



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:42 PM UTC

PDB ID : 7X8K / pdb_00007x8k
Title : Arabidopsis GDP-D-mannose pyrophosphorylase (VTC1) structure (product-bound)
Authors : Zhao, S.; Zhang, C.; Liu, L.
Deposited on : 2022-03-13
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

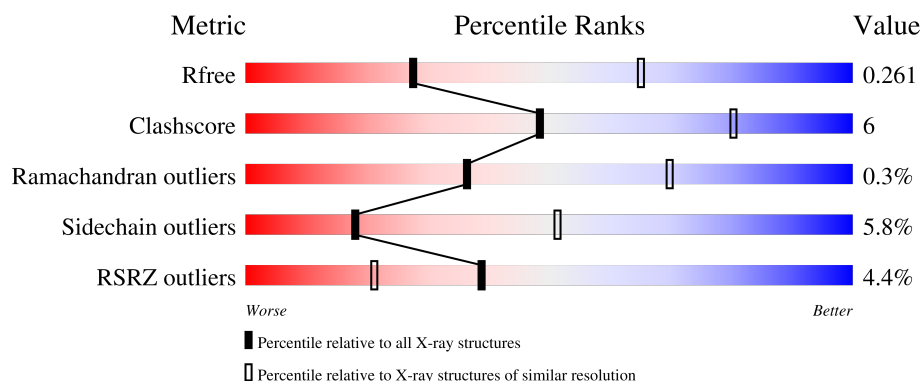
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	376	3% 82% 14% ..
1	B	376	2% 81% 15% ..
1	C	376	5% 75% 17% • 6%
1	D	376	7% 79% 13% • 6%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 11191 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 Mannose-1-phosphate guanylyltransferase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	365	Total	C	N	O	S	0	0	0
			2783	1788	466	513	16			
1	B	367	Total	C	N	O	S	0	0	0
			2805	1802	470	517	16			
1	C	355	Total	C	N	O	S	0	0	0
			2717	1746	456	500	15			
1	D	355	Total	C	N	O	S	0	0	0
			2697	1728	455	499	15			

There are 60 discrepancies between the modelled and reference sequences:

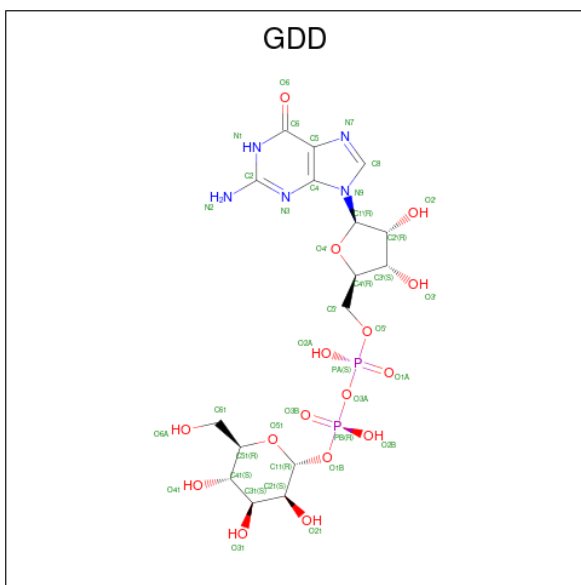
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	initiating methionine	UNP O22287
A	0	GLY	-	expression tag	UNP O22287
A	362	LYS	-	expression tag	UNP O22287
A	363	LEU	-	expression tag	UNP O22287
A	364	ALA	-	expression tag	UNP O22287
A	365	ALA	-	expression tag	UNP O22287
A	366	ALA	-	expression tag	UNP O22287
A	367	LEU	-	expression tag	UNP O22287
A	368	GLU	-	expression tag	UNP O22287
A	369	HIS	-	expression tag	UNP O22287
A	370	HIS	-	expression tag	UNP O22287
A	371	HIS	-	expression tag	UNP O22287
A	372	HIS	-	expression tag	UNP O22287
A	373	HIS	-	expression tag	UNP O22287
A	374	HIS	-	expression tag	UNP O22287
B	-1	MET	-	initiating methionine	UNP O22287
B	0	GLY	-	expression tag	UNP O22287
B	362	LYS	-	expression tag	UNP O22287
B	363	LEU	-	expression tag	UNP O22287
B	364	ALA	-	expression tag	UNP O22287
B	365	ALA	-	expression tag	UNP O22287

Continued on next page...

Continued from previous page...

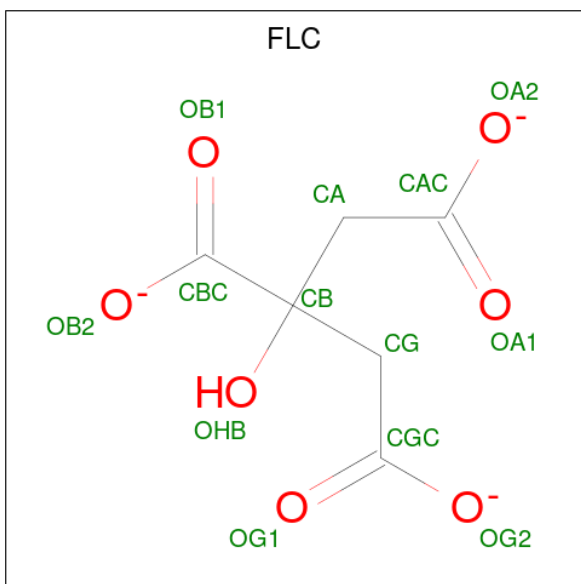
Chain	Residue	Modelled	Actual	Comment	Reference
B	366	ALA	-	expression tag	UNP O22287
B	367	LEU	-	expression tag	UNP O22287
B	368	GLU	-	expression tag	UNP O22287
B	369	HIS	-	expression tag	UNP O22287
B	370	HIS	-	expression tag	UNP O22287
B	371	HIS	-	expression tag	UNP O22287
B	372	HIS	-	expression tag	UNP O22287
B	373	HIS	-	expression tag	UNP O22287
B	374	HIS	-	expression tag	UNP O22287
C	-1	MET	-	initiating methionine	UNP O22287
C	0	GLY	-	expression tag	UNP O22287
C	362	LYS	-	expression tag	UNP O22287
C	363	LEU	-	expression tag	UNP O22287
C	364	ALA	-	expression tag	UNP O22287
C	365	ALA	-	expression tag	UNP O22287
C	366	ALA	-	expression tag	UNP O22287
C	367	LEU	-	expression tag	UNP O22287
C	368	GLU	-	expression tag	UNP O22287
C	369	HIS	-	expression tag	UNP O22287
C	370	HIS	-	expression tag	UNP O22287
C	371	HIS	-	expression tag	UNP O22287
C	372	HIS	-	expression tag	UNP O22287
C	373	HIS	-	expression tag	UNP O22287
C	374	HIS	-	expression tag	UNP O22287
D	-1	MET	-	initiating methionine	UNP O22287
D	0	GLY	-	expression tag	UNP O22287
D	362	LYS	-	expression tag	UNP O22287
D	363	LEU	-	expression tag	UNP O22287
D	364	ALA	-	expression tag	UNP O22287
D	365	ALA	-	expression tag	UNP O22287
D	366	ALA	-	expression tag	UNP O22287
D	367	LEU	-	expression tag	UNP O22287
D	368	GLU	-	expression tag	UNP O22287
D	369	HIS	-	expression tag	UNP O22287
D	370	HIS	-	expression tag	UNP O22287
D	371	HIS	-	expression tag	UNP O22287
D	372	HIS	-	expression tag	UNP O22287
D	373	HIS	-	expression tag	UNP O22287
D	374	HIS	-	expression tag	UNP O22287

- Molecule 2 is GUANOSINE-5'-DIPHOSPHATE-ALPHA-D-MANNOSE (CCD ID: GDD) (formula: $C_{16}H_{25}N_5O_{16}P_2$) (labeled as "Ligand of Interest" by depositor).



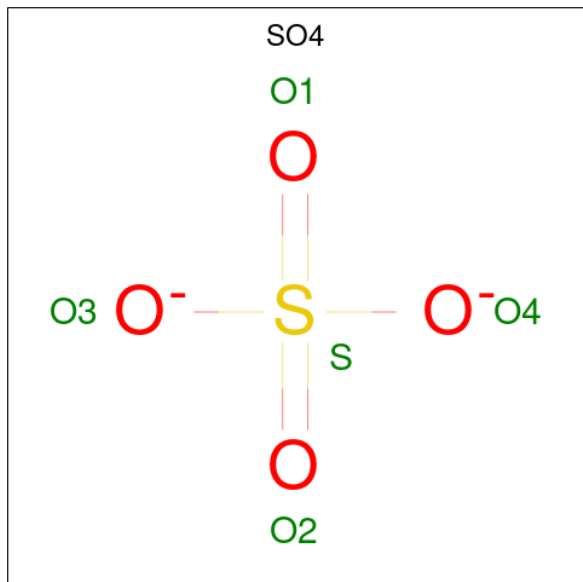
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			39	16	5	16	2		

- Molecule 3 is CITRATE ANION (CCD ID: FLC) (formula: $\text{C}_6\text{H}_5\text{O}_7$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 13 6 7	0	0
3	C	1	Total C O 13 6 7	0	0

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S) (labeled as "Ligand of Interest" by depositor).



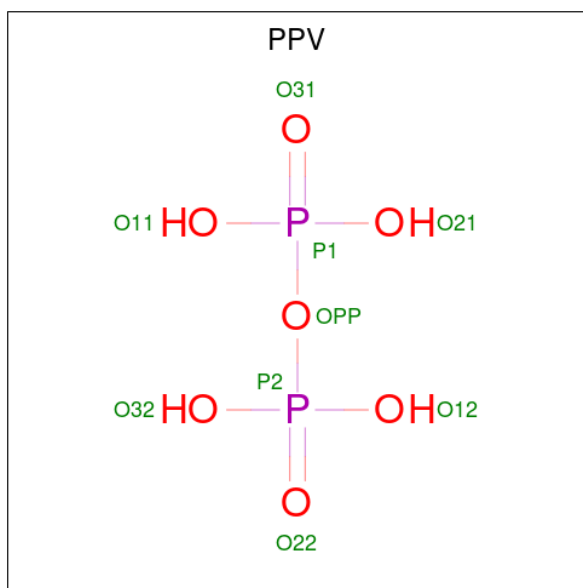
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total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

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is PYROPHOSPHATE (CCD ID: PPV) (formula: $\text{H}_4\text{O}_7\text{P}_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	O	P	0	0
			9	7	2		
5	D	1	Total	O	P	0	0
			9	7	2		

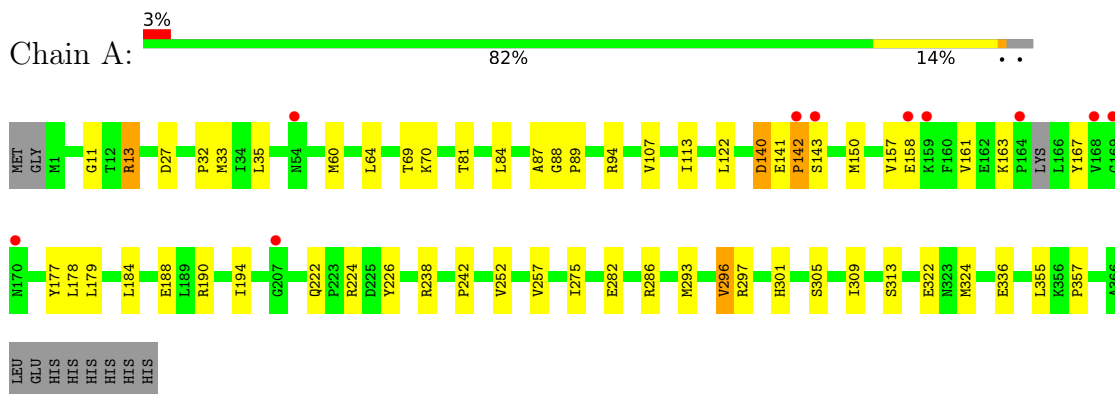
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	6	Total 6	O 6	0	0
6	B	1	Total 1	O 1	0	0
6	C	2	Total 2	O 2	0	0
6	D	2	Total 2	O 2	0	0

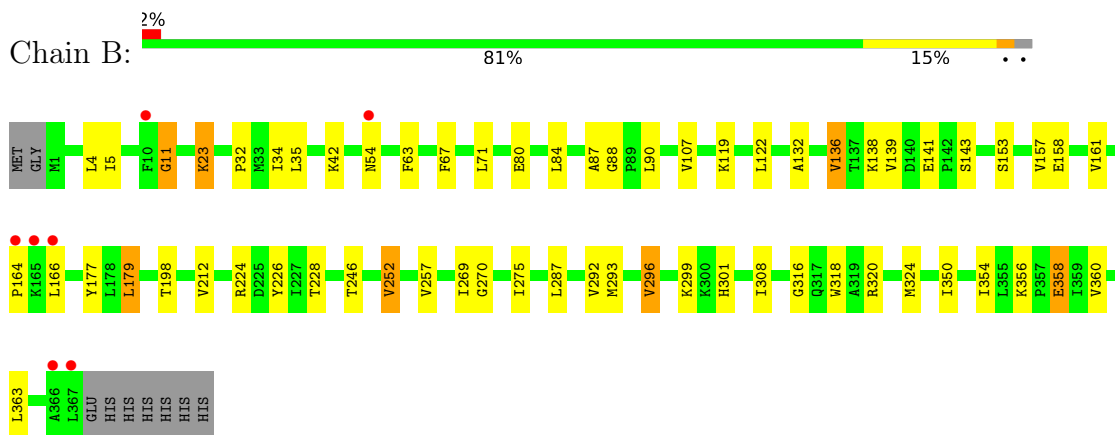
3 Residue-property plots [i](#)

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.

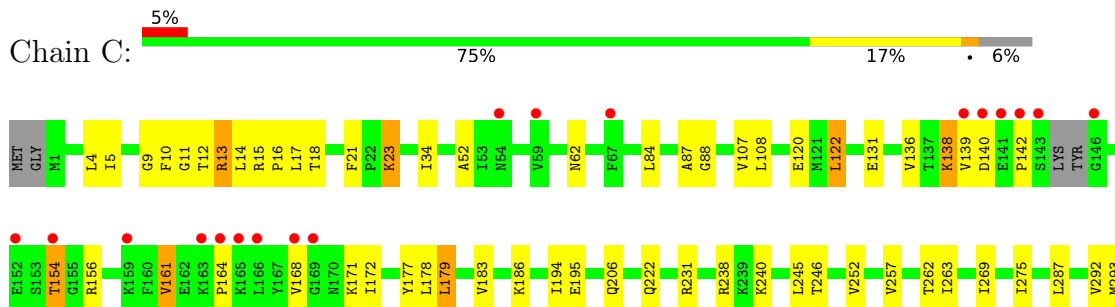
• Molecule 1: Mannose-1-phosphate guanylyltransferase 1

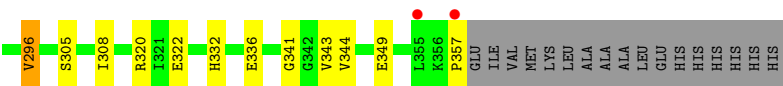


• Molecule 1: Mannose-1-phosphate guanylyltransferase 1

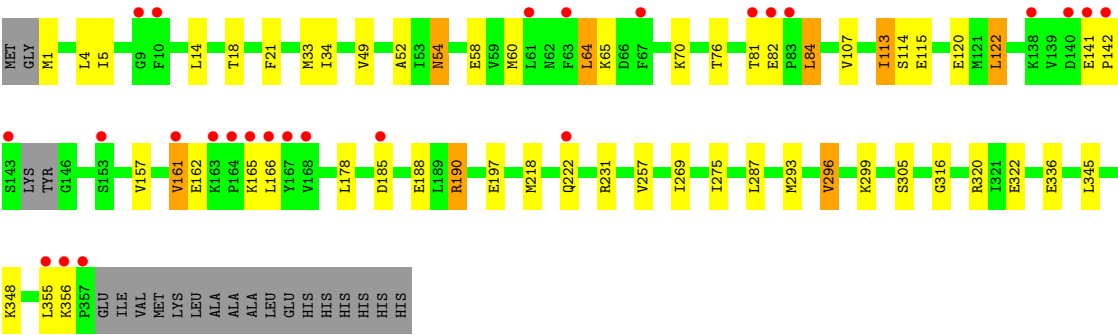
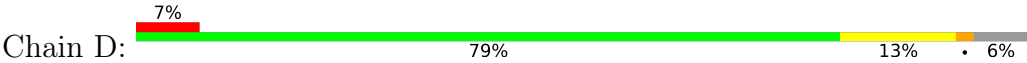


• Molecule 1: Mannose-1-phosphate guanylyltransferase 1





● Molecule 1: Mannose-1-phosphate guanylyltransferase 1



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	185.11Å 185.11Å 371.75Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.82 – 3.00 30.82 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.2 (30.82-3.00) 99.1 (30.82-3.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.40 (at 3.00Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.234 , 0.260 0.235 , 0.261	Depositor DCC
R_{free} test set	2451 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	54.2	Xtriage
Anisotropy	0.094	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 37.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	11191	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.83% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GDD, SO4, PPV, FLC

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	0.11	0/2836	0.33	0/3842
1	B	0.10	0/2859	0.31	0/3872
1	C	0.13	0/2770	0.34	0/3751
1	D	0.12	0/2748	0.37	0/3723
All	All	0.12	0/11213	0.34	0/15188

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2783	0	2877	33	0
1	B	2805	0	2908	32	0
1	C	2717	0	2812	40	0
1	D	2697	0	2778	28	0
2	A	39	0	23	1	0
3	A	13	0	5	1	0
3	C	13	0	5	3	0
4	A	30	0	0	1	0
4	B	25	0	0	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	20	0	0	1	0
4	D	20	0	0	1	0
5	B	9	0	0	0	0
5	D	9	0	0	0	0
6	A	6	0	0	0	0
6	B	1	0	0	0	0
6	C	2	0	0	0	0
6	D	2	0	0	0	0
All	All	11191	0	11408	125	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (125) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:401:GDD:O4'	2:A:401:GDD:C1'	1.63	1.23
1:C:11:GLY:HA2	3:C:401:FLC:HG1	1.52	0.90
1:A:301:HIS:HD2	1:B:301:HIS:HD2	1.28	0.81
1:A:11:GLY:HA2	3:A:402:FLC:HG1	1.67	0.76
1:C:156:ARG:HH12	1:C:206:GLN:HB3	1.54	0.72
1:A:84:LEU:HB3	1:A:88:GLY:HA3	1.70	0.71
1:B:84:LEU:HB3	1:B:88:GLY:HA3	1.71	0.70
1:B:143:SER:HA	1:B:164:PRO:HD2	1.73	0.70
1:A:70:LYS:NZ	1:C:349:GLU:OE2	2.25	0.68
1:C:13:ARG:HD2	1:C:222:GLN:HG2	1.76	0.67
1:A:140:ASP:OD1	1:A:140:ASP:N	2.21	0.65
1:D:113:ILE:HD11	1:D:218:MET:HB3	1.78	0.65
1:C:269:ILE:HG23	1:C:287:LEU:HB2	1.79	0.64
1:C:341:GLY:HA3	1:C:357:PRO:HA	1.80	0.63
1:C:161:VAL:HG21	1:C:168:VAL:HG21	1.79	0.63
1:D:188:GLU:HB2	1:D:190:ARG:HG2	1.80	0.63
1:B:356:LYS:HE3	1:B:358:GLU:HG3	1.83	0.61
1:D:5:ILE:HG21	1:D:34:ILE:HD11	1.84	0.60
1:C:84:LEU:HB3	1:C:88:GLY:HA3	1.84	0.58
1:A:13:ARG:HD2	1:A:222:GLN:HG2	1.84	0.58
1:A:282:GLU:OE2	1:A:297:ARG:NH1	2.37	0.57
1:C:12:THR:H	3:C:401:FLC:HA1	1.69	0.57
1:C:336:GLU:O	1:D:320:ARG:NH2	2.37	0.57
1:D:122:LEU:HD13	1:D:178:LEU:HD21	1.86	0.56
1:C:320:ARG:NH2	1:D:336:GLU:O	2.38	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:114:SER:OG	1:D:115:GLU:N	2.39	0.56
1:A:60:MET:HE2	1:A:64:LEU:HD11	1.88	0.55
1:B:54:ASN:ND2	1:B:80:GLU:OE1	2.39	0.55
1:B:42:LYS:NZ	1:B:71:LEU:O	2.38	0.54
1:D:82:GLU:O	1:D:84:LEU:HD22	2.08	0.54
1:C:5:ILE:HG21	1:C:34:ILE:HD11	1.90	0.53
1:B:11:GLY:H	1:B:23:LYS:HB2	1.74	0.53
1:B:299:LYS:HD2	1:B:316:GLY:HA2	1.91	0.53
1:A:94:ARG:HG3	1:A:184:LEU:HD13	1.91	0.52
1:A:188:GLU:HB2	1:A:190:ARG:HG2	1.90	0.52
1:D:190:ARG:NH2	1:D:197:GLU:OE1	2.42	0.52
1:B:138:LYS:NZ	4:B:504:SO4:O4	2.37	0.52
1:A:355:LEU:C	1:A:357:PRO:HD3	2.34	0.52
1:D:345:LEU:H	1:D:348:LYS:HZ1	1.56	0.52
1:A:32:PRO:HD2	1:A:35:LEU:HD12	1.91	0.51
1:D:299:LYS:HD2	1:D:316:GLY:HA2	1.93	0.51
1:C:257:VAL:HG22	1:C:275:ILE:HD12	1.92	0.51
1:C:332:HIS:HB2	1:C:349:GLU:HG2	1.92	0.51
1:C:263:ILE:HD11	1:C:275:ILE:HD13	1.91	0.51
1:B:5:ILE:HG21	1:B:34:ILE:HD11	1.92	0.50
1:D:33:MET:HE1	1:D:113:ILE:HG22	1.92	0.50
1:C:120:GLU:N	1:C:120:GLU:OE1	2.43	0.50
1:C:122:LEU:HD13	1:C:178:LEU:HD21	1.94	0.50
1:D:142:PRO:HB3	1:D:165:LYS:HD3	1.92	0.50
1:D:257:VAL:HG22	1:D:275:ILE:HD12	1.92	0.50
1:D:269:ILE:HD12	1:D:287:LEU:HD12	1.95	0.49
1:C:17:LEU:HD11	1:C:308:ILE:HG21	1.95	0.48
1:C:139:VAL:HG22	1:C:140:ASP:H	1.77	0.48
1:C:107:VAL:HB	1:C:177:TYR:HB2	1.95	0.48
1:B:269:ILE:HG23	1:B:287:LEU:HB2	1.96	0.48
1:C:131:GLU:OE1	1:C:186:LYS:NZ	2.42	0.48
1:A:336:GLU:O	1:B:320:ARG:NH2	2.47	0.47
1:B:32:PRO:HD2	1:B:35:LEU:HD12	1.96	0.47
1:D:4:LEU:HD11	1:D:52:ALA:HB2	1.95	0.47
1:C:10:PHE:HZ	1:C:15:ARG:HE	1.63	0.47
1:A:286:ARG:HB2	1:B:318:TRP:CE2	2.50	0.47
1:A:27:ASP:O	1:A:226:TYR:OH	2.28	0.47
1:C:138:LYS:HE2	1:C:138:LYS:HB2	1.60	0.47
1:A:305:SER:O	1:A:322:GLU:HA	2.15	0.46
1:B:136:VAL:HG12	1:B:212:VAL:HA	1.96	0.46
1:B:292:VAL:HG13	1:B:296:VAL:HG22	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:MET:HE1	1:A:113:ILE:HG22	1.97	0.46
1:A:257:VAL:HG22	1:A:275:ILE:HD12	1.97	0.46
1:D:120:GLU:OE1	1:D:120:GLU:N	2.46	0.46
1:B:350:ILE:HD12	1:B:354:ILE:HD11	1.98	0.46
1:C:9:GLY:H	3:C:401:FLC:CBC	2.29	0.45
1:D:60:MET:HE2	1:D:64:LEU:HD11	1.97	0.45
1:D:269:ILE:HG23	1:D:287:LEU:HB2	1.98	0.45
1:C:293:MET:O	1:C:296:VAL:HG13	2.16	0.45
1:C:305:SER:O	1:C:322:GLU:HA	2.16	0.44
1:A:140:ASP:C	1:A:142:PRO:HD3	2.42	0.44
1:A:141:GLU:C	1:A:143:SER:H	2.26	0.44
1:A:305:SER:OG	4:A:404:SO4:O2	2.33	0.44
1:C:23:LYS:HB3	1:C:23:LYS:HE3	1.77	0.44
1:D:231:ARG:NE	4:D:501:SO4:O4	2.39	0.44
1:C:14:LEU:HD12	1:C:23:LYS:HG2	2.00	0.43
1:B:257:VAL:HG22	1:B:275:ILE:HD12	2.01	0.43
1:D:305:SER:O	1:D:322:GLU:HA	2.19	0.43
1:A:87:ALA:HB2	1:A:194:ILE:HB	2.00	0.43
1:B:356:LYS:O	1:B:360:VAL:HG23	2.18	0.43
1:A:355:LEU:HB3	1:B:363:LEU:HD13	2.00	0.43
1:A:301:HIS:HD2	1:B:301:HIS:CD2	2.20	0.43
1:B:132:ALA:HB1	1:B:179:LEU:HD12	2.01	0.43
1:C:154:THR:HB	1:C:156:ARG:HG3	2.01	0.43
1:C:238:ARG:HE	1:C:245:LEU:HD12	1.84	0.43
1:A:293:MET:O	1:A:296:VAL:HG13	2.18	0.43
1:C:142:PRO:HB2	1:C:164:PRO:HG2	2.00	0.43
1:A:107:VAL:HB	1:A:177:TYR:HB2	2.01	0.43
1:B:226:TYR:HB2	1:B:308:ILE:HD11	2.01	0.42
1:C:292:VAL:HG13	1:C:296:VAL:HG22	2.00	0.42
1:C:18:THR:HA	1:C:21:PHE:O	2.19	0.42
1:B:293:MET:O	1:B:296:VAL:HG13	2.19	0.42
1:C:4:LEU:HD11	1:C:52:ALA:HB2	2.02	0.42
1:B:35:LEU:HD21	1:B:67:PHE:CG	2.54	0.42
1:D:70:LYS:HE3	1:D:70:LYS:HB2	1.83	0.42
1:D:293:MET:O	1:D:296:VAL:HG13	2.20	0.42
1:A:309:ILE:HG23	1:A:313:SER:HB2	2.02	0.42
1:B:358:GLU:H	1:B:358:GLU:HG2	1.36	0.42
1:A:141:GLU:O	1:A:143:SER:N	2.51	0.41
1:C:179:LEU:HB3	1:C:183:VAL:HG21	2.01	0.41
1:D:18:THR:HA	1:D:21:PHE:O	2.20	0.41
1:D:1:MET:HE1	1:D:122:LEU:HD21	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:LEU:HD12	1:A:178:LEU:HD21	2.02	0.41
1:B:119:LYS:HE3	1:B:119:LYS:HB3	1.88	0.41
1:B:107:VAL:HB	1:B:177:TYR:HB2	2.01	0.41
1:D:165:LYS:HG3	1:D:166:LEU:H	1.86	0.41
1:A:238:ARG:O	1:A:242:PRO:HG3	2.21	0.41
1:B:252:VAL:O	1:B:270:GLY:HA3	2.21	0.41
1:D:60:MET:O	1:D:64:LEU:HD22	2.21	0.41
1:A:84:LEU:HB2	1:A:89:PRO:HD3	2.01	0.40
1:B:4:LEU:HD23	1:B:90:LEU:HD22	2.03	0.40
1:B:224:ARG:HG3	1:B:324:MET:SD	2.61	0.40
1:C:231:ARG:NE	4:C:402:SO4:O2	2.54	0.40
1:C:240:LYS:HE2	1:C:240:LYS:HB3	1.91	0.40
1:A:224:ARG:HD3	1:A:324:MET:HG3	2.04	0.40
1:B:87:ALA:O	1:B:90:LEU:HB2	2.21	0.40
1:C:87:ALA:HB2	1:C:194:ILE:HB	2.02	0.40
1:A:70:LYS:HZ3	1:C:349:GLU:CD	2.23	0.40
1:C:16:PRO:HD3	1:C:343:VAL:HG13	2.04	0.40
1:D:54:ASN:HD22	1:D:54:ASN:C	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	361/376 (96%)	343 (95%)	16 (4%)	2 (1%)	21	56
1	B	365/376 (97%)	349 (96%)	15 (4%)	1 (0%)	36	70
1	C	351/376 (93%)	336 (96%)	15 (4%)	0	100	100
1	D	351/376 (93%)	329 (94%)	21 (6%)	1 (0%)	36	70
All	All	1428/1504 (95%)	1357 (95%)	67 (5%)	4 (0%)	36	70

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	161	VAL
1	B	11	GLY
1	A	167	TYR
1	A	142	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	307/321 (96%)	295 (96%)	12 (4%)	28	62
1	B	310/321 (97%)	292 (94%)	18 (6%)	18	51
1	C	302/321 (94%)	284 (94%)	18 (6%)	17	50
1	D	298/321 (93%)	276 (93%)	22 (7%)	13	42
All	All	1217/1284 (95%)	1147 (94%)	70 (6%)	18	51

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ARG
1	A	69	THR
1	A	81	THR
1	A	140	ASP
1	A	150	MET
1	A	157	VAL
1	A	158	GLU
1	A	161	VAL
1	A	163	LYS
1	A	179	LEU
1	A	252	VAL
1	A	296	VAL
1	B	23	LYS
1	B	63	PHE
1	B	122	LEU
1	B	136	VAL
1	B	139	VAL
1	B	141	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	153	SER
1	B	157	VAL
1	B	158	GLU
1	B	161	VAL
1	B	166	LEU
1	B	179	LEU
1	B	198	THR
1	B	228	THR
1	B	246	THR
1	B	252	VAL
1	B	296	VAL
1	B	358	GLU
1	C	13	ARG
1	C	23	LYS
1	C	62	ASN
1	C	108	LEU
1	C	122	LEU
1	C	136	VAL
1	C	138	LYS
1	C	154	THR
1	C	161	VAL
1	C	171	LYS
1	C	172	ILE
1	C	179	LEU
1	C	195	GLU
1	C	246	THR
1	C	252	VAL
1	C	262	THR
1	C	296	VAL
1	C	344	VAL
1	D	14	LEU
1	D	49	VAL
1	D	54	ASN
1	D	58	GLU
1	D	64	LEU
1	D	65	LYS
1	D	76	THR
1	D	81	THR
1	D	84	LEU
1	D	107	VAL
1	D	113	ILE
1	D	122	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	141	GLU
1	D	157	VAL
1	D	161	VAL
1	D	162	GLU
1	D	185	ASP
1	D	190	ARG
1	D	222	GLN
1	D	296	VAL
1	D	355	LEU
1	D	356	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	301	HIS
1	B	301	HIS
1	C	30	ASN
1	C	312	HIS
1	C	332	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

24 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	SO4	A	405	-	4,4,4	0.24	0	6,6,6	0.08	0
5	PPV	B	506	-	6,8,8	0.76	0	12,13,13	0.84	0
4	SO4	B	504	-	4,4,4	0.24	0	6,6,6	0.08	0
4	SO4	A	406	-	4,4,4	0.38	0	6,6,6	0.08	0
2	GDD	A	401	-	41,42,42	3.37	23 (56%)	62,65,65	1.45	9 (14%)
4	SO4	D	504	-	4,4,4	0.23	0	6,6,6	0.08	0
4	SO4	D	503	-	4,4,4	0.23	0	6,6,6	0.07	0
3	FLC	C	401	-	12,12,12	1.32	1 (8%)	17,17,17	1.64	4 (23%)
4	SO4	A	408	-	4,4,4	0.24	0	6,6,6	0.07	0
4	SO4	B	505	-	4,4,4	0.25	0	6,6,6	0.08	0
4	SO4	B	501	-	4,4,4	0.22	0	6,6,6	0.09	0
4	SO4	A	407	-	4,4,4	0.23	0	6,6,6	0.06	0
4	SO4	B	502	-	4,4,4	0.24	0	6,6,6	0.09	0
4	SO4	B	503	-	4,4,4	0.22	0	6,6,6	0.09	0
4	SO4	A	403	-	4,4,4	0.24	0	6,6,6	0.07	0
4	SO4	C	405	-	4,4,4	0.24	0	6,6,6	0.09	0
4	SO4	A	404	-	4,4,4	0.23	0	6,6,6	0.10	0
4	SO4	D	501	-	4,4,4	0.24	0	6,6,6	0.07	0
3	FLC	A	402	-	12,12,12	1.09	0	17,17,17	1.35	1 (5%)
4	SO4	C	402	-	4,4,4	0.24	0	6,6,6	0.09	0
4	SO4	D	502	-	4,4,4	0.23	0	6,6,6	0.07	0
4	SO4	C	404	-	4,4,4	0.24	0	6,6,6	0.10	0
4	SO4	C	403	-	4,4,4	0.24	0	6,6,6	0.07	0
5	PPV	D	505	-	6,8,8	0.83	0	12,13,13	0.93	1 (8%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PPV	B	506	-	-	1/6/6/6	-
2	GDD	A	401	-	-	5/23/59/59	0/4/4/4
3	FLC	A	402	-	-	9/16/16/16	-
3	FLC	C	401	-	-	9/16/16/16	-
5	PPV	D	505	-	-	0/6/6/6	-

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	GDD	O4'-C1'	9.49	1.63	1.42
2	A	401	GDD	C4-N3	6.64	1.49	1.34
2	A	401	GDD	C2'-C1'	-6.33	1.33	1.53
2	A	401	GDD	O4'-C4'	-6.26	1.31	1.45
2	A	401	GDD	PB-O3A	6.12	1.66	1.59
2	A	401	GDD	C2-N2	5.84	1.47	1.34
2	A	401	GDD	PA-O3A	5.55	1.65	1.59
2	A	401	GDD	C2-N3	4.96	1.45	1.33
2	A	401	GDD	PB-O1B	3.94	1.71	1.59
2	A	401	GDD	C2-N1	3.86	1.47	1.37
2	A	401	GDD	O2'-C2'	3.25	1.51	1.43
2	A	401	GDD	C5-N7	-3.18	1.32	1.39
2	A	401	GDD	O31-C31	2.83	1.50	1.43
2	A	401	GDD	C4-N9	-2.63	1.31	1.38
2	A	401	GDD	C6-N1	2.54	1.43	1.38
2	A	401	GDD	C41-C31	-2.38	1.46	1.52
2	A	401	GDD	C5-C6	2.38	1.53	1.44
2	A	401	GDD	PA-O5'	2.32	1.68	1.59
2	A	401	GDD	O6-C6	-2.16	1.19	1.23
2	A	401	GDD	O51-C11	2.16	1.47	1.41
3	C	401	FLC	CG-CB	-2.14	1.51	1.54
2	A	401	GDD	O3'-C3'	-2.12	1.37	1.43
2	A	401	GDD	O41-C41	2.02	1.48	1.43
2	A	401	GDD	C3'-C4'	2.00	1.58	1.53

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	GDD	C5-C4-N3	-5.01	120.42	128.39
2	A	401	GDD	C2-N3-C4	4.56	120.15	112.30
3	A	402	FLC	OB2-CBC-CB	3.33	119.54	113.14
2	A	401	GDD	N9-C8-N7	-3.08	107.70	113.40
3	C	401	FLC	CG-CB-CBC	-2.95	103.52	110.03
2	A	401	GDD	C2-N1-C6	-2.94	119.78	125.11
3	C	401	FLC	OB2-CBC-CB	2.93	118.76	113.14
2	A	401	GDD	N9-C4-N3	2.91	131.76	125.95
2	A	401	GDD	C5-C6-N1	2.56	119.77	113.25
2	A	401	GDD	O6-C6-C5	-2.45	120.07	126.53
3	C	401	FLC	CB-CG-CGC	-2.44	107.25	113.92
2	A	401	GDD	C8-N7-C5	2.17	108.13	104.26
2	A	401	GDD	O51-C11-O1B	-2.14	108.57	111.36
5	D	505	PPV	O21-P1-OPP	2.10	111.68	104.64

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	401	FLC	OA2-CAC-OA1	-2.02	118.14	123.33

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	GDD	C11-O1B-PB-O3A
3	A	402	FLC	CA-CB-CBC-OB1
3	A	402	FLC	CA-CB-CBC-OB2
3	A	402	FLC	OHB-CB-CBC-OB1
3	A	402	FLC	OHB-CB-CBC-OB2
3	A	402	FLC	CA-CB-CG-CGC
3	A	402	FLC	CBC-CB-CG-CGC
3	A	402	FLC	OHB-CB-CG-CGC
3	C	401	FLC	CG-CB-CBC-OB1
3	C	401	FLC	CG-CB-CBC-OB2
3	C	401	FLC	OHB-CB-CBC-OB1
3	C	401	FLC	OHB-CB-CBC-OB2
3	C	401	FLC	CBC-CB-CG-CGC
3	C	401	FLC	OHB-CB-CG-CGC
2	A	401	GDD	C3'-C4'-C5'-O5'
3	C	401	FLC	CA-CB-CG-CGC
2	A	401	GDD	O4'-C4'-C5'-O5'
3	A	402	FLC	CB-CA-CAC-OA1
3	A	402	FLC	CB-CA-CAC-OA2
5	B	506	PPV	P2-OPP-P1-O11
3	C	401	FLC	CA-CB-CBC-OB1
3	C	401	FLC	CA-CB-CBC-OB2
2	A	401	GDD	C41-C51-C61-O6A
2	A	401	GDD	O51-C51-C61-O6A

There are no ring outliers.

7 monomers are involved in 9 short contacts:

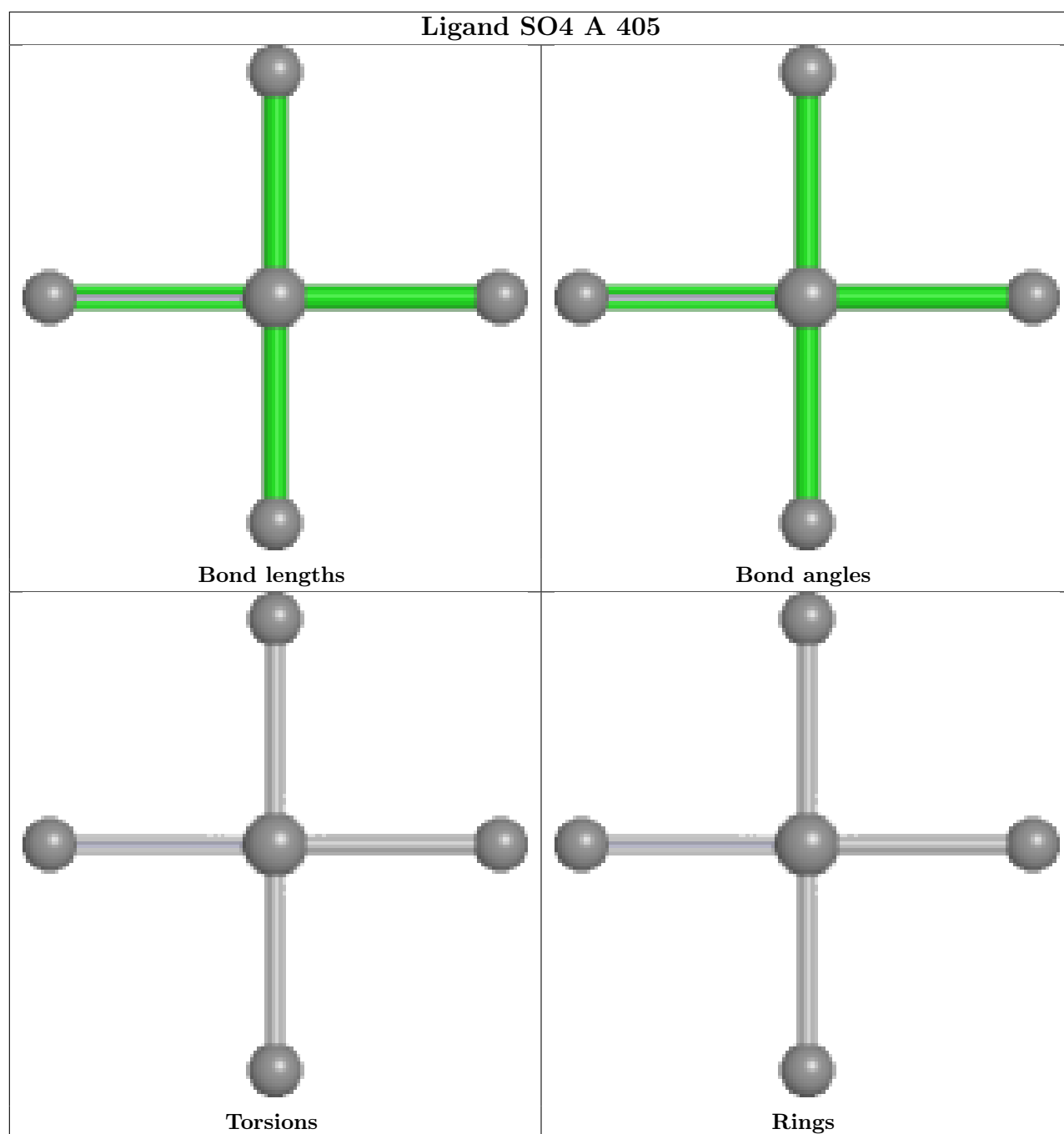
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	504	SO4	1	0
2	A	401	GDD	1	0
3	C	401	FLC	3	0
4	A	404	SO4	1	0
4	D	501	SO4	1	0
3	A	402	FLC	1	0

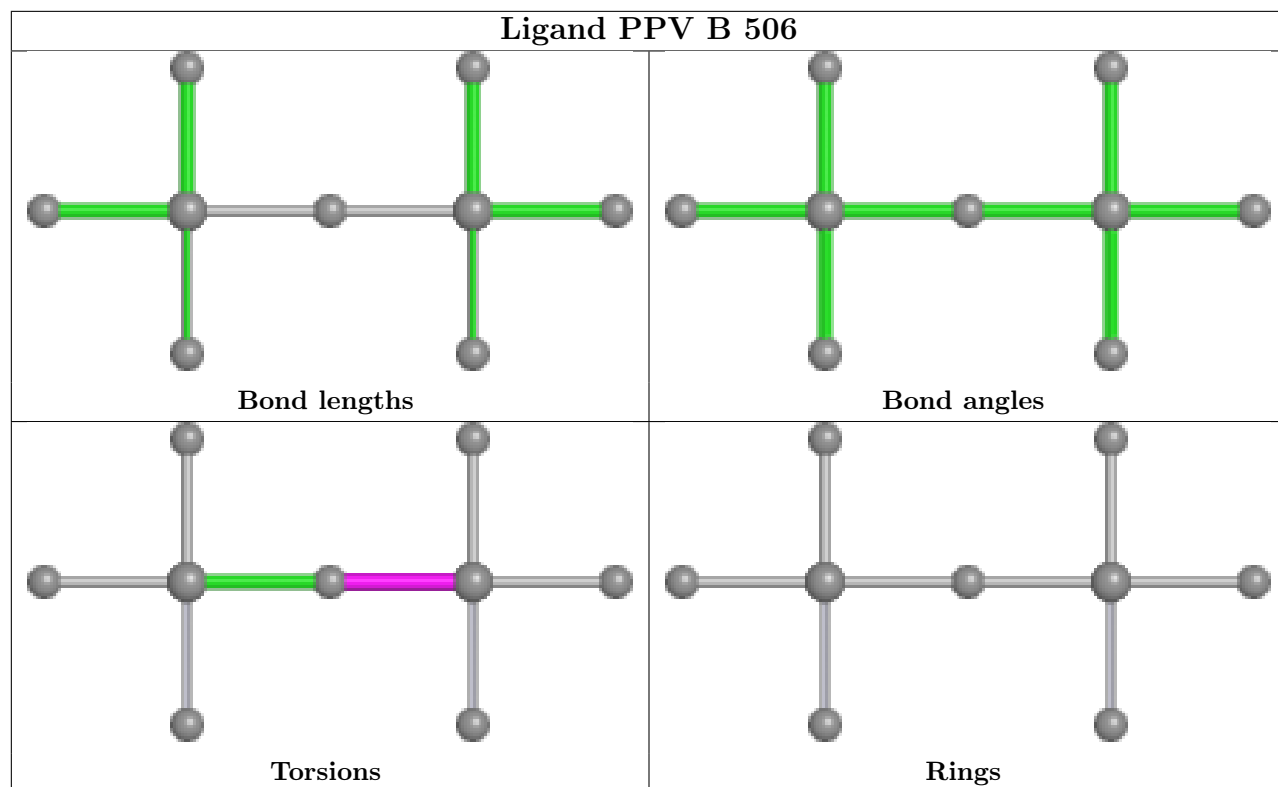
Continued on next page...

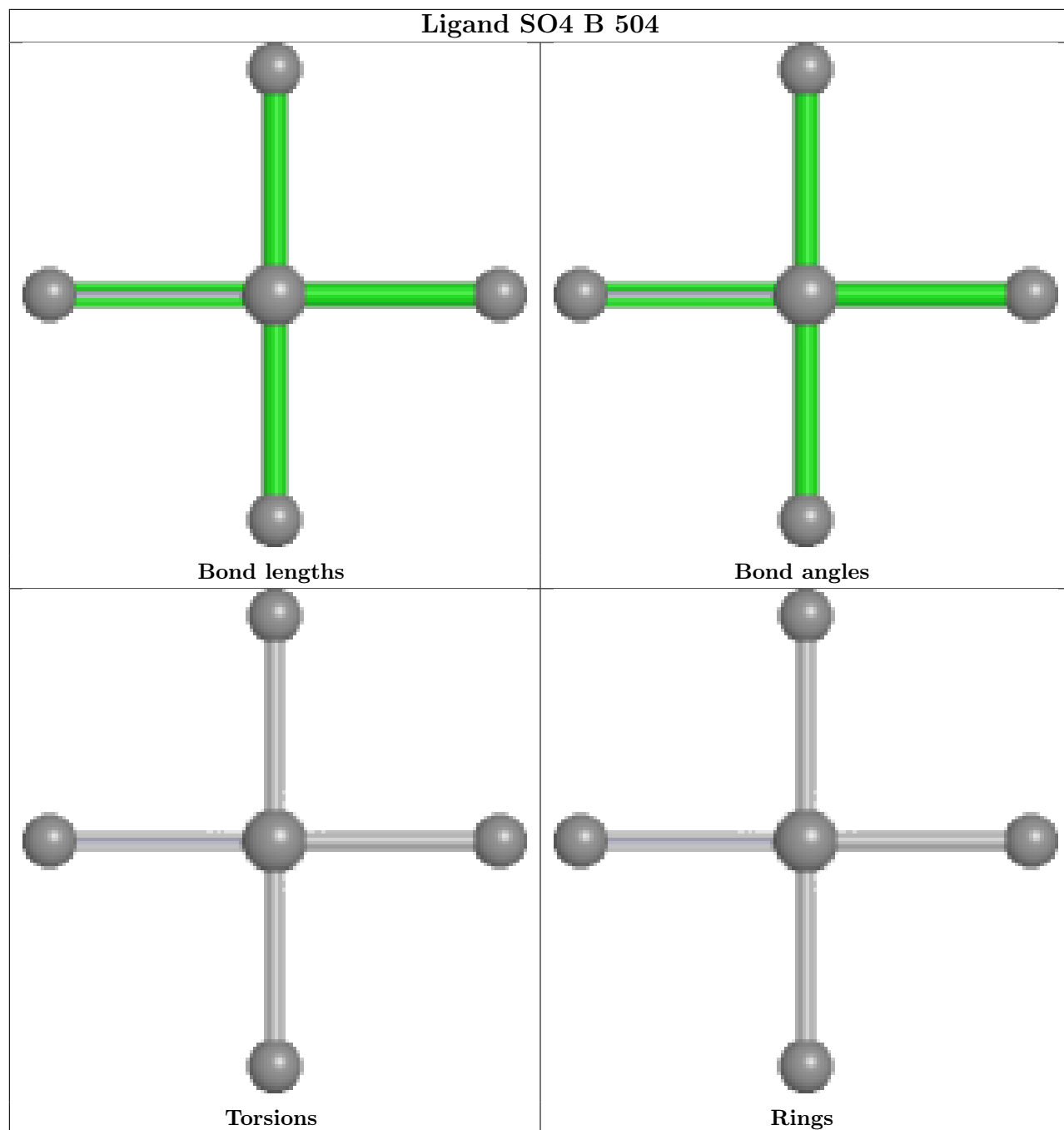
Continued from previous page...

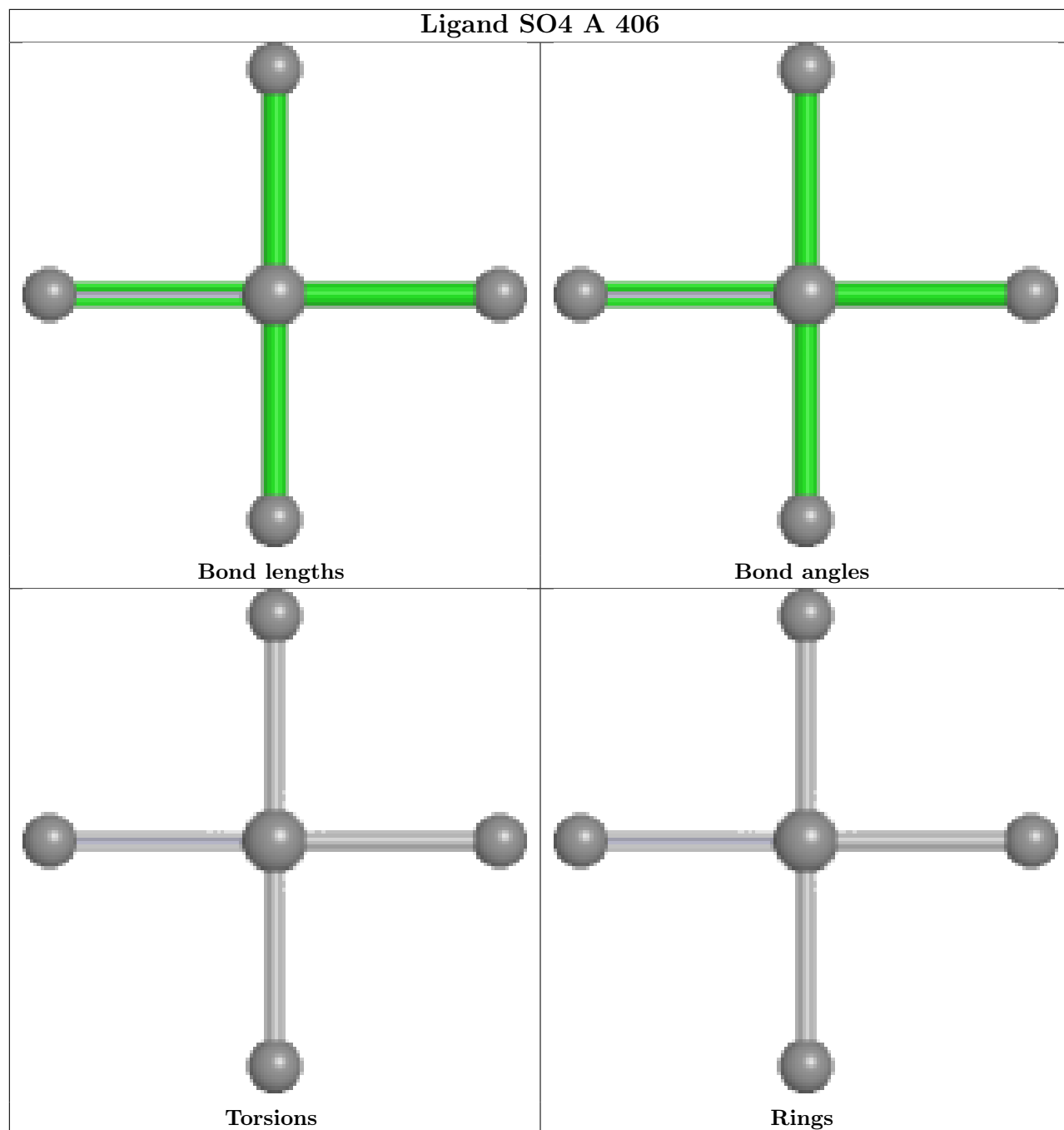
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	402	SO4	1	0

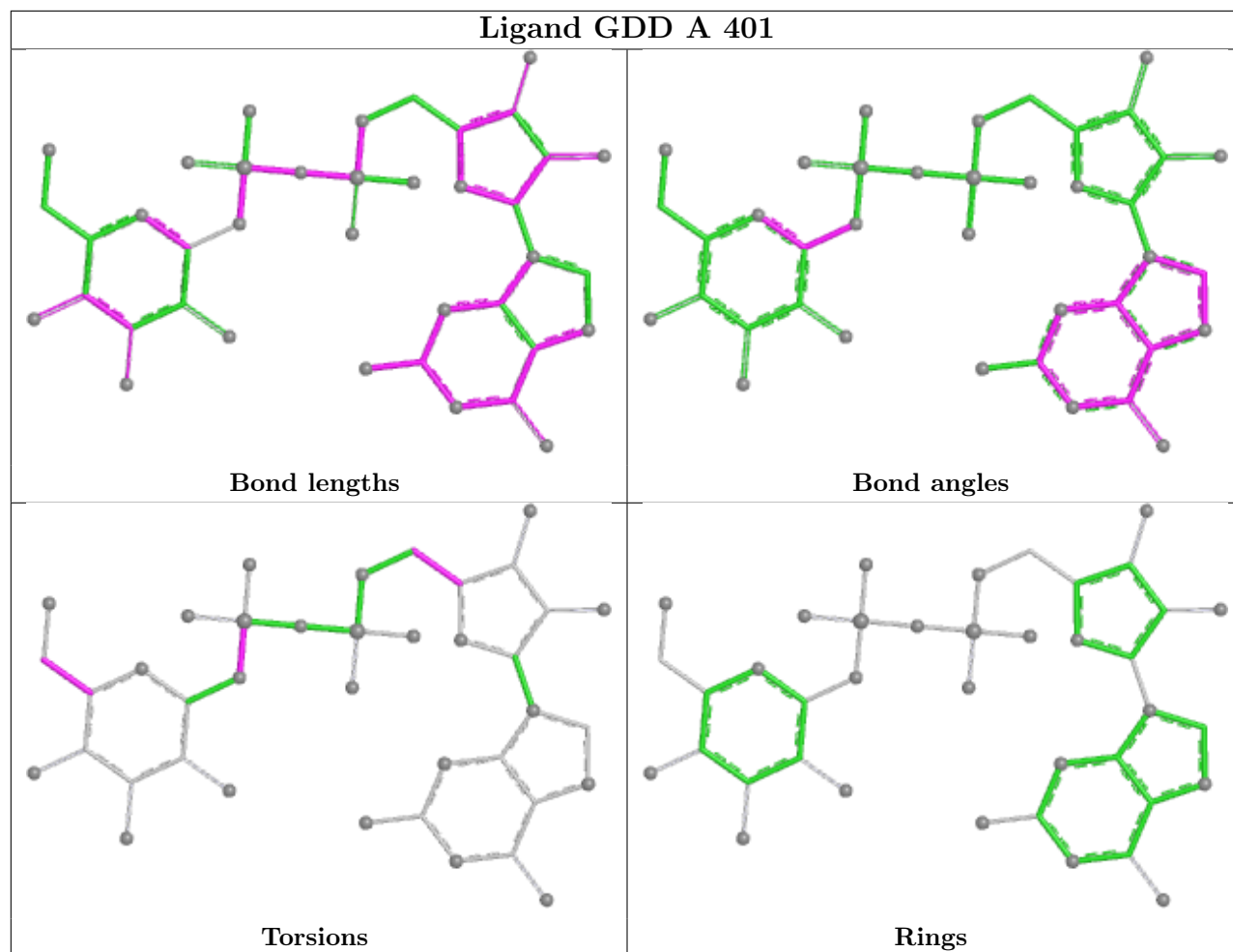
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

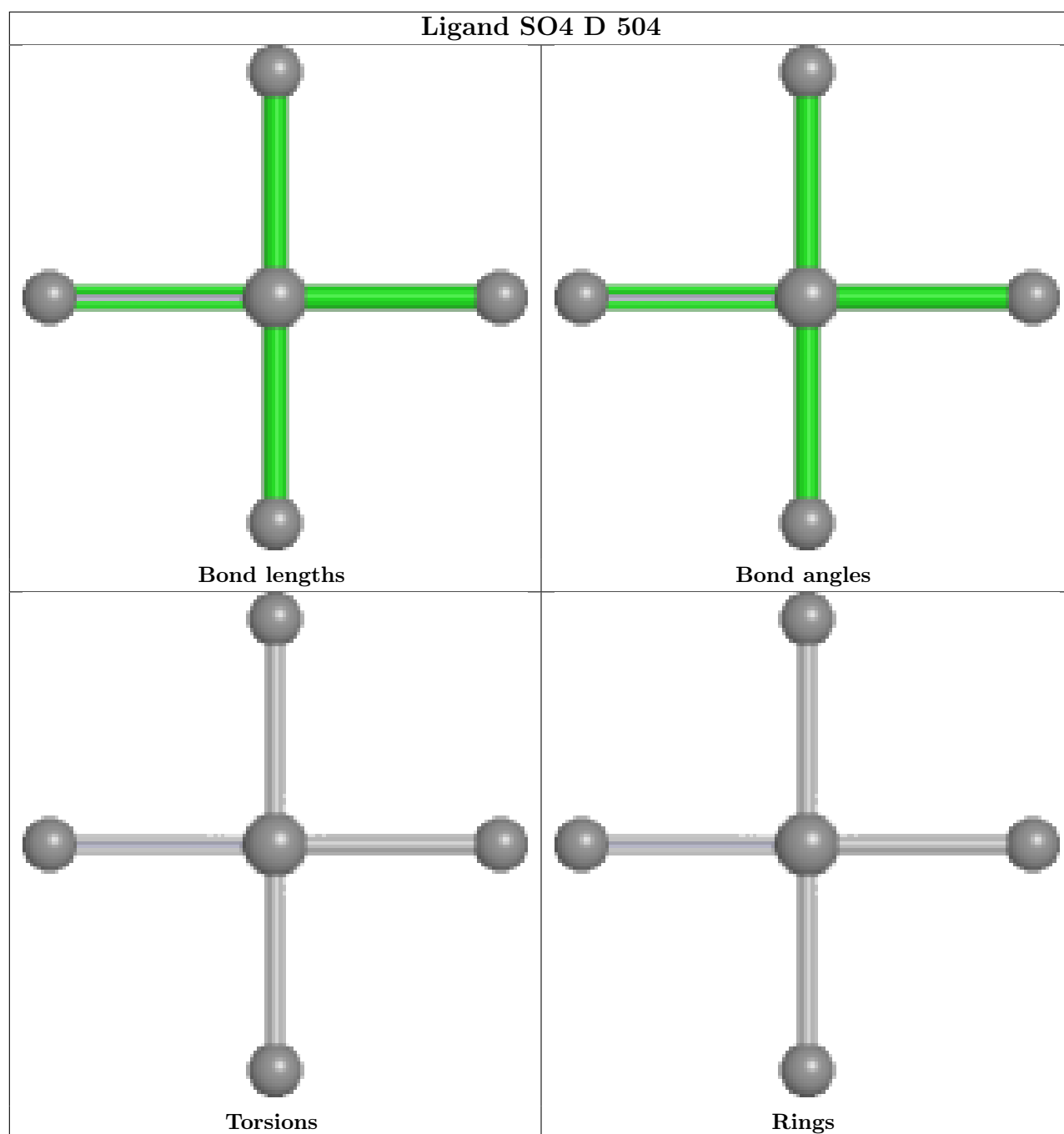


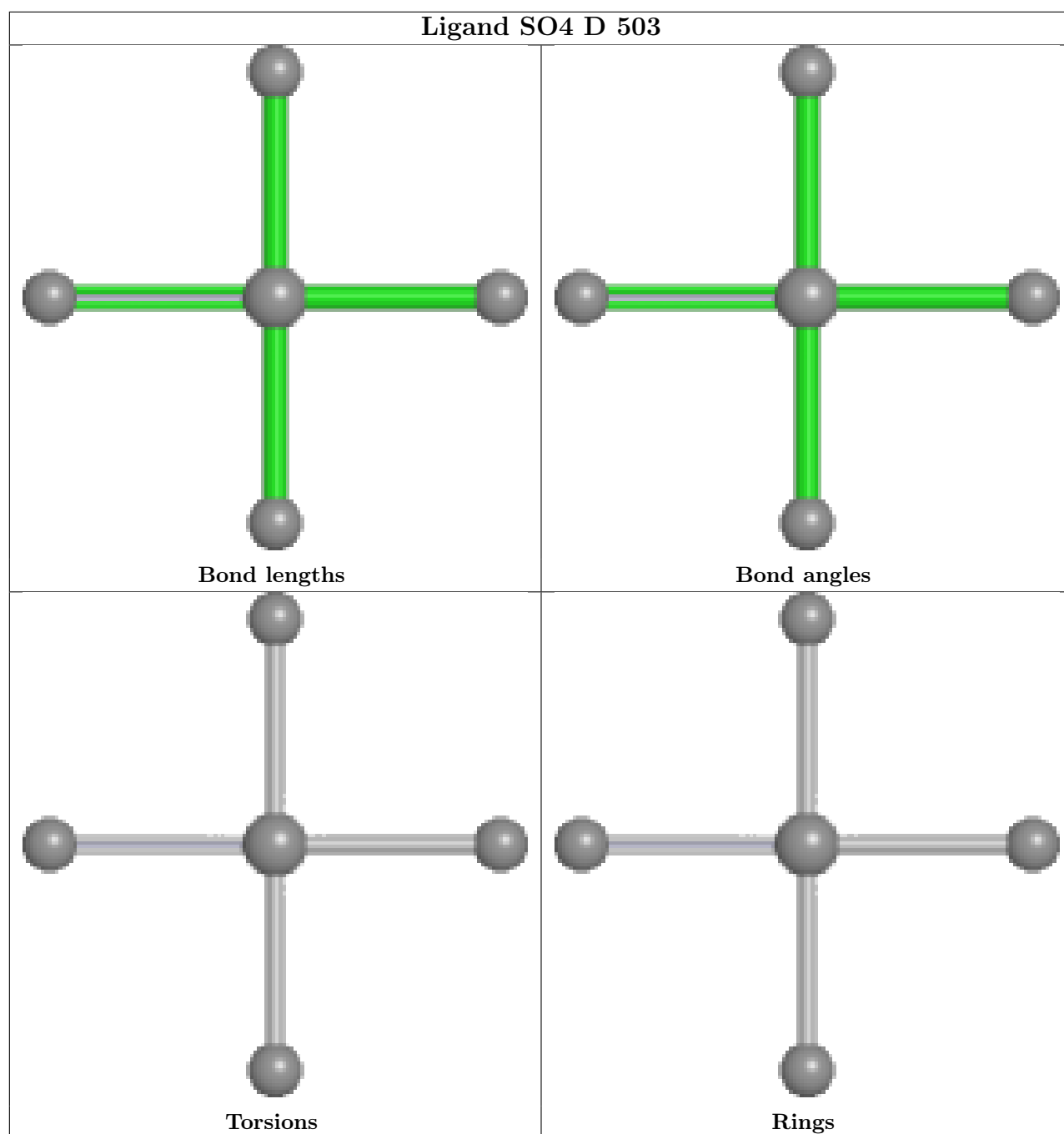


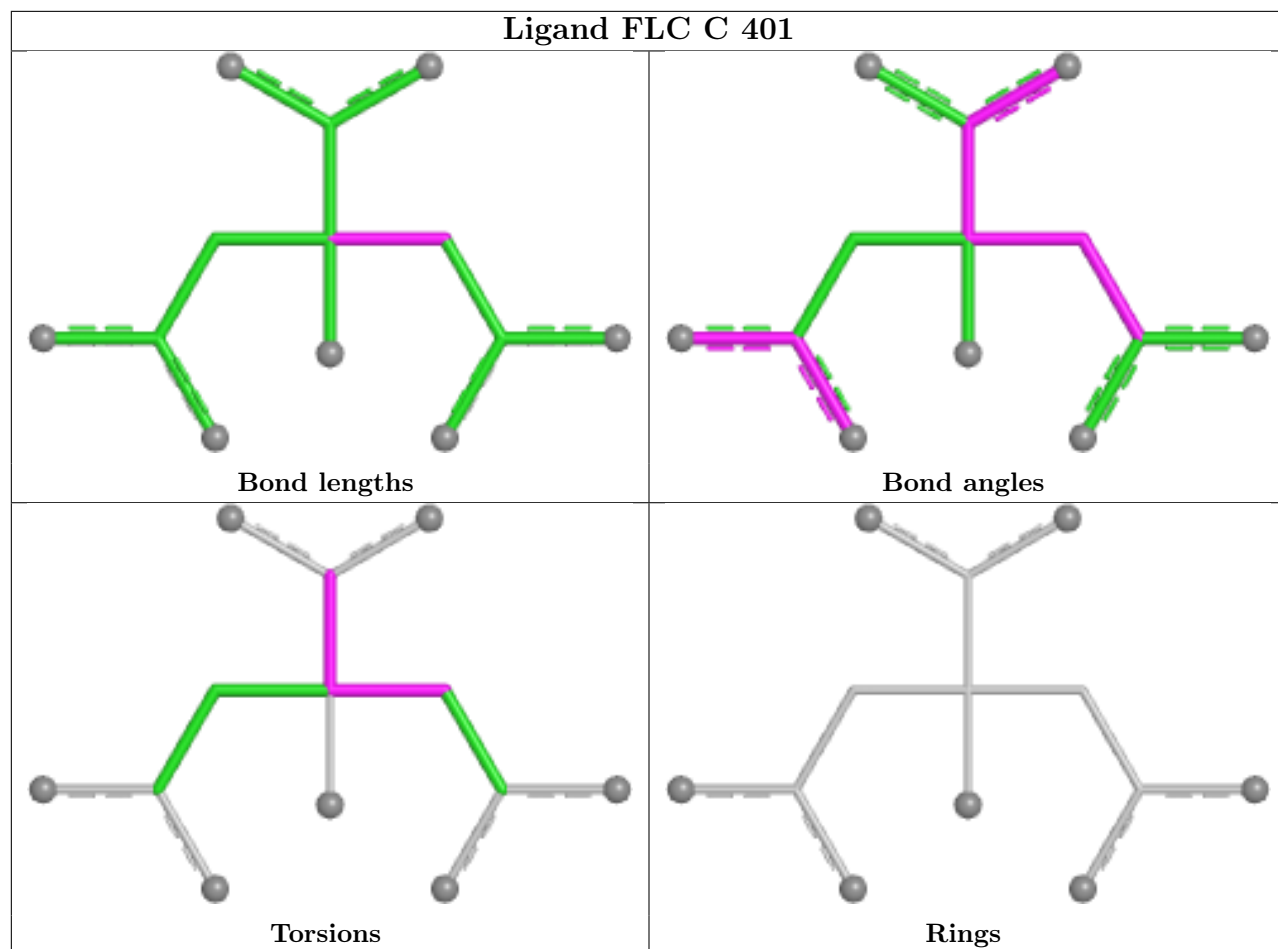


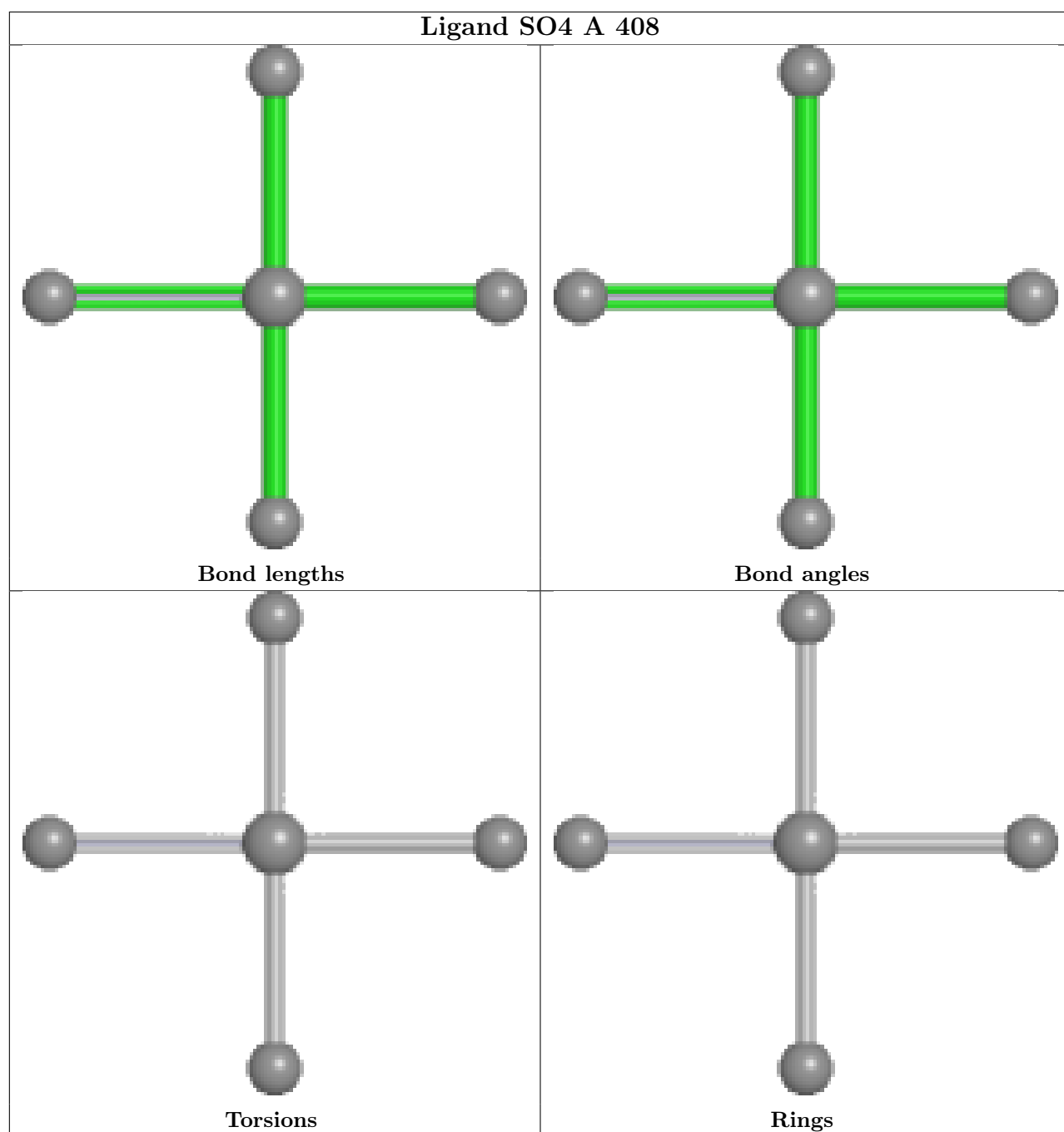


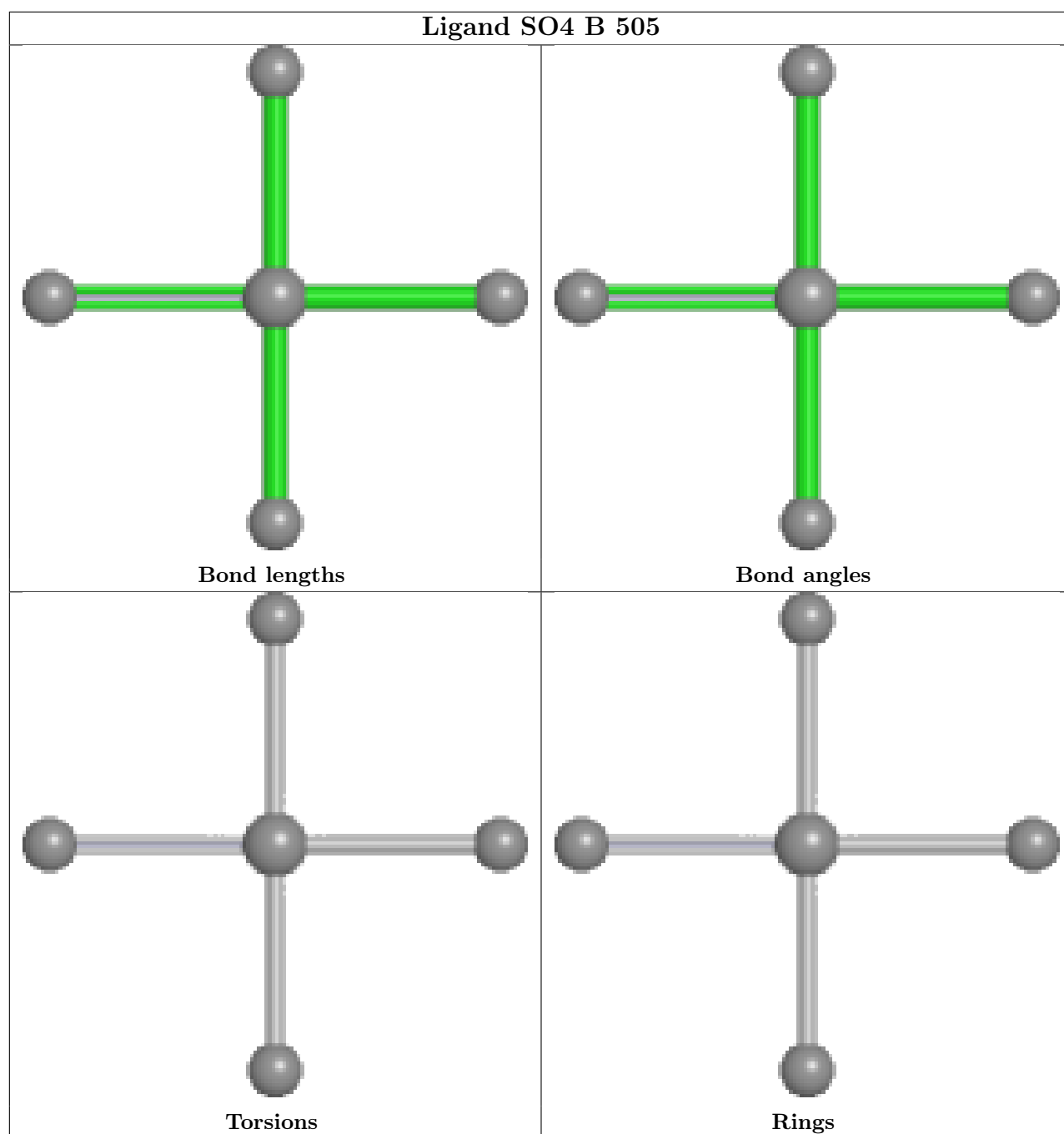


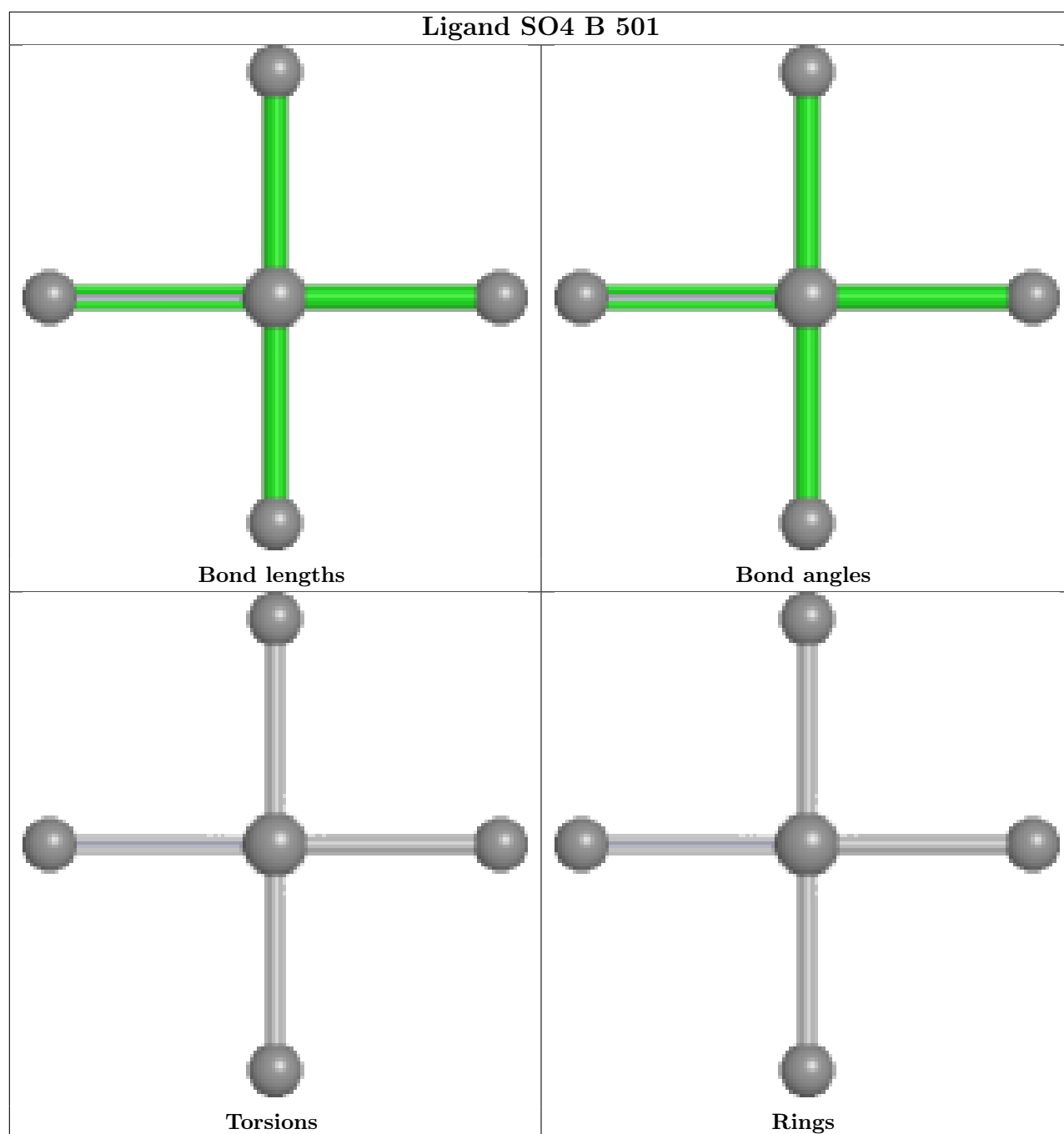


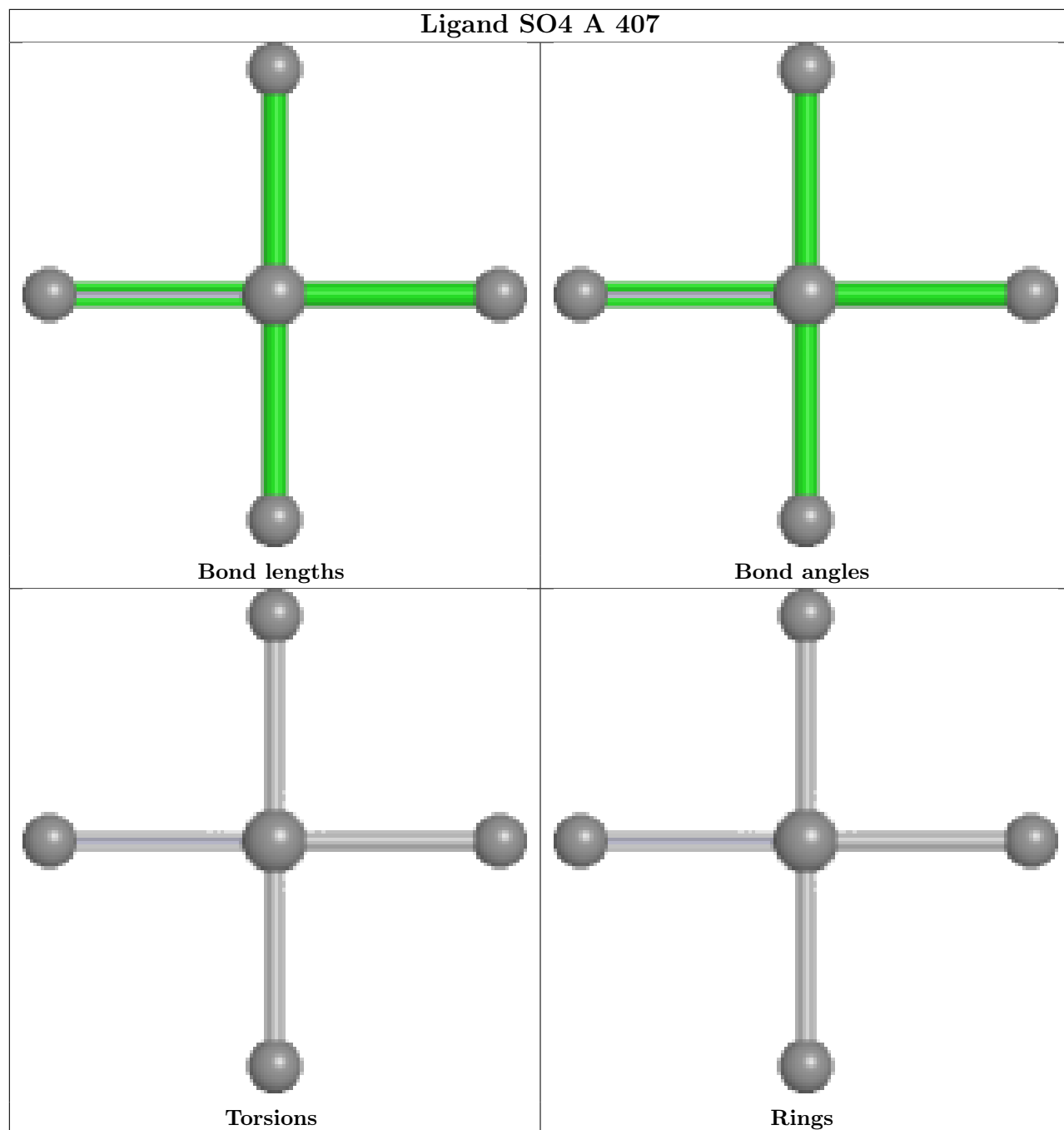


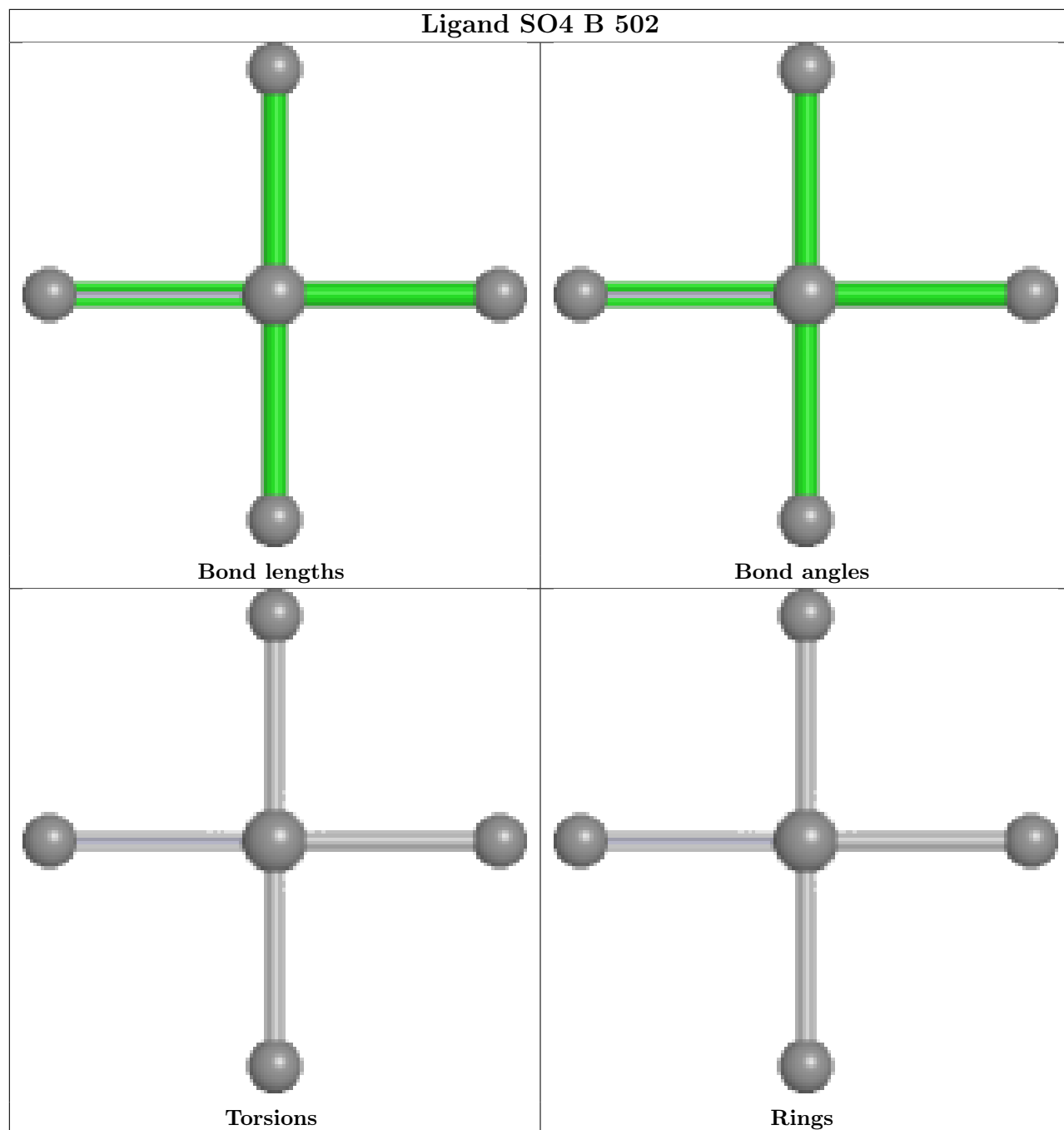


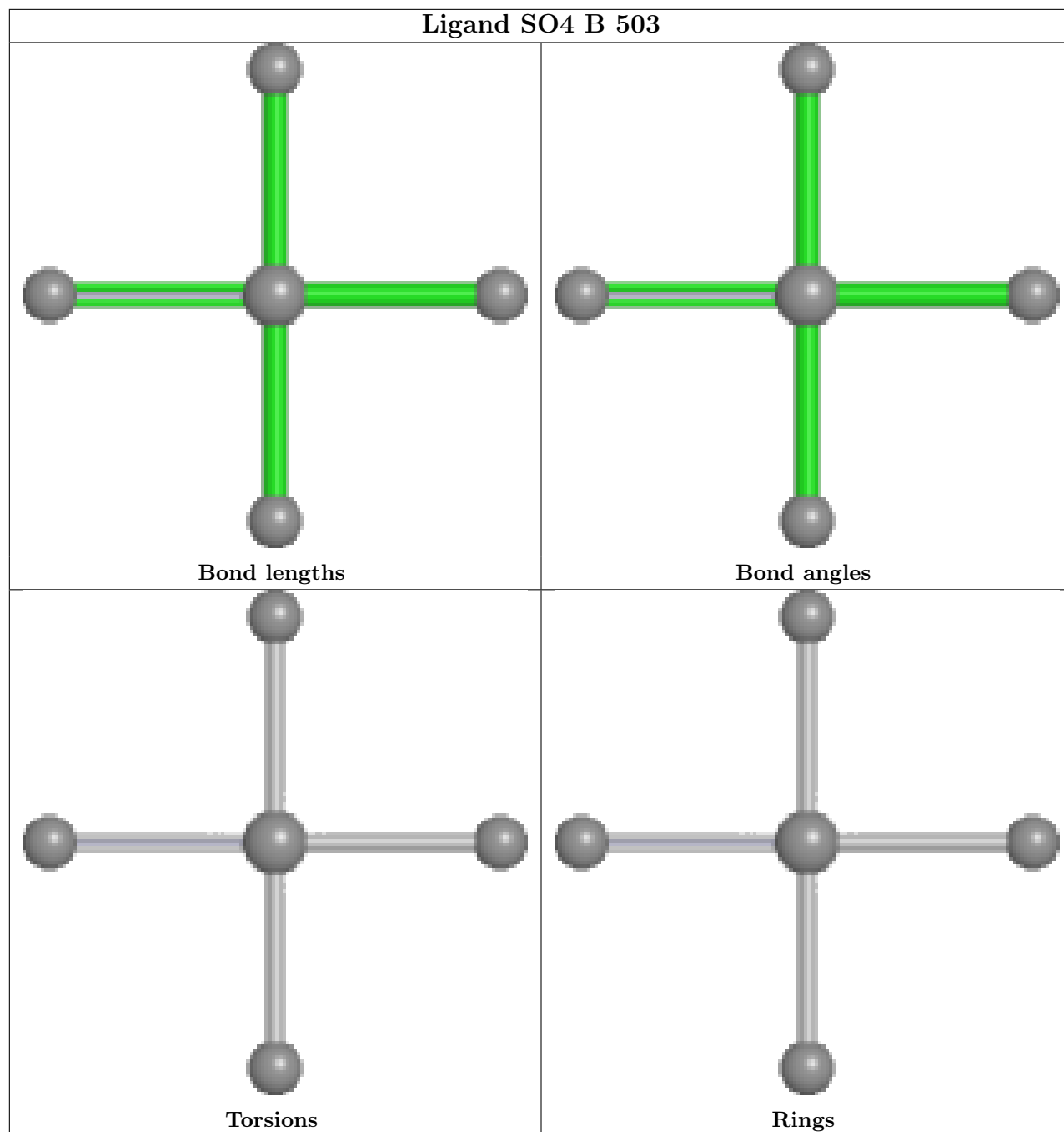


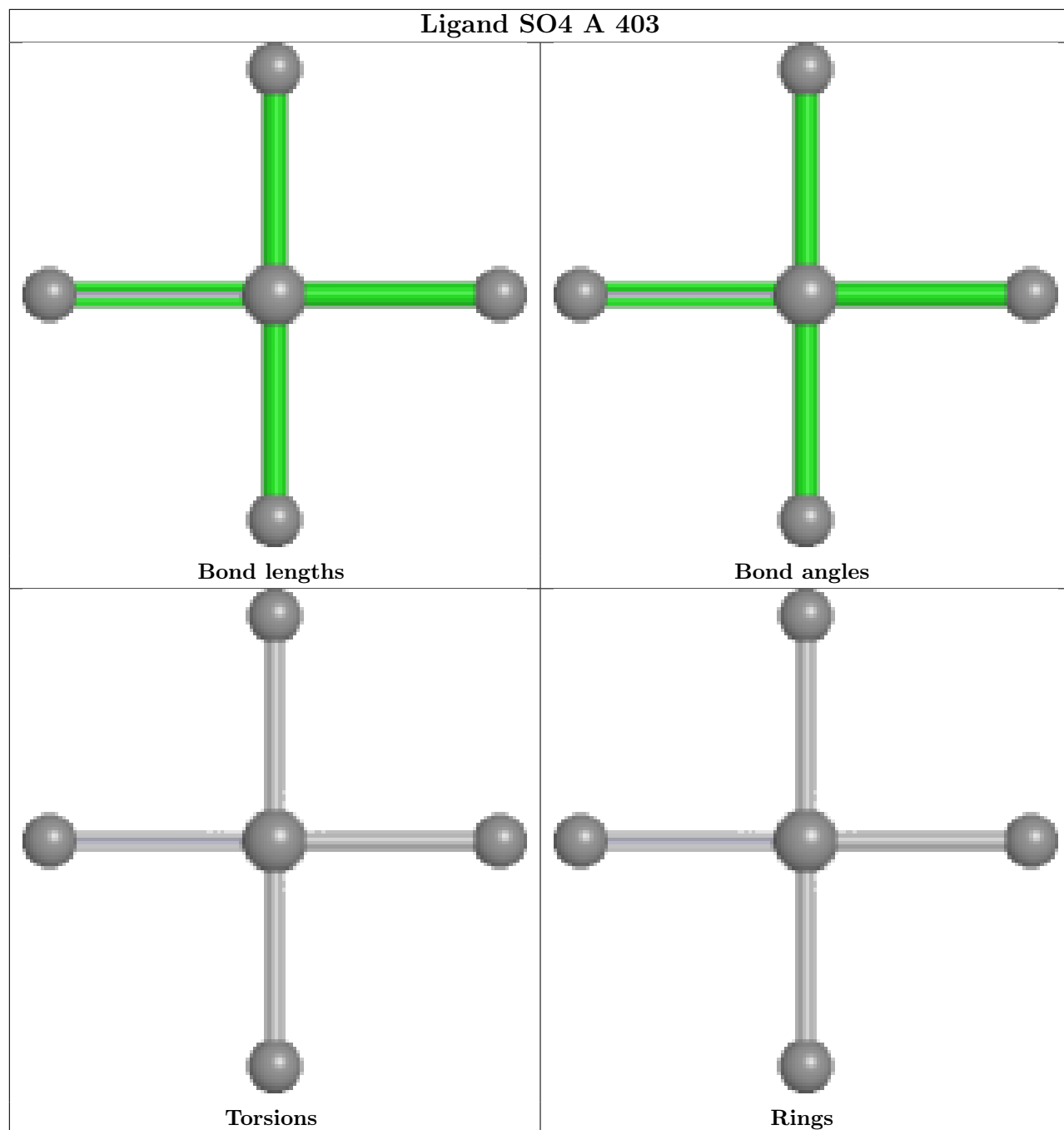


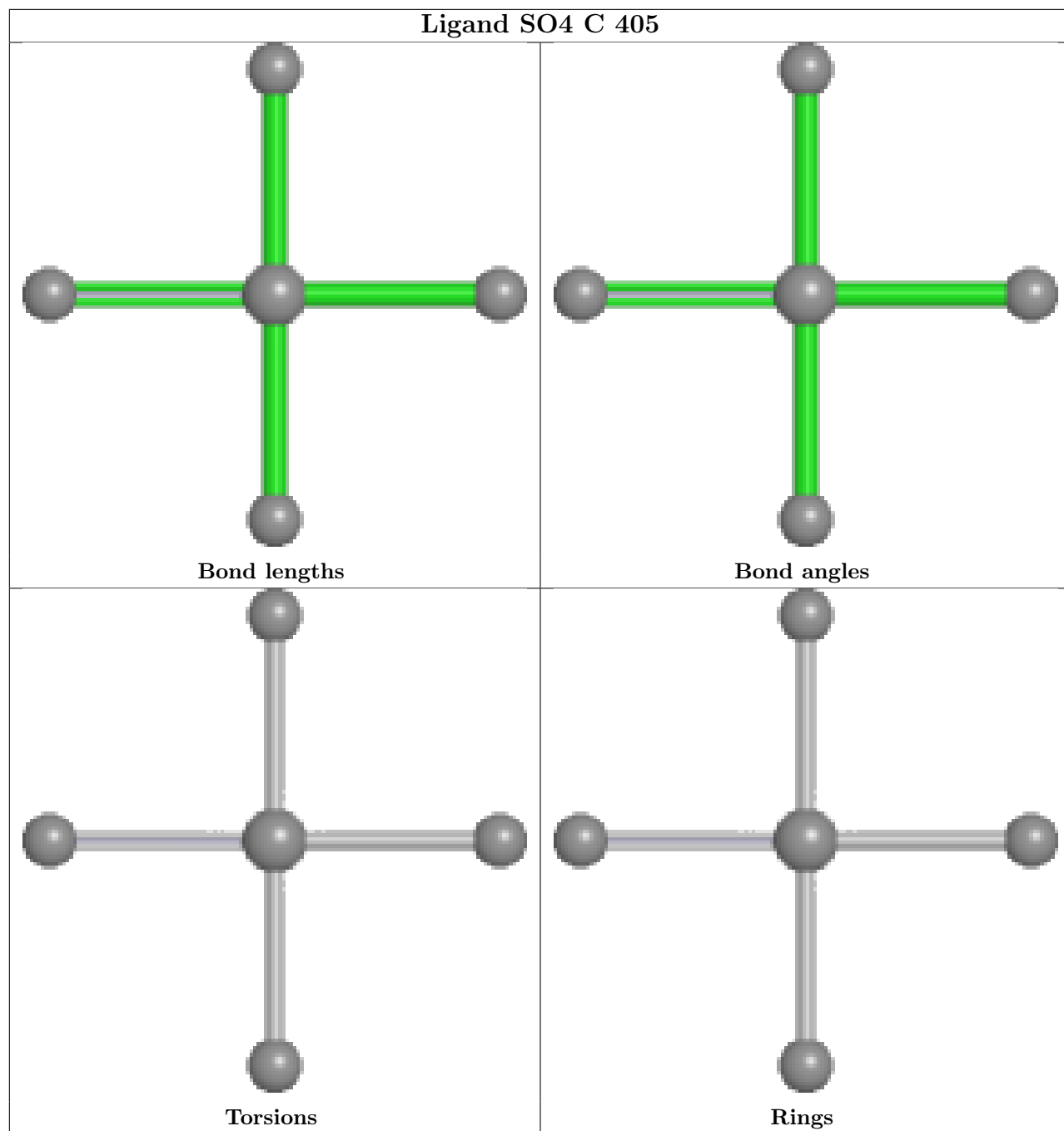


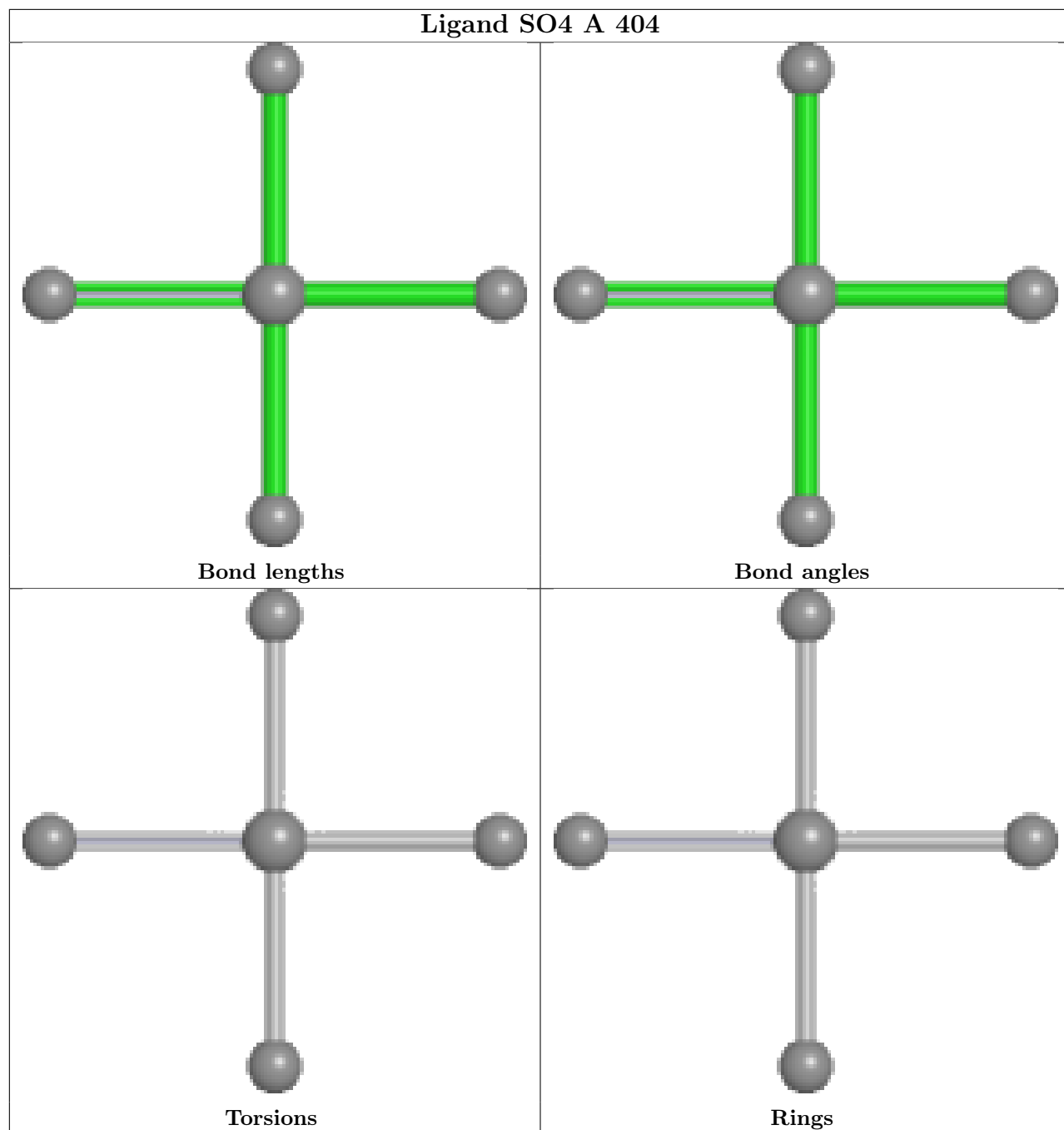


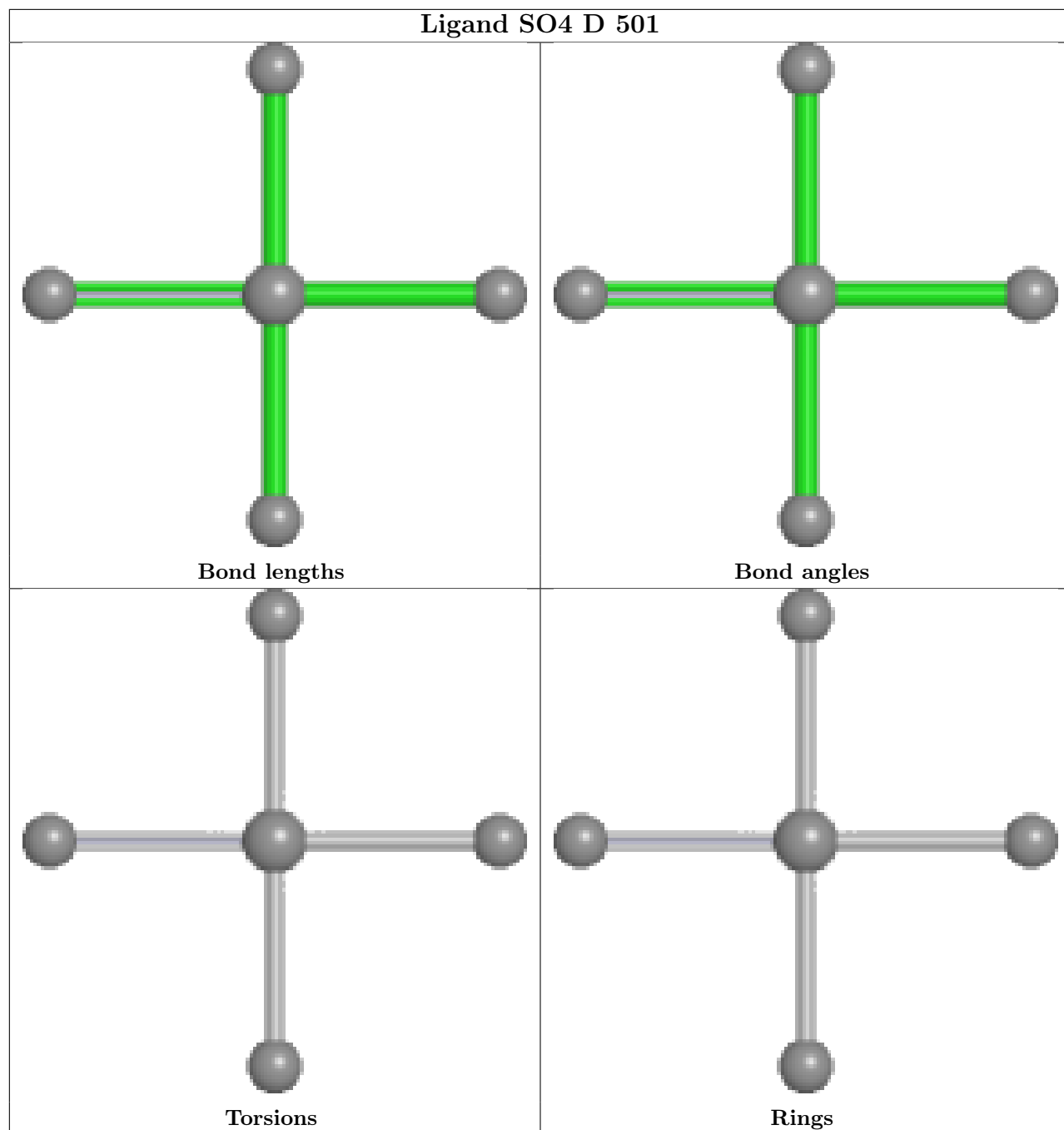


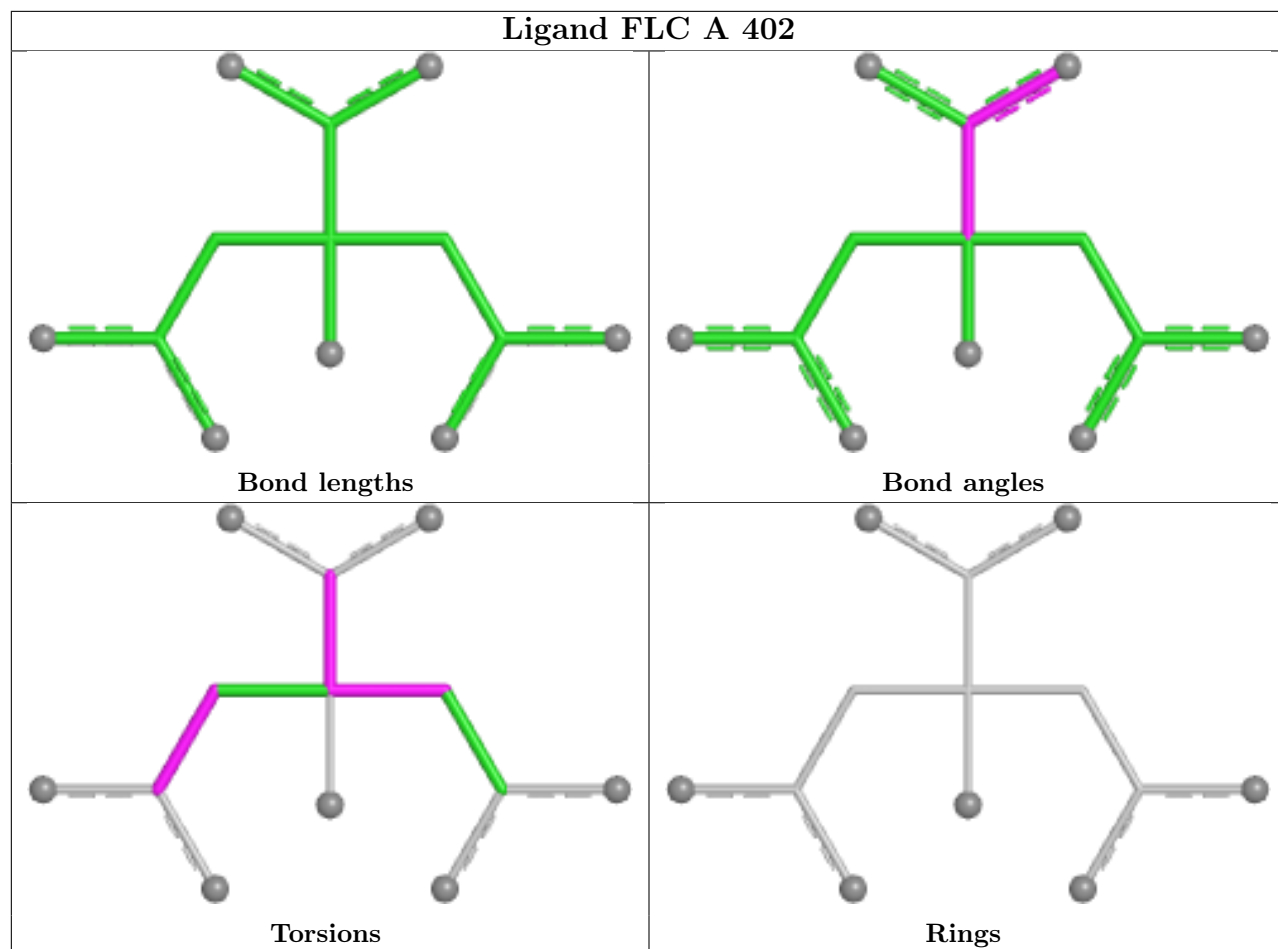


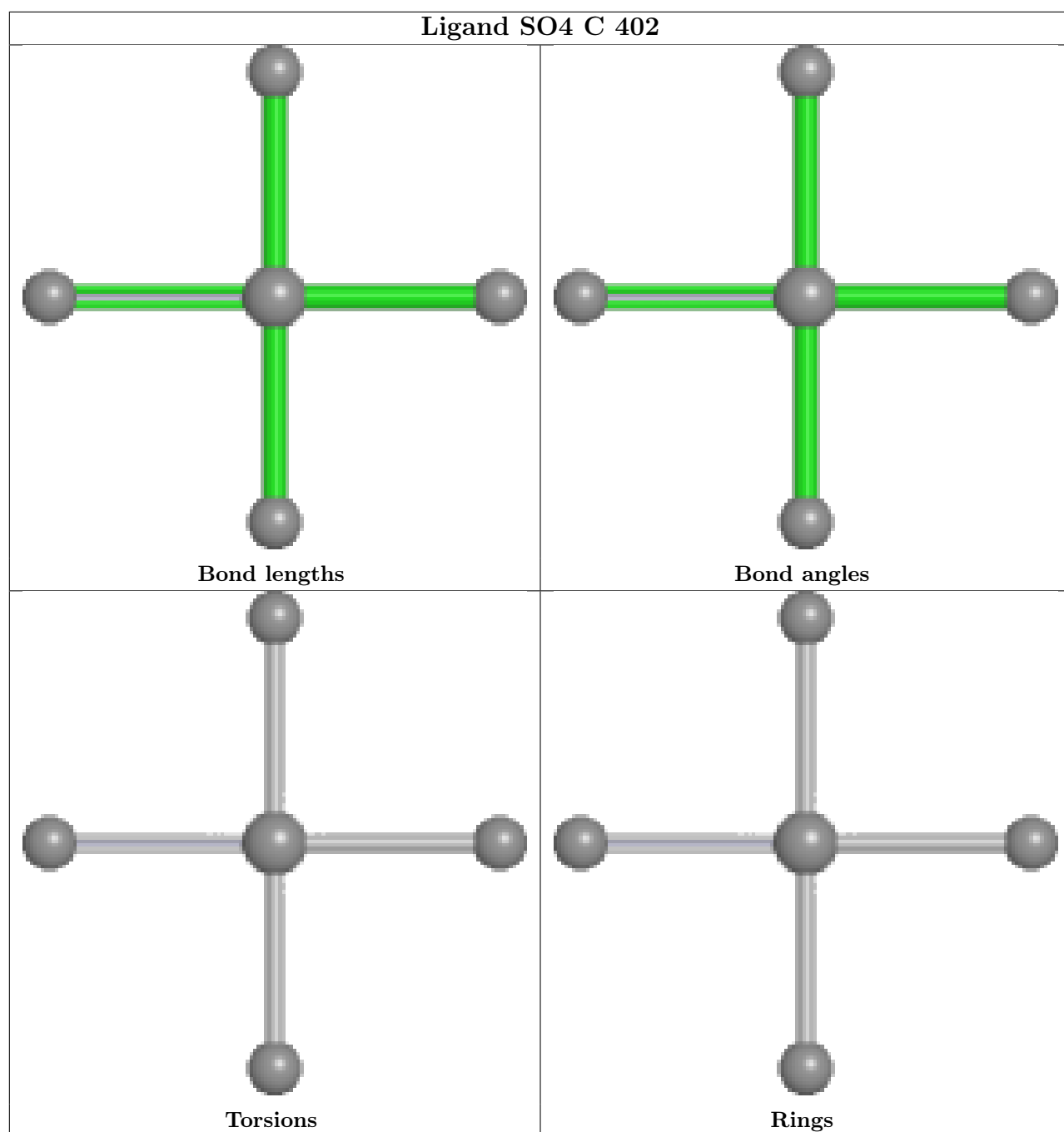


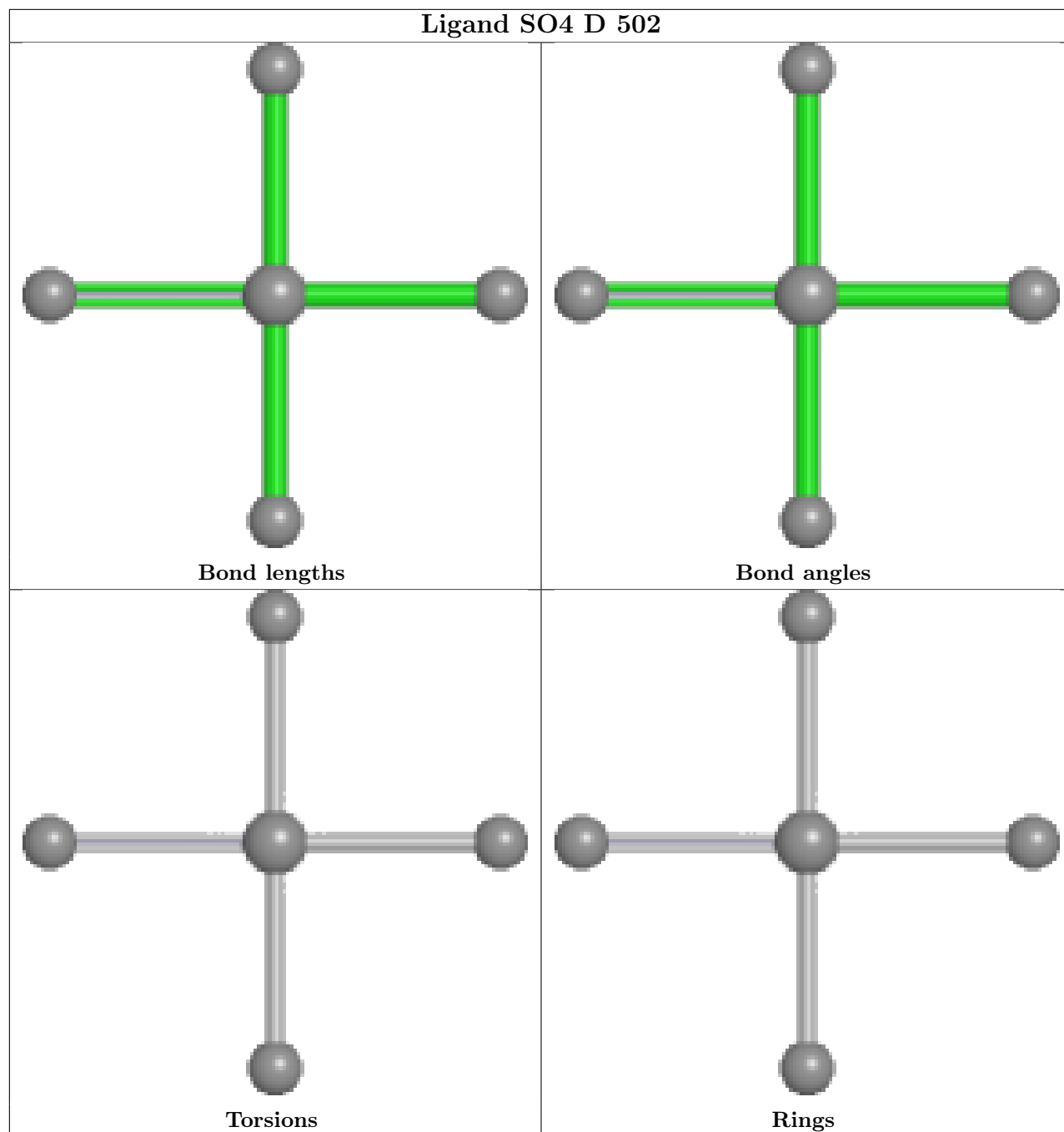


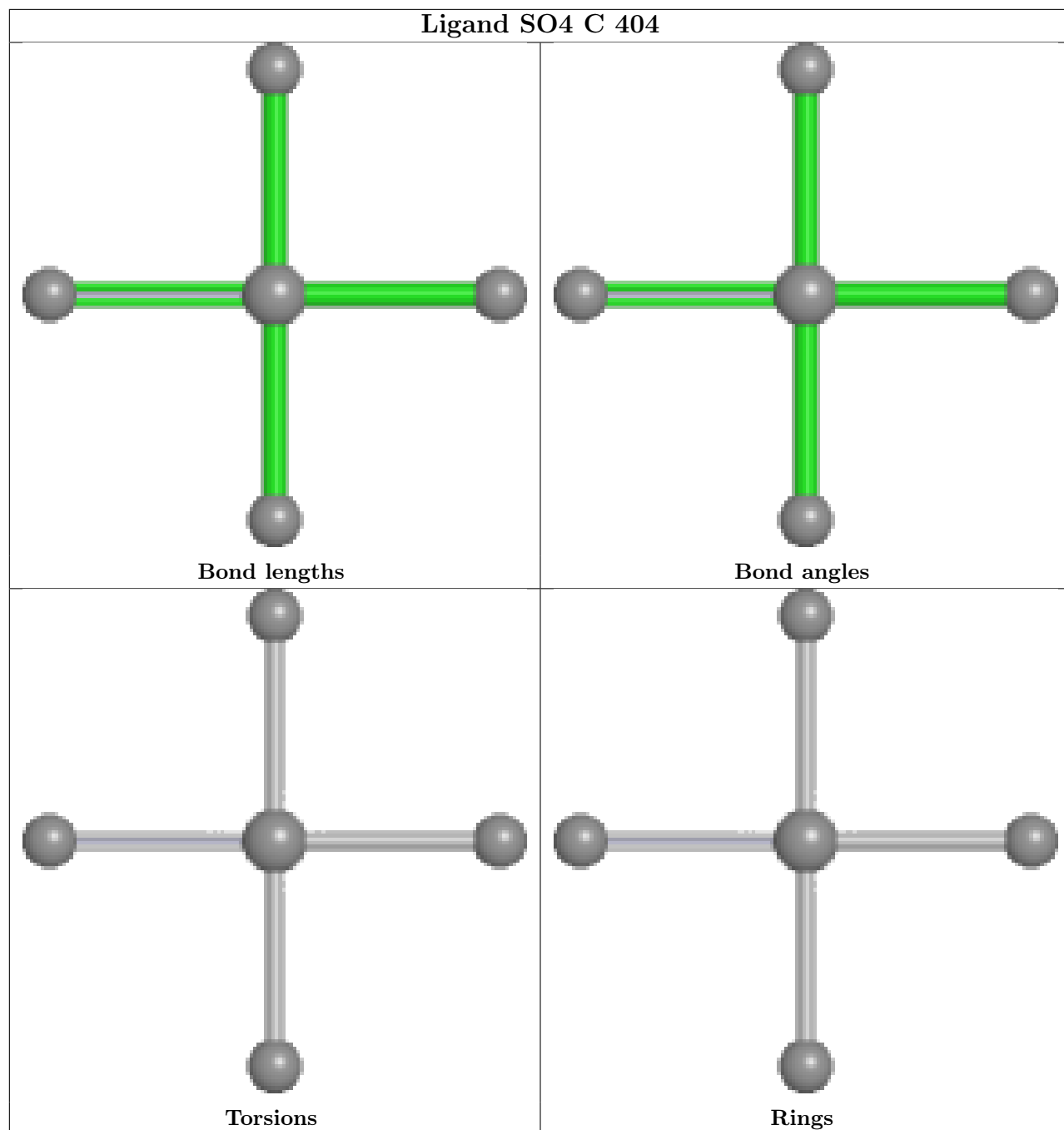


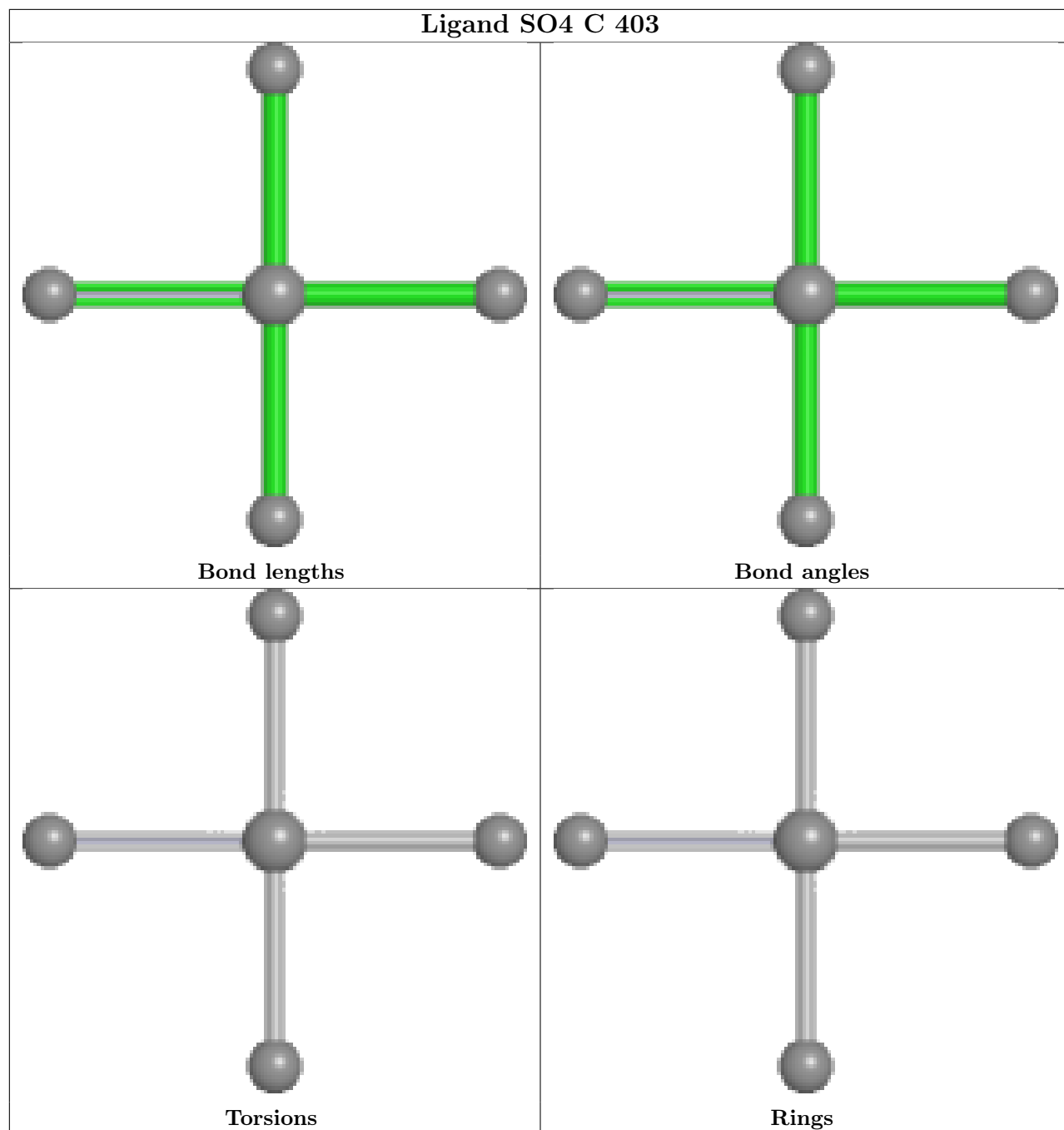


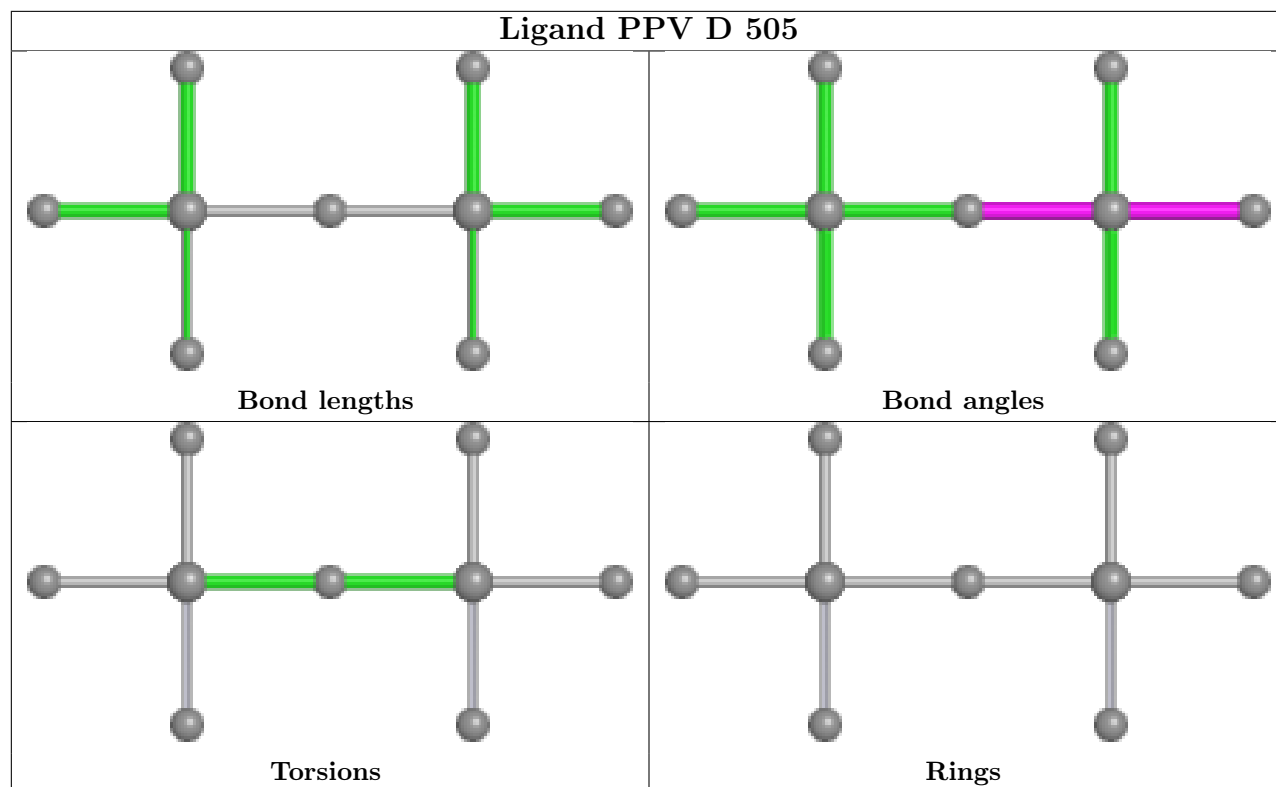












5.7 Other polymers [i](#)

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	365/376 (97%)	0.22	10 (2%) 56 33	28, 48, 86, 120	0
1	B	367/376 (97%)	0.16	7 (1%) 66 43	30, 54, 88, 119	0
1	C	355/376 (94%)	0.25	20 (5%) 30 15	27, 54, 110, 150	0
1	D	355/376 (94%)	0.46	26 (7%) 21 11	30, 63, 111, 128	0
All	All	1442/1504 (95%)	0.27	63 (4%) 39 21	27, 55, 96, 150	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	357	PRO	5.9
1	C	54	ASN	3.9
1	D	166	LEU	3.8
1	C	166	LEU	3.7
1	D	356	LYS	3.6
1	C	142	PRO	3.6
1	D	168	VAL	3.5
1	D	163	LYS	3.5
1	A	159	LYS	3.5
1	B	166	LEU	3.5
1	C	154	THR	3.4
1	D	164	PRO	3.4
1	D	67	PHE	3.2
1	A	169	GLY	3.2
1	D	161	VAL	3.2
1	D	143	SER	3.2
1	C	164	PRO	3.1
1	C	143	SER	3.1
1	D	142	PRO	3.1
1	D	355	LEU	3.1
1	C	152	GLU	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	54	ASN	2.9
1	D	9	GLY	2.9
1	A	207	GLY	2.8
1	B	165	LYS	2.8
1	C	140	ASP	2.7
1	D	167	TYR	2.7
1	C	355	LEU	2.7
1	A	158	GLU	2.6
1	D	141	GLU	2.6
1	D	153	SER	2.6
1	C	165	LYS	2.6
1	A	54	ASN	2.6
1	C	146	GLY	2.5
1	A	170	ASN	2.5
1	C	357	PRO	2.5
1	C	67	PHE	2.5
1	C	163	LYS	2.4
1	A	142	PRO	2.3
1	D	83	PRO	2.3
1	C	59	VAL	2.3
1	A	164	PRO	2.3
1	D	140	ASP	2.3
1	B	367	LEU	2.3
1	D	81	THR	2.3
1	C	141	GLU	2.2
1	B	366	ALA	2.2
1	D	185	ASP	2.2
1	C	139	VAL	2.2
1	D	82	GLU	2.2
1	D	165	LYS	2.2
1	A	143	SER	2.2
1	C	168	VAL	2.1
1	A	168	VAL	2.1
1	B	10	PHE	2.1
1	D	222	GLN	2.1
1	C	159	LYS	2.0
1	D	138	LYS	2.0
1	C	169	GLY	2.0
1	D	10	PHE	2.0
1	D	63	PHE	2.0
1	D	61	LEU	2.0
1	B	164	PRO	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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

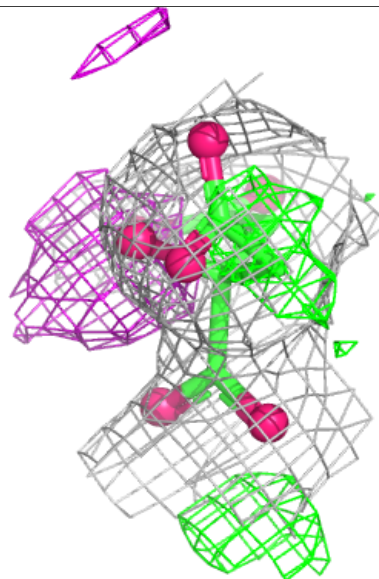
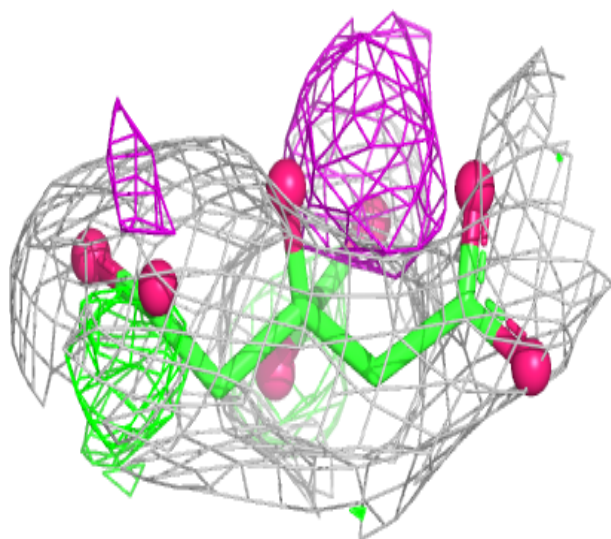
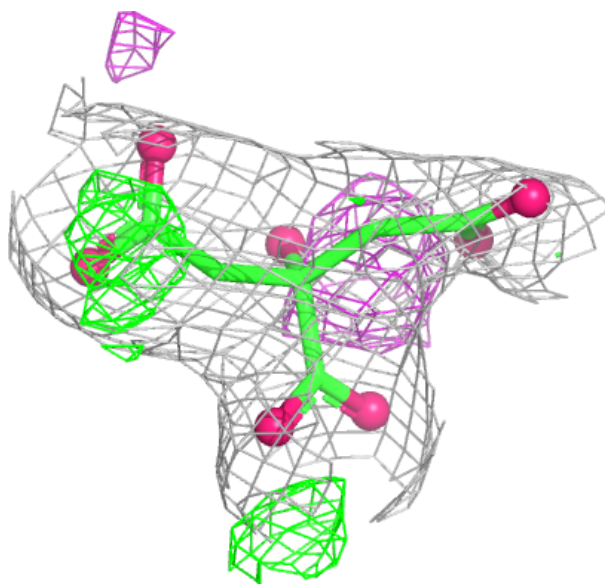
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	FLC	C	401	13/13	0.51	0.22	81,84,94,94	0
3	FLC	A	402	13/13	0.59	0.14	85,88,96,100	0
5	PPV	D	505	9/9	0.68	0.16	85,88,92,93	9
4	SO4	C	405	5/5	0.69	0.22	71,72,83,86	5
4	SO4	D	503	5/5	0.71	0.18	93,93,100,108	0
4	SO4	A	407	5/5	0.71	0.12	97,99,104,111	0
5	PPV	B	506	9/9	0.73	0.13	82,89,91,93	9
4	SO4	B	503	5/5	0.78	0.13	56,58,65,67	5
4	SO4	A	404	5/5	0.81	0.17	60,60,62,65	5
4	SO4	D	504	5/5	0.81	0.20	111,119,136,139	0
2	GDD	A	401	39/39	0.83	0.15	59,75,90,93	39
4	SO4	B	505	5/5	0.84	0.14	60,61,63,66	5
4	SO4	A	405	5/5	0.86	0.16	55,57,58,61	5
4	SO4	C	404	5/5	0.88	0.13	59,60,71,74	5
4	SO4	A	406	5/5	0.89	0.12	75,75,76,80	5
4	SO4	D	501	5/5	0.91	0.12	56,59,71,72	0
4	SO4	B	504	5/5	0.92	0.08	49,56,60,62	5
4	SO4	D	502	5/5	0.92	0.13	49,49,54,56	5
4	SO4	A	408	5/5	0.92	0.10	52,52,59,62	5
4	SO4	A	403	5/5	0.93	0.14	56,57,66,73	0
4	SO4	C	402	5/5	0.94	0.12	56,57,66,71	0
4	SO4	C	403	5/5	0.94	0.09	49,55,60,62	5
4	SO4	B	502	5/5	0.96	0.09	32,33,36,39	5
4	SO4	B	501	5/5	0.97	0.06	33,34,37,41	0

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

orientation to approximate a three-dimensional view.

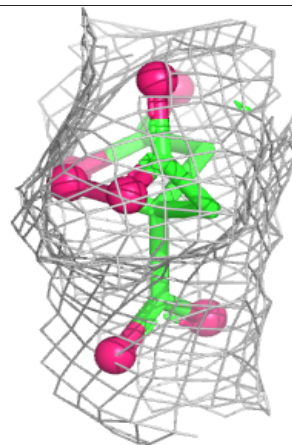
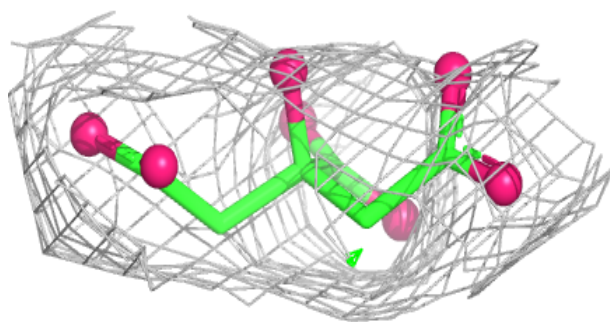
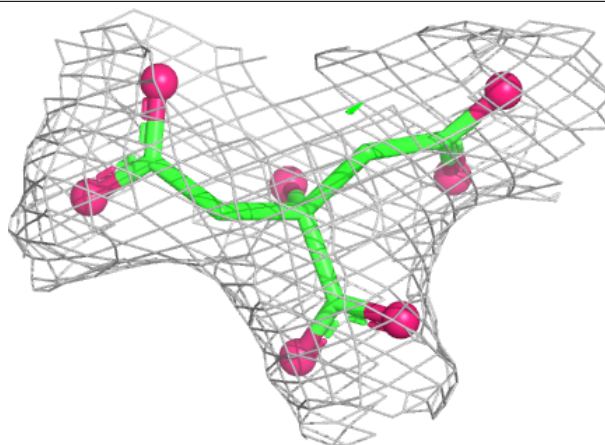
Electron density around FLC C 401:

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



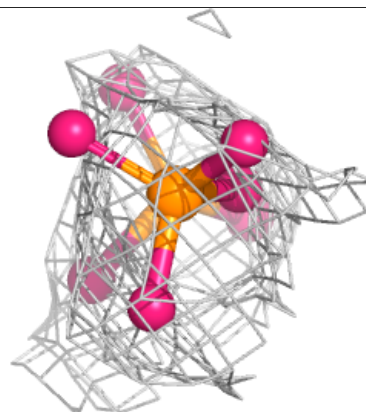
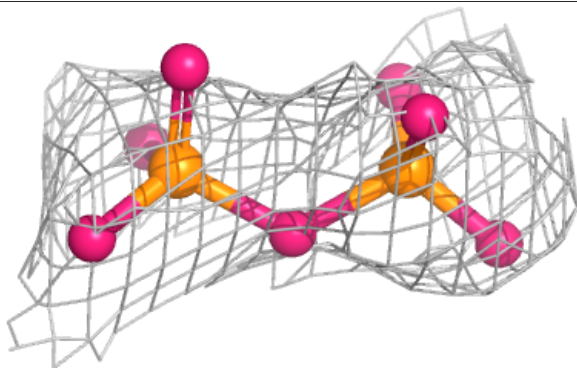
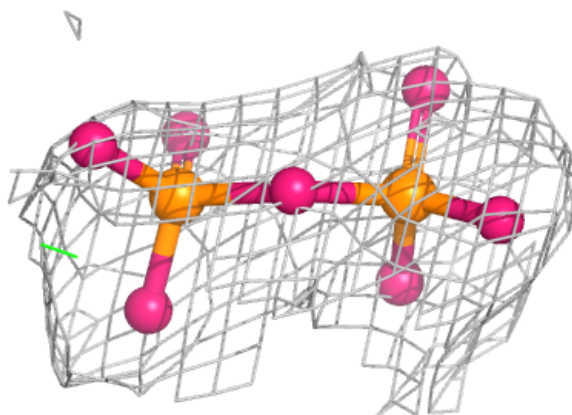
Electron density around FLC A 402:

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



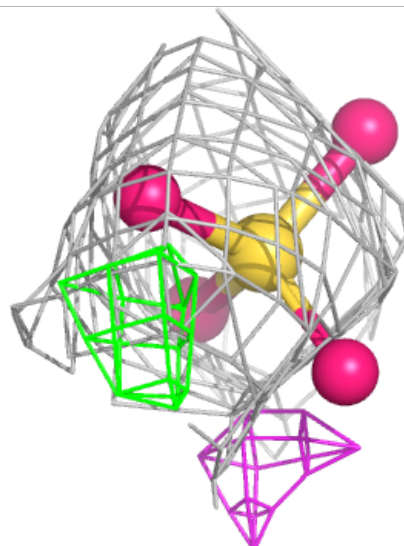
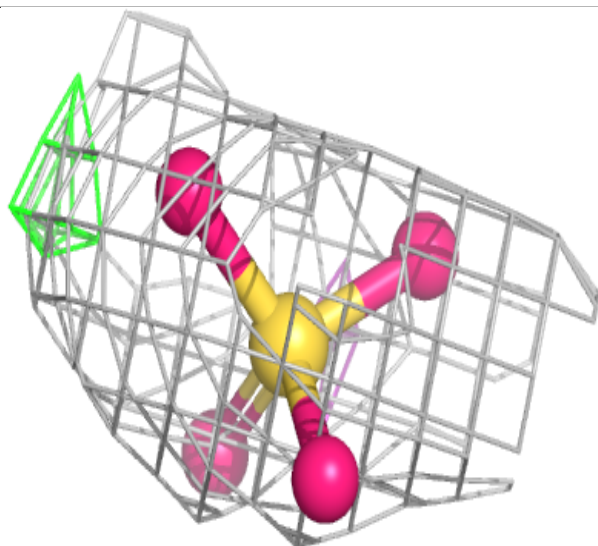
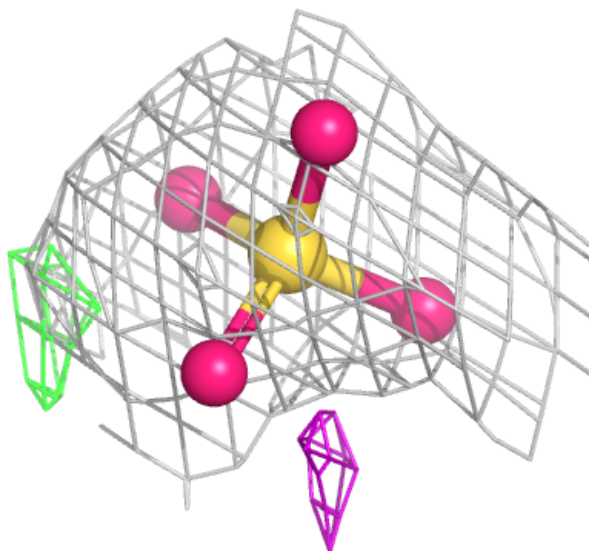
Electron density around PPV D 505:

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



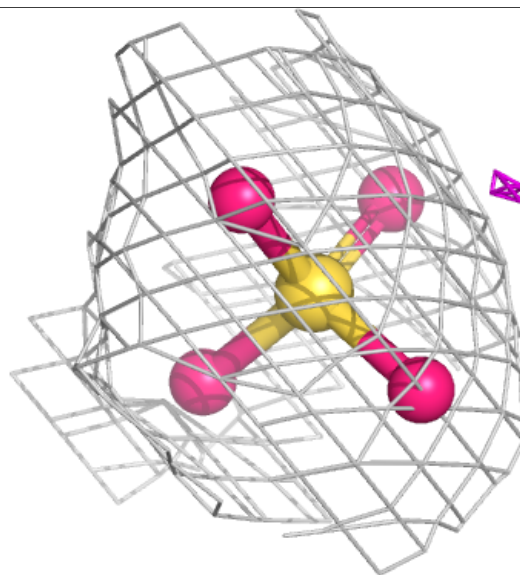
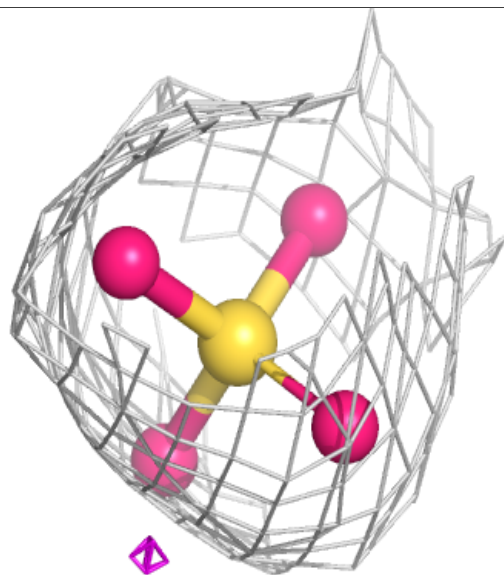
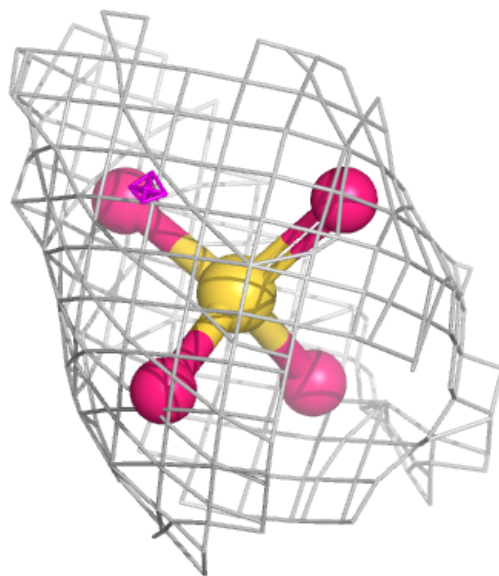
Electron density around SO4 C 405:

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



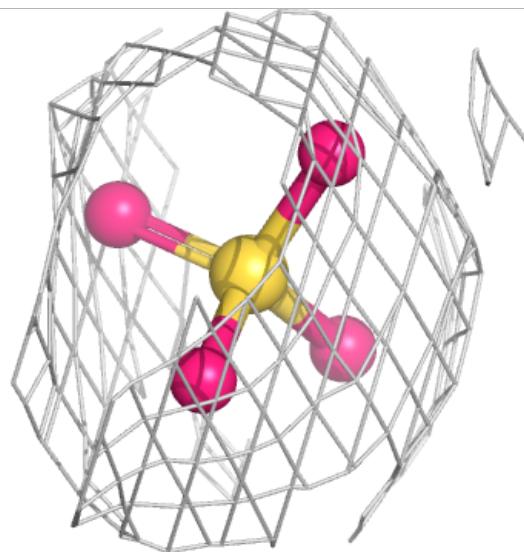
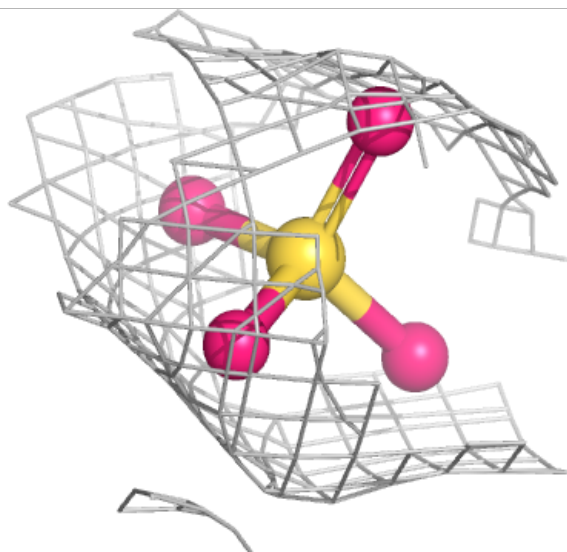
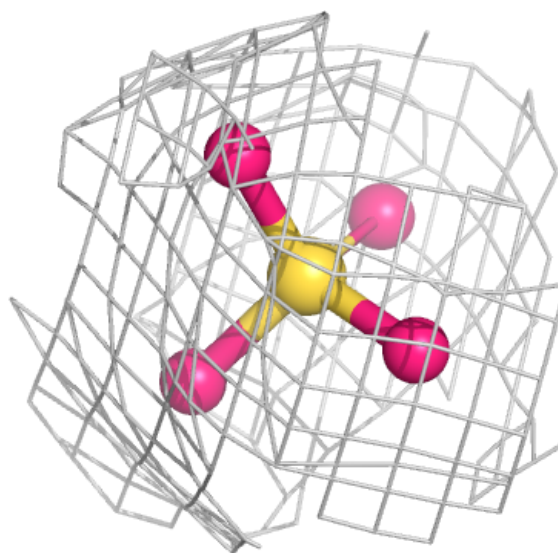
Electron density around SO4 D 503:

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



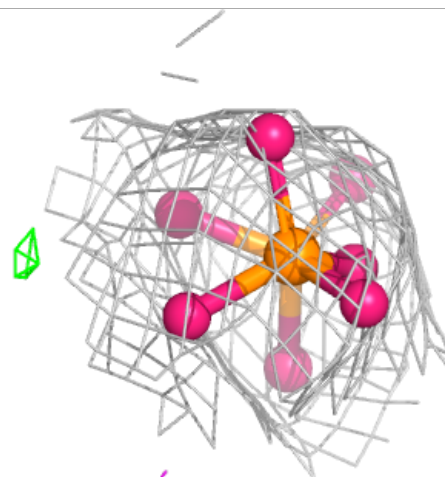
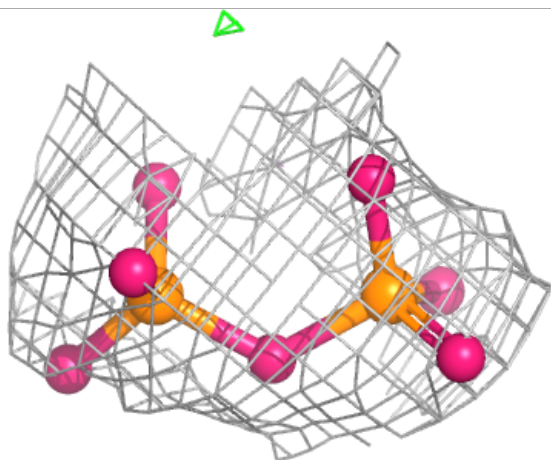
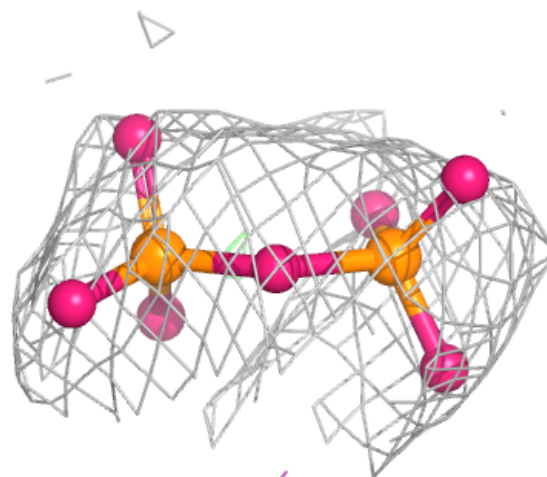
Electron density around SO4 A 407:

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



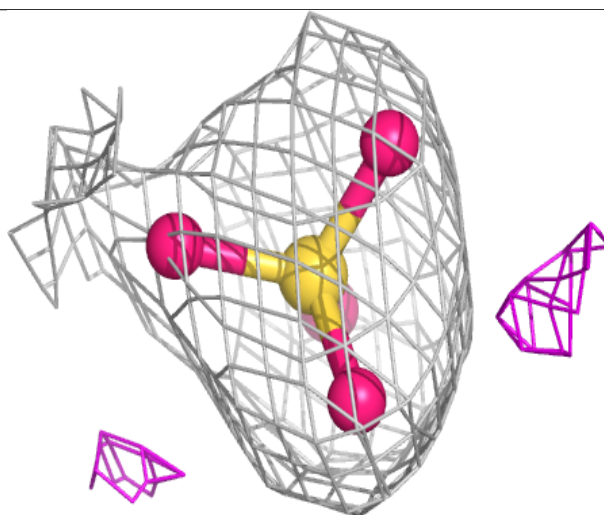
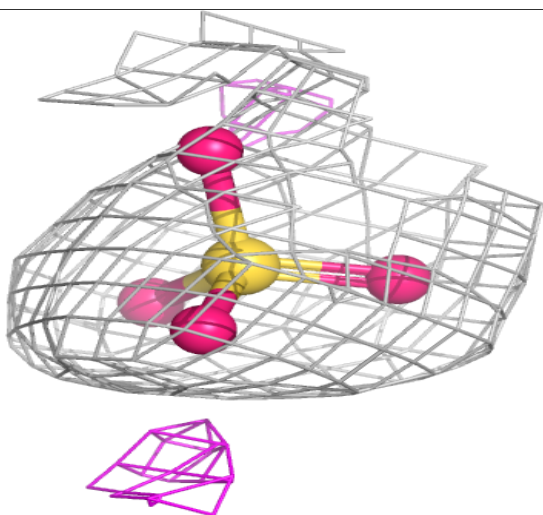
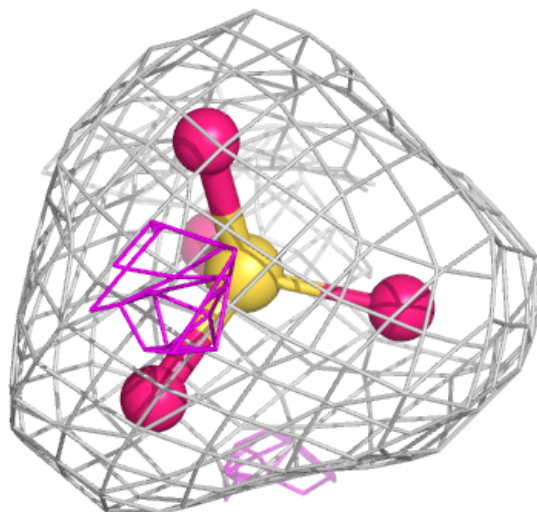
Electron density around PPV B 506:

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



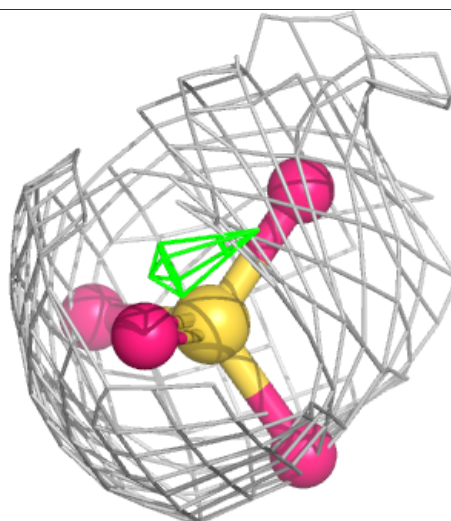
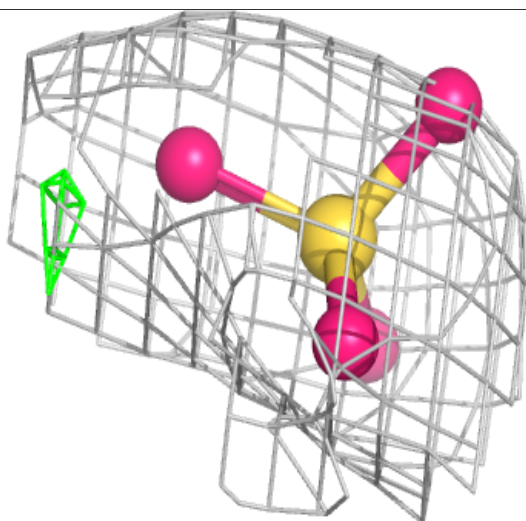
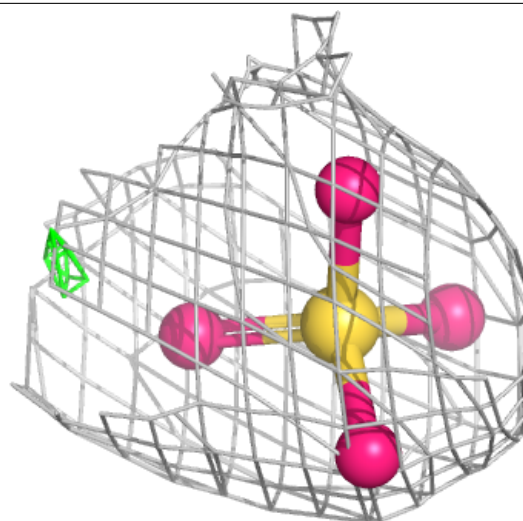
Electron density around SO4 B 503:

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



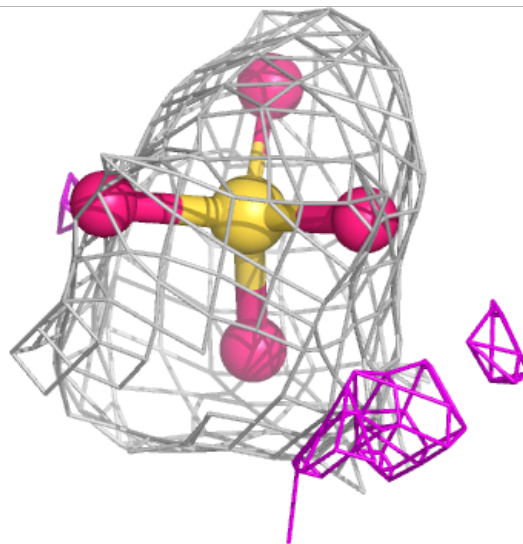
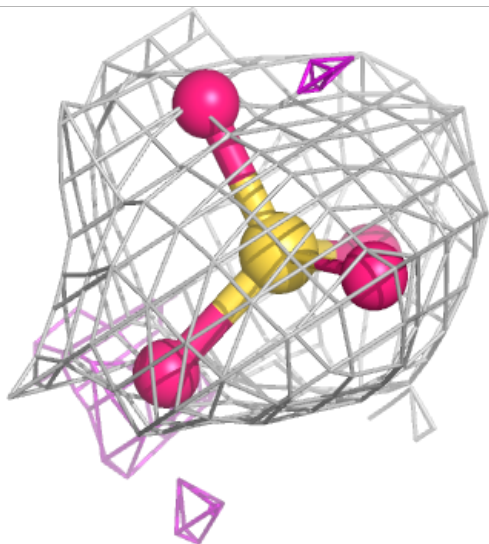
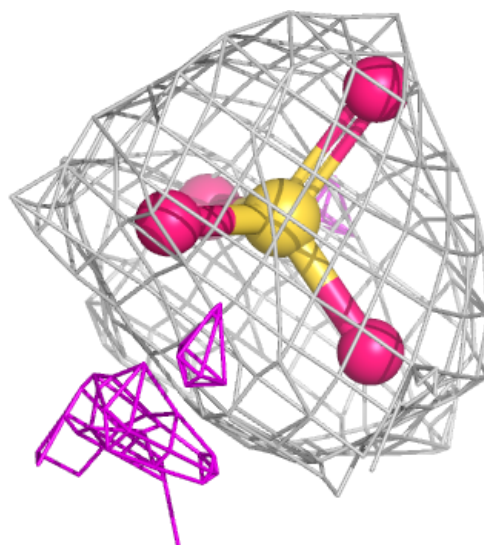
Electron density around SO4 A 404:

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



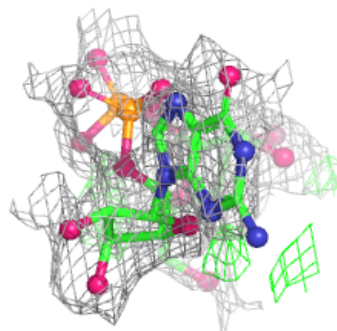
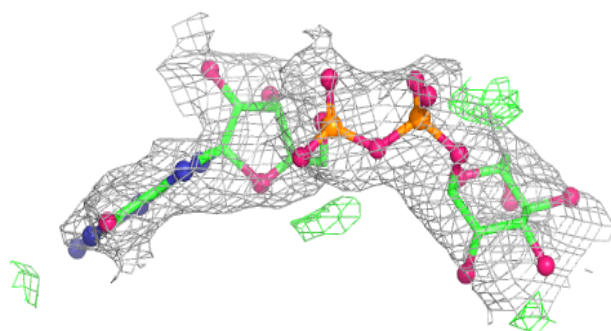
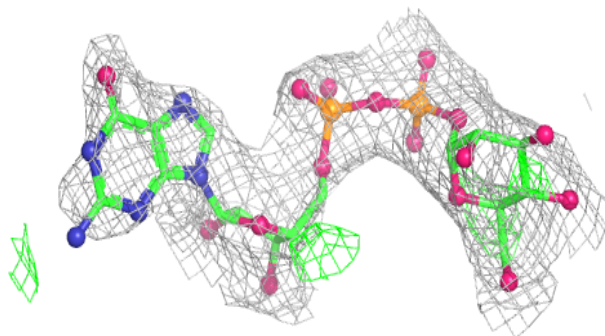
Electron density around SO4 D 504:

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

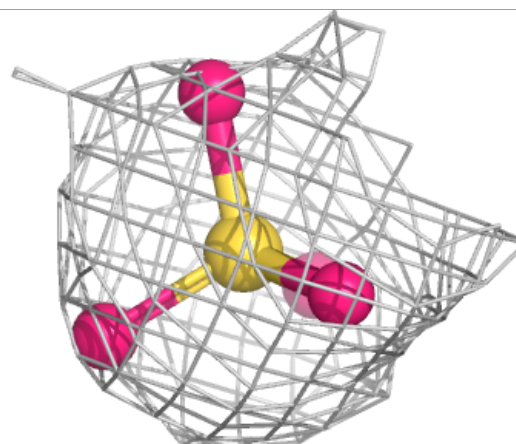
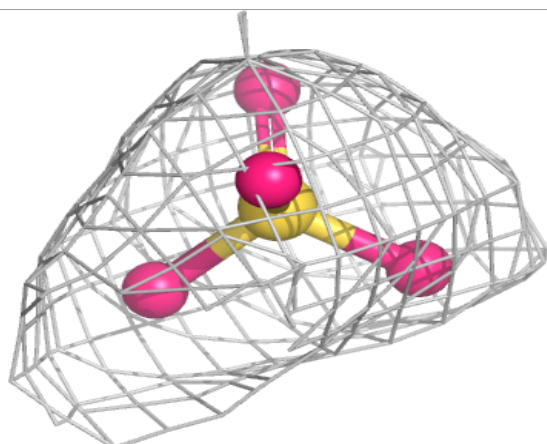
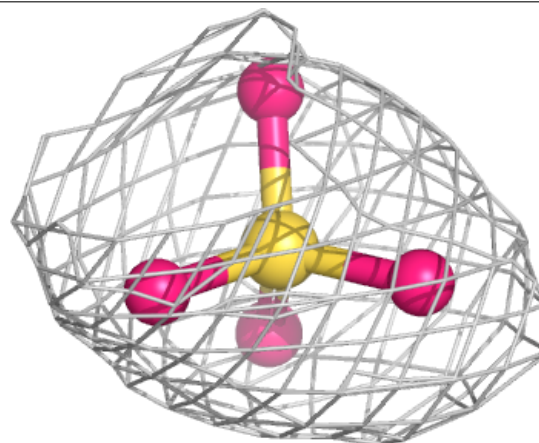


Electron density around GDD A 401:

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

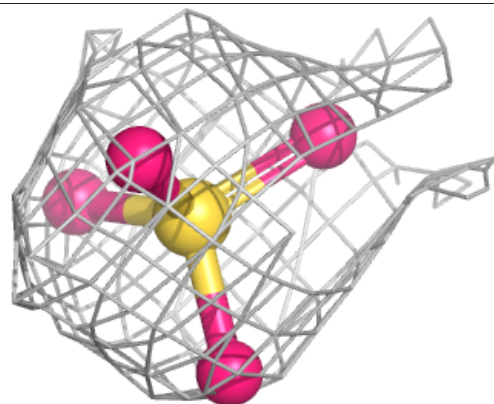
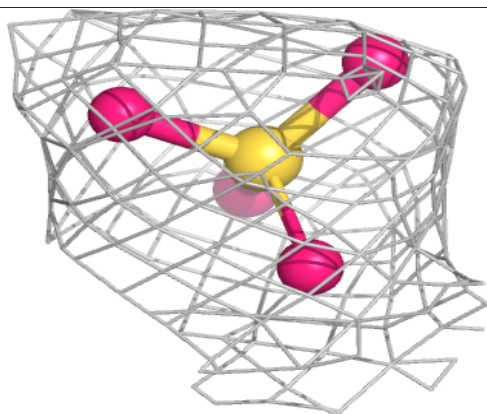
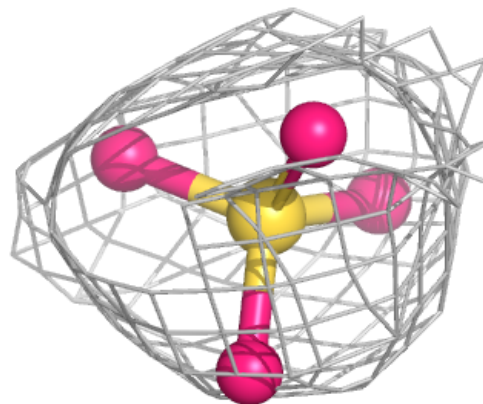
**Electron density around SO4 B 505:**

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



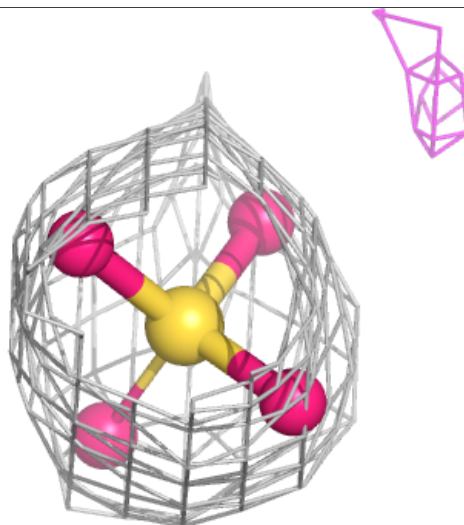
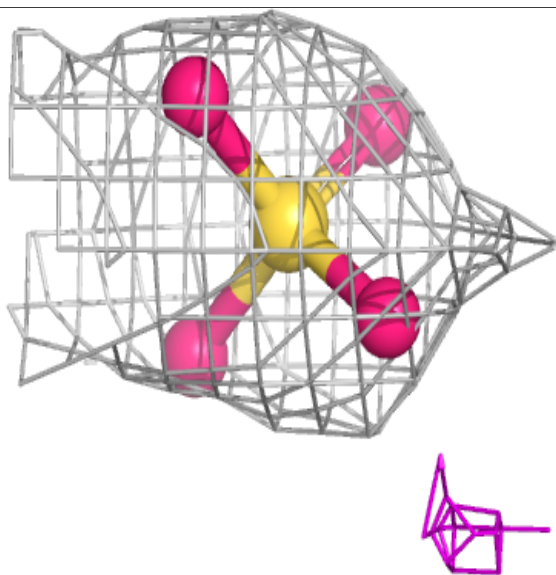
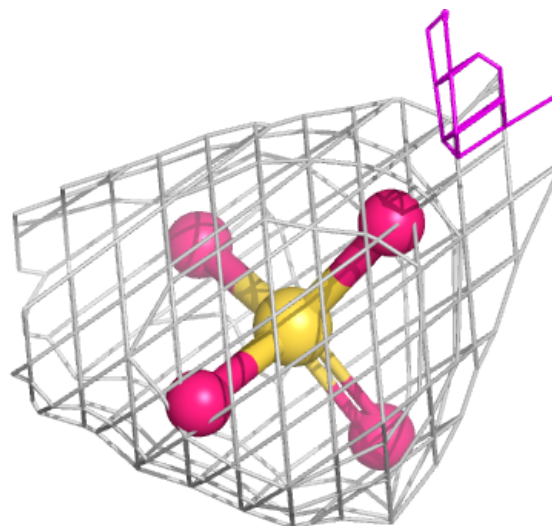
Electron density around SO4 A 405:

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



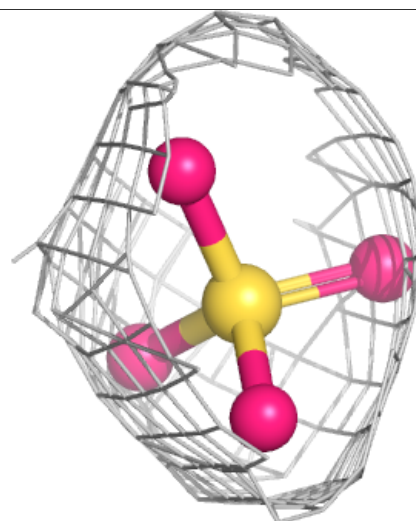
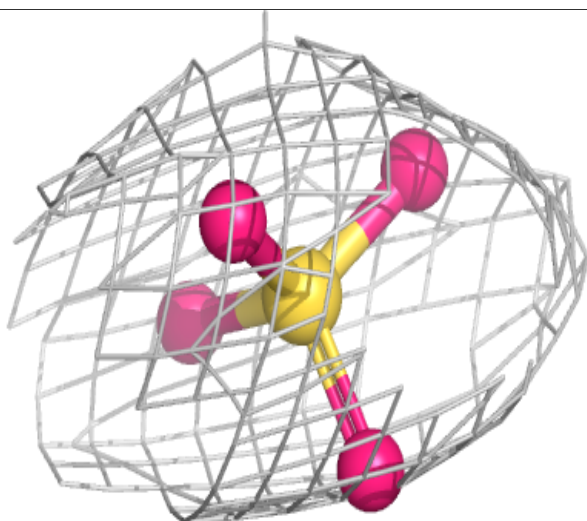
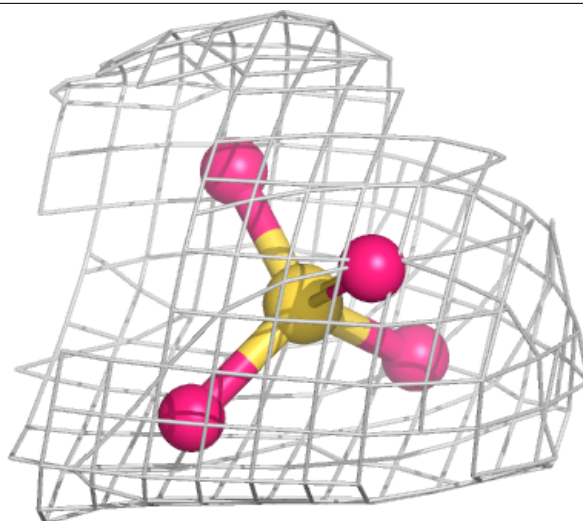
Electron density around SO4 C 404:

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



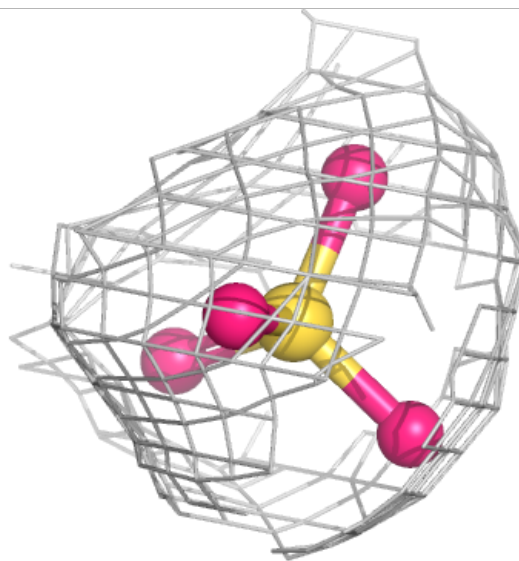
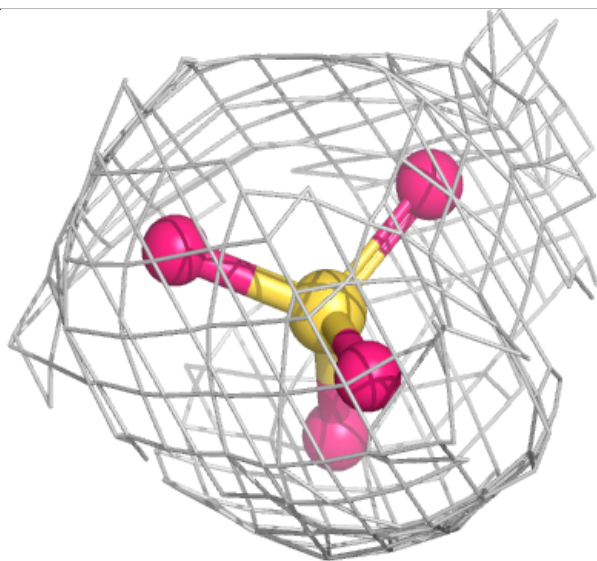
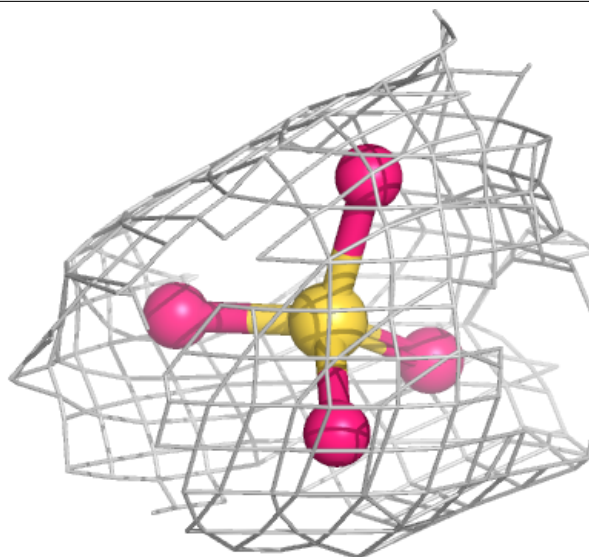
Electron density around SO4 A 406:

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



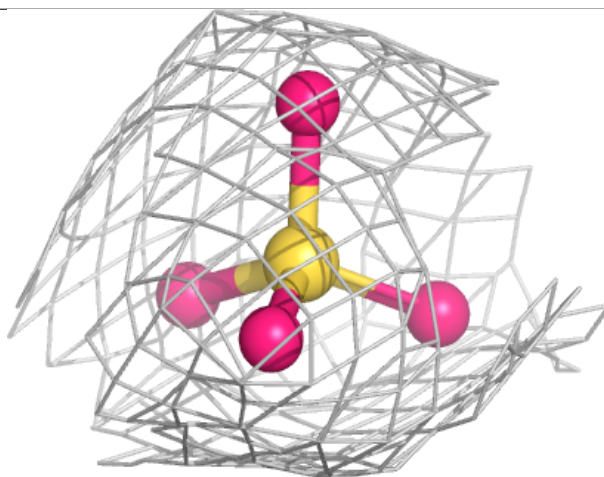
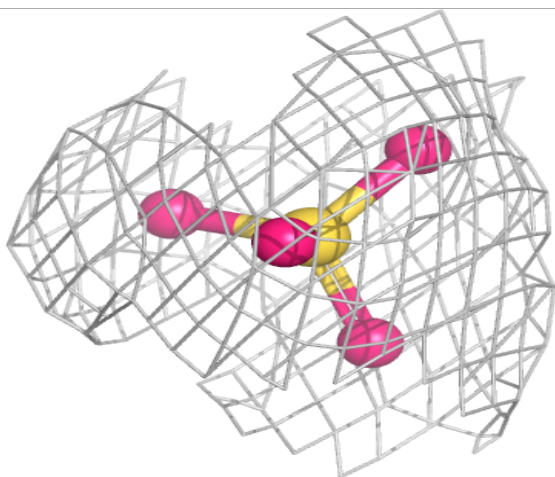
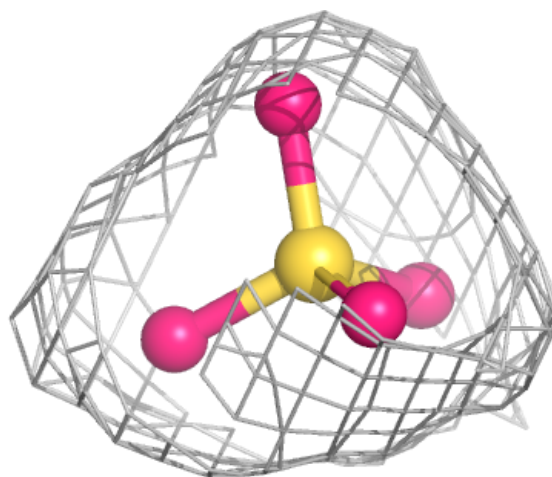
Electron density around SO4 D 501:

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



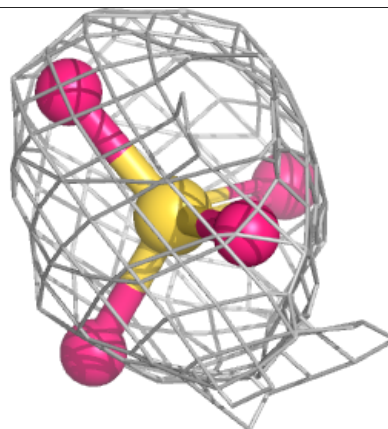
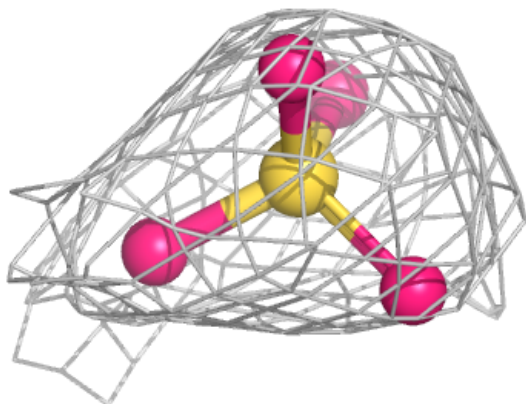
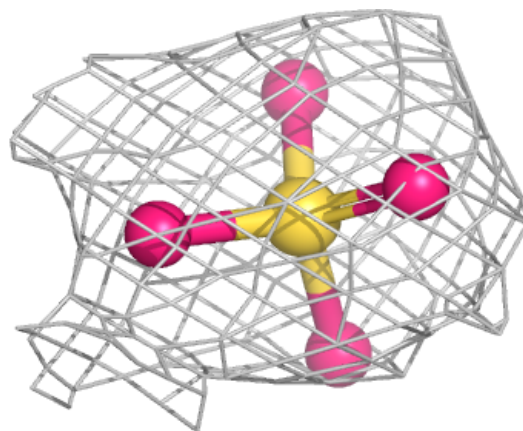
Electron density around SO4 B 504:

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



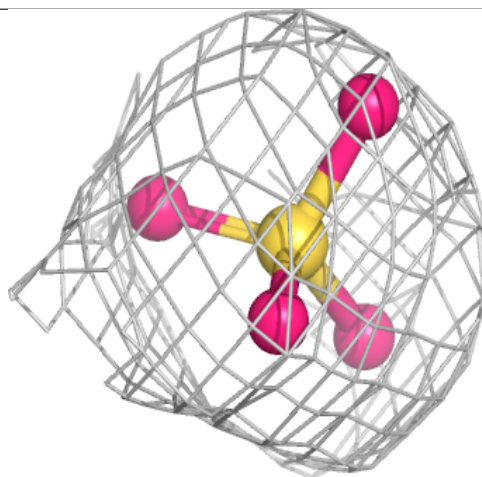
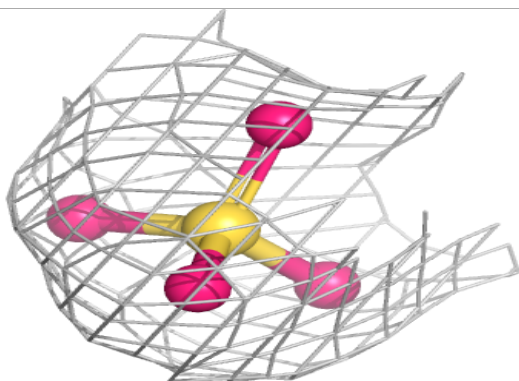
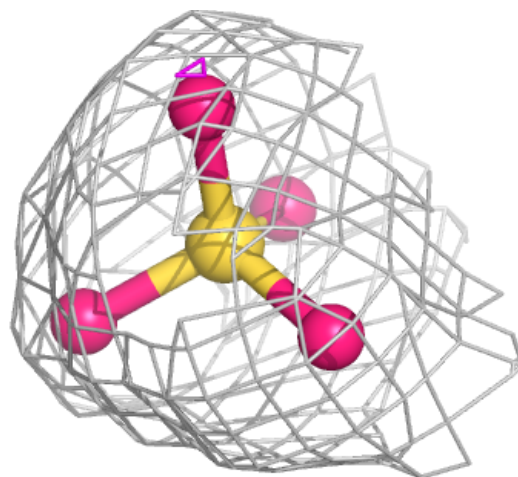
Electron density around SO4 D 502:

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



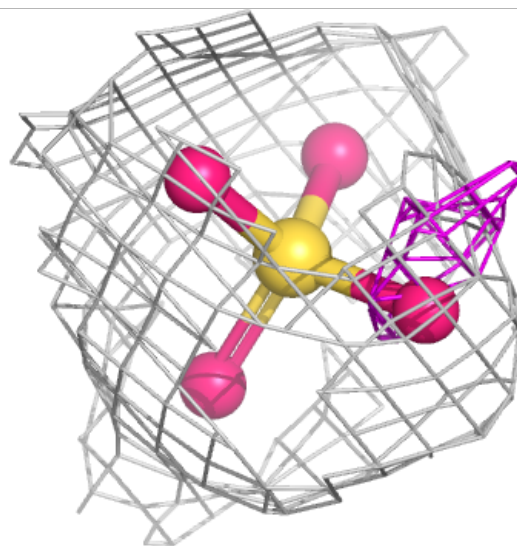
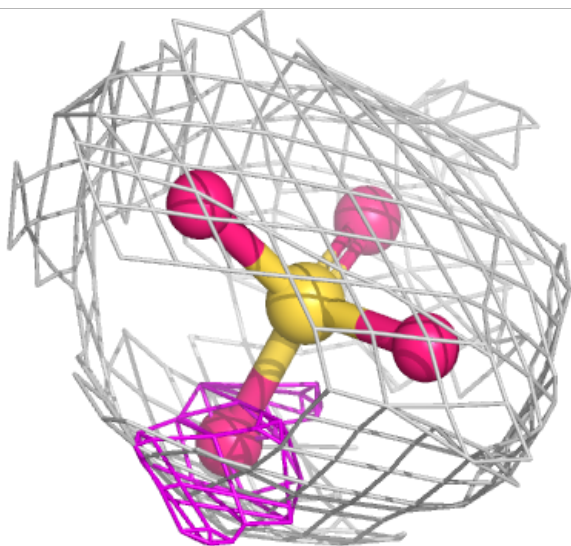
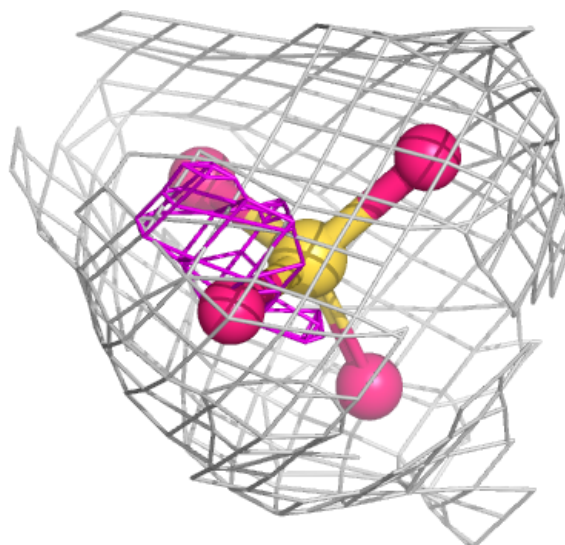
Electron density around SO4 A 408:

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



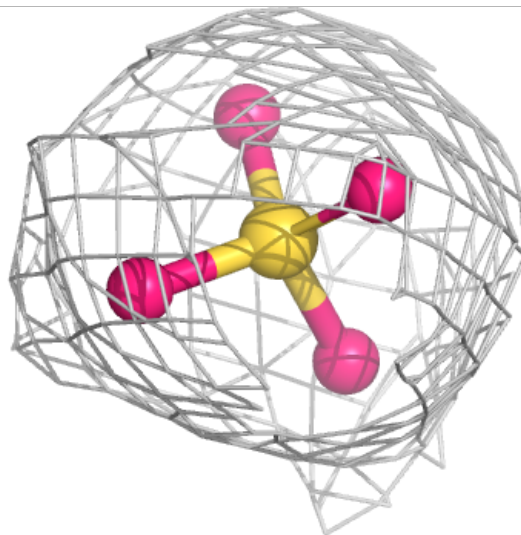
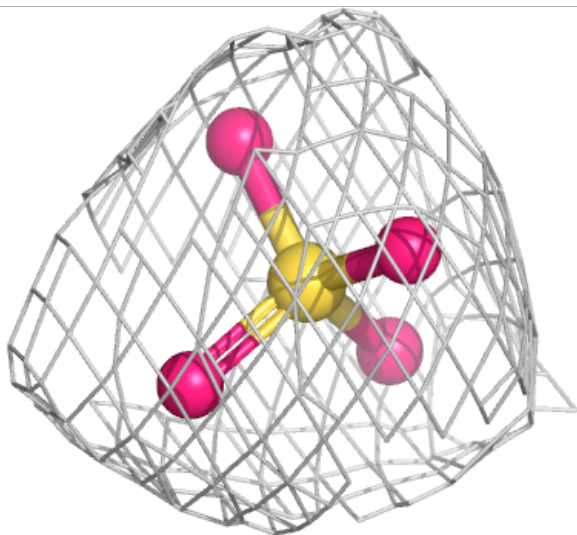
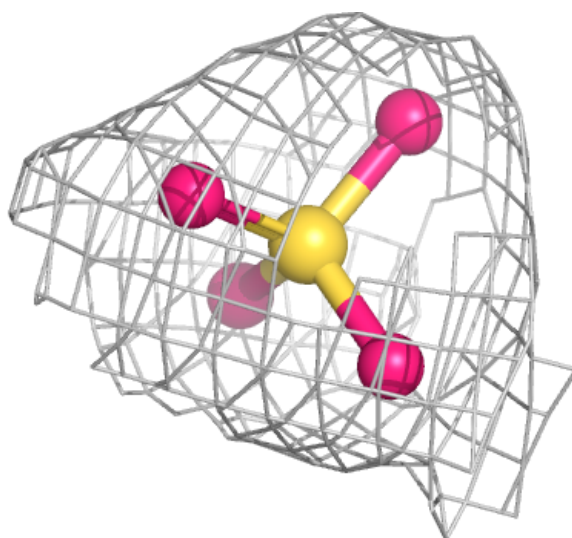
Electron density around SO4 A 403:

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



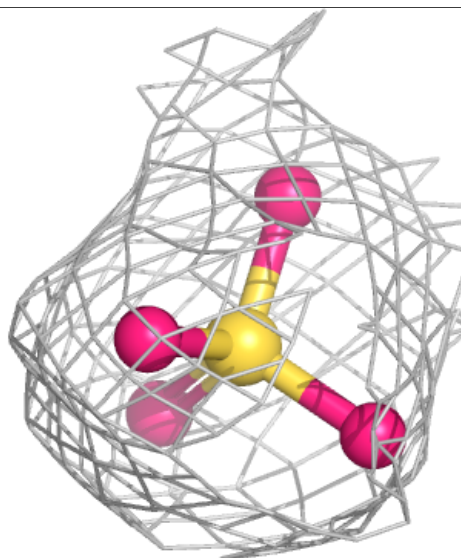
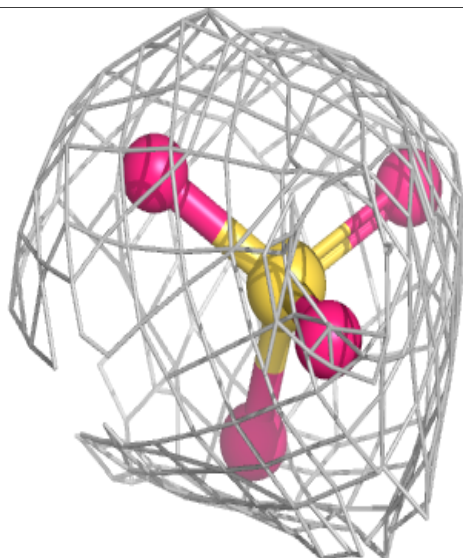
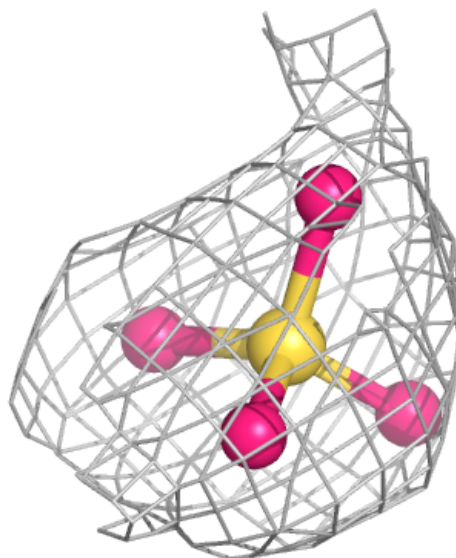
Electron density around SO4 C 402:

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



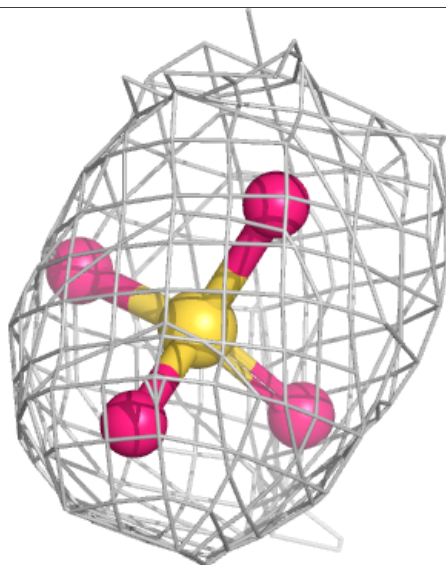
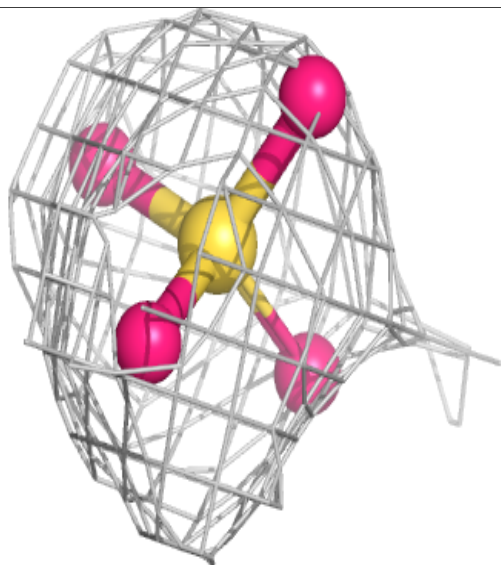
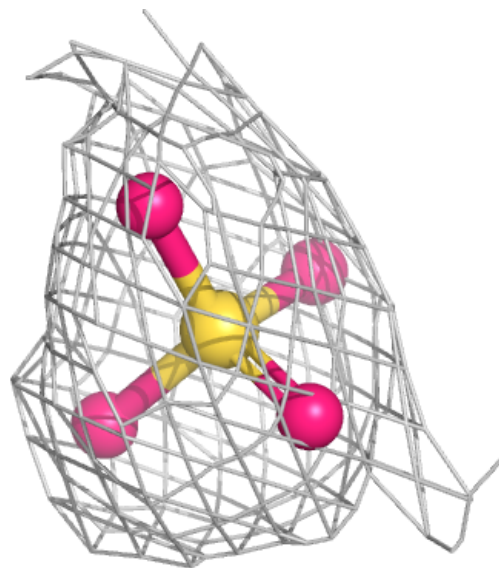
Electron density around SO4 C 403:

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



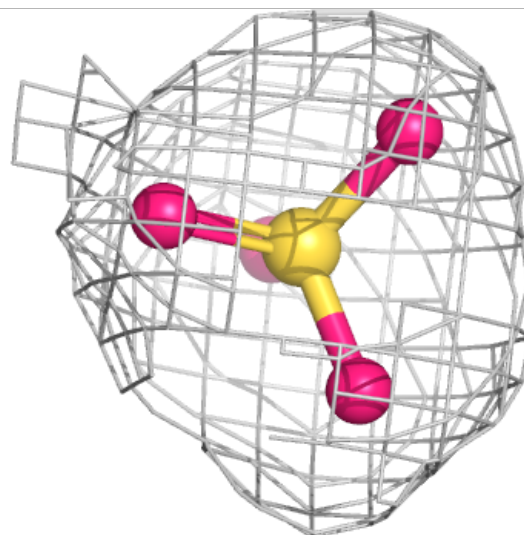
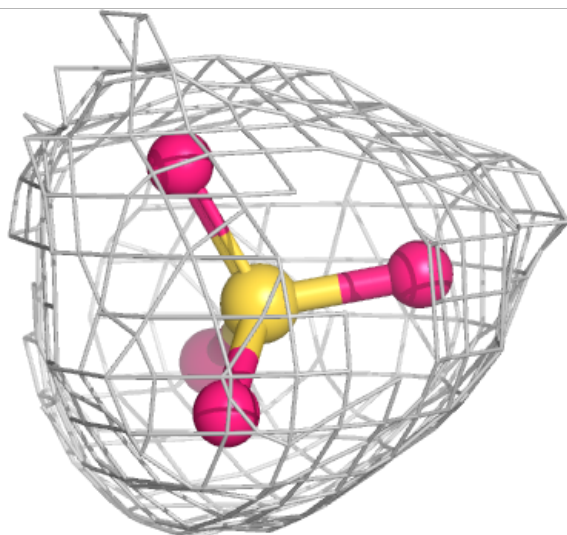
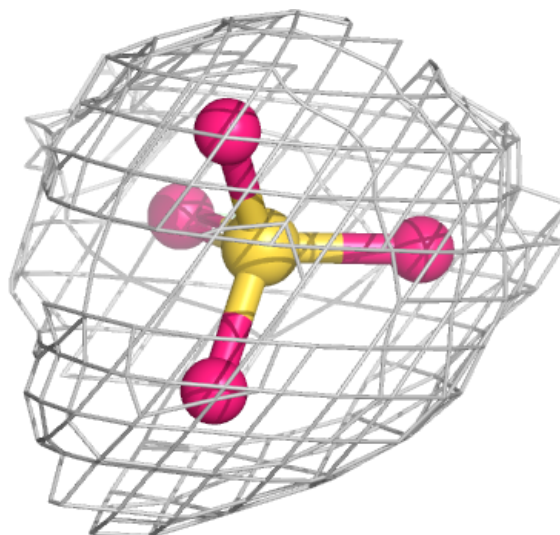
Electron density around SO4 B 502:

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



Electron density around SO4 B 501:

$2mF_o-DF_c$ (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.