3	SO4	L	403	5/5	0.80	0.19	123,125,129,130	0
3	SO4	C	402	5/5	0.80	0.12	95,96,101,103	0
3	SO4	J	403	5/5	0.80	0.23	112,114,121,121	0
3	SO4	K	402	5/5	0.80	0.11	114,117,121,124	0
3	SO4	K	403	5/5	0.80	0.19	95,107,112,116	0
3	SO4	Q	402	5/5	0.81	0.12	119,121,122,123	0
3	SO4	C	403	5/5	0.81	0.16	111,116,118,123	0
3	SO4	G	403	5/5	0.81	0.20	95,95,106,113	0
3	SO4	V	403	5/5	0.81	0.11	116,118,120,122	0
3	SO4	V	404	5/5	0.81	0.17	113,114,122,125	0
3	SO4	A	404	5/5	0.81	0.22	103,114,118,121	0
3	SO4	D	403	5/5	0.81	0.20	110,115,122,123	0
3	SO4	U	403	5/5	0.83	0.19	102,112,113,120	0
3	SO4	E	403	5/5	0.83	0.20	99,109,110,113	0
3	SO4	W	403	5/5	0.83	0.16	114,116,121,122	0
3	SO4	M	403	5/5	0.83	0.20	81,99,103,107	0
3	SO4	N	403	5/5	0.84	0.19	94,99,104,105	0
3	SO4	O	402	5/5	0.84	0.10	104,107,111,114	0
3	SO4	H	403	5/5	0.84	0.21	87,102,108,114	0
3	SO4	R	402	5/5	0.84	0.15	110,111,112,119	0
3	SO4	F	403	5/5	0.85	0.14	123,123,128,131	0
3	SO4	T	402	5/5	0.85	0.12	102,105,107,109	0
3	SO4	C	404	5/5	0.85	0.14	91,101,104,109	0
3	SO4	P	402	5/5	0.85	0.10	110,113,114,116	0
3	SO4	I	403	5/5	0.85	0.19	66,96,98,99	0
3	SO4	I	402	5/5	0.86	0.14	62,77,86,92	0
3	SO4	A	403	5/5	0.86	0.17	86,87,101,108	0
3	SO4	O	403	5/5	0.86	0.18	108,110,114,117	0
3	SO4	B	403	5/5	0.87	0.16	94,94,101,103	0
3	SO4	Q	403	5/5	0.87	0.17	85,103,106,108	0
3	SO4	P	403	5/5	0.87	0.18	107,107,116,118	0
3	SO4	N	402	5/5	0.88	0.12	107,107,108,111	0
3	SO4	M	402	5/5	0.88	0.09	103,104,105,110	0

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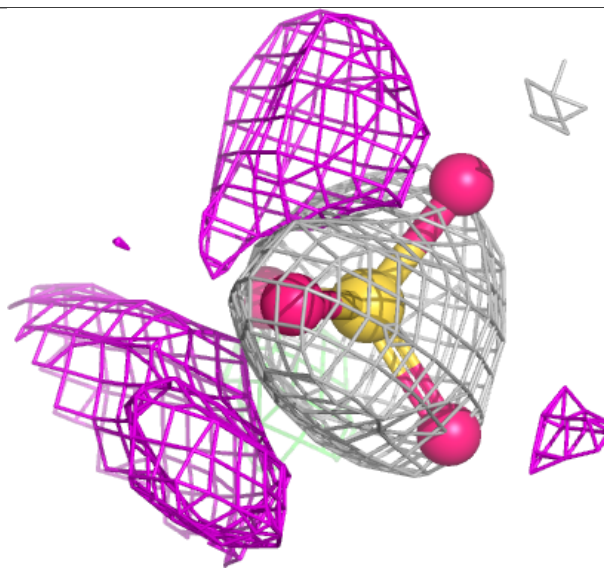
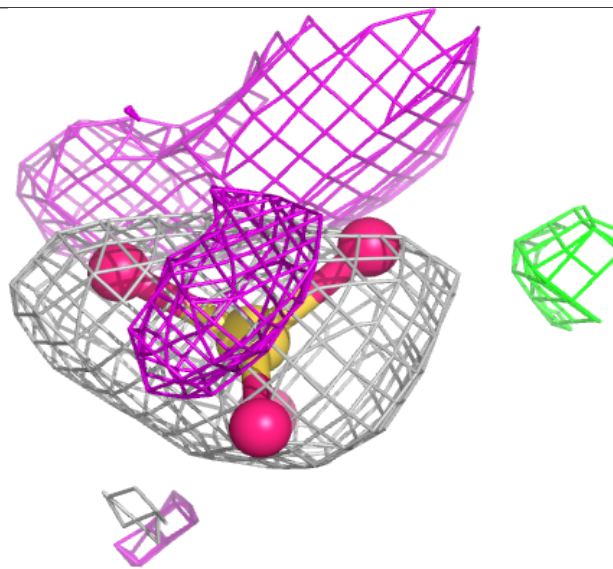
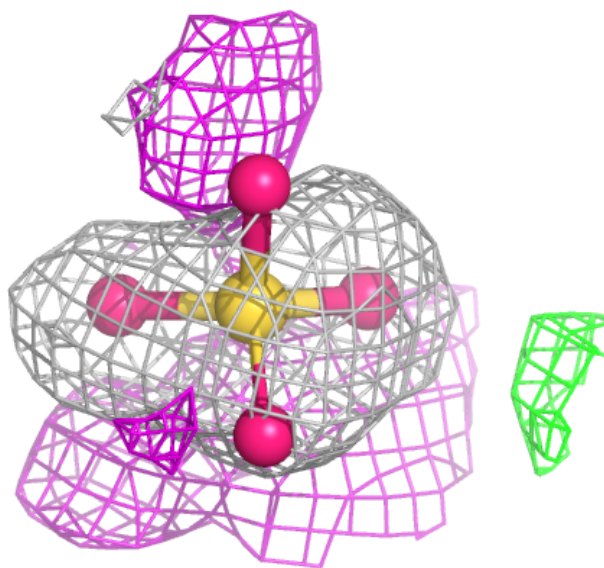
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	B	402	5/5	0.88	0.12	72,79,89,93	0
3	SO4	Z	402	5/5	0.88	0.09	97,102,104,109	0
3	SO4	J	402	5/5	0.89	0.10	91,98,98,107	0
2	FE	D	401	1/1	0.90	0.10	61,61,61,61	1
3	SO4	A	402	5/5	0.92	0.09	75,79,80,87	0
2	FE	V	402	1/1	0.92	0.09	59,59,59,59	1
2	FE	Z	401	1/1	0.93	0.06	43,43,43,43	1
2	FE	L	401	1/1	0.94	0.08	54,54,54,54	1
2	FE	O	401	1/1	0.94	0.10	48,48,48,48	1
2	FE	Q	401	1/1	0.95	0.07	42,42,42,42	1
2	FE	J	401	1/1	0.96	0.06	47,47,47,47	1
2	FE	E	401	1/1	0.96	0.07	50,50,50,50	1
2	FE	Y	401	1/1	0.96	0.04	59,59,59,59	1
2	FE	F	401	1/1	0.96	0.06	50,50,50,50	1
2	FE	C	401	1/1	0.97	0.04	44,44,44,44	1
2	FE	H	401	1/1	0.97	0.04	40,40,40,40	1
2	FE	T	401	1/1	0.97	0.04	46,46,46,46	1
2	FE	N	401	1/1	0.98	0.04	41,41,41,41	1
2	FE	U	401	1/1	0.98	0.04	42,42,42,42	1
2	FE	G	401	1/1	0.98	0.03	38,38,38,38	1
2	FE	W	401	1/1	0.98	0.04	52,52,52,52	1
2	FE	P	401	1/1	0.98	0.07	45,45,45,45	1
2	FE	M	401	1/1	0.98	0.04	39,39,39,39	1
2	FE	R	401	1/1	0.99	0.05	37,37,37,37	1
2	FE	A	401	1/1	0.99	0.03	40,40,40,40	1
2	FE	K	401	1/1	0.99	0.02	41,41,41,41	1
2	FE	B	401	1/1	0.99	0.03	37,37,37,37	1
2	FE	I	401	1/1	0.99	0.03	34,34,34,34	1

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.

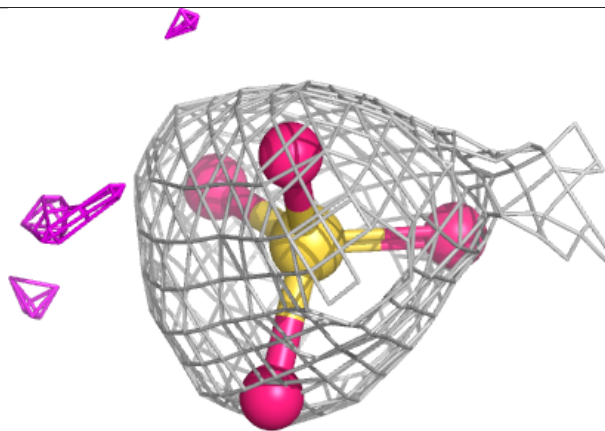
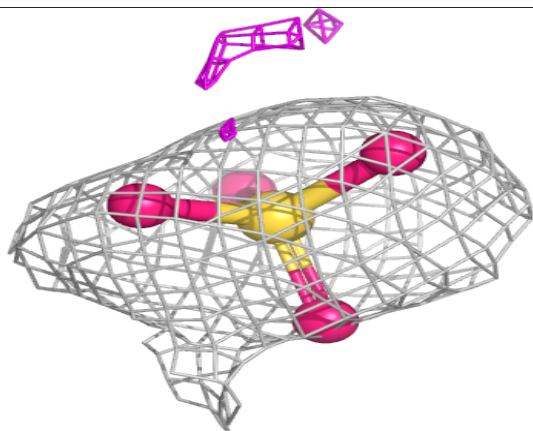
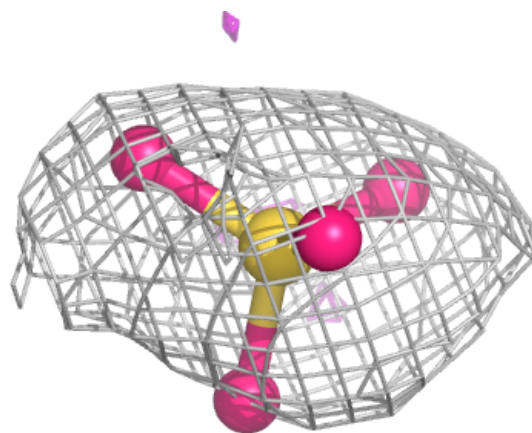
Electron density around SO4 V 401:

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



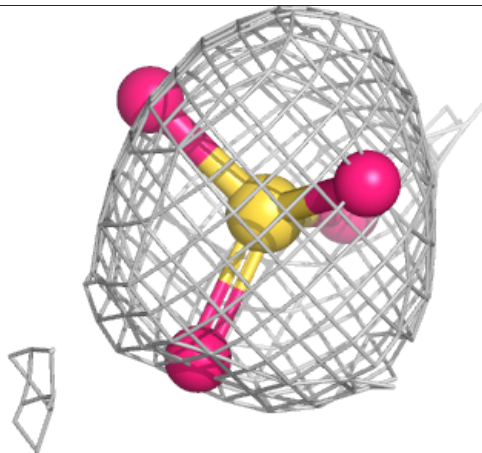
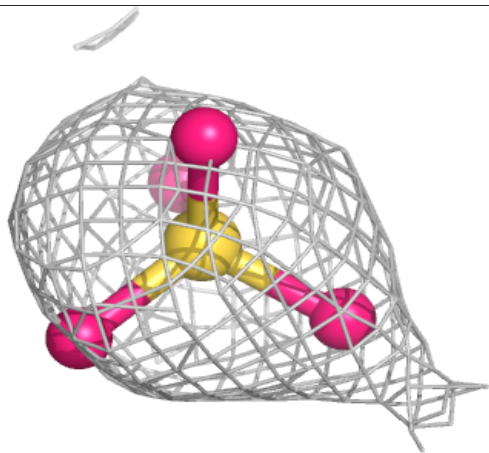
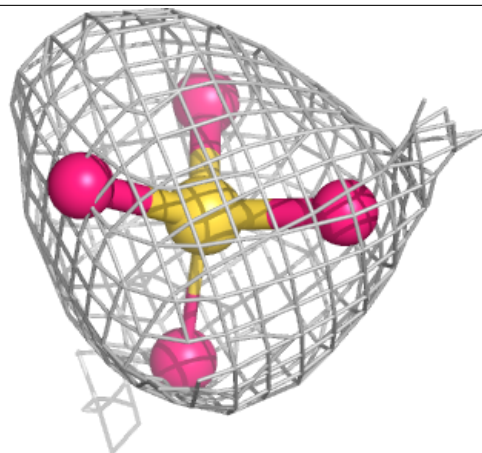
Electron density around SO4 F 402:

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



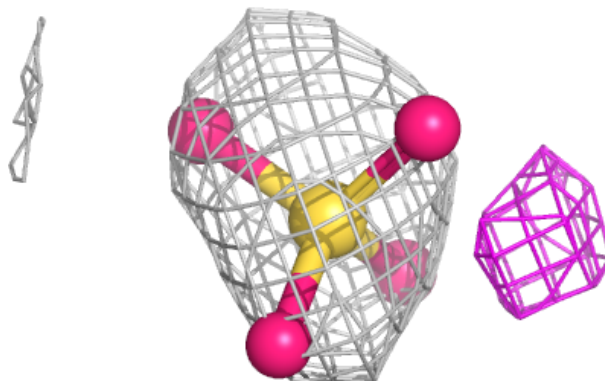
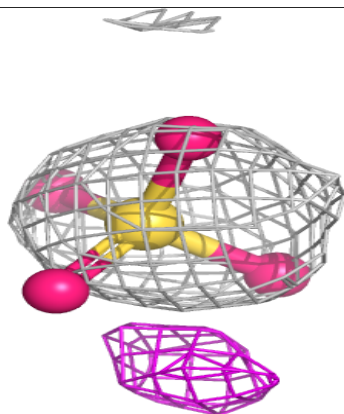
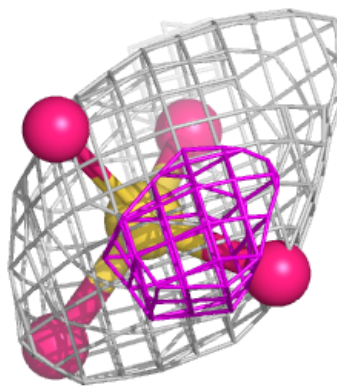
Electron density around SO4 Y 402:

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and green (positive)



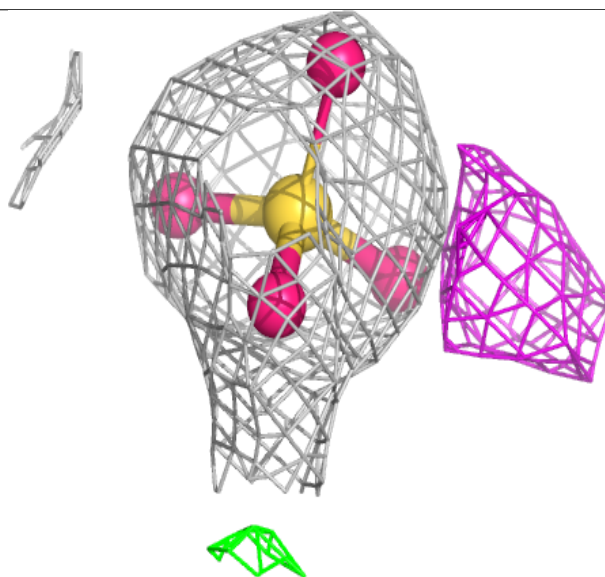
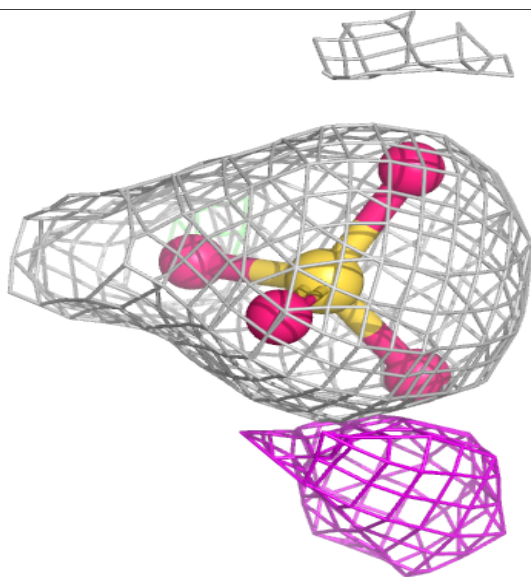
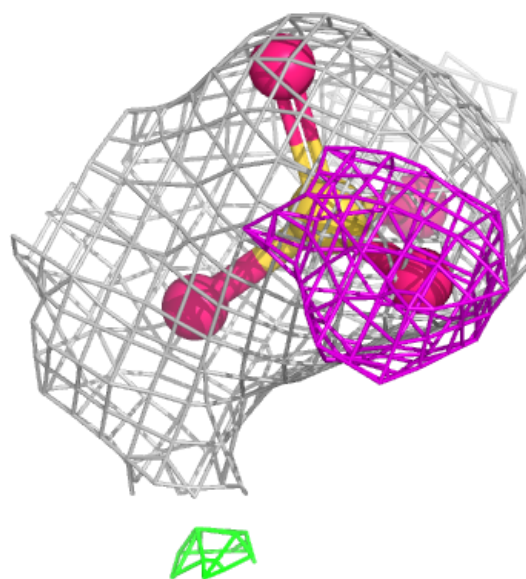
Electron density around SO4 E 402:

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and green (positive)



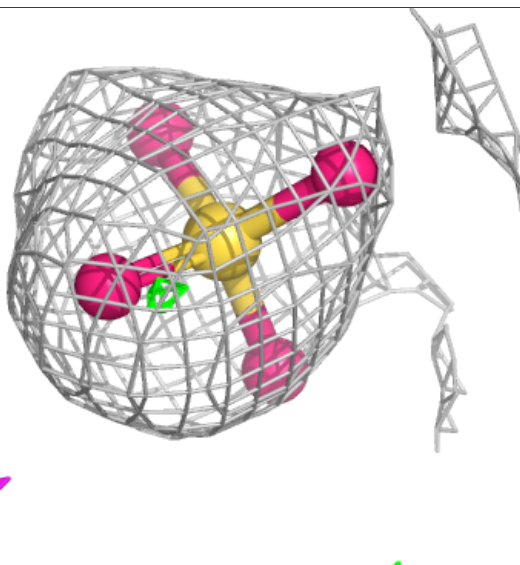
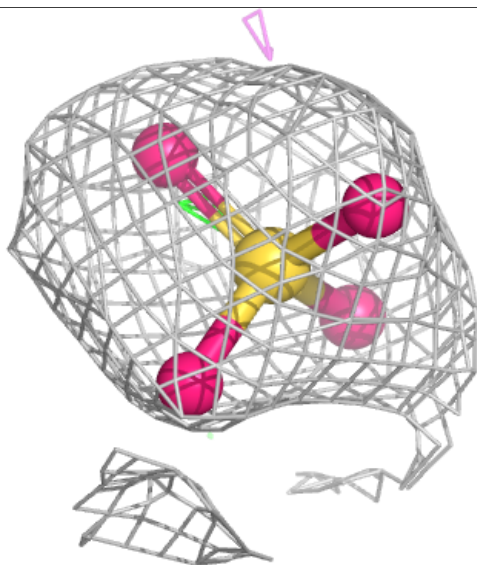
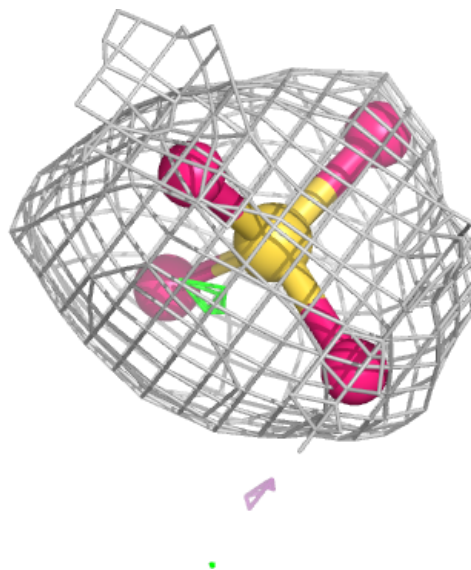
Electron density around SO4 G 402:

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



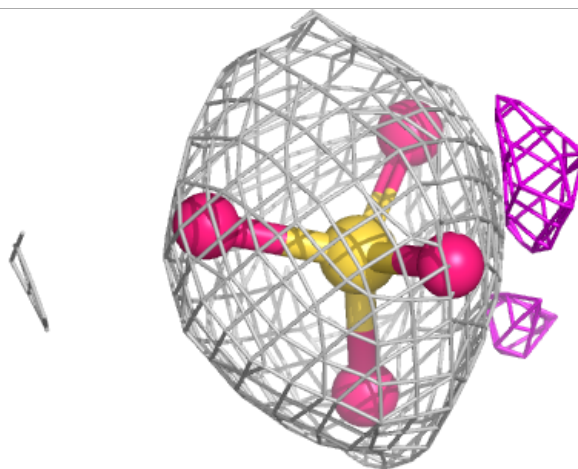
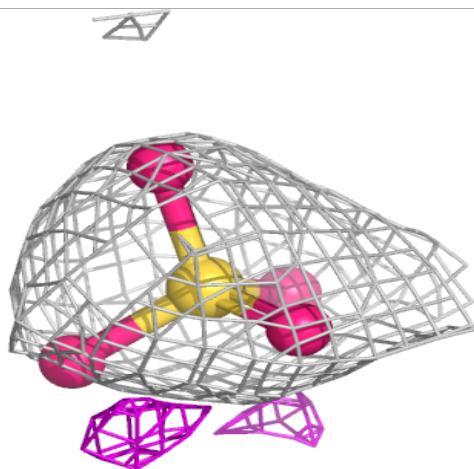
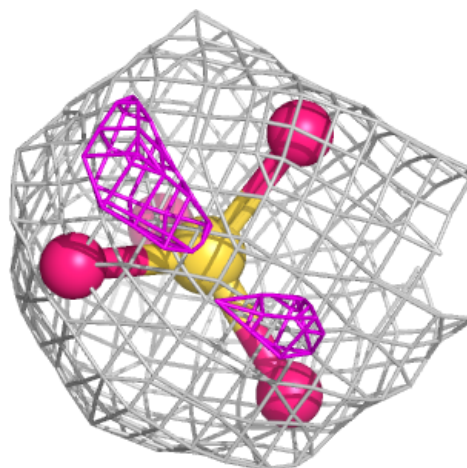
Electron density around SO4 H 402:

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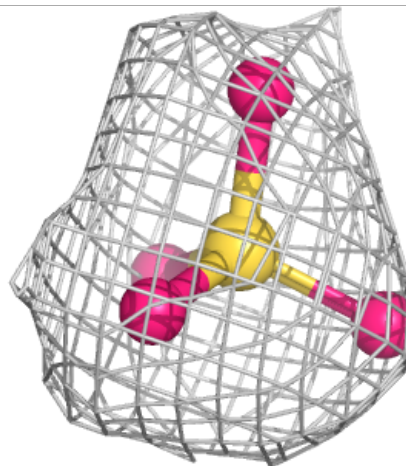
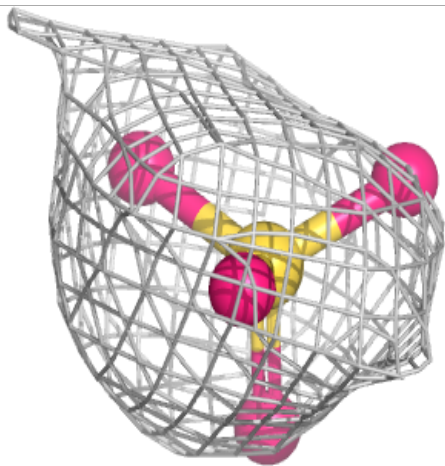
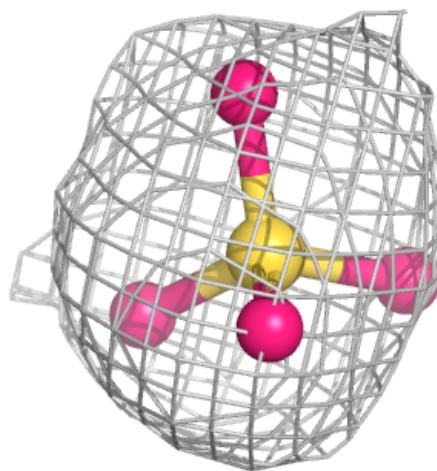
Electron density around SO4 U 402:

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and green (positive)



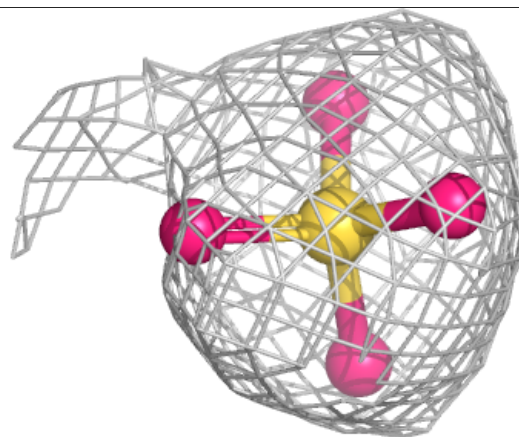
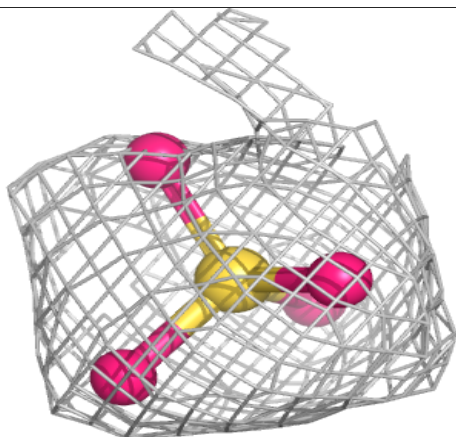
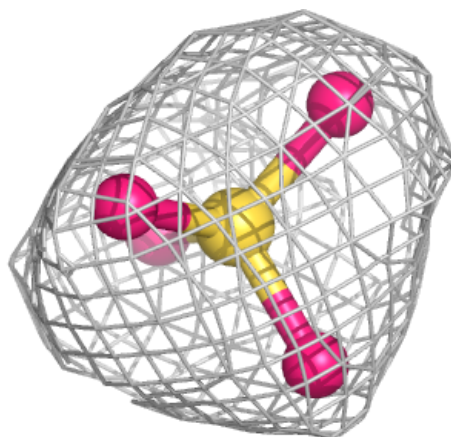
Electron density around SO4 D 402:

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and green (positive)

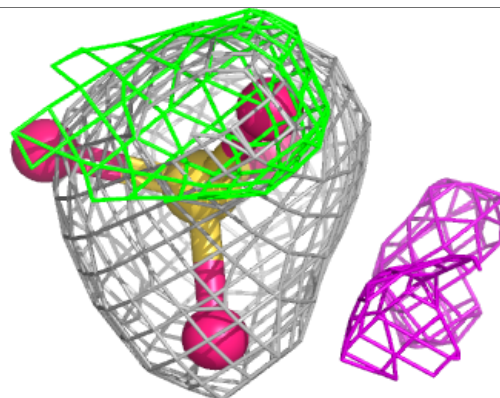
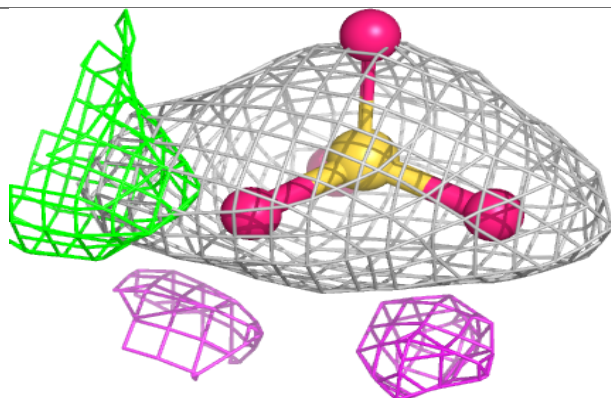
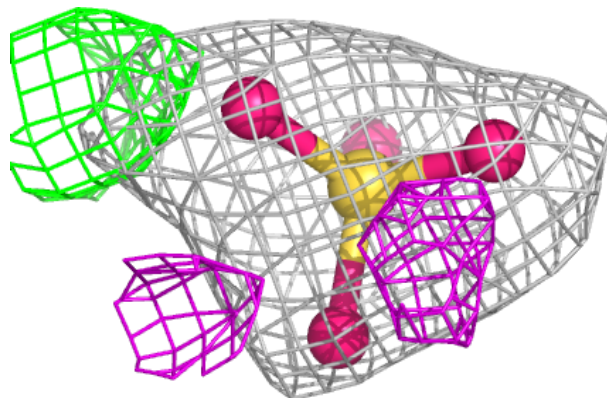


Electron density around SO4 W 402:

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and green (positive)

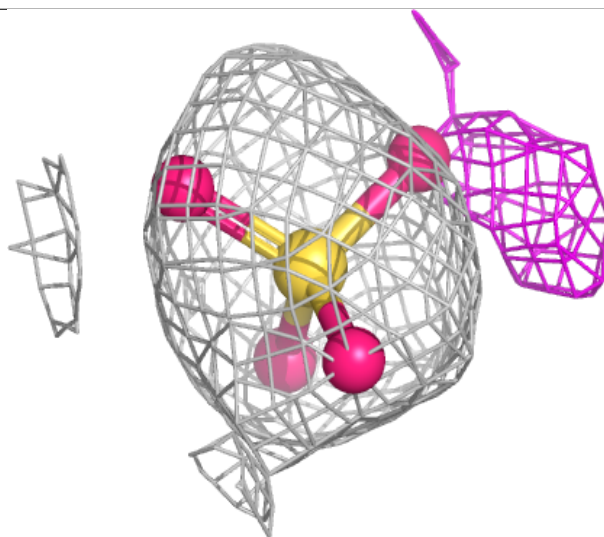
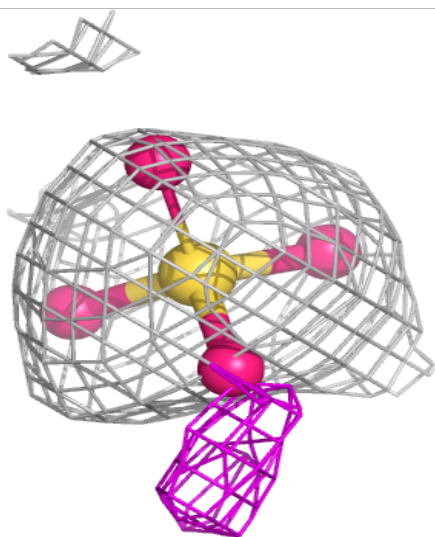
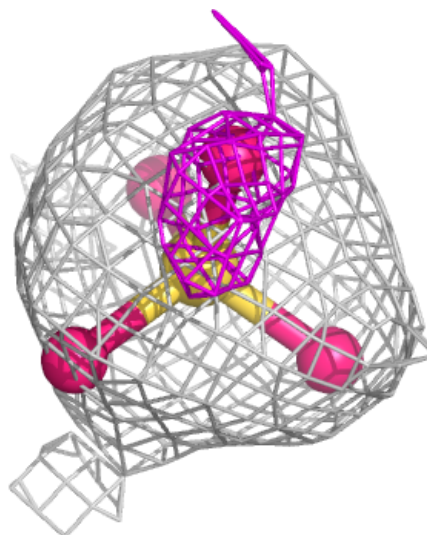
**Electron density around SO4 F 404:**

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and green (positive)



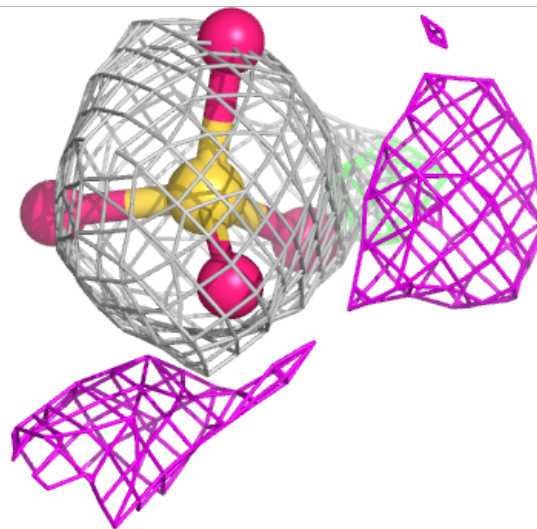
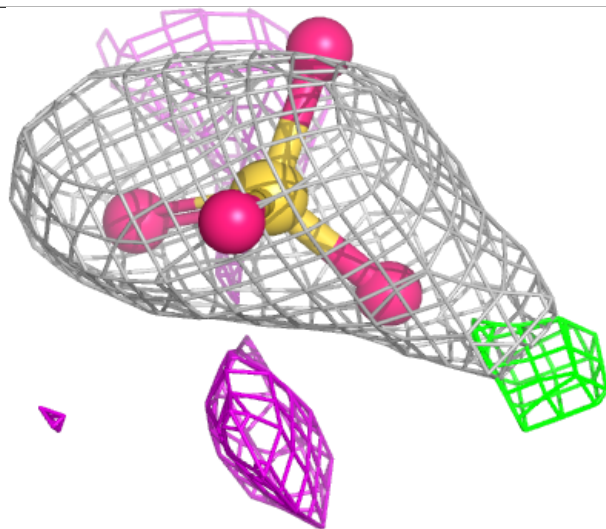
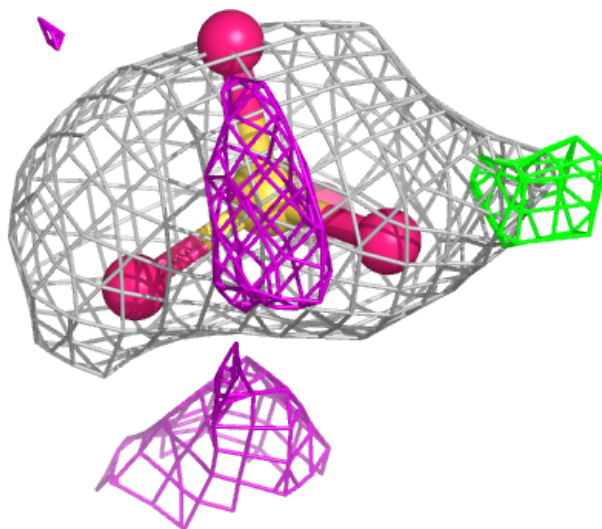
Electron density around SO4 L 402:

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



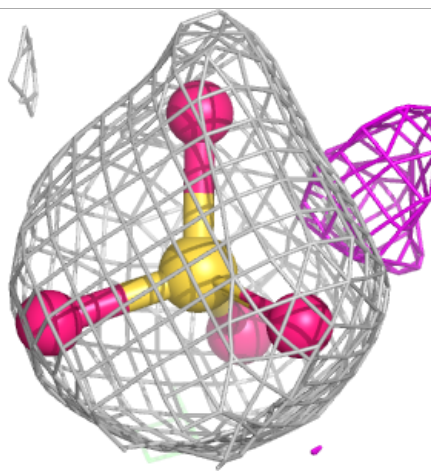
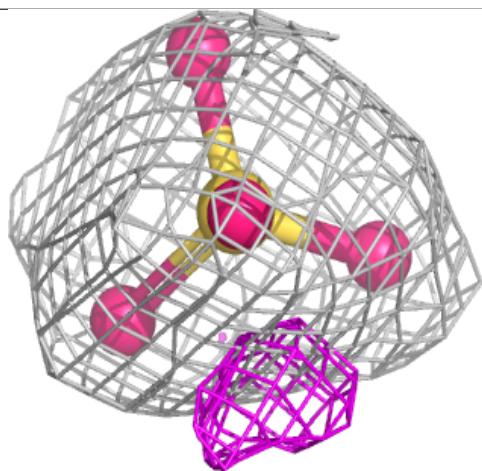
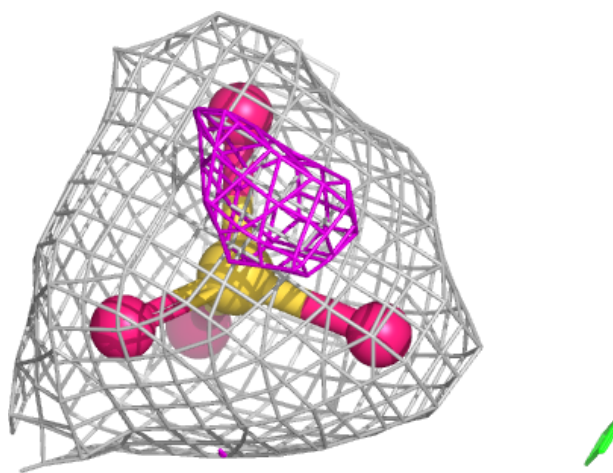
Electron density around SO4 L 403:

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



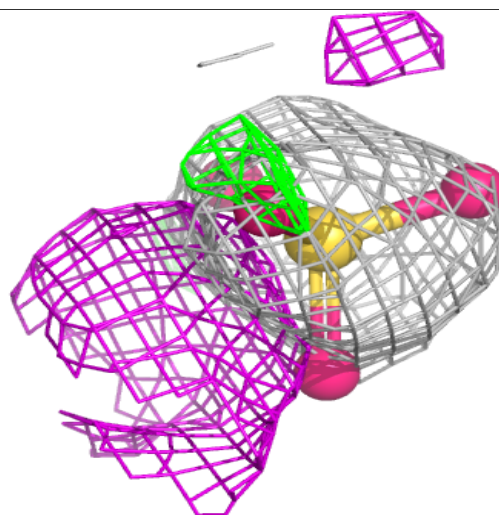
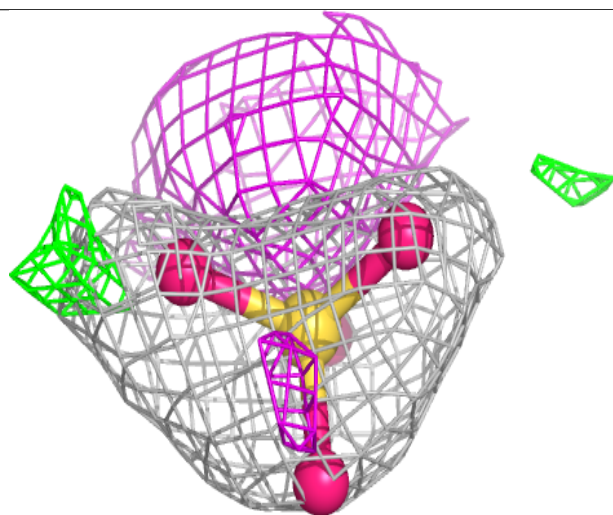
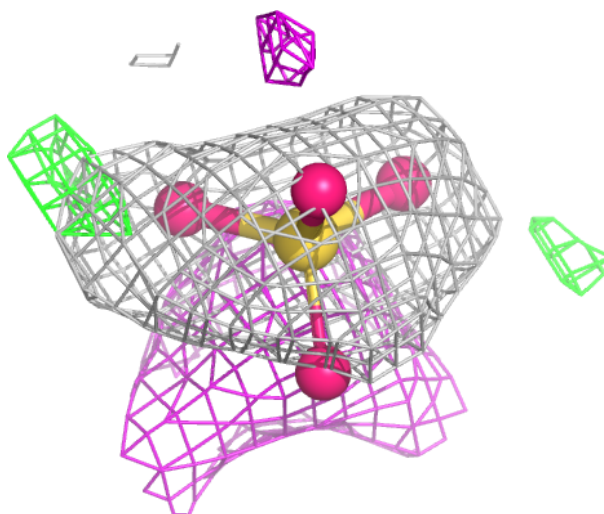
Electron density around SO4 C 402:

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



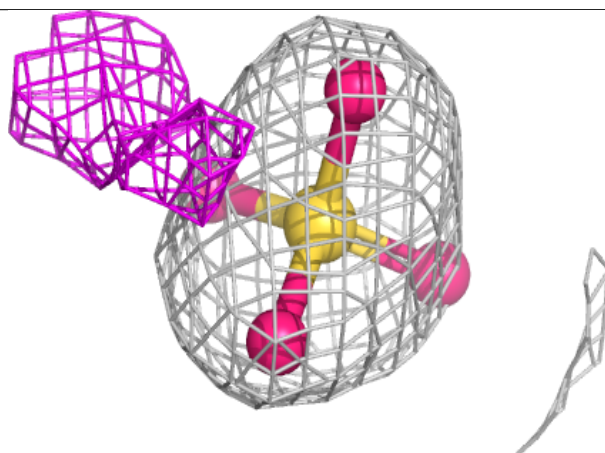
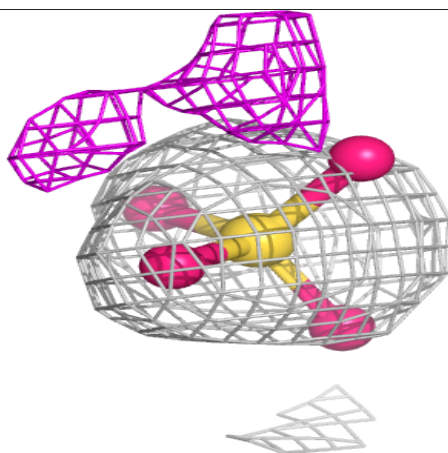
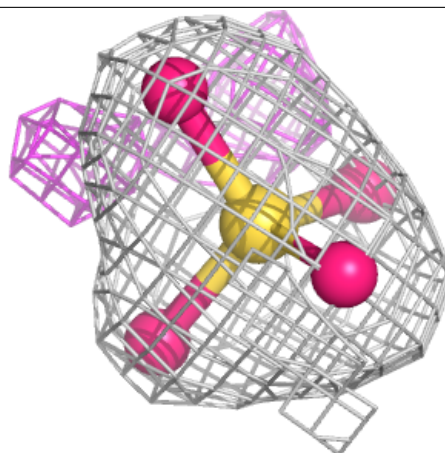
Electron density around SO4 J 403:

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



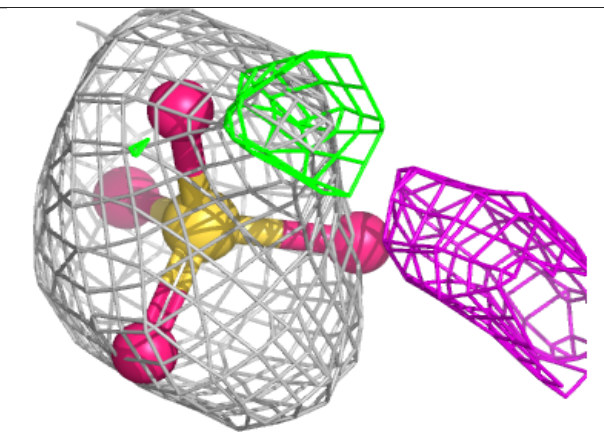
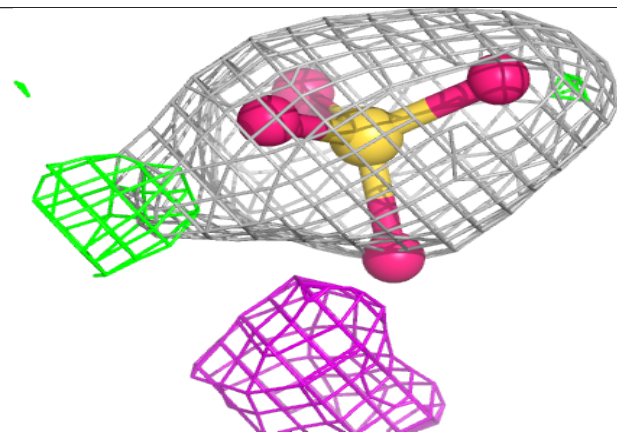
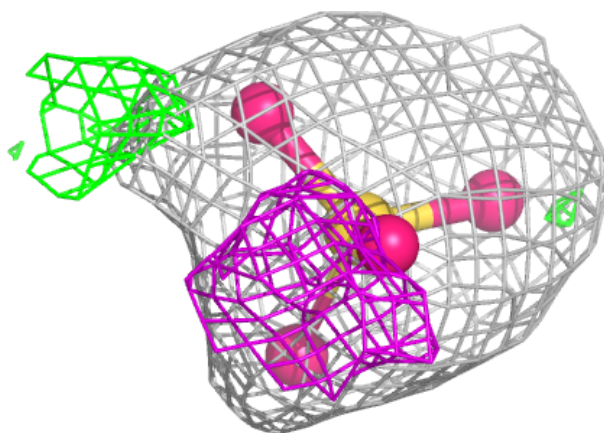
Electron density around SO4 K 402:

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



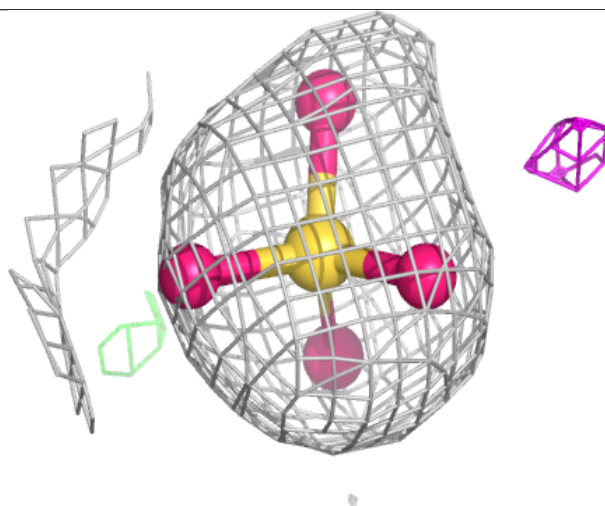
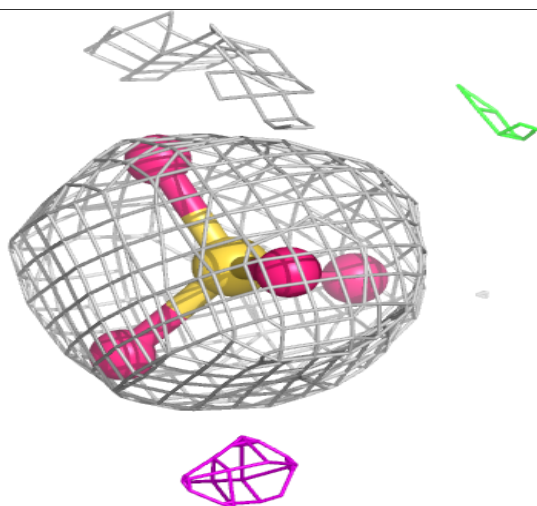
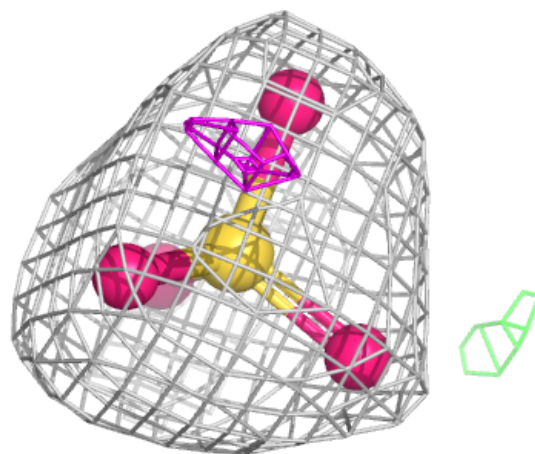
Electron density around SO4 K 403:

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



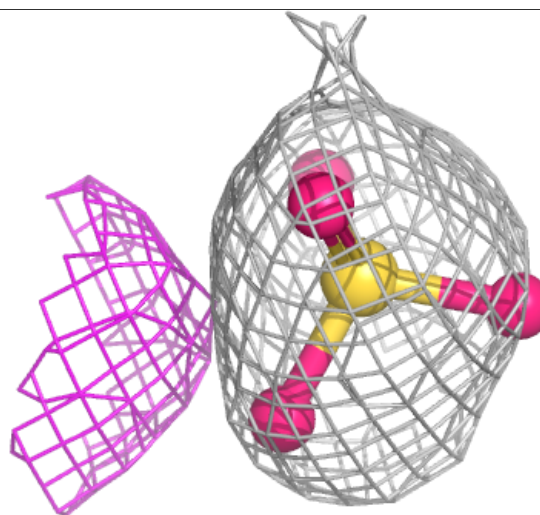
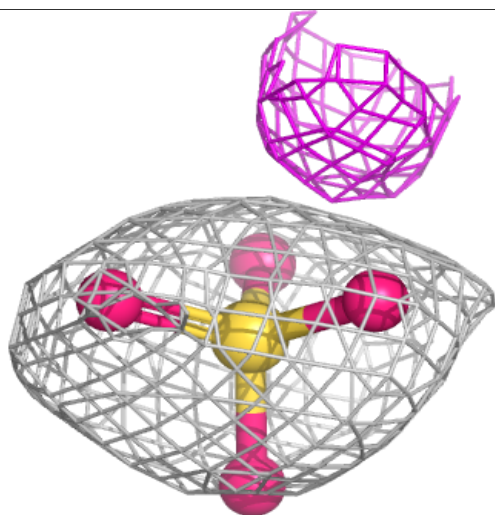
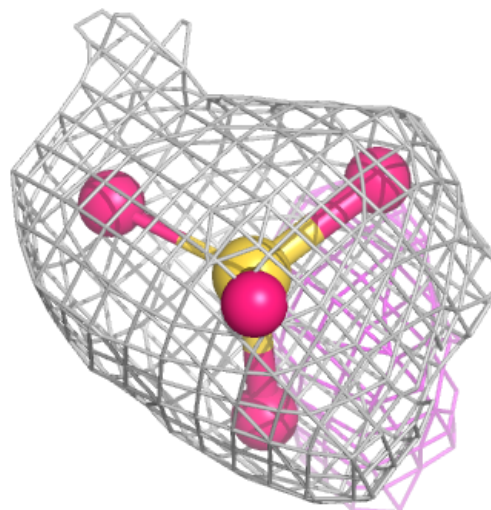
Electron density around SO4 Q 402:

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



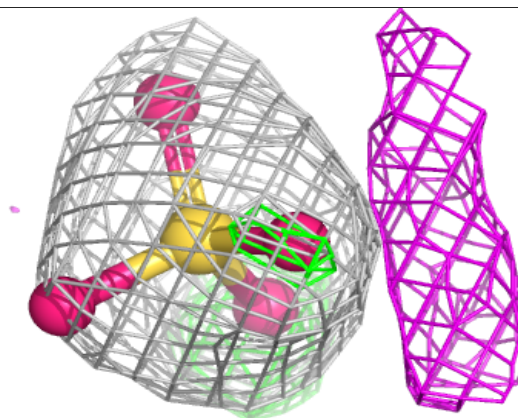
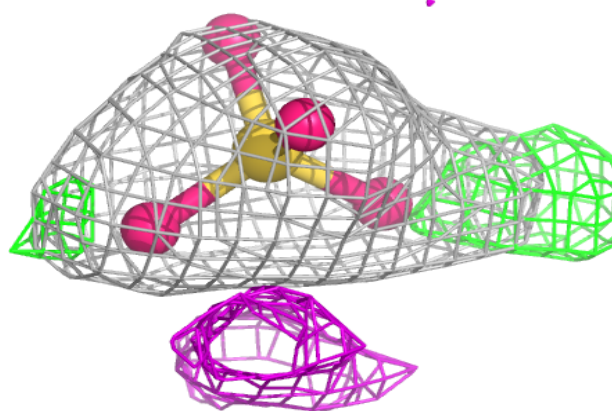
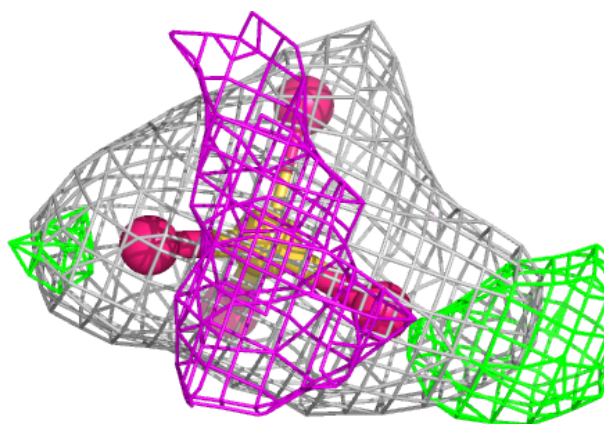
Electron density around SO4 C 403:

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



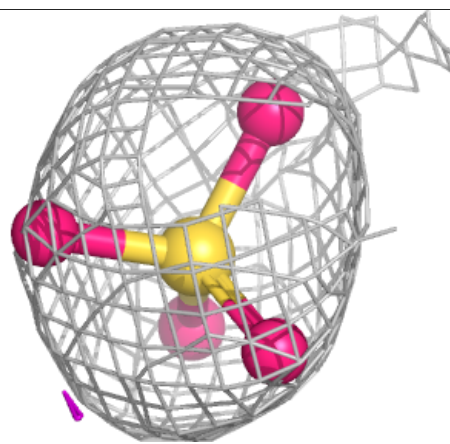
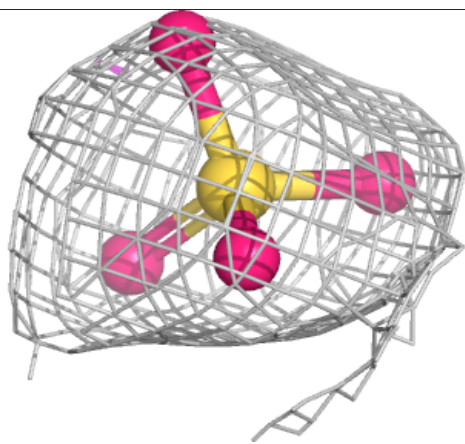
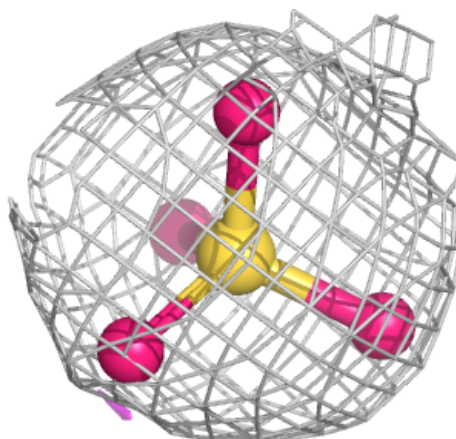
Electron density around SO4 G 403:

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



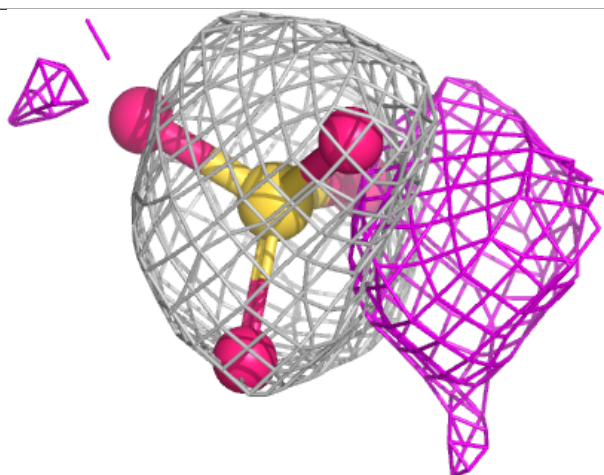
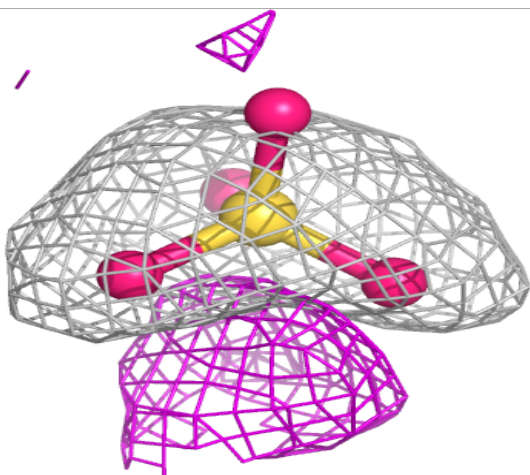
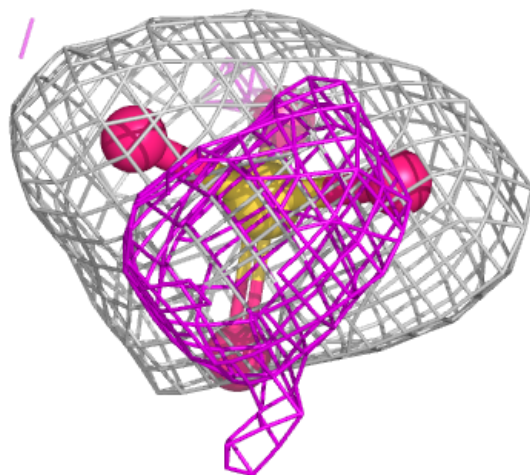
Electron density around SO4 V 403:

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



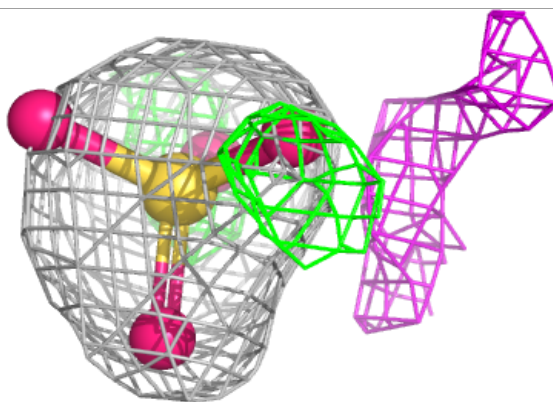
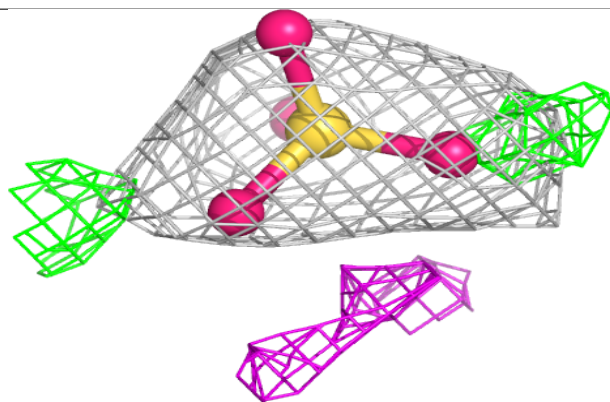
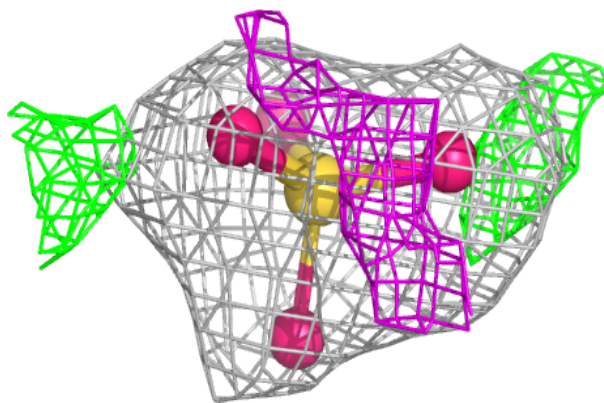
Electron density around SO4 V 404:

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



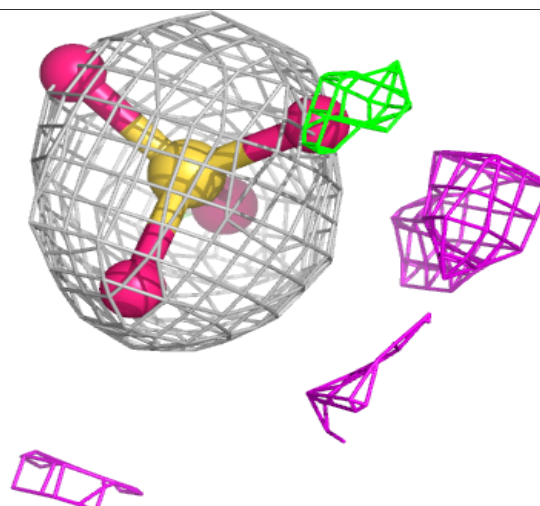
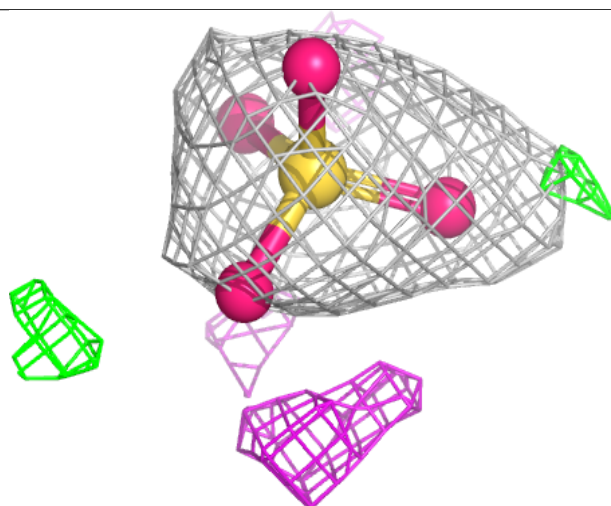
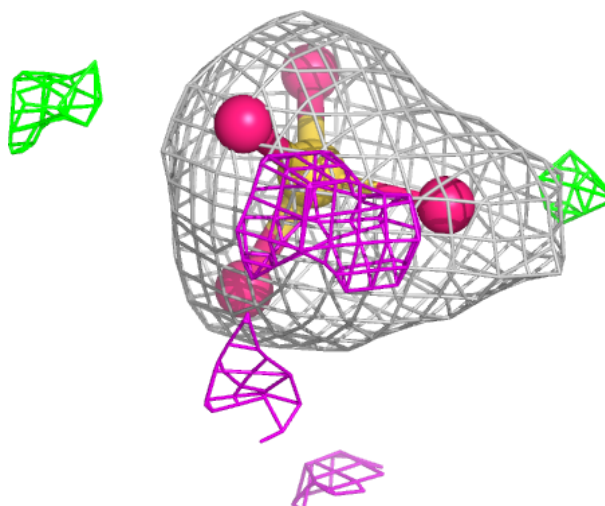
Electron density around SO4 A 404:

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



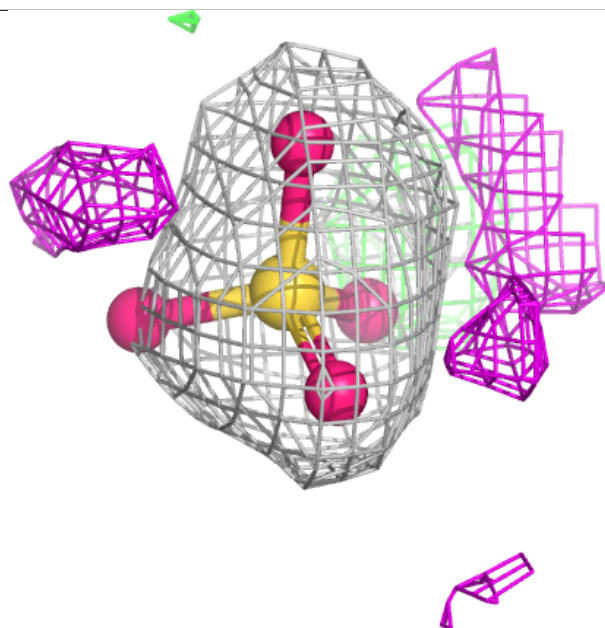
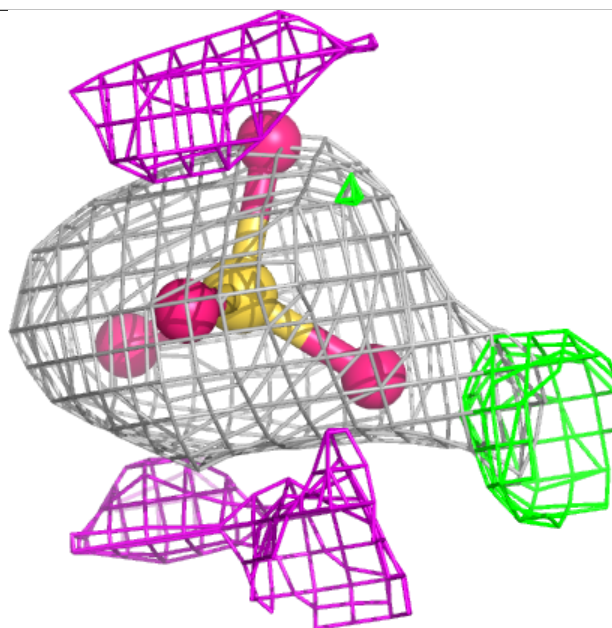
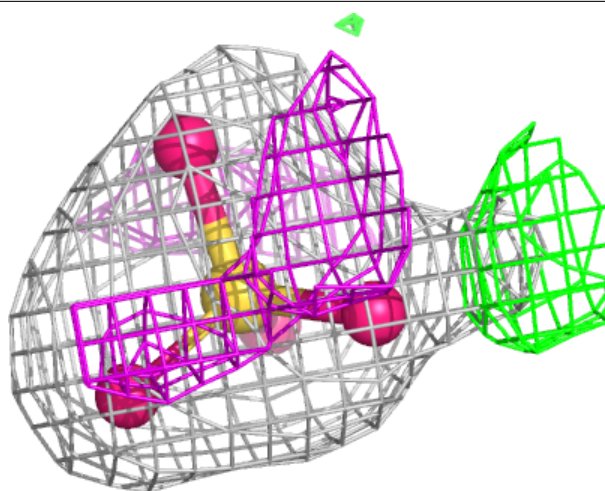
Electron density around SO4 D 403:

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



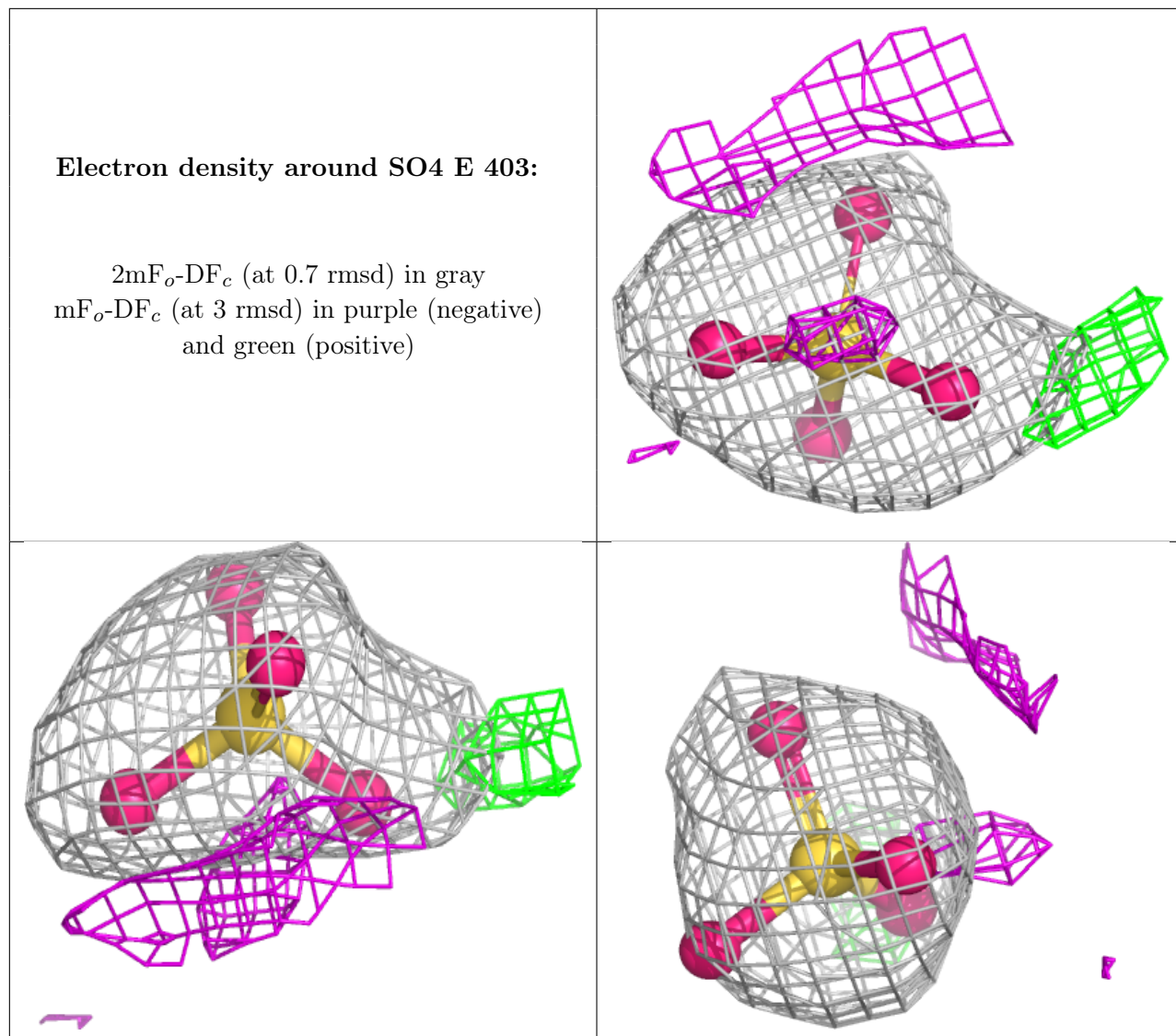
Electron density around SO4 U 403:

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



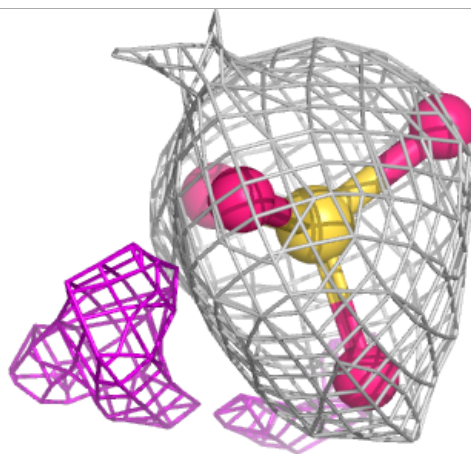
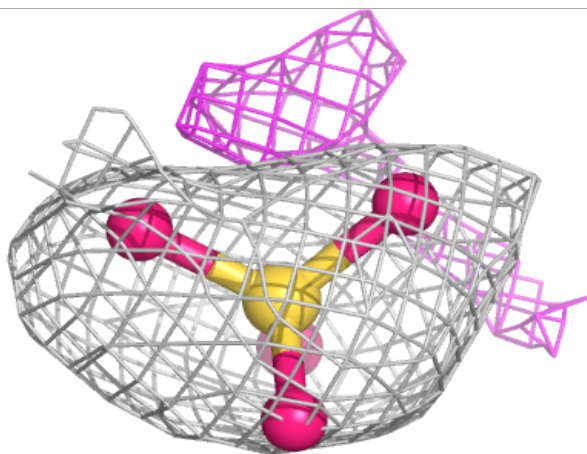
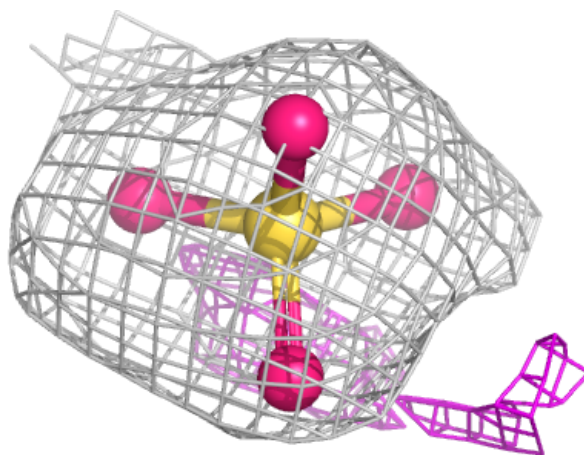
Electron density around SO4 E 403:

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



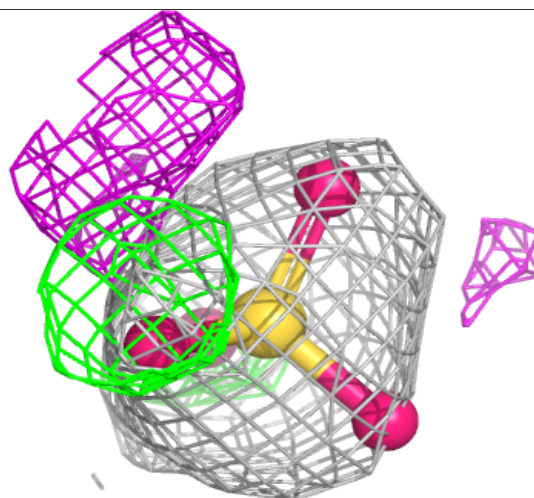
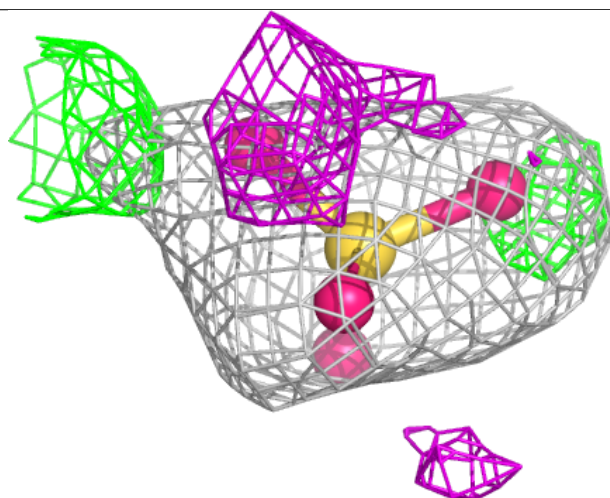
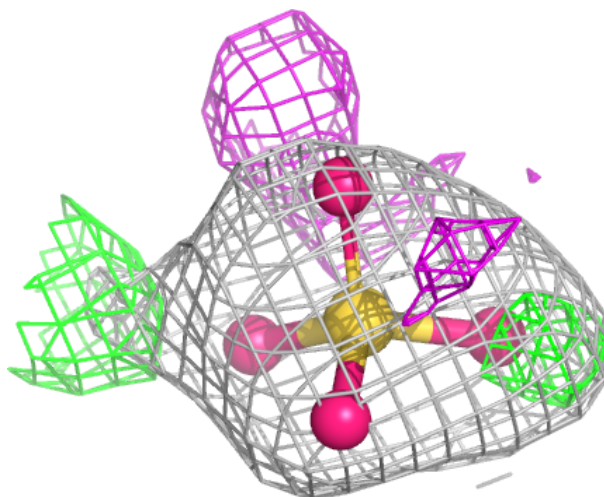
Electron density around SO4 W 403:

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



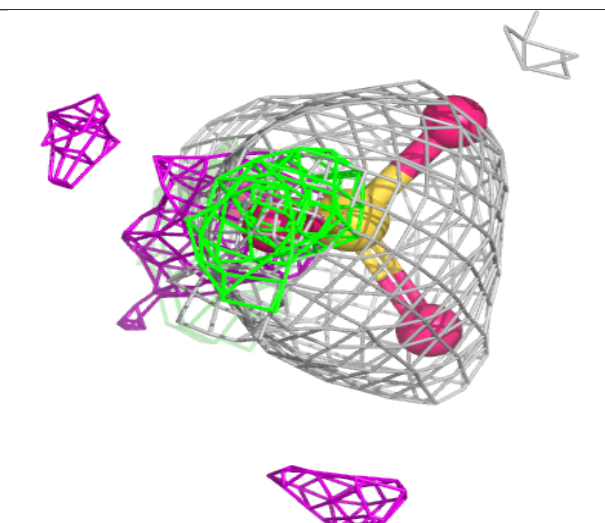
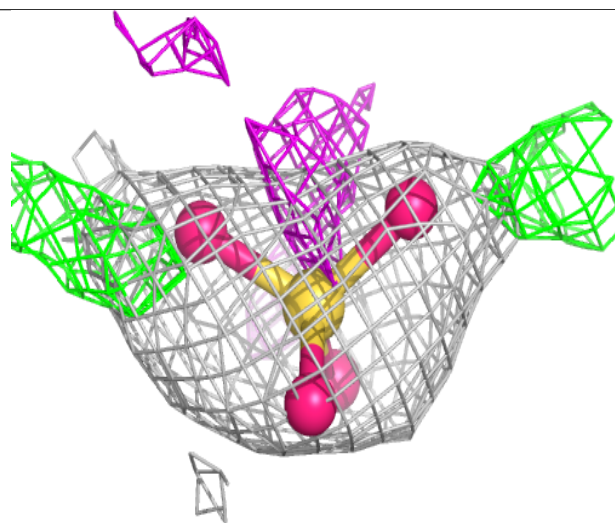
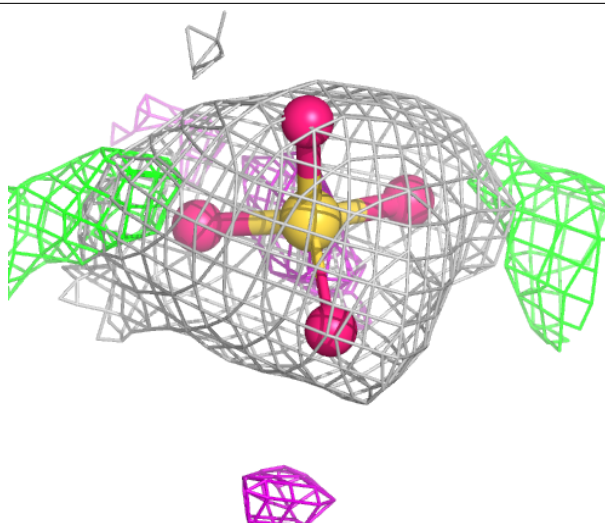
Electron density around SO4 M 403:

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



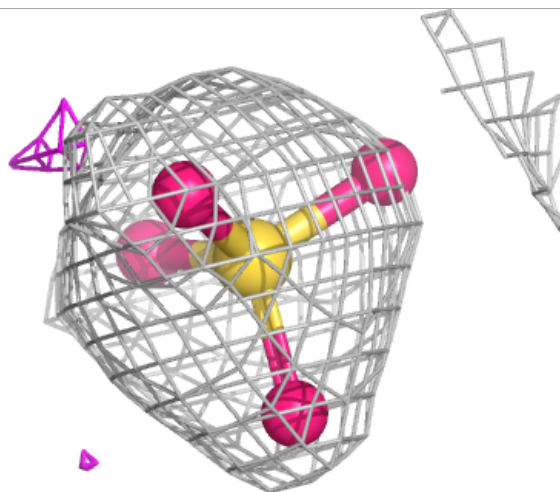
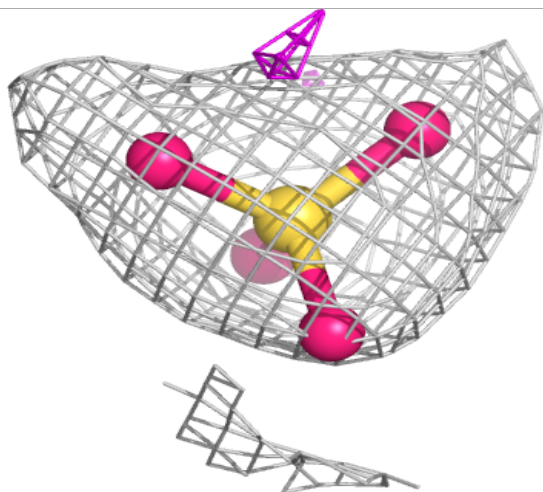
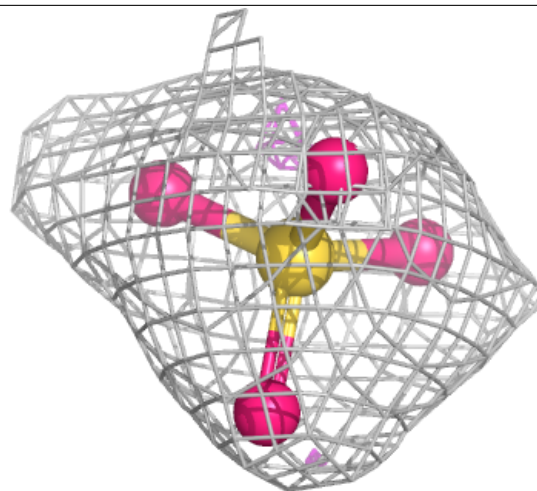
Electron density around SO4 N 403:

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



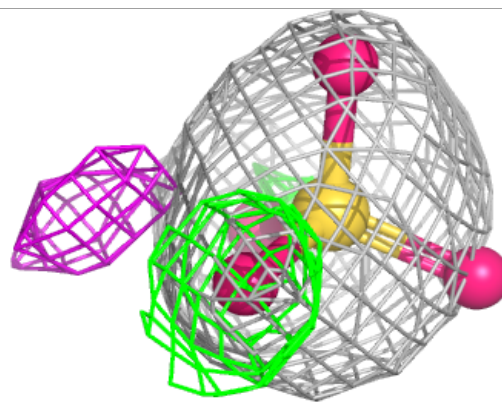
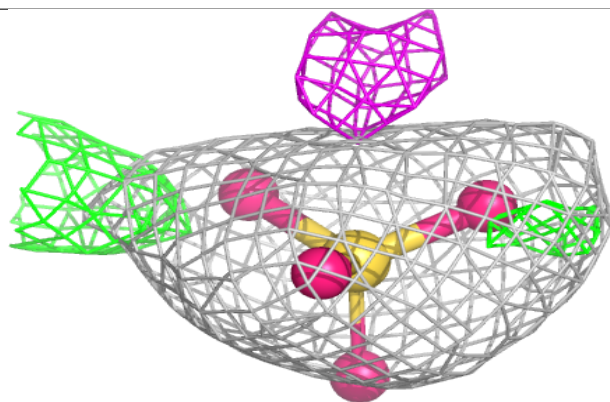
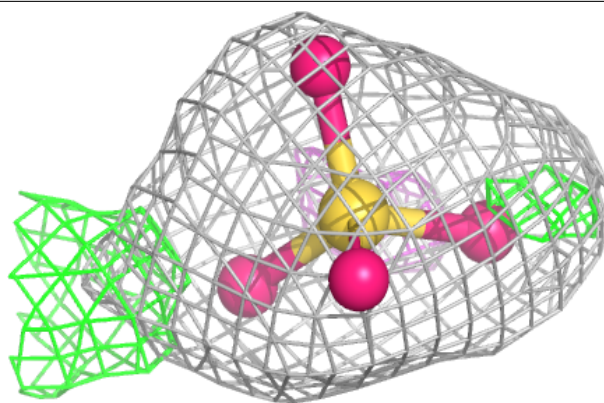
Electron density around SO4 O 402:

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



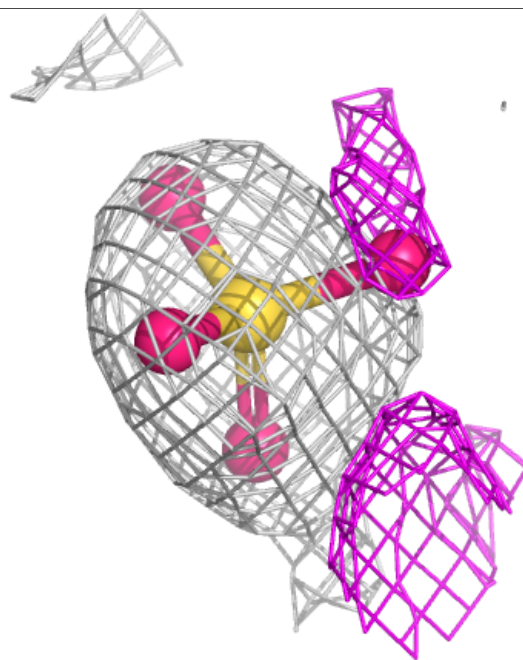
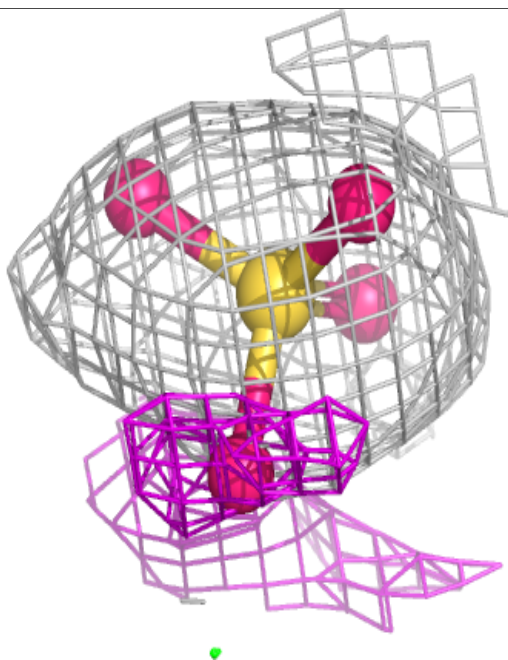
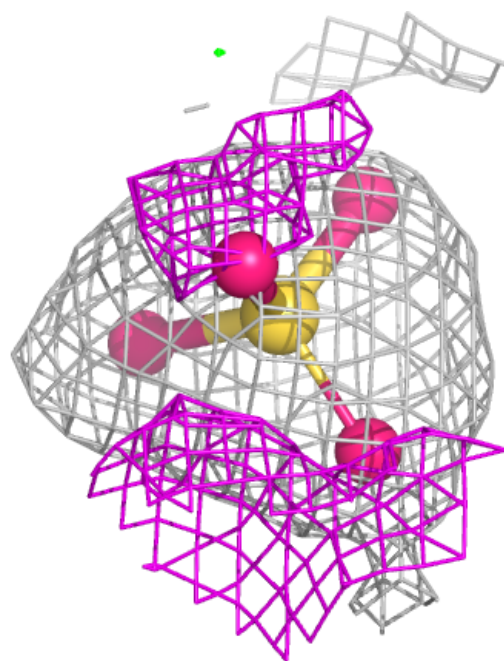
Electron density around SO4 H 403:

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



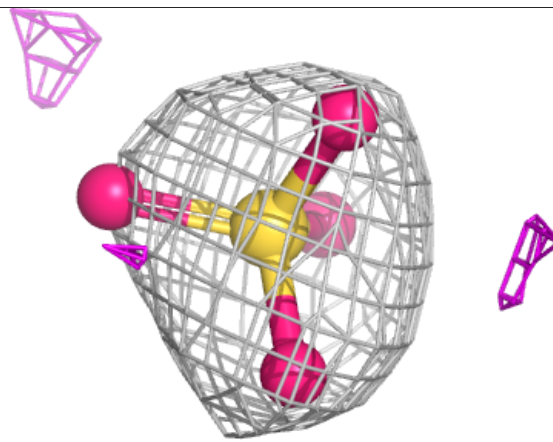
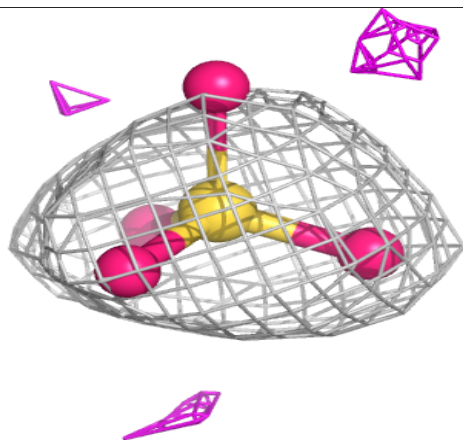
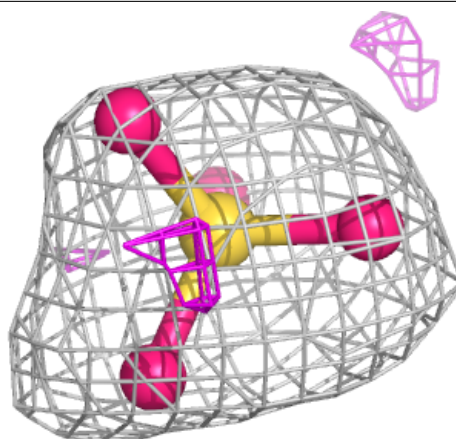
Electron density around SO4 R 402:

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



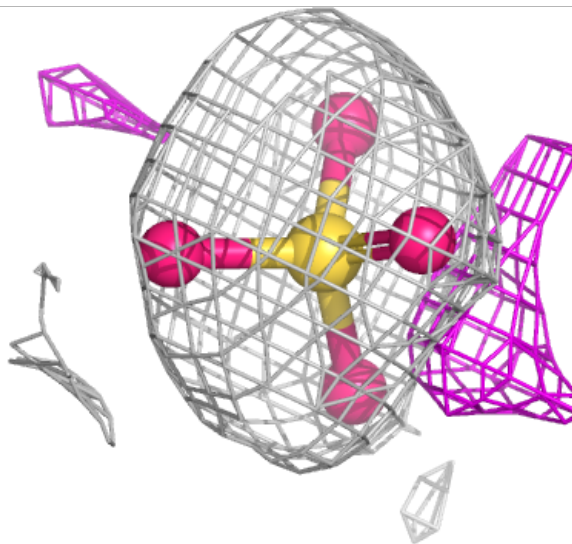
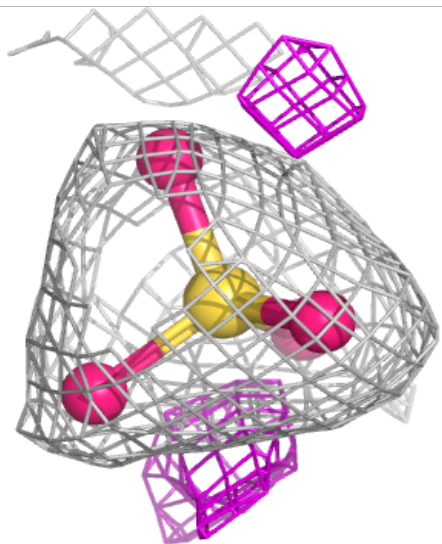
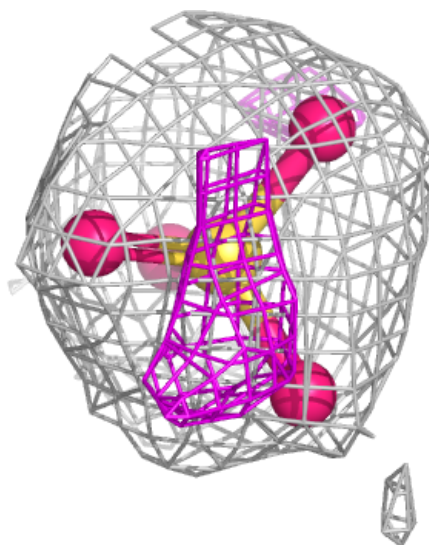
Electron density around SO4 F 403:

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



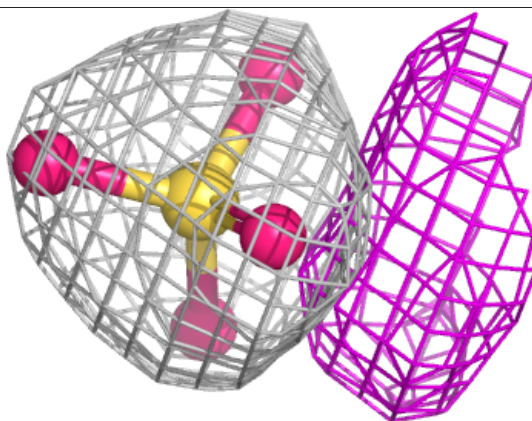
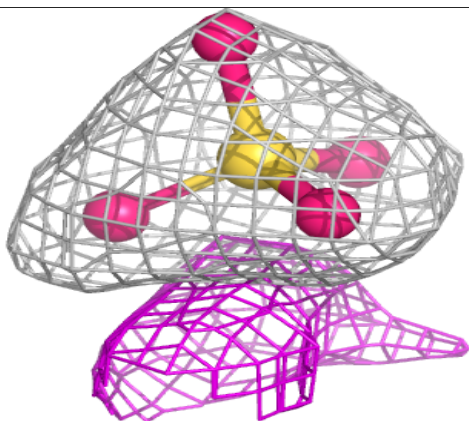
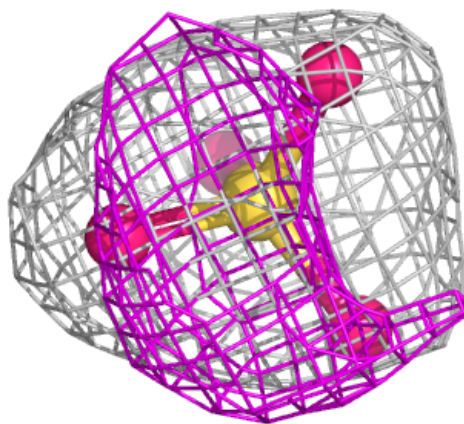
Electron density around SO4 T 402:

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



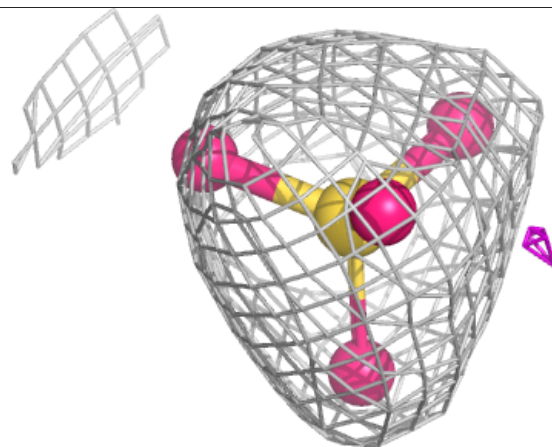
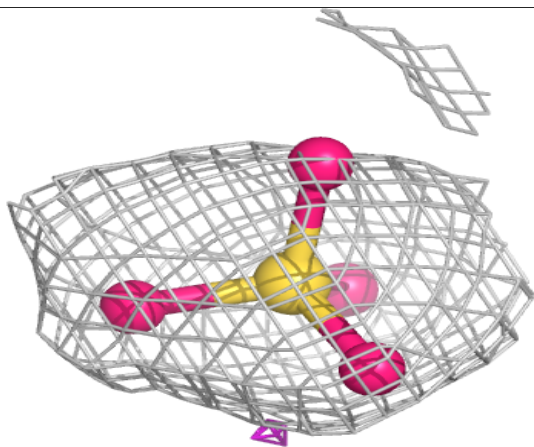
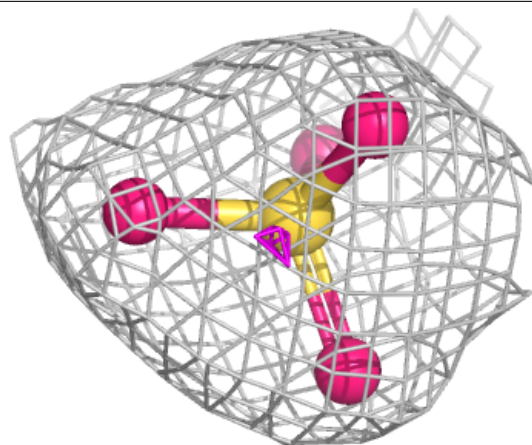
Electron density around SO4 C 404:

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



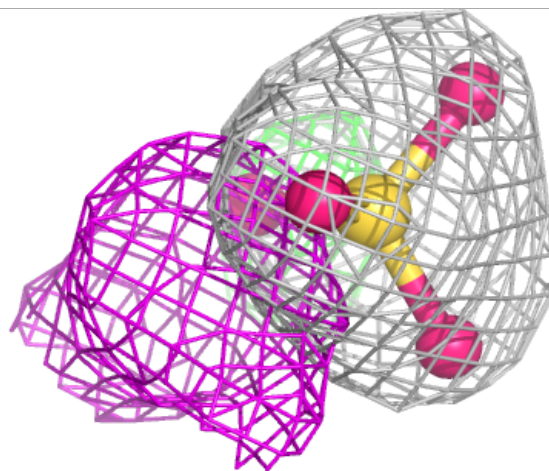
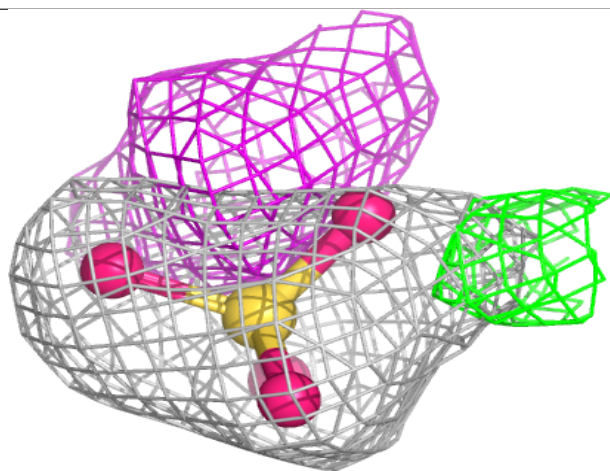
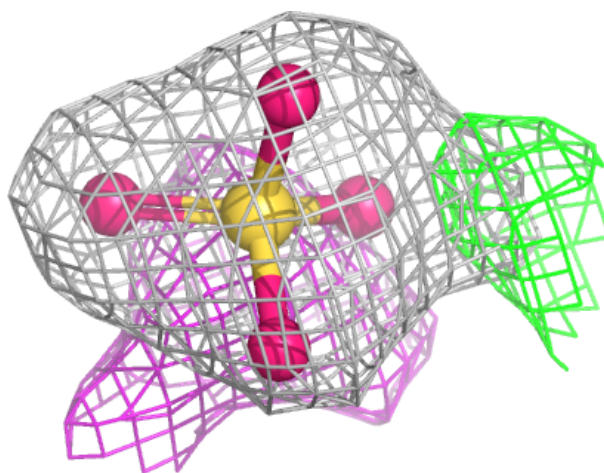
Electron density around SO4 P 402:

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



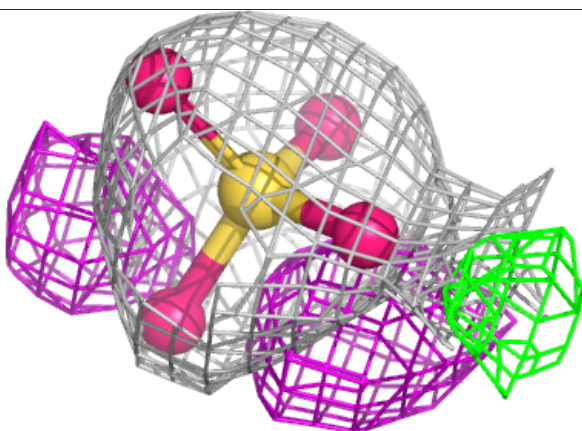
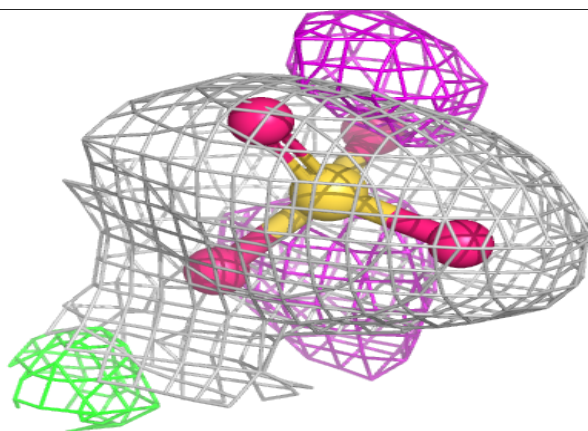
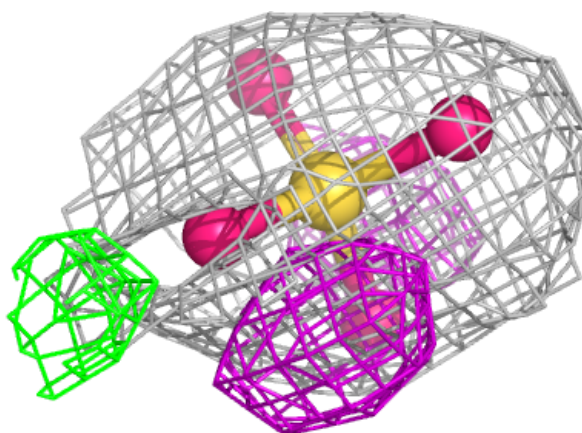
Electron density around SO4 I 403:

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



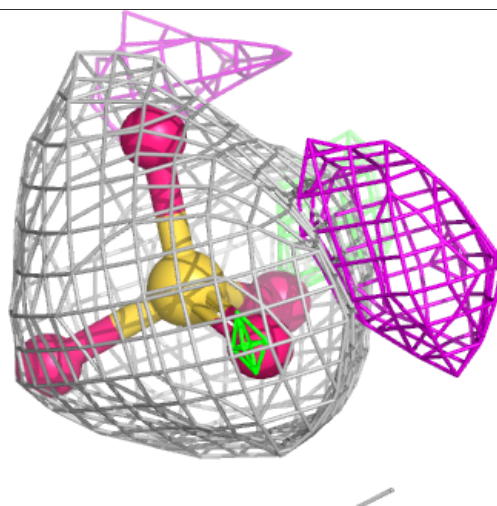
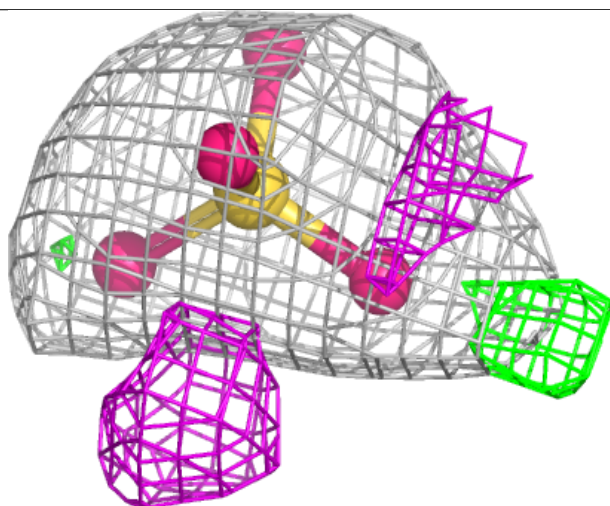
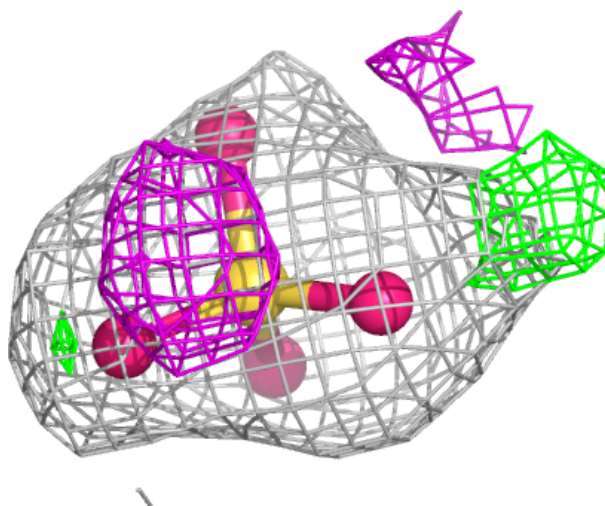
Electron density around SO4 I 402:

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



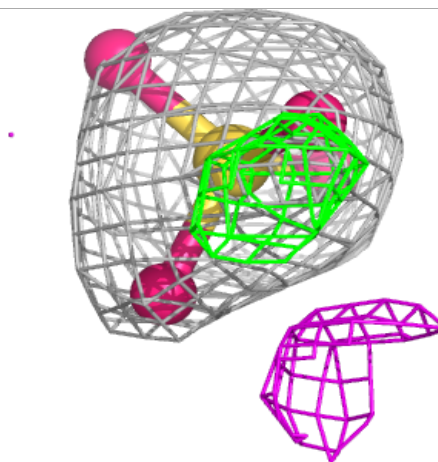
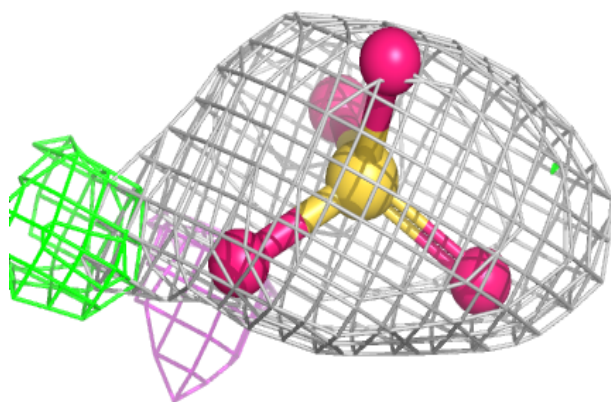
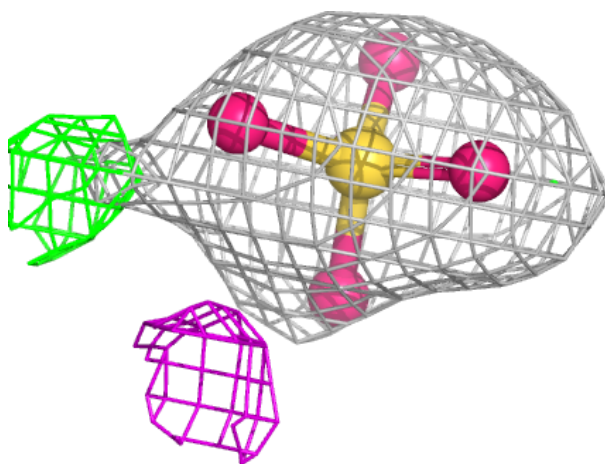
Electron density around SO4 A 403:

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



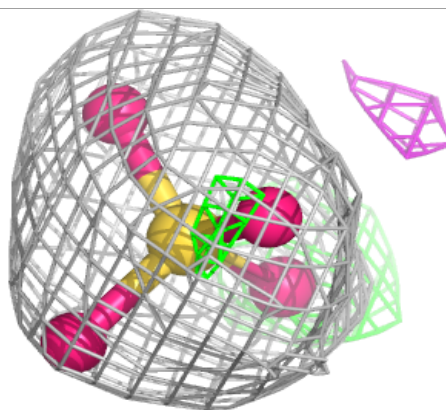
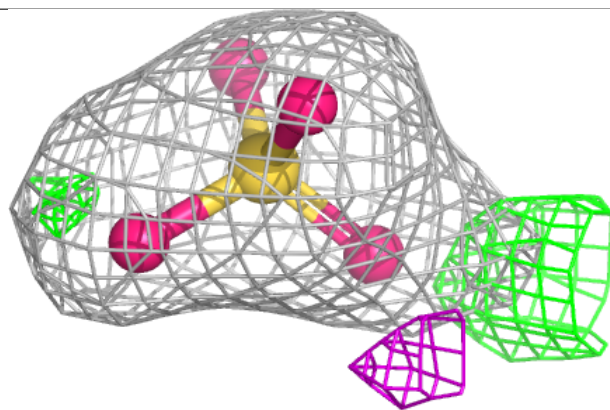
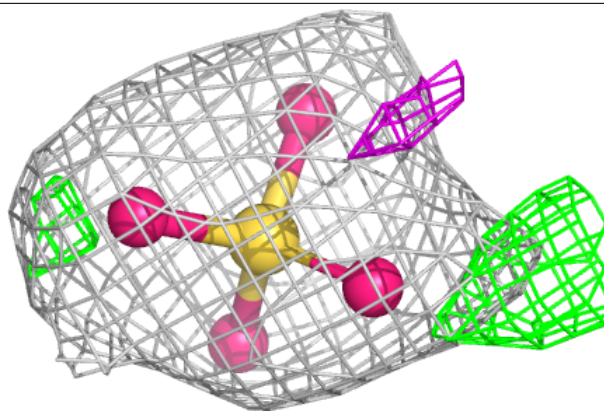
Electron density around SO4 O 403:

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

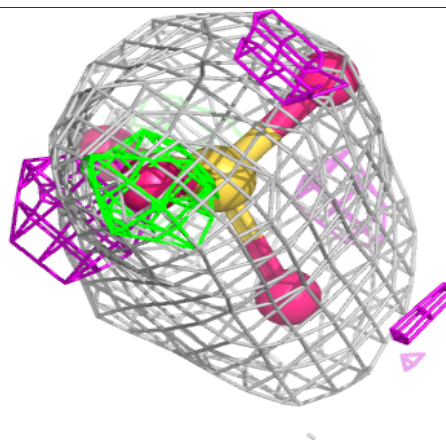
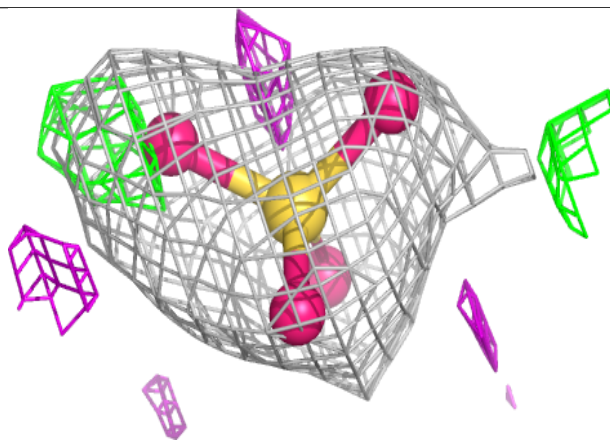
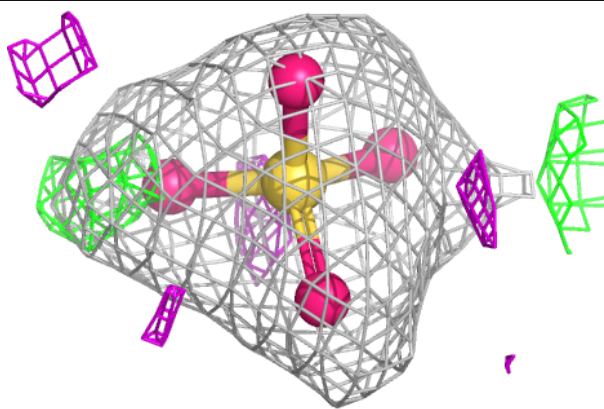


Electron density around SO4 B 403:

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

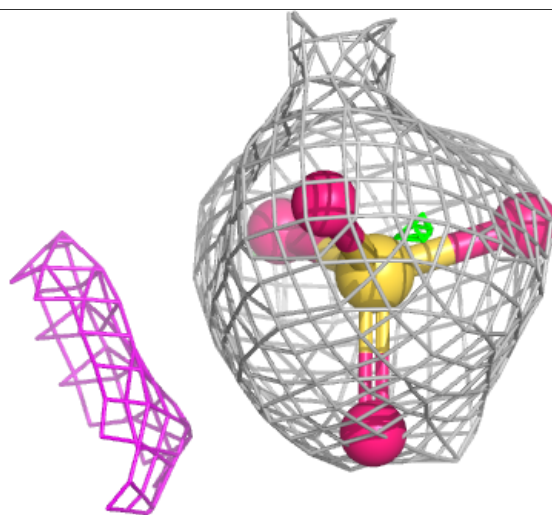
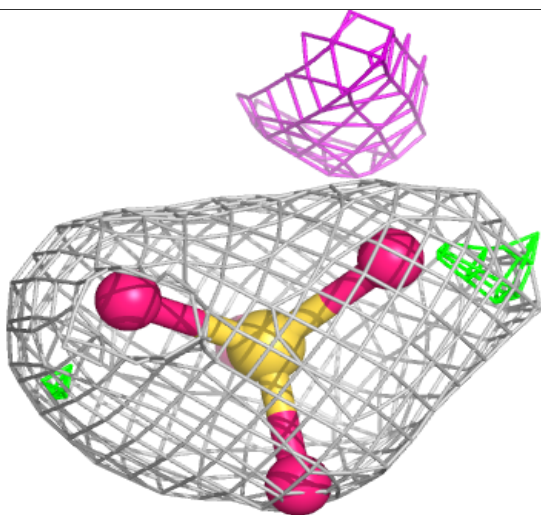
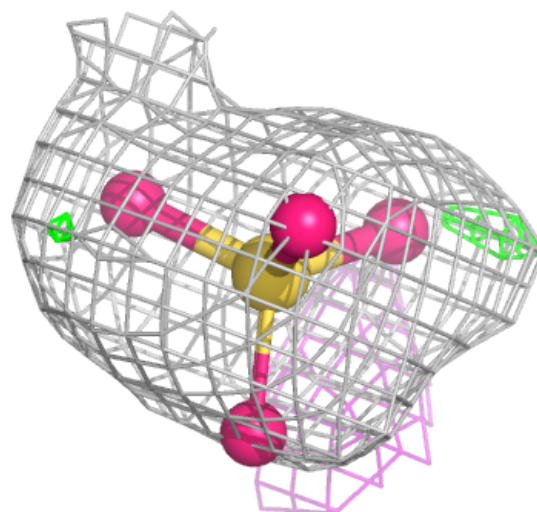
**Electron density around SO4 Q 403:**

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



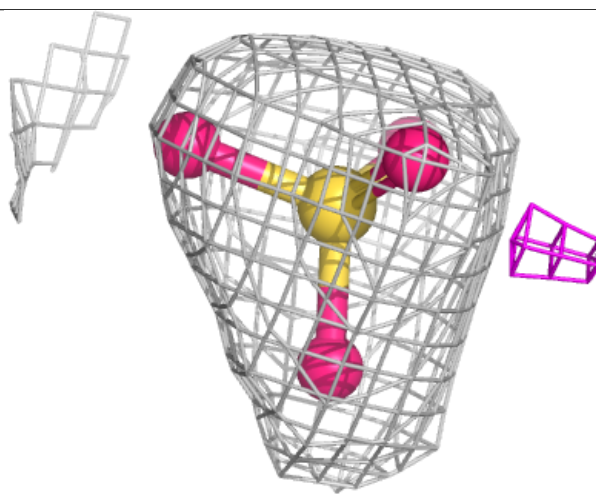
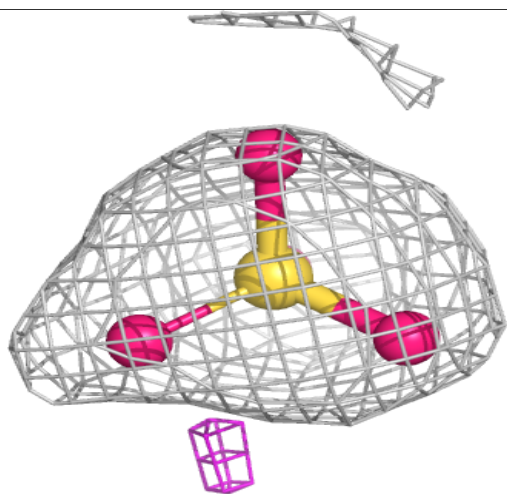
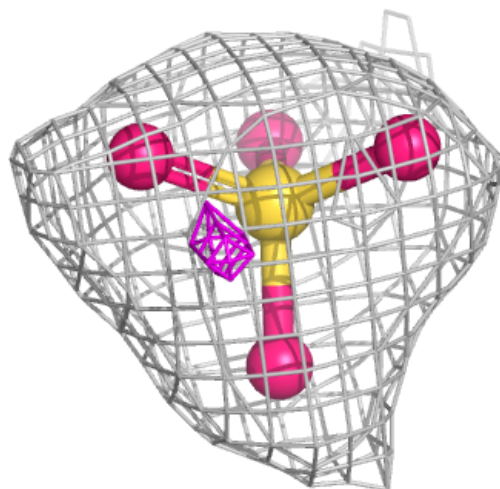
Electron density around SO4 P 403:

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



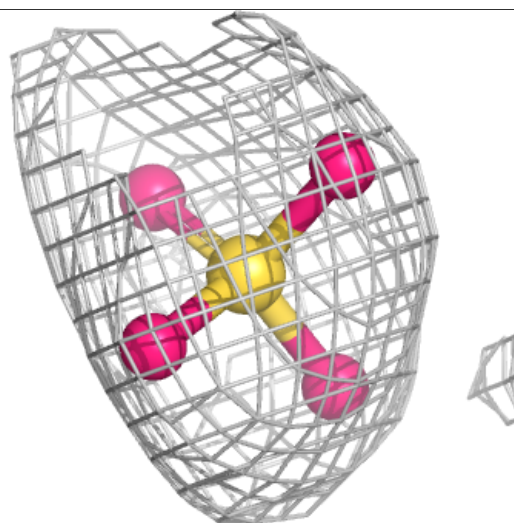
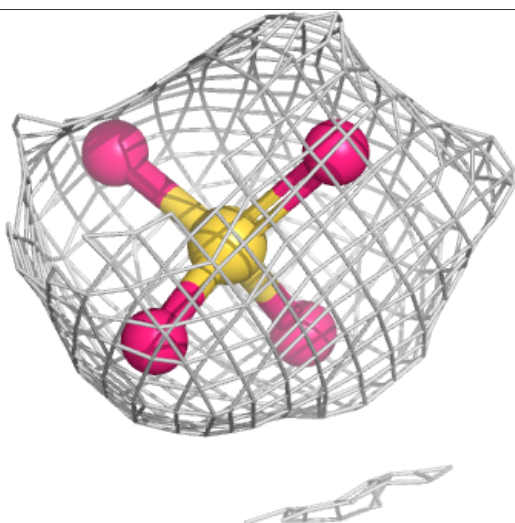
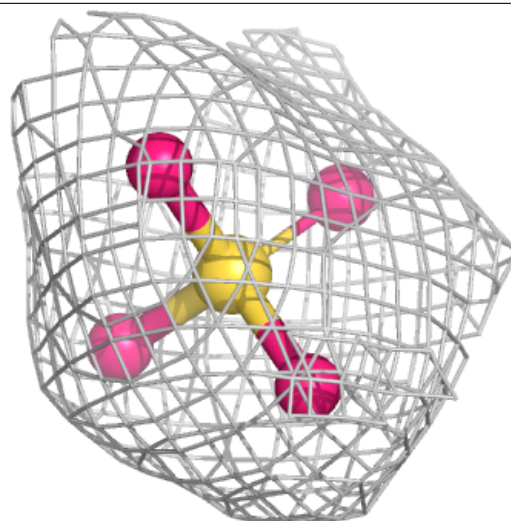
Electron density around SO4 N 402:

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



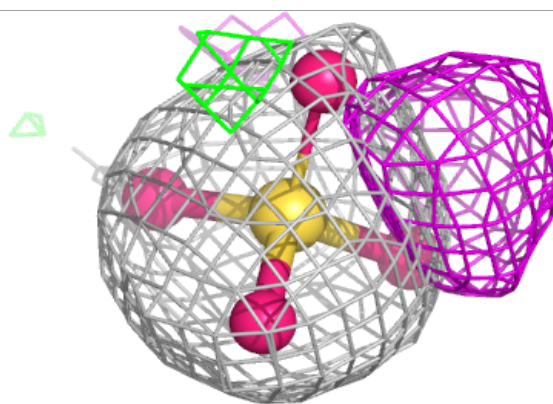
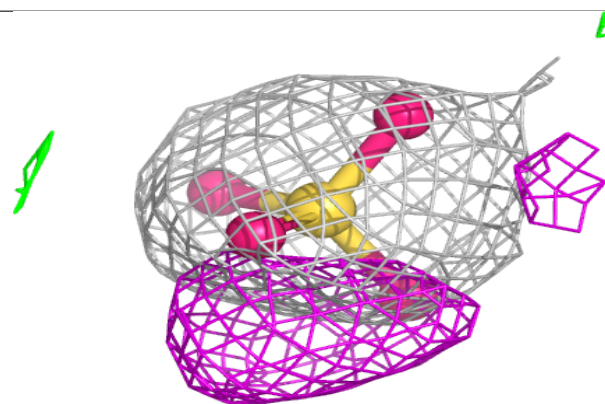
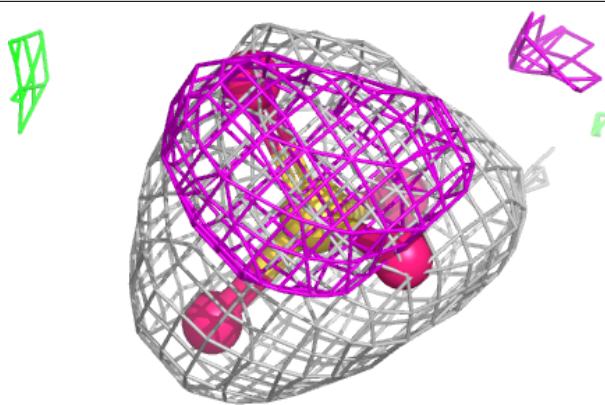
Electron density around SO4 M 402:

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



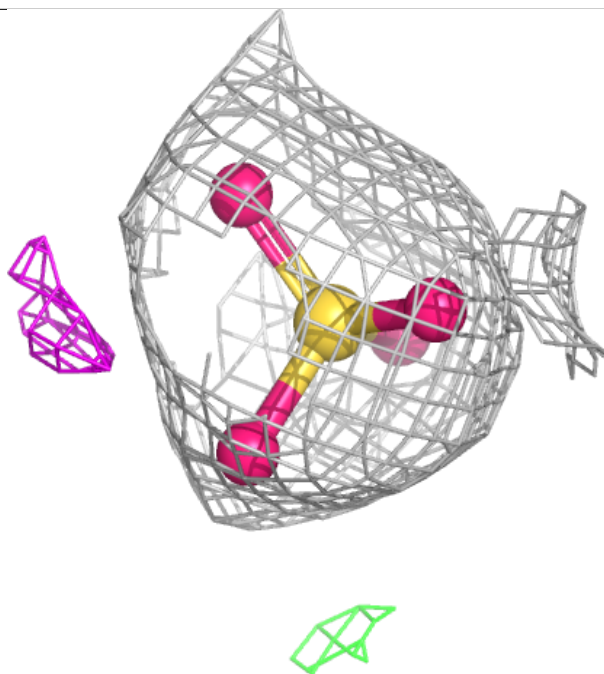
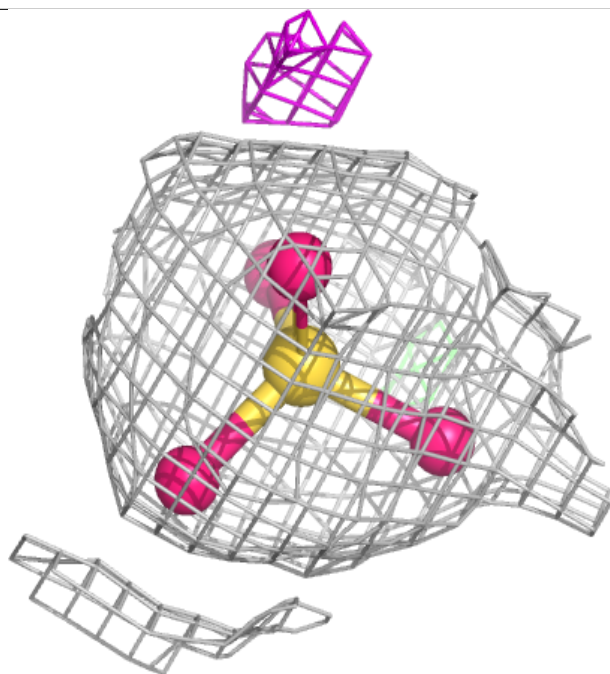
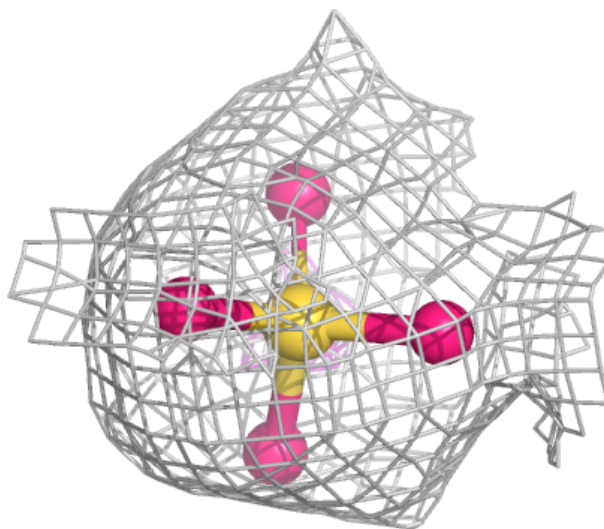
Electron density around SO4 B 402:

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



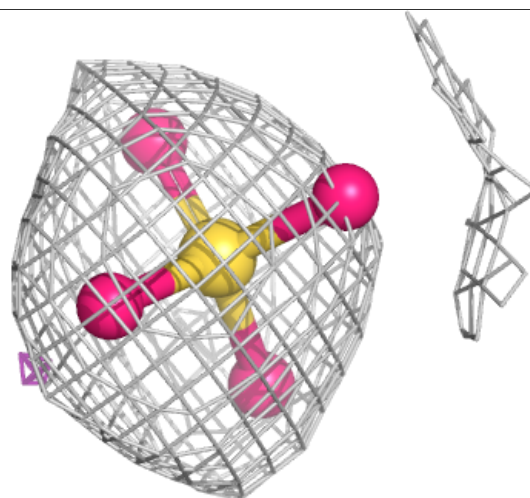
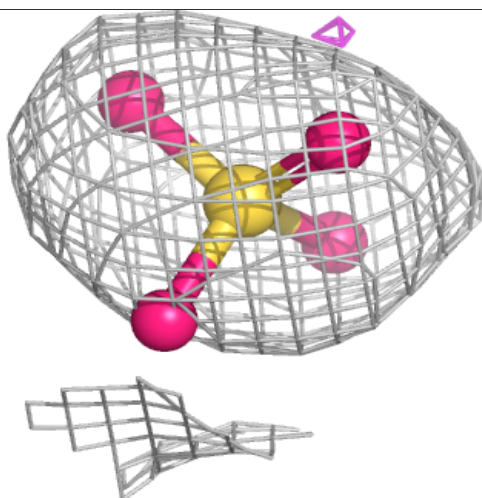
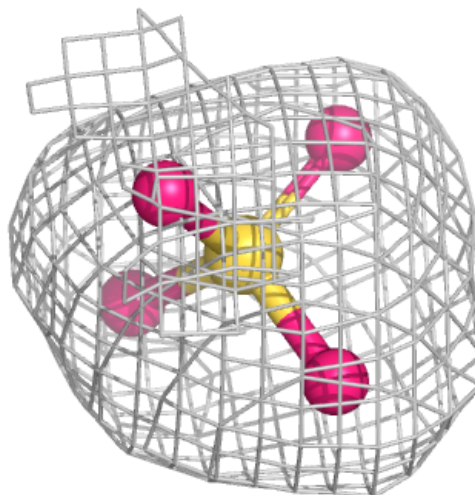
Electron density around SO4 Z 402:

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



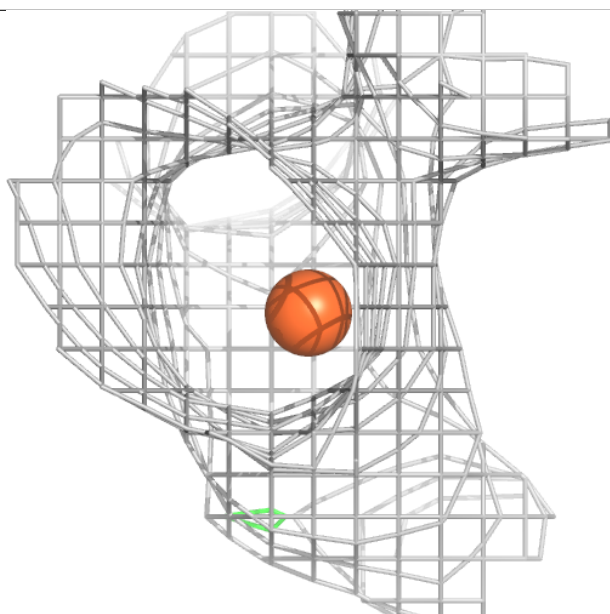
Electron density around SO4 J 402:

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



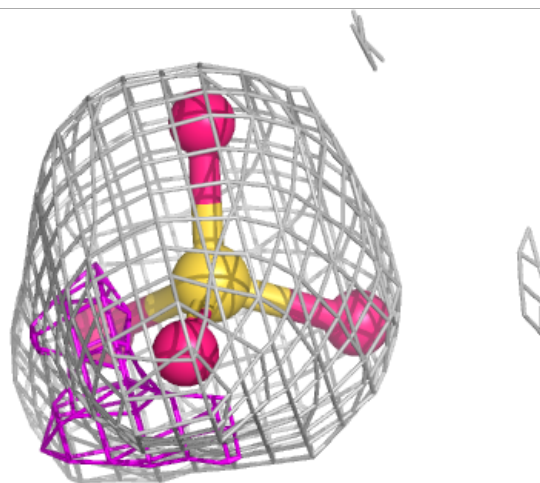
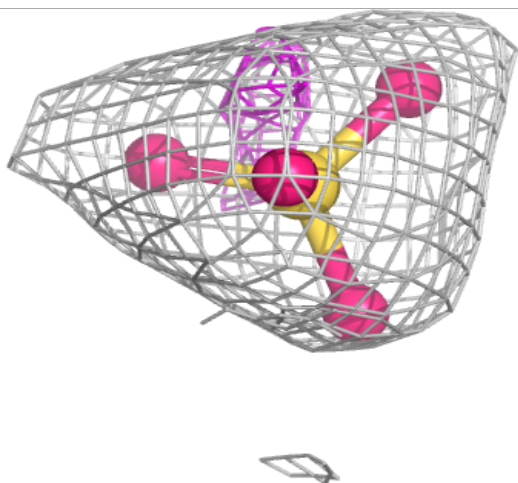
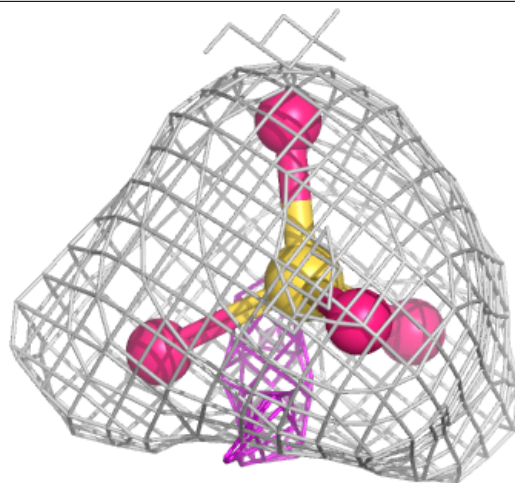
Electron density around FE D 401:

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



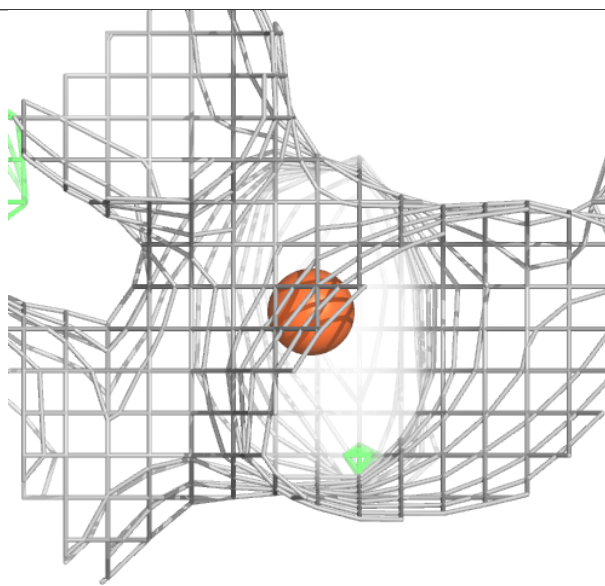
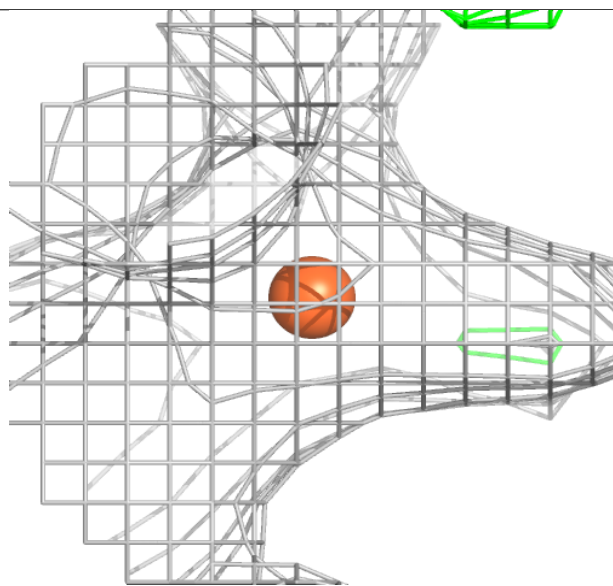
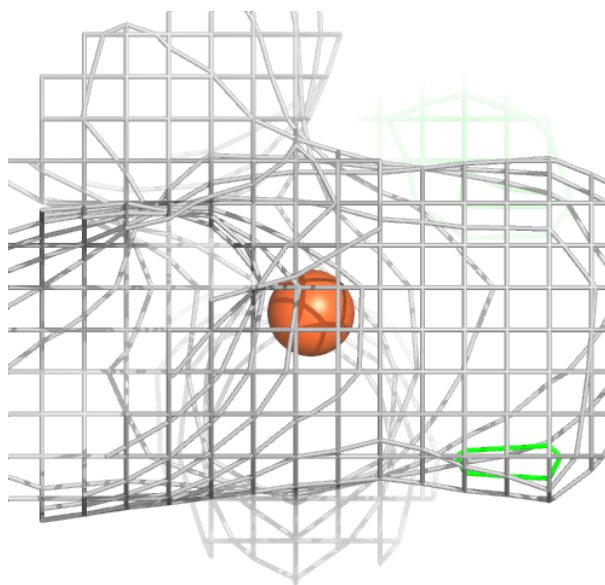
Electron density around SO4 A 402:

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



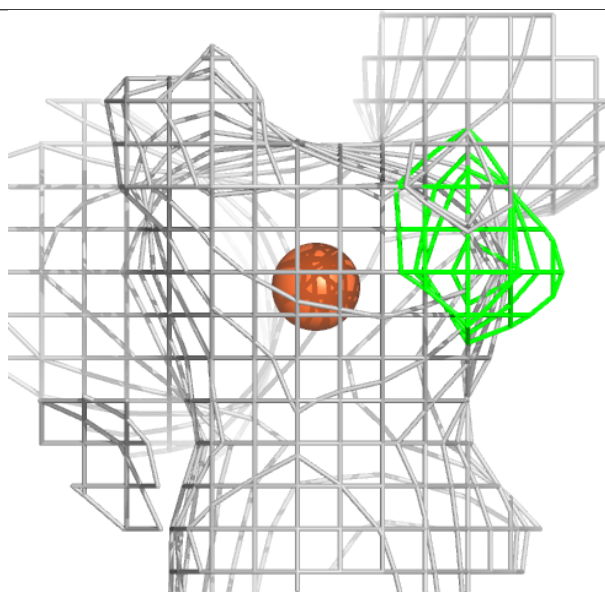
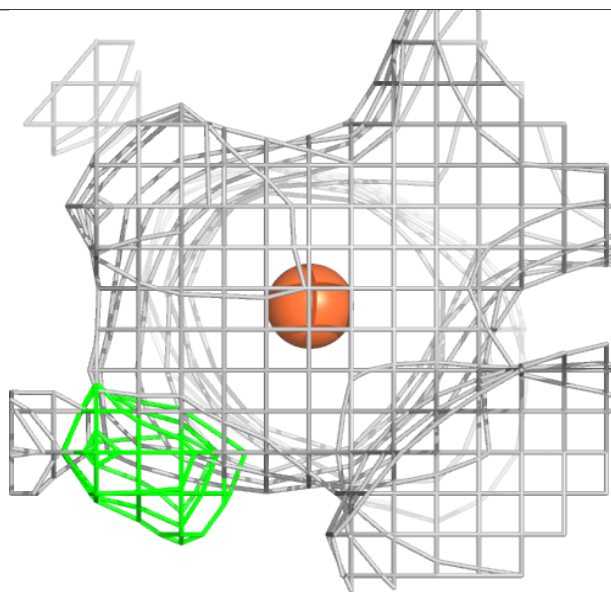
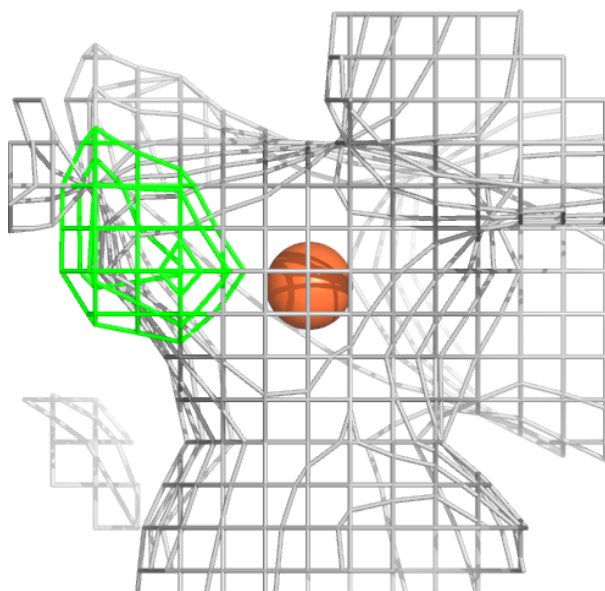
Electron density around FE V 402:

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



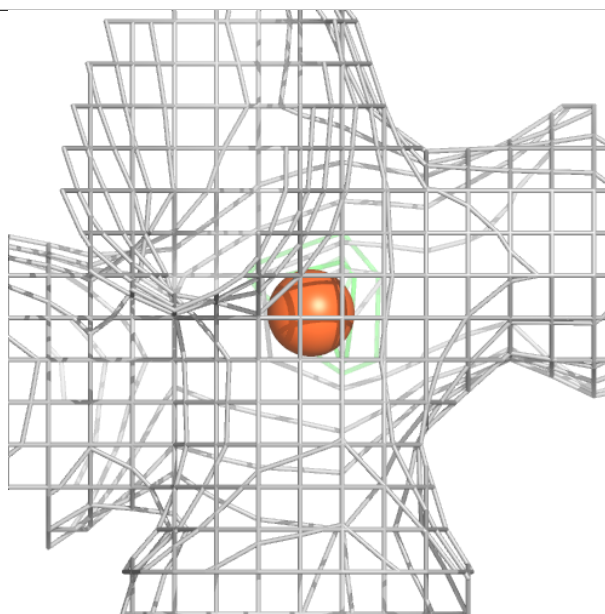
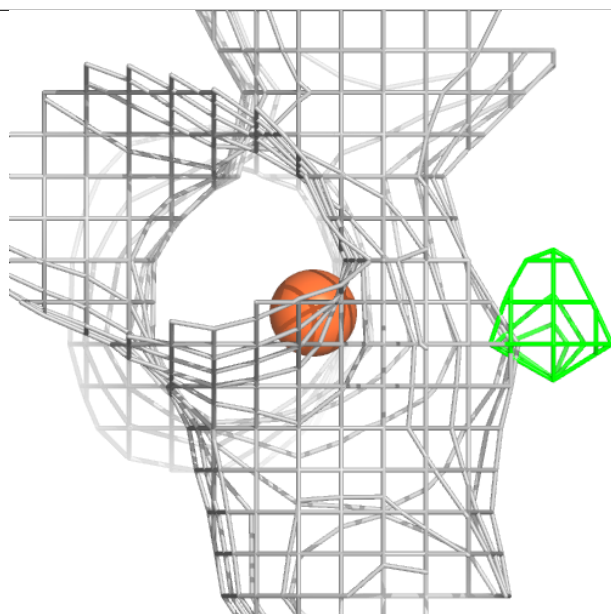
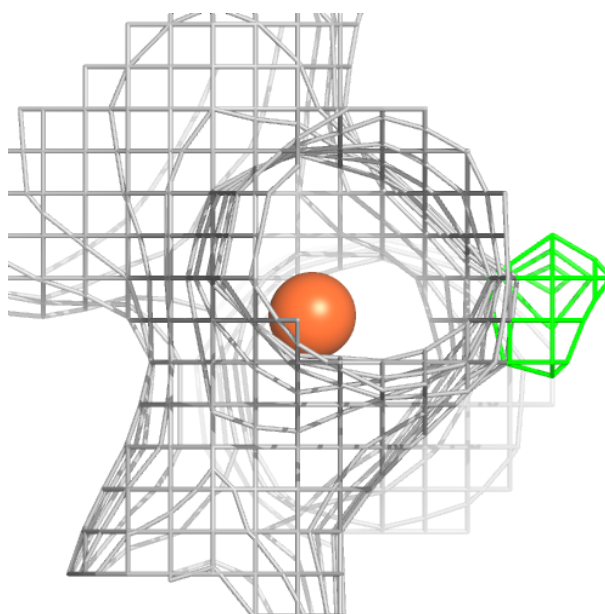
Electron density around FE Z 401:

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



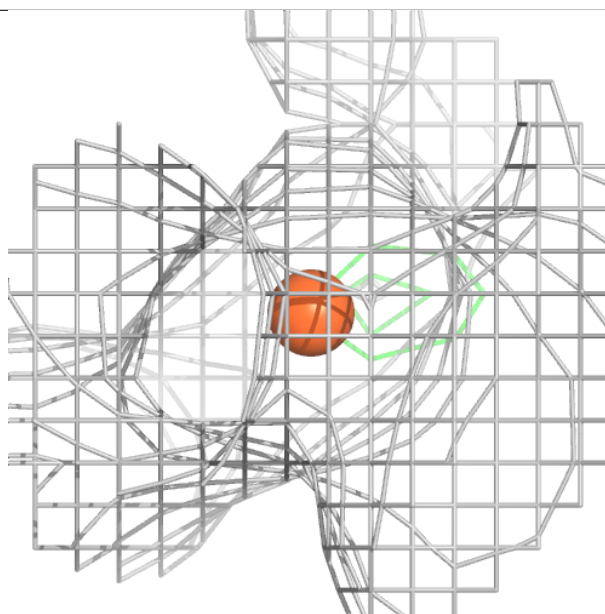
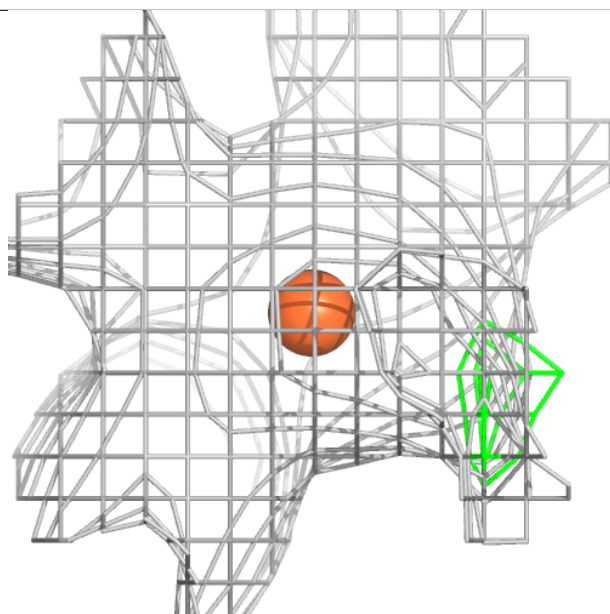
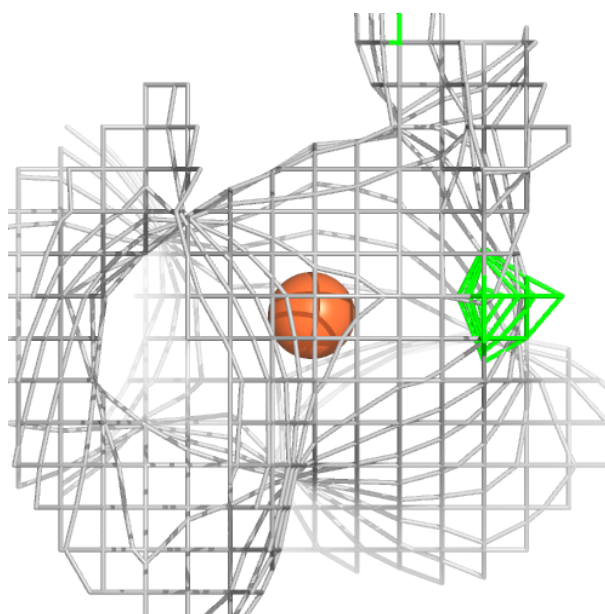
Electron density around FE L 401:

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



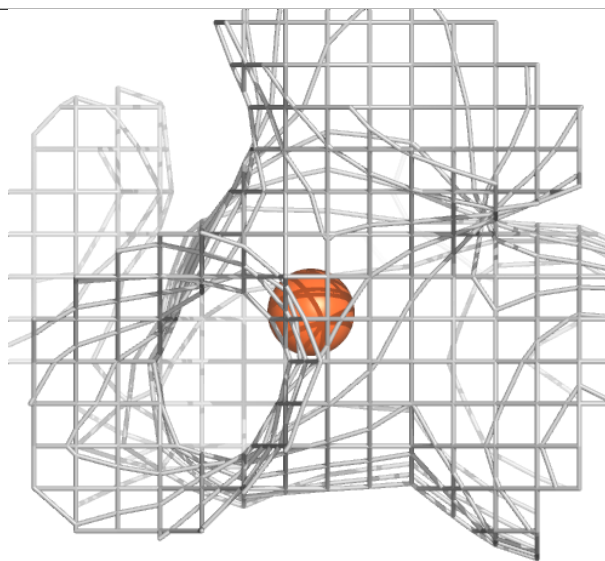
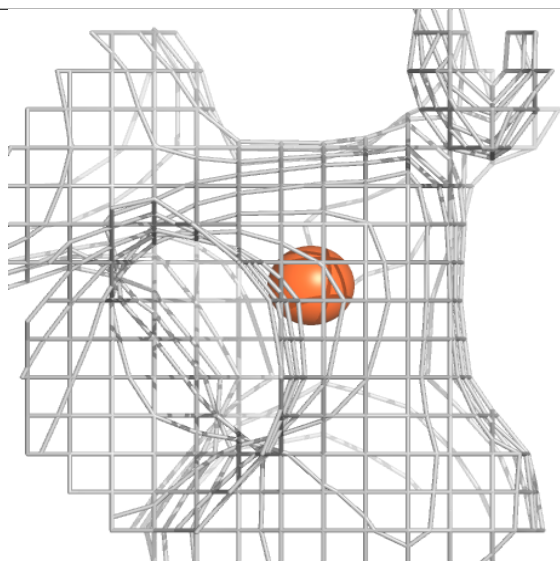
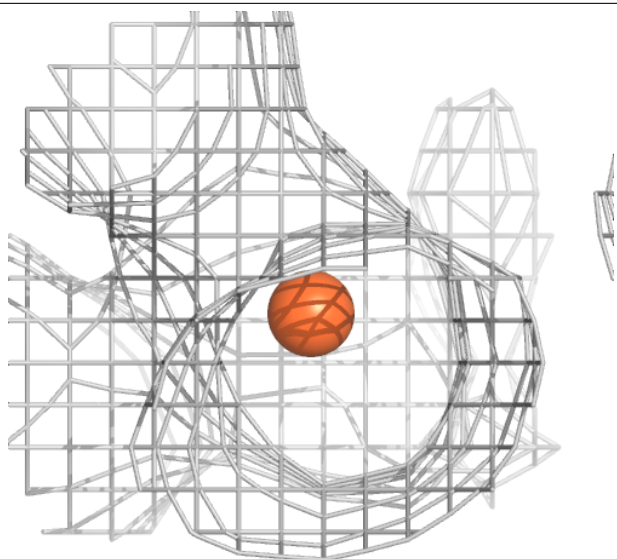
Electron density around FE O 401:

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



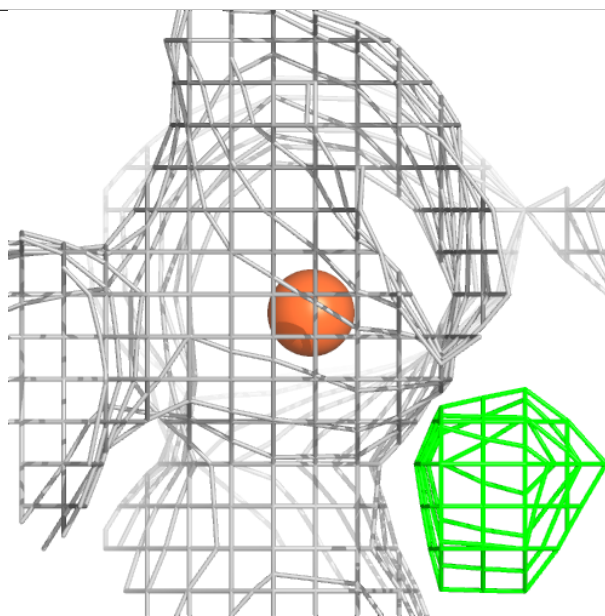
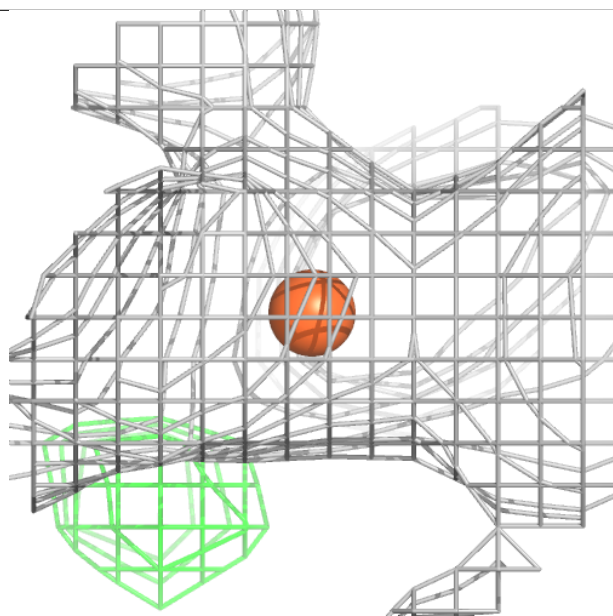
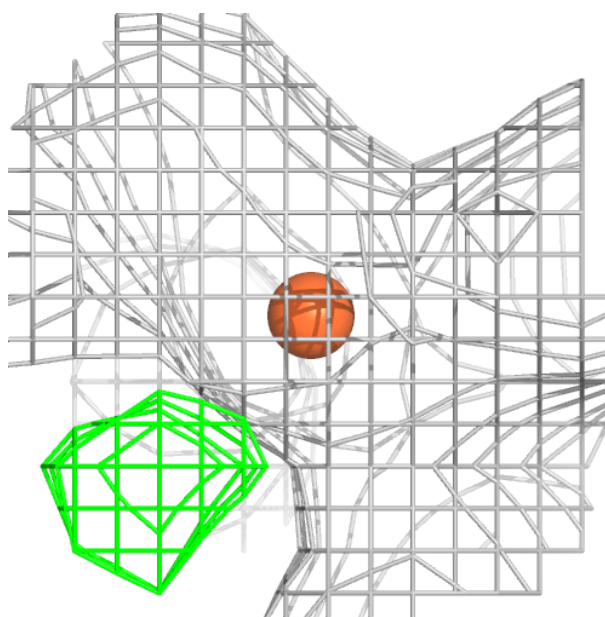
Electron density around FE Q 401:

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



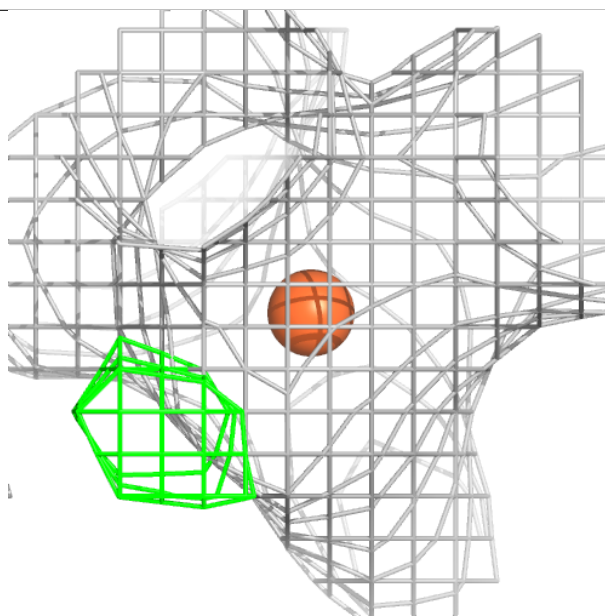
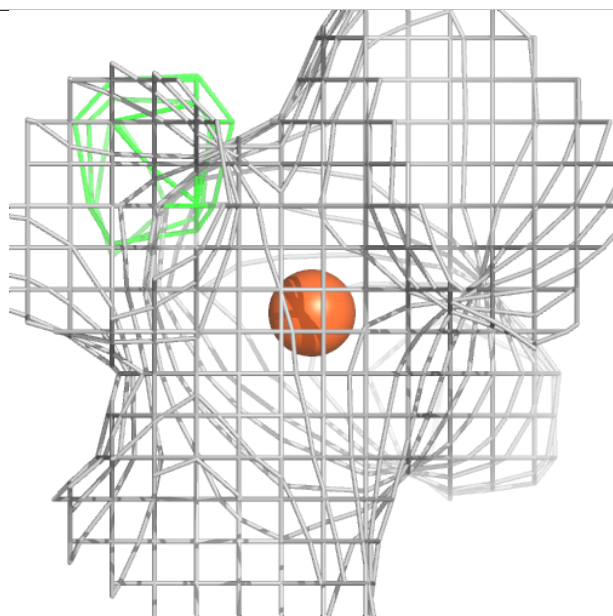
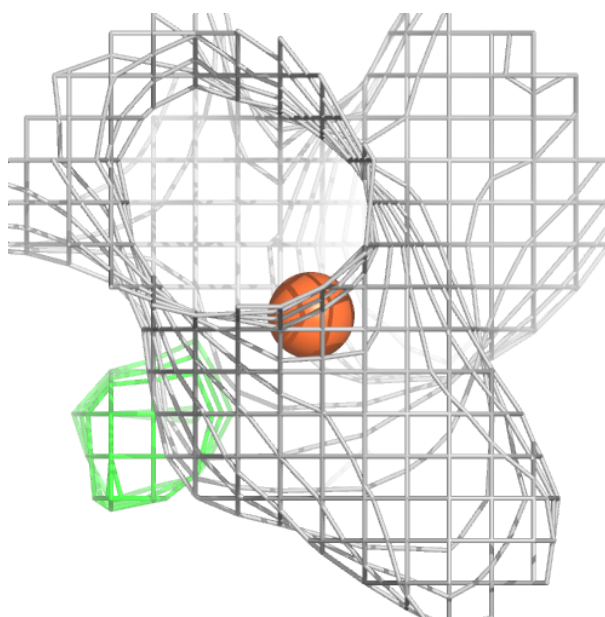
Electron density around FE J 401:

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



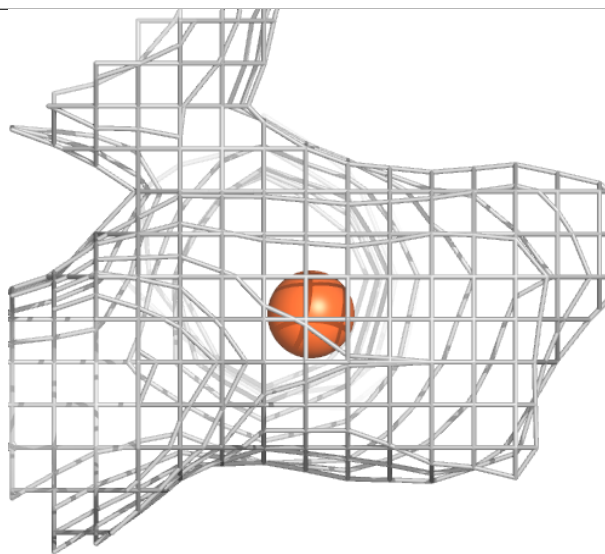
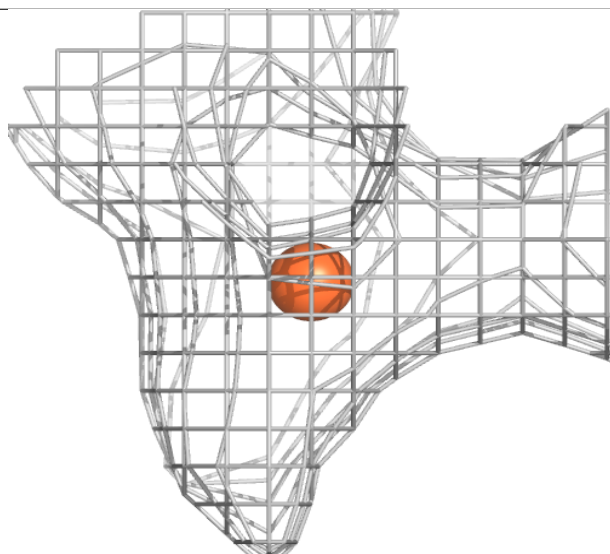
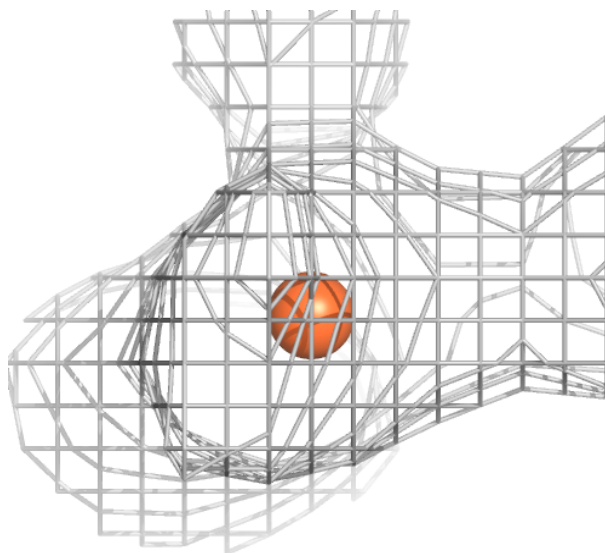
Electron density around FE E 401:

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



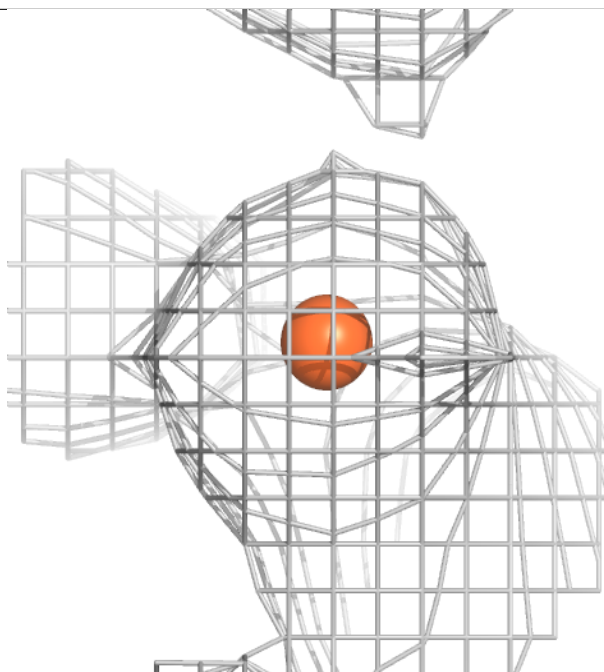
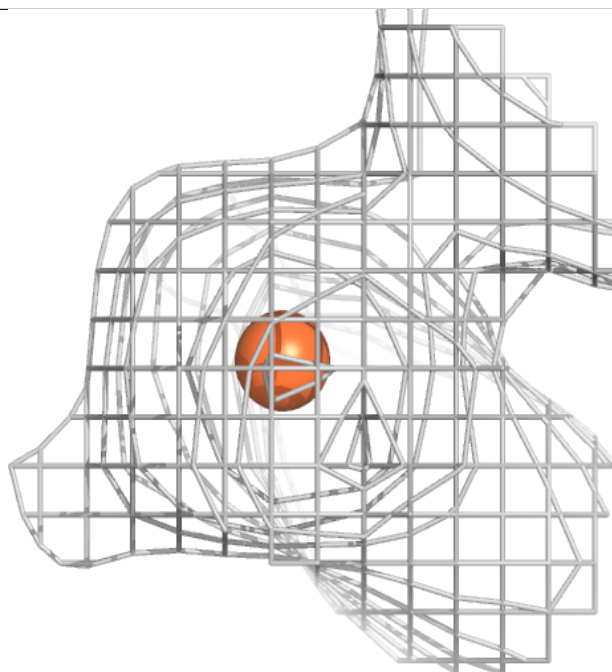
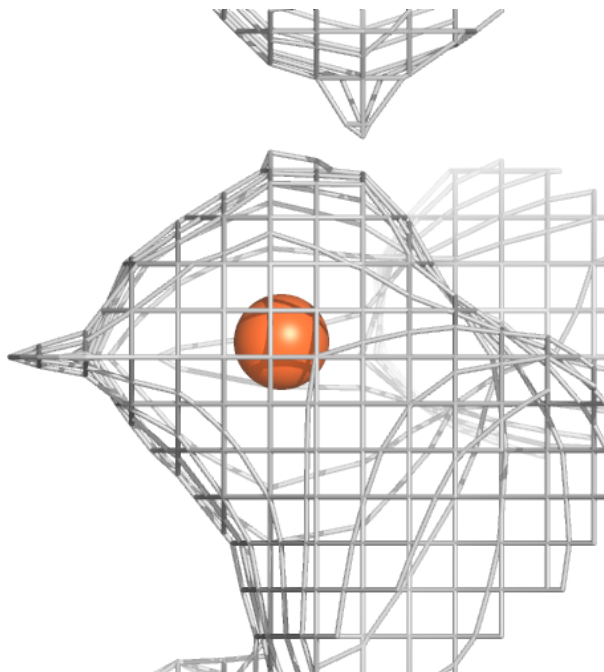
Electron density around FE Y 401:

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



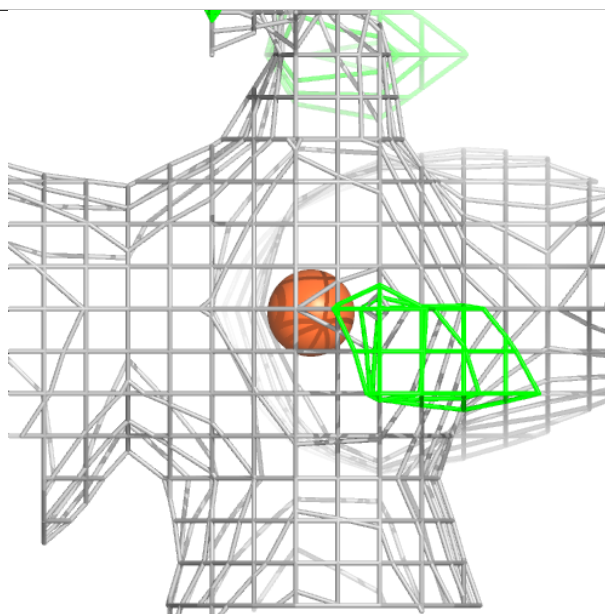
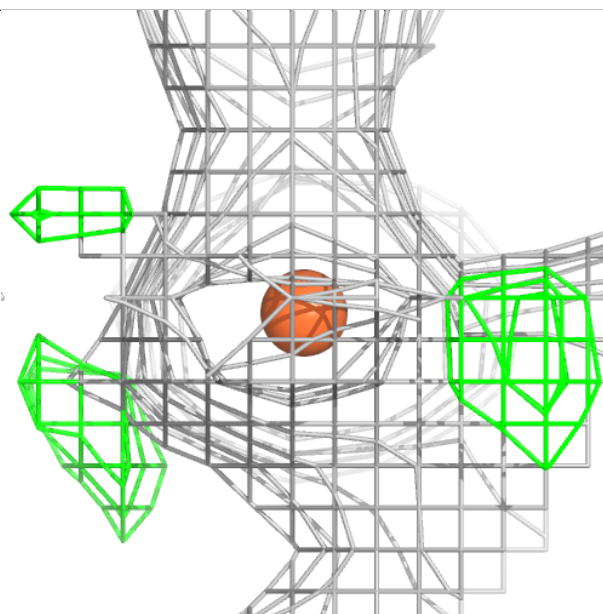
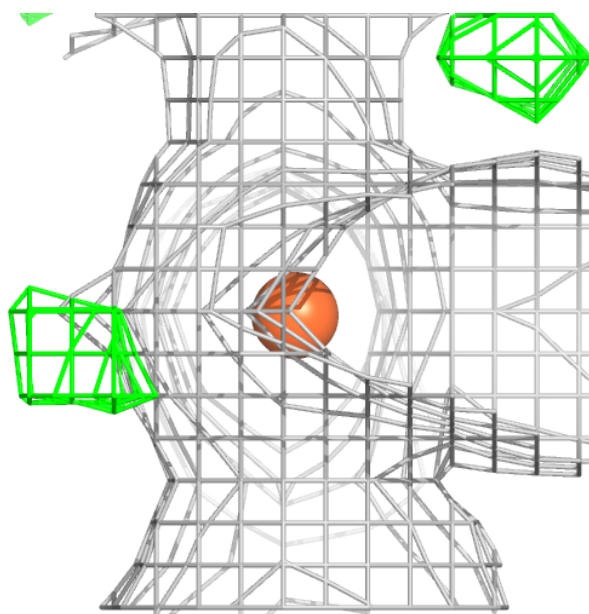
Electron density around FE F 401:

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



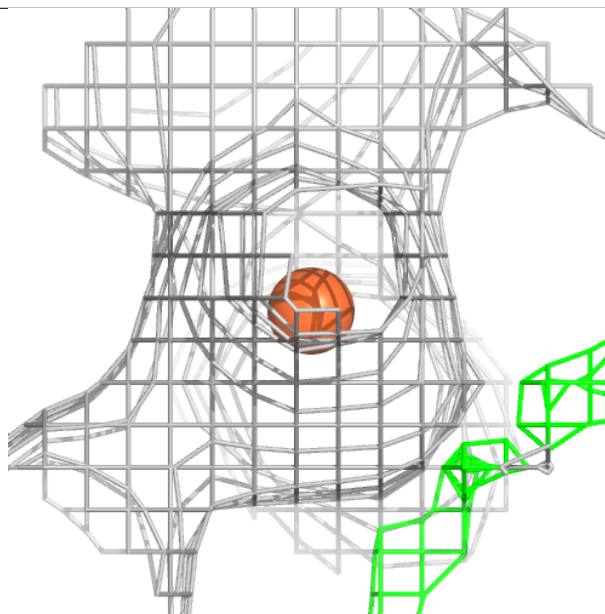
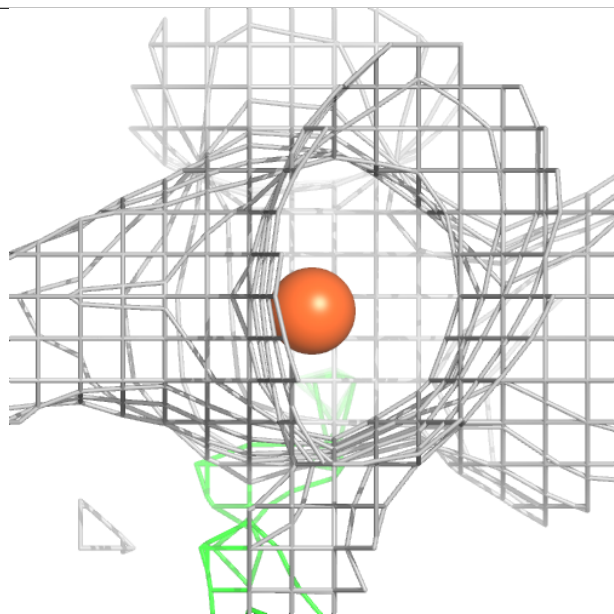
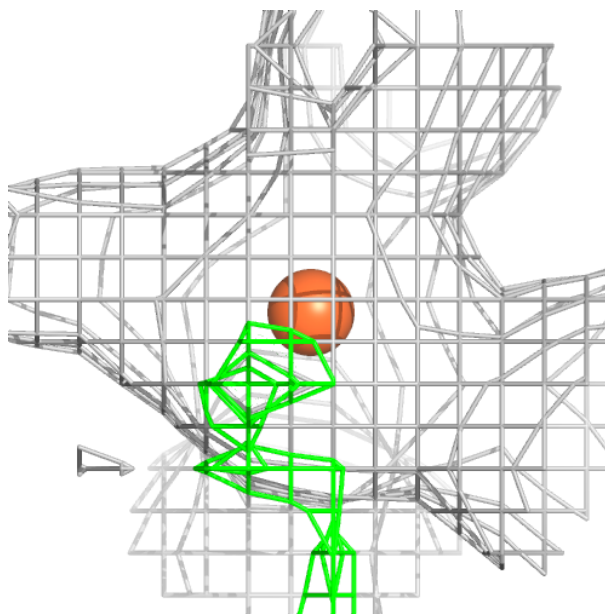
Electron density around FE C 401:

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



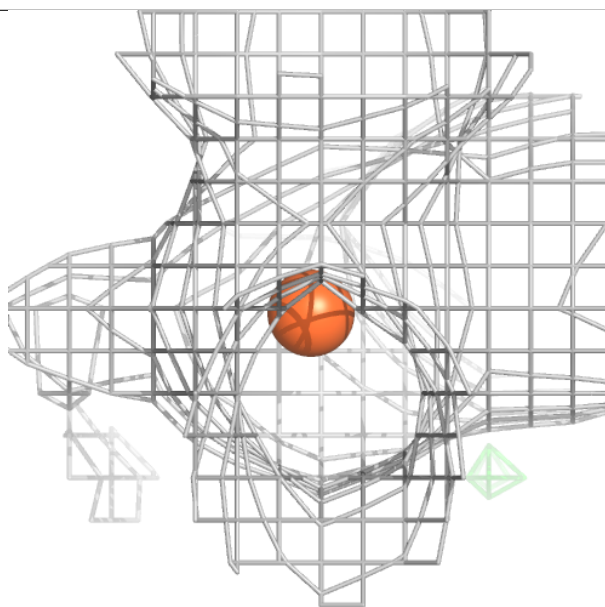
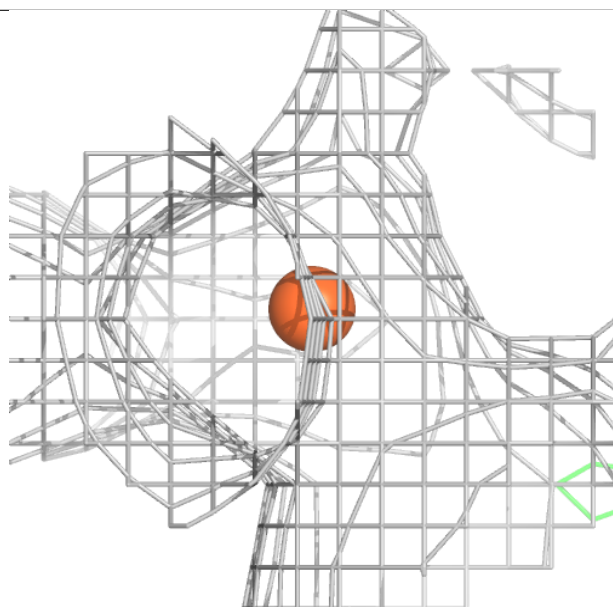
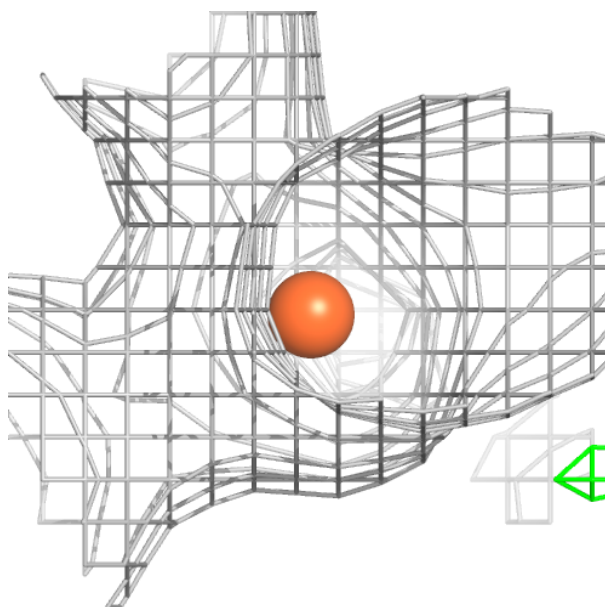
Electron density around FE H 401:

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



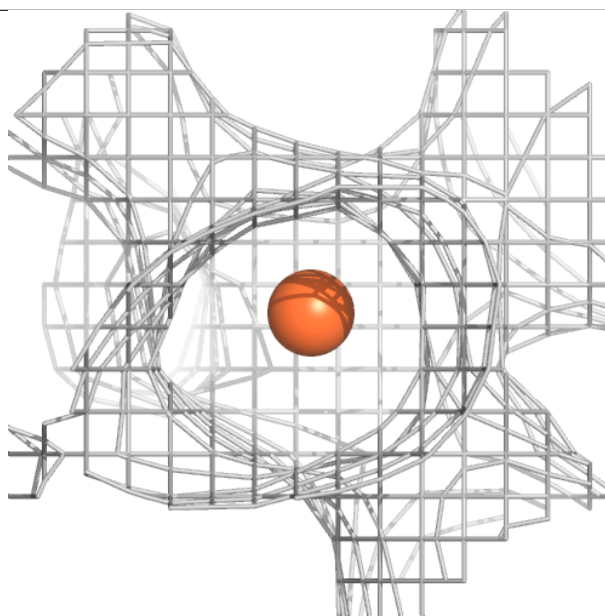
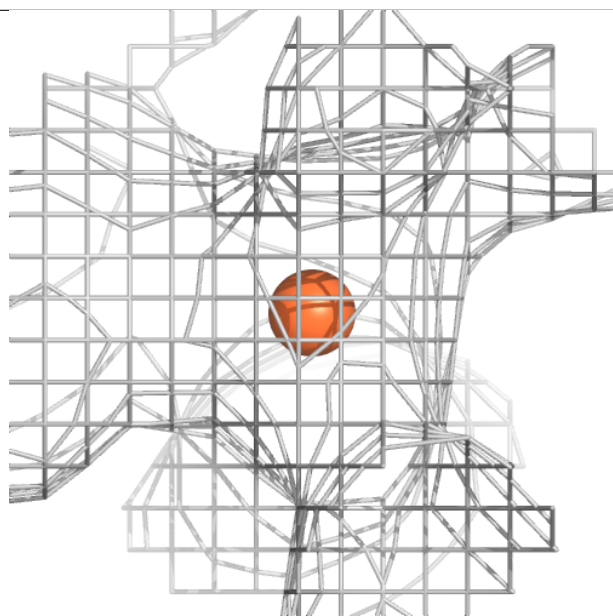
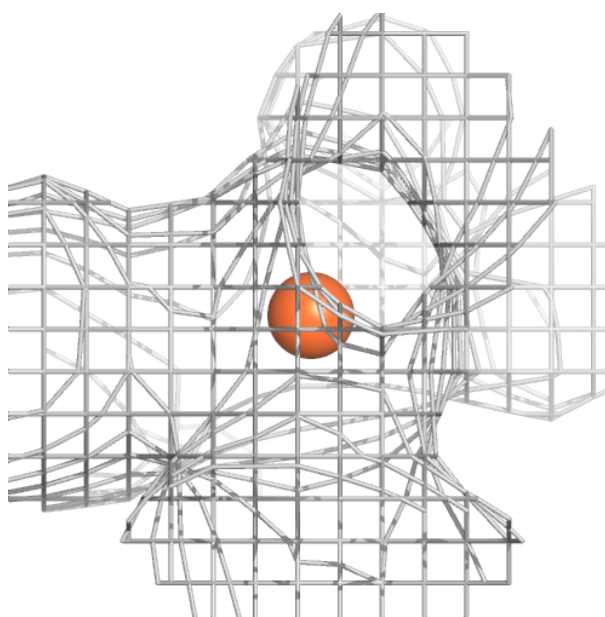
Electron density around FE T 401:

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



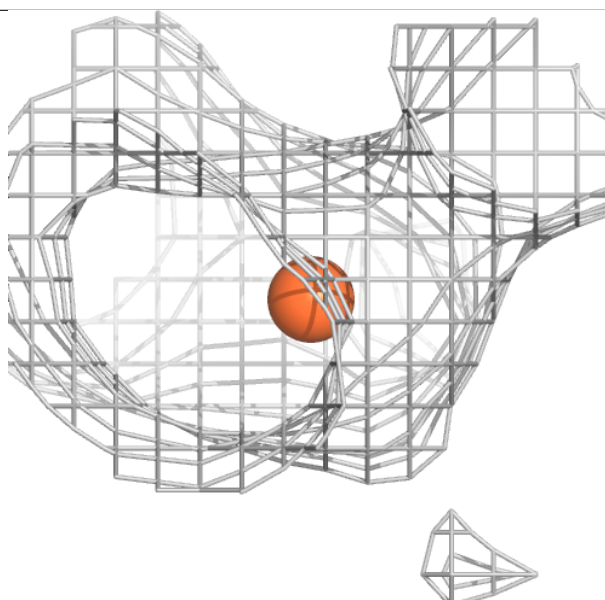
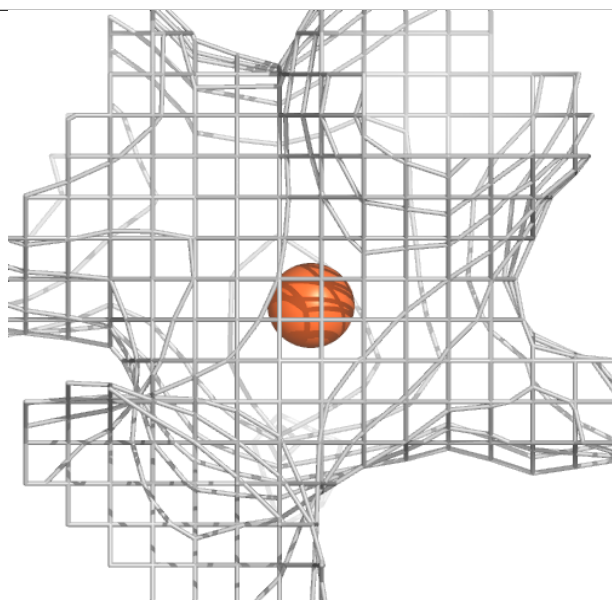
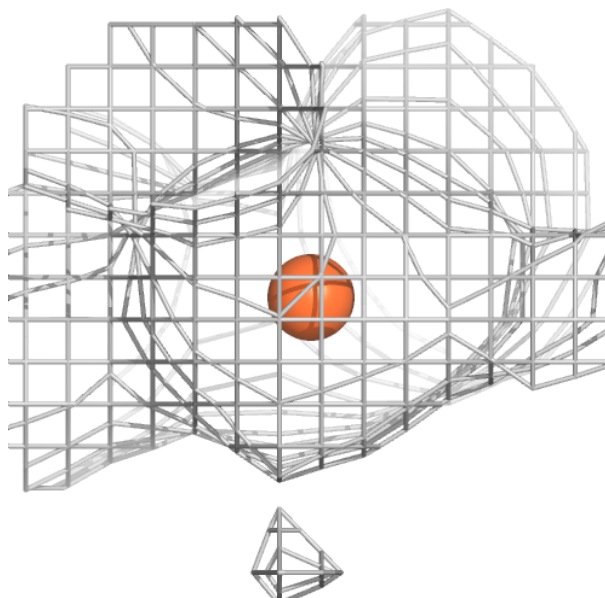
Electron density around FE N 401:

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



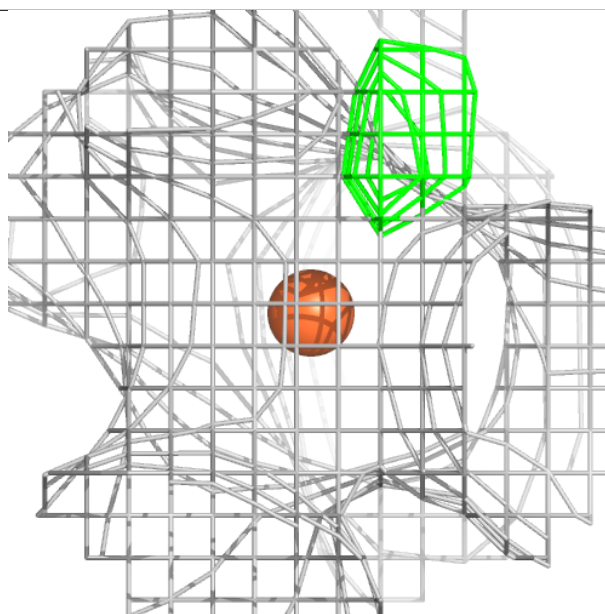
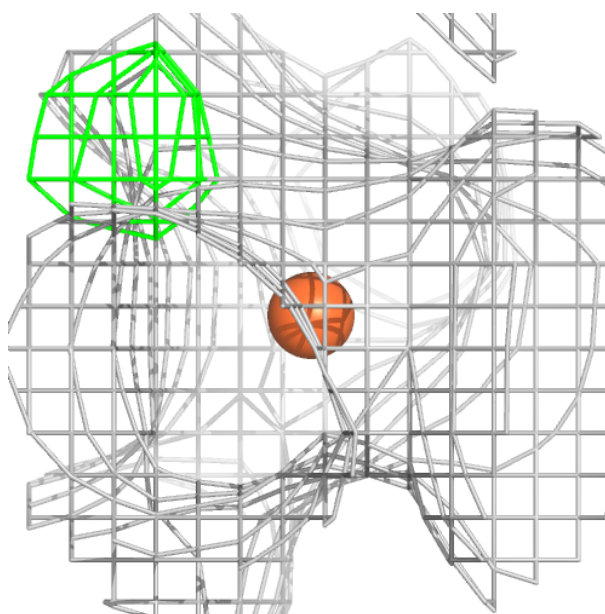
Electron density around FE U 401:

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



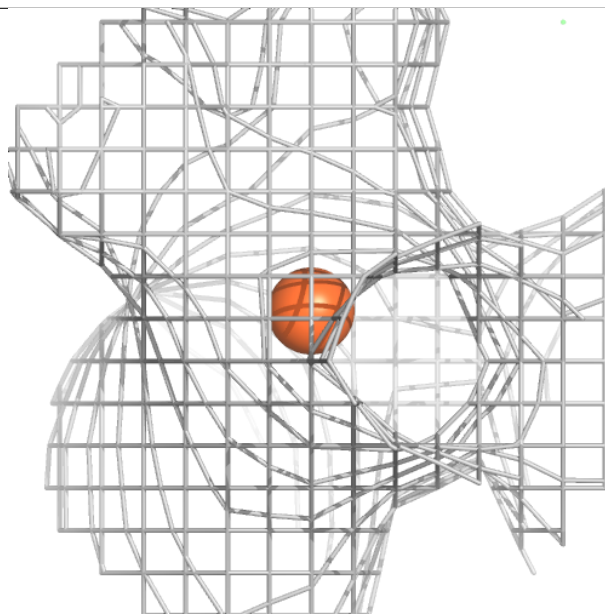
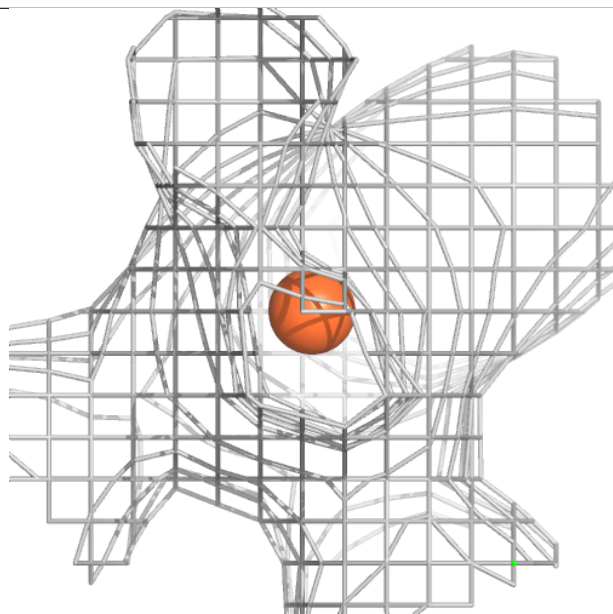
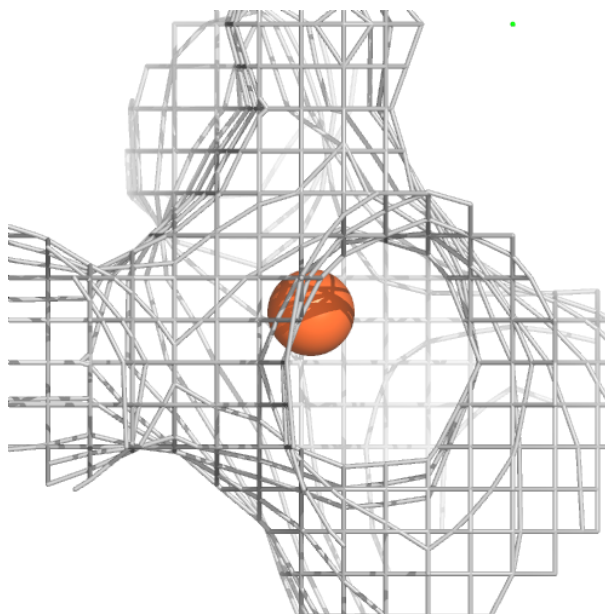
Electron density around FE G 401:

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



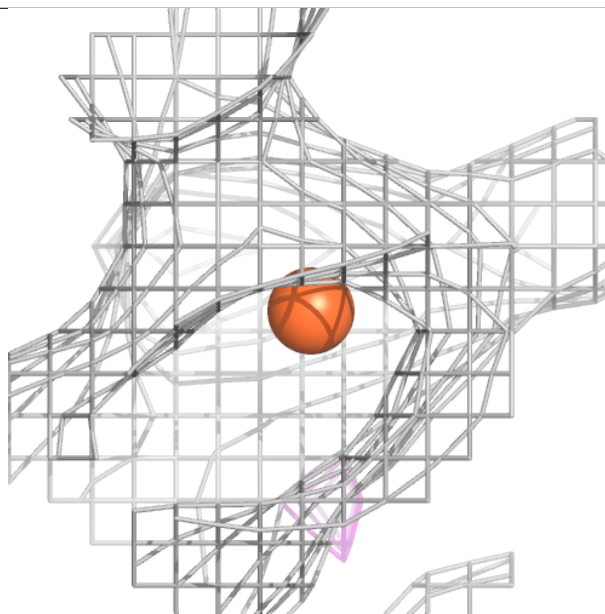
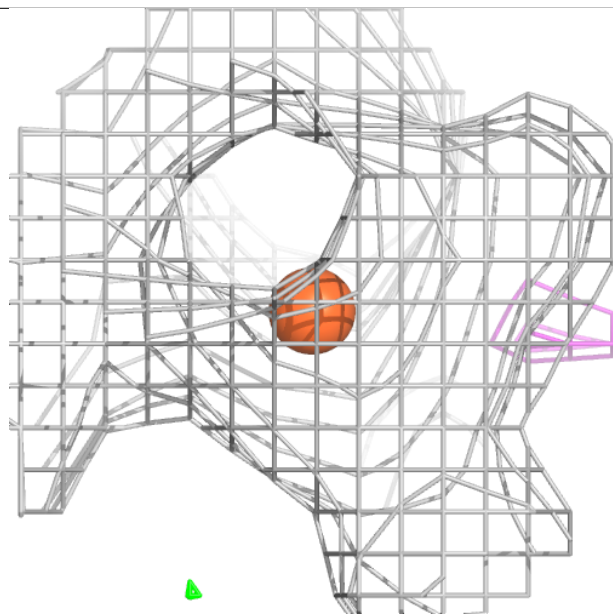
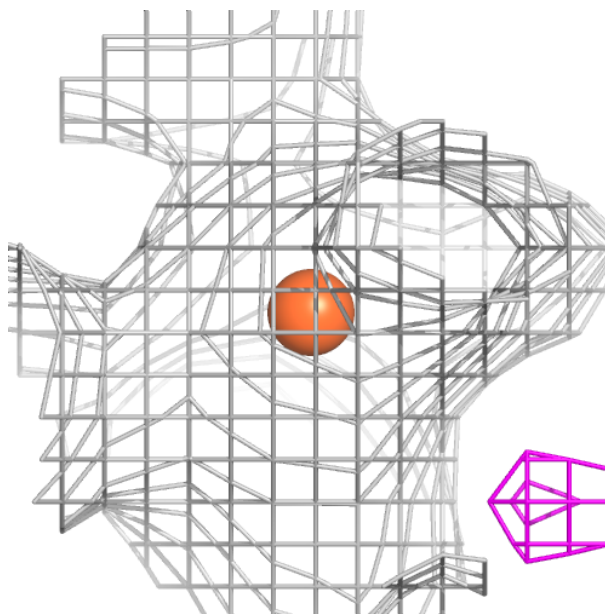
Electron density around FE W 401:

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



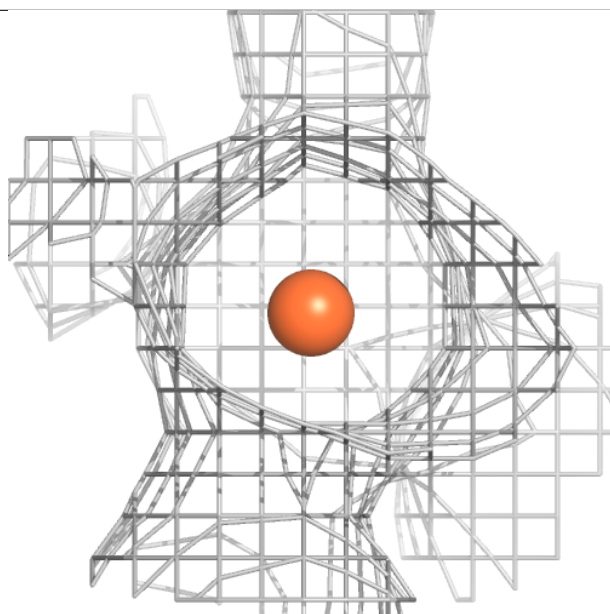
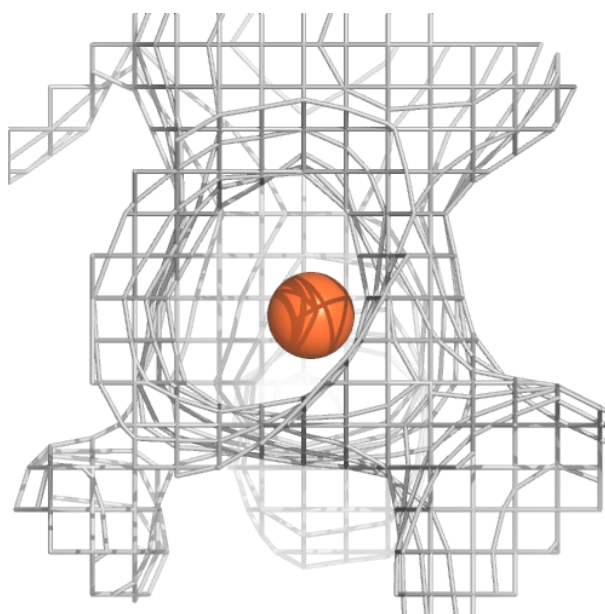
Electron density around FE P 401:

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



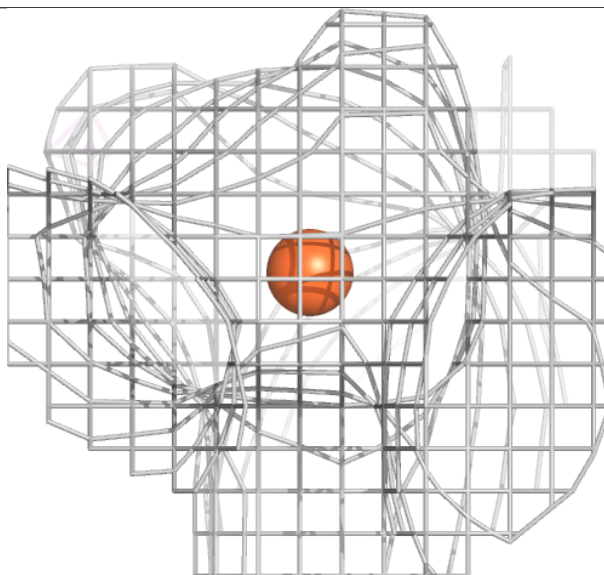
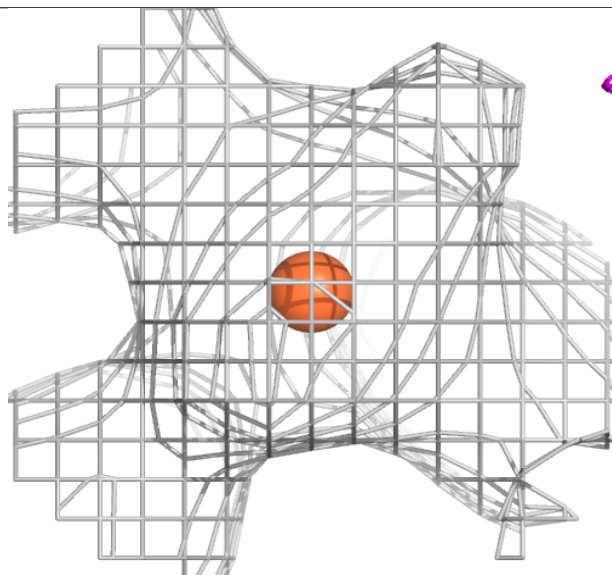
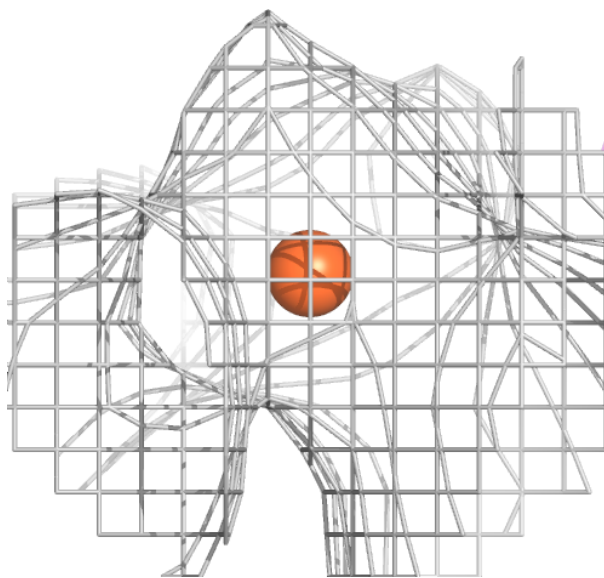
Electron density around FE M 401:

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



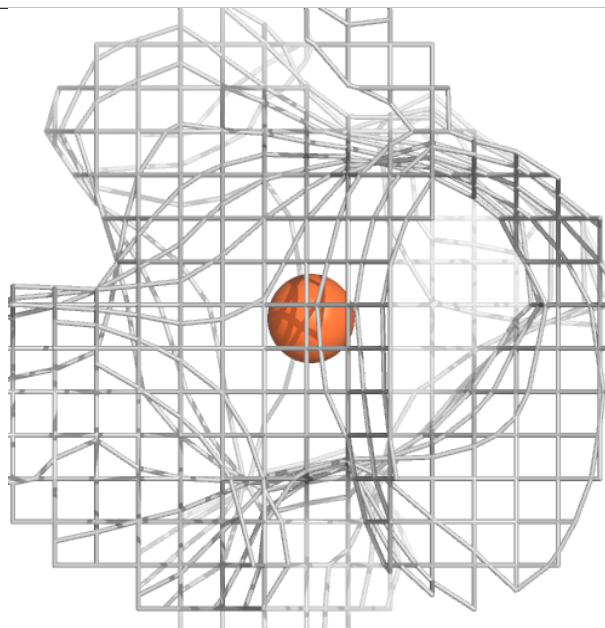
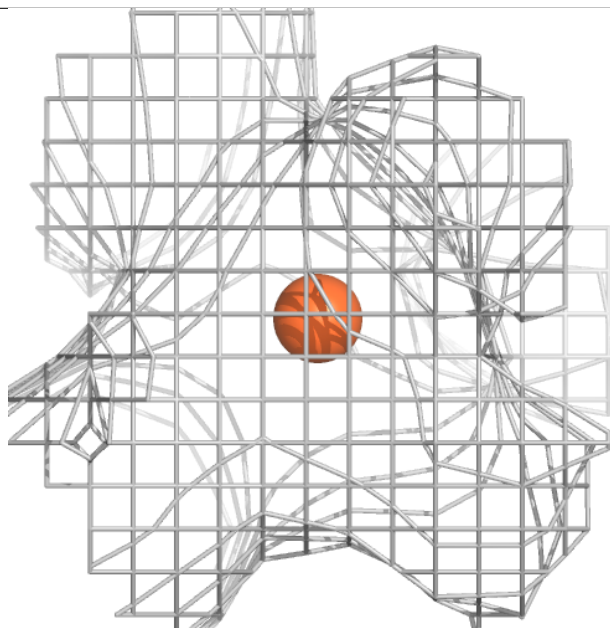
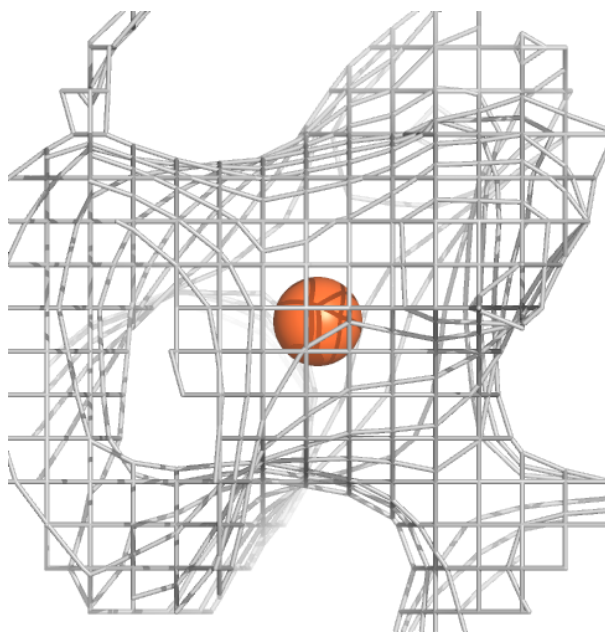
Electron density around FE R 401:

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



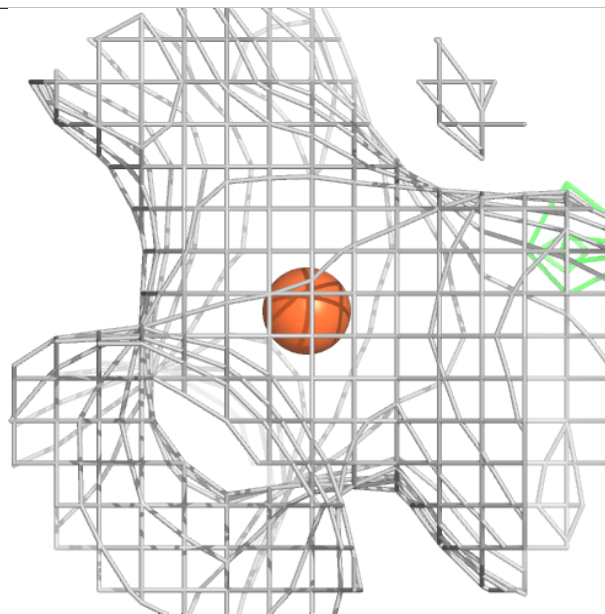
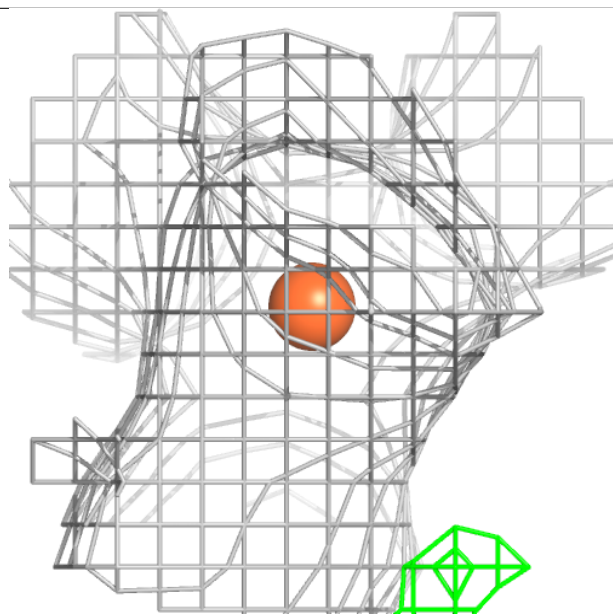
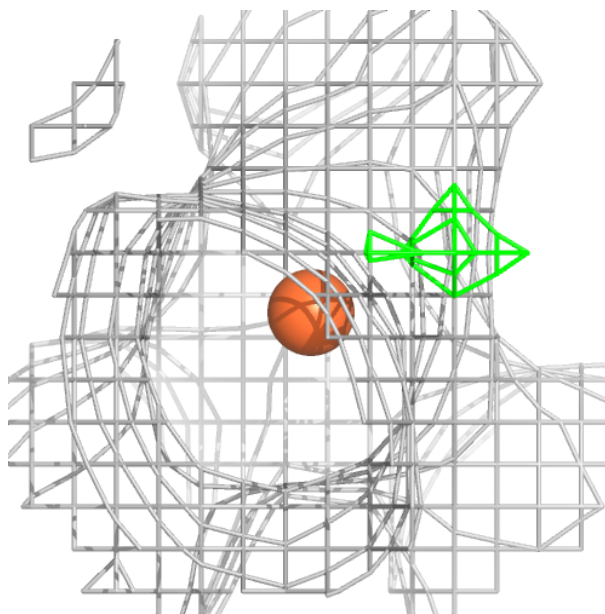
Electron density around FE A 401:

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



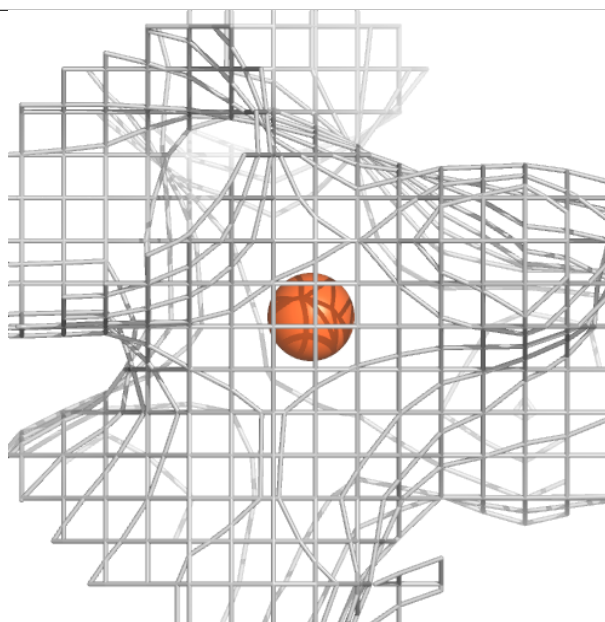
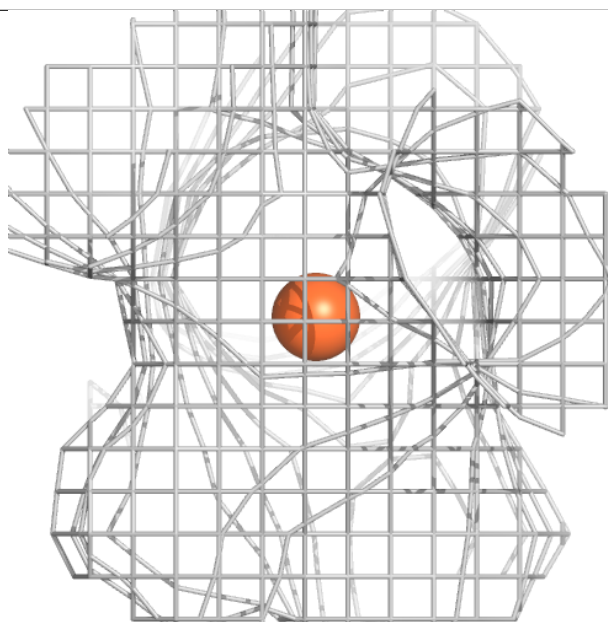
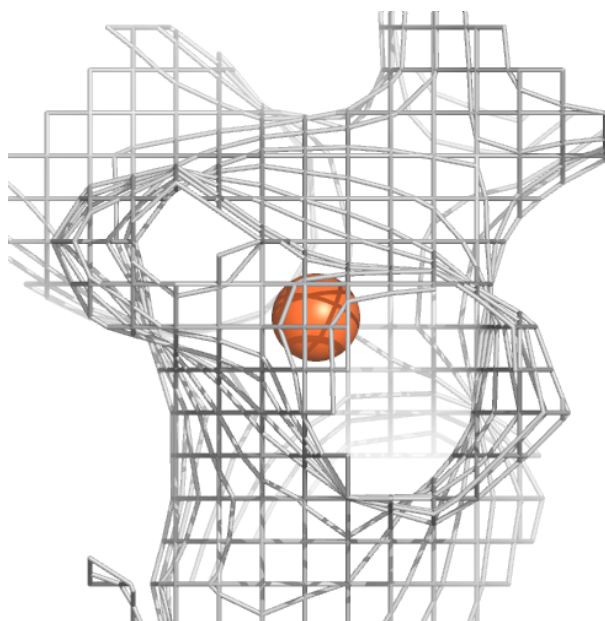
Electron density around FE K 401:

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



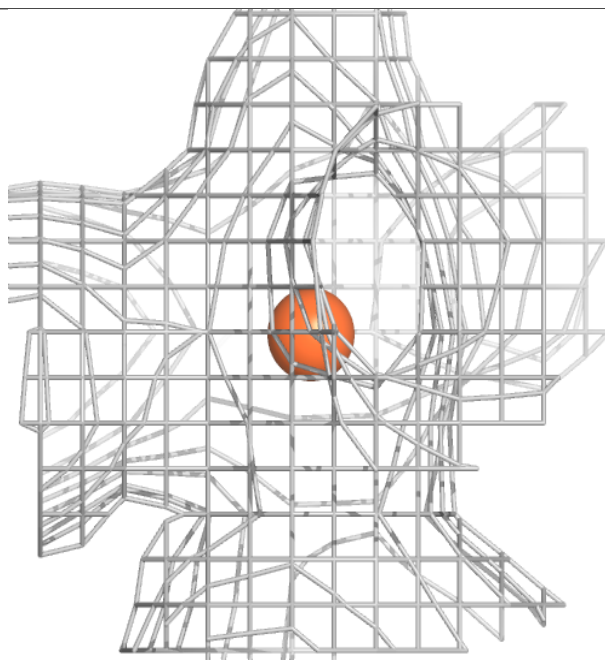
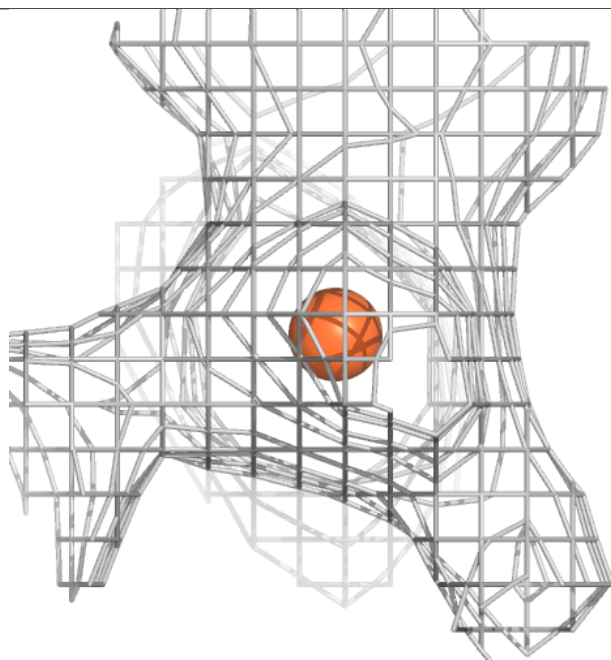
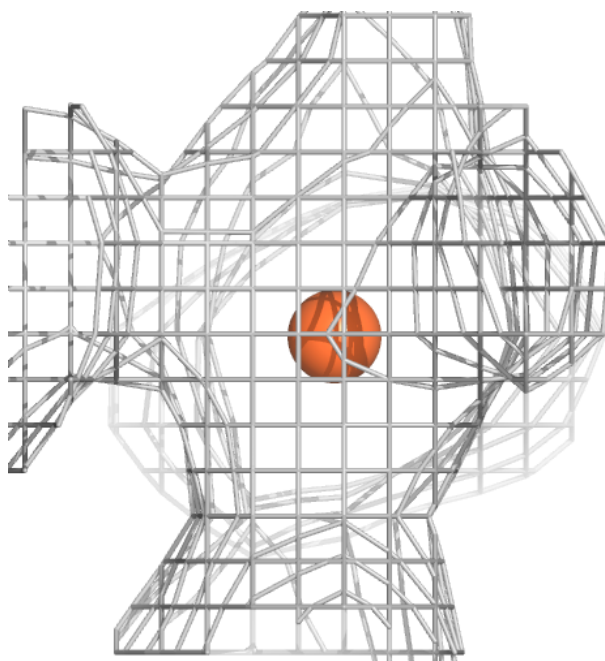
Electron density around FE B 401:

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



Electron density around FE I 401:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.