



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:32 PM UTC

PDB ID : 8FG8 / pdb_00008fg8
Title : Catalytic domain of GtfB in complex with inhibitor 2-[(2,4,5-Trihydroxyphenyl)methylidene]-1-benzofuran-3-one
Authors : Schormann, N.; Deivanayagam, C.; Velu, S.
Deposited on : 2022-12-12
Resolution : 2.35 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

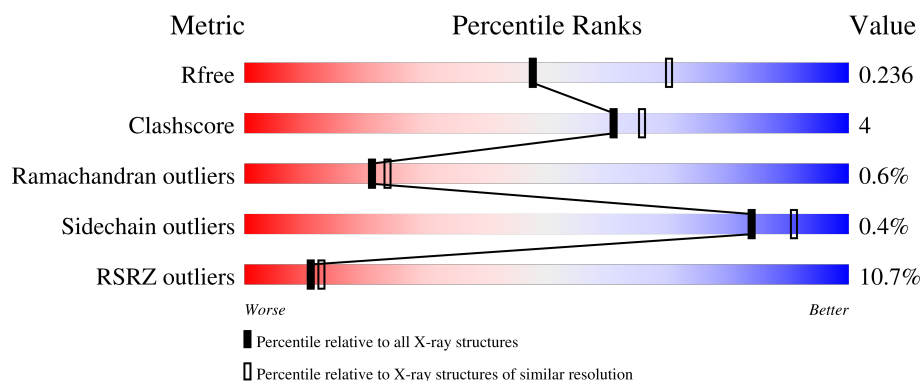
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	869	
1	B	869	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	BTB	A	1203	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 13759 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 Glucosyltransferase-I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	835	Total	C	N	O	S	0	0	0
			6595	4154	1132	1293	16			
1	B	824	Total	C	N	O	S	0	1	0
			6470	4074	1110	1270	16			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1052	LEU	-	expression tag	UNP P08987
A	1053	GLU	-	expression tag	UNP P08987
A	1054	HIS	-	expression tag	UNP P08987
A	1055	HIS	-	expression tag	UNP P08987
A	1056	HIS	-	expression tag	UNP P08987
A	1057	HIS	-	expression tag	UNP P08987
A	1058	HIS	-	expression tag	UNP P08987
A	1059	HIS	-	expression tag	UNP P08987
B	1052	LEU	-	expression tag	UNP P08987
B	1053	GLU	-	expression tag	UNP P08987
B	1054	HIS	-	expression tag	UNP P08987
B	1055	HIS	-	expression tag	UNP P08987
B	1056	HIS	-	expression tag	UNP P08987
B	1057	HIS	-	expression tag	UNP P08987
B	1058	HIS	-	expression tag	UNP P08987
B	1059	HIS	-	expression tag	UNP P08987

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

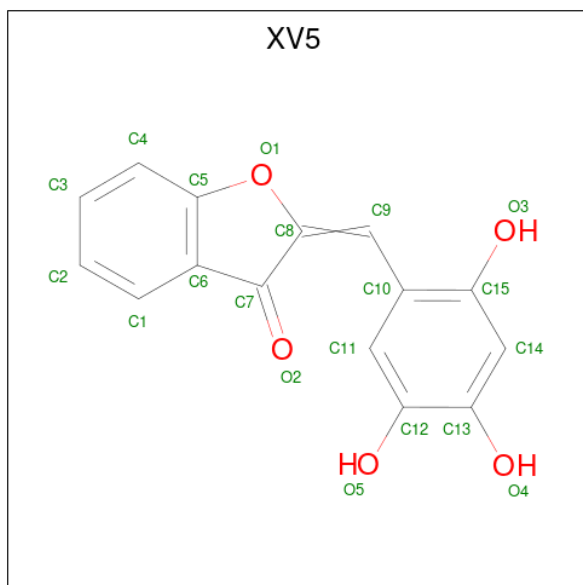
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Ca	0	0
			2	2		

- Molecule 3 is (2Z)-2-[(2,4,5-trihydroxyphenyl)methylidene]-1-benzofuran-3(2H)-one (CCD ID: XV5) (formula: C₁₅H₁₀O₅) (labeled as "Ligand of Interest" by depositor).



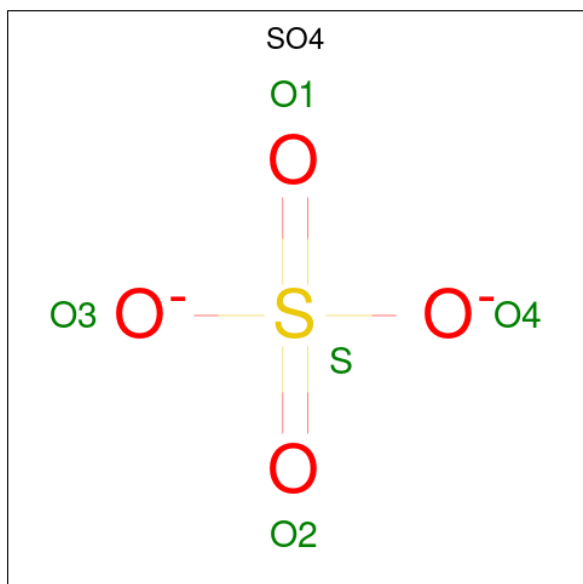
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			20	15	5		
3	B	1	Total	C	O	0	0
			20	15	5		

- Molecule 4 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: BTB) (formula: C₈H₁₉NO₅) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S) (labeled as "Ligand of Interest" by depositor).



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

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

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

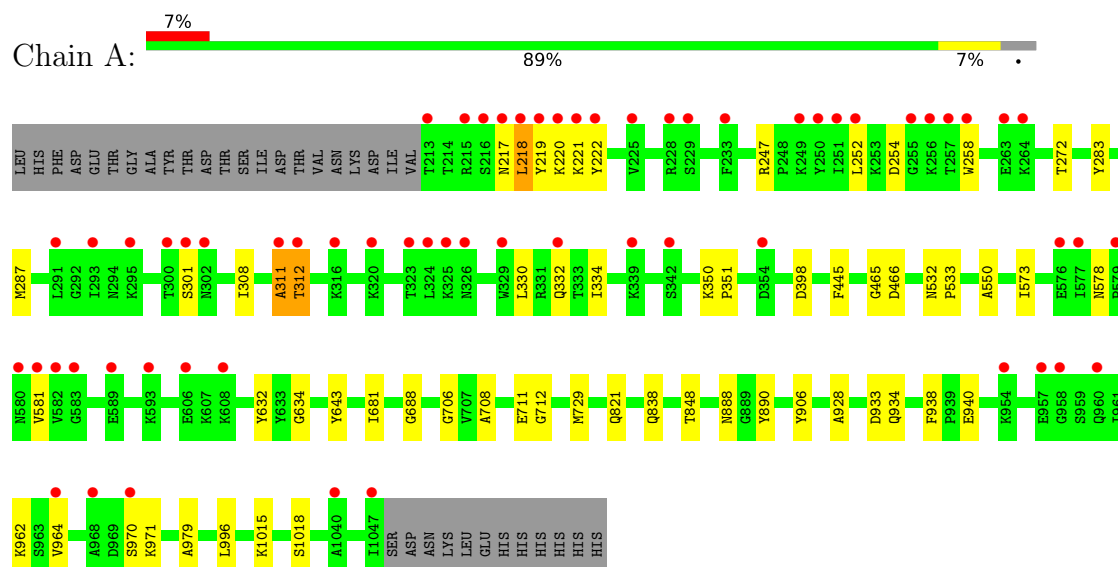
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	245	Total	O	0	0
			245	245		
6	B	258	Total	O	0	0
			258	258		

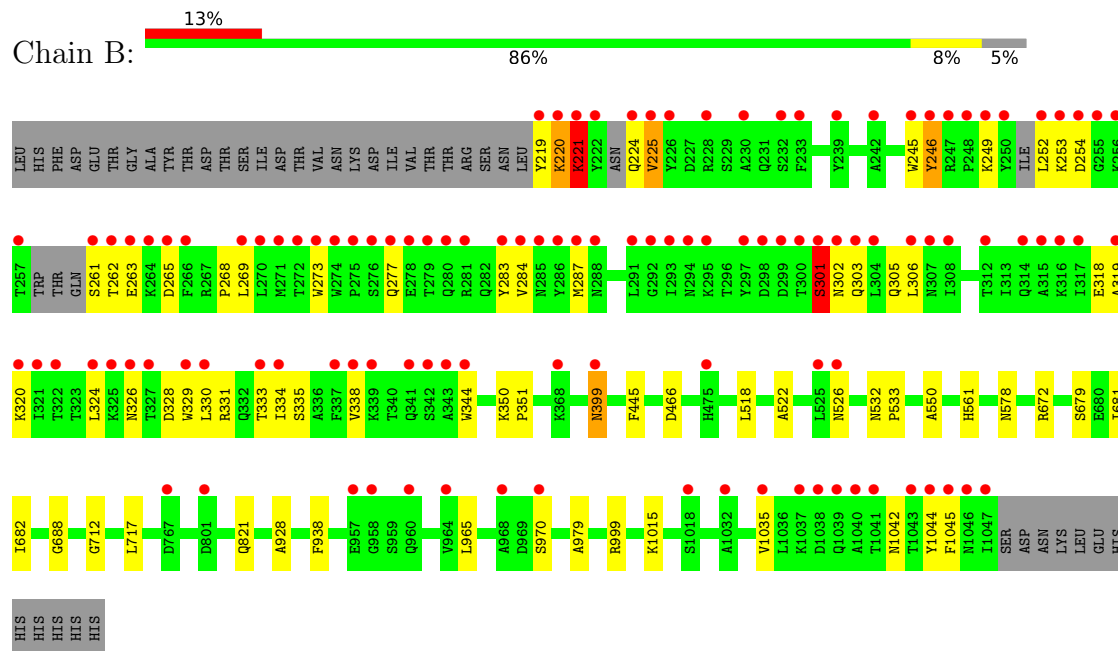
3 Residue-property plots

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

• Molecule 1: Glucosyltransferase-I



• Molecule 1: Glucosyltransferase-I



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 2 2	Depositor
Cell constants a, b, c, α , β , γ	150.46Å 150.46Å 304.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	73.04 – 2.35 73.04 – 2.35	Depositor EDS
% Data completeness (in resolution range)	96.1 (73.04-2.35) 96.1 (73.04-2.35)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.8.0257, PHENIX 1.16_3549	Depositor
R, R_{free}	0.205 , 0.233 0.208 , 0.236	Depositor DCC
R_{free} test set	6850 reflections (4.70%)	wwPDB-VP
Wilson B-factor (Å ²)	48.0	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 35.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13759	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.35% 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, CA, BTB, XV5

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	1.01	0/6734	1.34	8/9138 (0.1%)
1	B	1.00	0/6603	1.34	3/8958 (0.0%)
All	All	1.00	0/13337	1.34	11/18096 (0.1%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	221	LYS	N-CA-C	-7.71	105.83	114.62
1	A	398	ASP	CA-C-N	6.41	129.74	120.38
1	A	398	ASP	C-N-CA	6.41	129.74	120.38
1	A	688	GLY	CA-C-O	-6.16	118.22	122.22
1	A	311	ALA	N-CA-C	-5.48	103.25	110.43
1	B	688	GLY	CA-C-O	-5.27	118.79	122.22
1	A	712	GLY	CA-C-O	-5.24	117.01	121.57
1	B	712	GLY	CA-C-O	-5.24	117.01	121.57
1	A	711	GLU	CA-C-N	5.07	125.52	121.61
1	A	711	GLU	C-N-CA	5.07	125.52	121.61
1	A	706	GLY	CA-C-O	-5.04	118.54	122.52

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6595	0	6422	43	0
1	B	6470	0	6261	57	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
3	A	20	0	0	2	0
3	B	20	0	0	1	0
4	A	14	0	19	7	0
4	B	14	0	19	4	0
5	A	50	0	0	0	0
5	B	70	0	0	0	0
6	A	245	0	0	3	0
6	B	258	0	0	3	0
All	All	13759	0	12721	108	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 4.

All (108) 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:B:335:SER:O	1:B:338:VAL:HG12	1.84	0.76
1:B:284:VAL:HG21	1:B:306:LEU:HD22	1.69	0.74
1:A:838:GLN:HE22	1:A:848:THR:HG21	1.52	0.74
1:B:338:VAL:HG23	1:B:344:TRP:CE3	2.25	0.71
1:A:573:ILE:CG2	1:A:581:VAL:HG21	2.24	0.67
4:B:1203:BTB:O3	4:B:1203:BTB:O8	2.13	0.65
1:B:277:GLN:HG2	1:B:303:GLN:HG2	1.79	0.64
1:A:573:ILE:HG21	1:A:581:VAL:HG21	1.79	0.64
1:B:1042:ASN:HB3	6:B:1308:HOH:O	1.97	0.64
1:A:252:LEU:O	1:A:254:ASP:O	2.16	0.63
1:A:838:GLN:NE2	1:A:848:THR:HG21	2.13	0.63
1:B:219:TYR:O	1:B:221:LYS:N	2.27	0.60
1:B:320:LYS:HE3	1:B:324:LEU:HD11	1.82	0.60
1:B:329:TRP:O	1:B:333:THR:HG23	2.03	0.59
1:A:217:ASN:O	1:A:218:LEU:HB2	2.02	0.58
1:A:962:LYS:H	1:A:964:VAL:CG2	2.15	0.58
1:B:330:LEU:O	1:B:330:LEU:HD13	2.03	0.58
1:A:962:LYS:C	1:A:964:VAL:HG23	2.31	0.56
1:A:962:LYS:O	1:A:964:VAL:HG23	2.06	0.55
1:B:254:ASP:CG	1:B:319:ALA:HA	2.32	0.55
1:A:962:LYS:H	1:A:964:VAL:HG23	1.71	0.55
1:B:254:ASP:OD1	1:B:319:ALA:N	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:561:HIS:NE2	4:B:1203:BTB:H81	2.23	0.54
1:A:643:TYR:HB2	1:A:848:THR:HG22	1.90	0.54
1:A:332:GLN:NE2	1:B:329:TRP:HB2	2.22	0.54
4:B:1203:BTB:O1	4:B:1203:BTB:H62	2.08	0.54
1:B:965:LEU:HB2	1:B:1035:VAL:HG11	1.91	0.53
3:A:1202:XV5:C2	6:A:1536:HOH:O	2.57	0.53
1:A:218:LEU:CD2	1:A:272:THR:HB	2.38	0.53
3:A:1202:XV5:C2	6:A:1463:HOH:O	2.57	0.53
1:A:283:TYR:CE1	1:A:287:MET:HG3	2.44	0.52
1:B:330:LEU:O	1:B:334:ILE:HG22	2.10	0.52
1:B:326:ASN:ND2	1:B:328:ASP:HB2	2.25	0.52
1:B:254:ASP:OD1	1:B:318:GLU:C	2.53	0.51
1:A:578:ASN:O	1:A:581:VAL:HG23	2.11	0.51
1:B:1035:VAL:HG13	1:B:1044:TYR:CE2	2.45	0.51
1:B:329:TRP:CZ3	1:B:330:LEU:HD23	2.46	0.51
1:A:308:ILE:O	1:A:311:ALA:O	2.29	0.50
1:B:326:ASN:HD22	1:B:328:ASP:HB2	1.77	0.50
1:B:979:ALA:O	1:B:1015:LYS:HD2	2.11	0.50
1:A:330:LEU:O	1:A:334:ILE:HG12	2.12	0.50
1:A:218:LEU:HG	1:A:219:TYR:N	2.26	0.50
1:B:399:ASN:ND2	6:B:1306:HOH:O	2.44	0.50
1:B:254:ASP:OD1	1:B:319:ALA:HA	2.12	0.49
1:B:252:LEU:HD23	1:B:252:LEU:O	2.12	0.49
1:B:221:LYS:O	1:B:249:LYS:HE3	2.12	0.49
1:A:332:GLN:HE22	1:B:329:TRP:HB2	1.78	0.49
4:A:1203:BTB:O3	4:A:1203:BTB:C7	2.61	0.49
1:A:848:THR:OG1	1:A:906:TYR:HB3	2.13	0.49
1:B:224:GLN:O	1:B:225:VAL:HG22	2.12	0.49
1:A:222:TYR:HB3	1:A:258:TRP:CZ3	2.48	0.48
1:B:283:TYR:CE1	1:B:287:MET:HG3	2.48	0.48
1:A:979:ALA:O	1:A:1015:LYS:HD2	2.14	0.48
1:A:933:ASP:HB3	1:A:934:GLN:OE1	2.14	0.48
1:B:320:LYS:NZ	1:B:324:LEU:HD21	2.29	0.47
1:B:261:SER:C	1:B:263:GLU:H	2.22	0.47
1:A:938:PHE:CD2	1:A:970:SER:HA	2.50	0.47
1:B:225:VAL:HA	1:B:246:TYR:HE2	1.79	0.47
1:B:329:TRP:CH2	1:B:330:LEU:HD23	2.50	0.47
1:B:532:ASN:N	1:B:533:PRO:CD	2.79	0.46
1:B:302:ASN:O	1:B:303:GLN:C	2.59	0.46
1:B:254:ASP:OD1	1:B:319:ALA:CA	2.64	0.45
1:B:938:PHE:CD2	1:B:970:SER:HA	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1203:BTB:O3	4:A:1203:BTB:H71	2.16	0.45
4:A:1203:BTB:H51	4:A:1203:BTB:O4	2.17	0.45
1:A:550:ALA:HB3	1:A:821:GLN:HB3	1.99	0.45
1:A:890:TYR:CD2	4:A:1203:BTB:H72	2.52	0.45
1:B:350:LYS:HB3	1:B:351:PRO:HA	1.99	0.45
1:B:225:VAL:HA	1:B:246:TYR:CE2	2.53	0.44
1:A:888:ASN:O	1:A:906:TYR:OH	2.31	0.44
1:B:550:ALA:HB3	1:B:821:GLN:HB3	2.00	0.44
1:A:218:LEU:HG	1:A:219:TYR:H	1.81	0.43
1:B:268:PRO:HG3	1:B:330:LEU:HD12	1.99	0.43
1:A:220:LYS:C	1:A:222:TYR:H	2.26	0.43
1:B:252:LEU:O	1:B:254:ASP:N	2.41	0.43
1:A:970:SER:O	1:A:1018:SER:HA	2.18	0.43
1:B:269:LEU:HD21	1:B:273:TRP:CE3	2.54	0.43
1:B:245:TRP:CZ2	1:B:331:ARG:HG2	2.53	0.43
1:B:320:LYS:CE	1:B:324:LEU:HD11	2.46	0.43
1:B:681:ILE:HD12	1:B:681:ILE:C	2.44	0.43
1:A:532:ASN:N	1:A:533:PRO:CD	2.82	0.42
4:A:1203:BTB:O4	4:A:1203:BTB:C5	2.68	0.42
1:B:578:ASN:OD1	1:B:578:ASN:C	2.62	0.42
1:B:261:SER:N	1:B:265:ASP:CB	2.83	0.42
1:B:526:ASN:C	6:B:1319:HOH:O	2.62	0.42
1:B:466:ASP:OD2	1:B:999:ARG:HD2	2.20	0.42
1:A:445:PHE:CG	1:A:928:ALA:HB2	2.54	0.42
1:A:311:ALA:O	1:A:312:THR:CB	2.68	0.42
1:B:221:LYS:HZ3	1:B:221:LYS:HG3	1.77	0.41
1:B:301:SER:HB3	1:B:302:ASN:H	1.75	0.41
1:A:465:GLY:HA3	6:A:1348:HOH:O	2.20	0.41
1:B:672:ARG:O	1:B:682:ILE:HA	2.21	0.41
4:A:1203:BTB:H81	4:A:1203:BTB:H52	1.92	0.41
3:B:1202:XV5:O1	3:B:1202:XV5:O3	2.38	0.41
1:A:220:LYS:HG2	1:A:221:LYS:H	1.86	0.41
1:A:466:ASP:HB3	1:A:996:LEU:CD2	2.51	0.41
1:A:632:TYR:CE2	1:A:634:GLY:HA3	2.56	0.41
1:A:708:ALA:HB2	1:A:729:MET:HE1	2.02	0.41
1:A:350:LYS:HB3	1:A:351:PRO:HA	2.03	0.41
1:A:681:ILE:HD12	1:A:681:ILE:C	2.46	0.40
1:A:890:TYR:CD1	4:A:1203:BTB:H12	2.56	0.40
1:A:578:ASN:OD1	1:A:578:ASN:C	2.64	0.40
1:A:940:GLU:HB2	1:A:971:LYS:HB2	2.03	0.40
1:B:561:HIS:NE2	4:B:1203:BTB:C8	2.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:445:PHE:CG	1:B:928:ALA:HB2	2.56	0.40
1:B:518:LEU:HD12	1:B:522:ALA:HB3	2.04	0.40
1:B:338:VAL:CG2	1:B:344:TRP:CE3	3.00	0.40
1:B:679:SER:HB3	1:B:717:LEU:HD13	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	833/869 (96%)	799 (96%)	31 (4%)	3 (0%)	30	34
1	B	817/869 (94%)	784 (96%)	26 (3%)	7 (1%)	14	14
All	All	1650/1738 (95%)	1583 (96%)	57 (4%)	10 (1%)	21	24

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	218	LEU
1	B	301	SER
1	B	305	GLN
1	A	301	SER
1	B	220	LYS
1	B	262	THR
1	B	1045	PHE
1	B	225	VAL
1	B	253	LYS
1	A	312	THR

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	706/738 (96%)	705 (100%)	1 (0%)	88	94
1	B	686/738 (93%)	681 (99%)	5 (1%)	76	86
All	All	1392/1476 (94%)	1386 (100%)	6 (0%)	84	91

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	247	ARG
1	B	220	LYS
1	B	221	LYS
1	B	246	TYR
1	B	301	SER
1	B	399	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	277	GLN
1	A	326	ASN
1	A	341	GLN
1	A	386	ASN
1	A	455	ASN
1	A	527	GLN
1	A	532	ASN
1	A	537	ASN
1	A	735	ASN
1	A	756	GLN
1	A	785	GLN
1	A	977	GLN
1	B	238	HIS
1	B	386	ASN
1	B	532	ASN
1	B	537	ASN

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Mol	Chain	Res	Type
1	B	735	ASN
1	B	785	GLN
1	B	855	ASN
1	B	977	GLN

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](#)

Of 31 ligands modelled in this entry, 3 are monoatomic - leaving 28 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	$\# Z > 2$
5	SO4	A	1208	-	4,4,4	0.29	0	6,6,6	0.12	0
5	SO4	B	1204	-	4,4,4	0.29	0	6,6,6	0.24	0
5	SO4	B	1213	-	4,4,4	0.30	0	6,6,6	0.18	0
5	SO4	A	1204	-	4,4,4	0.31	0	6,6,6	0.09	0
5	SO4	B	1206	-	4,4,4	0.31	0	6,6,6	0.10	0
5	SO4	A	1211	-	4,4,4	0.31	0	6,6,6	0.05	0
5	SO4	A	1209	-	4,4,4	0.28	0	6,6,6	0.17	0
5	SO4	B	1214	-	4,4,4	0.32	0	6,6,6	0.16	0
5	SO4	B	1210	-	4,4,4	0.30	0	6,6,6	0.11	0
5	SO4	B	1205	-	4,4,4	0.31	0	6,6,6	0.11	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	SO4	B	1216	-	4,4,4	0.34	0	6,6,6	0.11	0
5	SO4	A	1212	-	4,4,4	0.27	0	6,6,6	0.15	0
5	SO4	B	1211	-	4,4,4	0.28	0	6,6,6	0.11	0
4	BTB	A	1203	-	13,13,13	1.74	1 (7%)	7,16,16	1.22	1 (14%)
5	SO4	B	1215	-	4,4,4	0.34	0	6,6,6	0.09	0
3	XV5	A	1202	-	22,22,22	0.40	0	32,32,32	0.59	0
5	SO4	B	1207	-	4,4,4	0.32	0	6,6,6	0.08	0
3	XV5	B	1202	2	22,22,22	0.41	0	32,32,32	0.61	0
5	SO4	A	1213	-	4,4,4	0.28	0	6,6,6	0.06	0
5	SO4	A	1207	-	4,4,4	0.31	0	6,6,6	0.18	0
5	SO4	B	1208	-	4,4,4	0.31	0	6,6,6	0.09	0
5	SO4	B	1209	-	4,4,4	0.24	0	6,6,6	0.14	0
5	SO4	B	1217	-	4,4,4	0.32	0	6,6,6	0.05	0
5	SO4	A	1206	-	4,4,4	0.32	0	6,6,6	0.05	0
4	BTB	B	1203	2	13,13,13	1.41	1 (7%)	7,16,16	1.06	1 (14%)
5	SO4	B	1212	-	4,4,4	0.28	0	6,6,6	0.10	0
5	SO4	A	1210	-	4,4,4	0.31	0	6,6,6	0.09	0
5	SO4	A	1205	-	4,4,4	0.31	0	6,6,6	0.09	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
4	BTB	A	1203	-	-	10/21/21/21	-
3	XV5	B	1202	2	-	4/4/16/16	0/3/3/3
4	BTB	B	1203	2	-	6/21/21/21	-
3	XV5	A	1202	-	-	4/4/16/16	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1203	BTB	C2-N	6.16	1.60	1.48
4	B	1203	BTB	C2-N	4.96	1.58	1.48

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1203	BTB	O4-C4-C2	2.34	116.91	111.40
4	A	1203	BTB	O4-C4-C2	2.26	116.73	111.40

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1202	XV5	C7-C8-C9-C10
3	A	1202	XV5	O1-C8-C9-C10
3	A	1202	XV5	C11-C10-C9-C8
3	A	1202	XV5	C15-C10-C9-C8
3	B	1202	XV5	C7-C8-C9-C10
3	B	1202	XV5	O1-C8-C9-C10
3	B	1202	XV5	C11-C10-C9-C8
3	B	1202	XV5	C15-C10-C9-C8
4	A	1203	BTB	C1-C2-C3-O3
4	A	1203	BTB	C1-C2-C4-O4
4	A	1203	BTB	C3-C2-C4-O4
4	A	1203	BTB	N-C2-C4-O4
4	A	1203	BTB	C4-C2-N-C5
4	A	1203	BTB	C8-C7-N-C5
4	B	1203	BTB	O1-C1-C2-C4
4	B	1203	BTB	C1-C2-C3-O3
4	B	1203	BTB	N-C2-C4-O4
4	B	1203	BTB	C1-C2-C4-O4
4	B	1203	BTB	C3-C2-C4-O4
4	A	1203	BTB	N-C7-C8-O8
4	A	1203	BTB	C1-C2-N-C5
4	A	1203	BTB	C3-C2-N-C5
4	B	1203	BTB	N-C2-C3-O3
4	A	1203	BTB	O1-C1-C2-C4

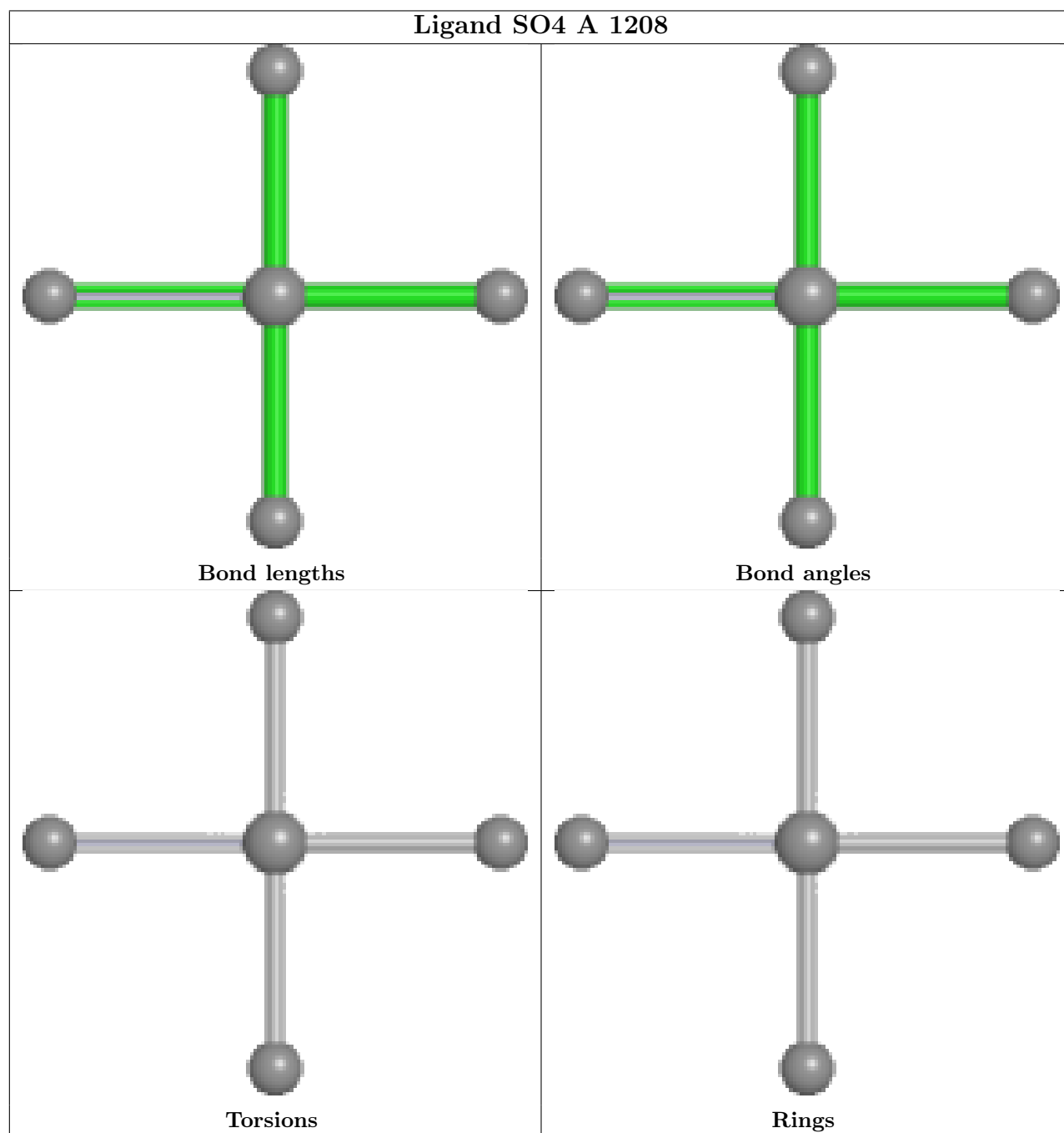
There are no ring outliers.

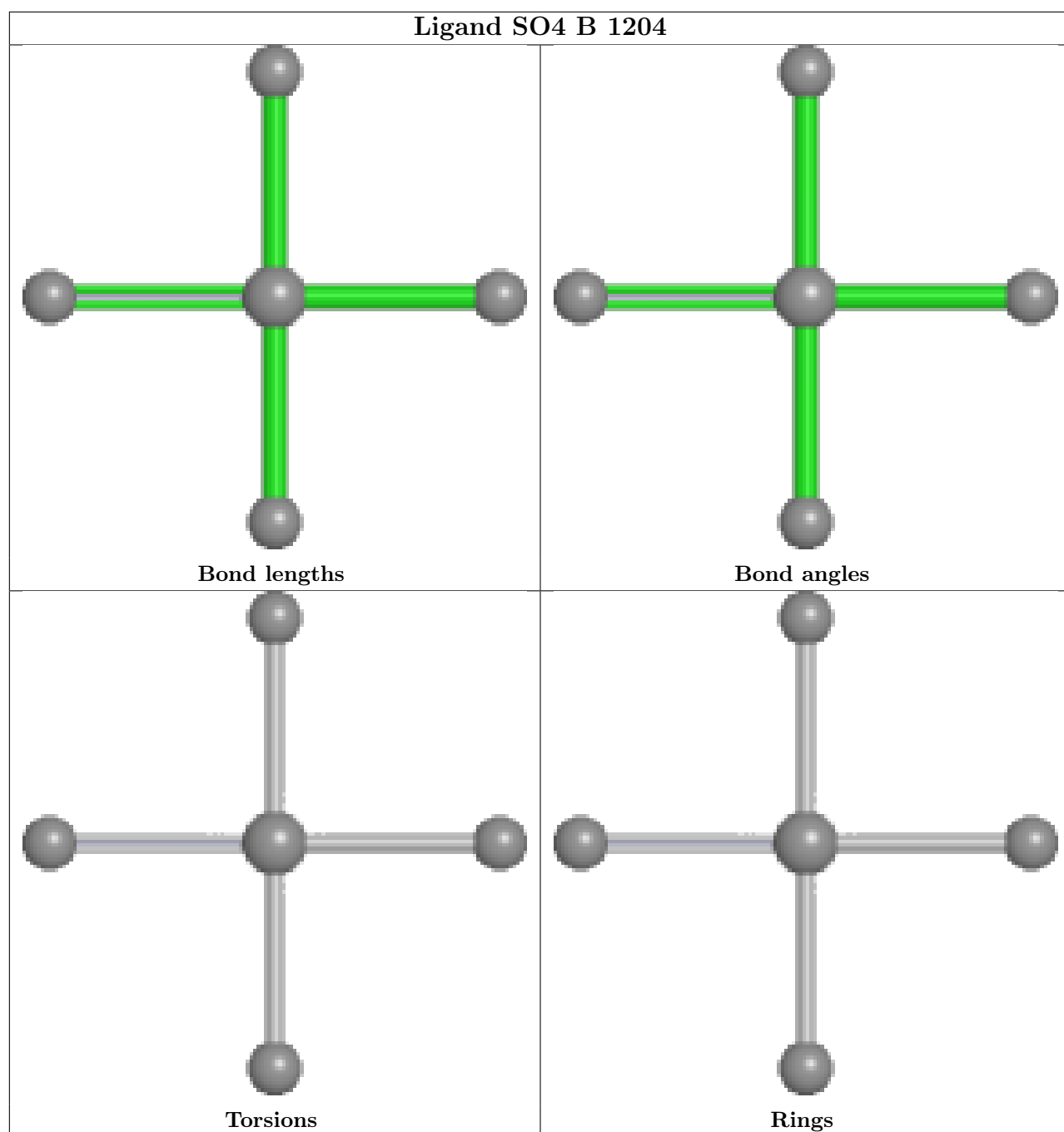
4 monomers are involved in 14 short contacts:

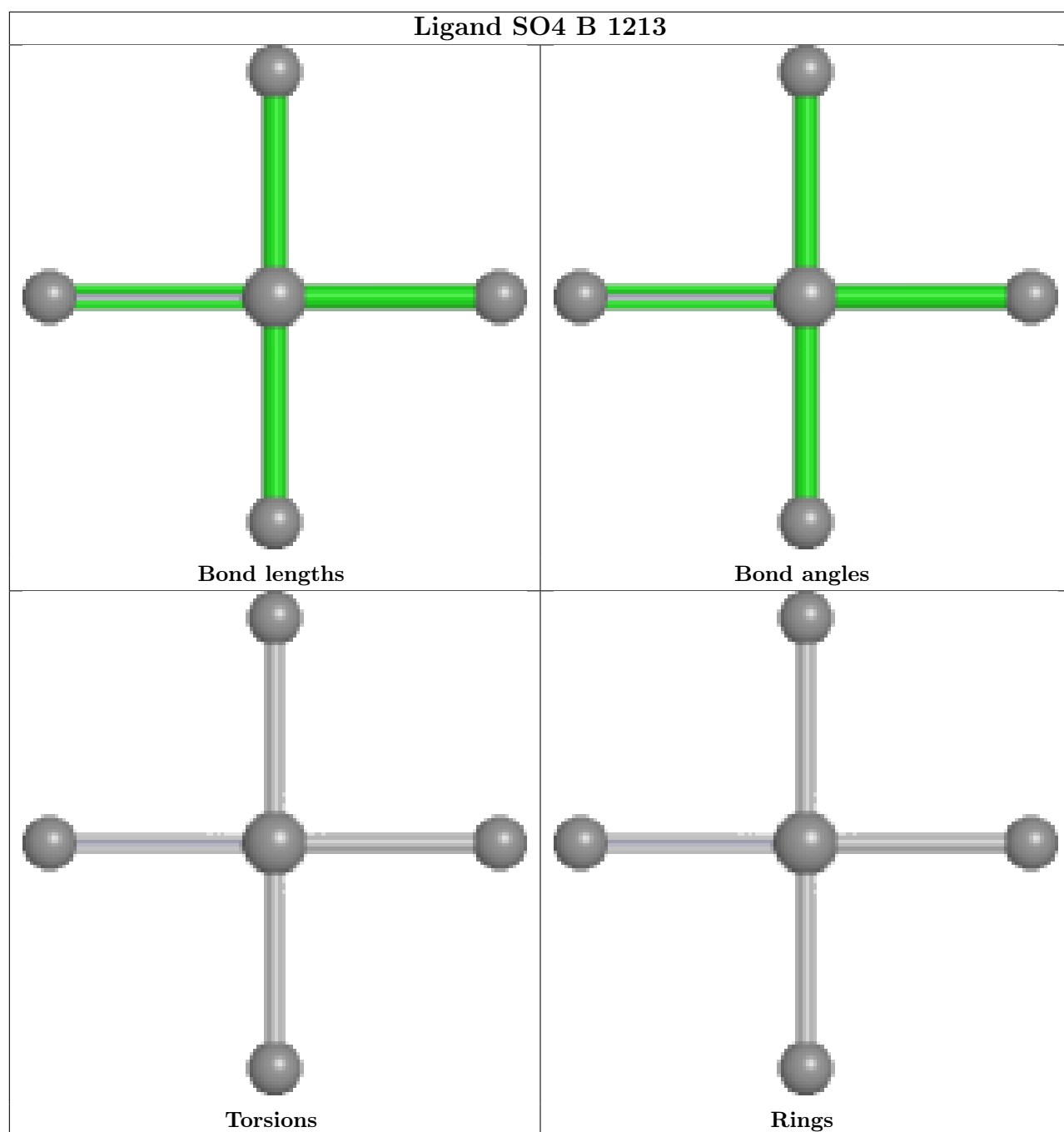
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1203	BTB	7	0
3	A	1202	XV5	2	0
3	B	1202	XV5	1	0
4	B	1203	BTB	4	0

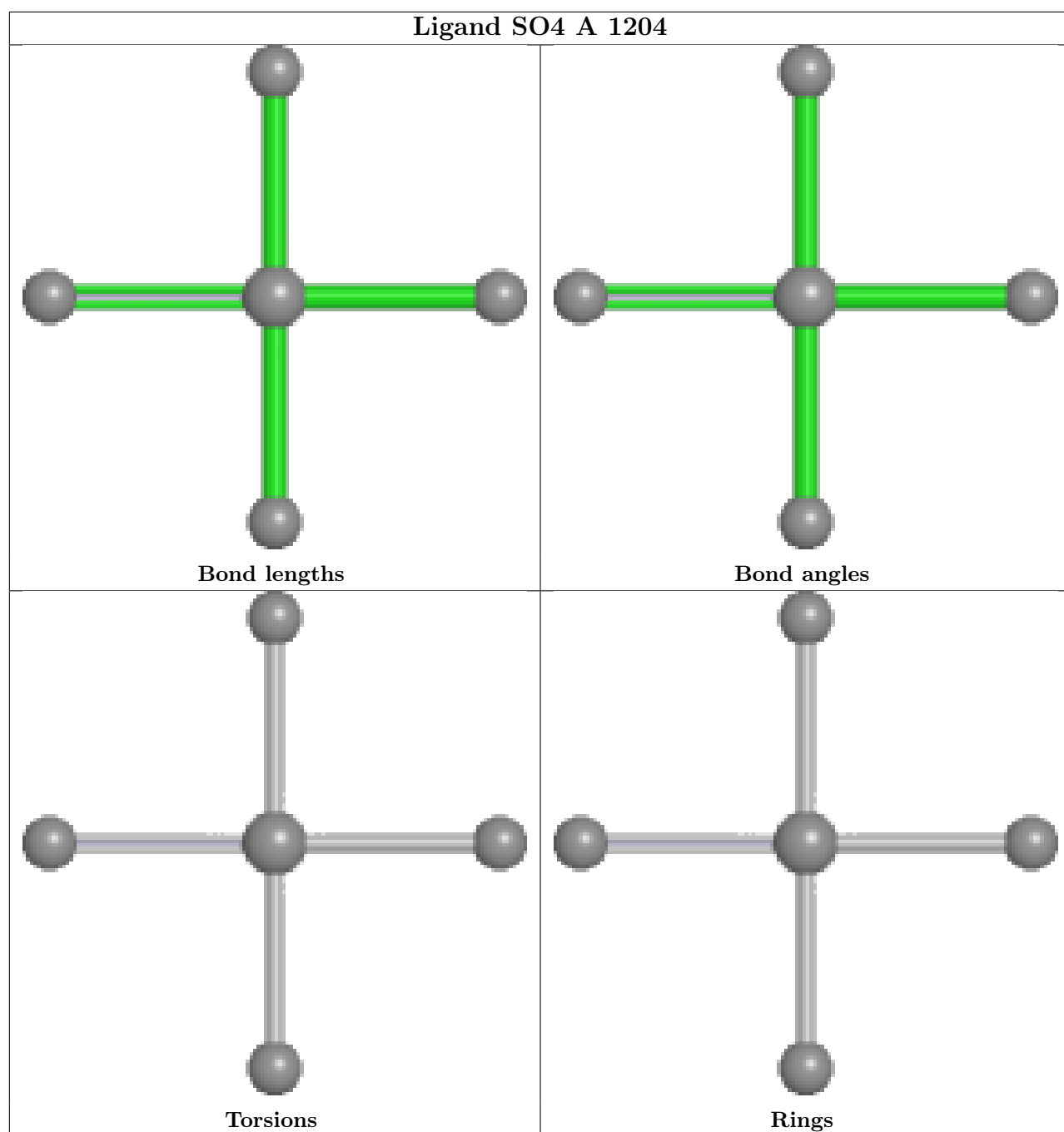
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

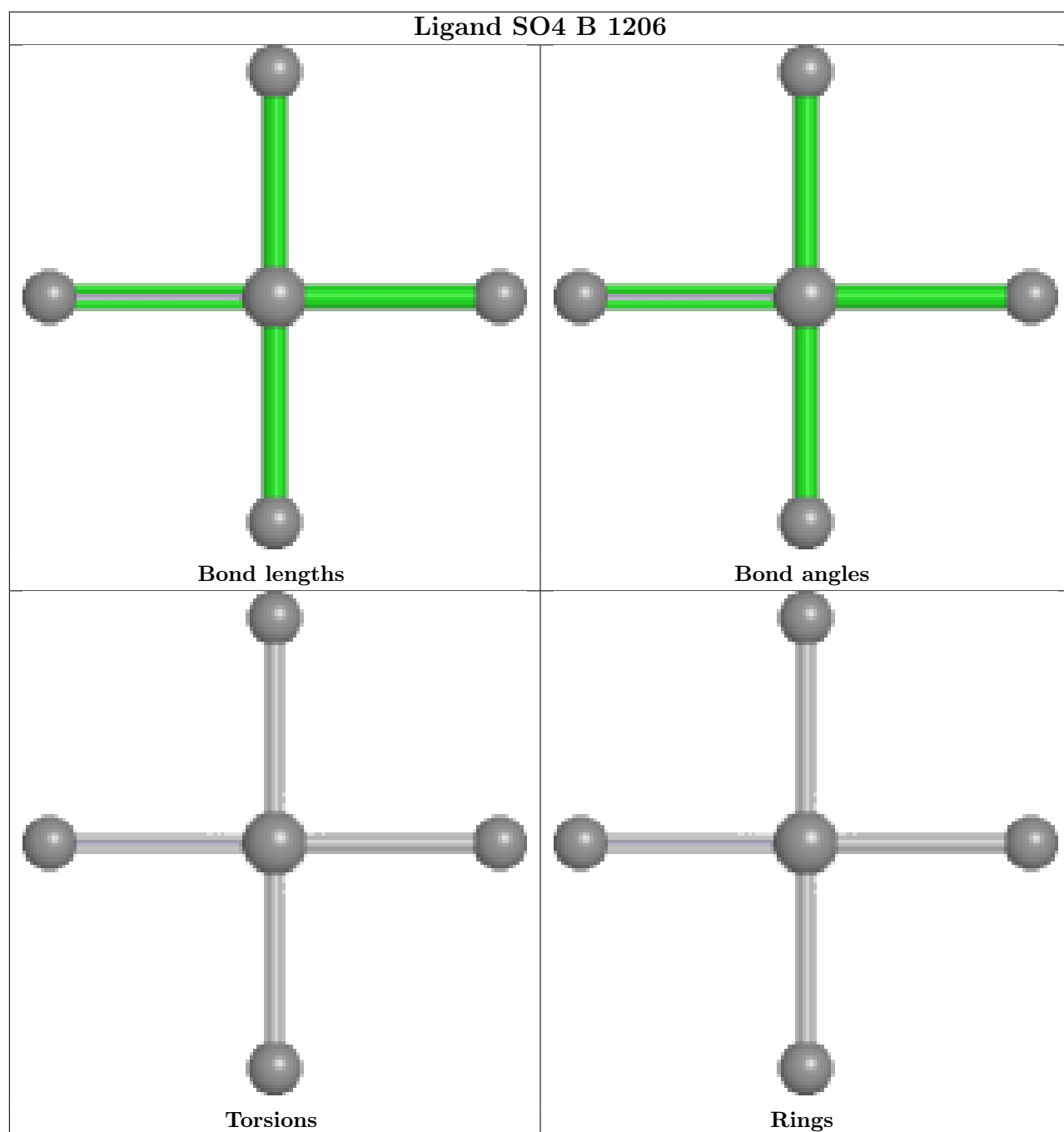
highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified 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.

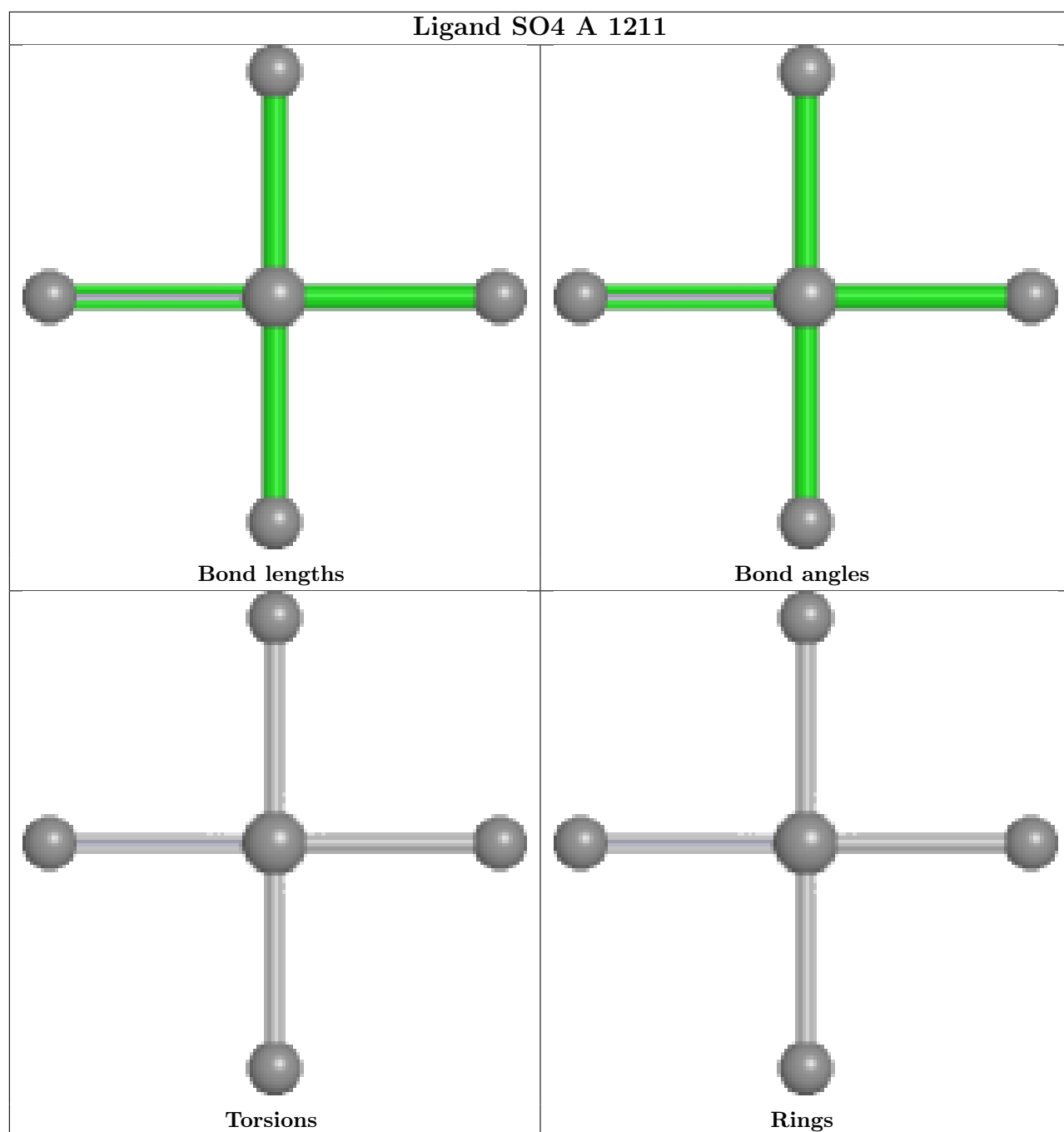


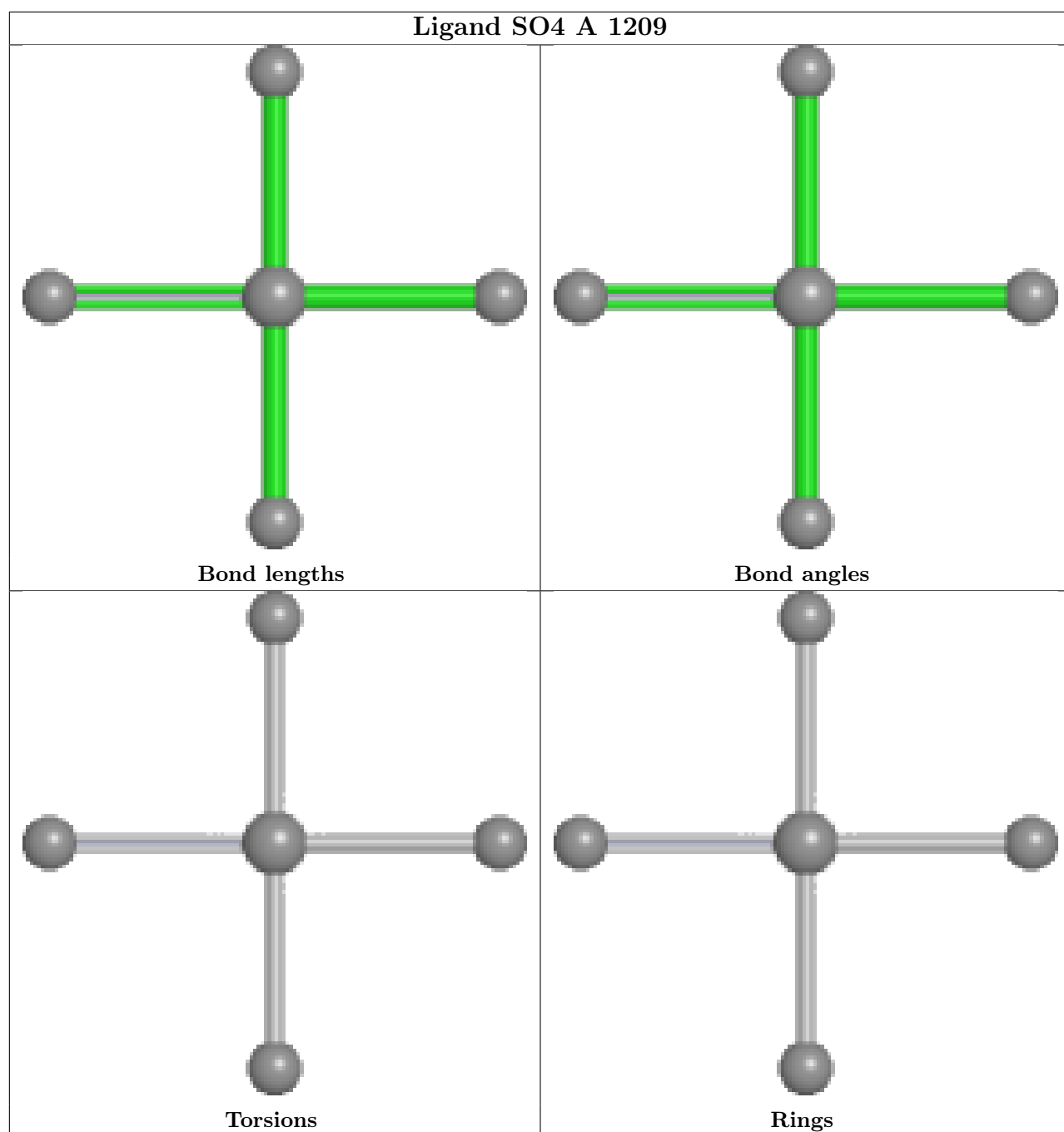


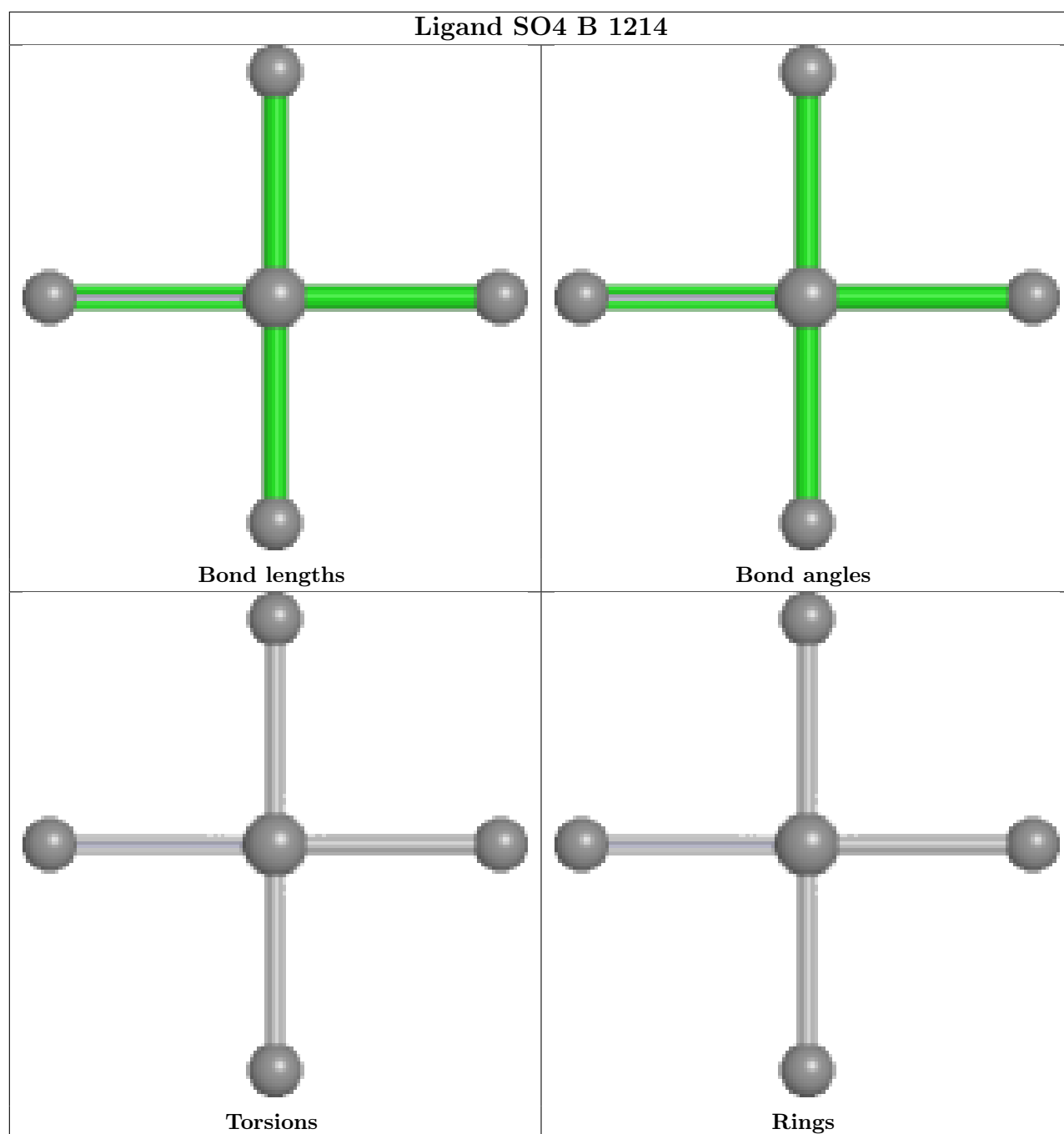


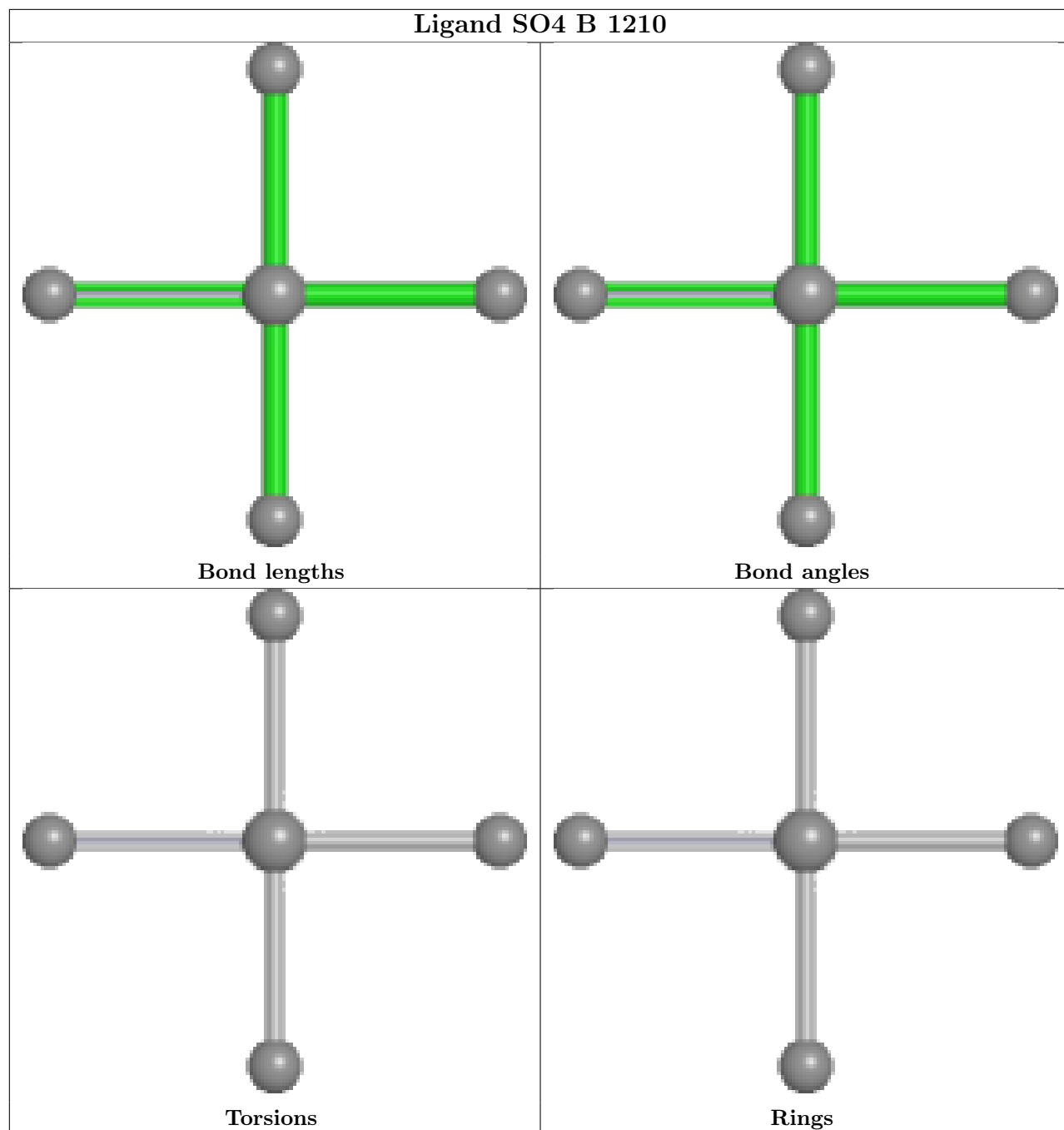


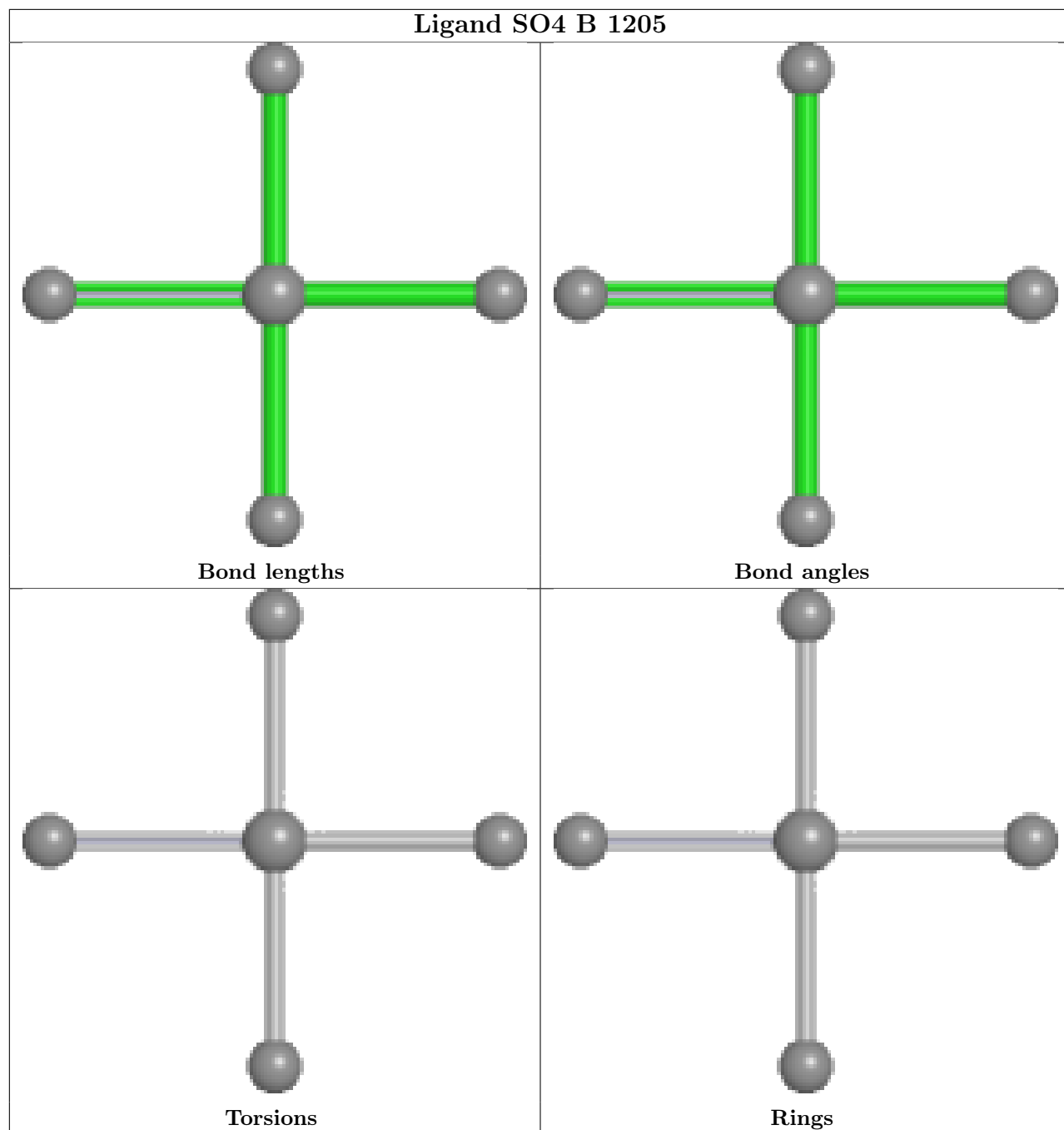


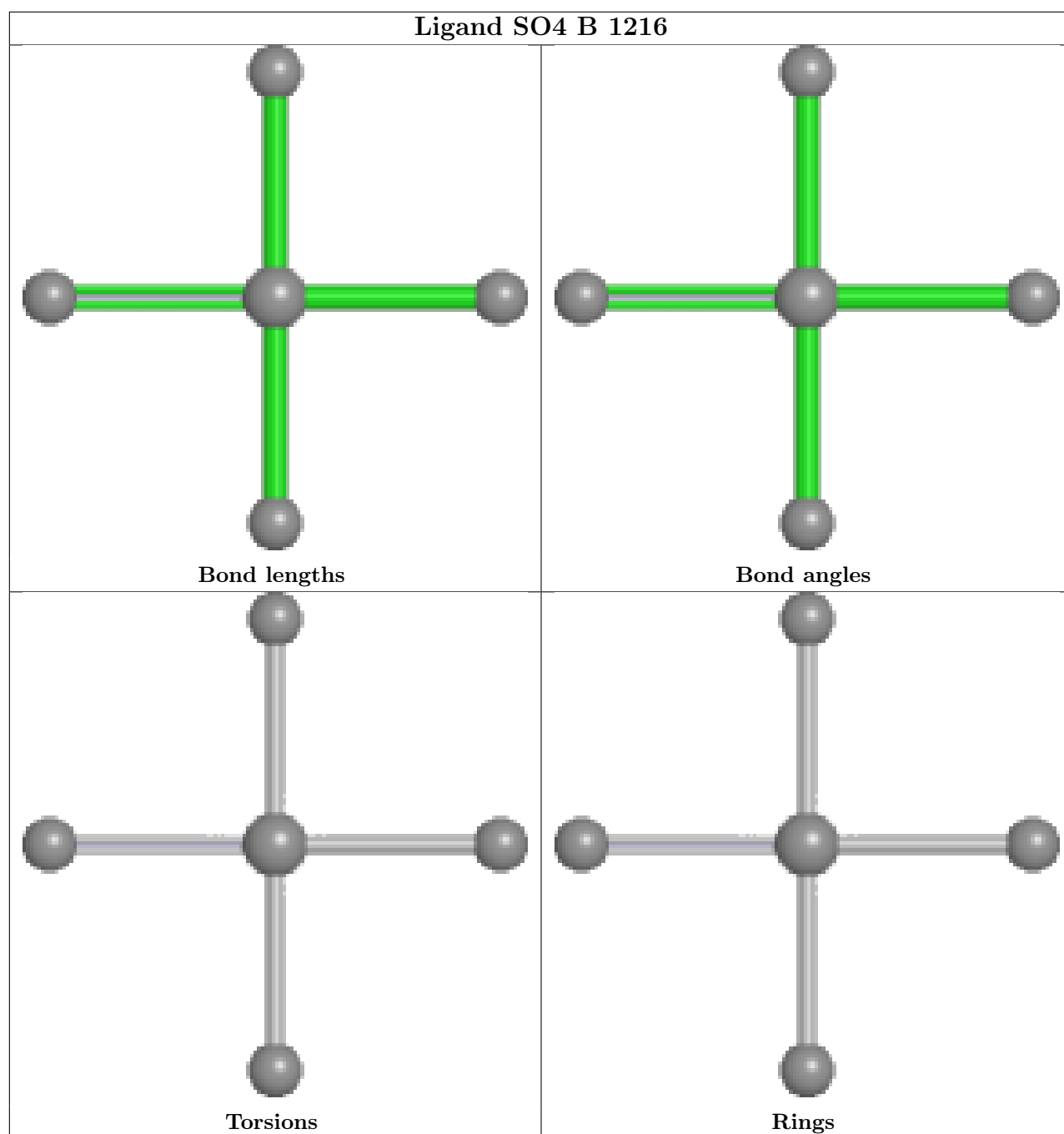


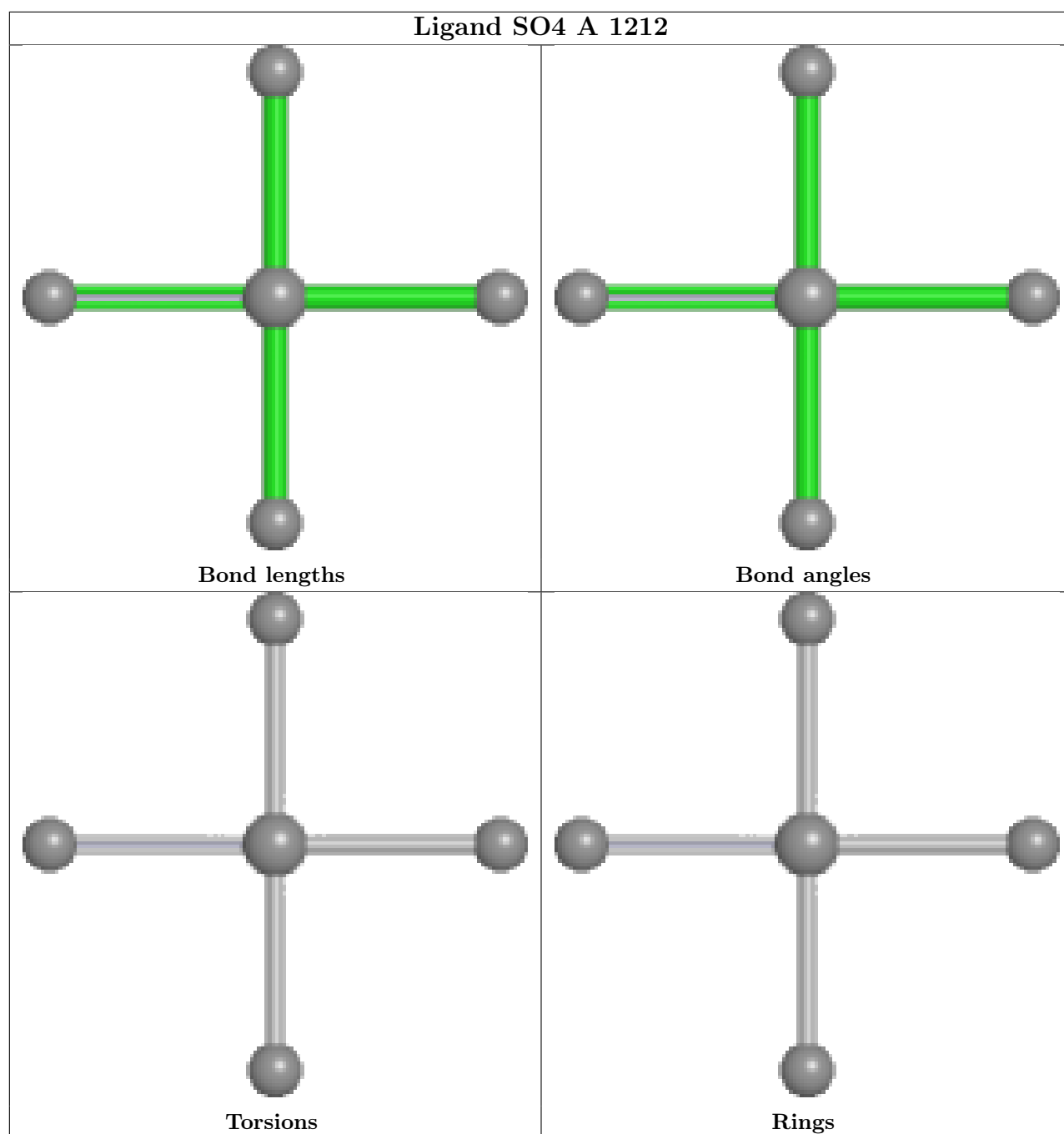


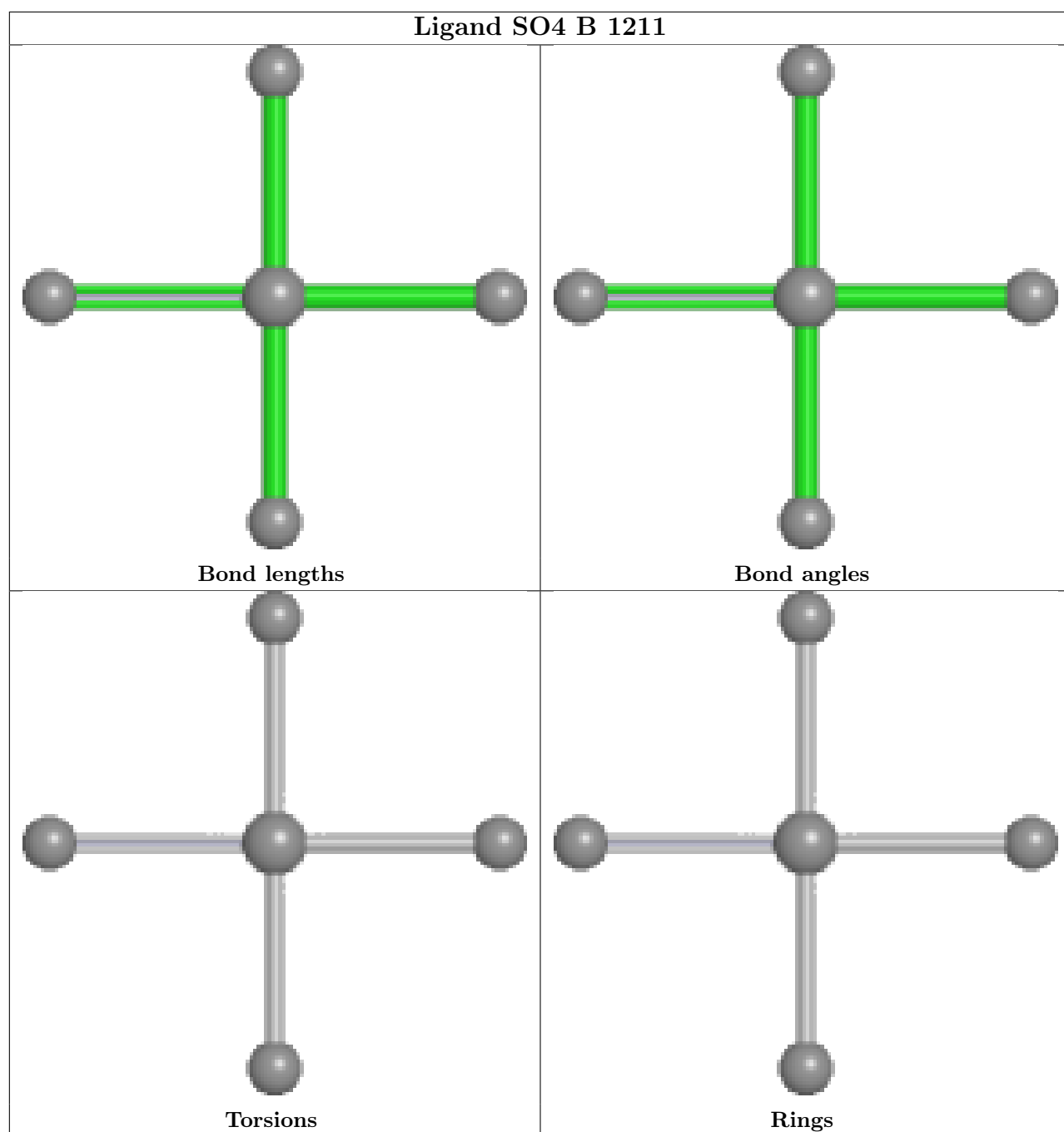


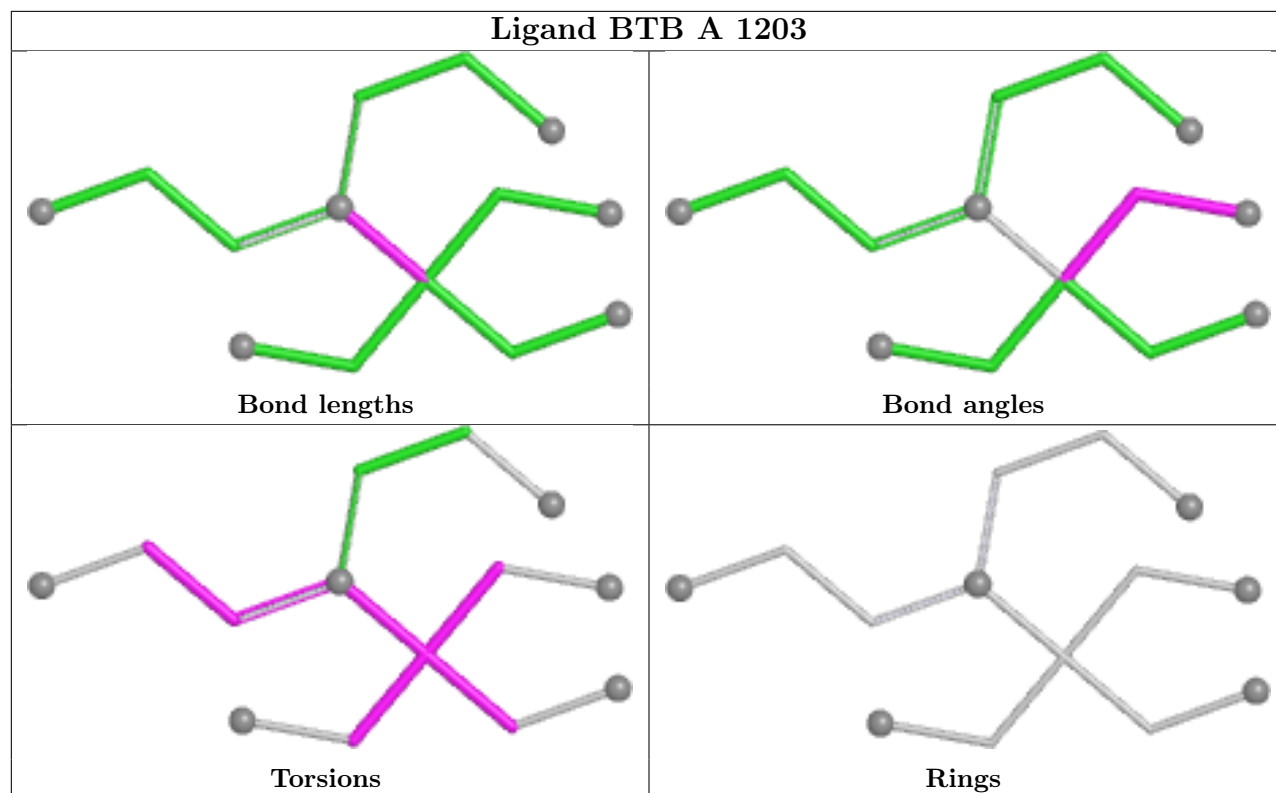


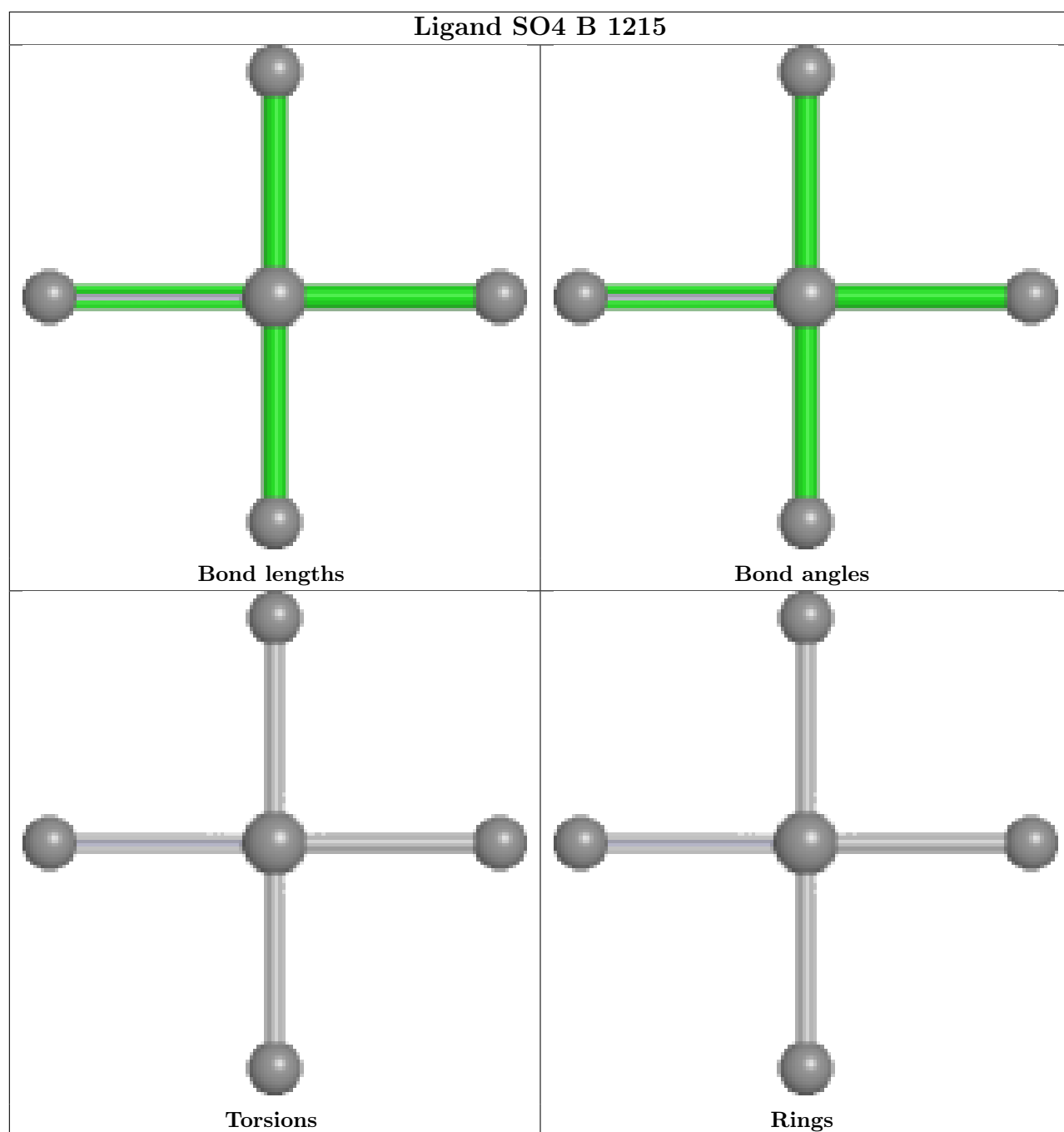


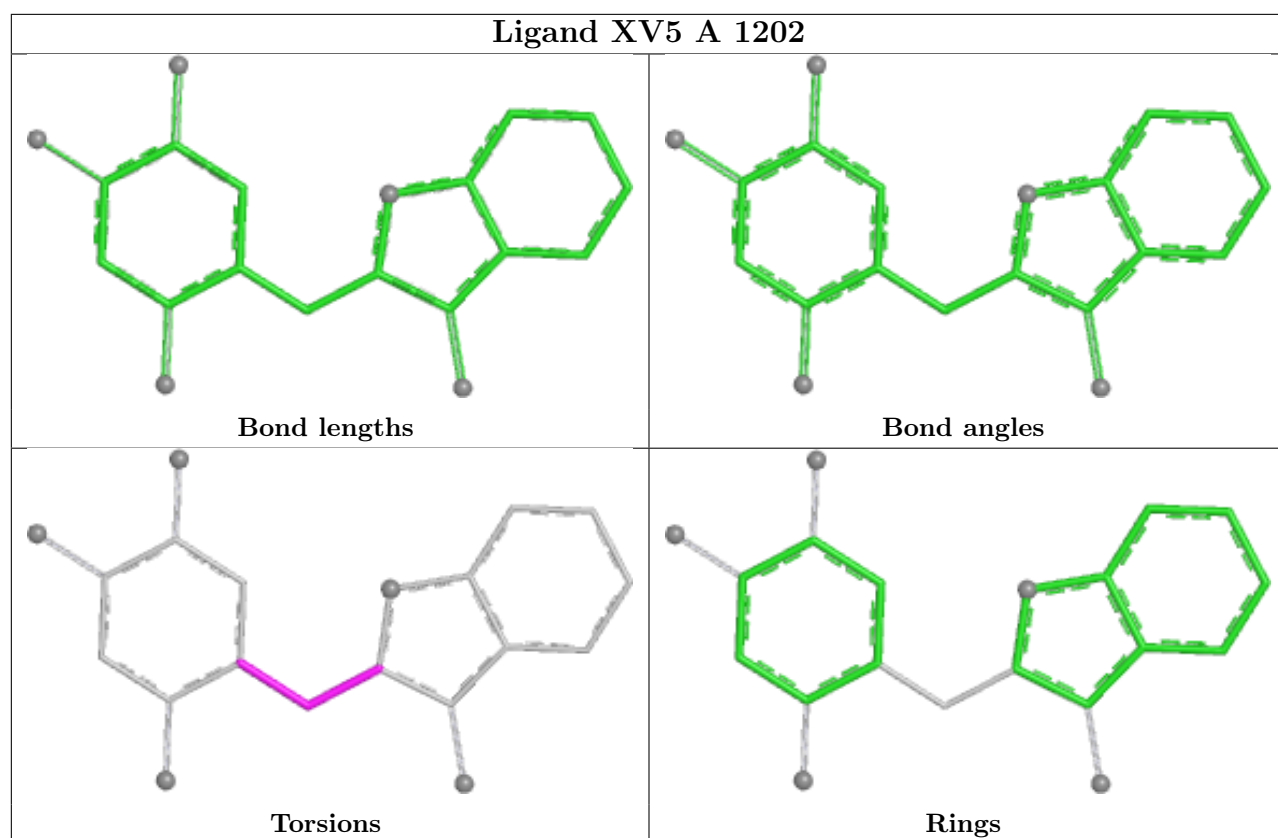


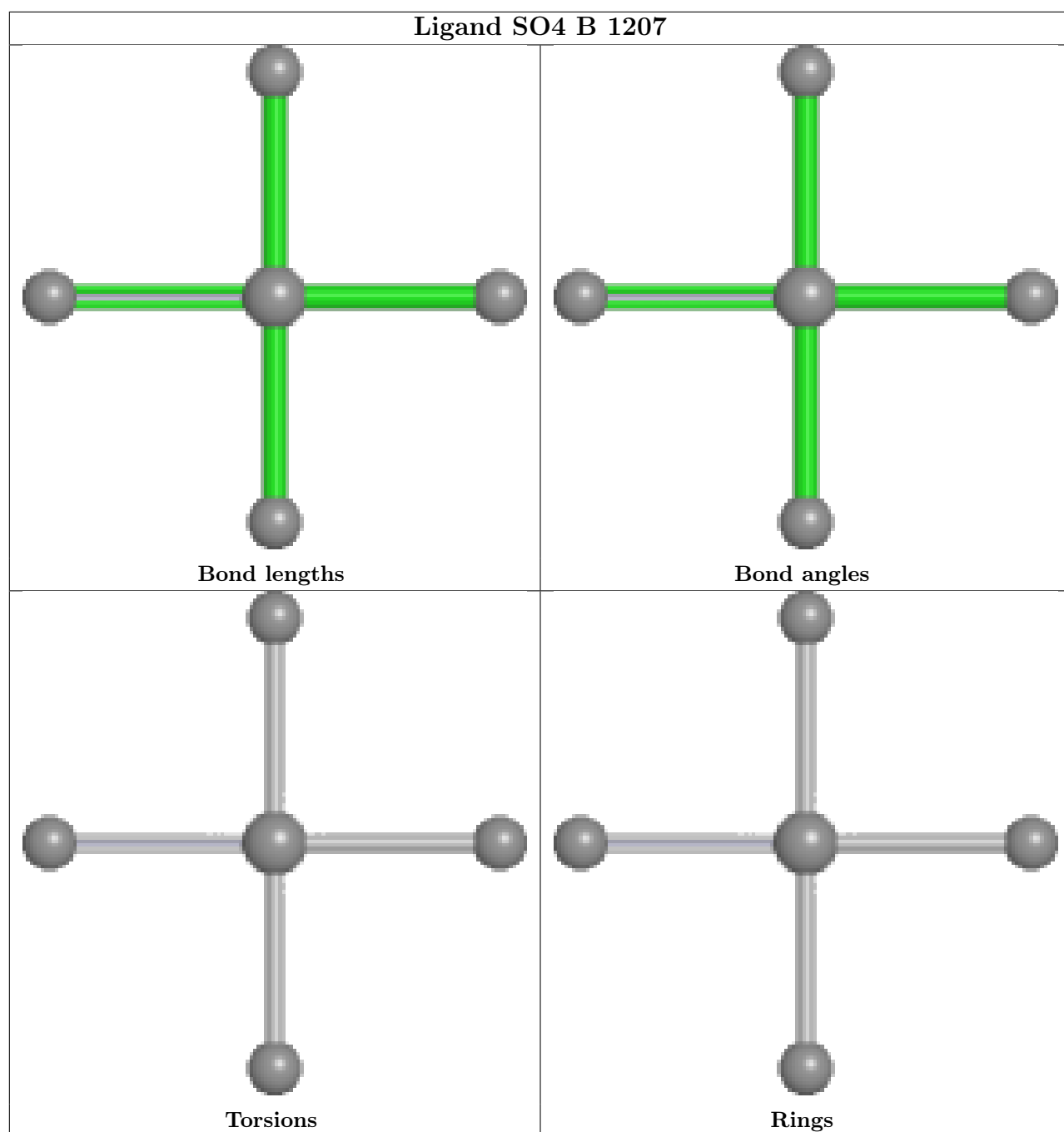


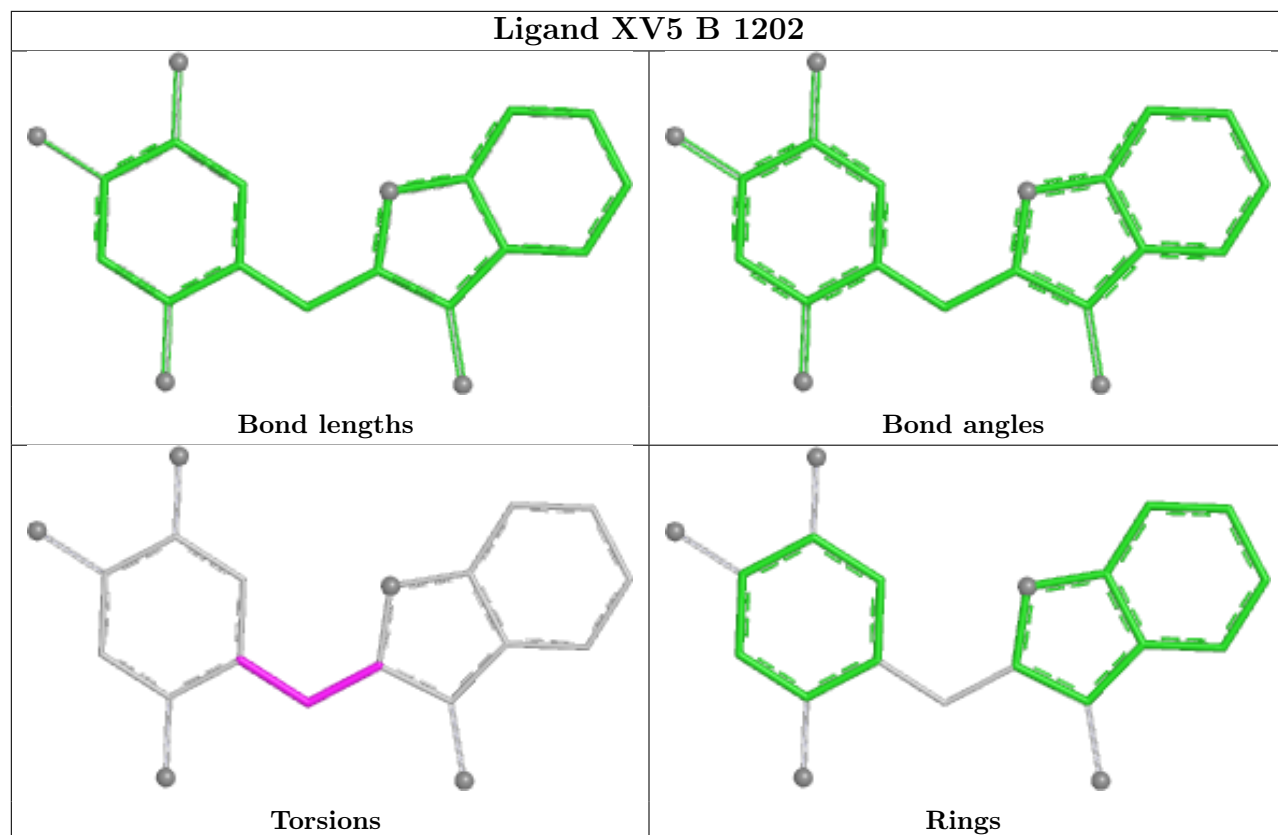


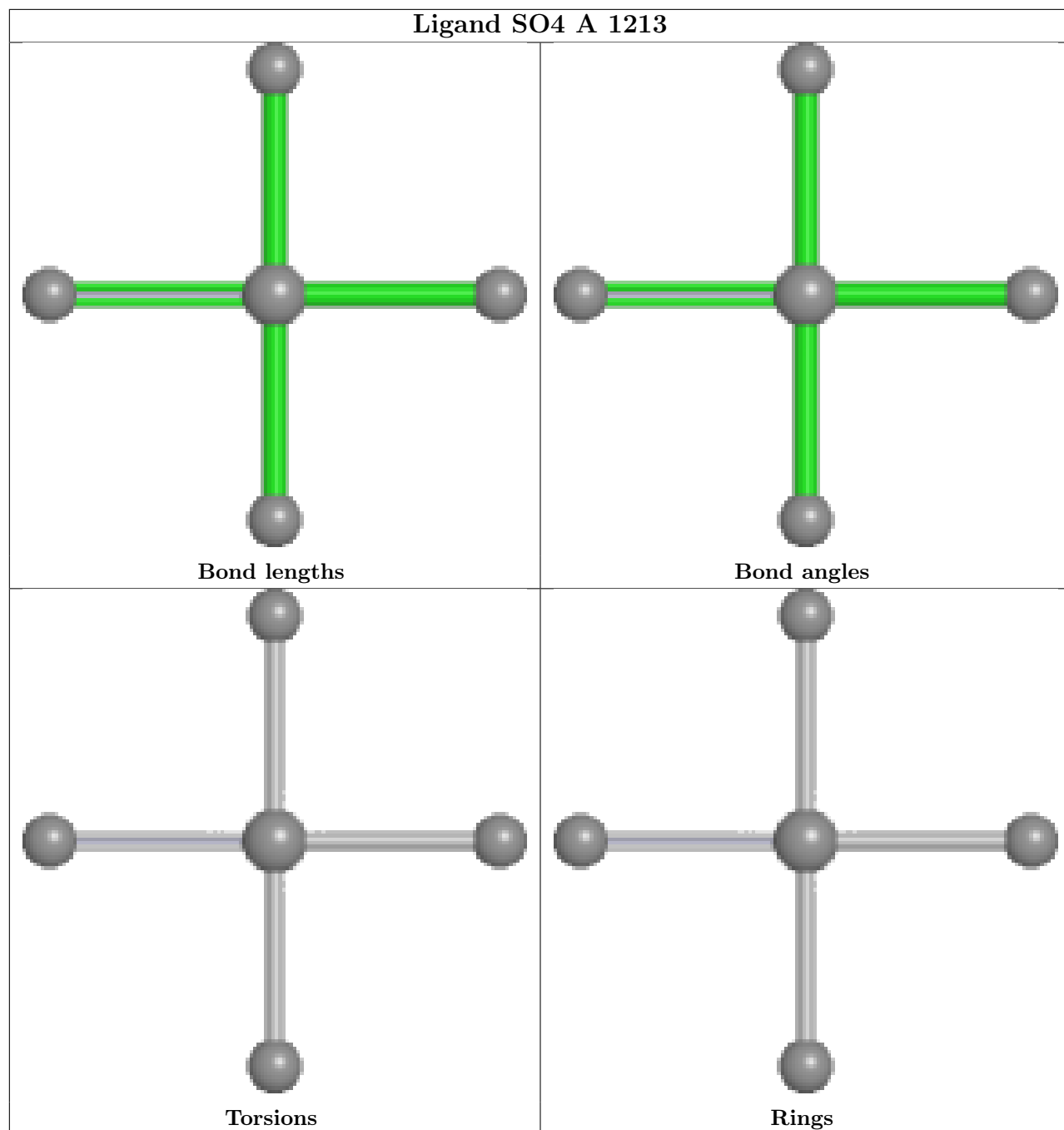


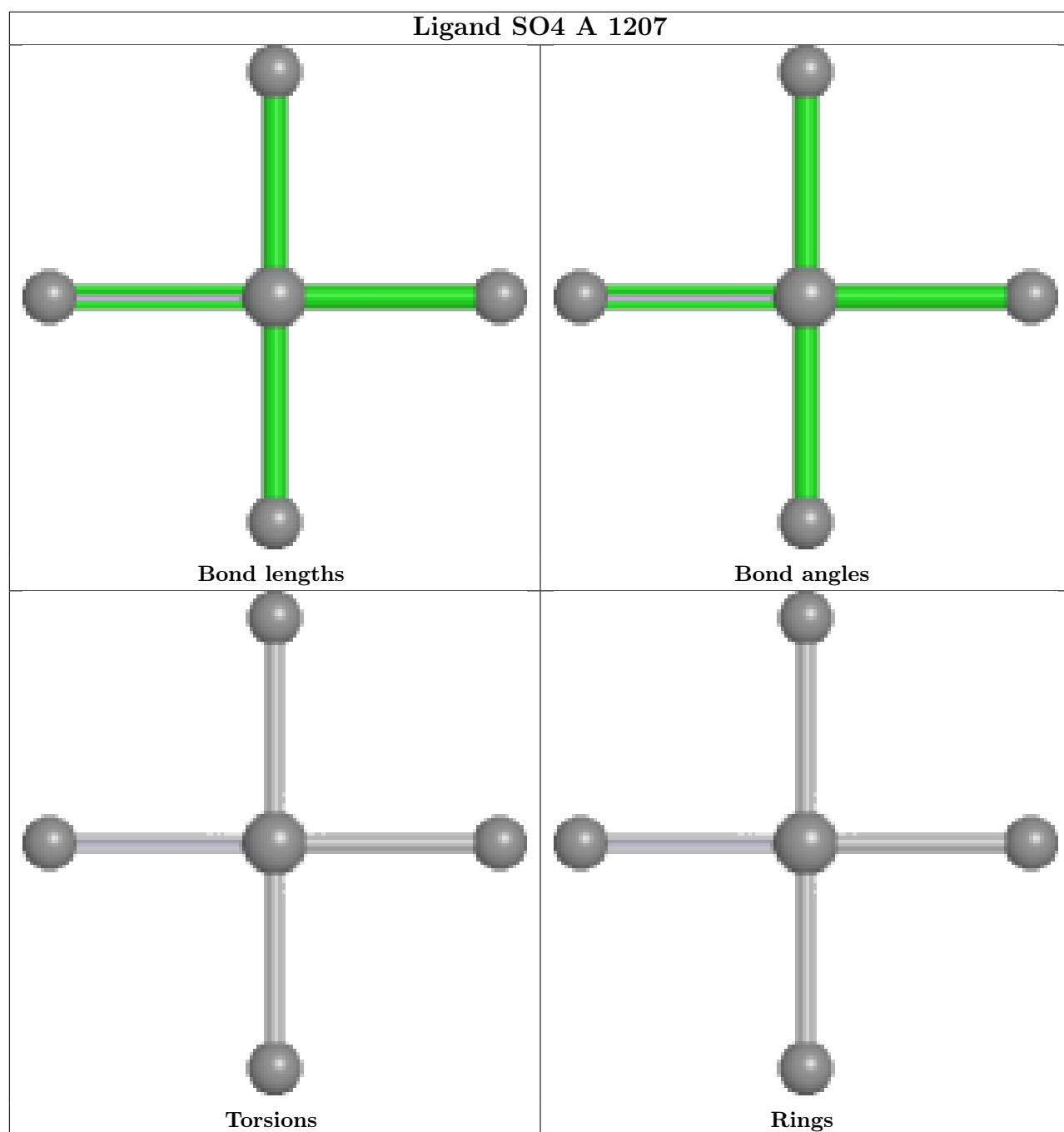


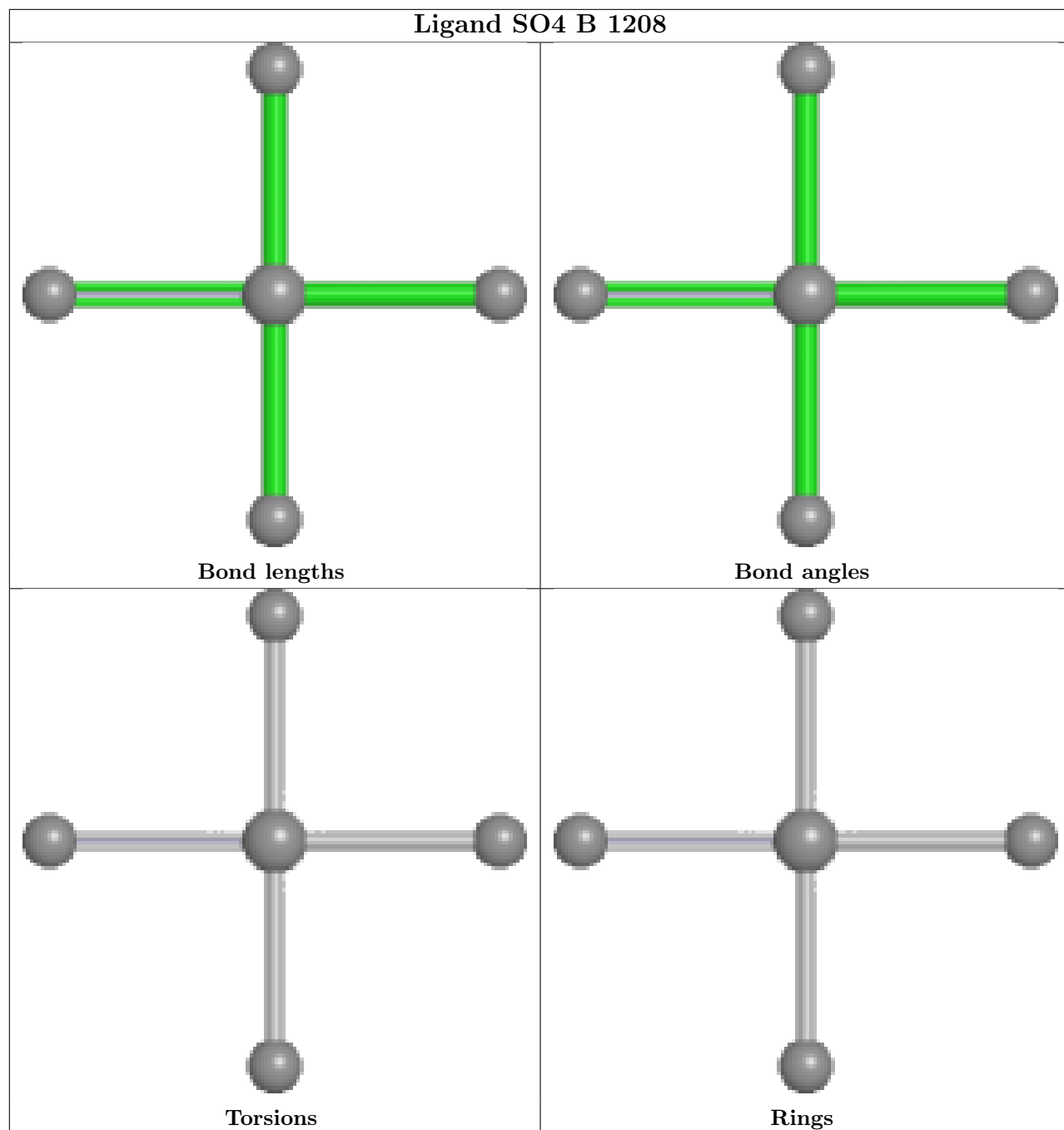


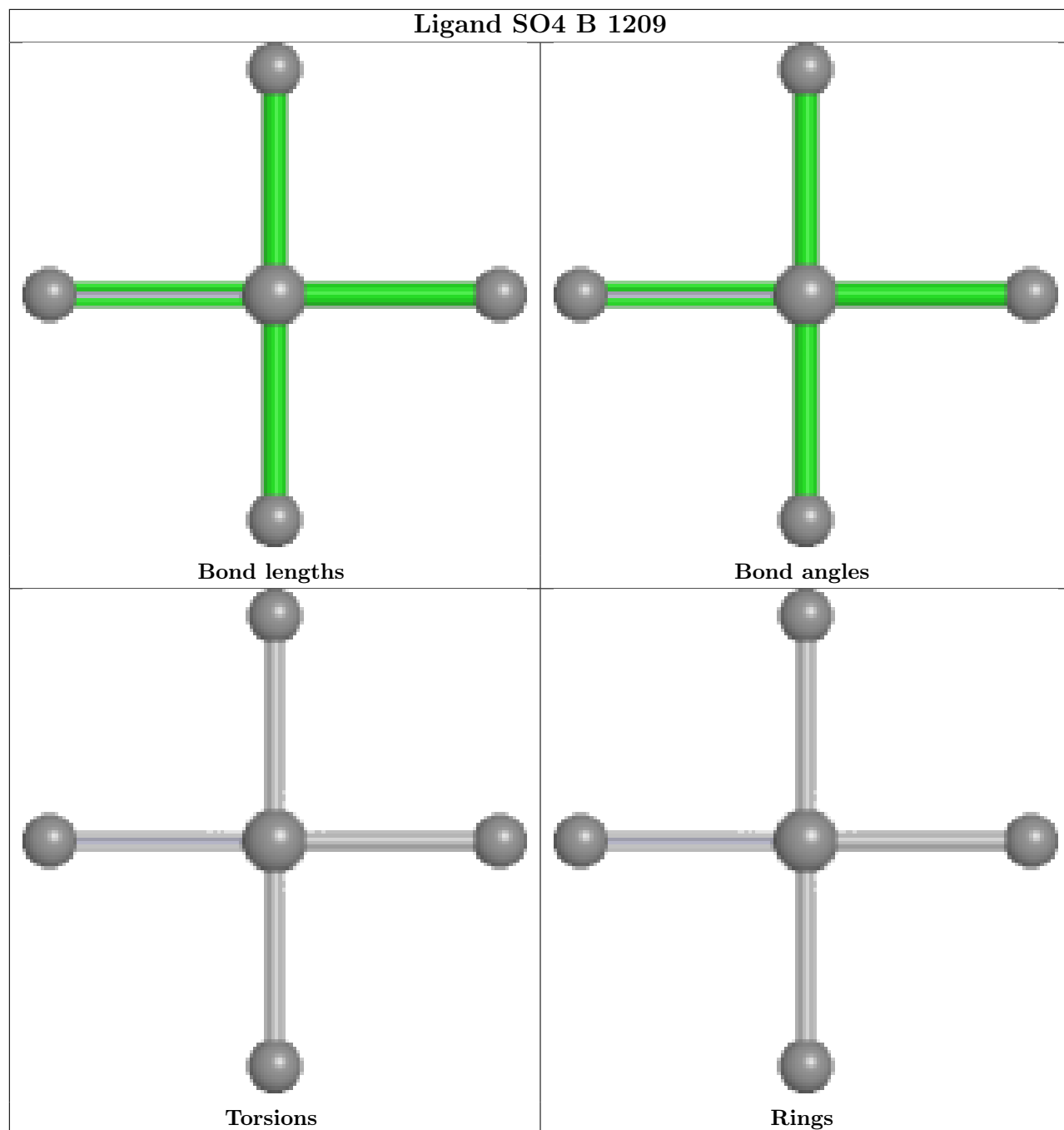


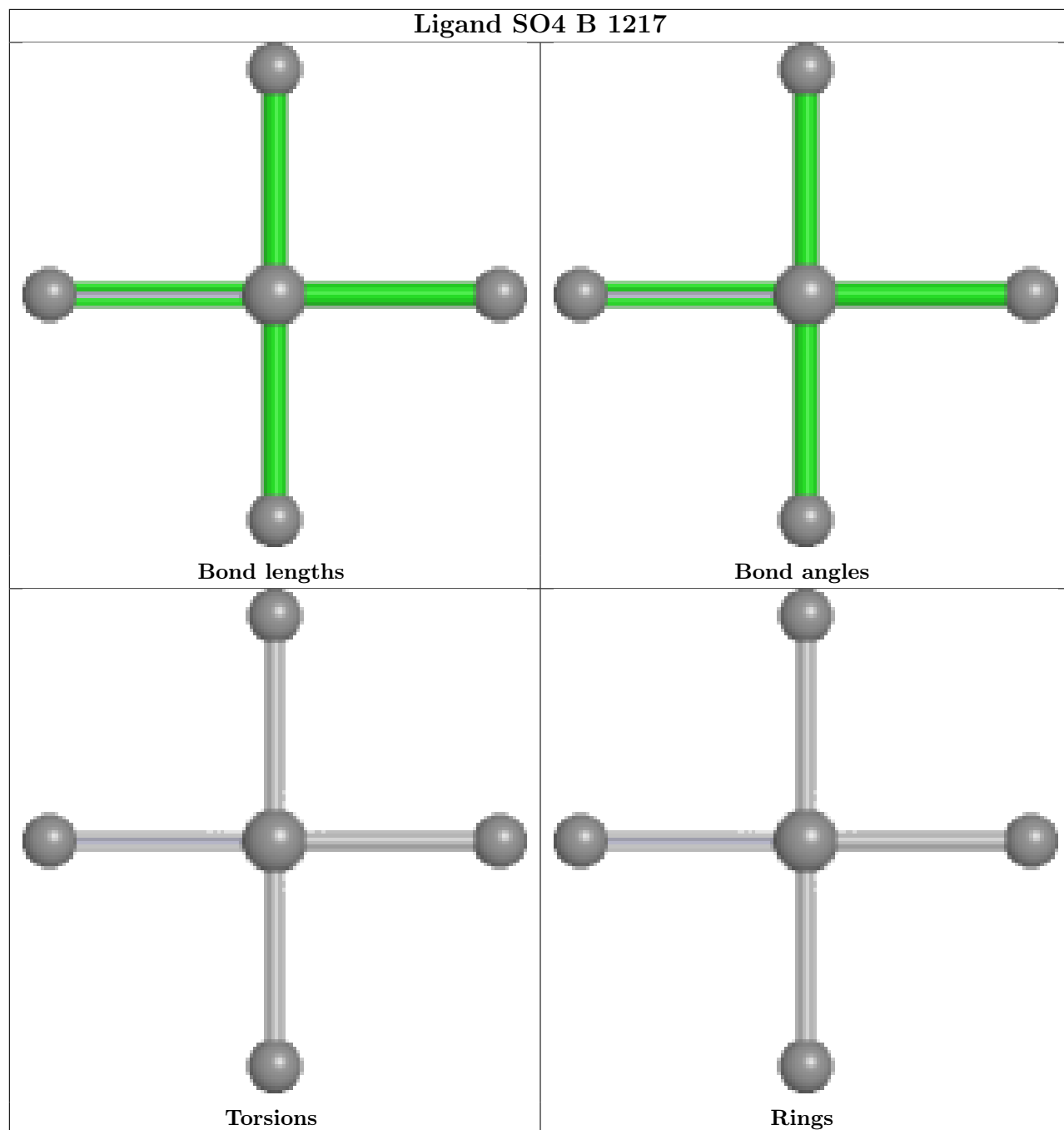


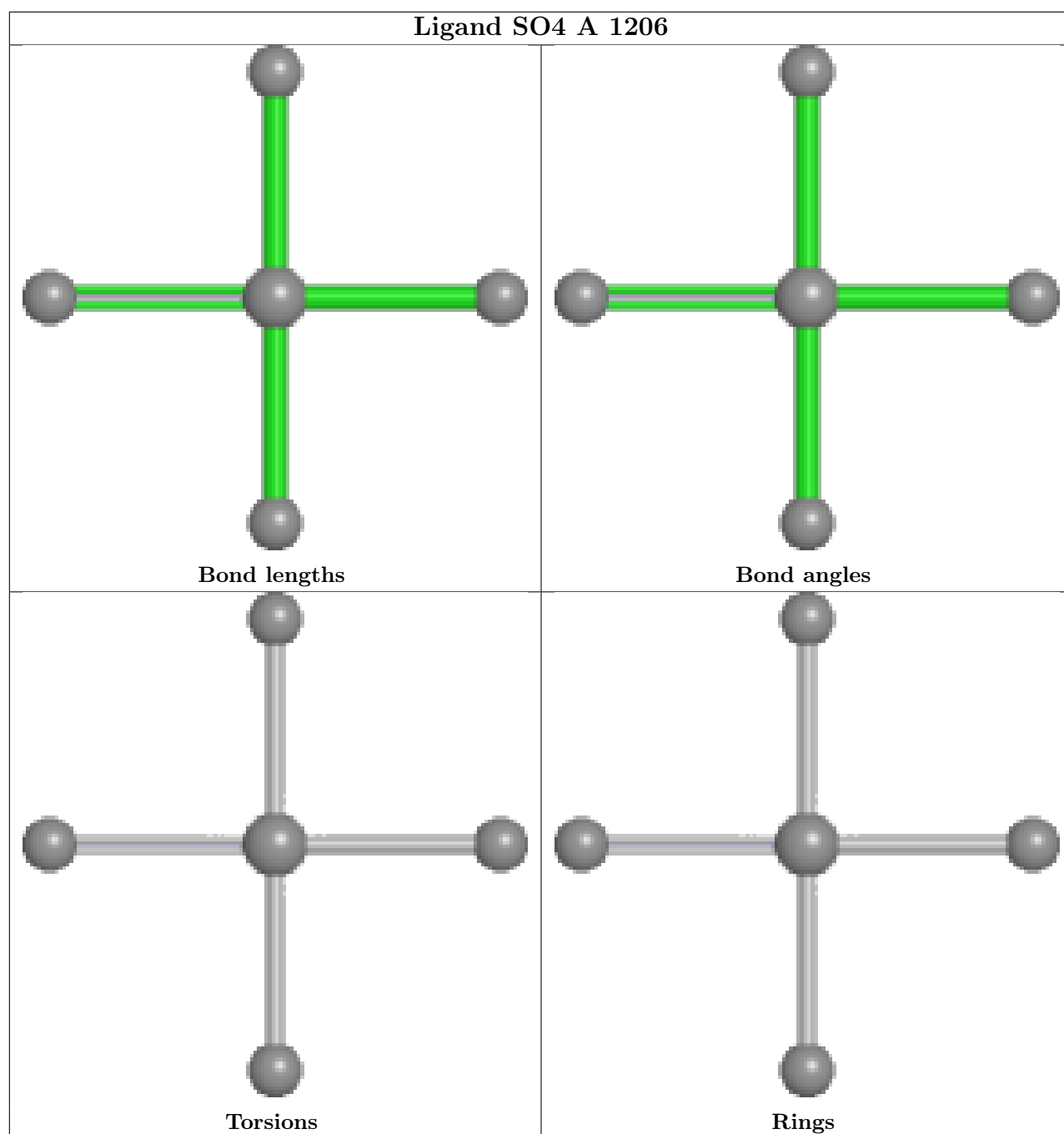


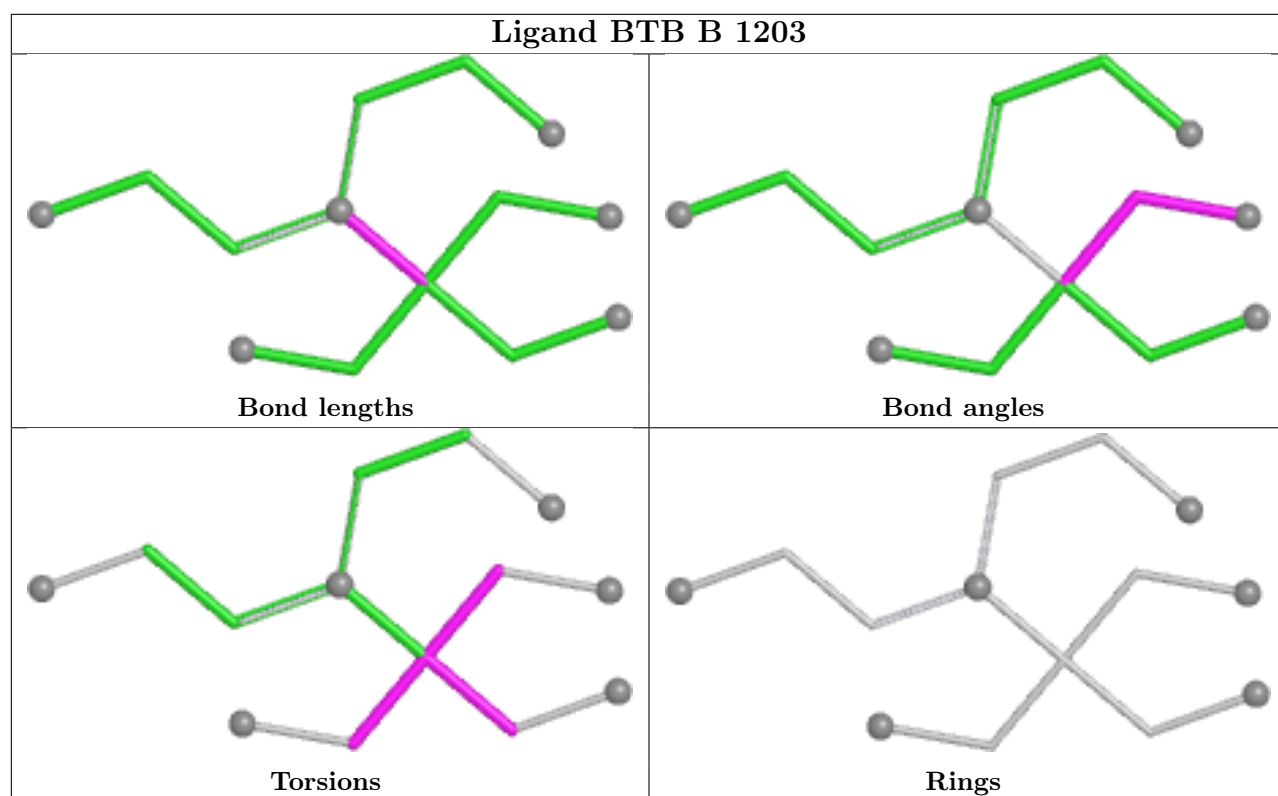


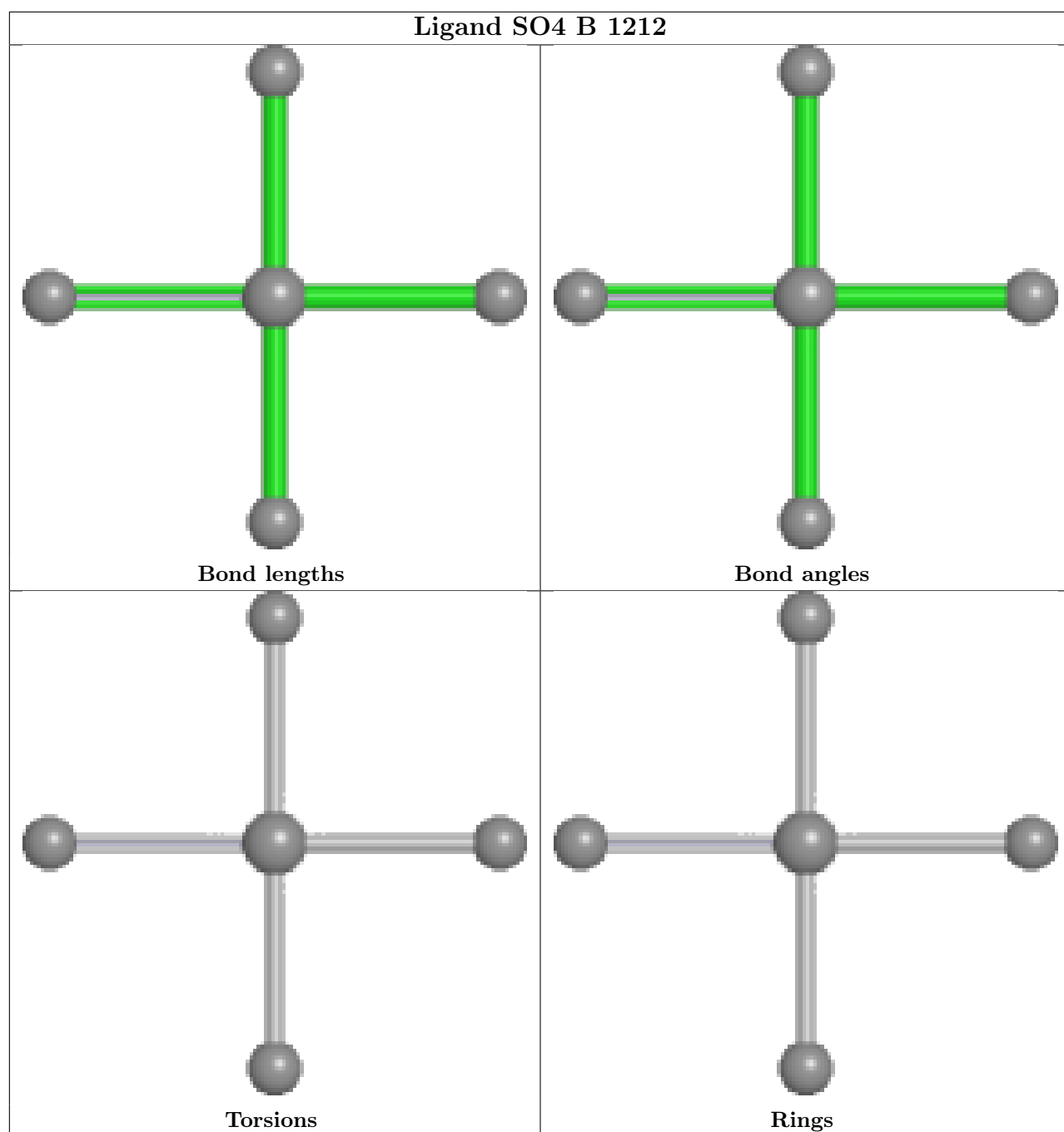


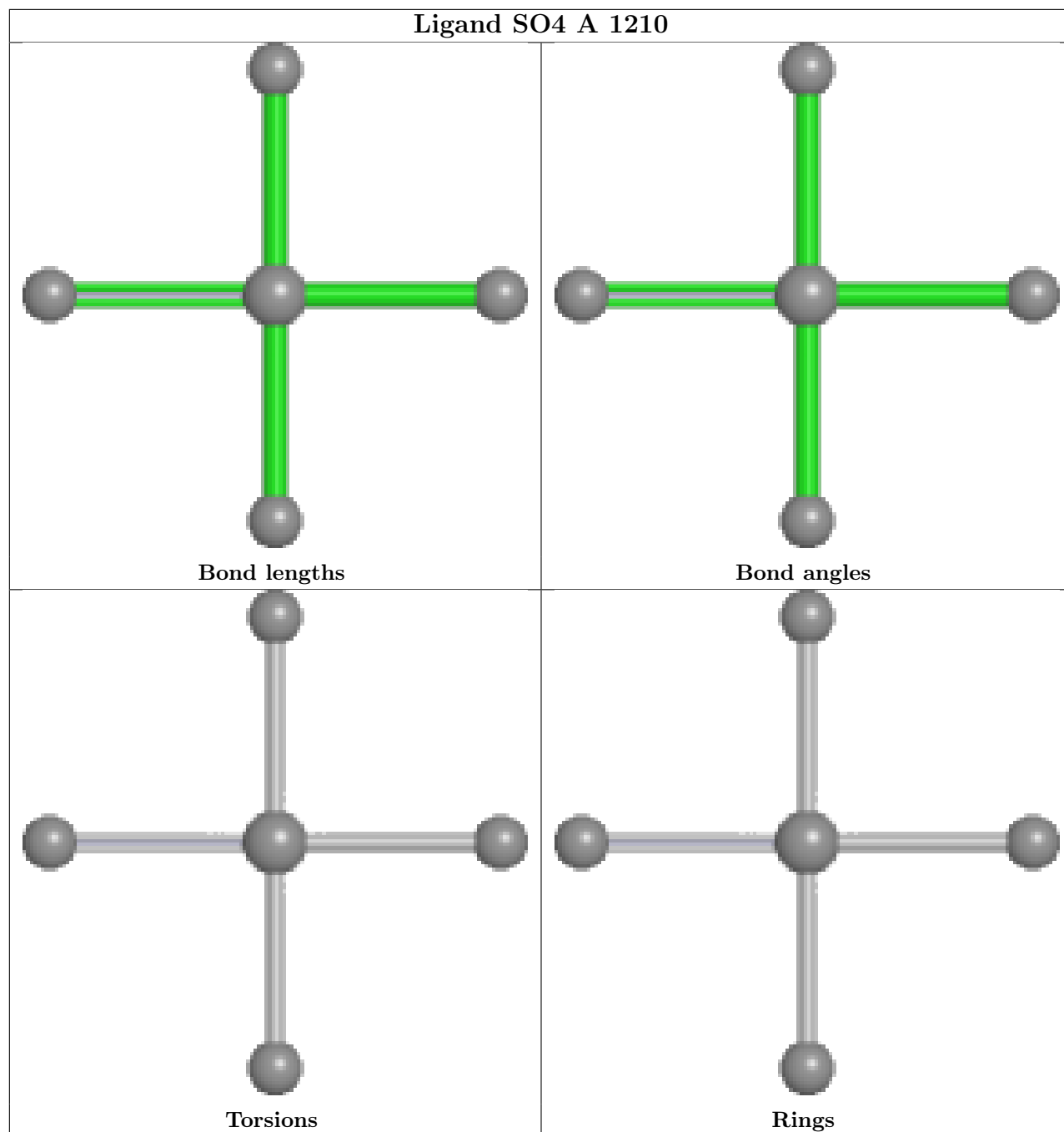


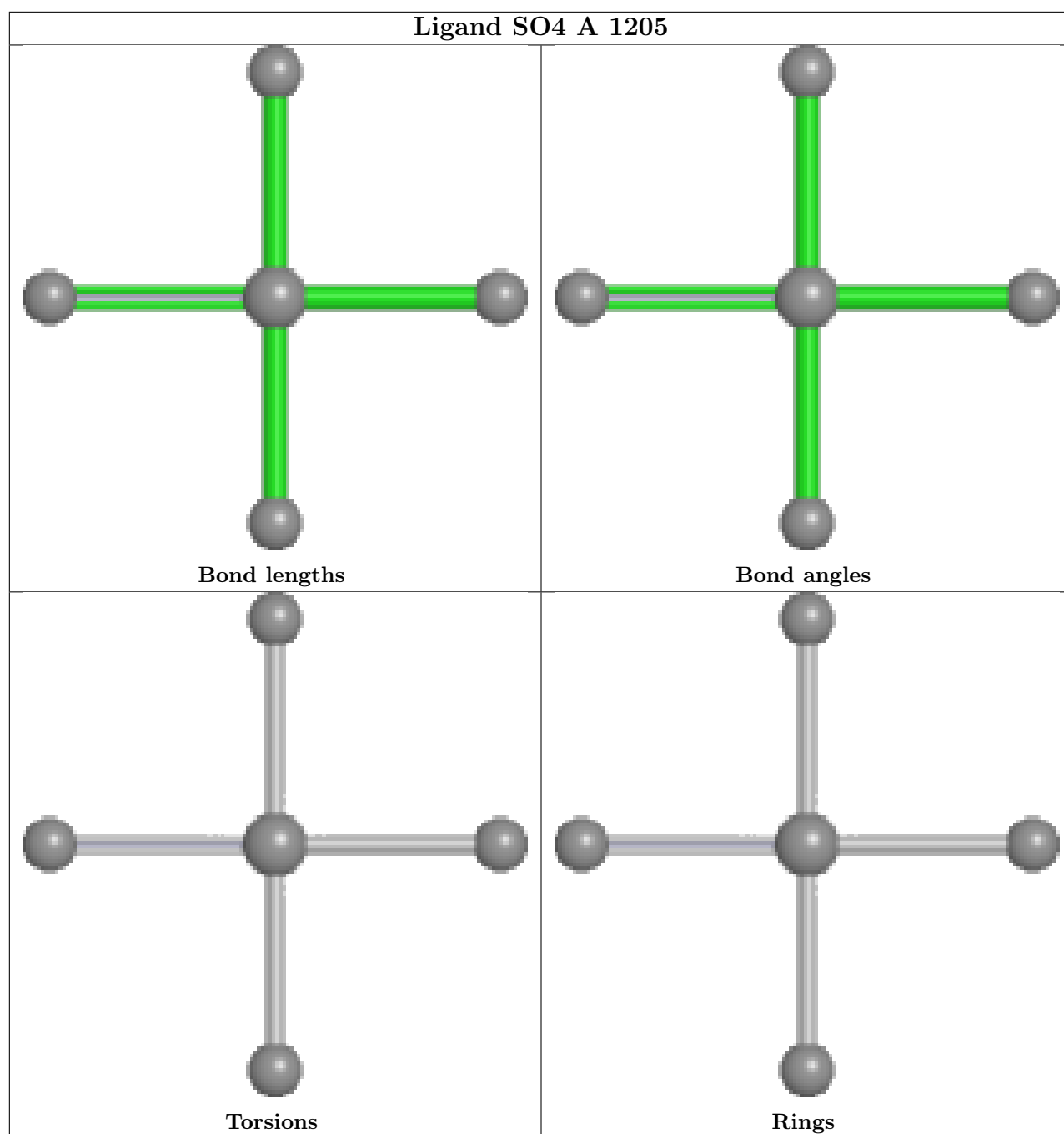












5.7 Other polymers [i](#)

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	835/869 (96%)	0.42	62 (7%)	20 23	34, 52, 92, 132	0
1	B	824/869 (94%)	0.52	116 (14%)	6 7	20, 49, 113, 145	1 (0%)
All	All	1659/1738 (95%)	0.47	178 (10%)	11 13	20, 50, 107, 145	1 (0%)

All (178) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	222	TYR	10.0
1	B	224	GLN	9.5
1	B	252	LEU	8.5
1	A	218	LEU	8.3
1	B	304	LEU	8.2
1	B	219	TYR	8.1
1	B	257	THR	7.6
1	B	271	MET	6.7
1	B	300	THR	6.5
1	B	1045	PHE	6.2
1	B	279	THR	6.2
1	B	250	TYR	6.1
1	B	262	THR	5.7
1	A	213	THR	5.6
1	B	225	VAL	5.4
1	B	306	LEU	5.2
1	B	327	THR	5.1
1	B	970	SER	4.9
1	B	220	LYS	4.9
1	B	272	THR	4.9
1	B	292	GLY	4.7
1	B	291	LEU	4.6
1	B	1047	ILE	4.6
1	B	325	LYS	4.5

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Mol	Chain	Res	Type	RSRZ
1	A	1047	ILE	4.4
1	B	280	GLN	4.4
1	A	255	GLY	4.4
1	B	270	LEU	4.2
1	B	246	TYR	4.2
1	B	242	ALA	4.2
1	B	253	LYS	4.1
1	B	293	ILE	4.1
1	B	399	ASN	4.1
1	A	295	LYS	4.0
1	A	251	ILE	3.9
1	B	329	TRP	3.9
1	B	286	TYR	3.8
1	A	221	LYS	3.8
1	B	287	MET	3.8
1	B	1037	LYS	3.8
1	B	269	LEU	3.8
1	B	316	LYS	3.7
1	B	284	VAL	3.7
1	B	299	ASP	3.6
1	B	326	ASN	3.6
1	B	248	PRO	3.6
1	B	295	LYS	3.6
1	A	219	TYR	3.6
1	A	970	SER	3.6
1	B	337	PHE	3.6
1	B	221	LYS	3.5
1	B	333	THR	3.5
1	A	577	ILE	3.5
1	B	324	LEU	3.5
1	B	275	PRO	3.4
1	B	254	ASP	3.4
1	B	273	TRP	3.4
1	B	266	PHE	3.4
1	B	283	TYR	3.3
1	A	957	GLU	3.3
1	B	475[A]	HIS	3.3
1	B	256	LYS	3.3
1	A	339	LYS	3.3
1	B	245	TRP	3.3
1	B	302	ASN	3.3
1	A	332	GLN	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	329	TRP	3.3
1	B	1041	THR	3.2
1	B	958	GLY	3.2
1	B	233	PHE	3.2
1	B	334	ILE	3.2
1	B	264	LYS	3.2
1	B	1040	ALA	3.2
1	B	1043	THR	3.2
1	B	249	LYS	3.1
1	B	1046	ASN	3.1
1	B	274	TRP	3.1
1	A	958	GLY	3.1
1	B	226	TYR	3.0
1	B	308	ILE	3.0
1	B	228	ARG	3.0
1	B	320	LYS	3.0
1	A	1040	ALA	3.0
1	A	293	ILE	3.0
1	B	343	ALA	3.0
1	B	1044	TYR	3.0
1	A	229	SER	3.0
1	B	255	GLY	3.0
1	B	288	ASN	3.0
1	B	1038	ASP	3.0
1	A	300	THR	2.9
1	A	264	LYS	2.9
1	B	232	SER	2.8
1	B	297	TYR	2.8
1	A	233	PHE	2.8
1	B	276	SER	2.8
1	A	291	LEU	2.8
1	A	968	ALA	2.8
1	A	263	GLU	2.8
1	A	217	ASN	2.8
1	B	265	ASP	2.8
1	A	324	LEU	2.8
1	B	230	ALA	2.8
1	B	344	TRP	2.7
1	A	320	LYS	2.7
1	A	325	LYS	2.7
1	B	330	LEU	2.7
1	B	314	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	278	GLU	2.7
1	A	316	LYS	2.7
1	B	964	VAL	2.7
1	B	281	ARG	2.7
1	B	960	GLN	2.6
1	B	312	THR	2.6
1	B	339	LYS	2.6
1	A	583	GLY	2.5
1	B	321	ILE	2.5
1	B	1039	GLN	2.5
1	B	1032	ALA	2.5
1	A	579	PRO	2.5
1	A	593	LYS	2.5
1	A	312	THR	2.5
1	B	322	THR	2.5
1	A	589	GLU	2.5
1	A	215	ARG	2.5
1	A	249	LYS	2.5
1	A	576	GLU	2.4
1	A	581	VAL	2.4
1	B	285	ASN	2.4
1	B	303	GLN	2.4
1	B	341	GLN	2.4
1	B	261	SER	2.4
1	A	228	ARG	2.4
1	A	326	ASN	2.4
1	B	247	ARG	2.4
1	B	801	ASP	2.4
1	B	1035	VAL	2.4
1	B	239	TYR	2.4
1	B	368	LYS	2.4
1	A	606	GLU	2.4
1	A	216	SER	2.3
1	B	342	SER	2.3
1	B	338	VAL	2.3
1	A	222	TYR	2.3
1	B	263	GLU	2.3
1	B	294	ASN	2.3
1	A	311	ALA	2.3
1	A	342	SER	2.3
1	A	257	THR	2.3
1	B	319	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	1018	SER	2.2
1	A	225	VAL	2.2
1	B	525	LEU	2.2
1	B	315	ALA	2.2
1	B	301	SER	2.2
1	A	258	TRP	2.2
1	B	526	ASN	2.2
1	B	767	ASP	2.2
1	B	957	GLU	2.2
1	A	954	LYS	2.2
1	A	323	THR	2.2
1	B	968	ALA	2.2
1	A	964	VAL	2.2
1	A	582	VAL	2.1
1	A	220	LYS	2.1
1	A	250	TYR	2.1
1	A	256	LYS	2.1
1	A	301	SER	2.1
1	A	960	GLN	2.1
1	A	354	ASP	2.1
1	A	580	ASN	2.1
1	B	307	ASN	2.1
1	B	277	GLN	2.0
1	A	302	ASN	2.0
1	B	317	ILE	2.0
1	A	252	LEU	2.0
1	B	298	ASP	2.0
1	A	608	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

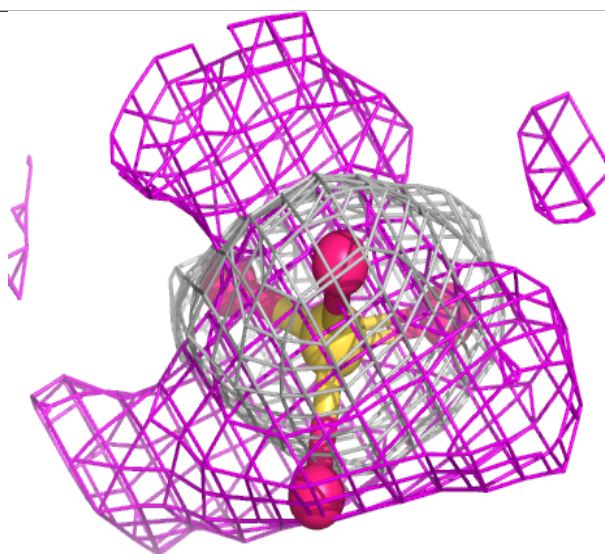
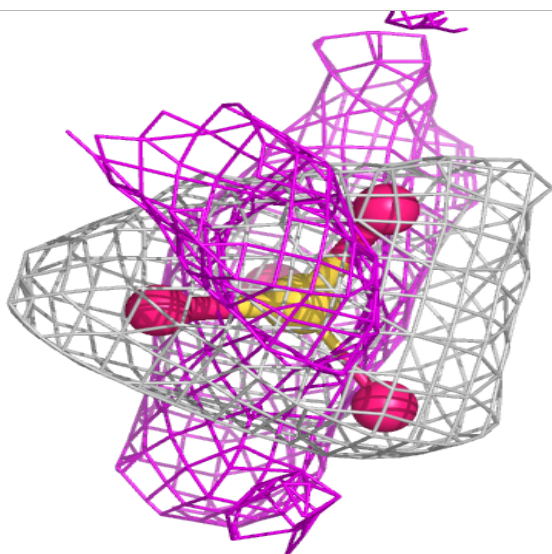
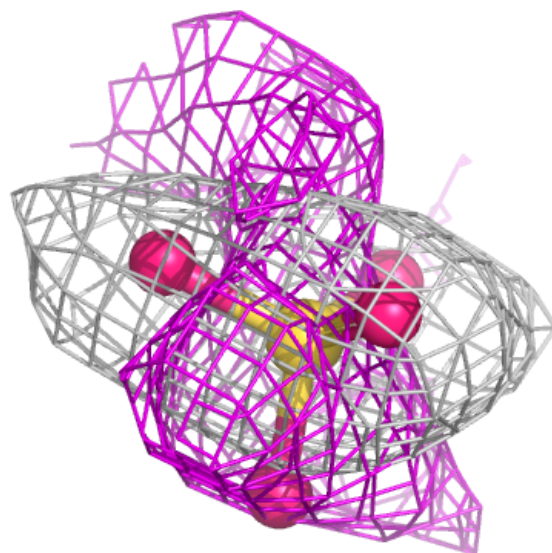
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	SO4	A	1212	5/5	0.59	0.14	79,85,101,104	0
5	SO4	A	1211	5/5	0.67	0.13	101,107,115,115	0
5	SO4	A	1207	5/5	0.68	0.14	105,107,116,125	0
5	SO4	A	1205	5/5	0.70	0.12	113,122,125,127	0
5	SO4	A	1206	5/5	0.73	0.12	107,118,124,125	0
5	SO4	B	1206	5/5	0.74	0.13	106,114,122,124	0
5	SO4	B	1208	5/5	0.77	0.11	85,87,98,101	0
5	SO4	B	1215	5/5	0.77	0.09	103,105,112,122	0
5	SO4	B	1204	5/5	0.78	0.18	68,78,103,111	0
5	SO4	A	1210	5/5	0.78	0.14	84,99,104,109	0
5	SO4	B	1214	5/5	0.79	0.12	90,103,108,112	0
5	SO4	B	1207	5/5	0.79	0.11	108,111,117,122	0
5	SO4	B	1209	5/5	0.80	0.23	90,103,118,126	0
3	XV5	B	1202	20/20	0.81	0.21	62,81,90,91	0
5	SO4	B	1213	5/5	0.81	0.11	86,91,98,100	0
3	XV5	A	1202	20/20	0.82	0.22	72,84,95,100	0
5	SO4	A	1213	5/5	0.82	0.14	85,97,100,105	0
5	SO4	A	1208	5/5	0.86	0.11	87,97,100,109	0
5	SO4	A	1209	5/5	0.86	0.12	68,74,94,104	0
5	SO4	B	1210	5/5	0.87	0.12	94,98,107,107	0
5	SO4	B	1212	5/5	0.88	0.10	80,83,92,97	0
5	SO4	B	1211	5/5	0.88	0.12	81,82,88,95	0
5	SO4	B	1217	5/5	0.88	0.13	111,112,122,126	0
5	SO4	B	1216	5/5	0.89	0.13	94,112,115,122	0
4	BTB	B	1203	14/14	0.89	0.20	52,70,78,82	0
2	CA	B	1218	1/1	0.90	0.15	85,85,85,85	0
4	BTB	A	1203	14/14	0.93	0.15	52,77,86,97	0
5	SO4	A	1204	5/5	0.94	0.07	70,71,80,80	0
5	SO4	B	1205	5/5	0.96	0.10	67,69,73,76	0
2	CA	A	1201	1/1	0.99	0.05	40,40,40,40	0
2	CA	B	1201	1/1	1.00	0.02	42,42,42,42	0

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

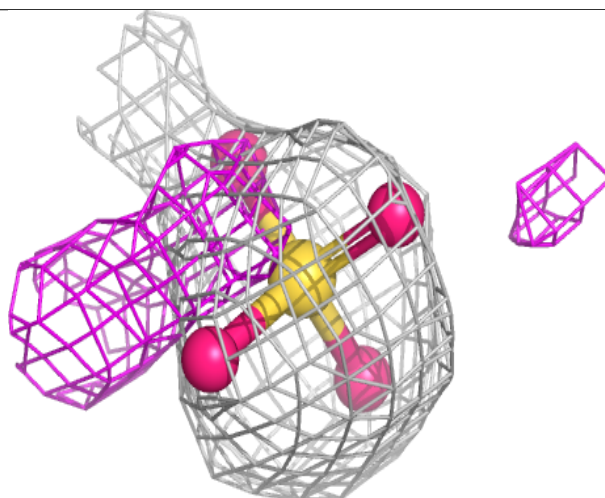
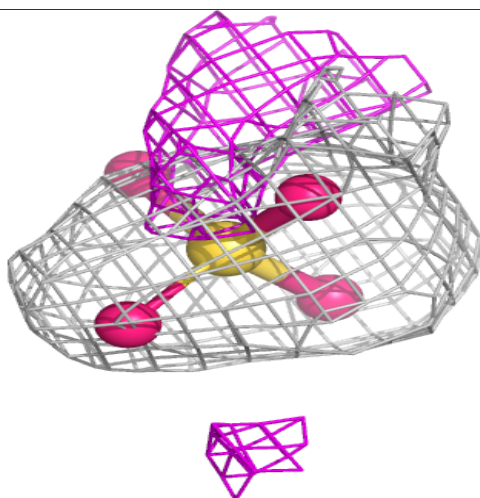
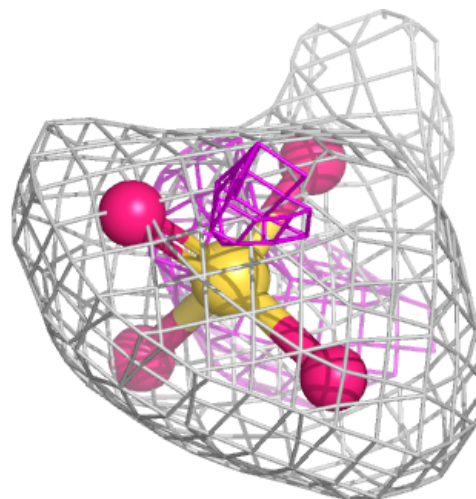
Electron density around SO4 A 1212:

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



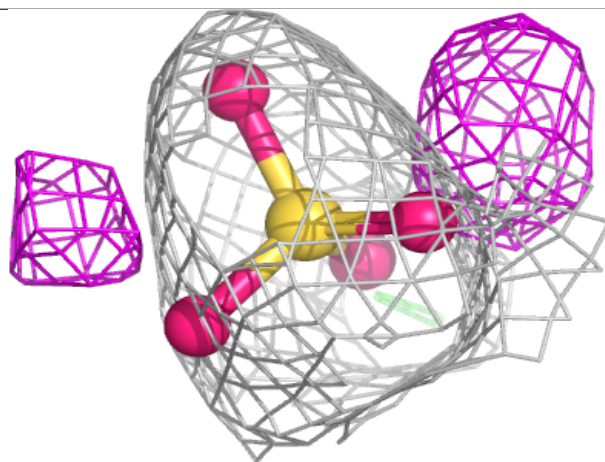
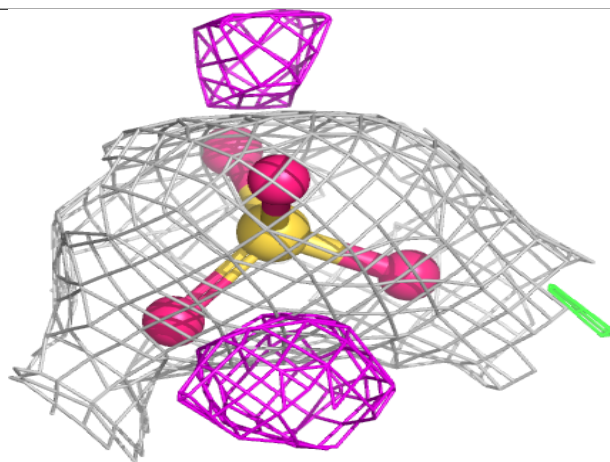
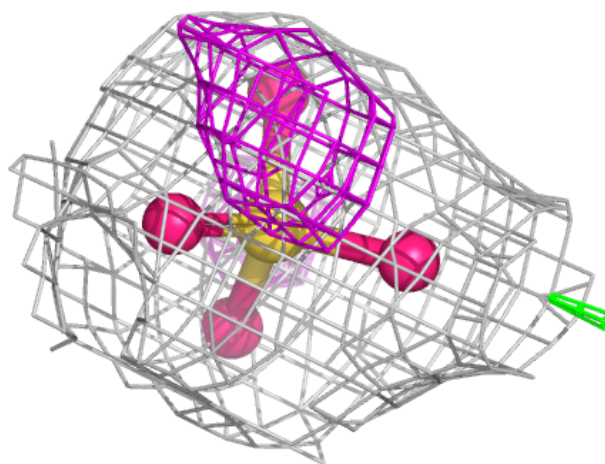
Electron density around SO4 A 1211:

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and green (positive)



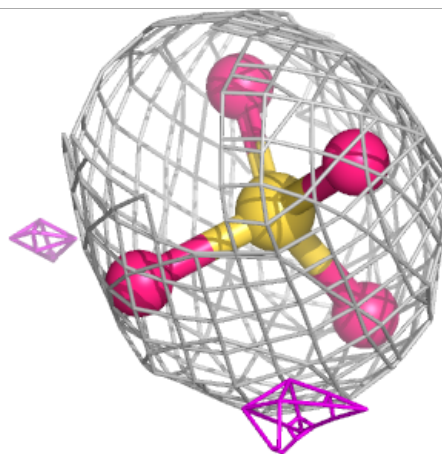
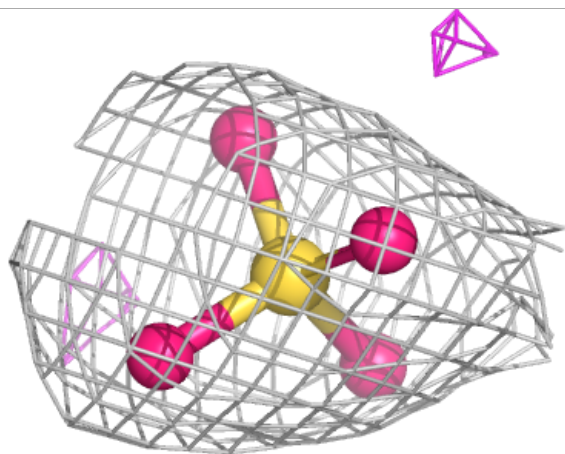
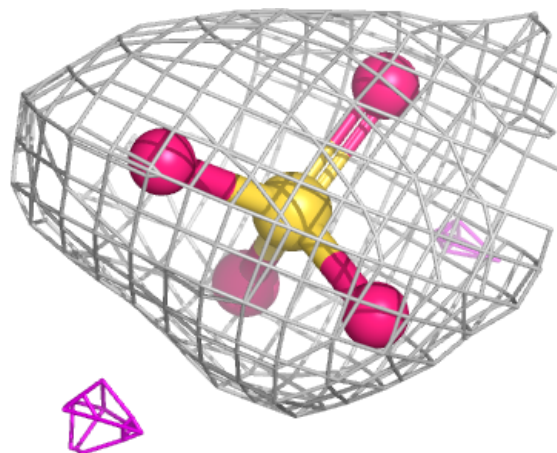
Electron density around SO4 A 1207:

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



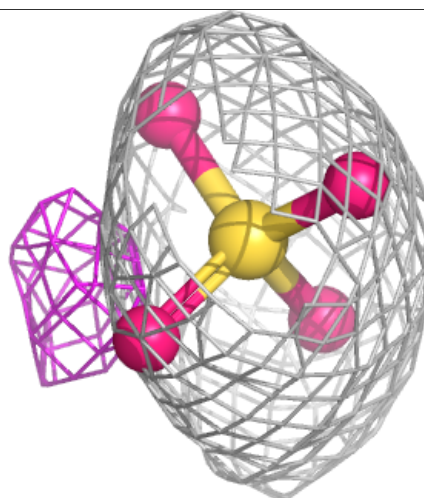
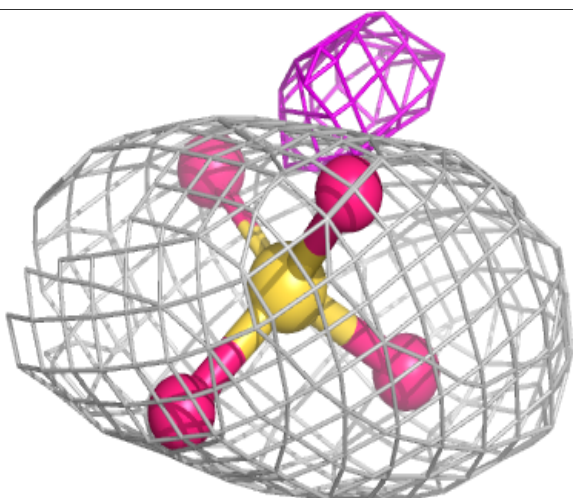
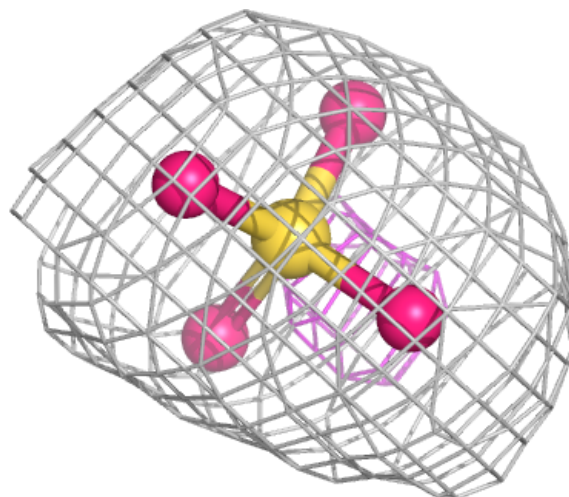
Electron density around SO4 A 1205:

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



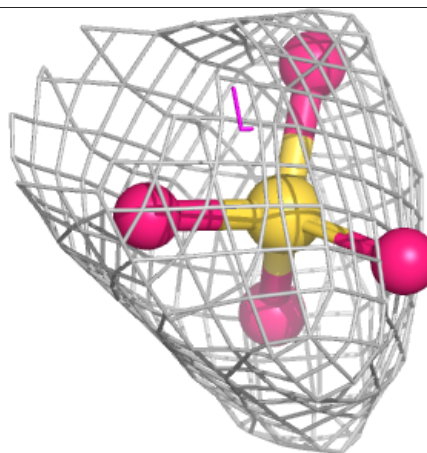
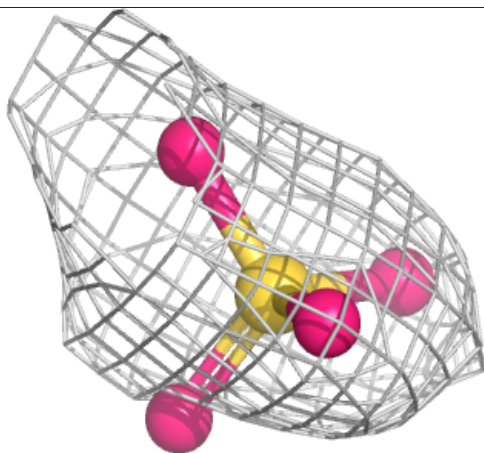
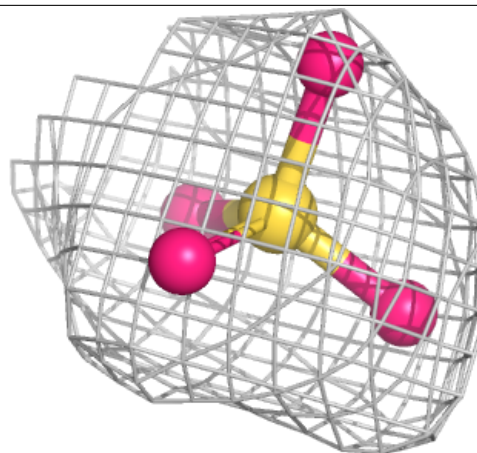
Electron density around SO4 A 1206:

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and green (positive)



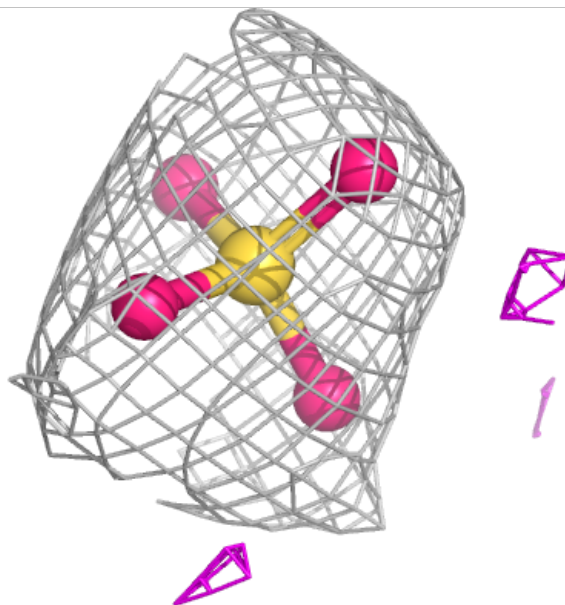
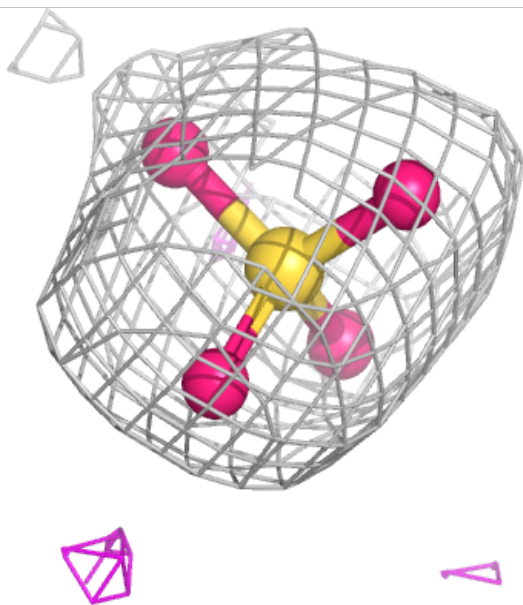
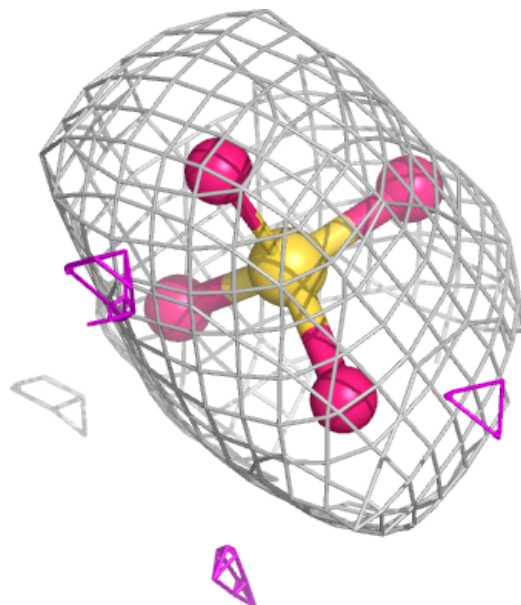
Electron density around SO4 B 1206:

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



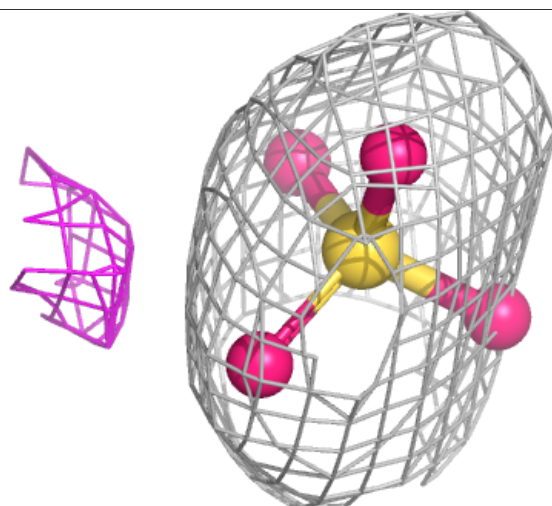
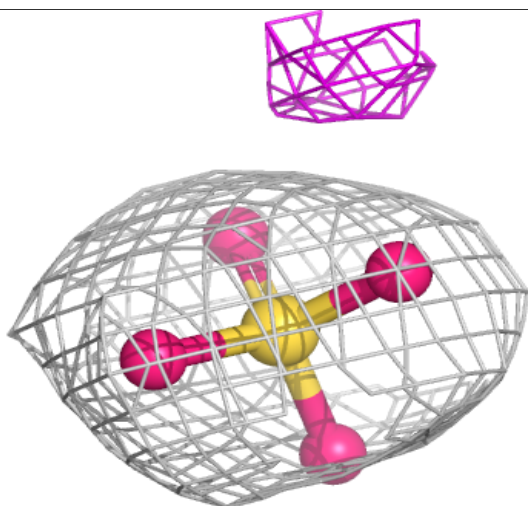
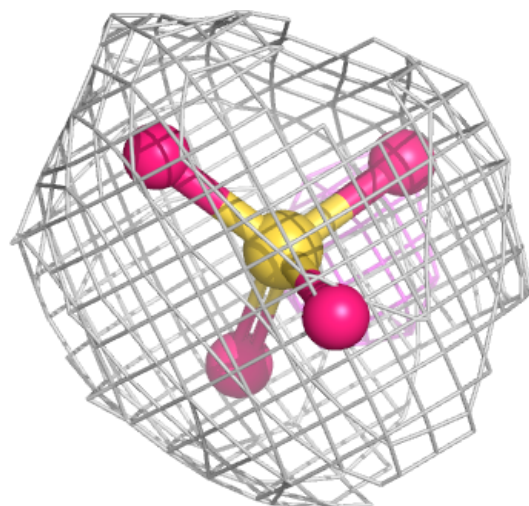
Electron density around SO4 B 1208:

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



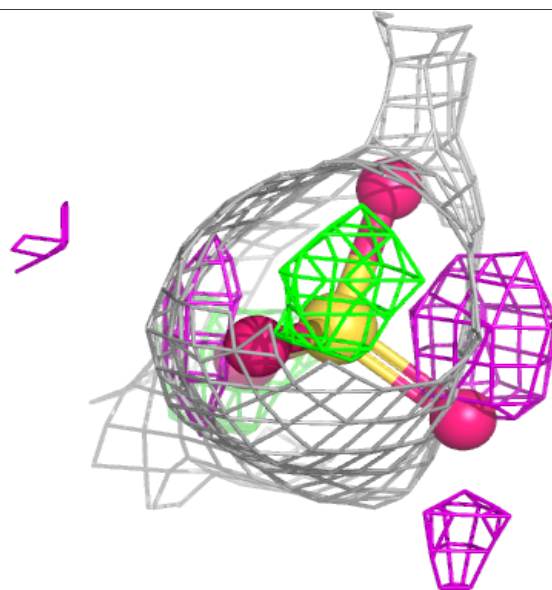
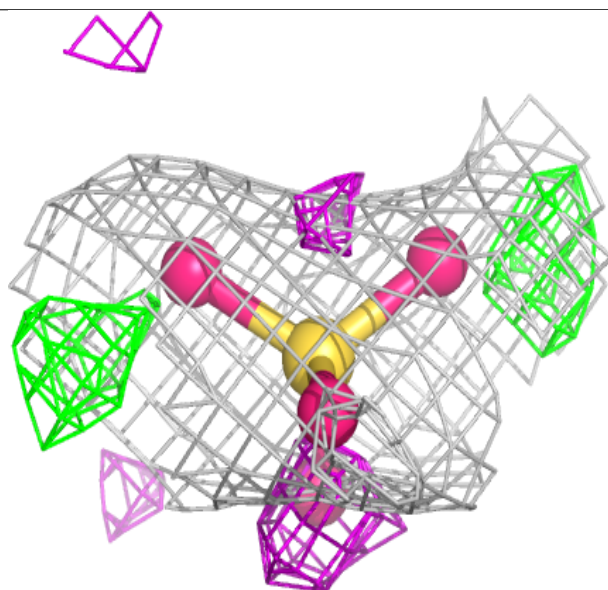
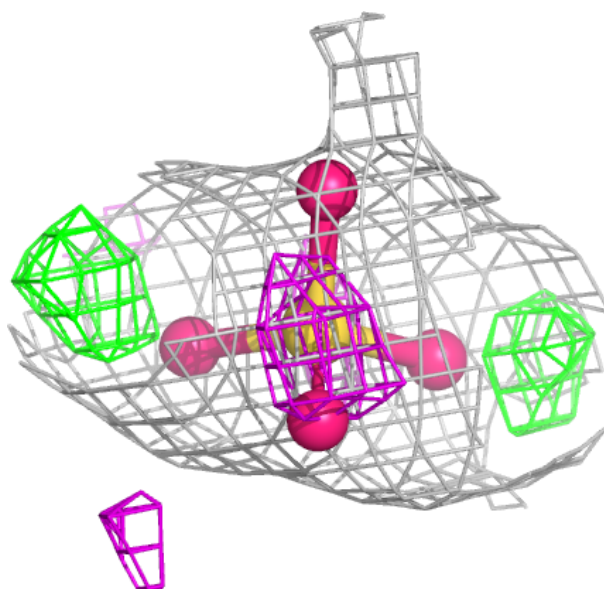
Electron density around SO4 B 1215:

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



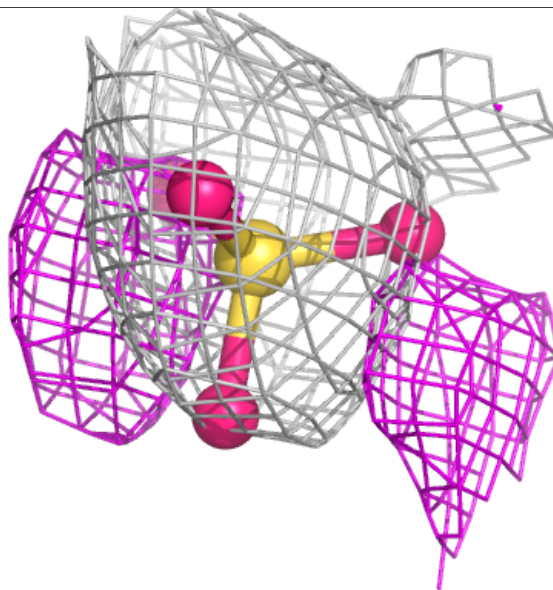
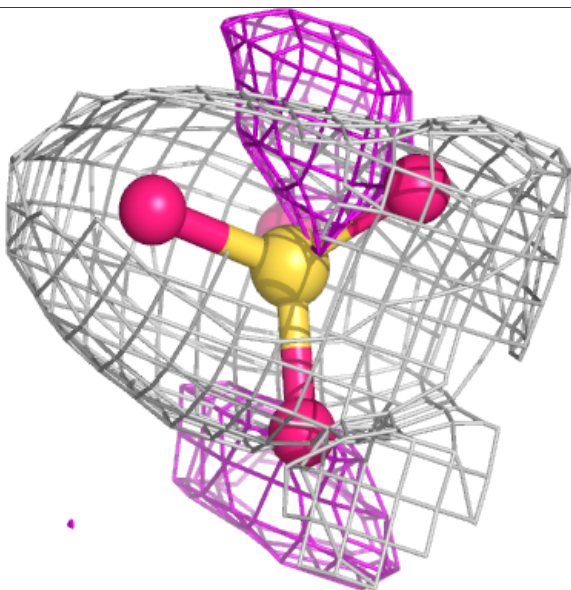
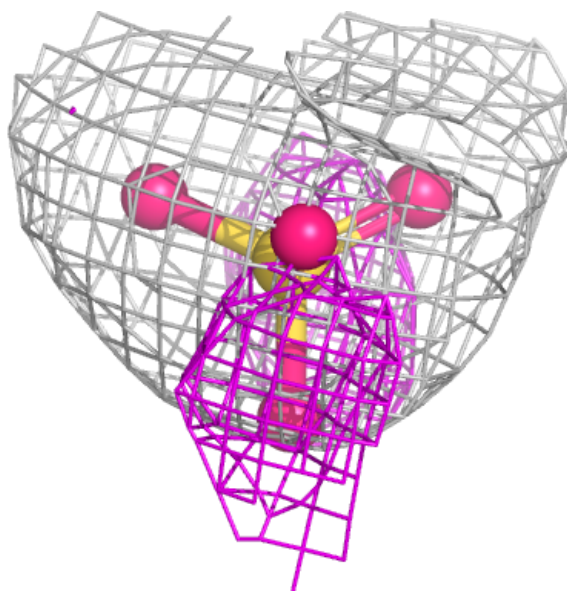
Electron density around SO4 B 1204:

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and green (positive)



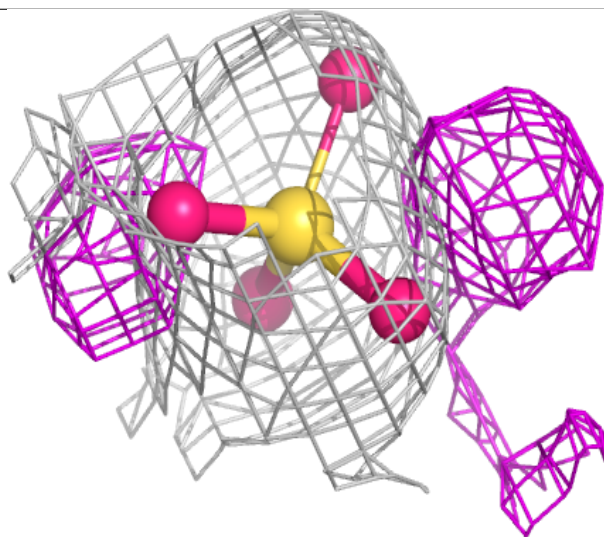
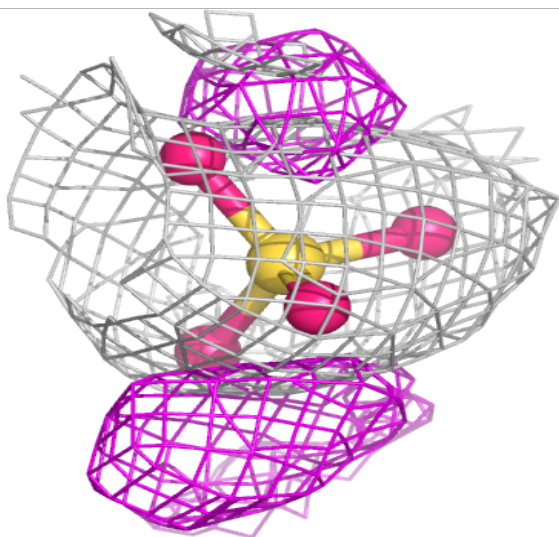
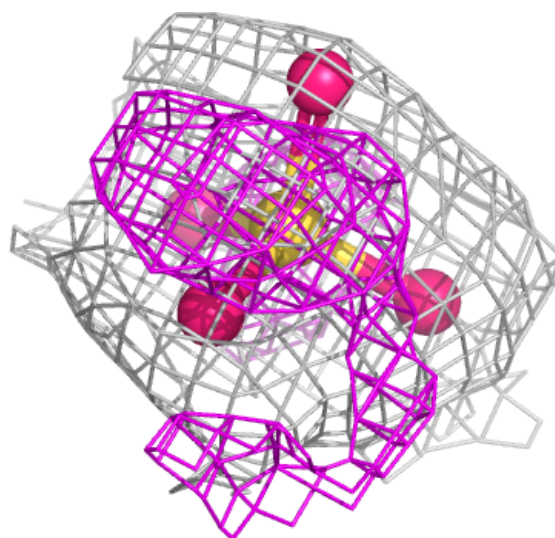
Electron density around SO4 A 1210:

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



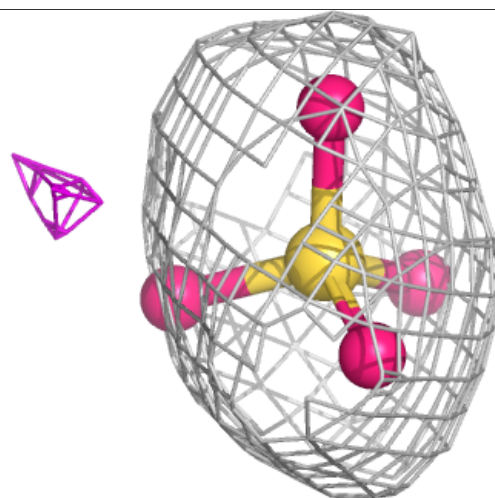
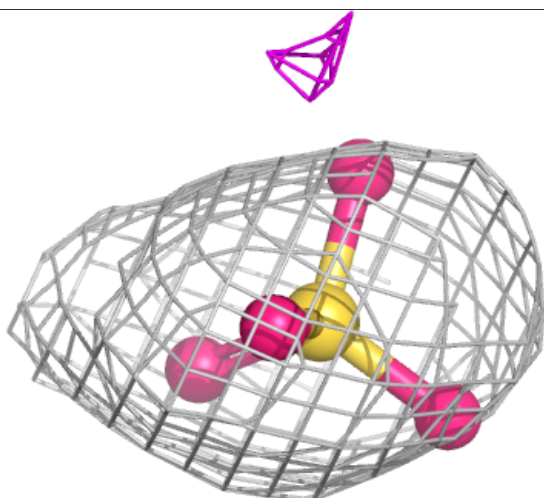
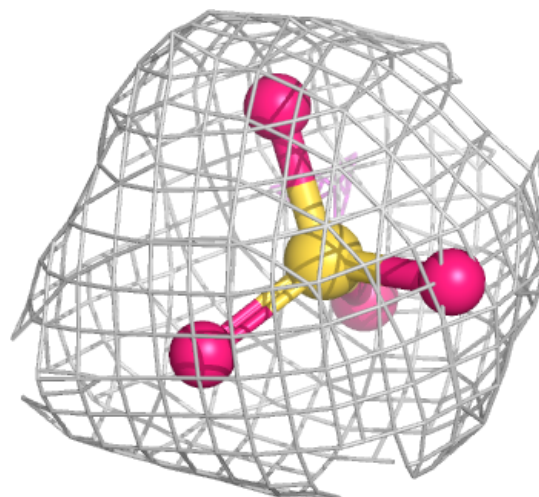
Electron density around SO4 B 1214:

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and green (positive)



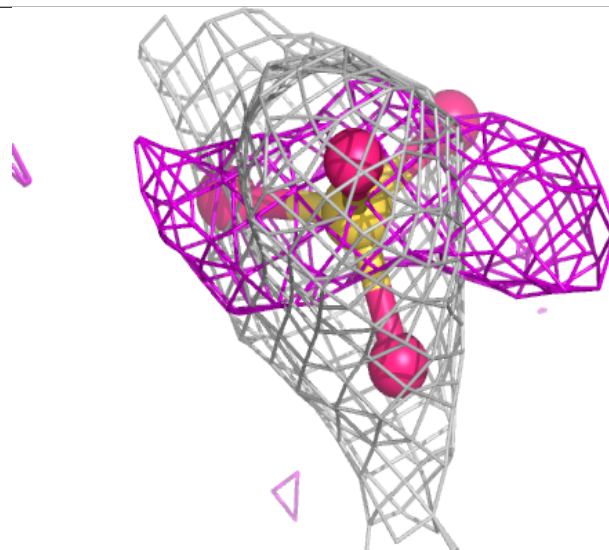
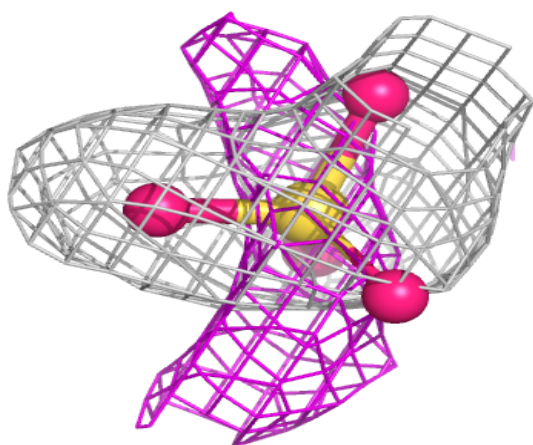
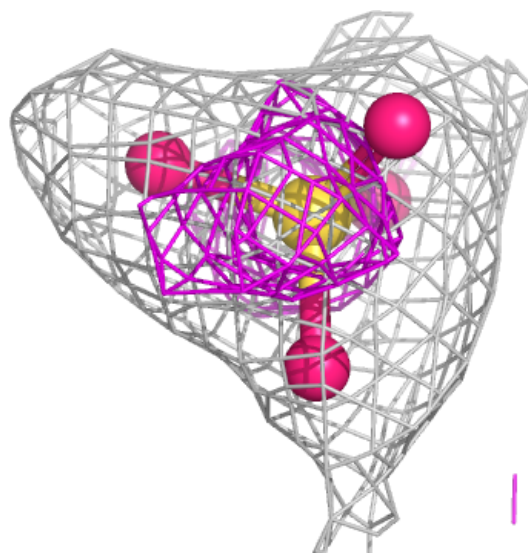
Electron density around SO4 B 1207:

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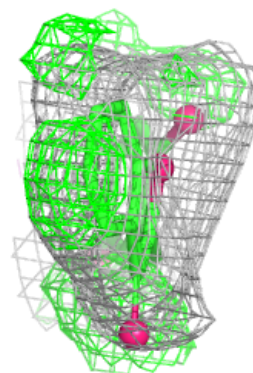
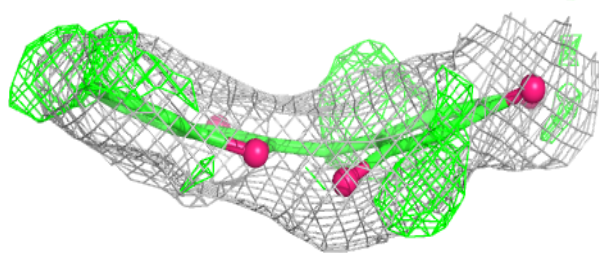
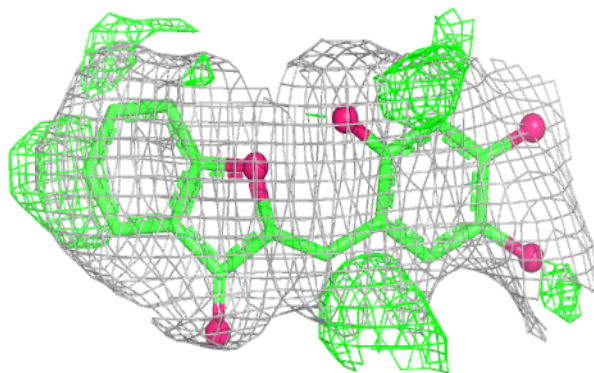
Electron density around SO4 B 1209:

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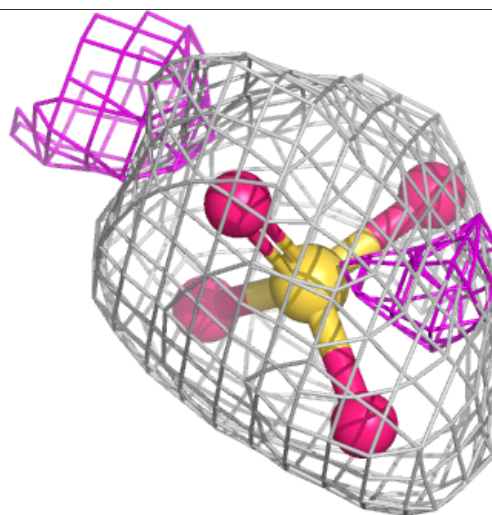
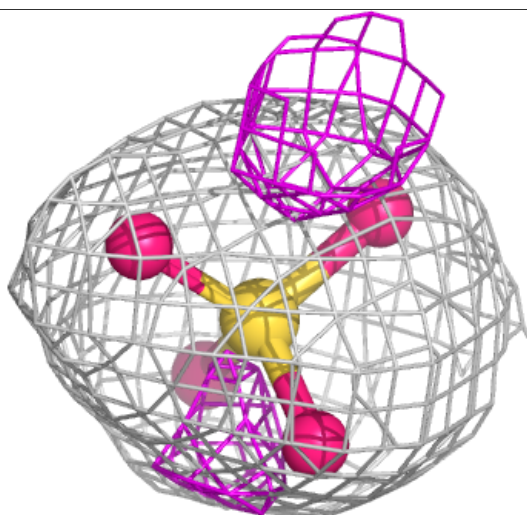
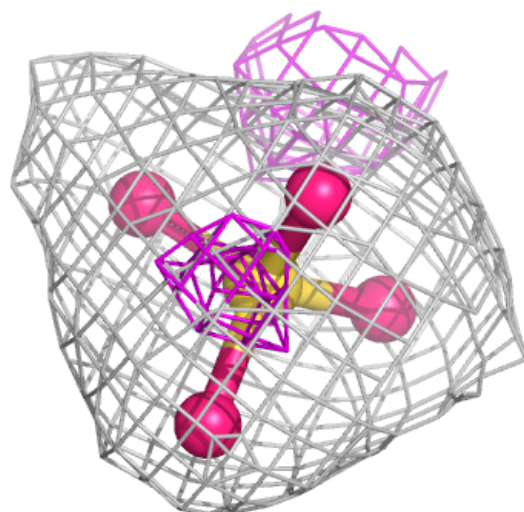
Electron density around XV5 B 1202:

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



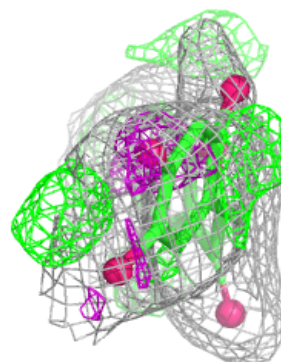
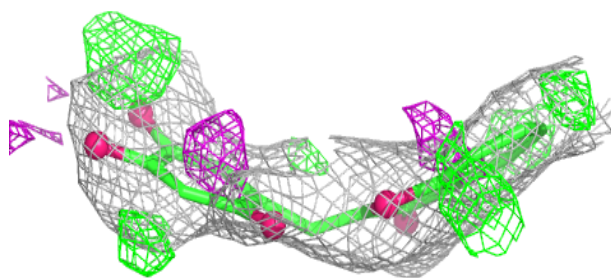
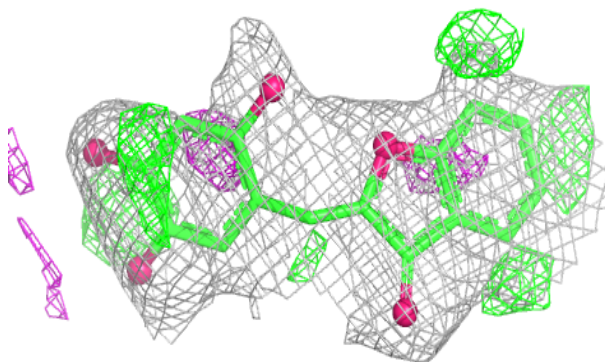
Electron density around SO4 B 1213:

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



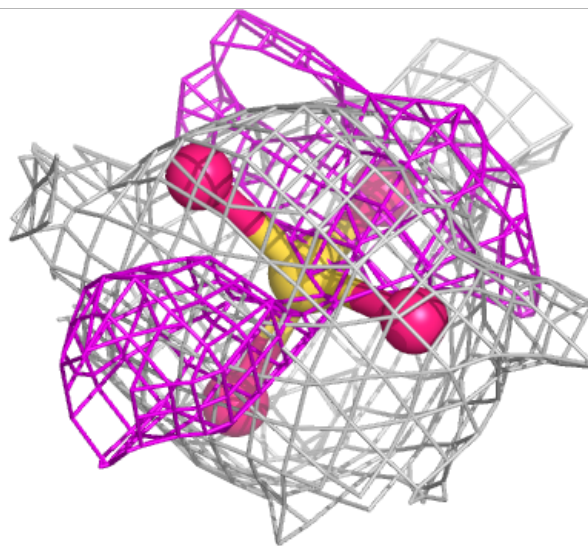
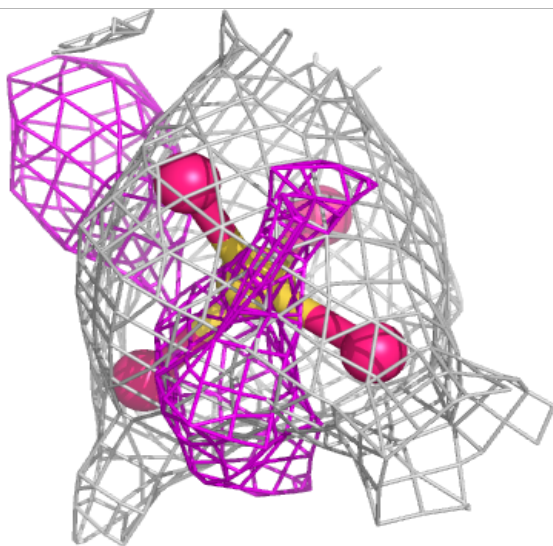
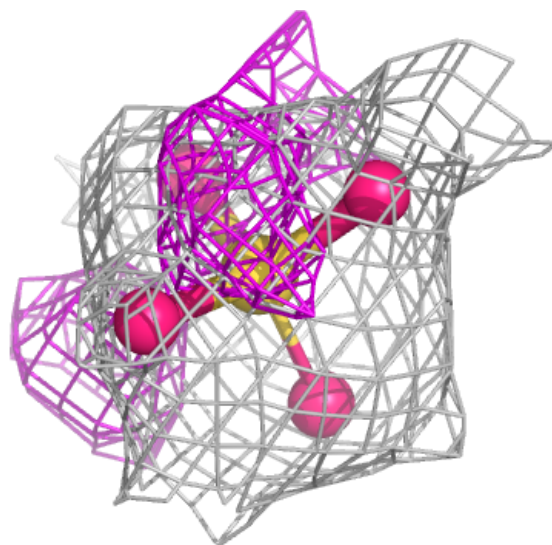
Electron density around XV5 A 1202:

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and green (positive)



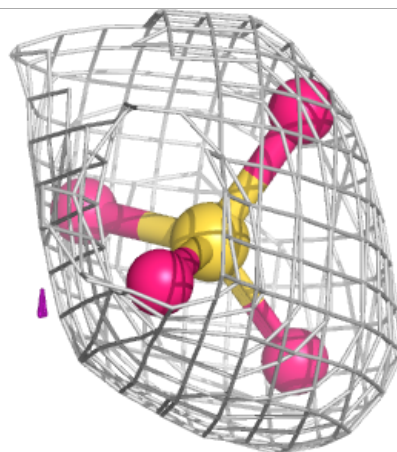
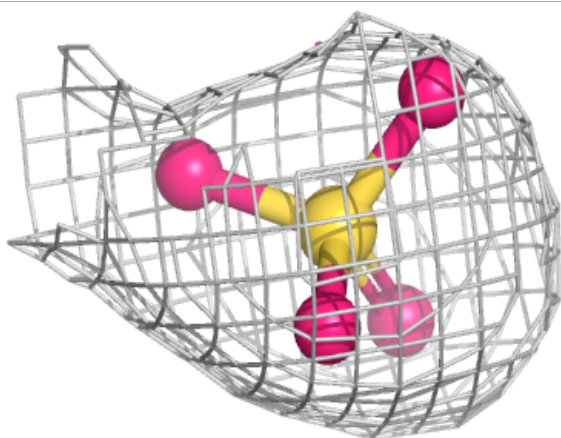
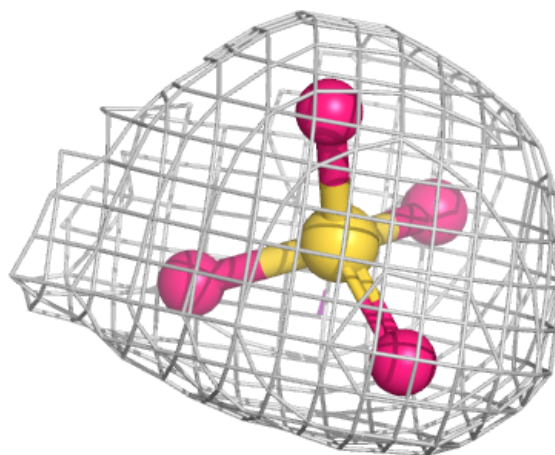
Electron density around SO4 A 1213:

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



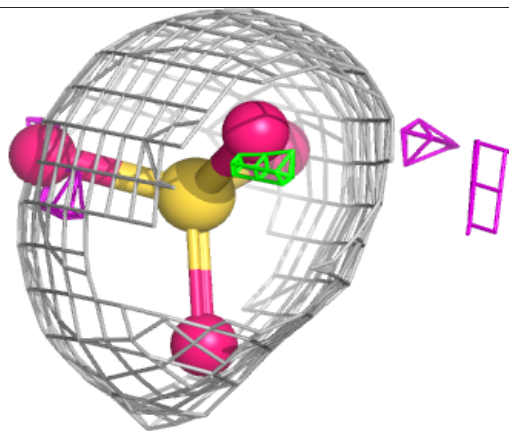
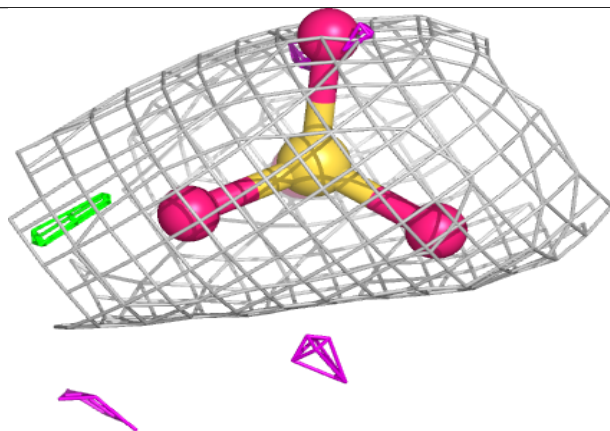
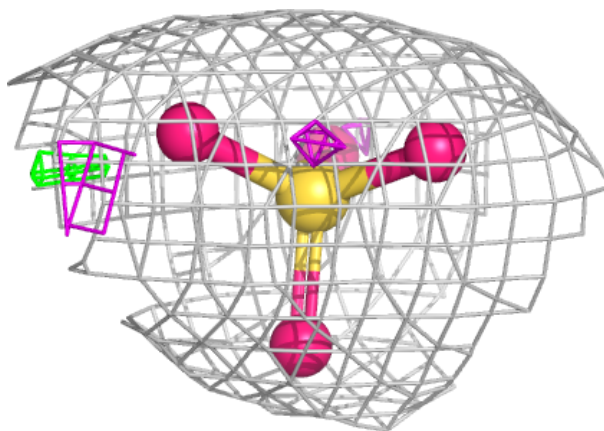
Electron density around SO4 A 1208:

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



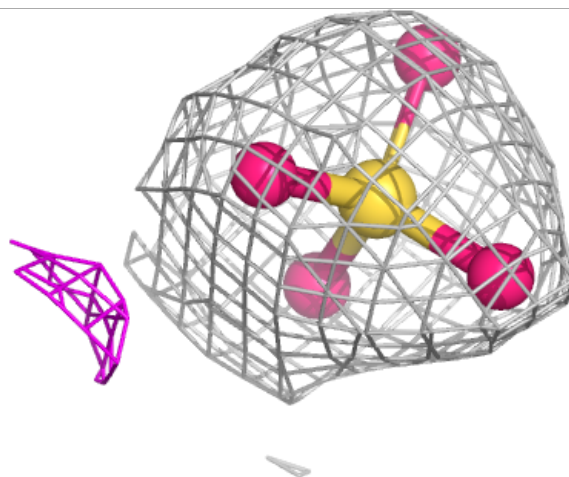
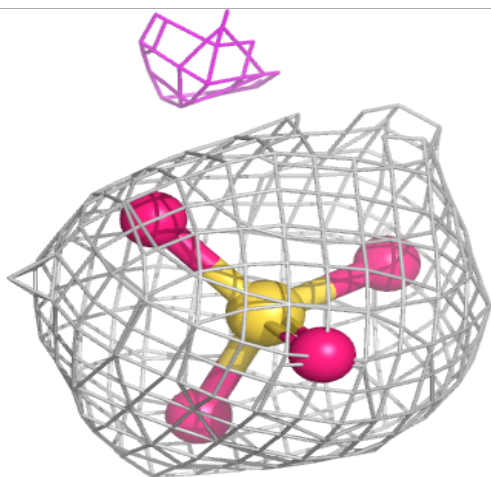
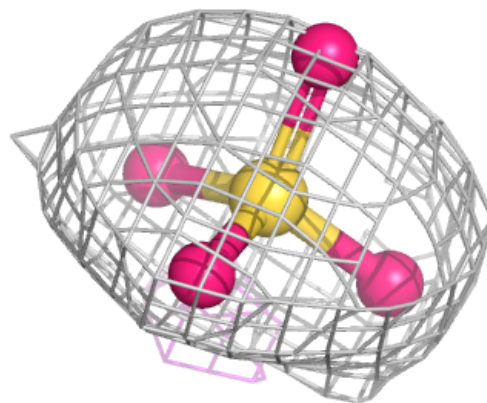
Electron density around SO4 A 1209:

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



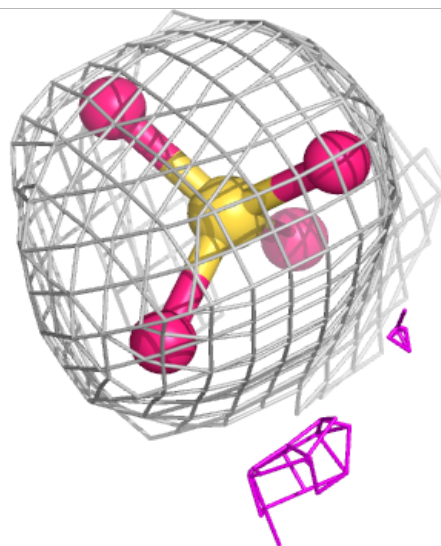
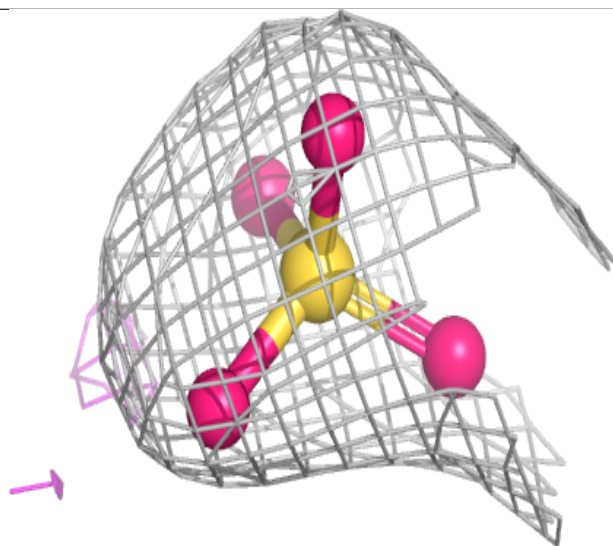
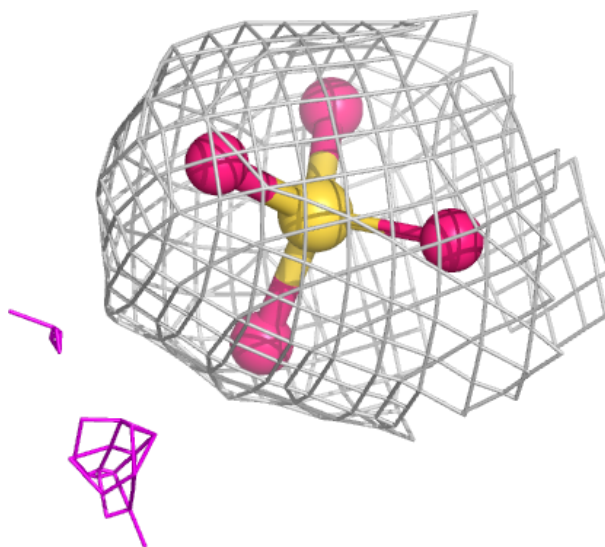
Electron density around SO4 B 1210:

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



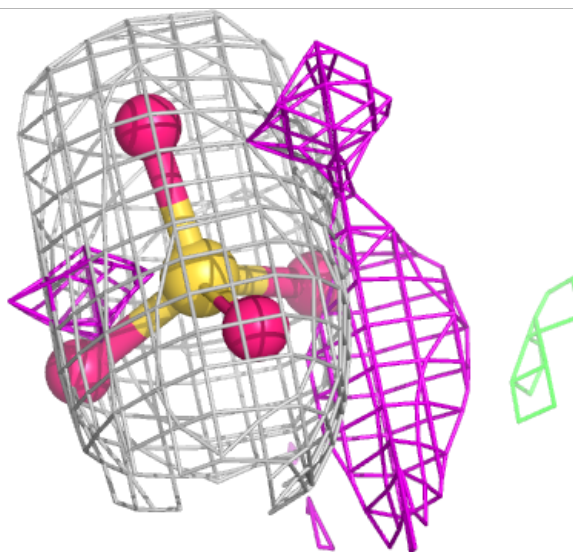
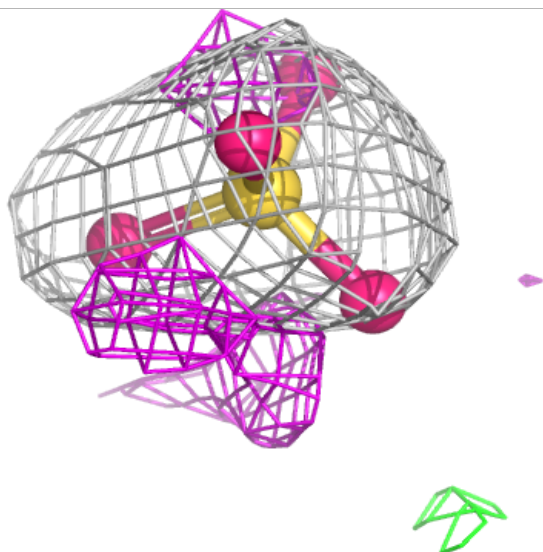
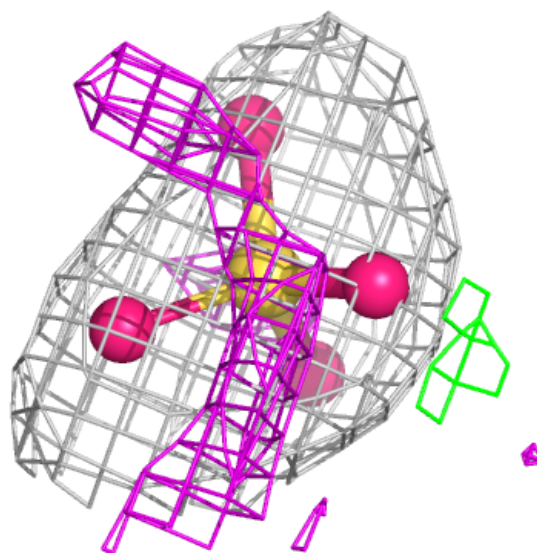
Electron density around SO4 B 1212:

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



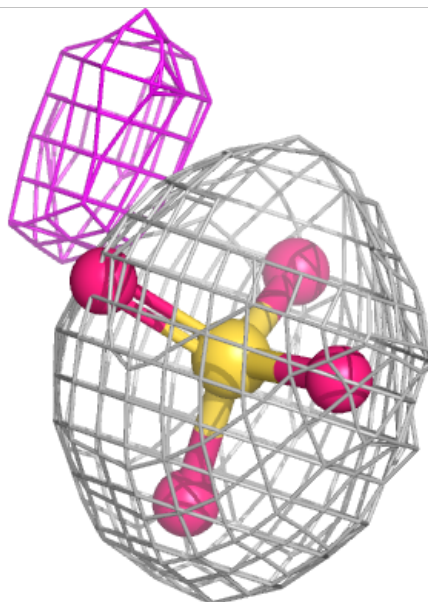
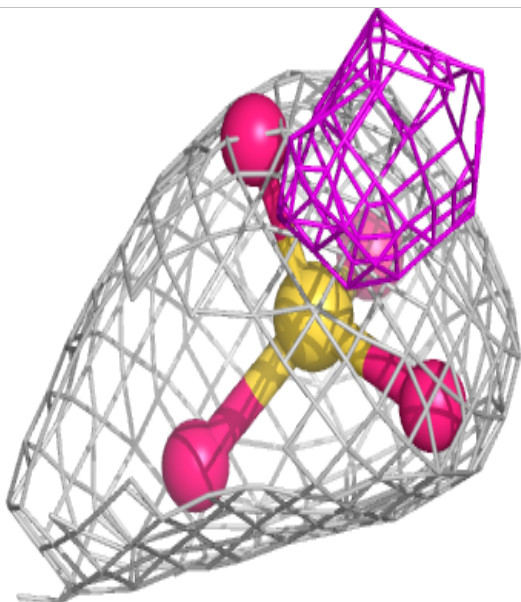
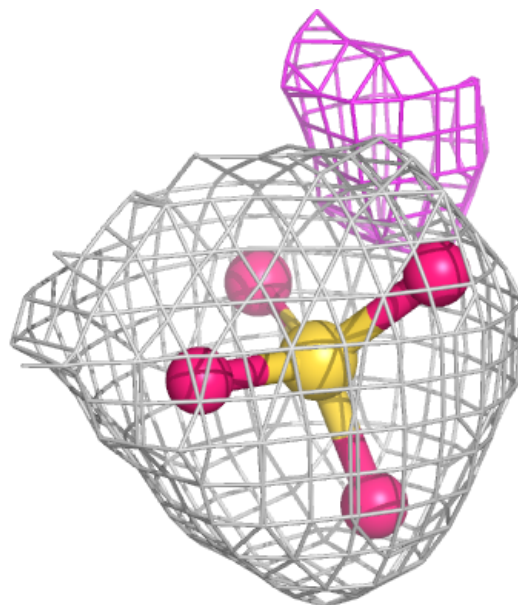
Electron density around SO4 B 1211:

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



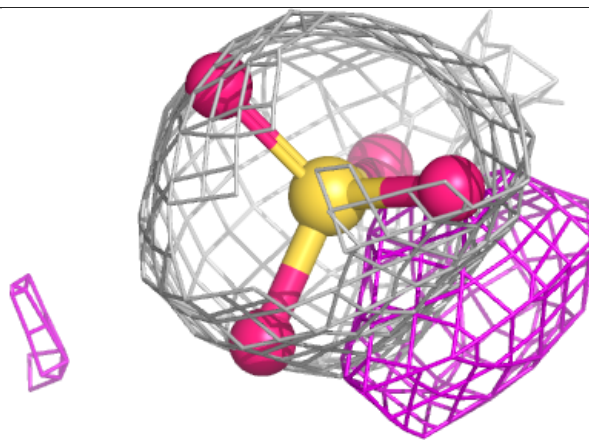
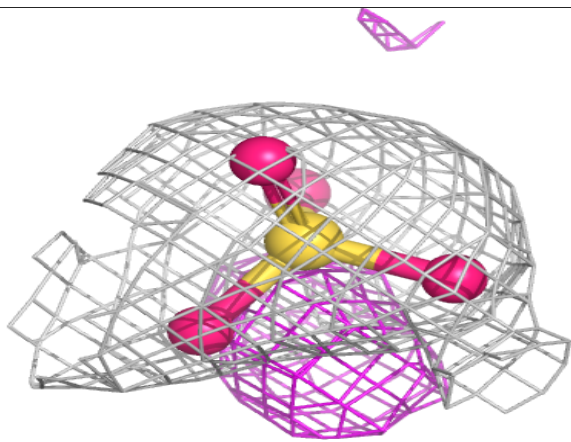
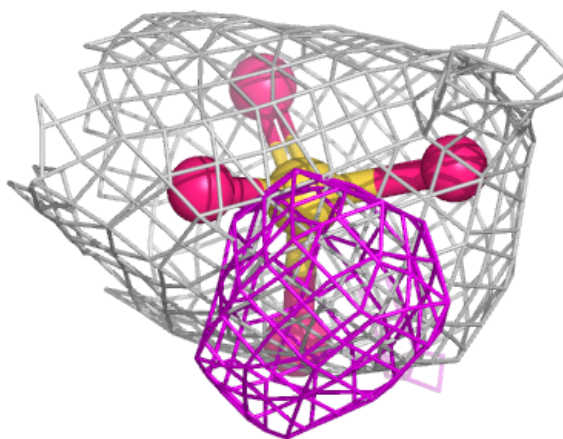
Electron density around SO4 B 1217:

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



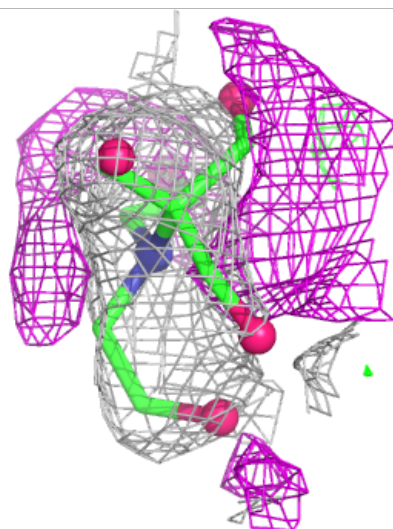
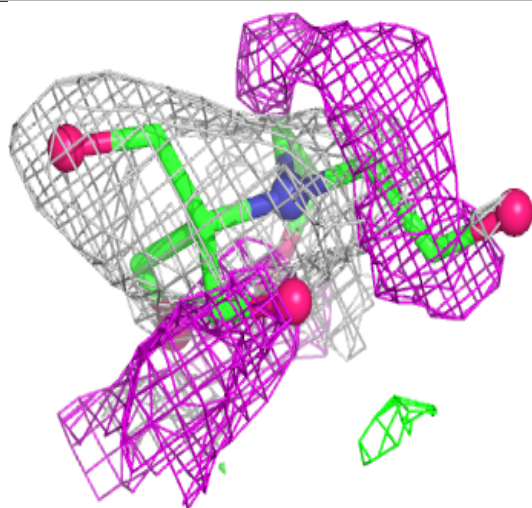
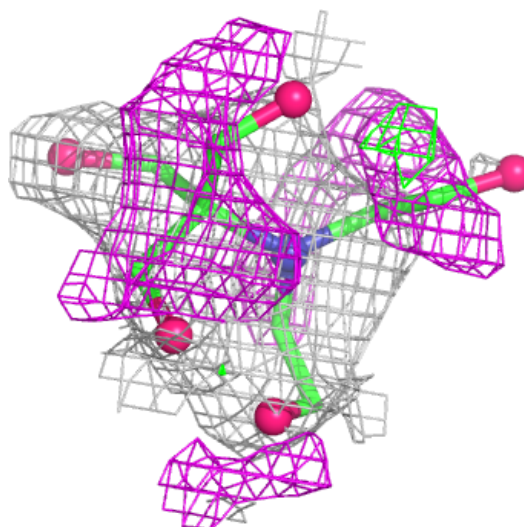
Electron density around SO4 B 1216:

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



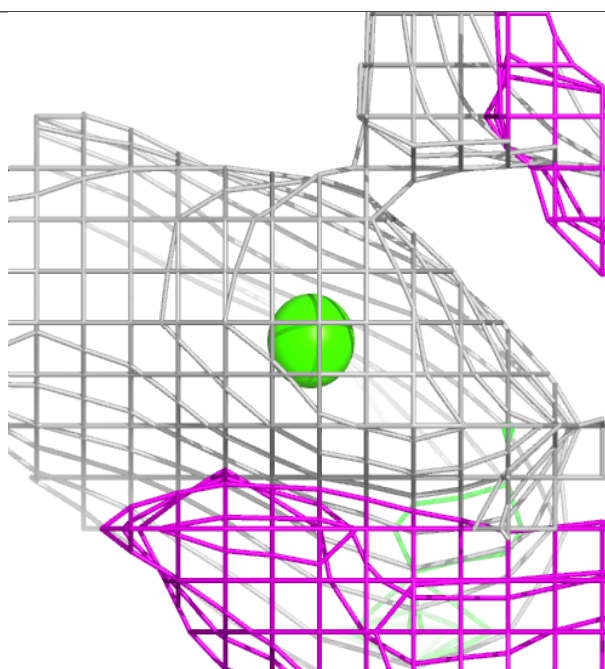
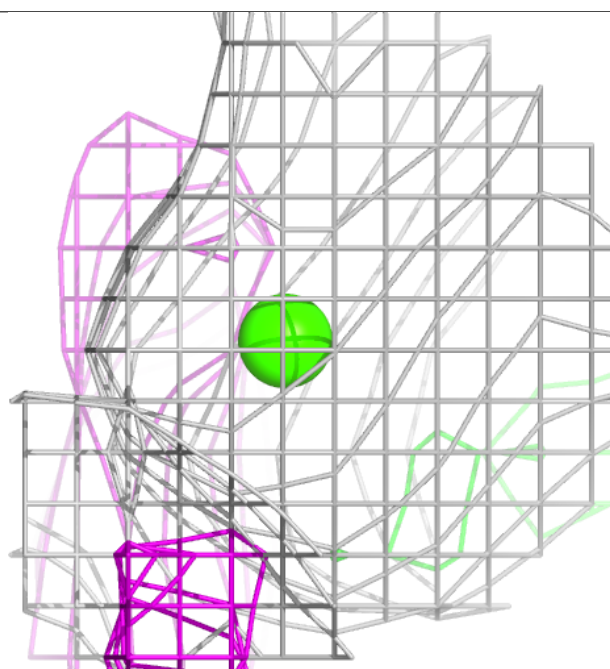
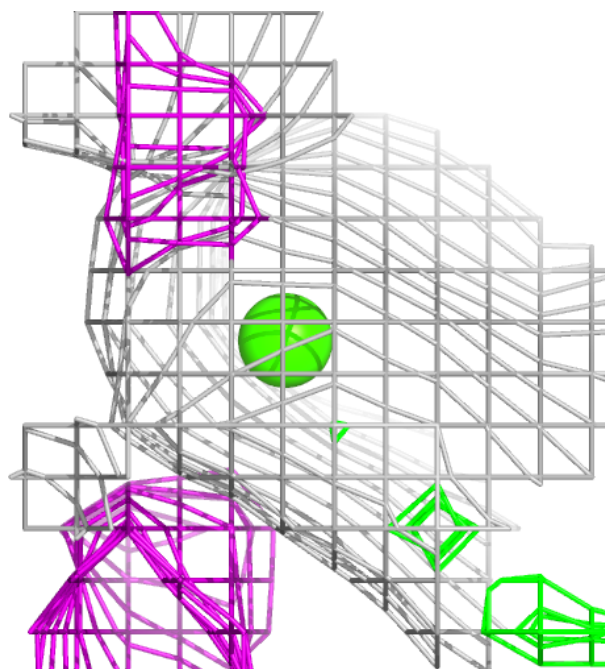
Electron density around BTB B 1203:

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



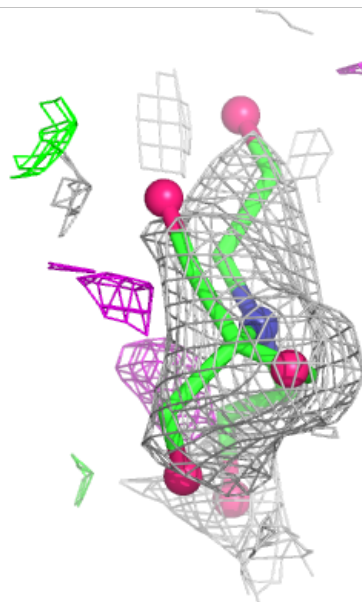
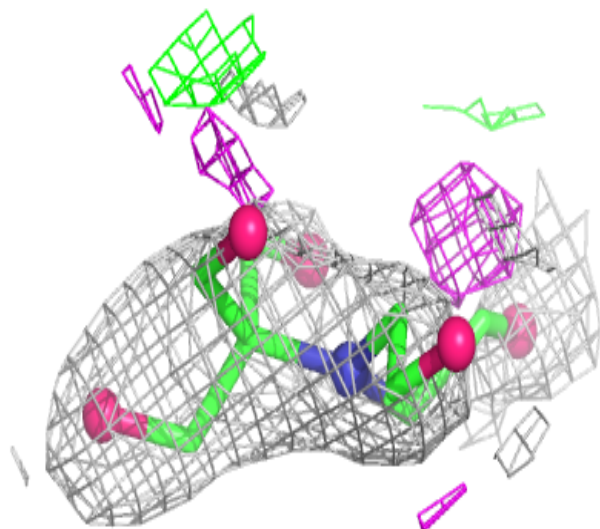
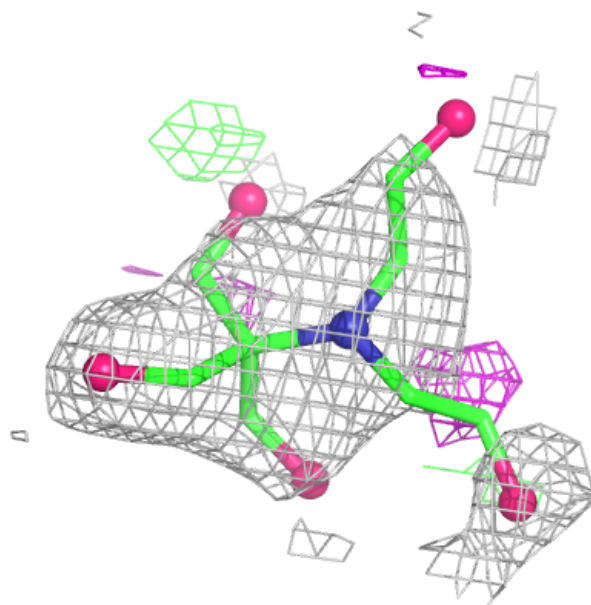
Electron density around CA B 1218:

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



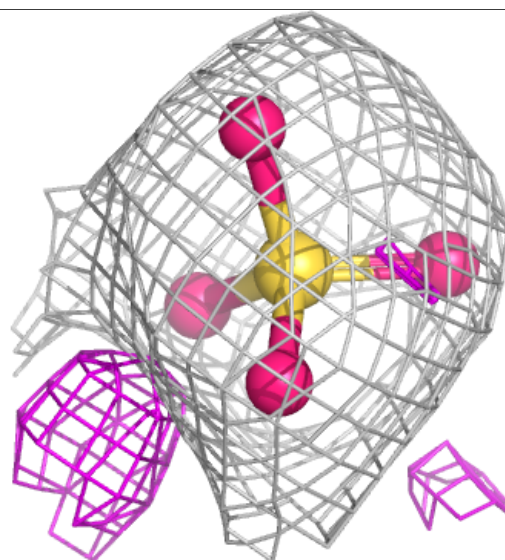
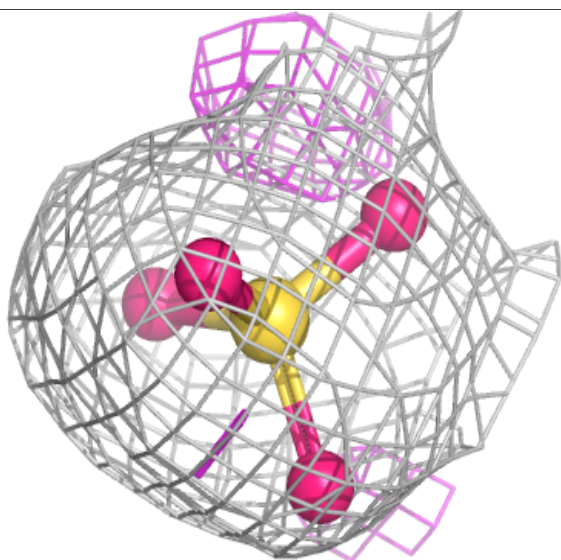
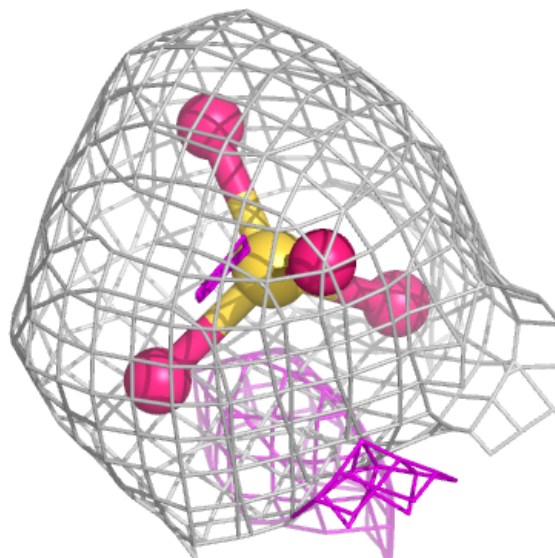
Electron density around BTB A 1203:

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



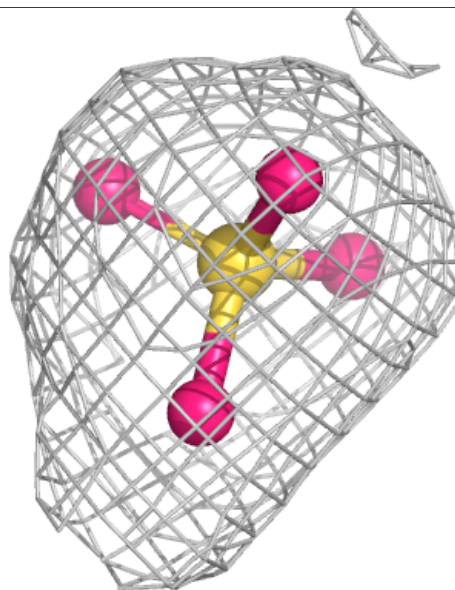
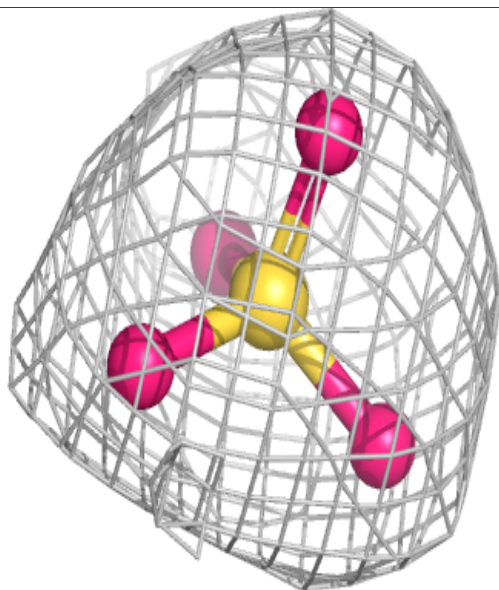
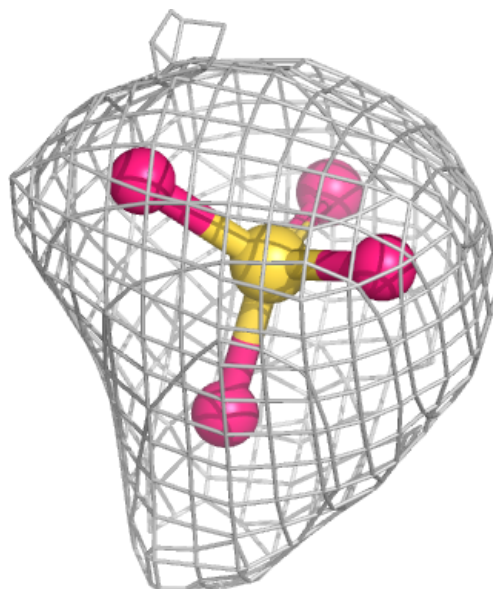
Electron density around SO4 A 1204:

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



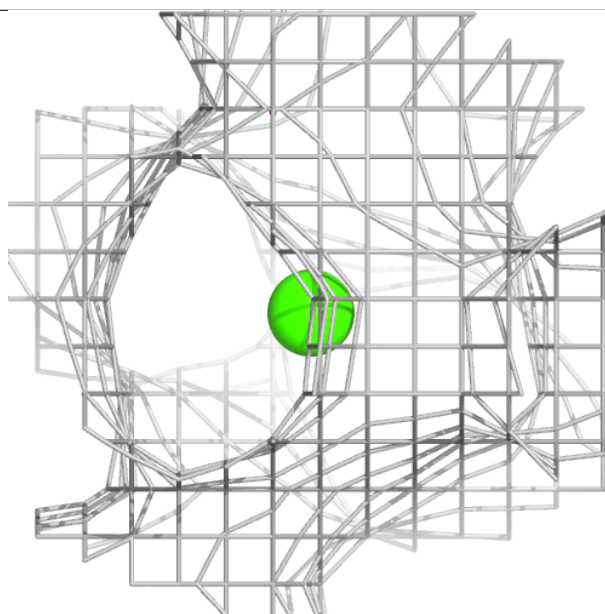
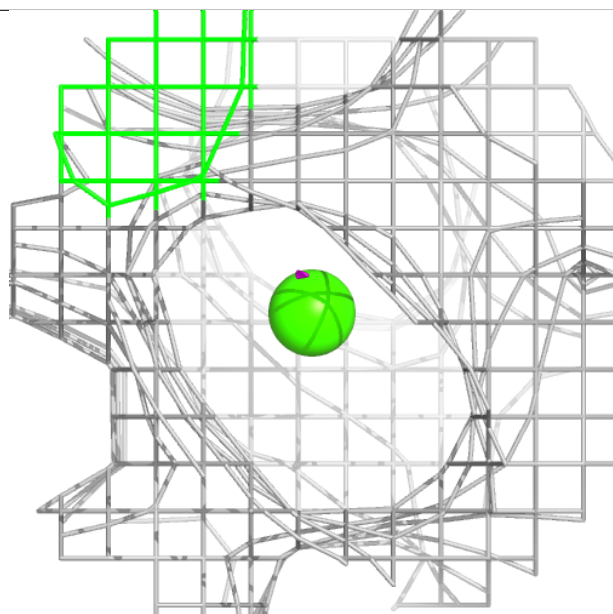
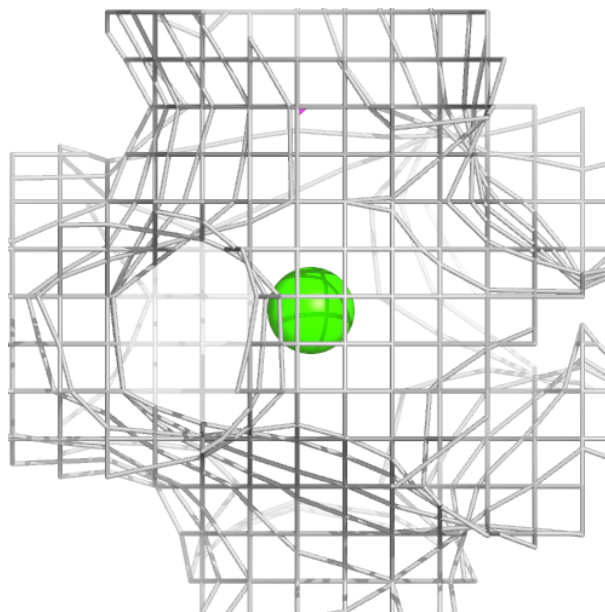
Electron density around SO4 B 1205:

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



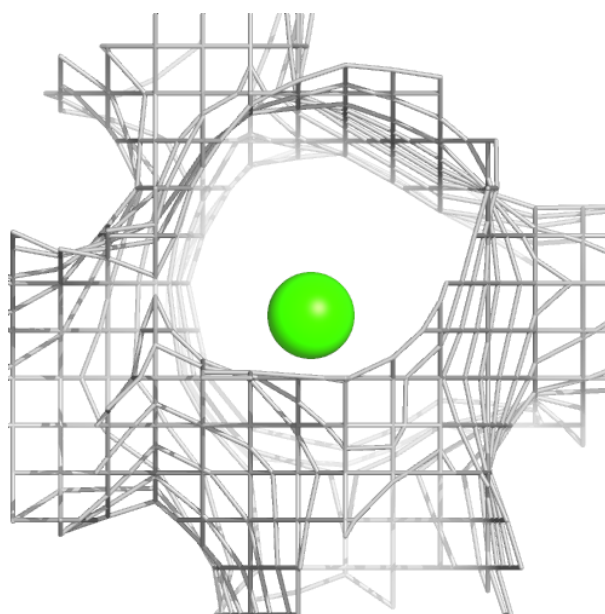
Electron density around CA A 1201:

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



Electron density around CA B 1201:

$2mF_o-DF_c$ (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.