wwPDB X-ray Structure Validation Summary Report (i)

Feb 28, 2023 – 12:36 PM EST

PDB ID	:	8FF9
Title	:	Crystal structure of Apo Dps protein (PA0962) from Pseudomonas aeruginosa (orthorhombic form)
Authors	:	Lovell, S.; Kashipathy, M.M.; Battaile, K.P.; Rivera, M.
Deposited on	:	2022-12-08
Resolution	:	1.70 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

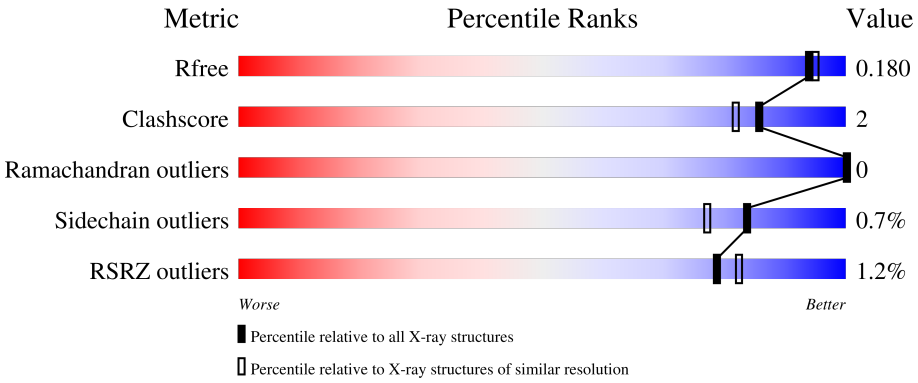
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.32.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.32.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 <=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	156	94% 6%
1	B	156	91% 9%
1	C	156	3% 94% 6%
1	D	156	97%
1	E	156	94% 6%

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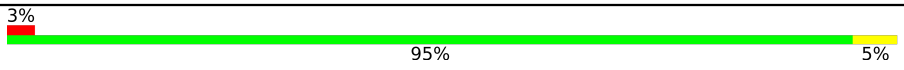
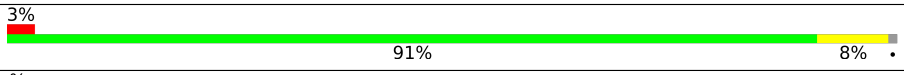
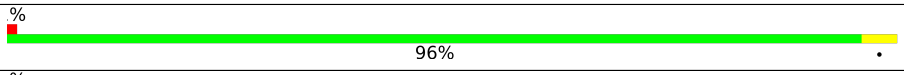
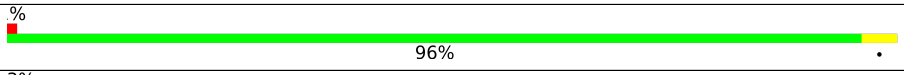
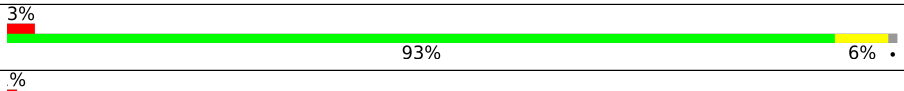
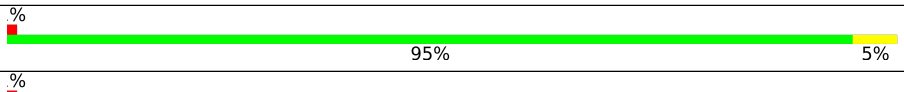
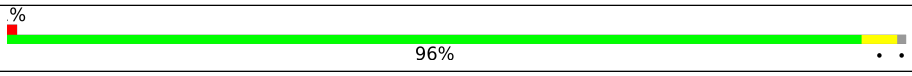
Mol	Chain	Length	Quality of chain
1	F	156	
1	G	156	
1	H	156	
1	I	156	
1	J	156	
1	K	156	
1	L	156	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 17441 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 Probable dna-binding stress protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	155	Total	C	N	O	S	0	1	0
			1211	770	207	228	6			
1	B	156	Total	C	N	O	S	0	3	0
			1232	784	209	233	6			
1	C	156	Total	C	N	O	S	0	2	0
			1224	778	209	231	6			
1	D	155	Total	C	N	O	S	0	2	0
			1229	780	210	233	6			
1	E	155	Total	C	N	O	S	0	2	0
			1219	774	207	232	6			
1	F	156	Total	C	N	O	S	0	0	0
			1211	769	208	228	6			
1	G	155	Total	C	N	O	S	0	1	0
			1211	770	207	228	6			
1	H	156	Total	C	N	O	S	0	1	0
			1227	776	209	236	6			
1	I	156	Total	C	N	O	S	0	3	0
			1235	782	211	236	6			
1	J	155	Total	C	N	O	S	0	1	0
			1211	770	207	228	6			
1	K	156	Total	C	N	O	S	0	2	0
			1238	783	211	238	6			
1	L	155	Total	C	N	O	S	0	3	0
			1229	779	210	235	5			

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Cl	0	0
			2	2		
2	B	2	Total	Cl	0	0
			2	2		

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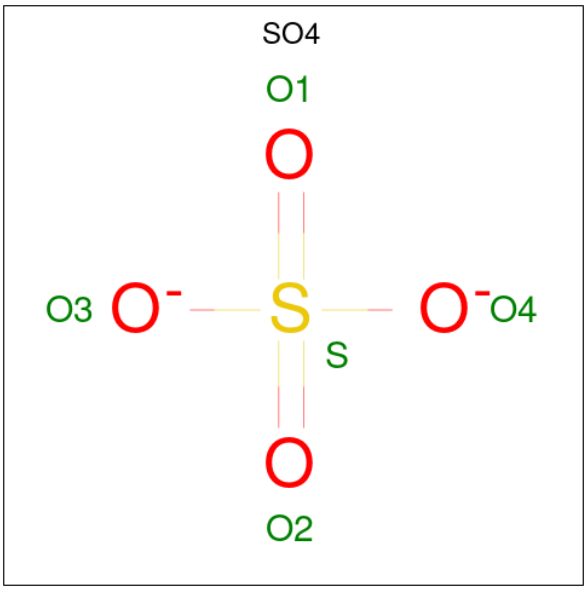
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	2	Total Cl 2 2	0	0
2	D	2	Total Cl 2 2	0	0
2	E	2	Total Cl 2 2	0	0
2	F	2	Total Cl 2 2	0	0
2	G	2	Total Cl 2 2	0	0
2	H	2	Total Cl 2 2	0	0
2	I	2	Total Cl 2 2	0	0
2	J	2	Total Cl 2 2	0	0
2	K	2	Total Cl 2 2	0	0
2	L	2	Total Cl 2 2	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S) (labeled as "Ligand of Interest" by depositor).



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

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

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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	G	1	Total O S 5 4 1	0	0
3	G	1	Total O S 5 4 1	0	0
3	G	1	Total O S 5 4 1	0	0
3	G	1	Total O S 5 4 1	0	0
3	G	1	Total O S 5 4 1	0	0
3	G	1	Total O S 5 4 1	0	0
3	G	1	Total O S 5 4 1	0	0
3	G	1	Total O S 5 4 1	0	0
3	H	1	Total O S 5 4 1	0	0
3	H	1	Total O S 5 4 1	0	0
3	H	1	Total O S 5 4 1	0	0
3	H	1	Total O S 5 4 1	0	0
3	H	1	Total O S 5 4 1	0	0
3	H	1	Total O S 5 4 1	0	0
3	I	1	Total O S 5 4 1	0	0
3	I	1	Total O S 5 4 1	0	0
3	I	1	Total O S 5 4 1	0	0
3	I	1	Total O S 5 4 1	0	0
3	I	1	Total O S 5 4 1	0	0
3	I	1	Total O S 5 4 1	0	0
3	J	1	Total O S 5 4 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	J	1	Total O S 5 4 1	0	0
3	J	1	Total O S 5 4 1	0	0
3	J	1	Total O S 5 4 1	0	0
3	J	1	Total O S 5 4 1	0	0
3	J	1	Total O S 5 4 1	0	0
3	J	1	Total O S 5 4 1	0	0
3	K	1	Total O S 5 4 1	0	0
3	K	1	Total O S 5 4 1	0	0
3	K	1	Total O S 5 4 1	0	0
3	K	1	Total O S 5 4 1	0	0
3	K	1	Total O S 5 4 1	0	0
3	K	1	Total O S 5 4 1	0	0
3	L	1	Total O S 5 4 1	0	0
3	L	1	Total O S 5 4 1	0	0
3	L	1	Total O S 5 4 1	0	0
3	L	1	Total O S 5 4 1	0	0
3	L	1	Total O S 5 4 1	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	2	Total Na 2 2	0	0
4	C	2	Total Na 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	2	Total Na 2 2	0	0
4	E	2	Total Na 2 2	0	0
4	G	1	Total Na 1 1	0	0
4	I	1	Total Na 1 1	0	0
4	K	2	Total Na 2 2	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	191	Total O 191 191	0	0
5	B	213	Total O 213 213	0	0
5	C	167	Total O 167 167	0	0
5	D	221	Total O 221 221	0	0
5	E	187	Total O 187 187	0	0
5	F	175	Total O 175 175	0	0
5	G	178	Total O 178 178	0	0
5	H	198	Total O 198 198	0	0
5	I	204	Total O 204 204	0	0
5	J	178	Total O 178 178	0	0
5	K	206	Total O 206 206	0	0
5	L	205	Total O 205 205	0	0

3 Residue-property plots (i)

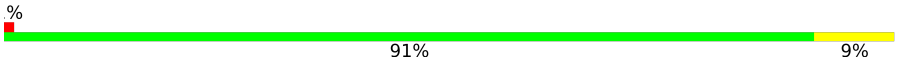
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

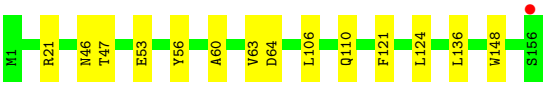
• Molecule 1: Probable dna-binding stress protein

Chain A:

• Molecule 1: Probable dna-binding stress protein

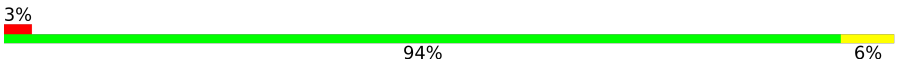
Chain B:

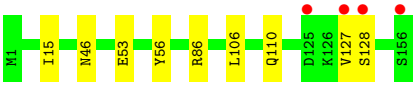




• Molecule 1: Probable dna-binding stress protein

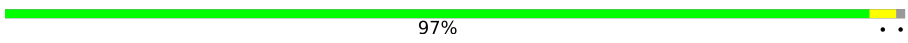
Chain C:





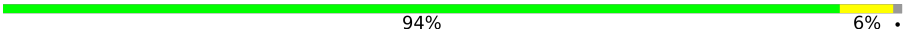
• Molecule 1: Probable dna-binding stress protein

Chain D:



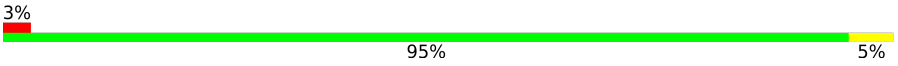
• Molecule 1: Probable dna-binding stress protein

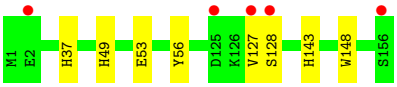
Chain E:



• Molecule 1: Probable dna-binding stress protein

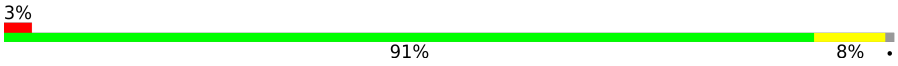
Chain F:

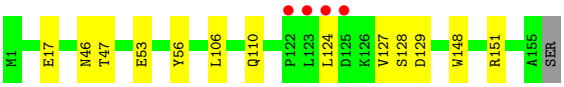




• Molecule 1: Probable dna-binding stress protein

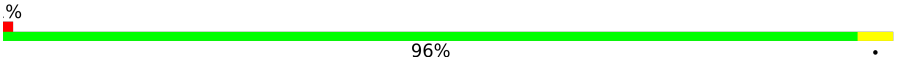
Chain G:





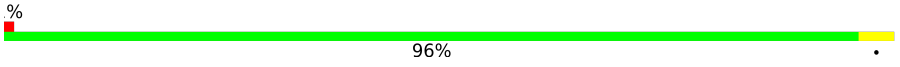
• Molecule 1: Probable dna-binding stress protein

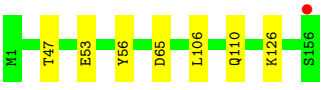
Chain H:



• Molecule 1: Probable dna-binding stress protein

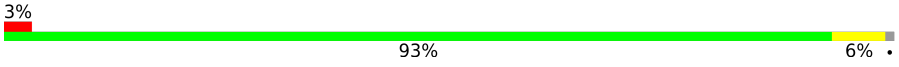
Chain I:

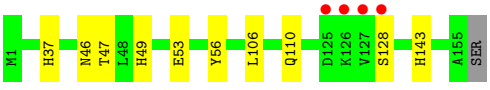




• Molecule 1: Probable dna-binding stress protein

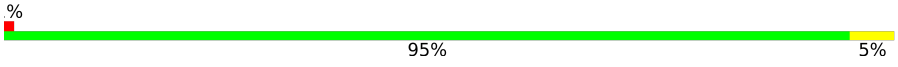
Chain J:





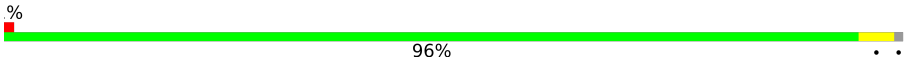
• Molecule 1: Probable dna-binding stress protein

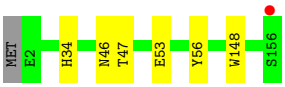
Chain K:



• Molecule 1: Probable dna-binding stress protein

Chain L:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	129.54Å 129.82Å 156.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.43 – 1.70 48.43 – 1.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.43-1.70) 100.0 (48.43-1.70)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.93 (at 1.70Å)	Xtriage
Refinement program	PHENIX dev_3959	Depositor
R, R_{free}	0.146 , 0.170 0.158 , 0.180	Depositor DCC
R_{free} test set	14417 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	21.6	Xtriage
Anisotropy	0.033	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 43.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.010 for k,h,-l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	17441	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.82% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: CL, SO4, NA

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	0.43	0/1237	0.64	0/1681
1	B	0.46	0/1264	0.66	0/1715
1	C	0.48	0/1253	0.65	0/1700
1	D	0.48	0/1258	0.64	0/1707
1	E	0.46	0/1248	0.66	0/1696
1	F	0.44	0/1234	0.63	0/1675
1	G	0.44	0/1237	0.64	0/1681
1	H	0.48	0/1253	0.65	0/1701
1	I	0.45	0/1267	0.64	0/1719
1	J	0.45	0/1237	0.63	0/1681
1	K	0.48	0/1267	0.66	0/1717
1	L	0.45	0/1261	0.64	0/1711
All	All	0.46	0/15016	0.64	0/20384

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

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	1211	0	1197	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1232	0	1228	10	0
1	C	1224	0	1215	6	0
1	D	1229	0	1227	4	0
1	E	1219	0	1203	6	0
1	F	1211	0	1193	5	0
1	G	1211	0	1197	9	0
1	H	1227	0	1210	6	0
1	I	1235	0	1228	5	0
1	J	1211	0	1197	9	0
1	K	1238	0	1232	5	0
1	L	1229	0	1220	4	0
2	A	2	0	0	0	0
2	B	2	0	0	1	0
2	C	2	0	0	0	0
2	D	2	0	0	1	0
2	E	2	0	0	0	0
2	F	2	0	0	1	0
2	G	2	0	0	0	0
2	H	2	0	0	1	0
2	I	2	0	0	0	0
2	J	2	0	0	1	0
2	K	2	0	0	0	0
2	L	2	0	0	0	0
3	A	40	0	0	1	0
3	B	45	0	0	0	0
3	C	25	0	0	1	0
3	D	45	0	0	0	0
3	E	25	0	0	0	0
3	F	35	0	0	0	0
3	G	40	0	0	1	0
3	H	30	0	0	0	0
3	I	30	0	0	0	0
3	J	35	0	0	0	0
3	K	30	0	0	0	0
3	L	25	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
4	E	2	0	0	0	0
4	G	1	0	0	0	0
4	I	1	0	0	0	0
4	K	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	191	0	0	1	0
5	B	213	0	0	4	0
5	C	167	0	0	2	0
5	D	221	0	0	0	0
5	E	187	0	0	2	0
5	F	175	0	0	0	0
5	G	178	0	0	3	0
5	H	198	0	0	2	0
5	I	204	0	0	2	0
5	J	178	0	0	2	0
5	K	206	0	0	1	0
5	L	205	0	0	1	0
All	All	17441	0	14547	66	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 2.

The worst 5 of 66 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:C:86:ARG:NH2	5:C:301:HOH:O	2.21	0.69
1:B:64[A]:ASP:OD1	1:L:34:HIS:NE2	2.27	0.65
2:B:204:CL:CL	5:B:438:HOH:O	2.54	0.59
1:I:126:LYS:NZ	5:I:303:HOH:O	2.31	0.56
1:H:34:HIS:NE2	1:K:64[A]:ASP:OD1	2.34	0.56

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	154/156 (99%)	151 (98%)	3 (2%)	0	100	100
1	B	157/156 (101%)	156 (99%)	1 (1%)	0	100	100
1	C	156/156 (100%)	153 (98%)	3 (2%)	0	100	100
1	D	155/156 (99%)	153 (99%)	2 (1%)	0	100	100
1	E	155/156 (99%)	152 (98%)	3 (2%)	0	100	100
1	F	154/156 (99%)	150 (97%)	4 (3%)	0	100	100
1	G	154/156 (99%)	151 (98%)	3 (2%)	0	100	100
1	H	155/156 (99%)	152 (98%)	3 (2%)	0	100	100
1	I	157/156 (101%)	155 (99%)	2 (1%)	0	100	100
1	J	154/156 (99%)	152 (99%)	2 (1%)	0	100	100
1	K	156/156 (100%)	154 (99%)	2 (1%)	0	100	100
1	L	156/156 (100%)	153 (98%)	3 (2%)	0	100	100
All	All	1863/1872 (100%)	1832 (98%)	31 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	124/129 (96%)	123 (99%)	1 (1%)	81	74
1	B	128/129 (99%)	126 (98%)	2 (2%)	62	48
1	C	126/129 (98%)	125 (99%)	1 (1%)	81	74
1	D	129/129 (100%)	129 (100%)	0	100	100
1	E	126/129 (98%)	125 (99%)	1 (1%)	81	74
1	F	123/129 (95%)	122 (99%)	1 (1%)	81	74
1	G	124/129 (96%)	123 (99%)	1 (1%)	81	74
1	H	128/129 (99%)	128 (100%)	0	100	100
1	I	130/129 (101%)	130 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	J	124/129 (96%)	123 (99%)	1 (1%)	81 74
1	K	131/129 (102%)	130 (99%)	1 (1%)	81 74
1	L	129/129 (100%)	128 (99%)	1 (1%)	81 74
All	All	1522/1548 (98%)	1512 (99%)	10 (1%)	84 77

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	128	SER
1	K	121	PHE
1	L	148	TRP
1	C	128	SER
1	E	148	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 117 ligands modelled in this entry, 36 are monoatomic - leaving 81 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	SO4	B	205	-	4,4,4	0.20	0	6,6,6	0.32	0
3	SO4	K	205	-	4,4,4	0.15	0	6,6,6	0.14	0
3	SO4	F	206	-	4,4,4	0.15	0	6,6,6	0.16	0
3	SO4	B	206	-	4,4,4	0.14	0	6,6,6	0.27	0
3	SO4	K	208	-	4,4,4	0.23	0	6,6,6	0.29	0
3	SO4	B	211	-	4,4,4	0.12	0	6,6,6	0.22	0
3	SO4	A	206	-	4,4,4	0.22	0	6,6,6	0.14	0
3	SO4	A	210	-	4,4,4	0.76	0	6,6,6	0.25	0
3	SO4	K	209	-	4,4,4	1.07	0	6,6,6	0.30	0
3	SO4	C	207	-	4,4,4	0.15	0	6,6,6	0.10	0
3	SO4	I	205	-	4,4,4	0.18	0	6,6,6	0.08	0
3	SO4	G	204	-	4,4,4	0.15	0	6,6,6	0.45	0
3	SO4	L	206	-	4,4,4	0.15	0	6,6,6	0.33	0
3	SO4	G	207	-	4,4,4	0.14	0	6,6,6	0.16	0
3	SO4	J	207	-	4,4,4	0.14	0	6,6,6	0.20	0
3	SO4	G	206	-	4,4,4	0.18	0	6,6,6	0.32	0
3	SO4	J	206	-	4,4,4	0.18	0	6,6,6	0.20	0
3	SO4	D	213	-	4,4,4	0.17	0	6,6,6	0.18	0
3	SO4	H	205	-	4,4,4	0.18	0	6,6,6	0.26	0
3	SO4	I	204	-	4,4,4	0.13	0	6,6,6	0.10	0
3	SO4	J	204	-	4,4,4	0.13	0	6,6,6	0.11	0
3	SO4	B	212	-	4,4,4	0.18	0	6,6,6	0.25	0
3	SO4	D	211	-	4,4,4	0.14	0	6,6,6	0.23	0
3	SO4	K	206	-	4,4,4	0.13	0	6,6,6	0.17	0
3	SO4	B	213	-	4,4,4	0.16	0	6,6,6	0.09	0
3	SO4	D	208	-	4,4,4	0.15	0	6,6,6	0.13	0
3	SO4	G	208	-	4,4,4	0.13	0	6,6,6	0.26	0
3	SO4	G	209	-	4,4,4	0.13	0	6,6,6	0.16	0
3	SO4	J	209	-	4,4,4	0.12	0	6,6,6	0.13	0
3	SO4	C	205	-	4,4,4	0.21	0	6,6,6	0.08	0
3	SO4	B	207	-	4,4,4	0.21	0	6,6,6	0.22	0
3	SO4	H	207	-	4,4,4	0.17	0	6,6,6	0.19	0
3	SO4	L	207	-	4,4,4	0.17	0	6,6,6	0.08	0
3	SO4	A	205	-	4,4,4	0.19	0	6,6,6	0.22	0
3	SO4	D	207	-	4,4,4	0.13	0	6,6,6	0.11	0
3	SO4	E	207	-	4,4,4	0.18	0	6,6,6	0.06	0
3	SO4	D	206	-	4,4,4	0.14	0	6,6,6	0.30	0
3	SO4	I	209	-	4,4,4	0.15	0	6,6,6	0.12	0
3	SO4	E	206	-	4,4,4	0.22	0	6,6,6	0.15	0
3	SO4	H	208	-	4,4,4	0.17	0	6,6,6	0.11	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	SO4	D	212	-	4,4,4	0.22	0	6,6,6	0.41	0
3	SO4	H	204	-	4,4,4	0.24	0	6,6,6	0.20	0
3	SO4	G	210	-	4,4,4	0.11	0	6,6,6	0.20	0
3	SO4	A	204	-	4,4,4	0.19	0	6,6,6	0.31	0
3	SO4	K	210	-	4,4,4	0.24	0	6,6,6	0.19	0
3	SO4	I	207	-	4,4,4	0.15	0	6,6,6	0.11	0
3	SO4	I	208	-	4,4,4	0.17	0	6,6,6	0.25	0
3	SO4	B	209	-	4,4,4	0.16	0	6,6,6	0.33	0
3	SO4	F	209	-	4,4,4	0.15	0	6,6,6	0.25	0
3	SO4	H	206	-	4,4,4	0.13	0	6,6,6	0.12	0
3	SO4	F	204	-	4,4,4	0.14	0	6,6,6	0.22	0
3	SO4	A	203	-	4,4,4	0.16	0	6,6,6	0.17	0
3	SO4	I	206	-	4,4,4	0.19	0	6,6,6	0.17	0
3	SO4	E	205	-	4,4,4	0.15	0	6,6,6	0.26	0
3	SO4	B	210	-	4,4,4	0.13	0	6,6,6	0.21	0
3	SO4	J	208	-	4,4,4	0.88	0	6,6,6	0.37	0
3	SO4	J	203	-	4,4,4	0.18	0	6,6,6	0.23	0
3	SO4	E	208	-	4,4,4	0.14	0	6,6,6	0.12	0
3	SO4	J	205	-	4,4,4	0.13	0	6,6,6	0.19	0
3	SO4	E	209	-	4,4,4	0.15	0	6,6,6	0.08	0
3	SO4	C	206	-	4,4,4	0.16	0	6,6,6	0.14	0
3	SO4	G	205	-	4,4,4	0.18	0	6,6,6	0.16	0
3	SO4	L	205	-	4,4,4	0.15	0	6,6,6	0.14	0
3	SO4	A	207	-	4,4,4	0.09	0	6,6,6	0.14	0
3	SO4	L	204	-	4,4,4	0.18	0	6,6,6	0.25	0
3	SO4	A	208	-	4,4,4	0.18	0	6,6,6	0.16	0
3	SO4	F	207	-	4,4,4	0.84	0	6,6,6	0.14	0
3	SO4	C	209	-	4,4,4	0.14	0	6,6,6	0.23	0
3	SO4	D	210	-	4,4,4	0.31	0	6,6,6	0.37	0
3	SO4	D	209	-	4,4,4	0.15	0	6,6,6	0.10	0
3	SO4	F	203	-	4,4,4	0.20	0	6,6,6	0.41	0
3	SO4	F	208	-	4,4,4	0.18	0	6,6,6	0.19	0
3	SO4	C	208	-	4,4,4	0.15	0	6,6,6	0.20	0
3	SO4	B	208	-	4,4,4	0.26	0	6,6,6	0.16	0
3	SO4	F	205	-	4,4,4	0.13	0	6,6,6	0.24	0
3	SO4	A	209	-	4,4,4	0.15	0	6,6,6	0.10	0
3	SO4	H	203	-	4,4,4	0.10	0	6,6,6	0.38	0
3	SO4	G	211	-	4,4,4	0.15	0	6,6,6	0.11	0
3	SO4	D	205	-	4,4,4	0.13	0	6,6,6	0.36	0
3	SO4	K	207	-	4,4,4	0.10	0	6,6,6	0.08	0
3	SO4	L	203	-	4,4,4	1.22	0	6,6,6	0.28	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

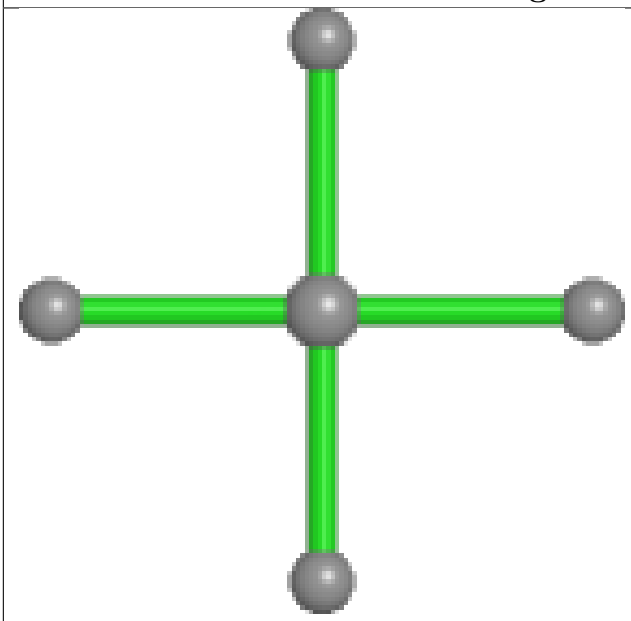
There are no ring outliers.

3 monomers are involved in 3 short contacts:

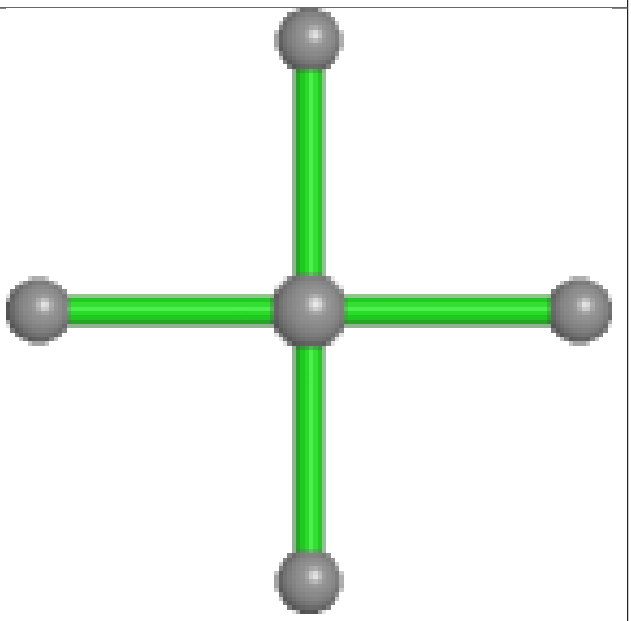
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	206	SO4	1	0
3	G	210	SO4	1	0
3	C	208	SO4	1	0

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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

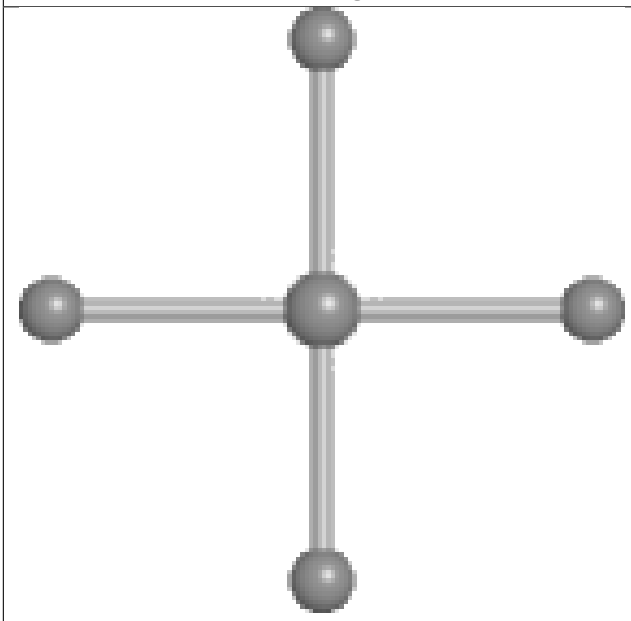
Ligand SO4 B 205



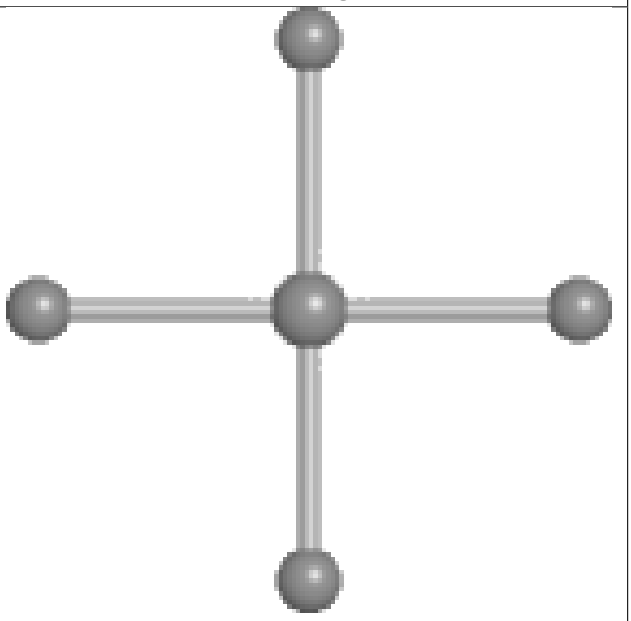
Bond lengths



Bond angles

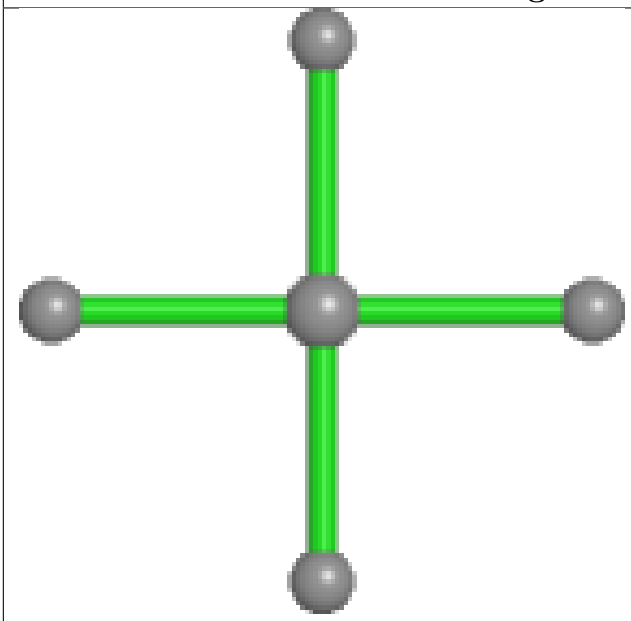


Torsions

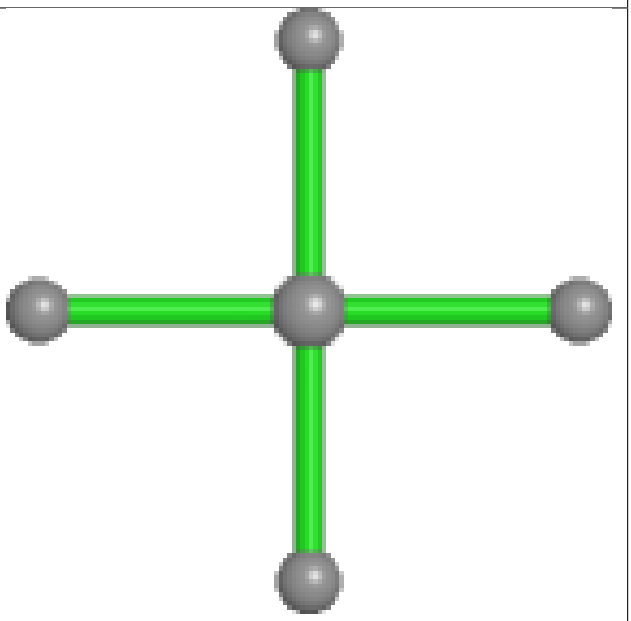


Rings

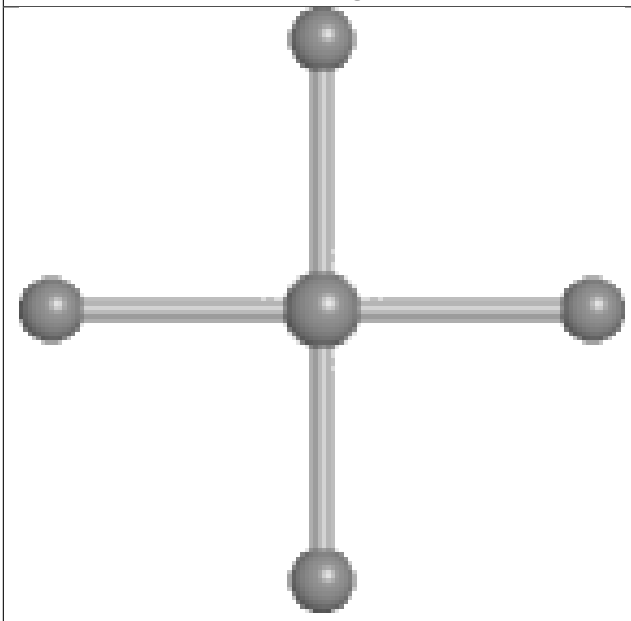
Ligand SO4 K 205



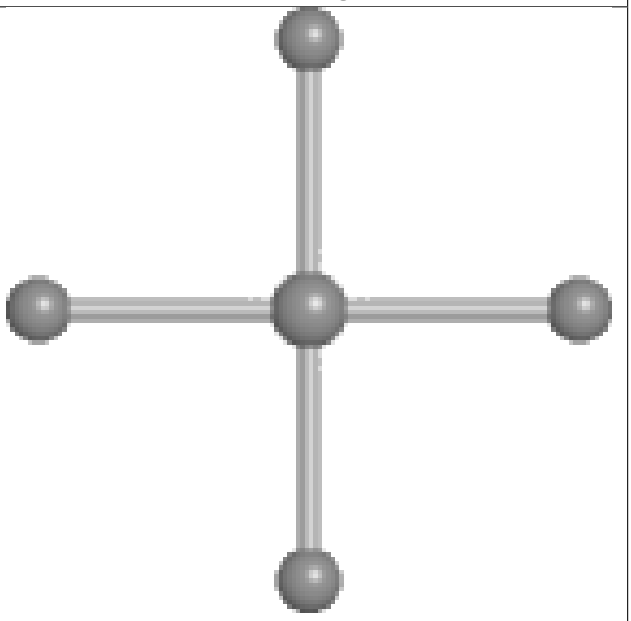
Bond lengths



Bond angles

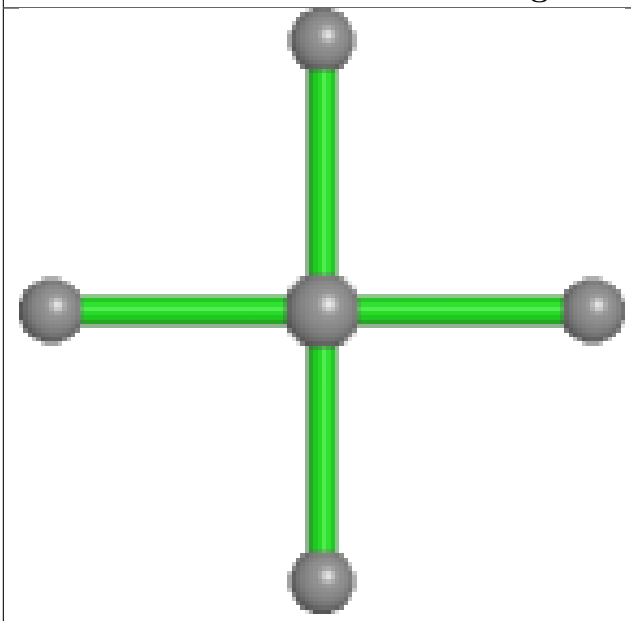


Torsions

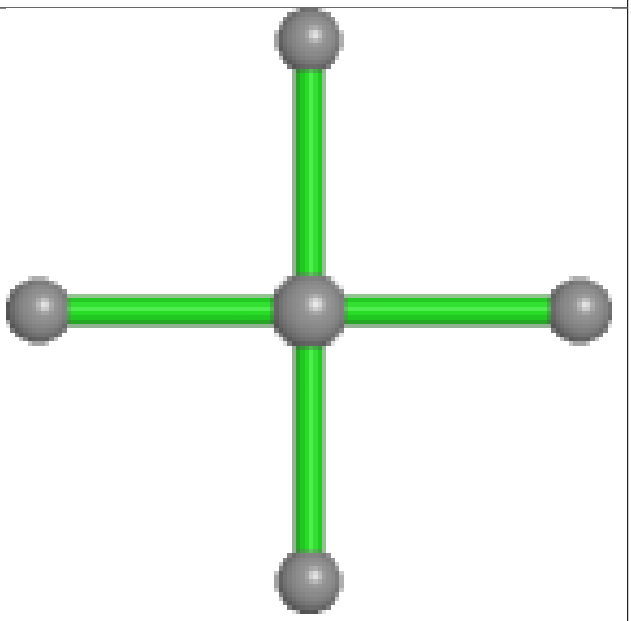


Rings

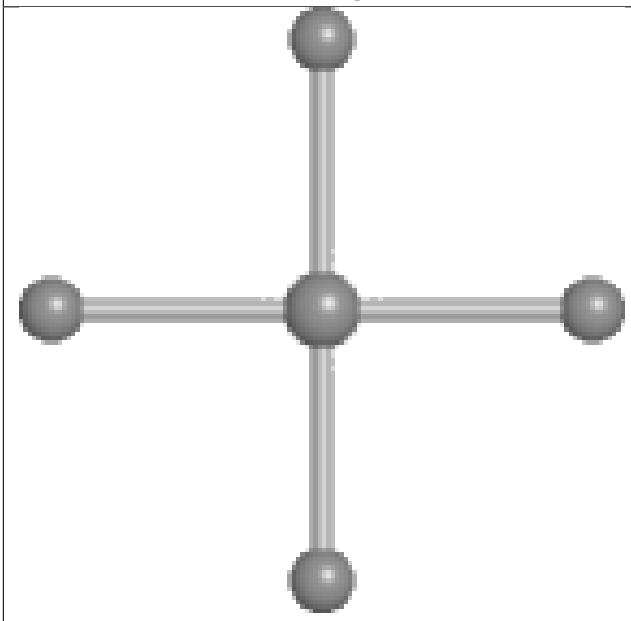
Ligand SO4 F 206



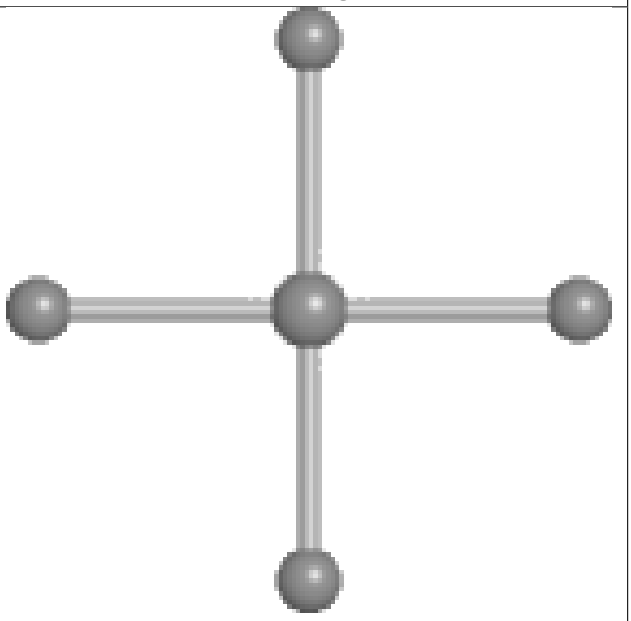
Bond lengths



Bond angles

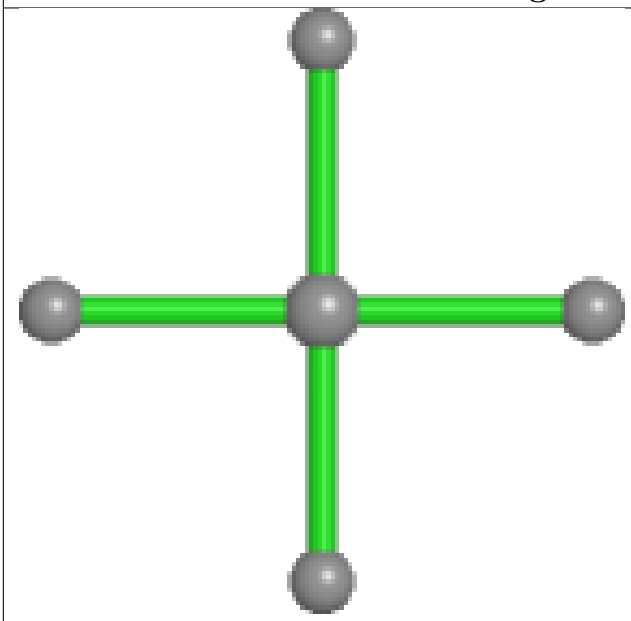


Torsions



Rings

Ligand SO4 B 206



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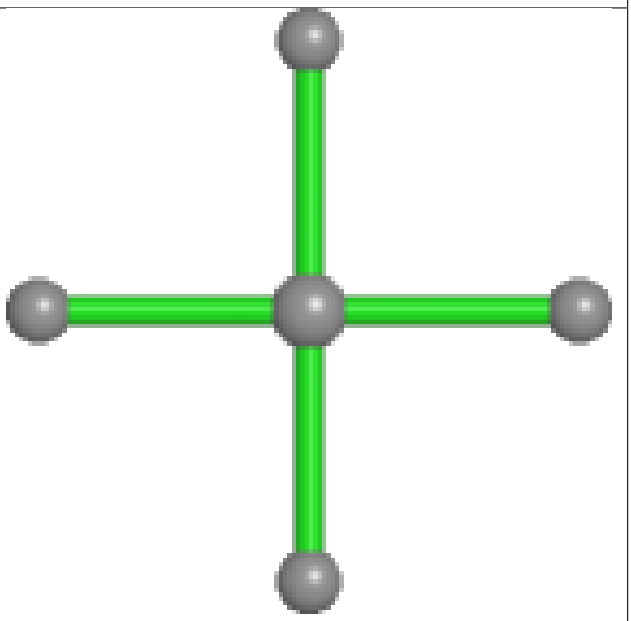
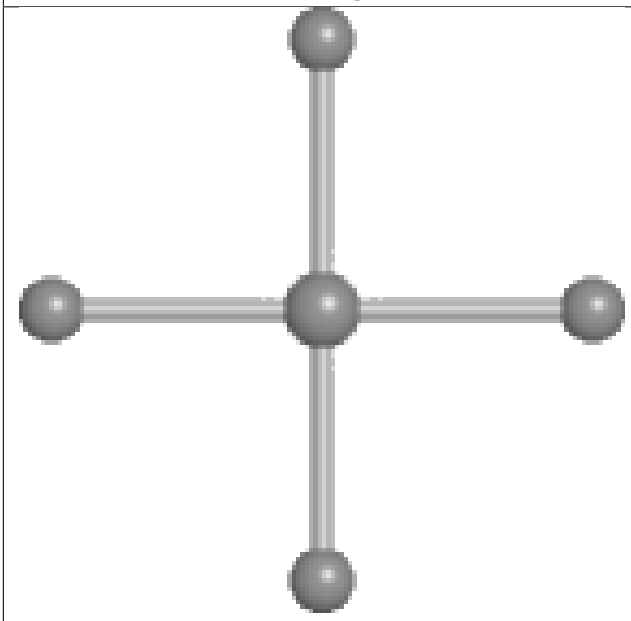
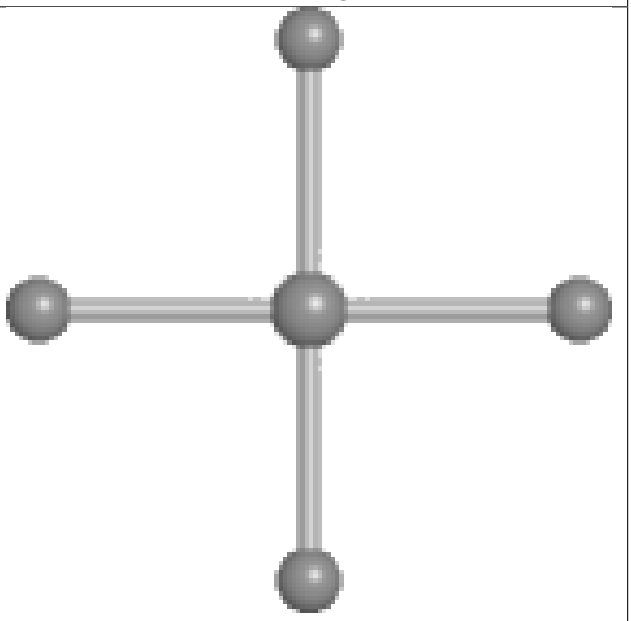


Bond angles

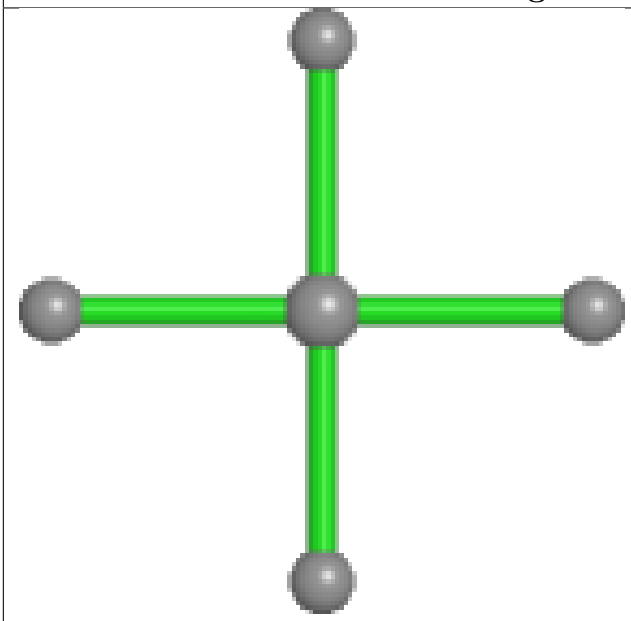


Torsions



Rings

Ligand SO4 K 208



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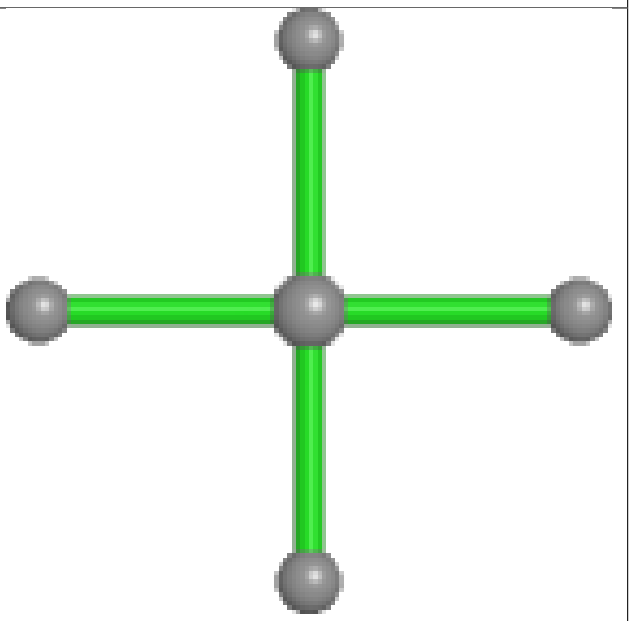
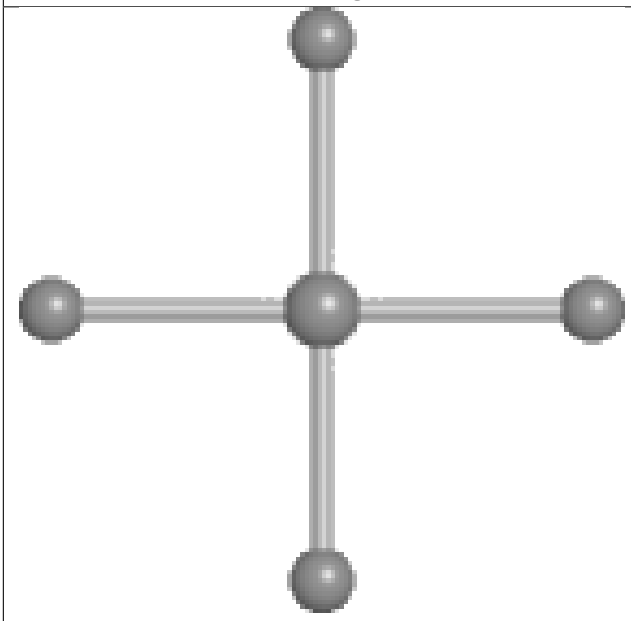
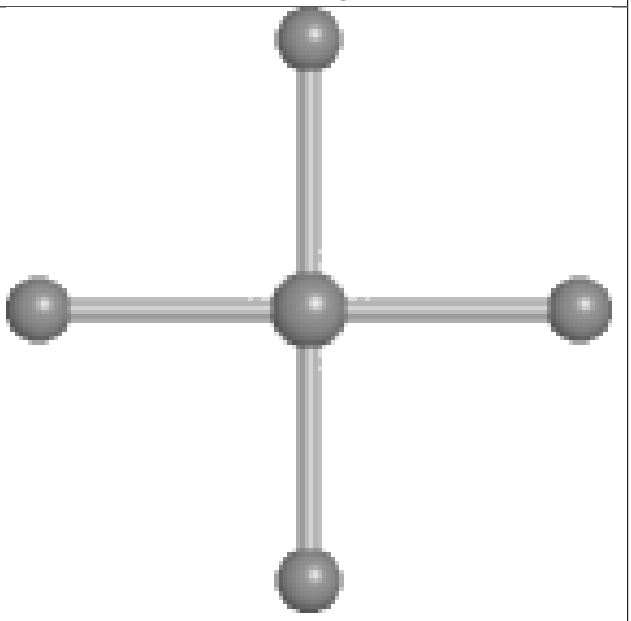


Bond angles

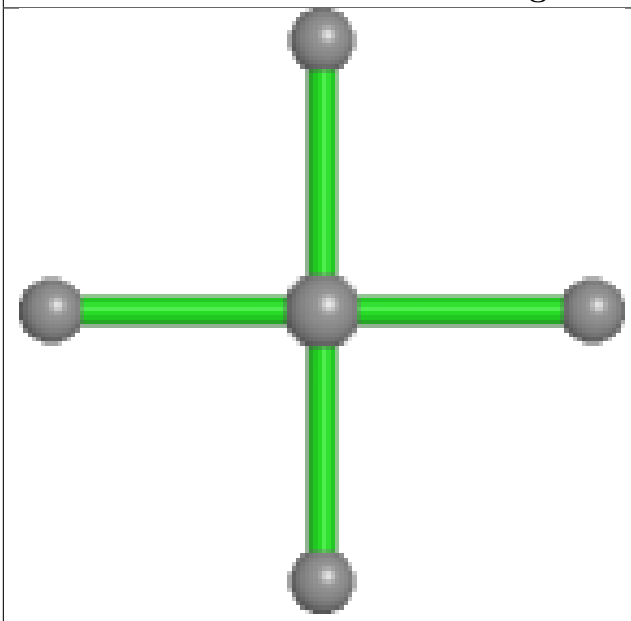


Torsions



Rings

Ligand SO4 B 211



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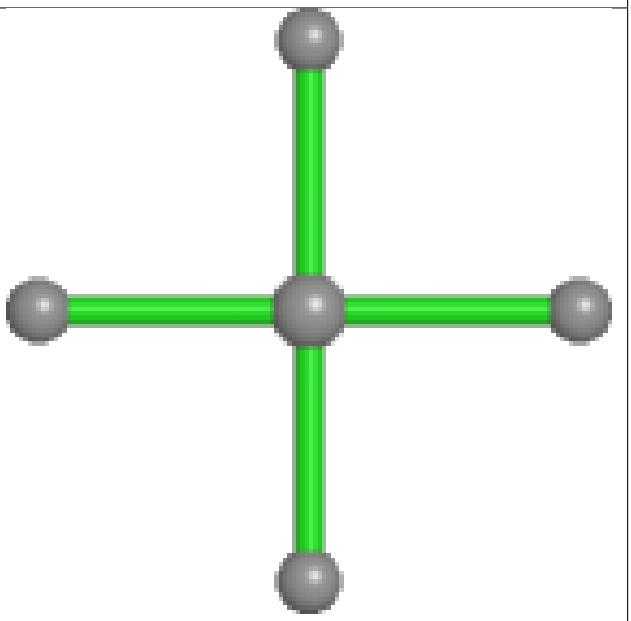
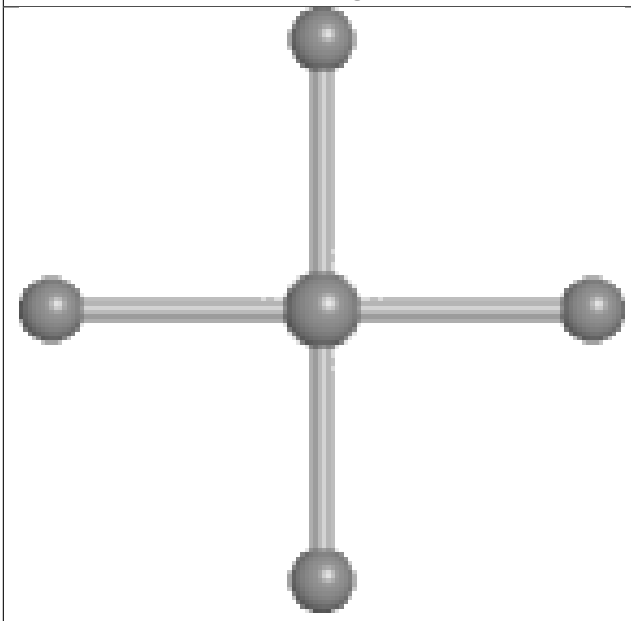


Bond angles



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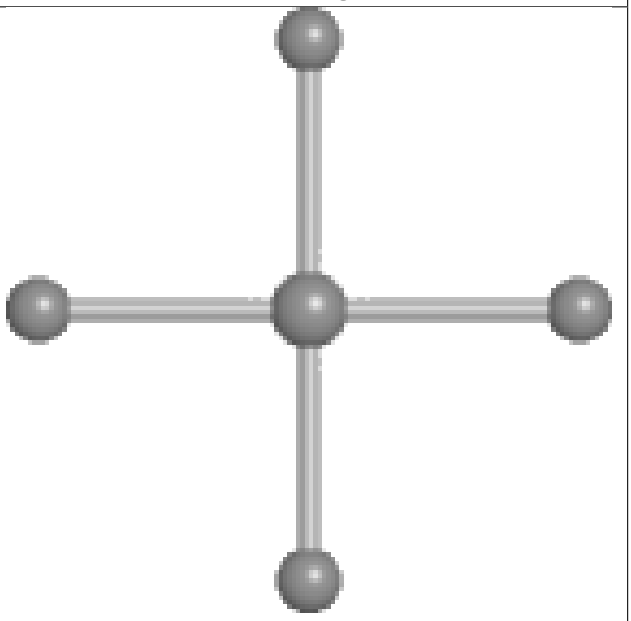
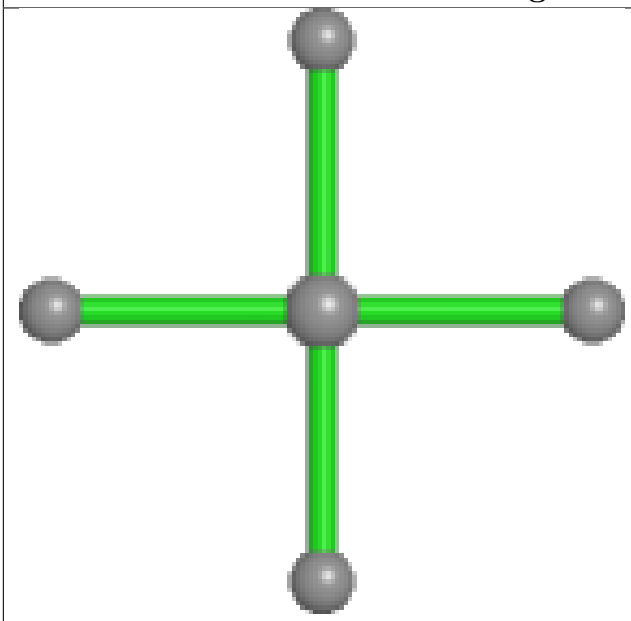


Rings

Ligand SO4 A 206



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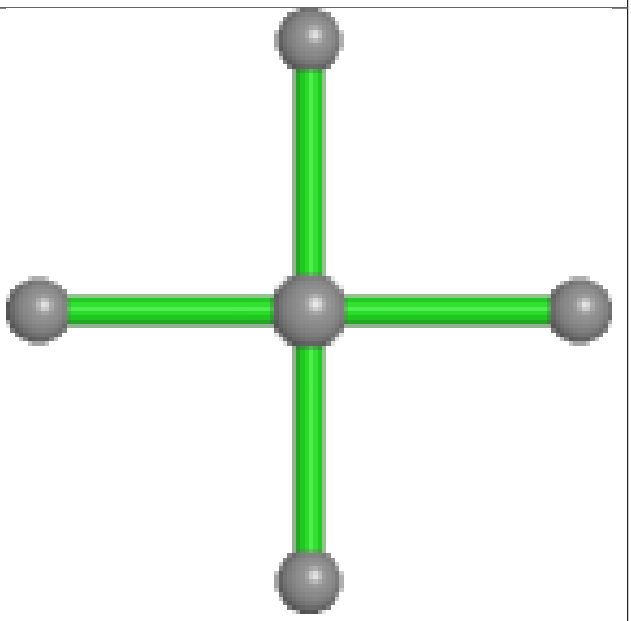
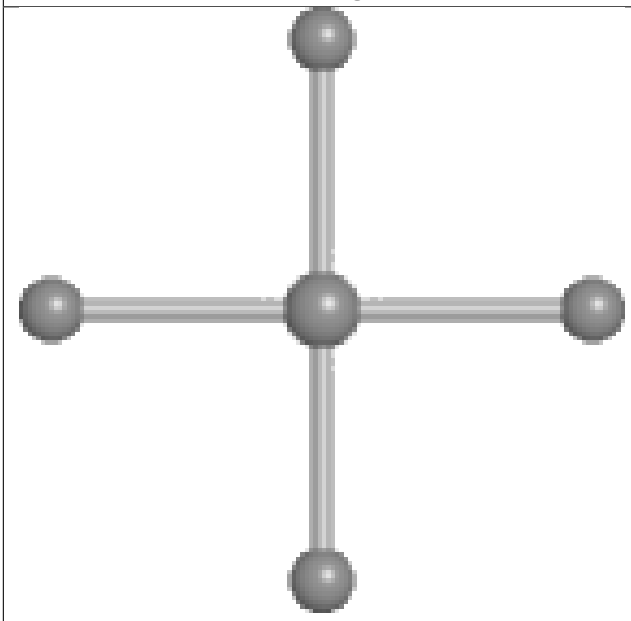


Bond angles



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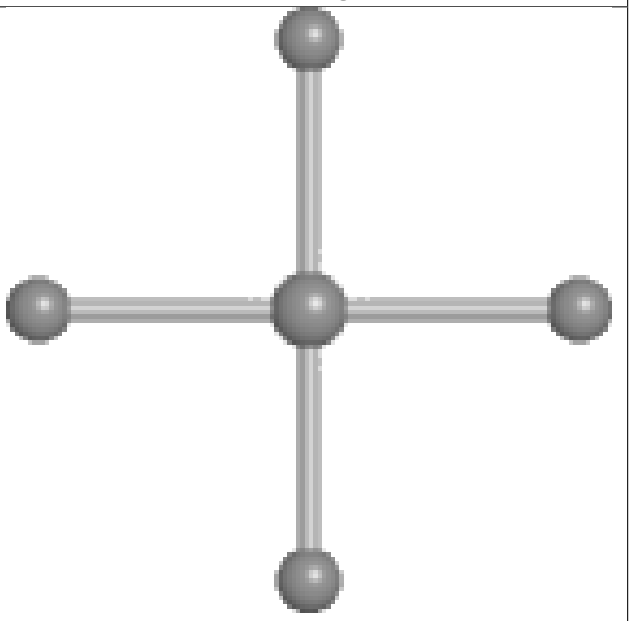
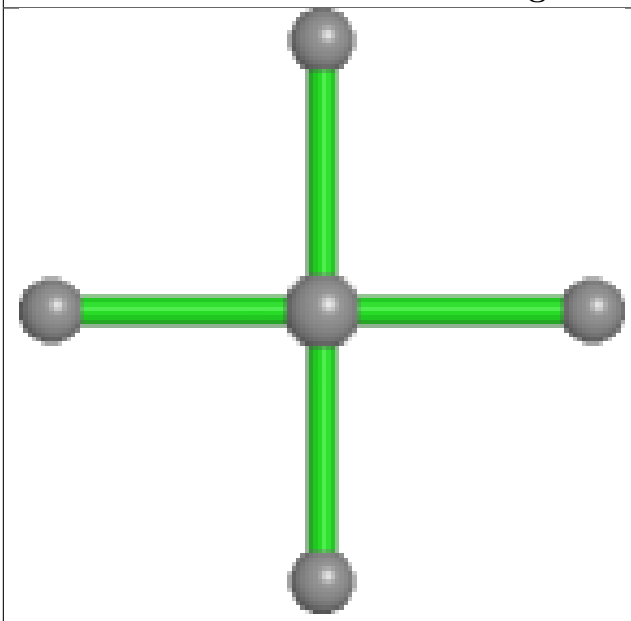
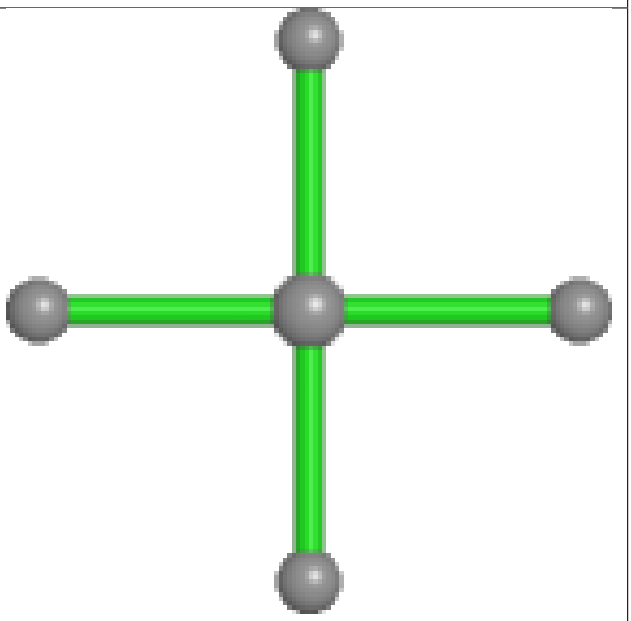


Rings

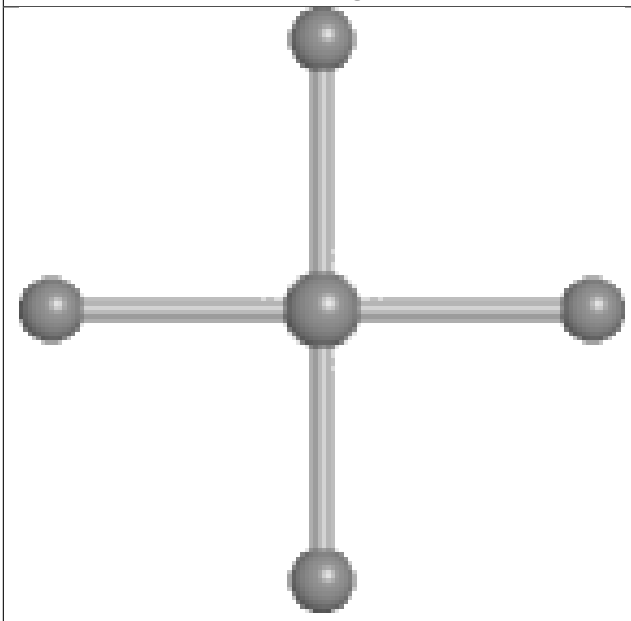
Ligand SO4 A 210



Bond lengths



Bond angles



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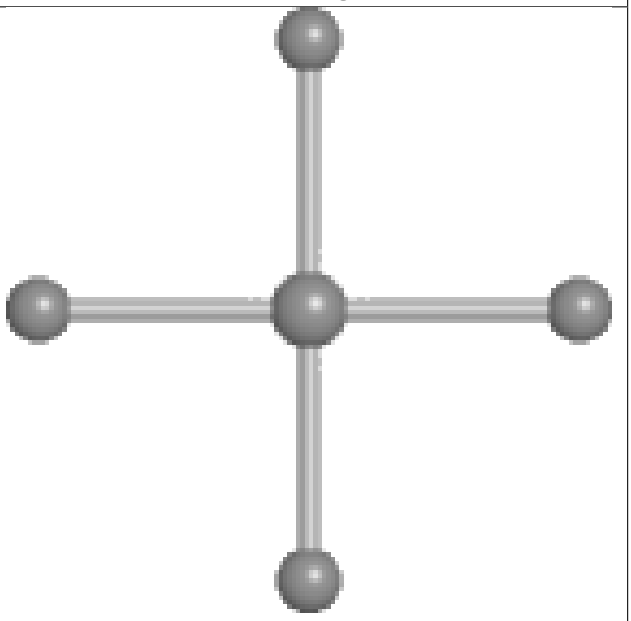
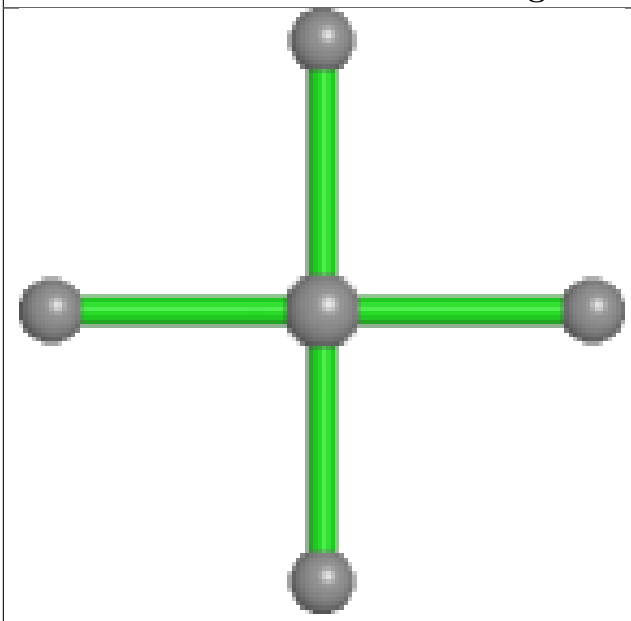


Rings

Ligand SO4 K 209



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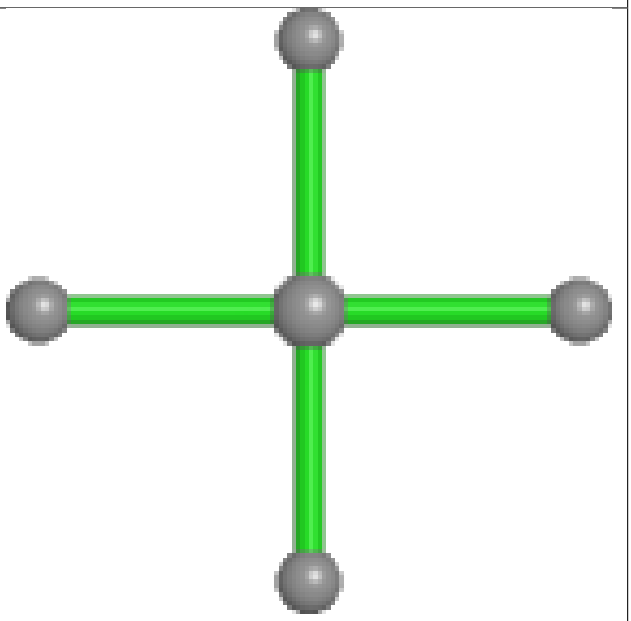
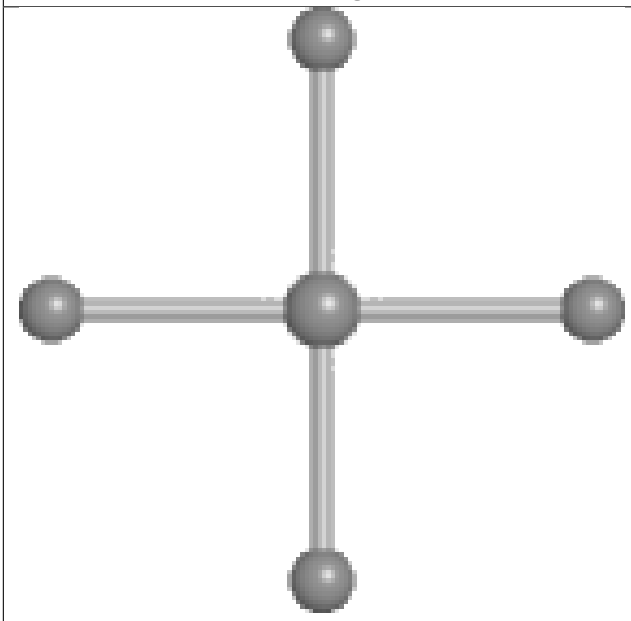


Bond angles



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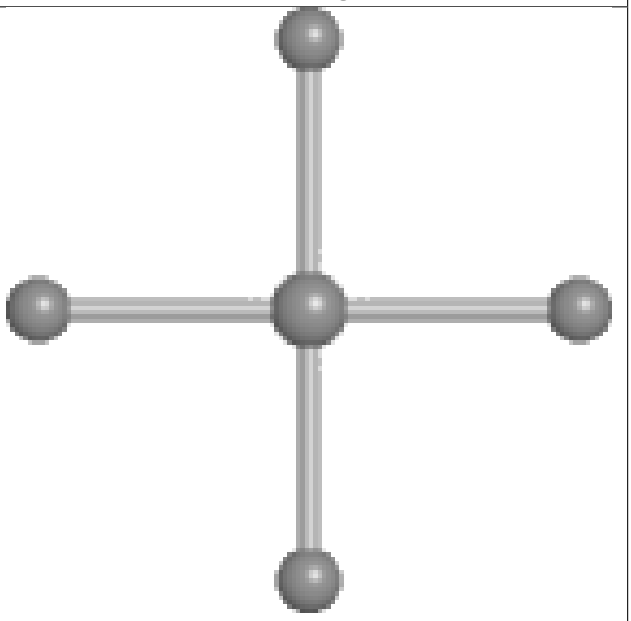
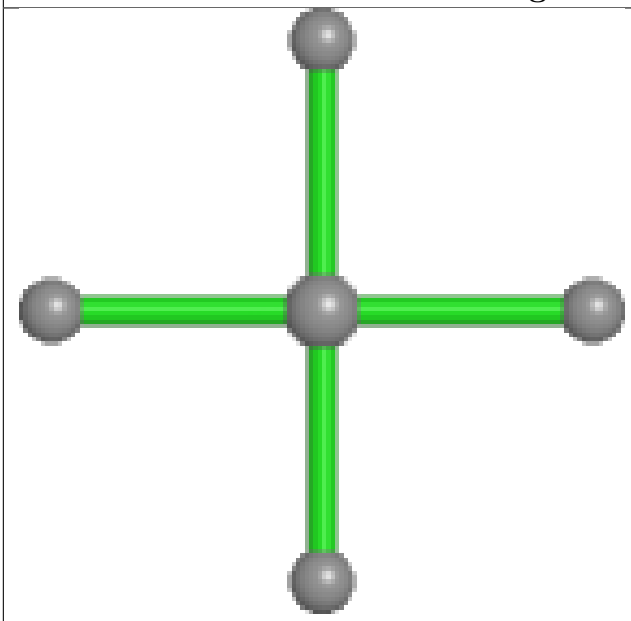


Rings

Ligand SO4 C 207



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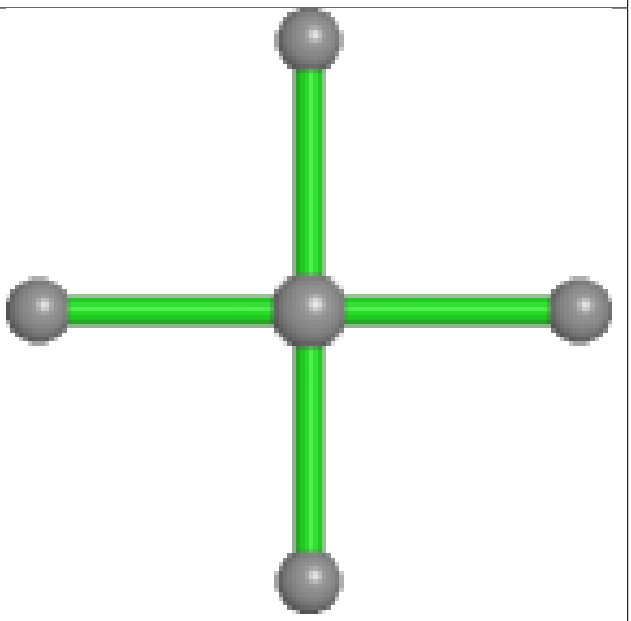
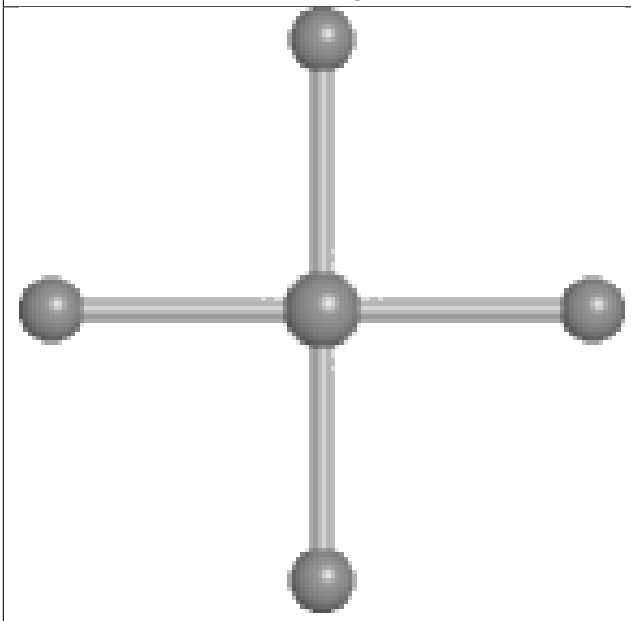
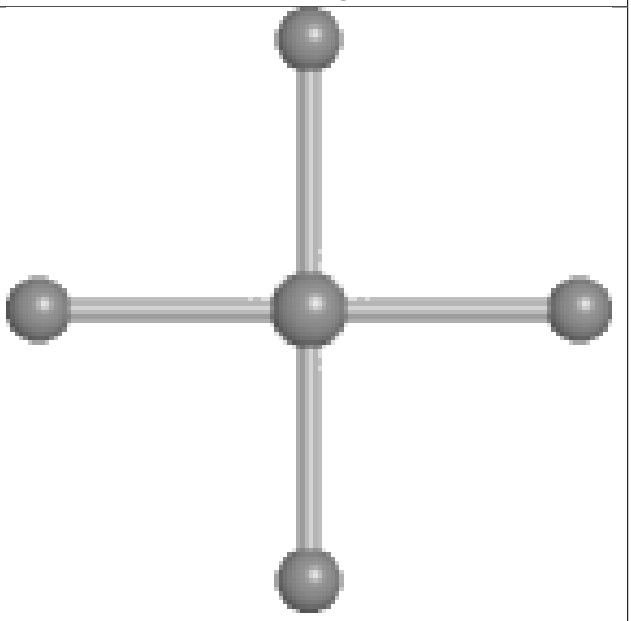


Bond angles

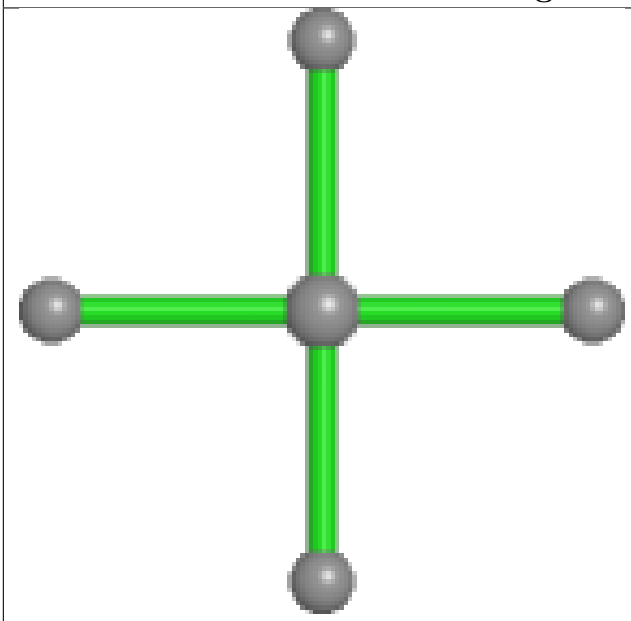


Torsions



Rings

Ligand SO4 I 205



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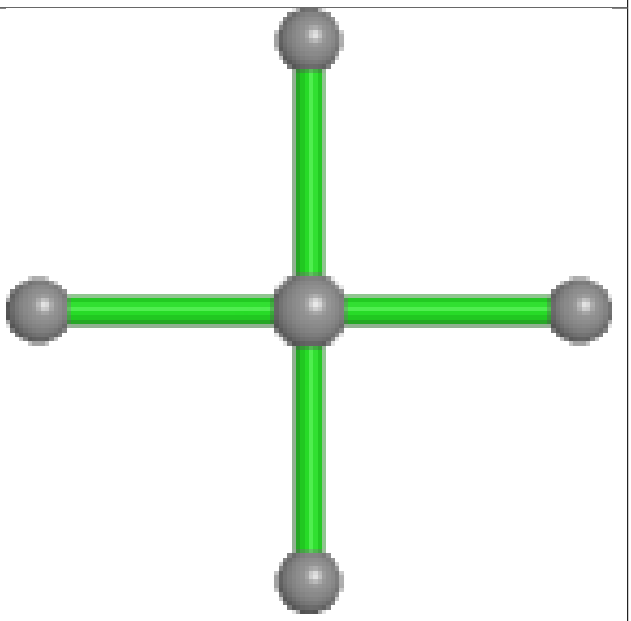
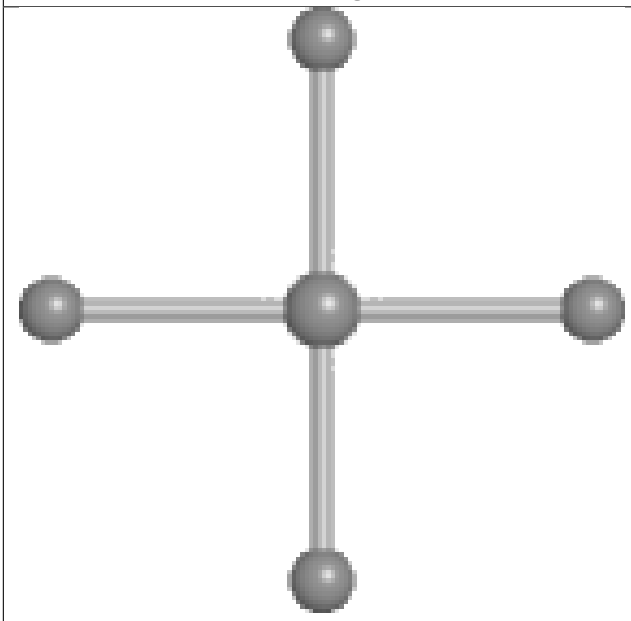


Bond angles



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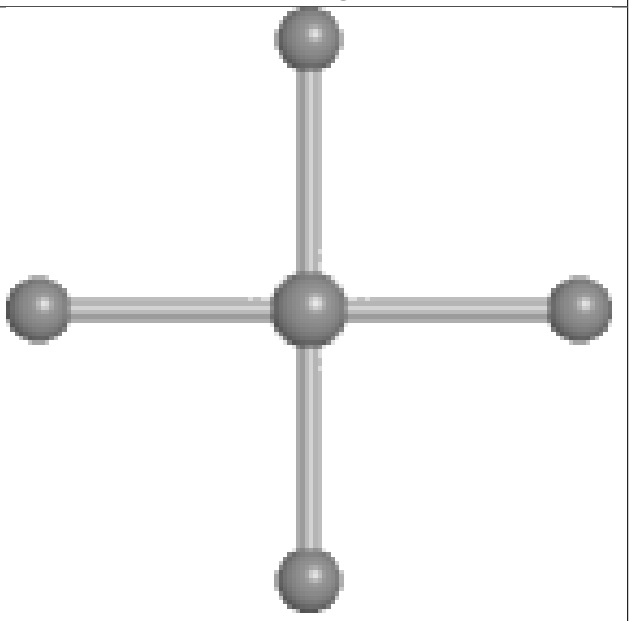
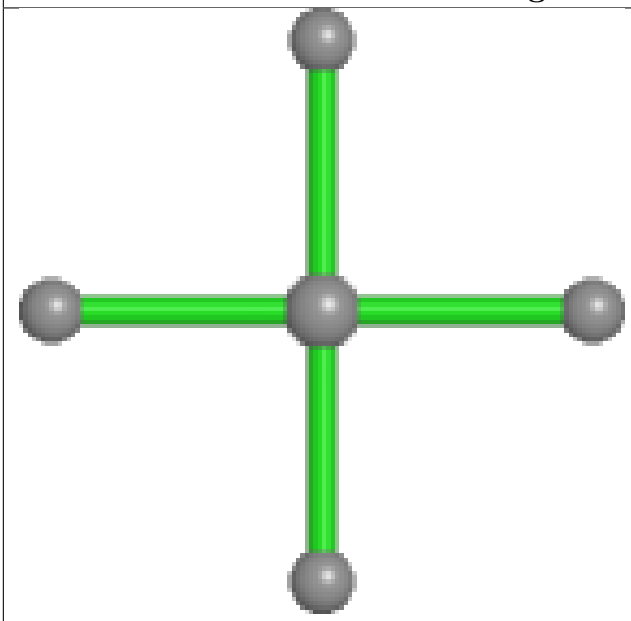
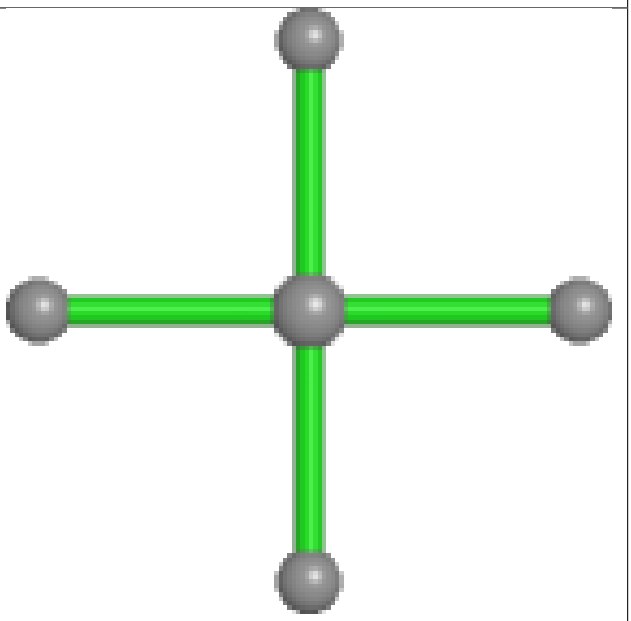


Rings

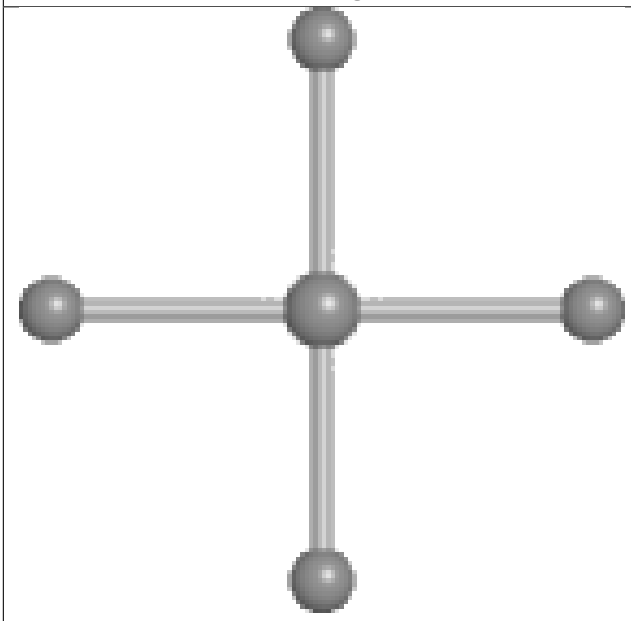
Ligand SO4 G 204



Bond lengths



Bond angles



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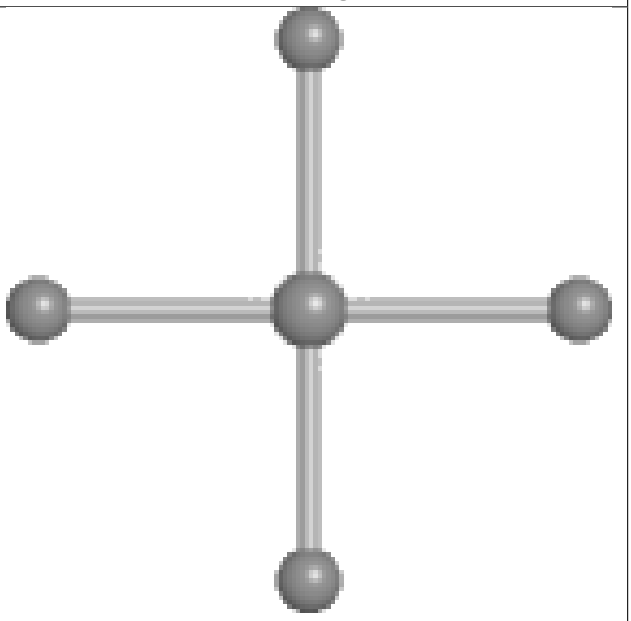
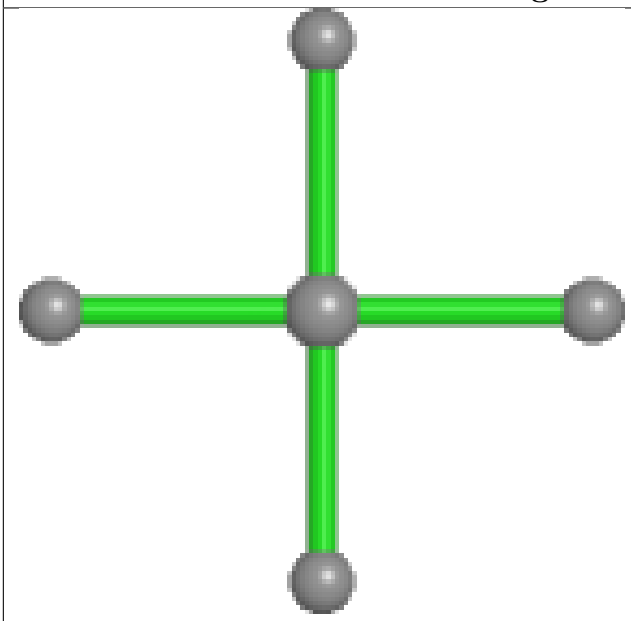


Rings

Ligand SO4 L 206



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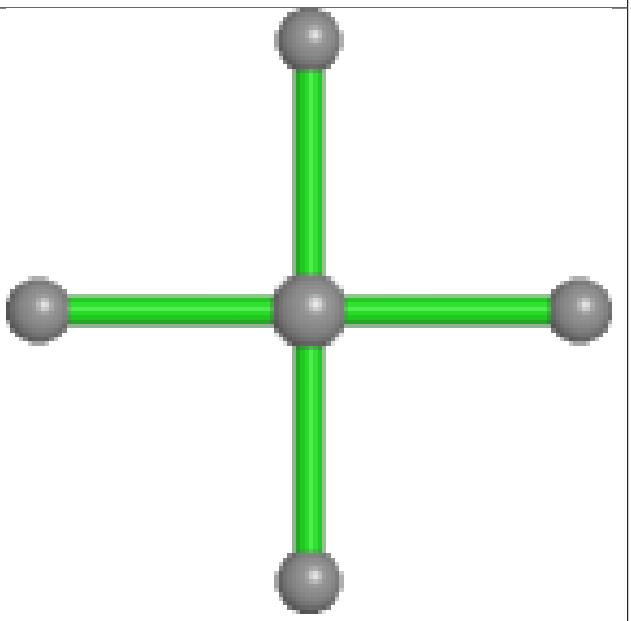

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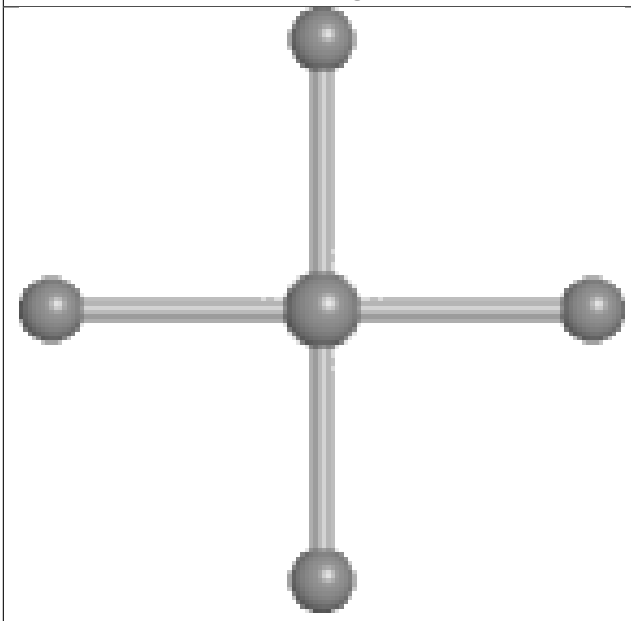

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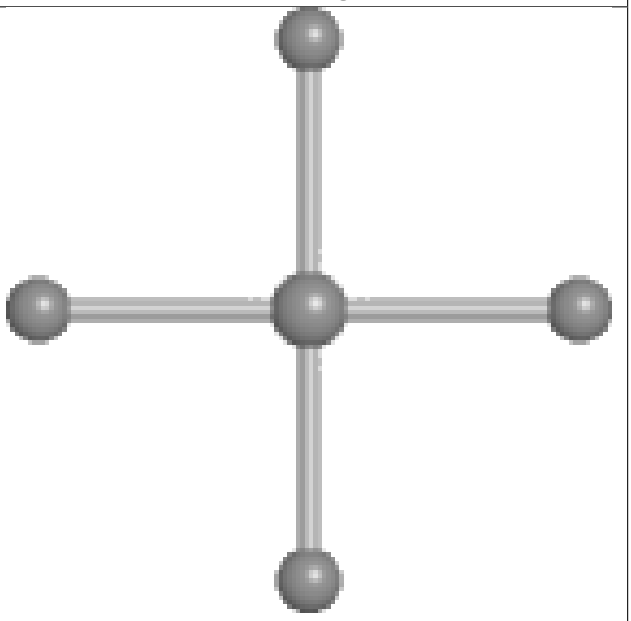
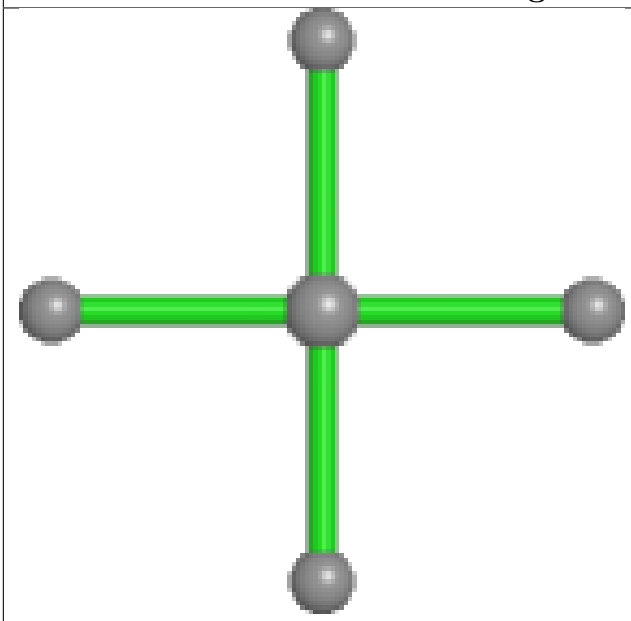


Rings

Ligand SO4 G 207



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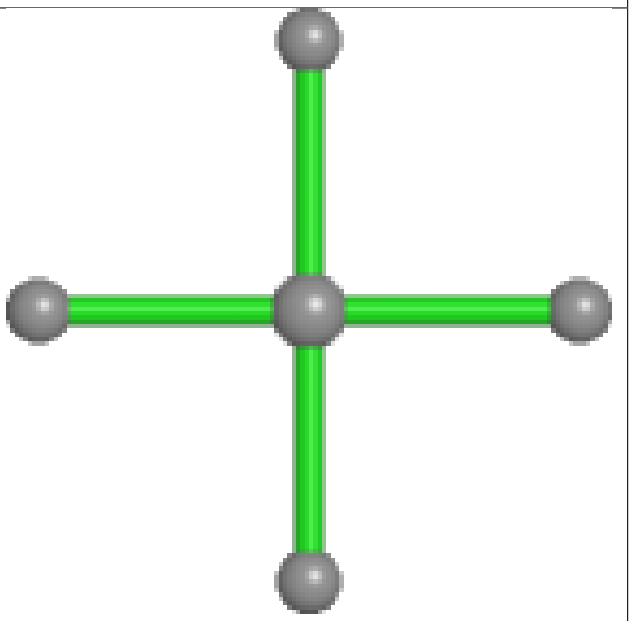

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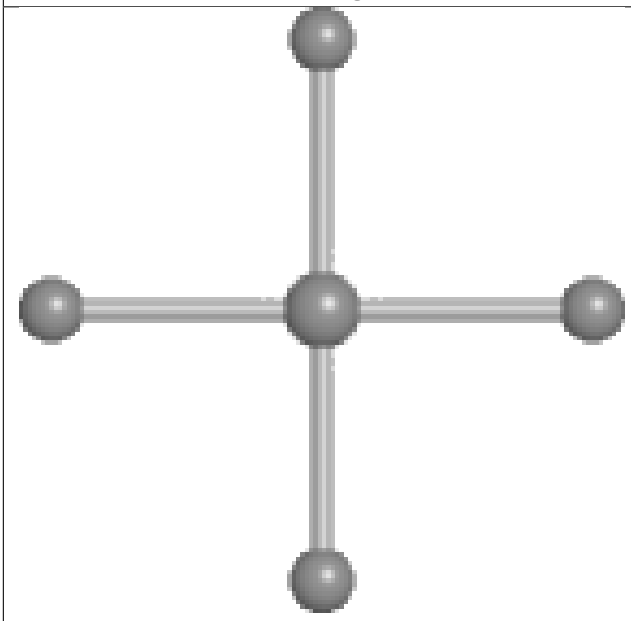

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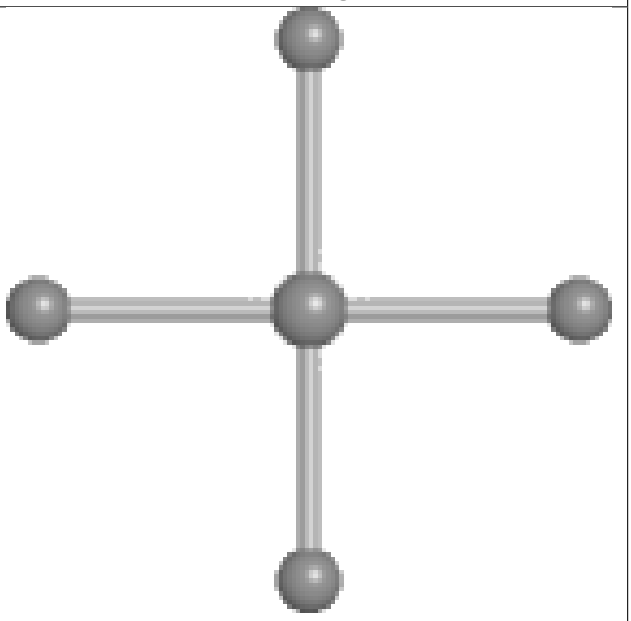
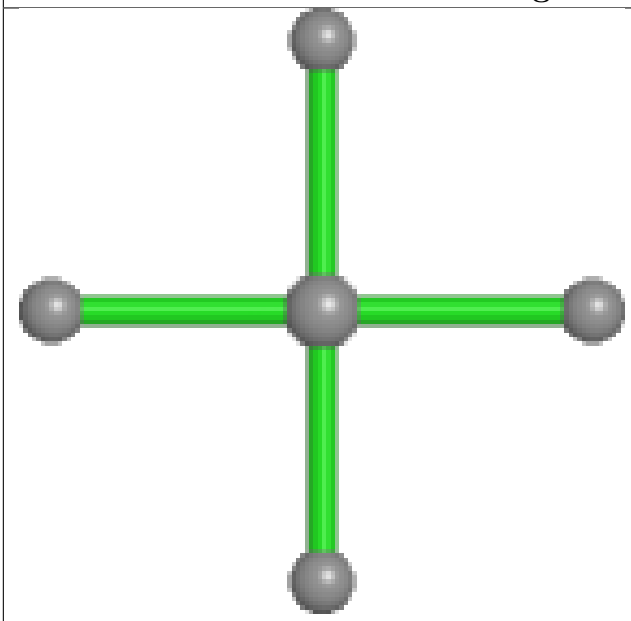


Rings

Ligand SO4 J 207



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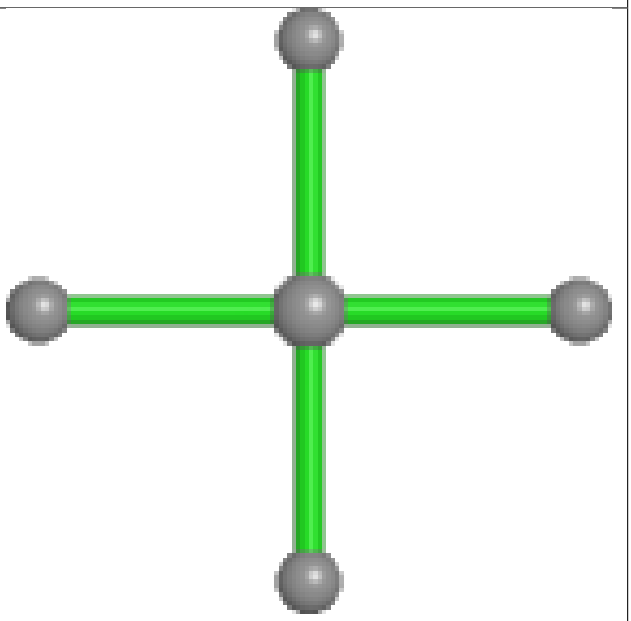

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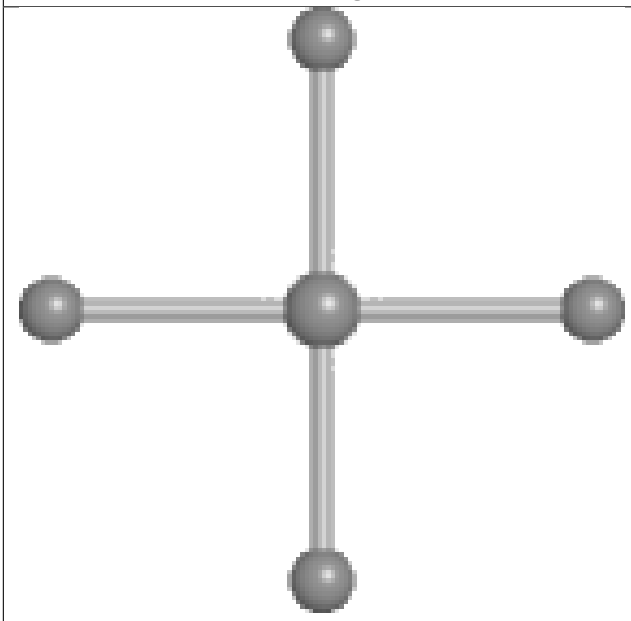

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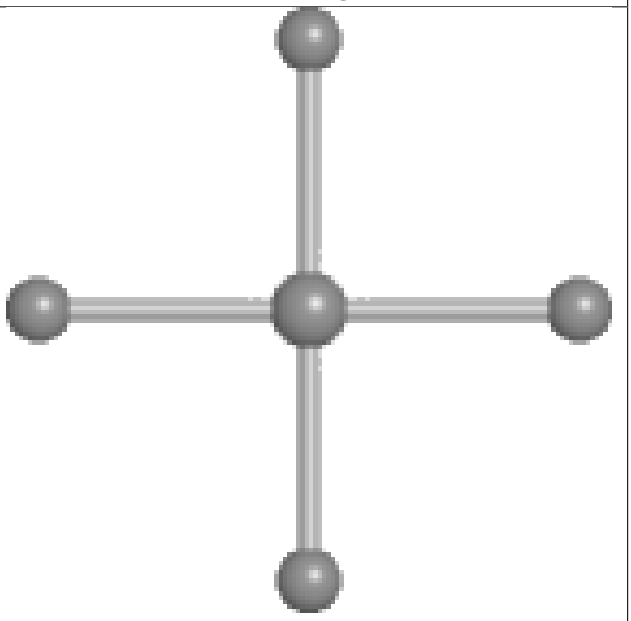
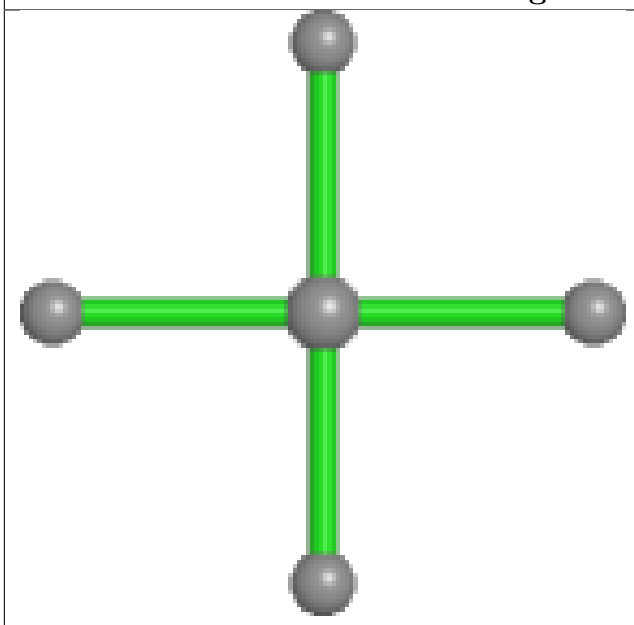


Rings

Ligand SO4 G 206



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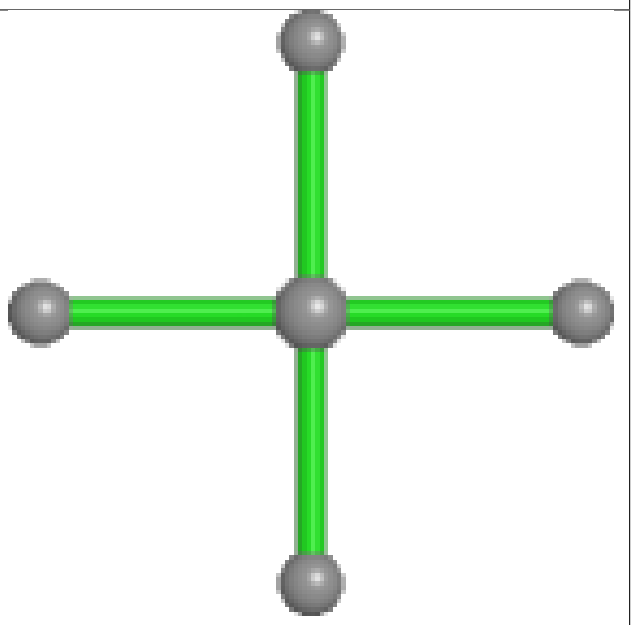
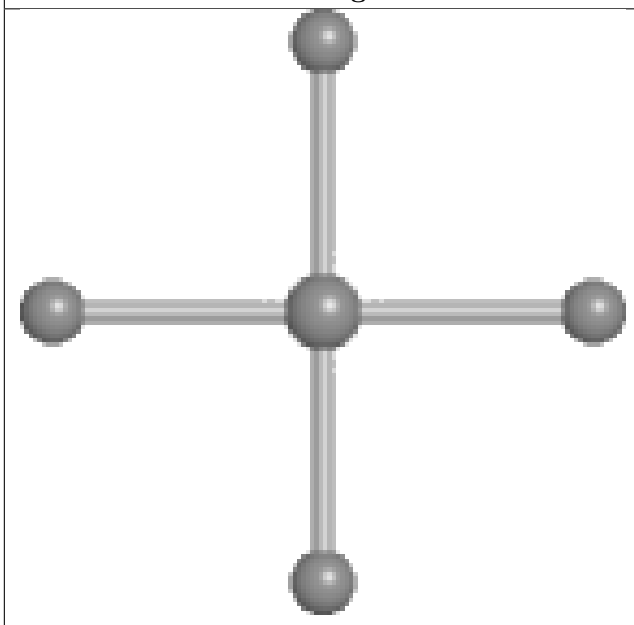
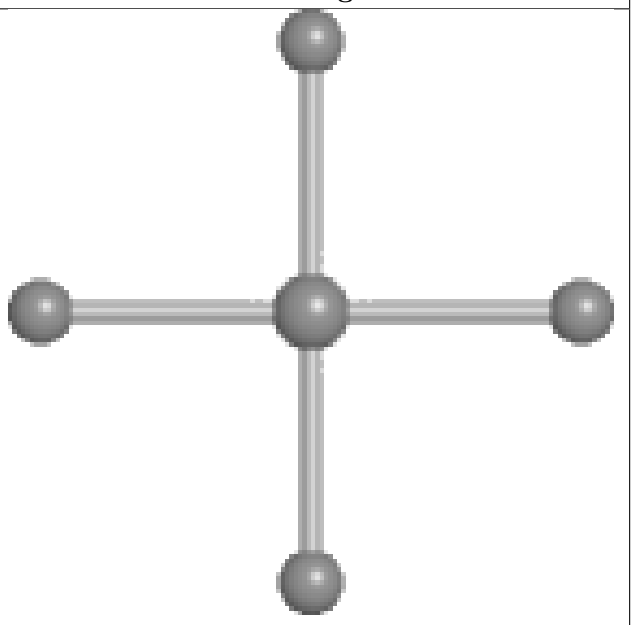


Bond angles

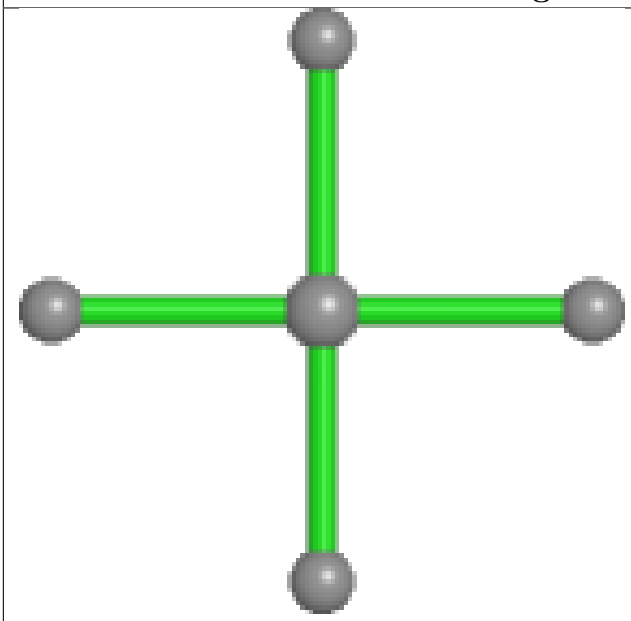


Torsions



Rings

Ligand SO4 J 206



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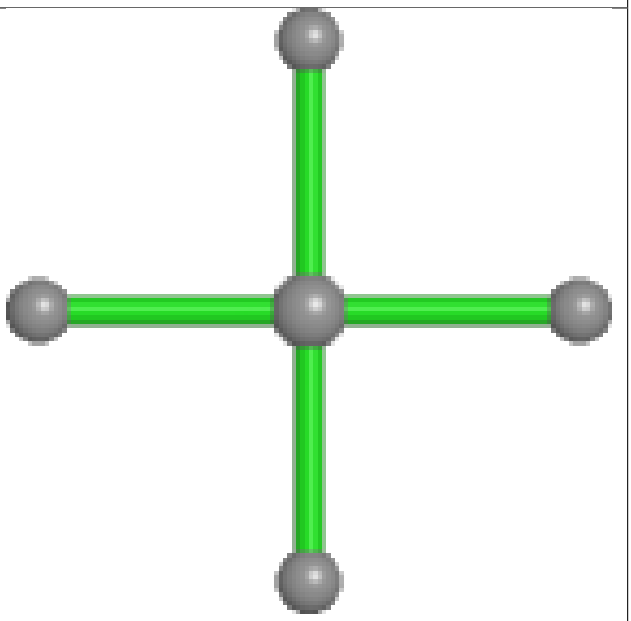
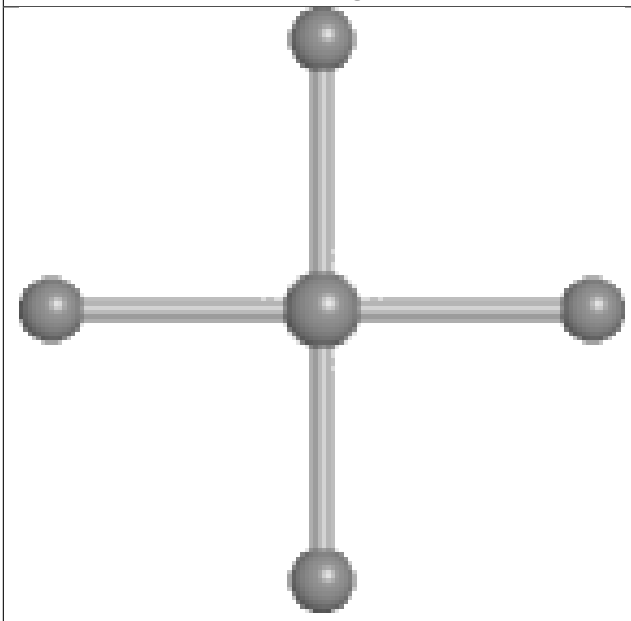
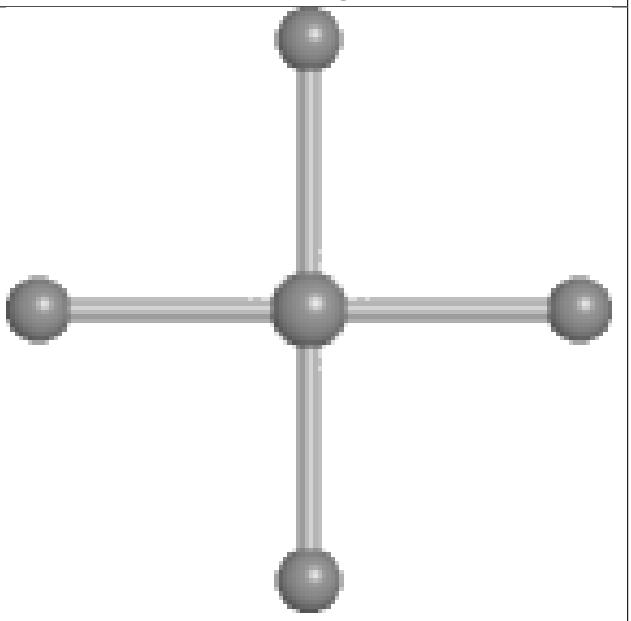


Bond angles

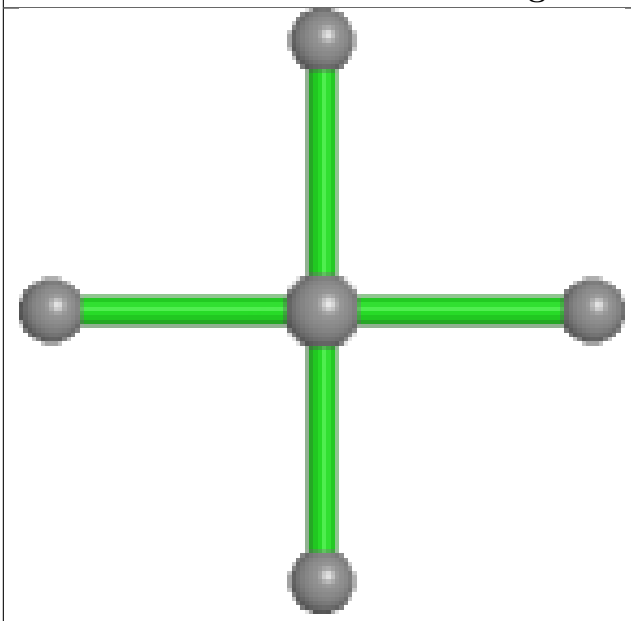


Torsions

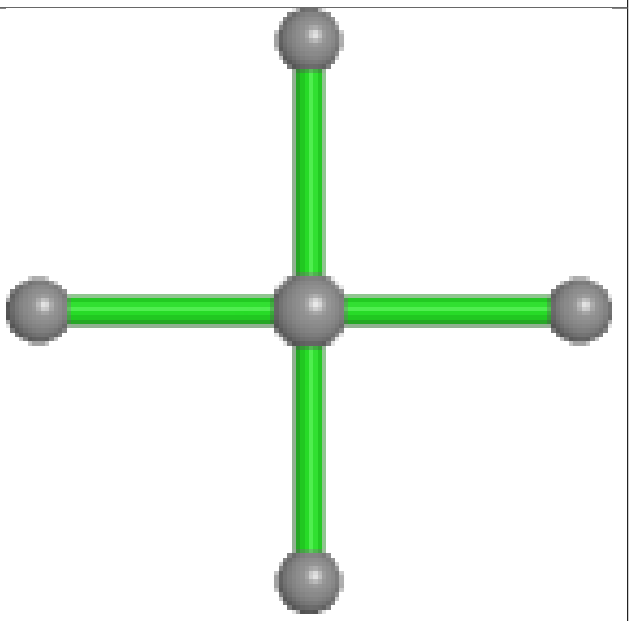


Rings

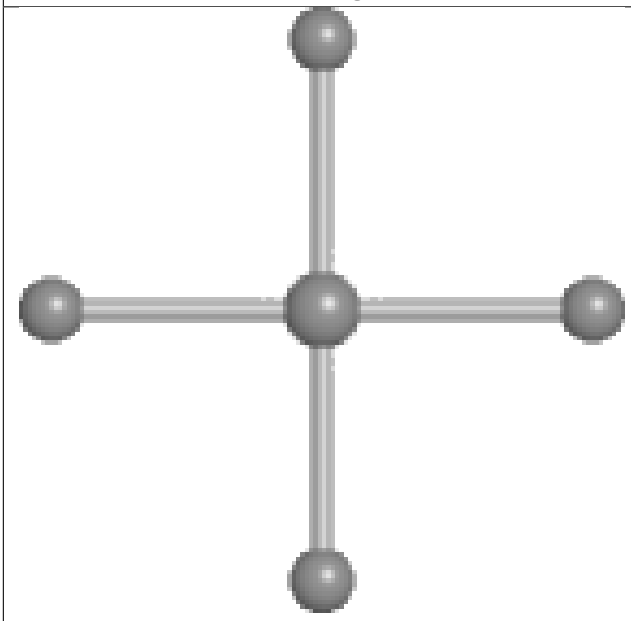
Ligand SO4 D 213



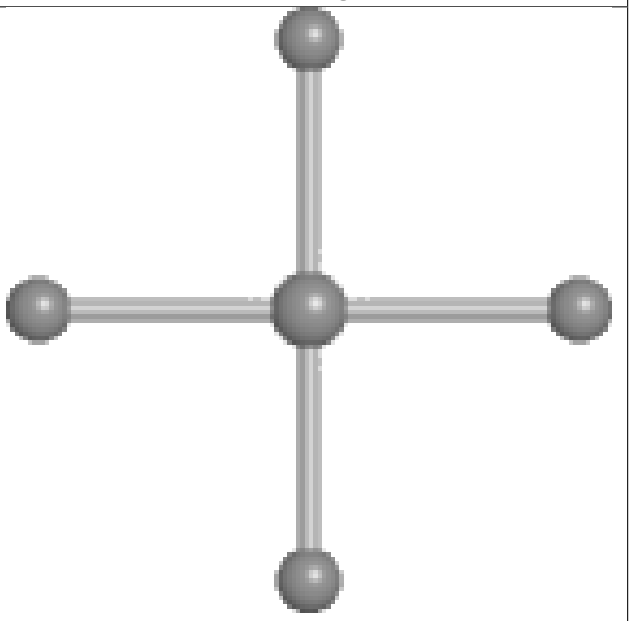
Bond lengths



Bond angles

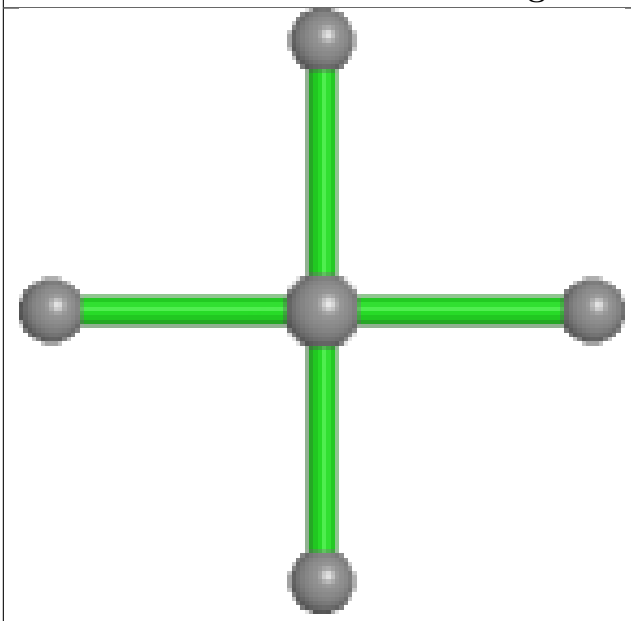


Torsions

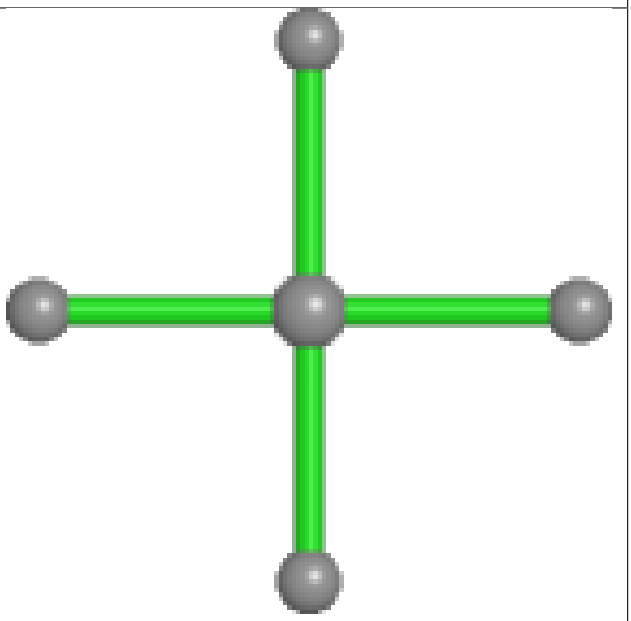


Rings

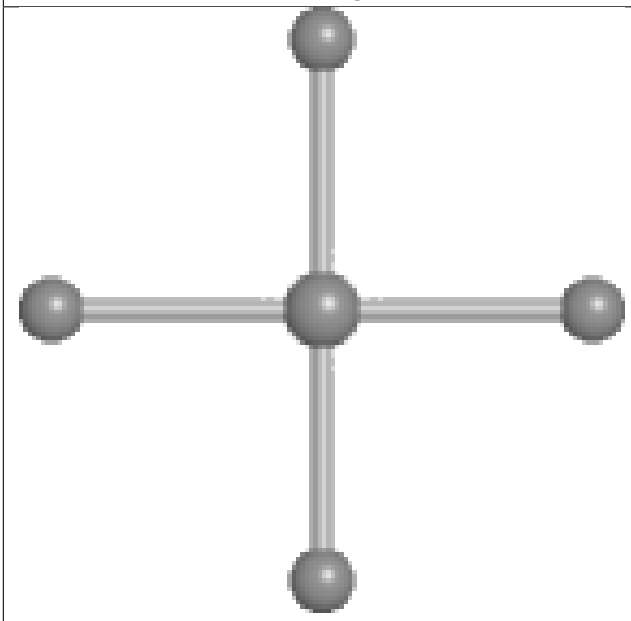
Ligand SO4 H 205



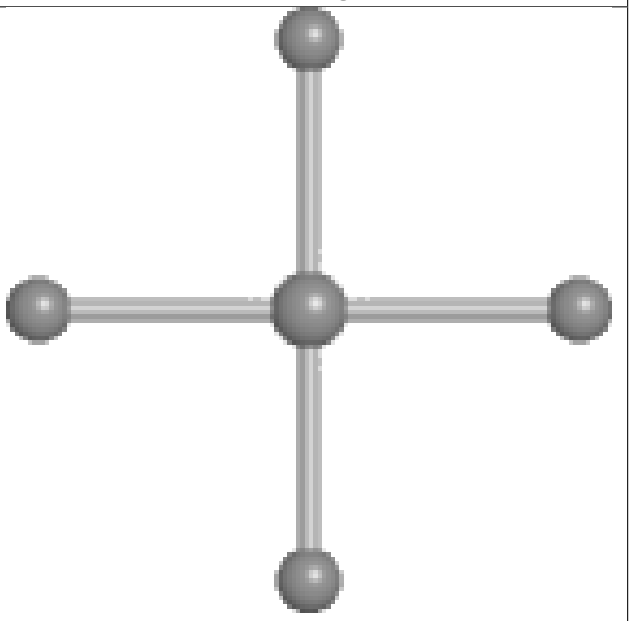
Bond lengths



Bond angles

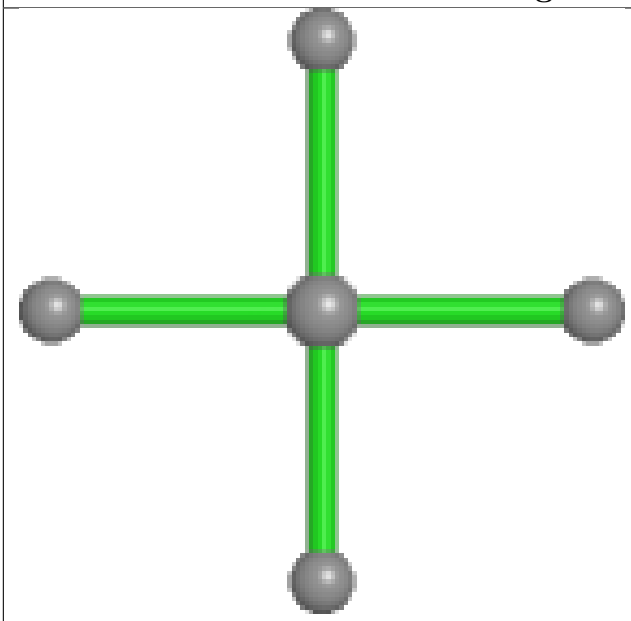


Torsions



Rings

Ligand SO4 I 204



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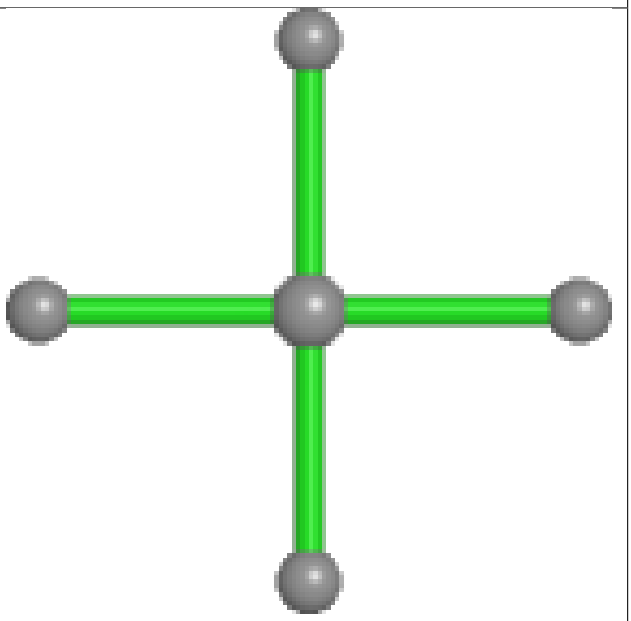
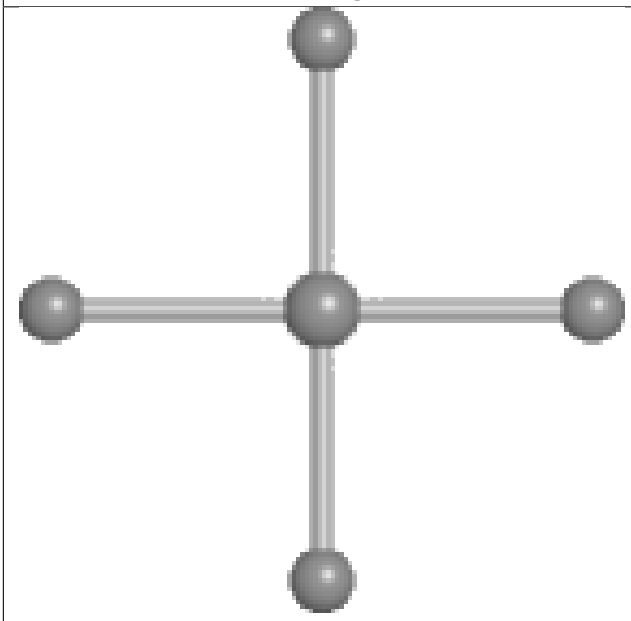
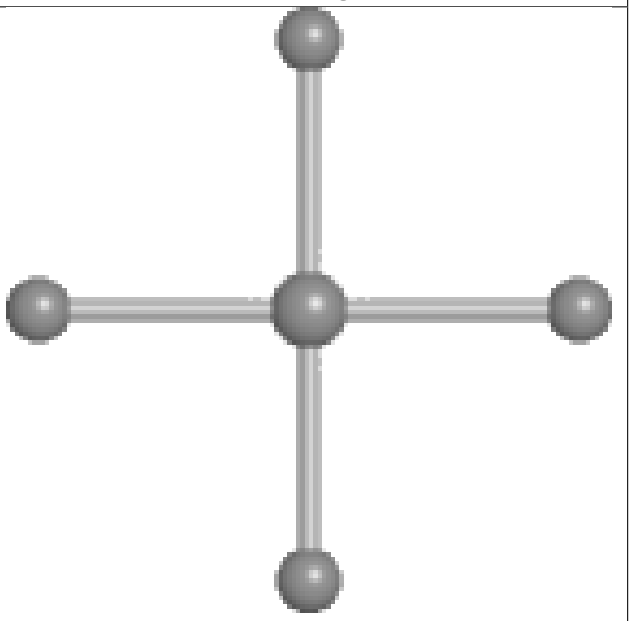


Bond angles

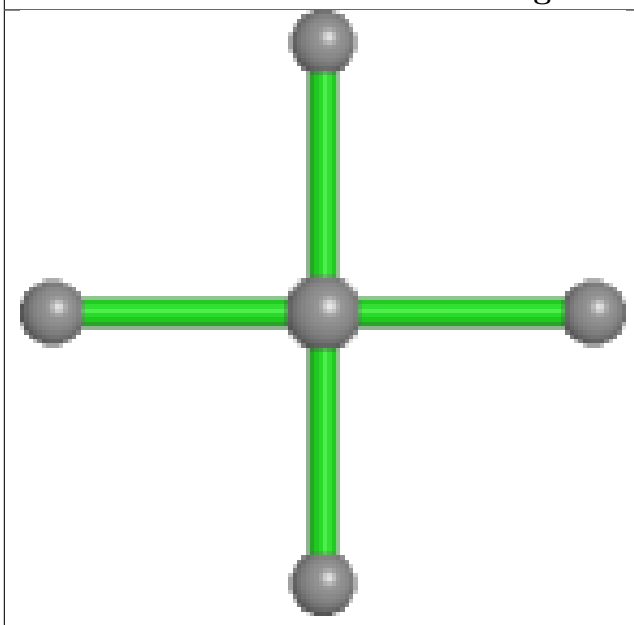


Torsions



Rings

Ligand SO4 J 204



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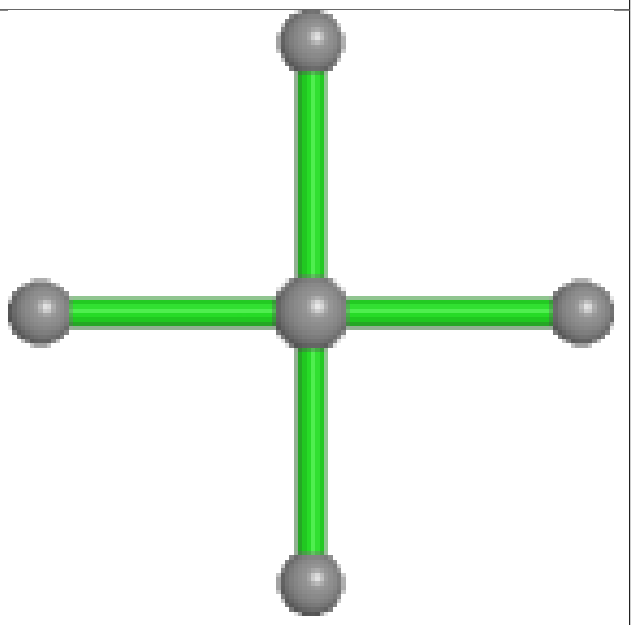
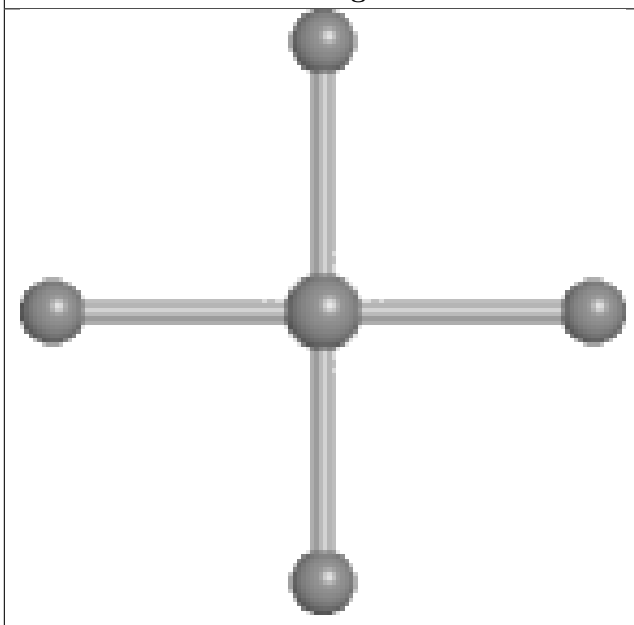


Bond angles



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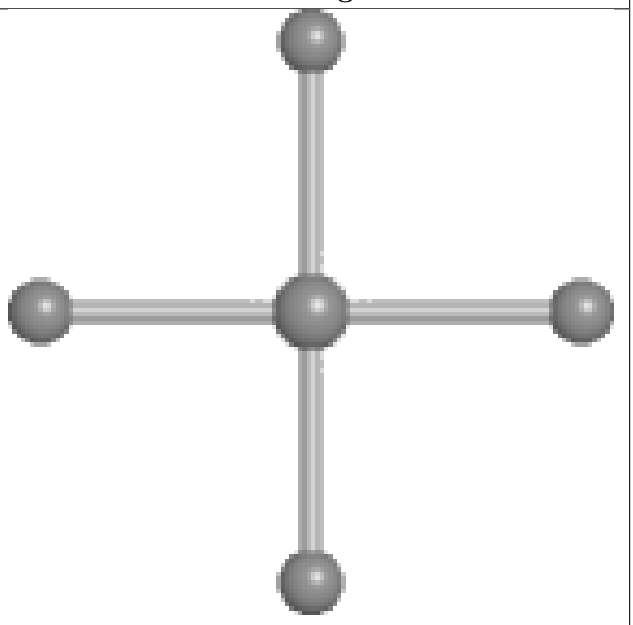
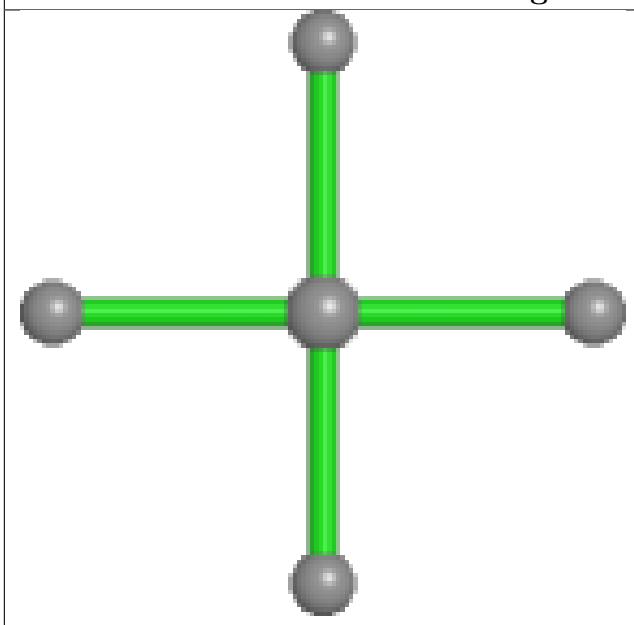


Rings

Ligand SO4 B 212



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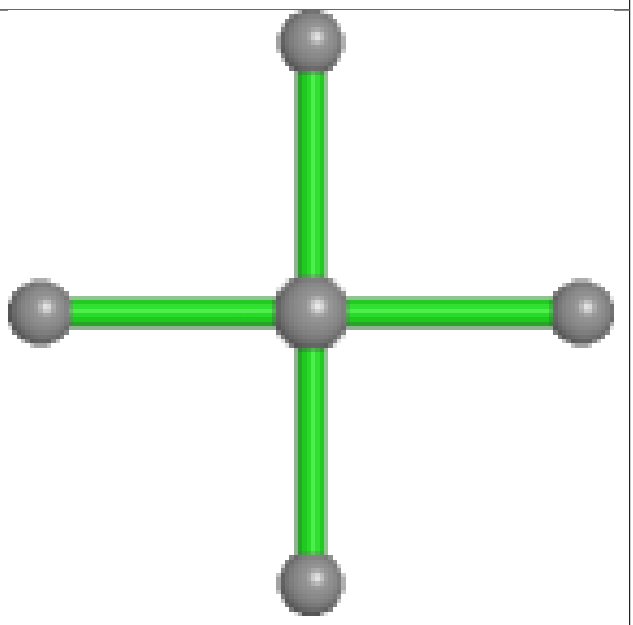
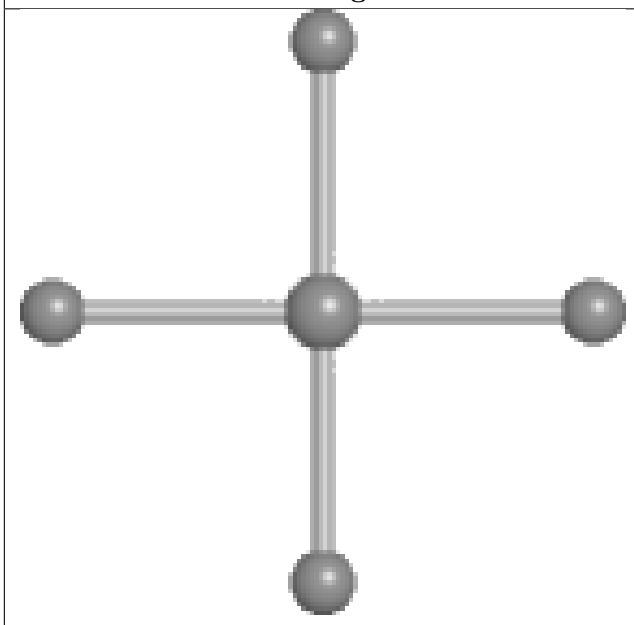
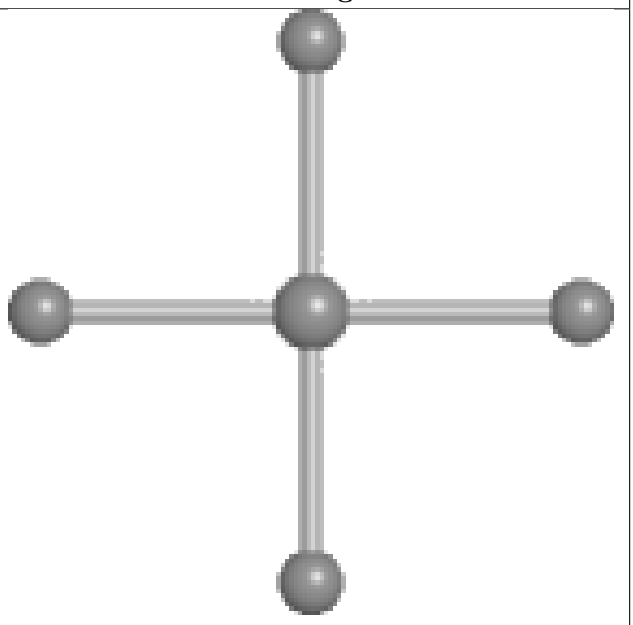


Bond angles

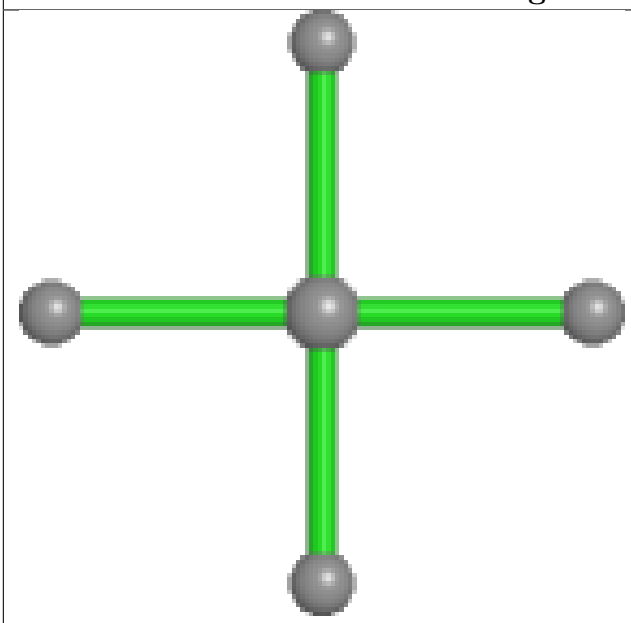


Torsions



Rings

Ligand SO4 D 211



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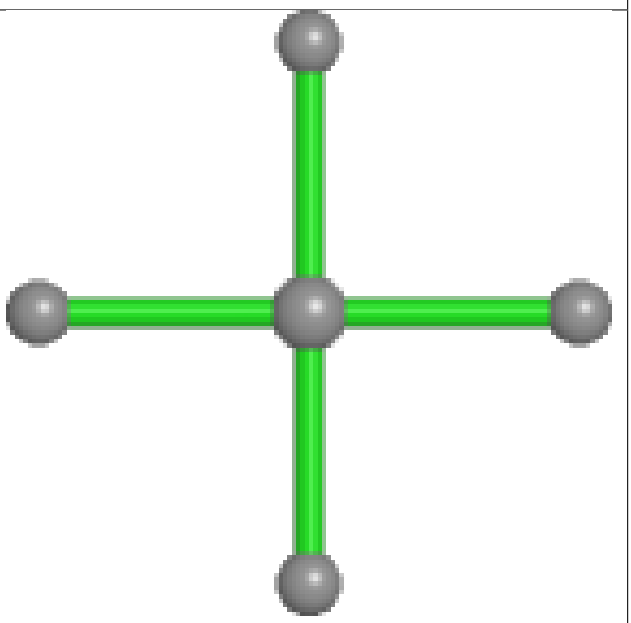
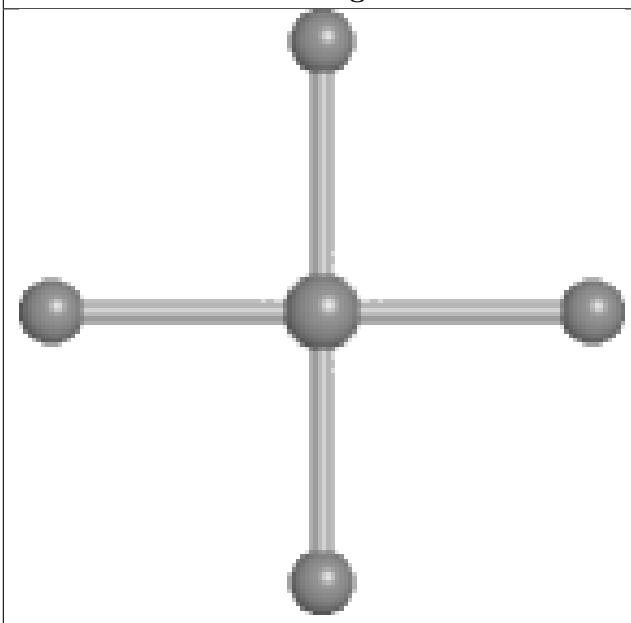


Bond angles



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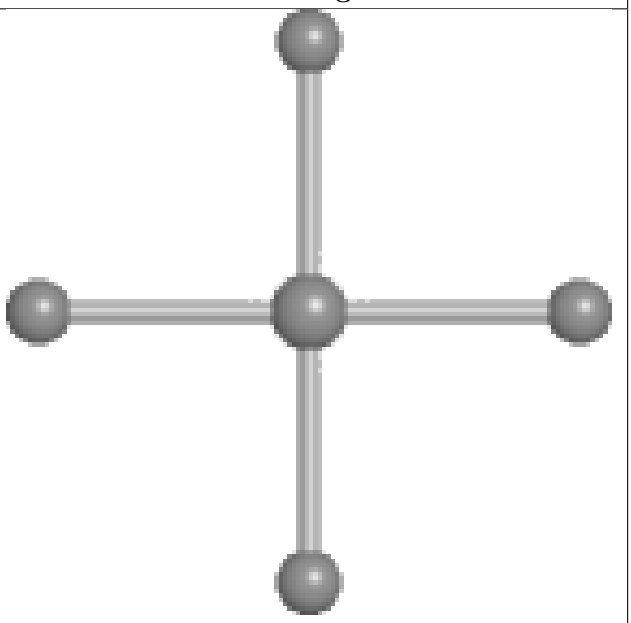
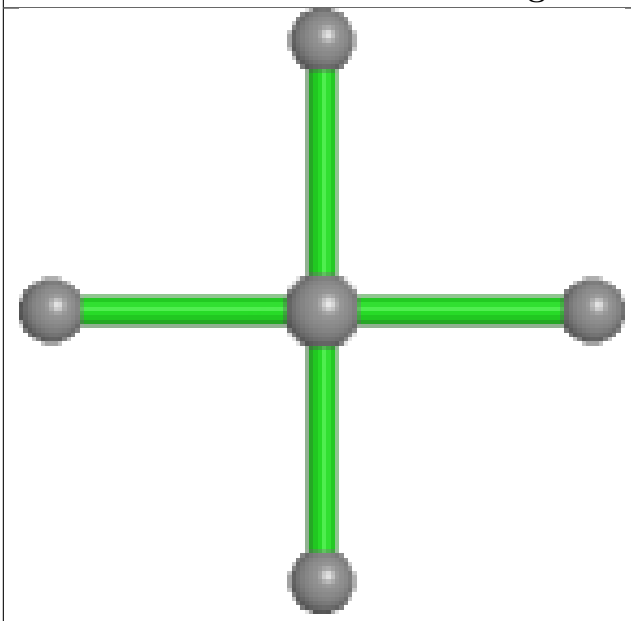
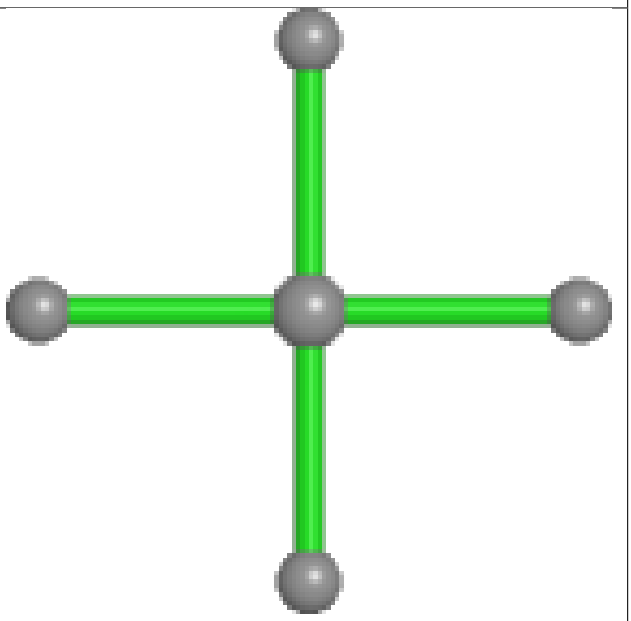


Rings

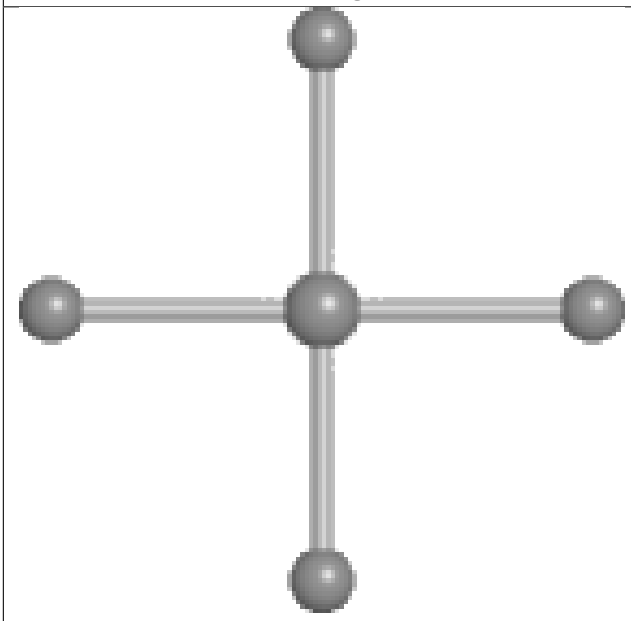
Ligand SO4 K 206



Bond lengths



Bond angles



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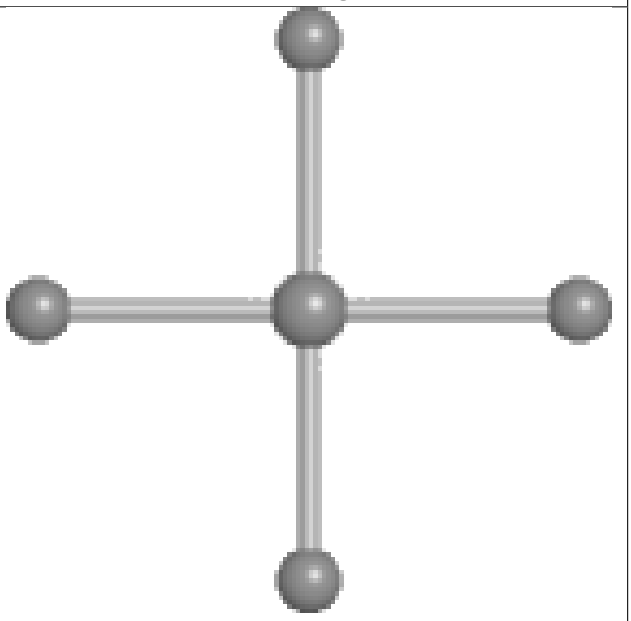
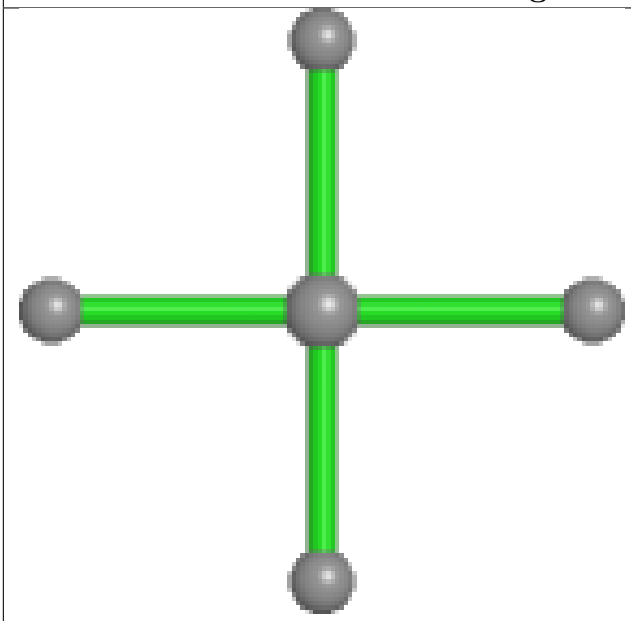


Rings

Ligand SO4 B 213



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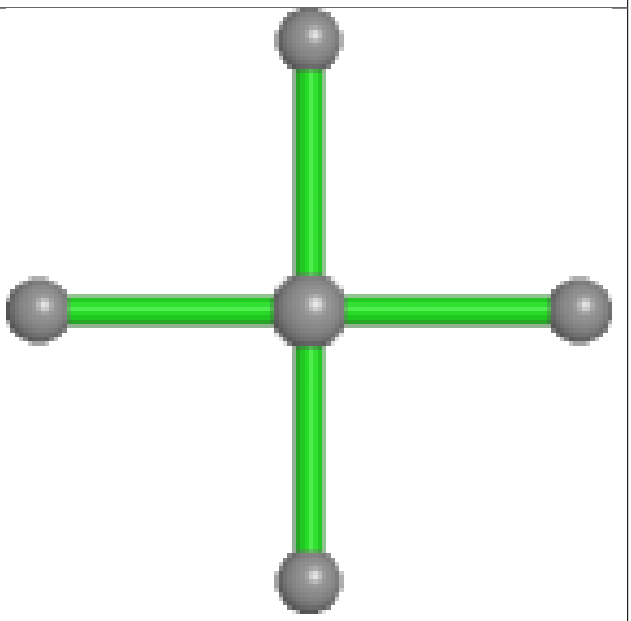
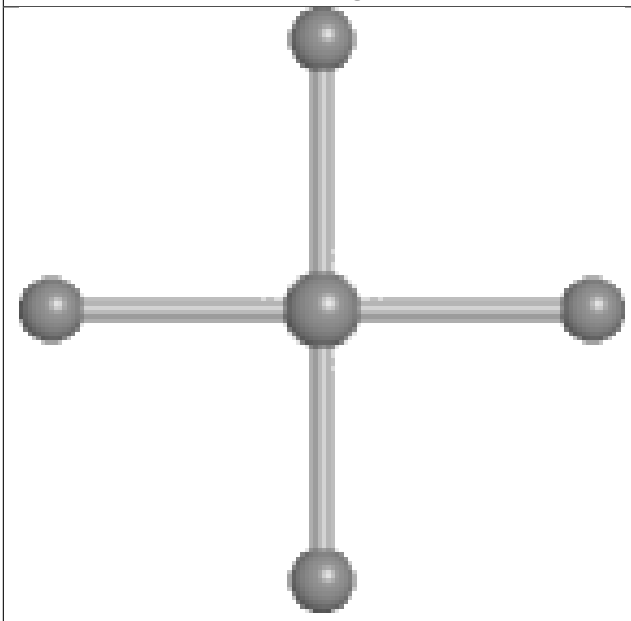


Bond angles



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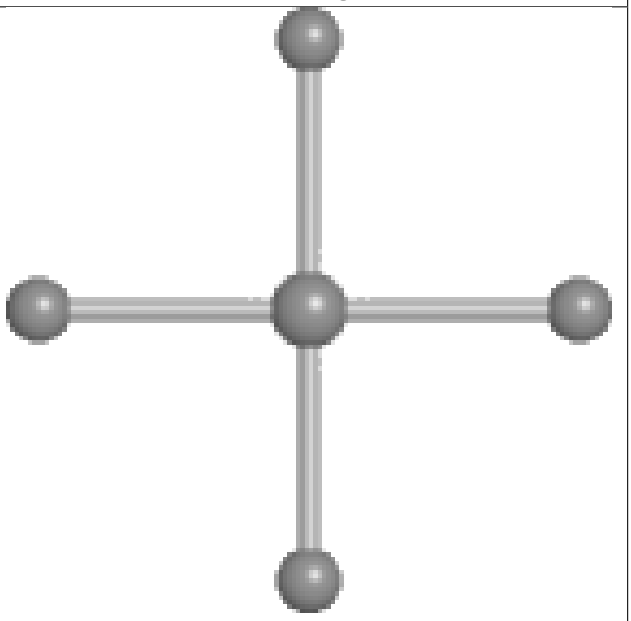
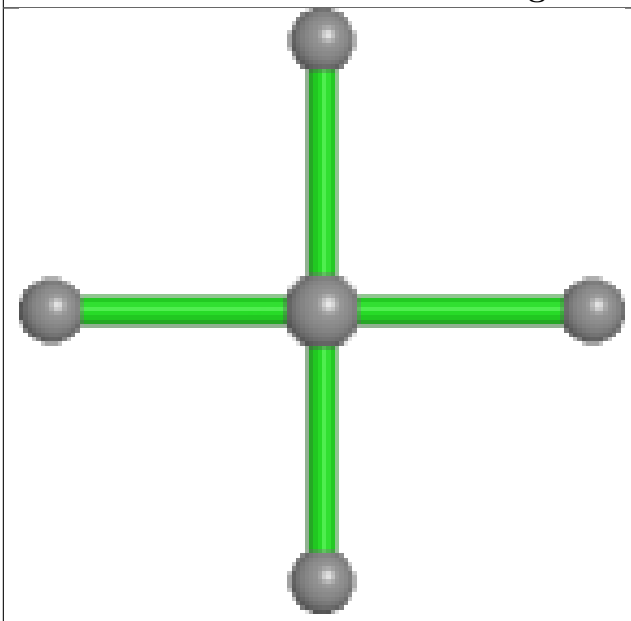
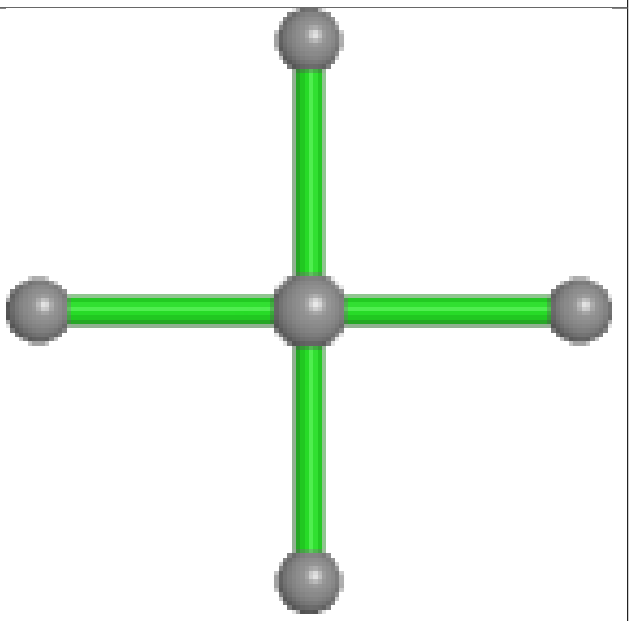


Rings

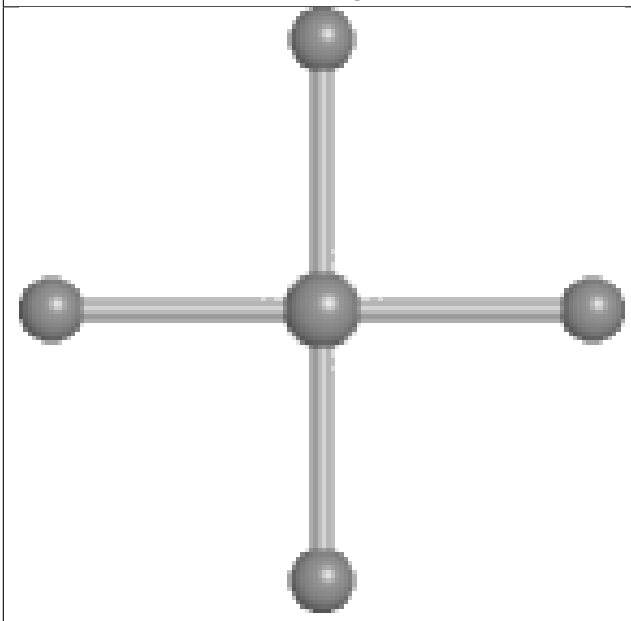
Ligand SO4 D 208



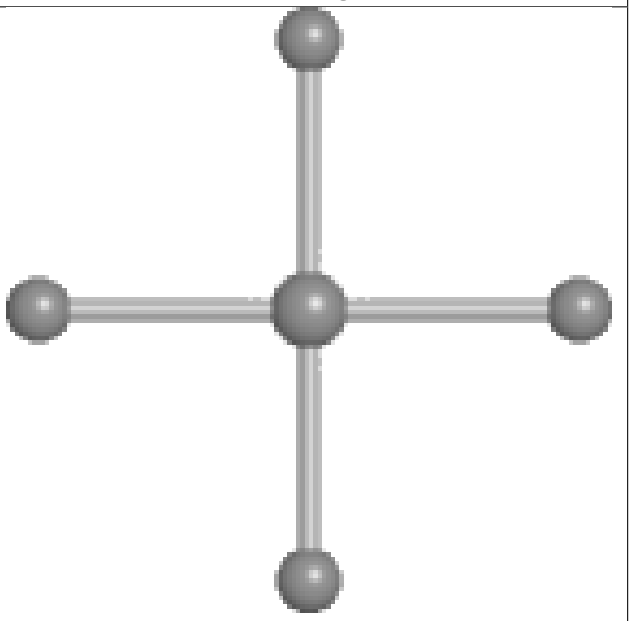
Bond lengths



Bond angles

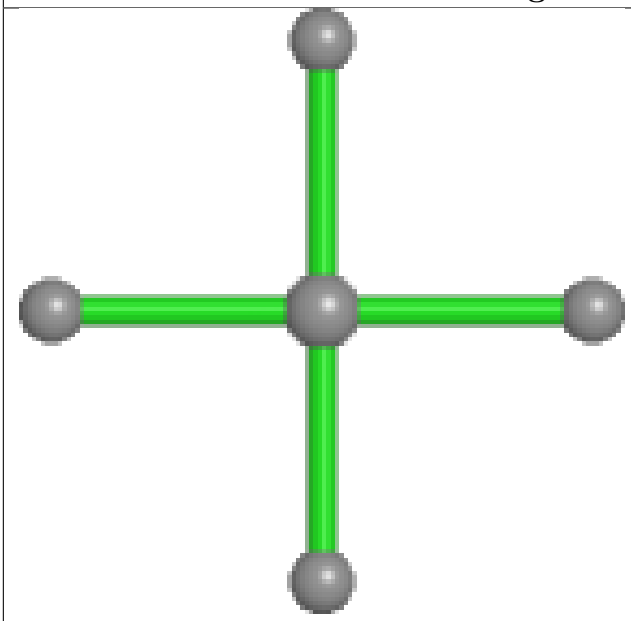


Torsions



Rings

Ligand SO4 G 208



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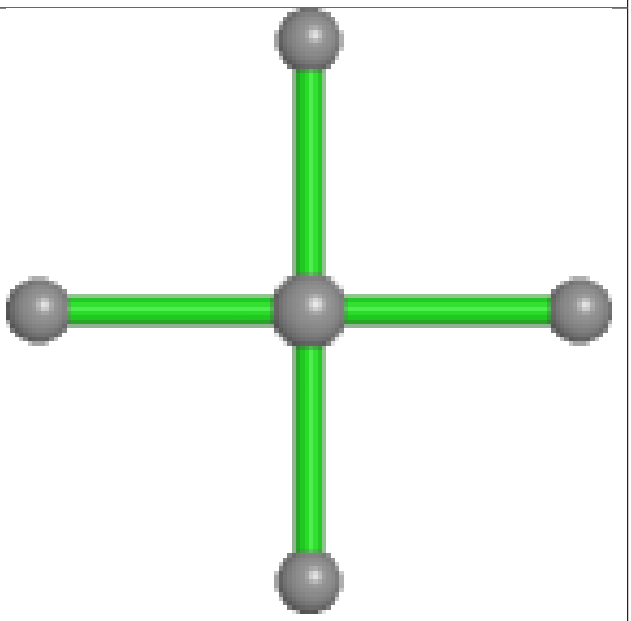
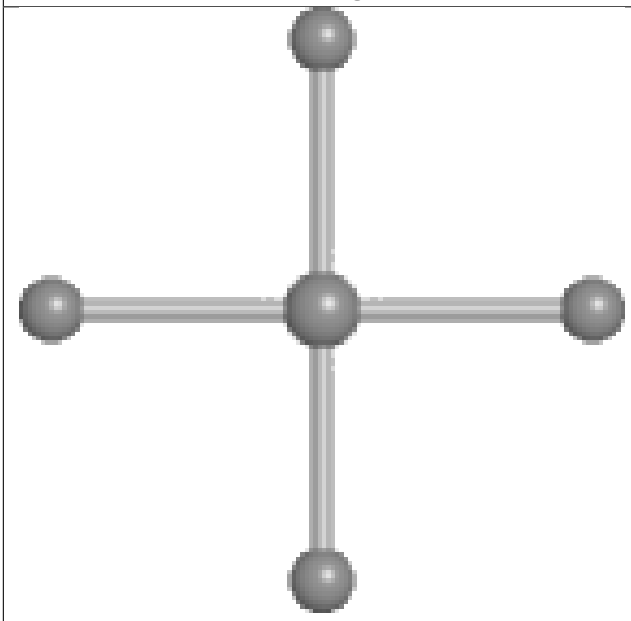


Bond angles



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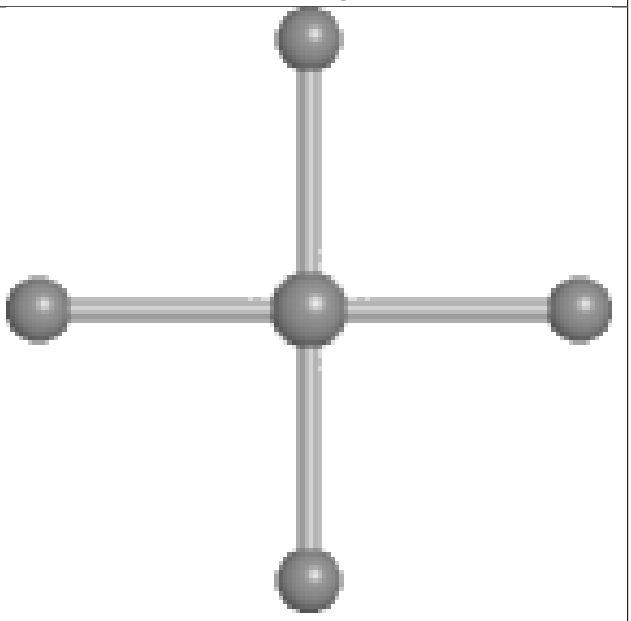
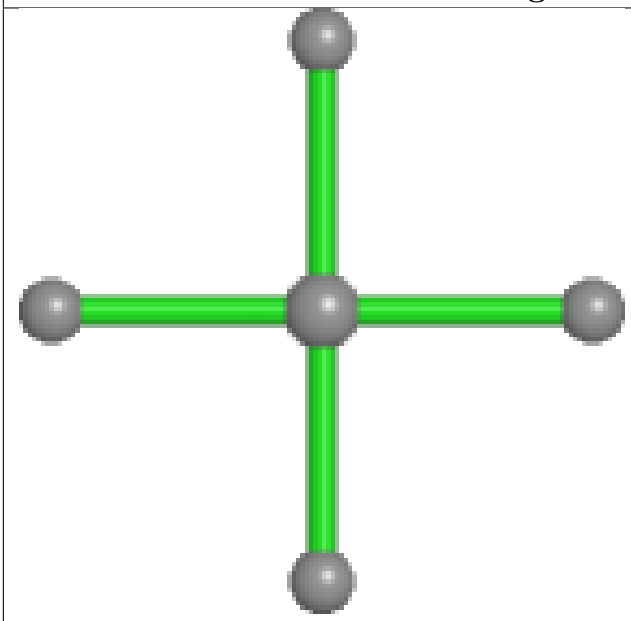
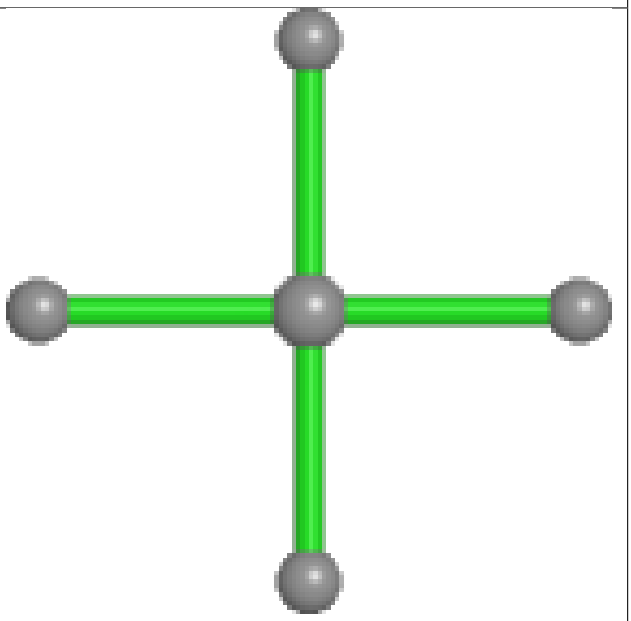


Rings

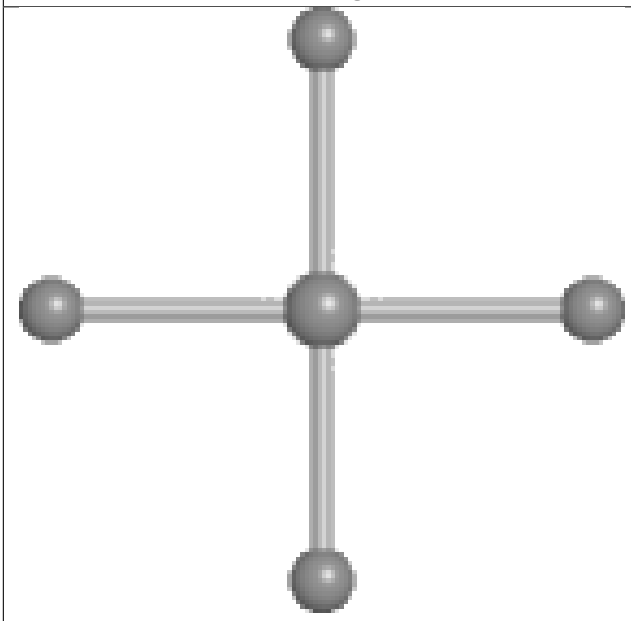
Ligand SO4 G 209



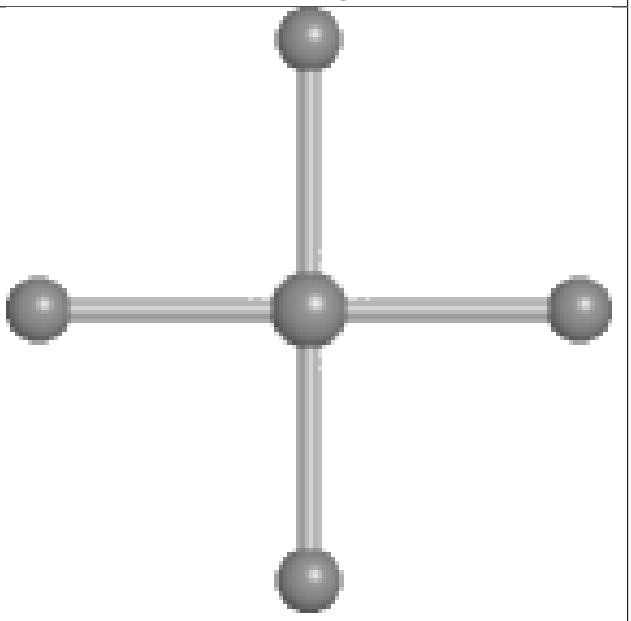
Bond lengths



Bond angles

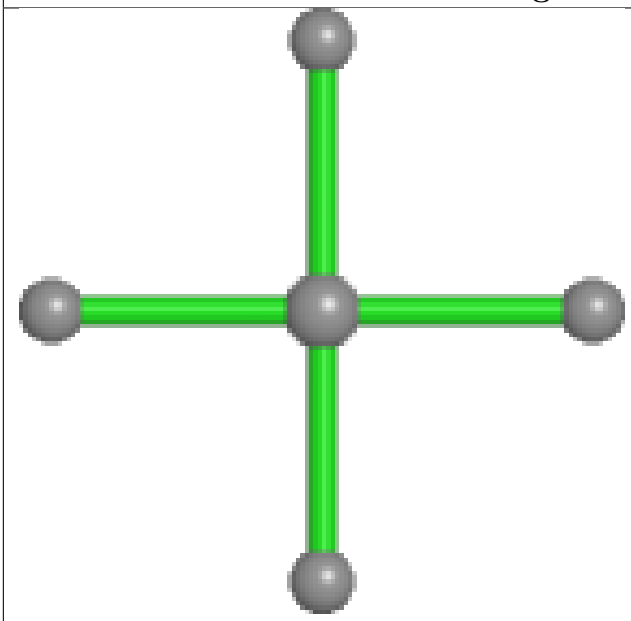


Torsions

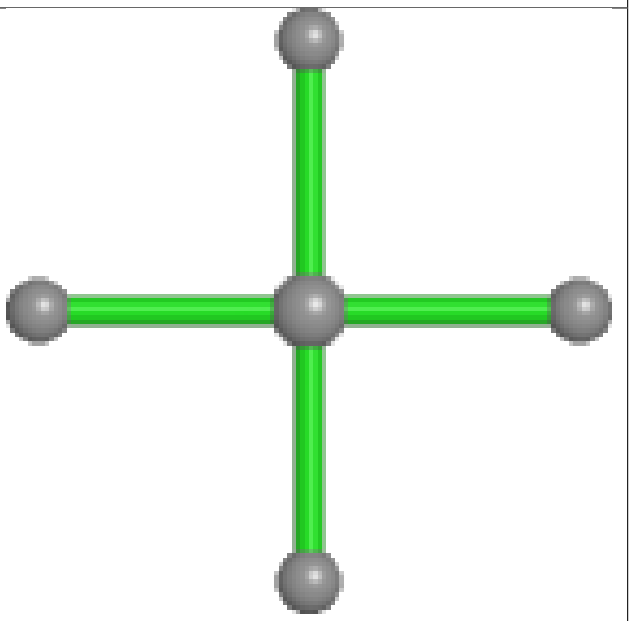


Rings

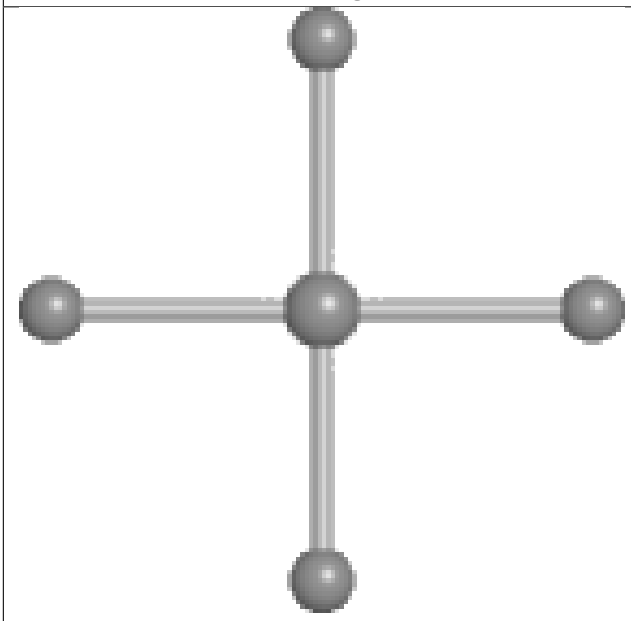
Ligand SO4 J 209



Bond lengths



Bond angles



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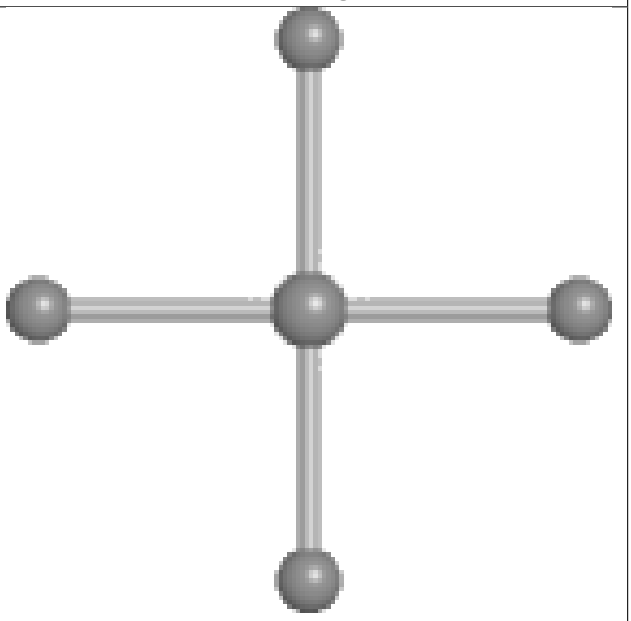
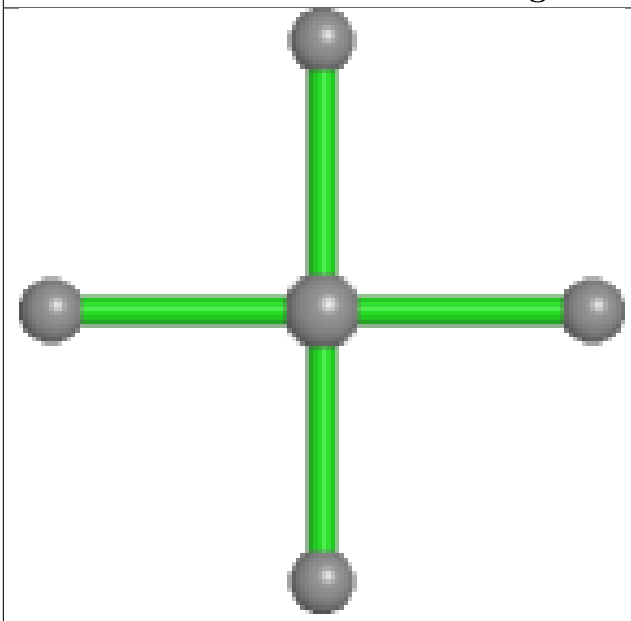
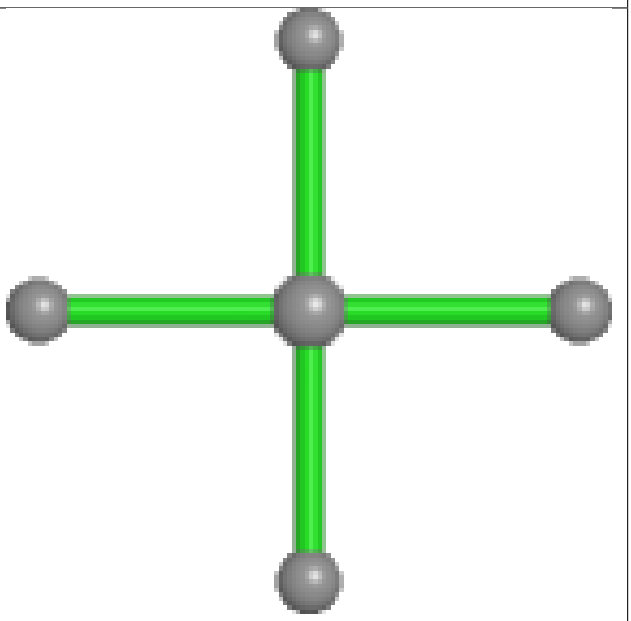


Rings

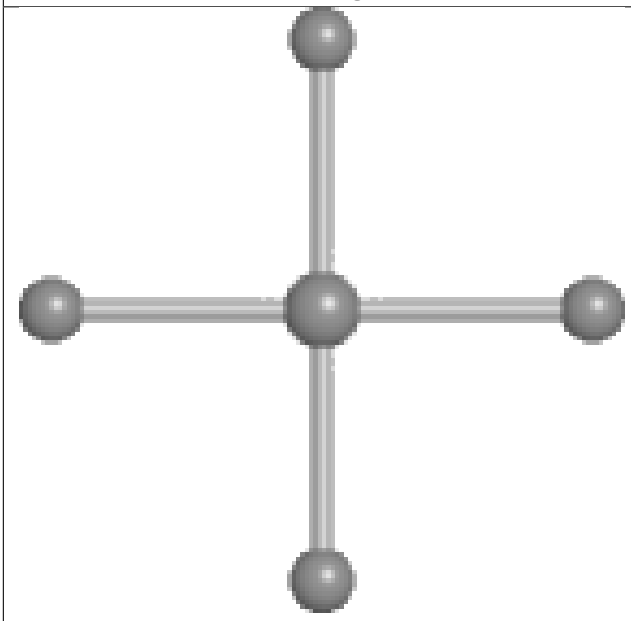
Ligand SO4 C 205



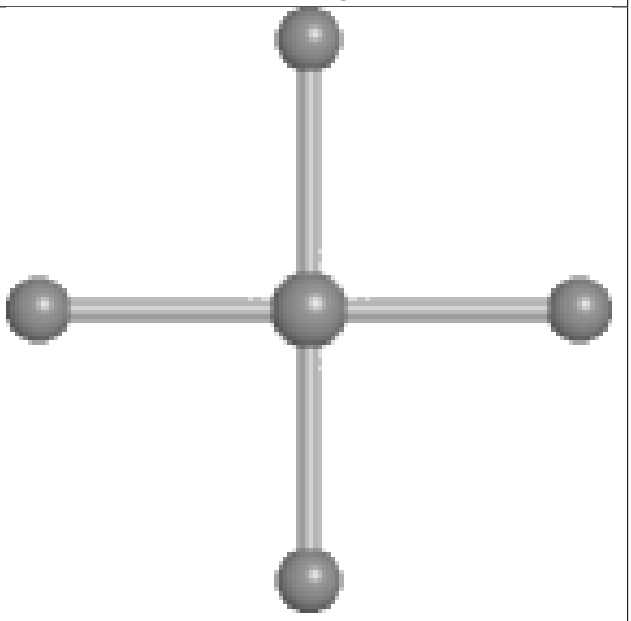
Bond lengths



Bond angles

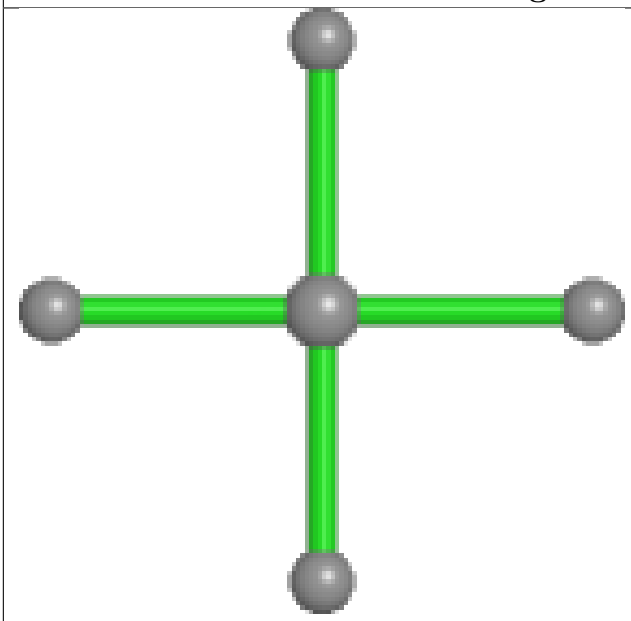


Torsions

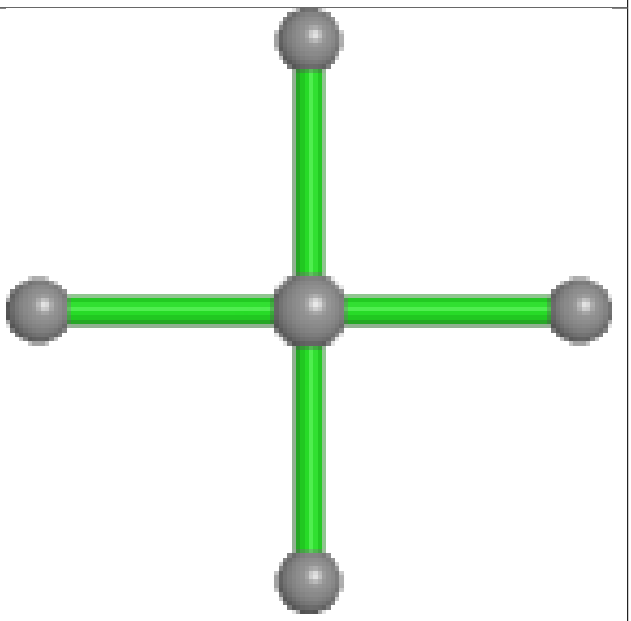


Rings

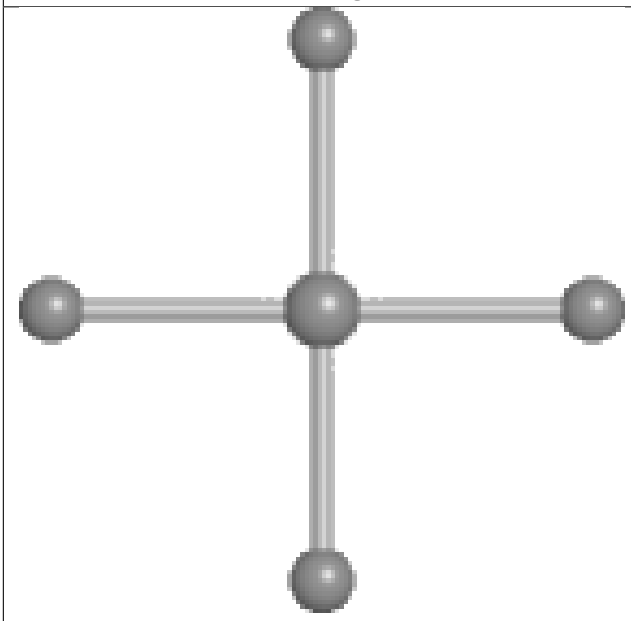
Ligand SO4 B 207



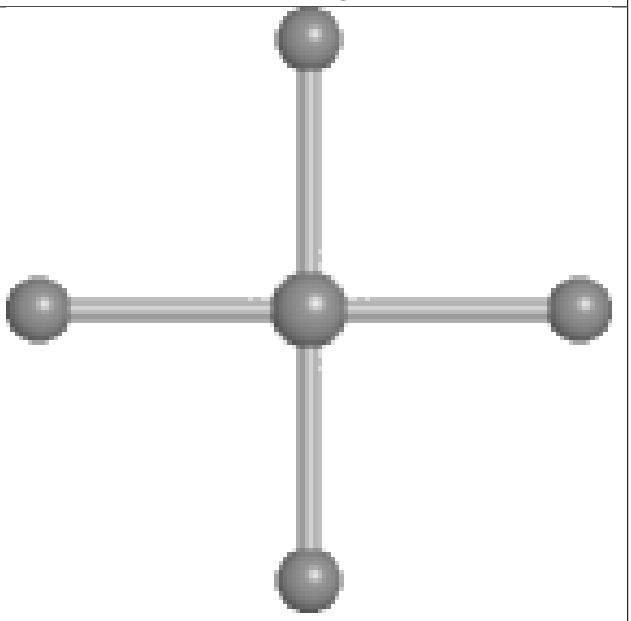
Bond lengths



Bond angles

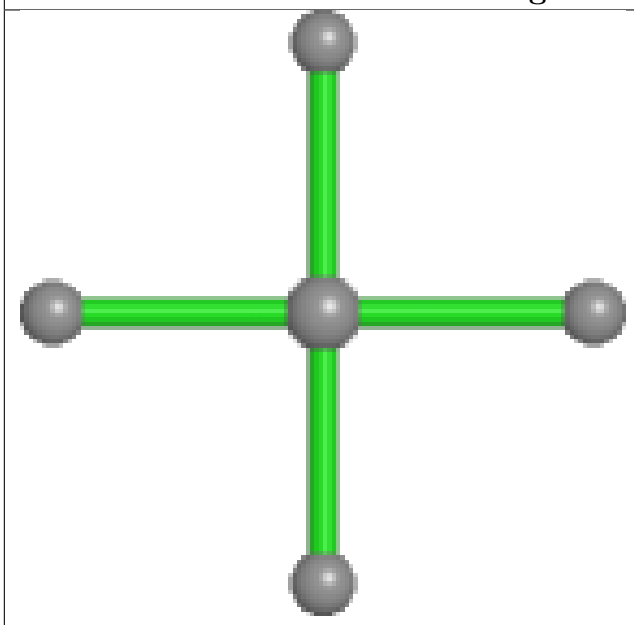


Torsions

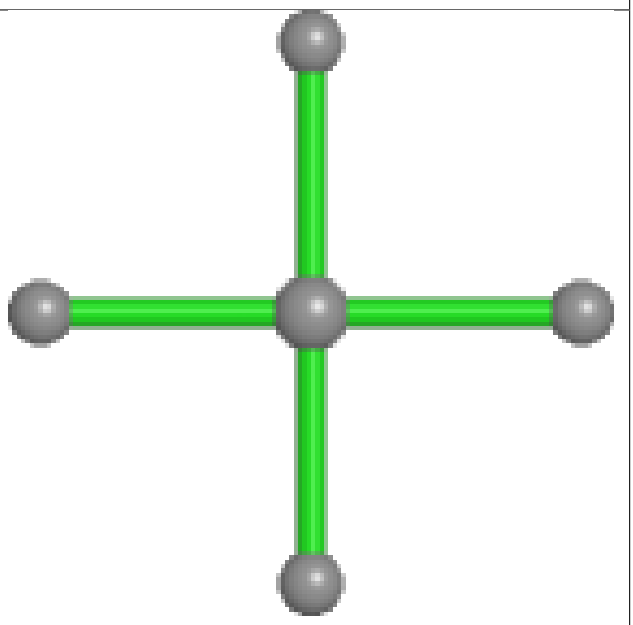


Rings

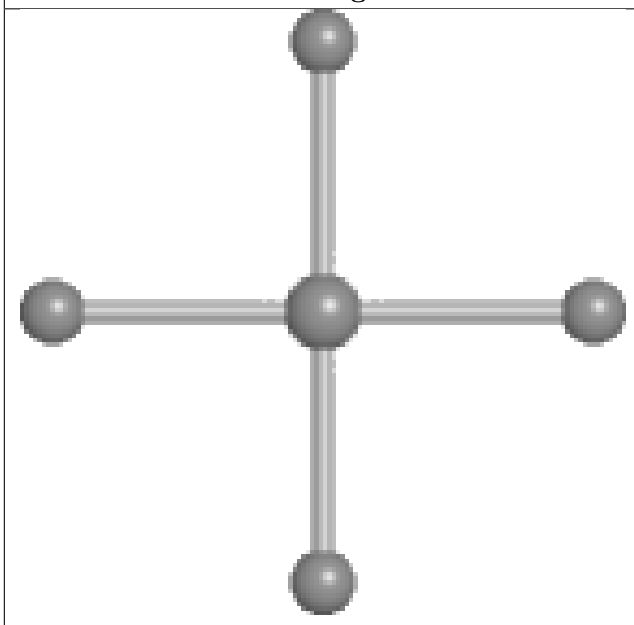
Ligand SO4 H 207



Bond lengths



Bond angles



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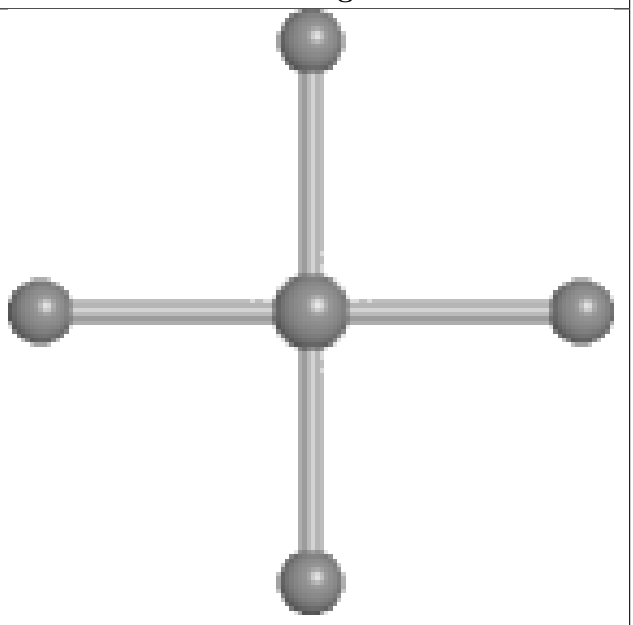
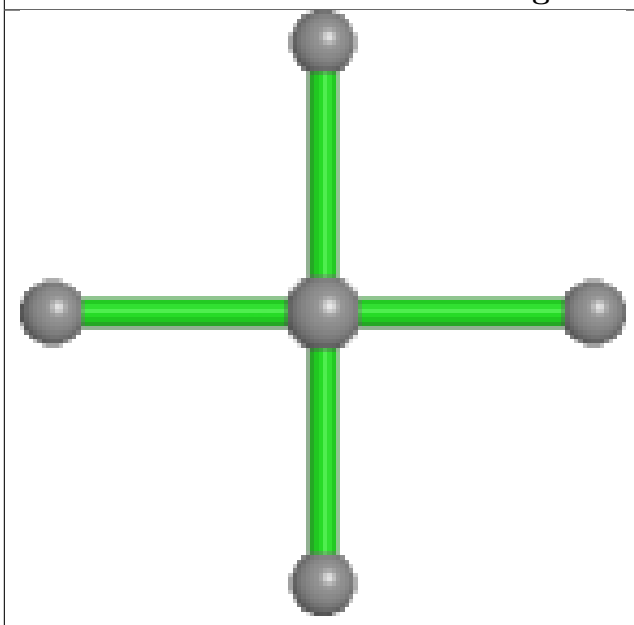


Rings

Ligand SO4 L 207



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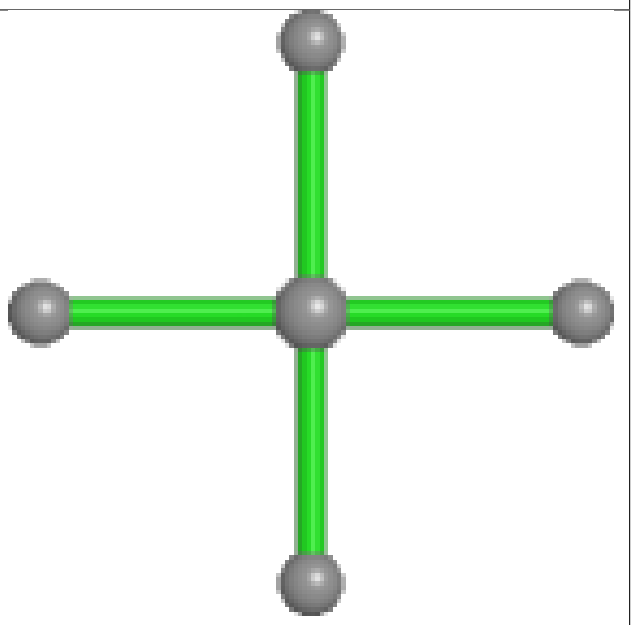

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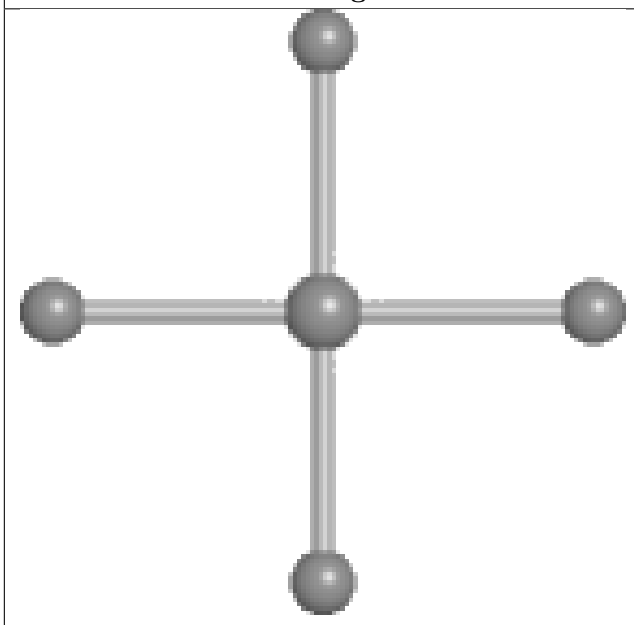

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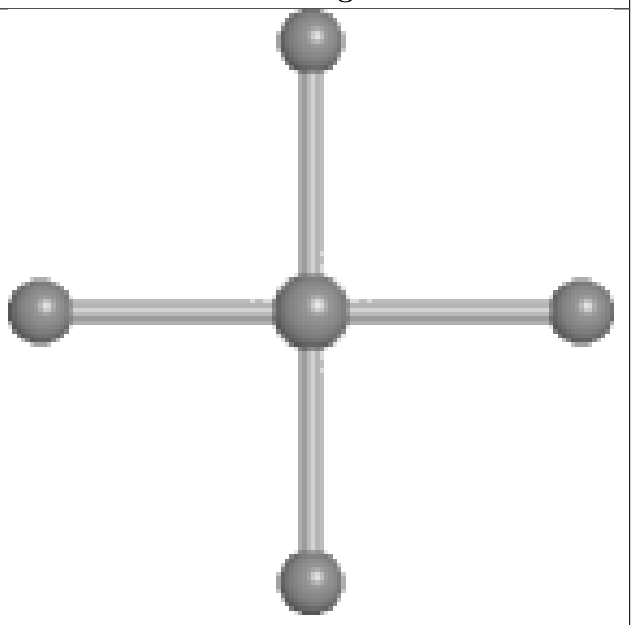
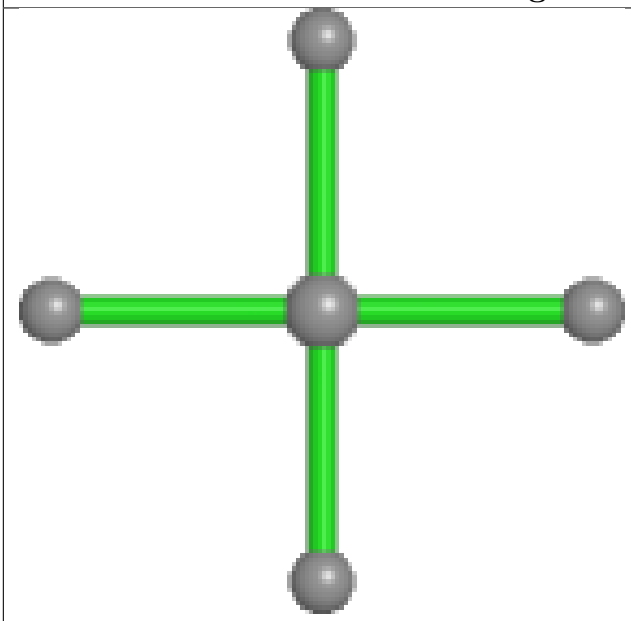


Rings

Ligand SO4 A 205



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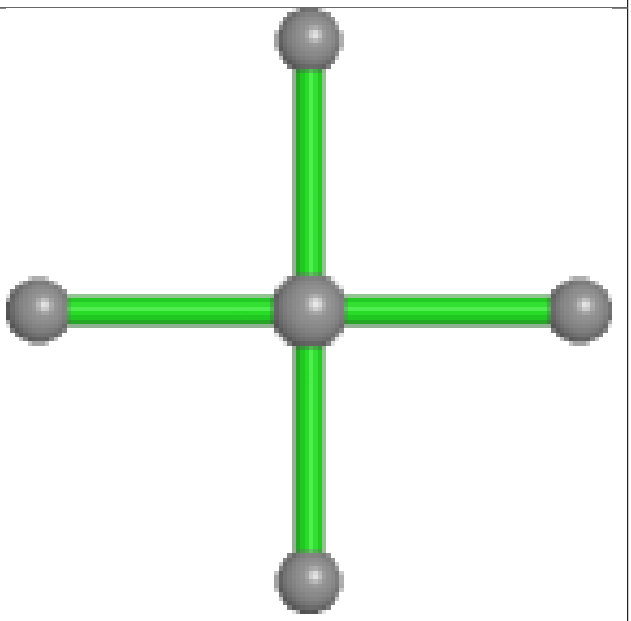
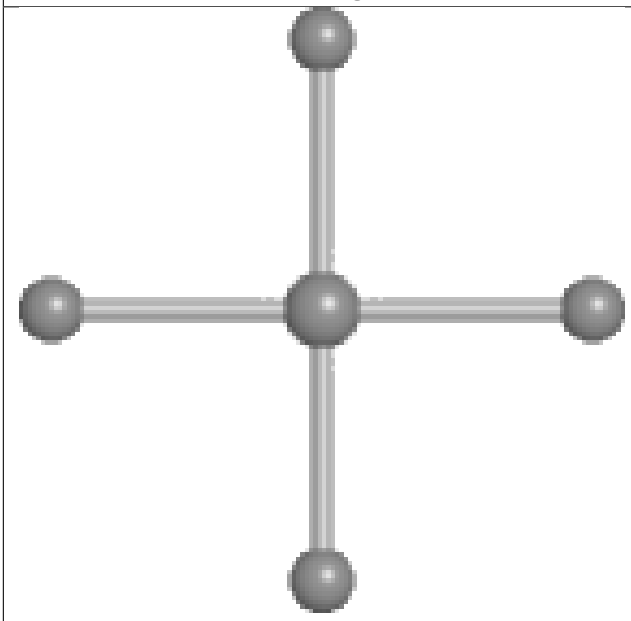


Bond angles



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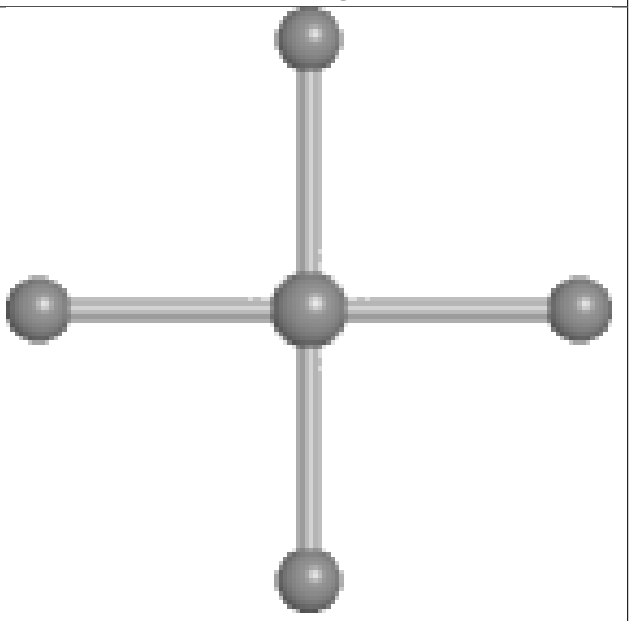
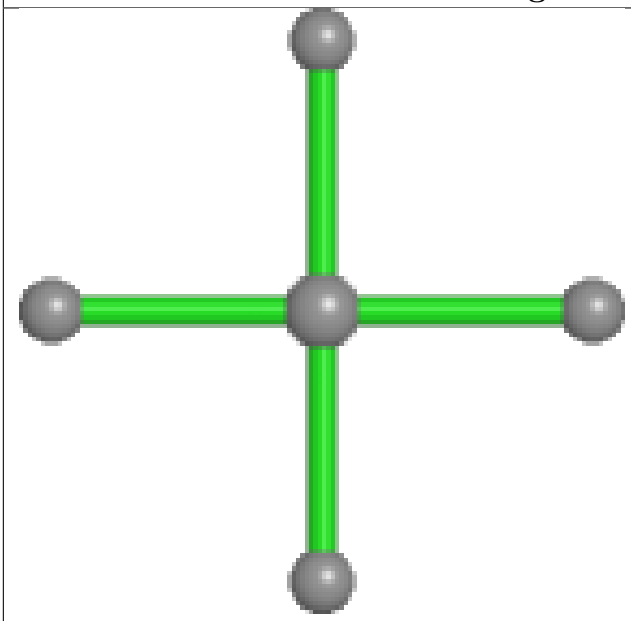


Rings

Ligand SO4 D 207



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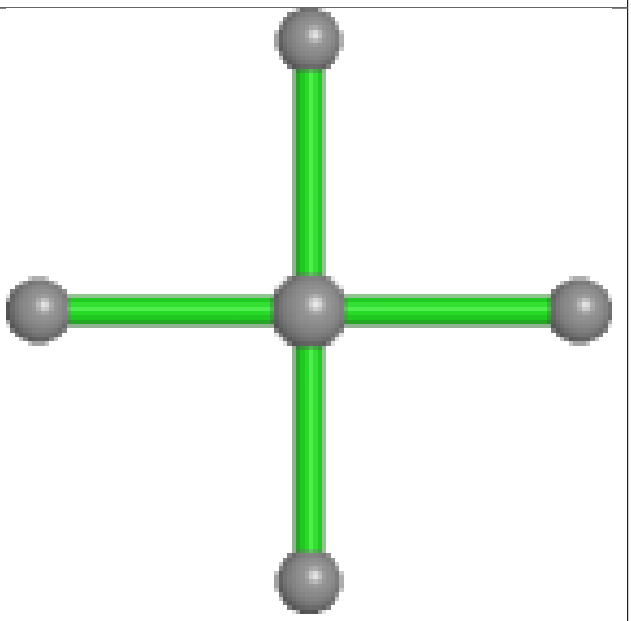
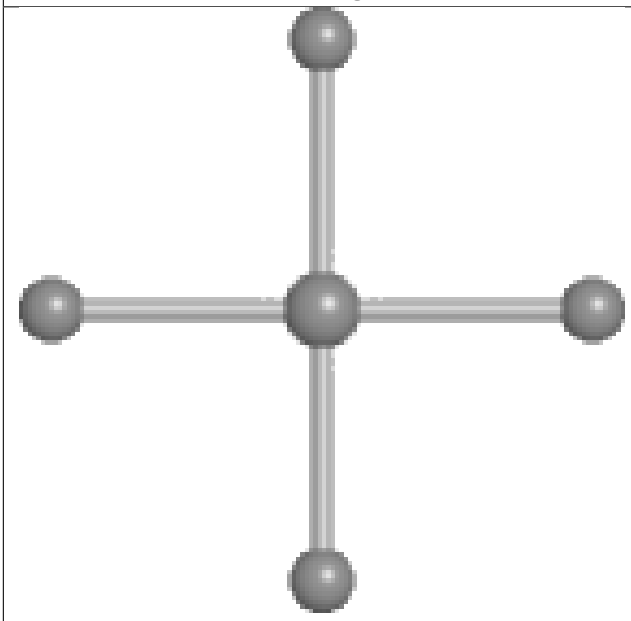


Bond angles



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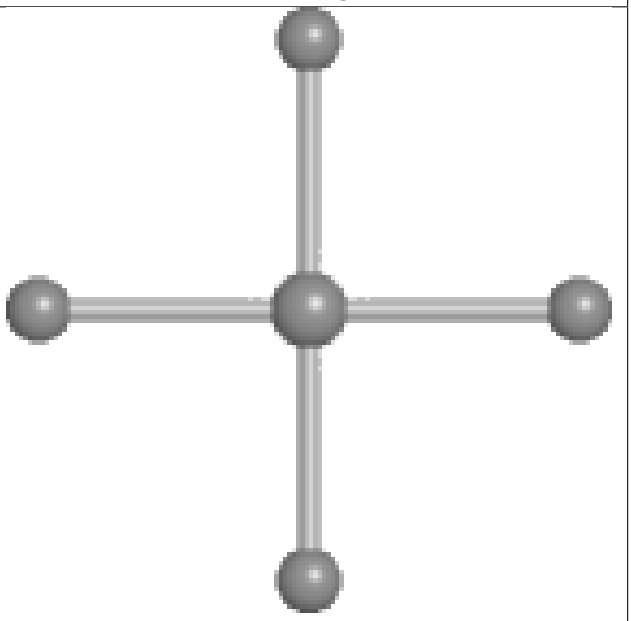
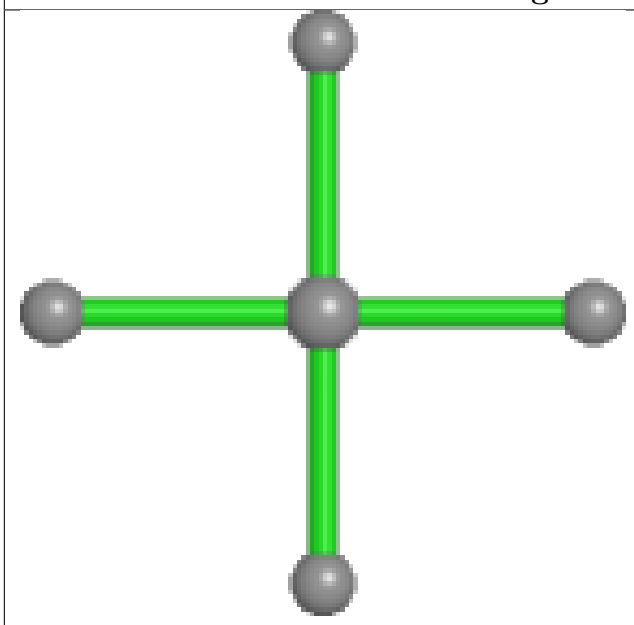


Rings

Ligand SO4 E 207



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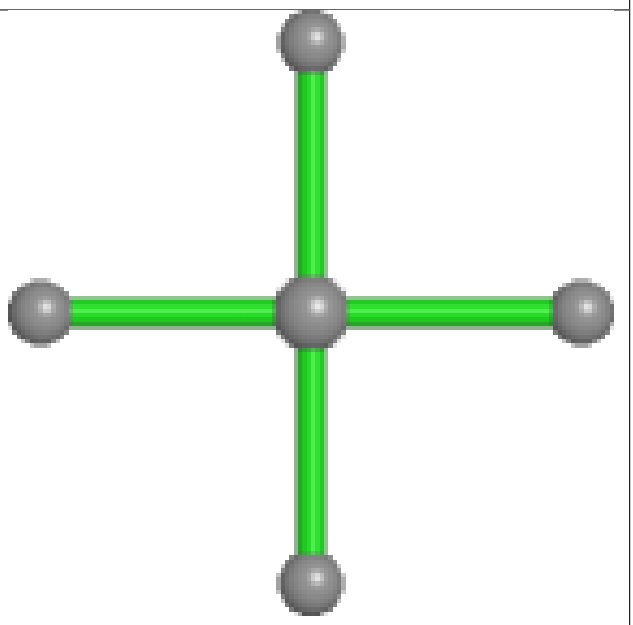
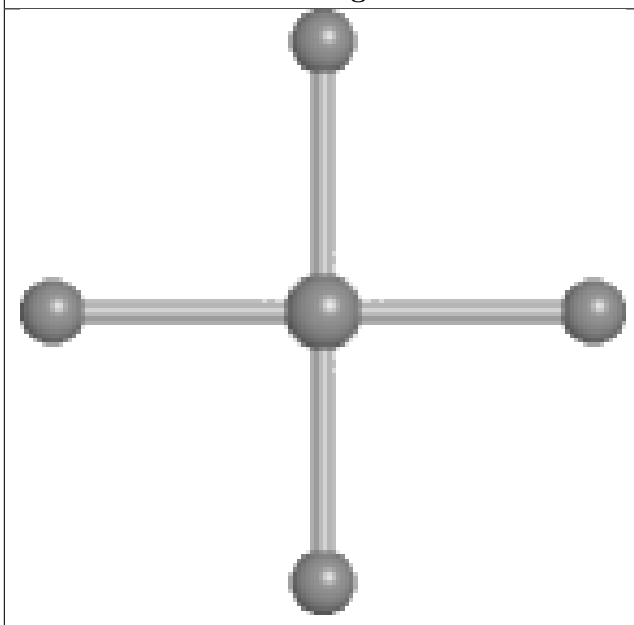


Bond angles



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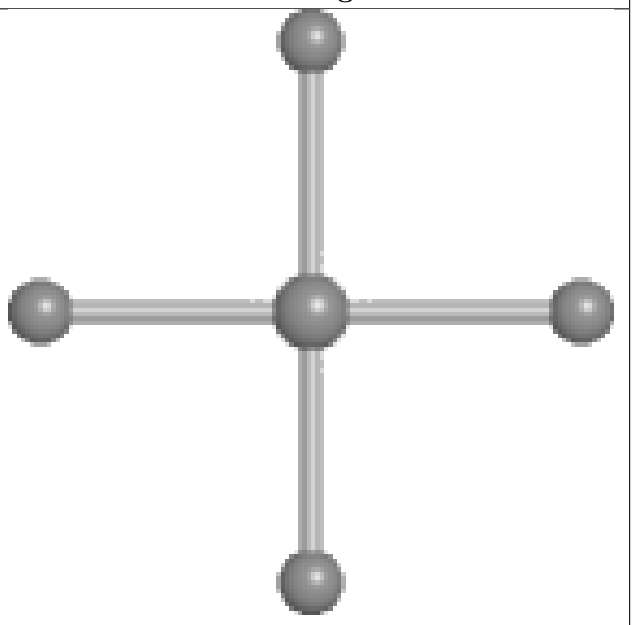
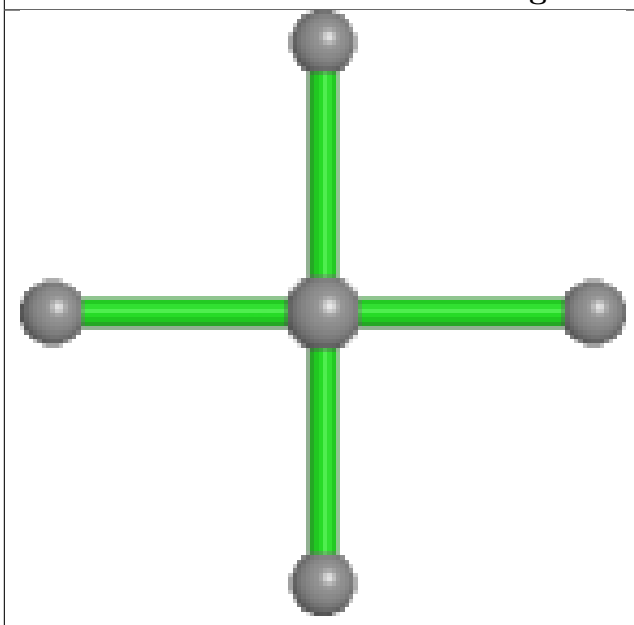


Rings

Ligand SO4 D 206



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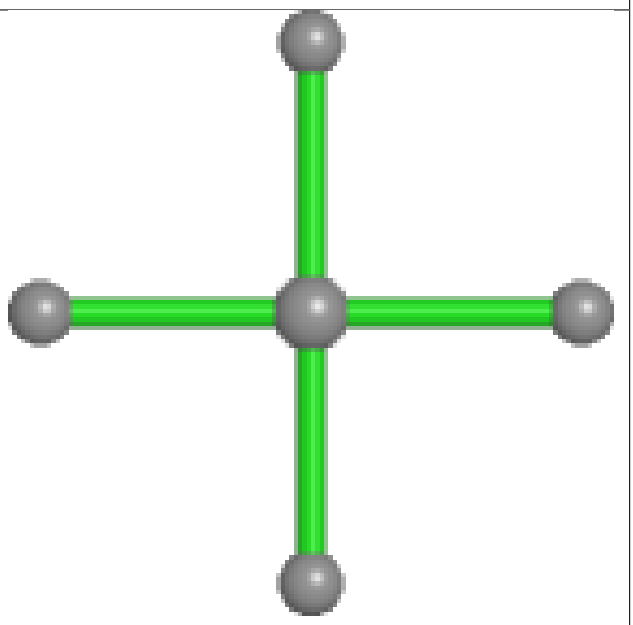
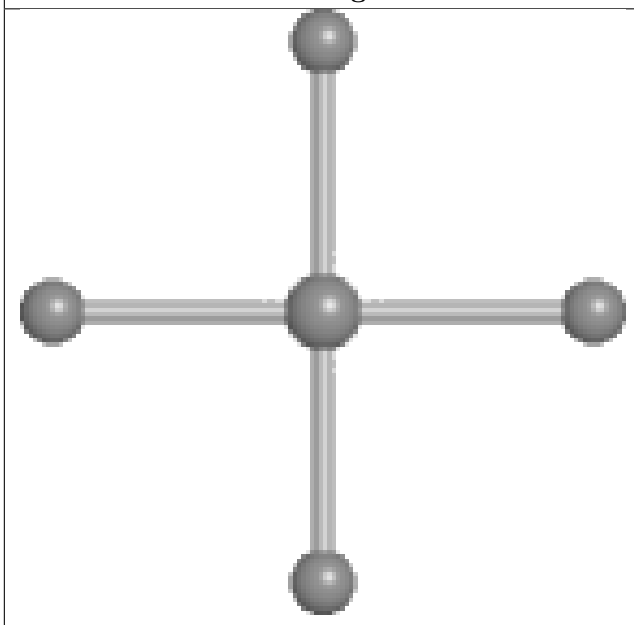


Bond angles



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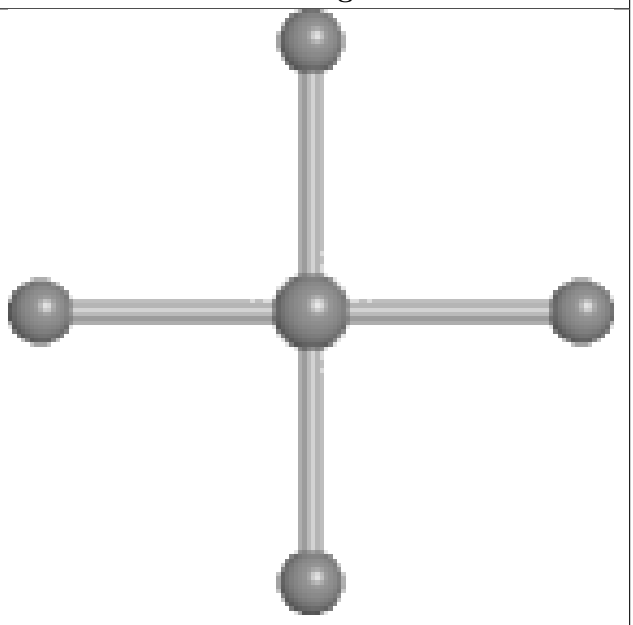
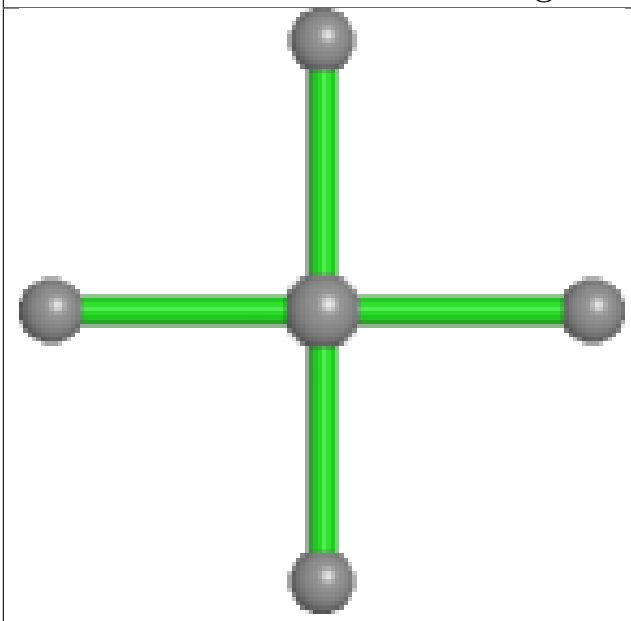


Rings

Ligand SO4 I 209



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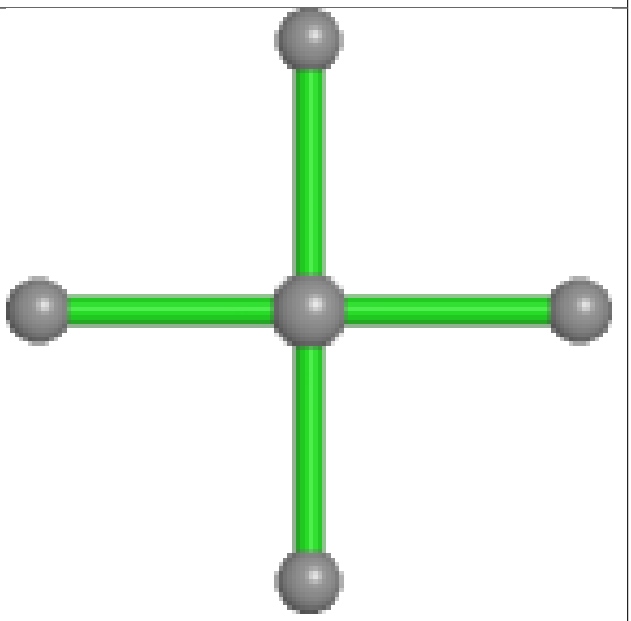
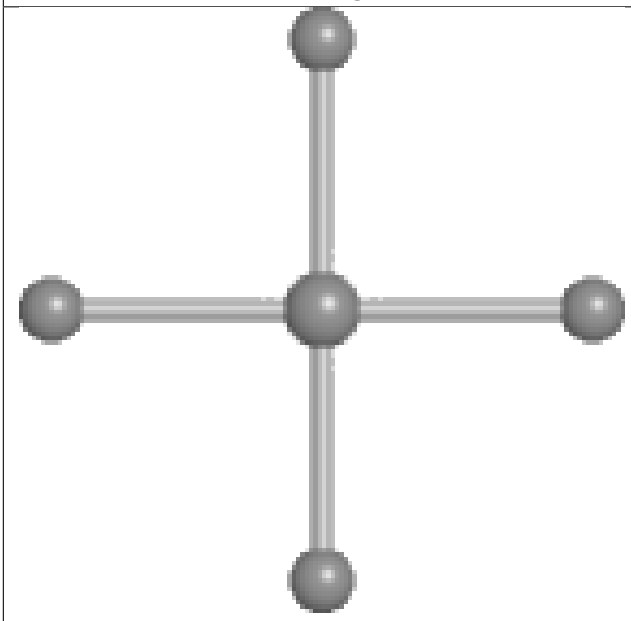


Bond angles



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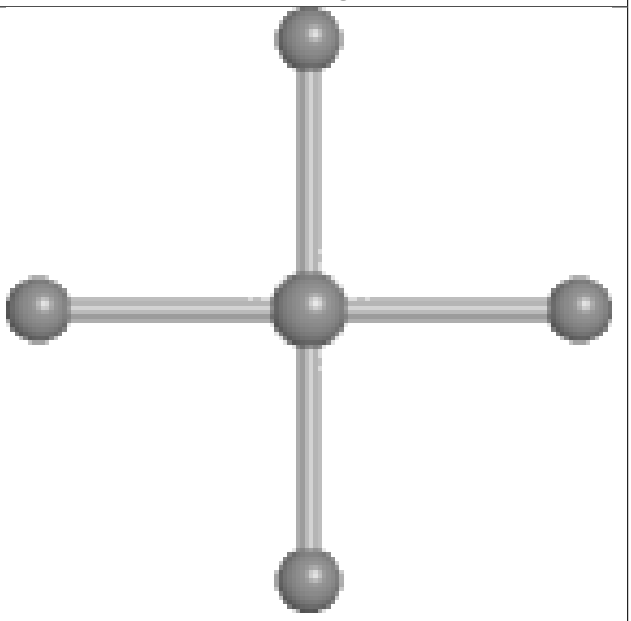
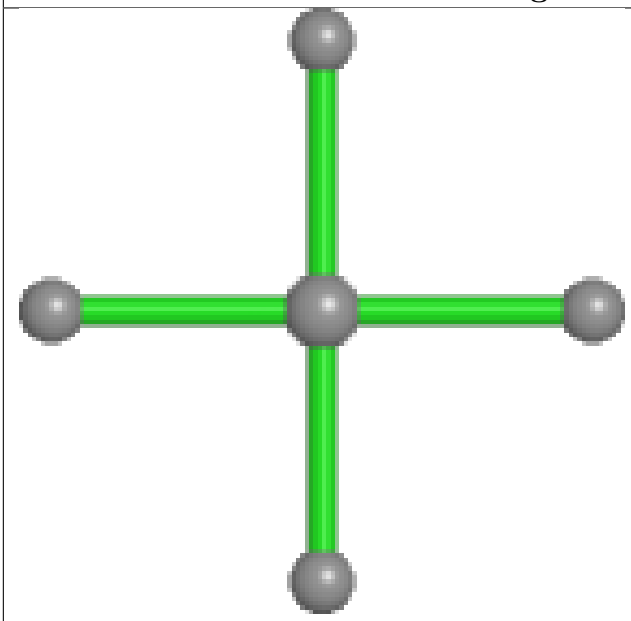


Rings

Ligand SO4 E 206



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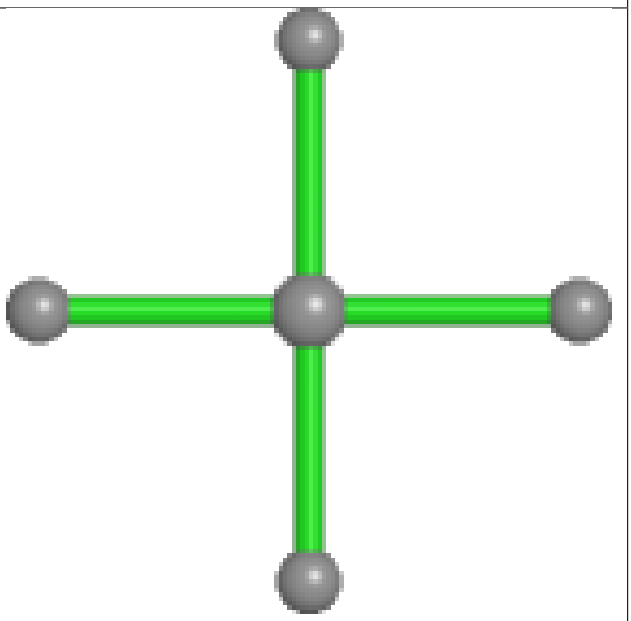
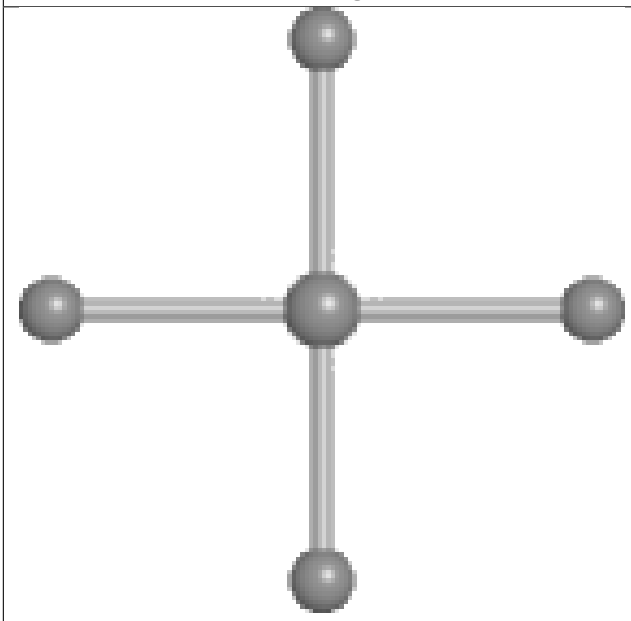


Bond angles



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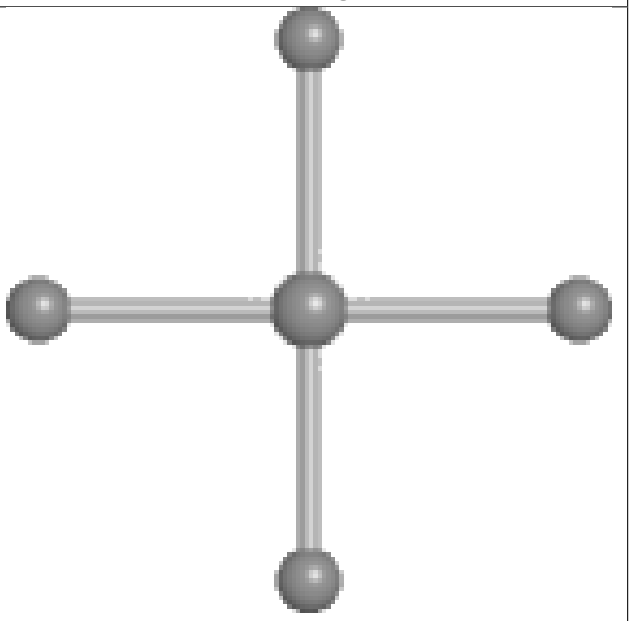
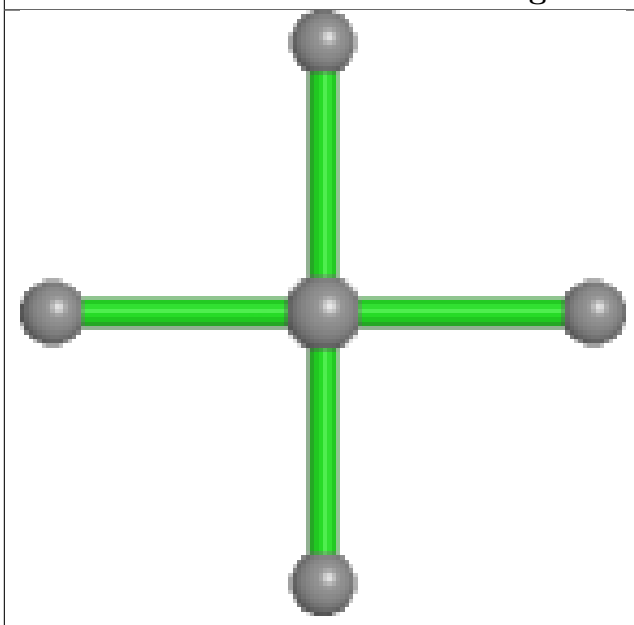


Rings

Ligand SO4 H 208



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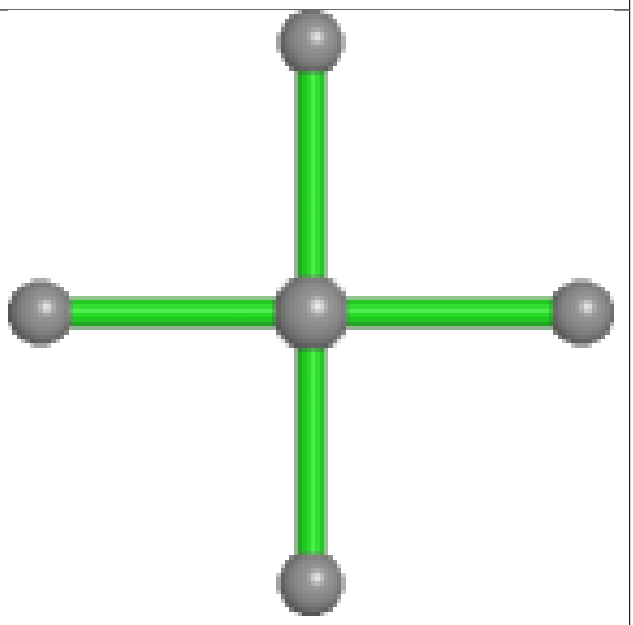
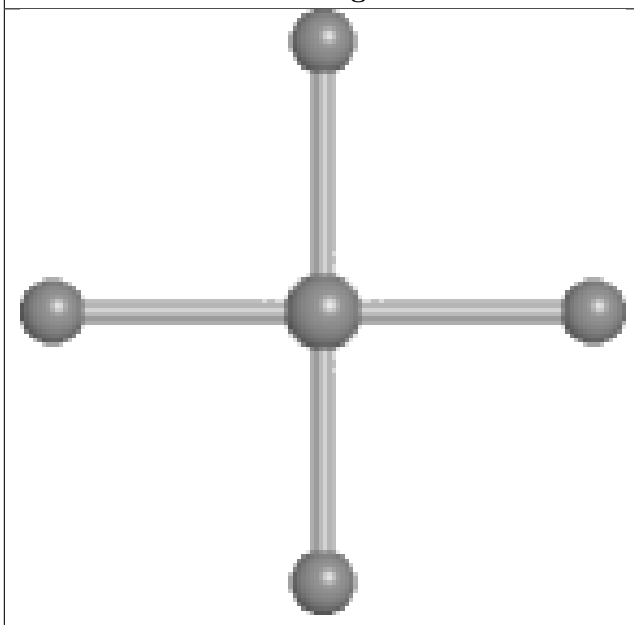


Bond angles



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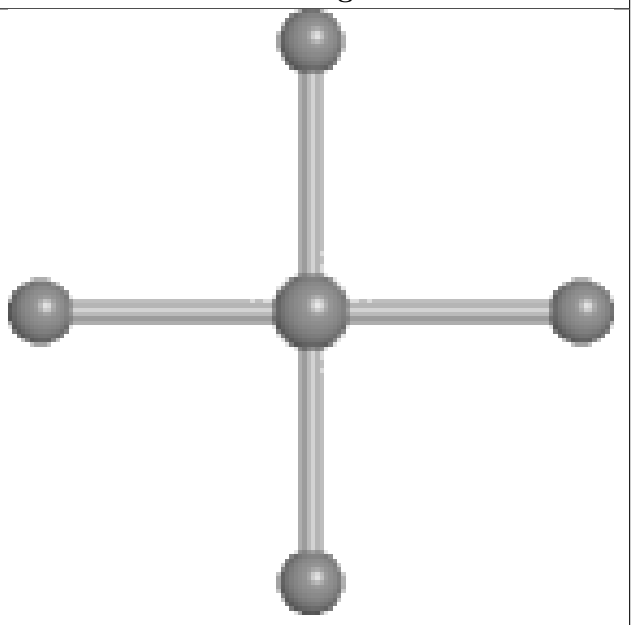
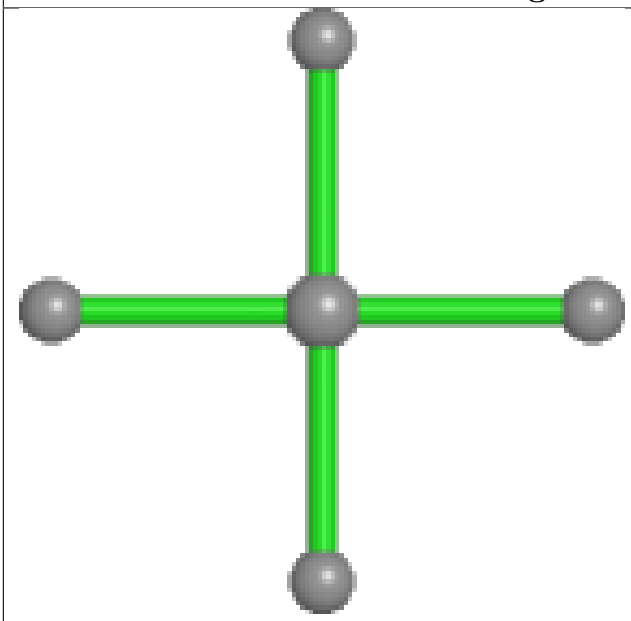
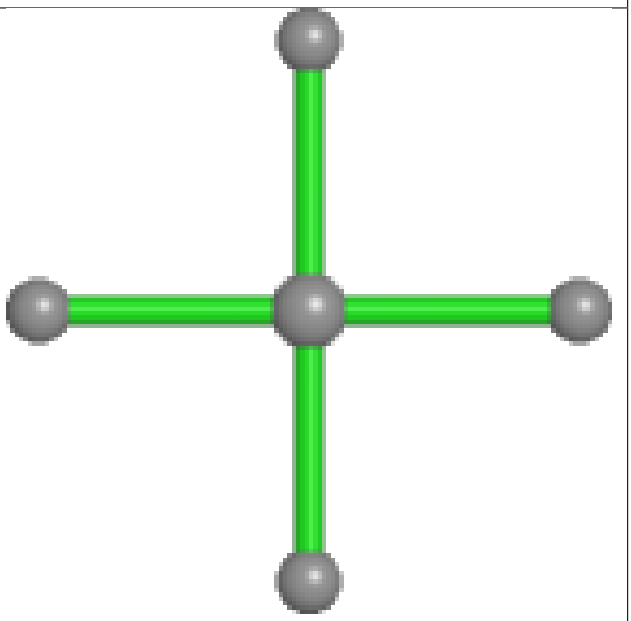


Rings

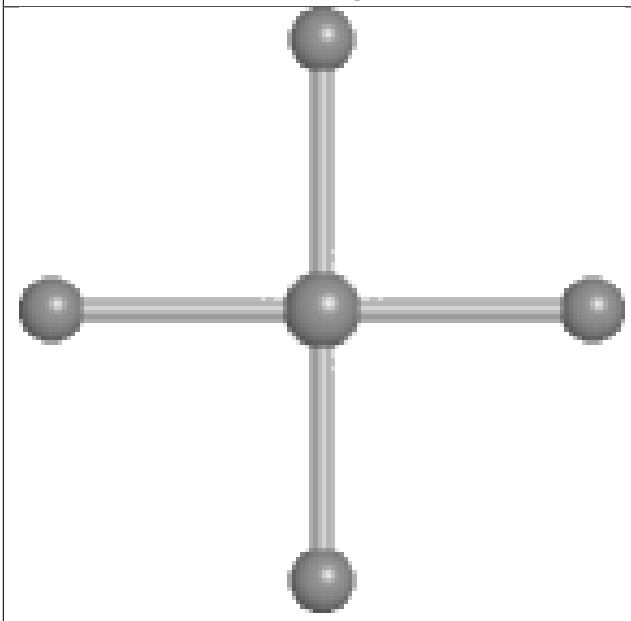
Ligand SO4 D 212



Bond lengths



Bond angles



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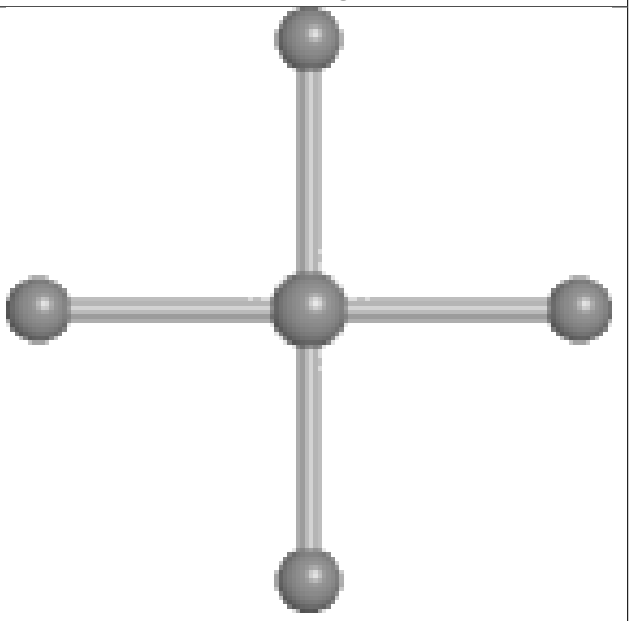
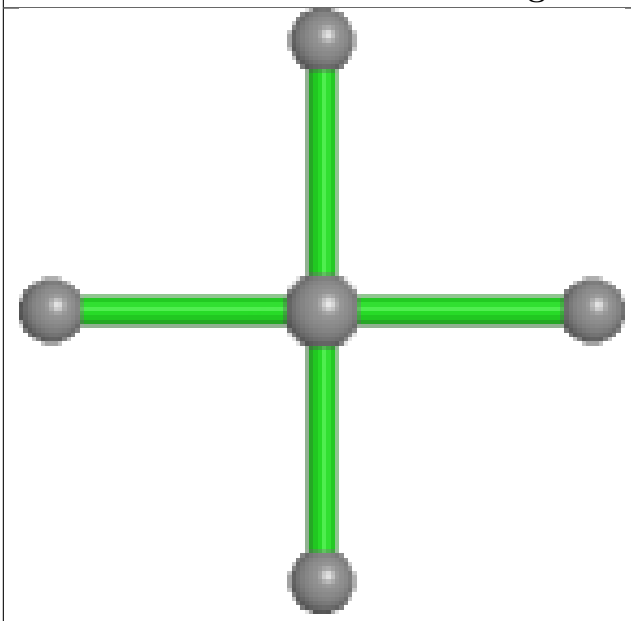


Rings

Ligand SO4 H 204



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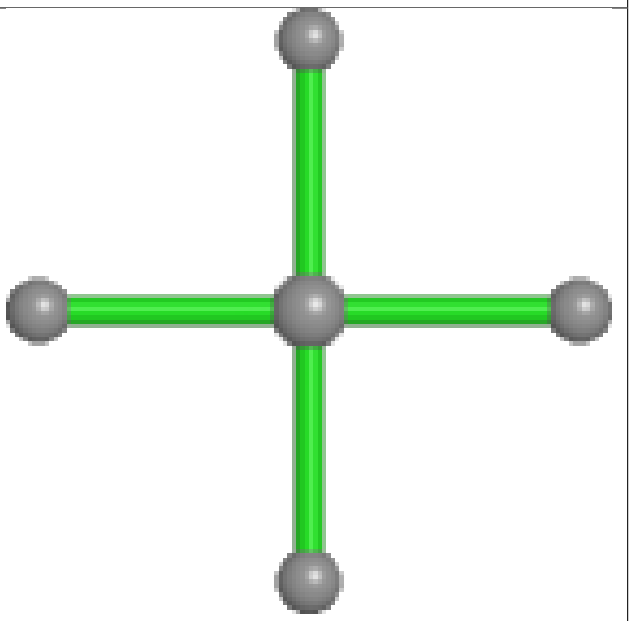

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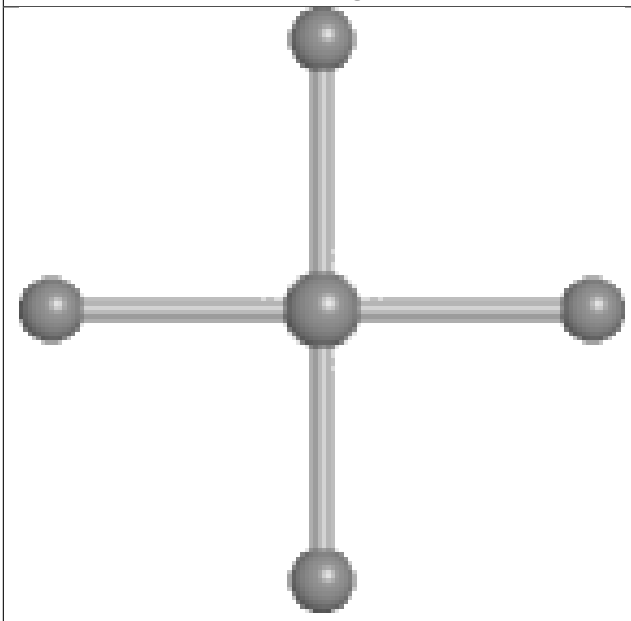

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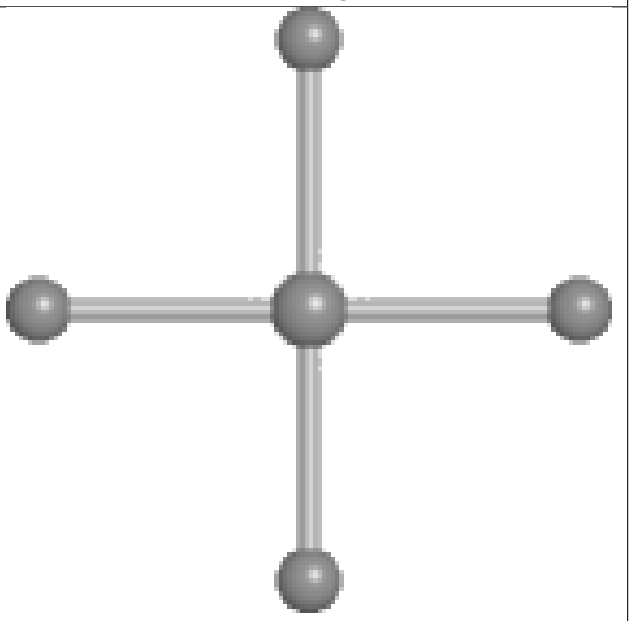
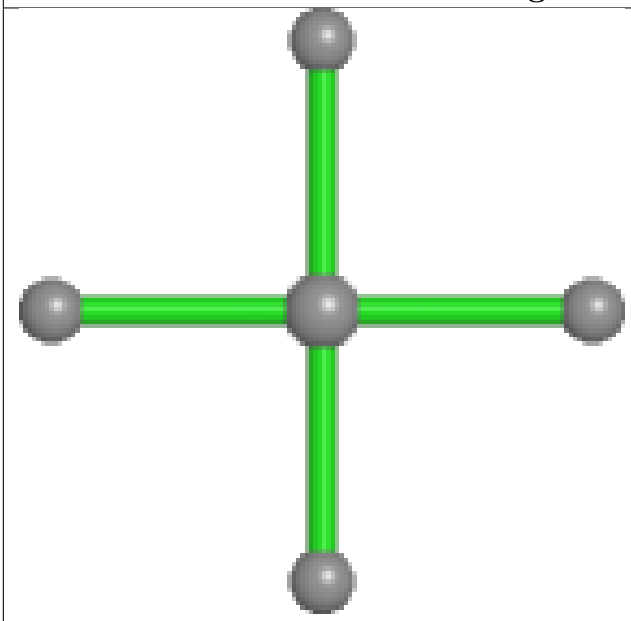


Rings

Ligand SO4 G 210



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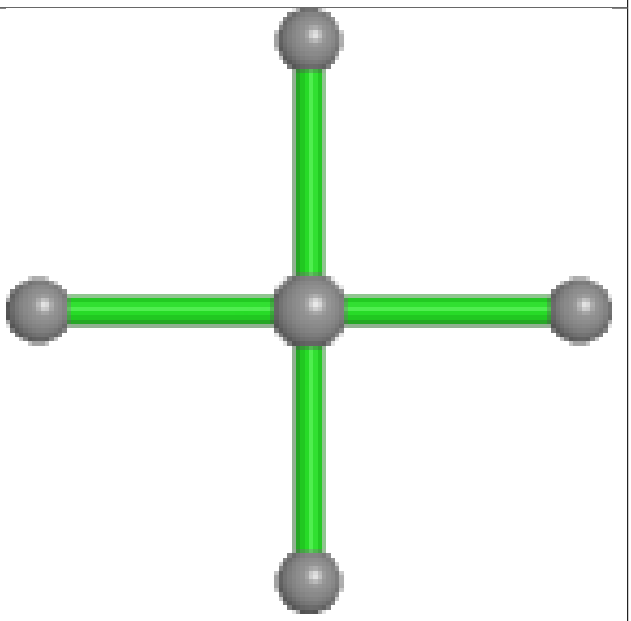
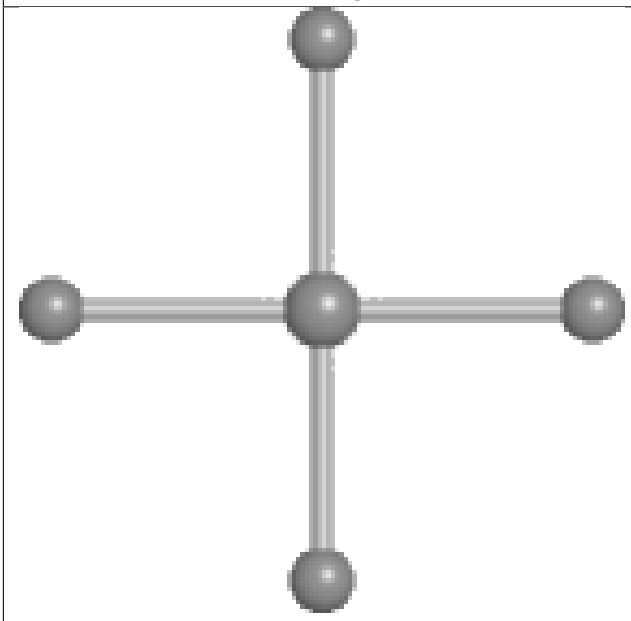


Bond angles



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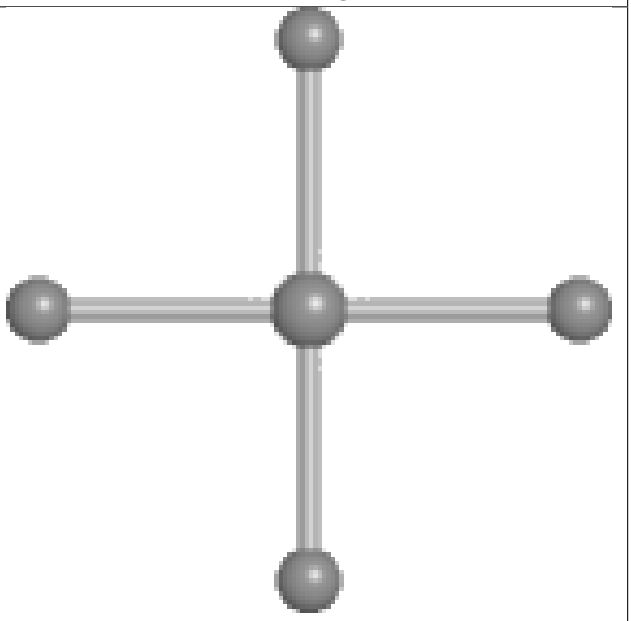
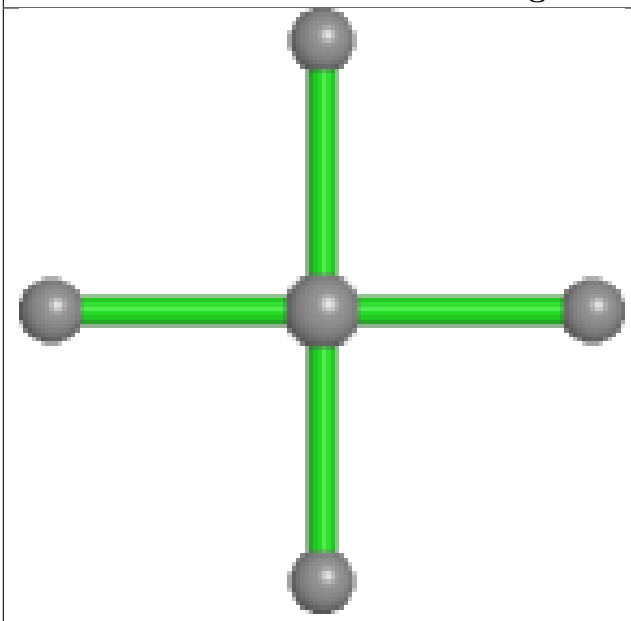


Rings

Ligand SO4 A 204



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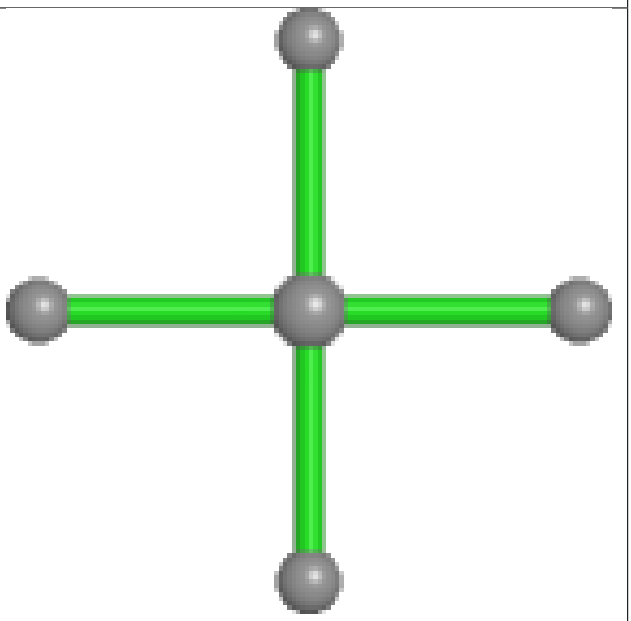
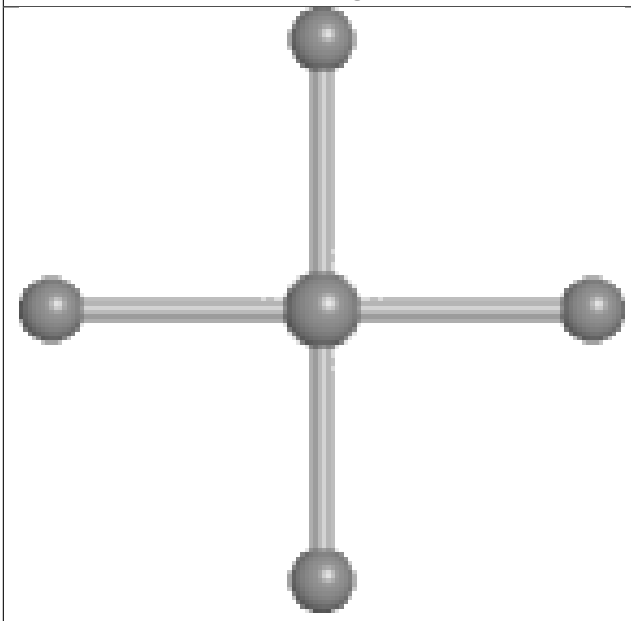


Bond angles



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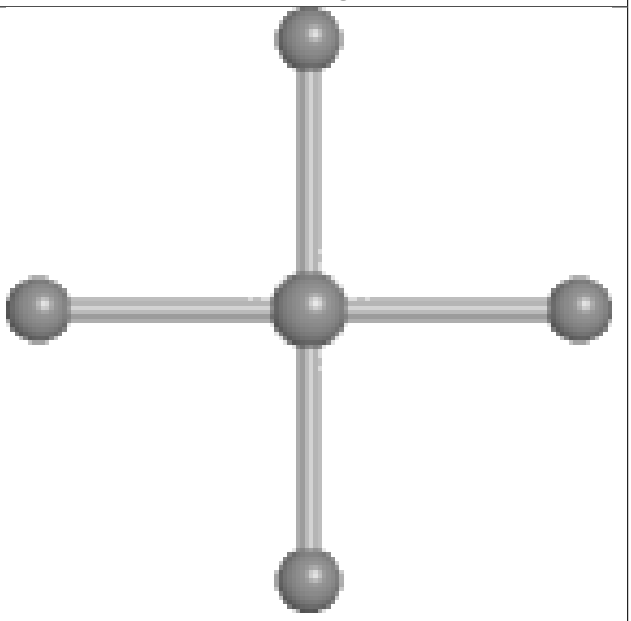
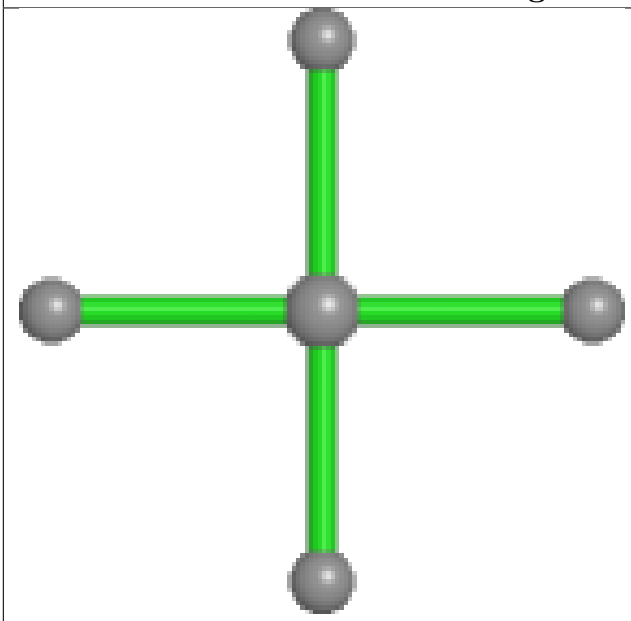
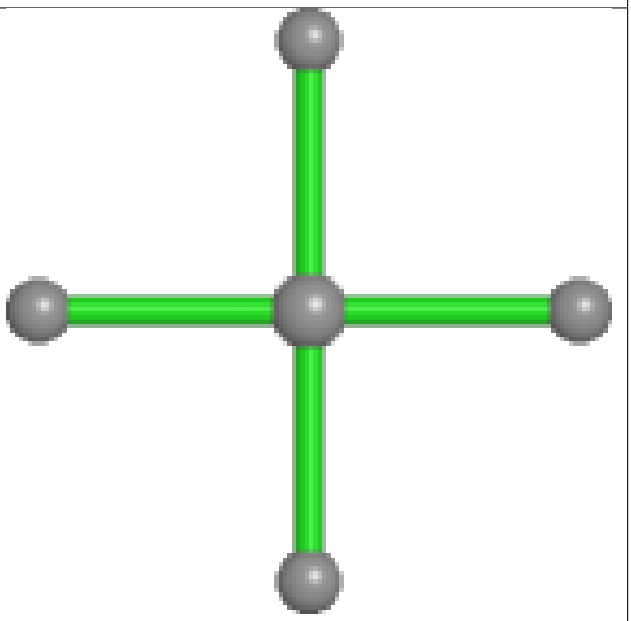


Rings

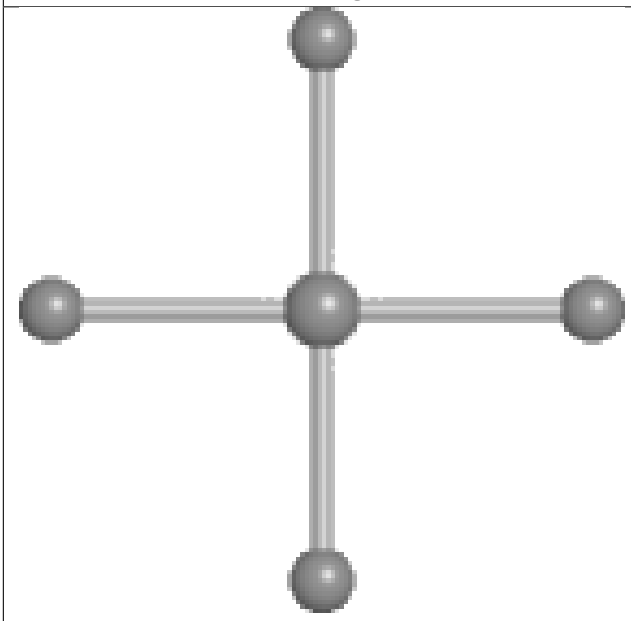
Ligand SO4 K 210



Bond lengths



Bond angles



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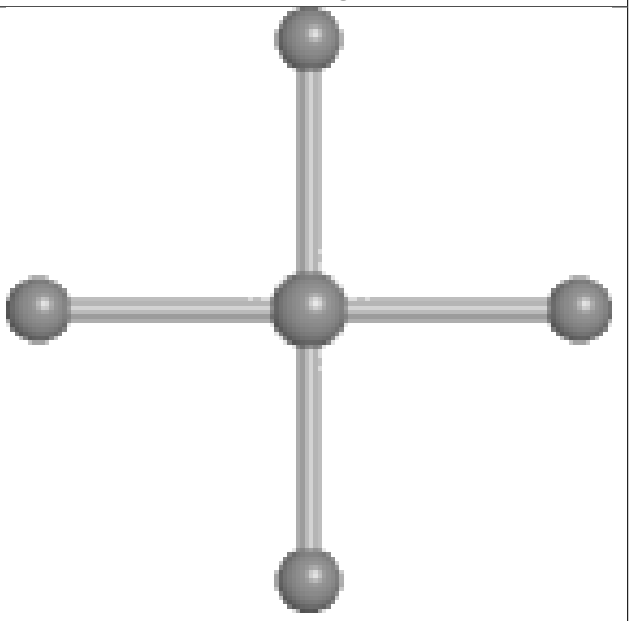
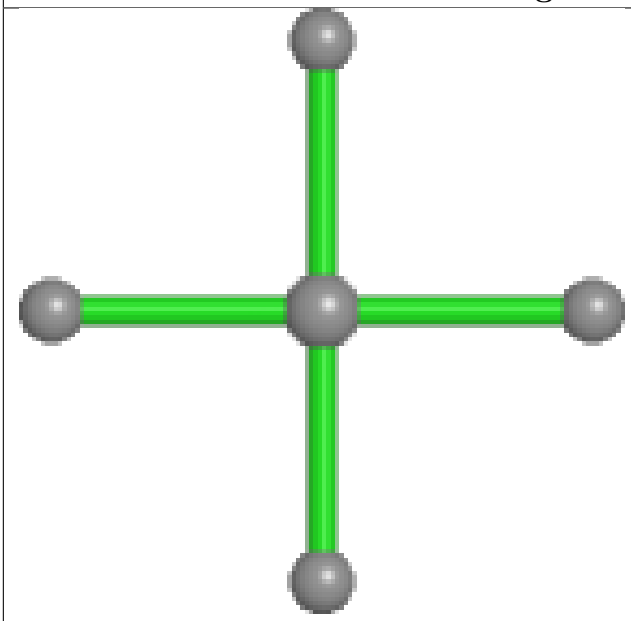
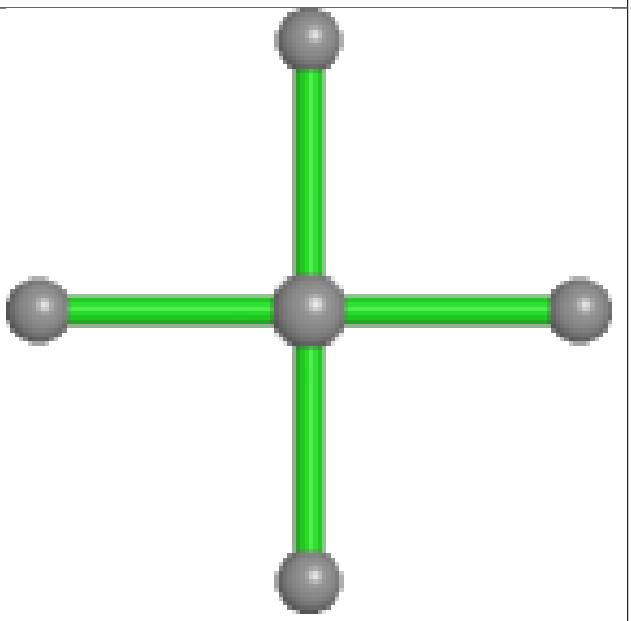


Rings

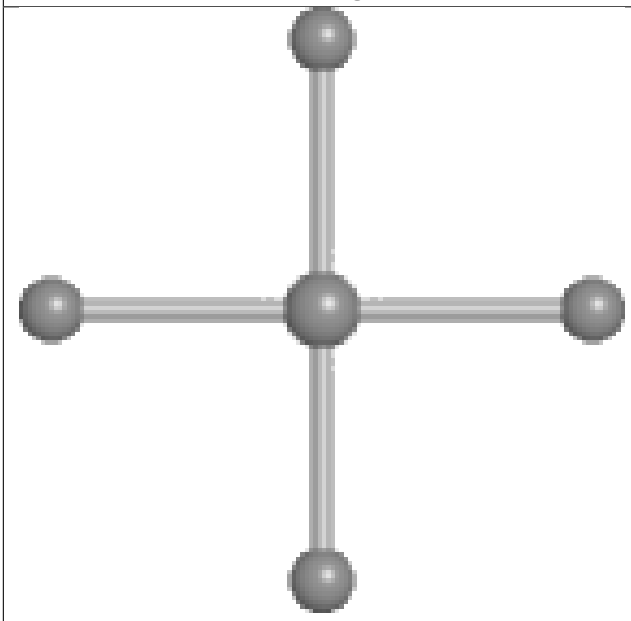
Ligand SO4 I 207



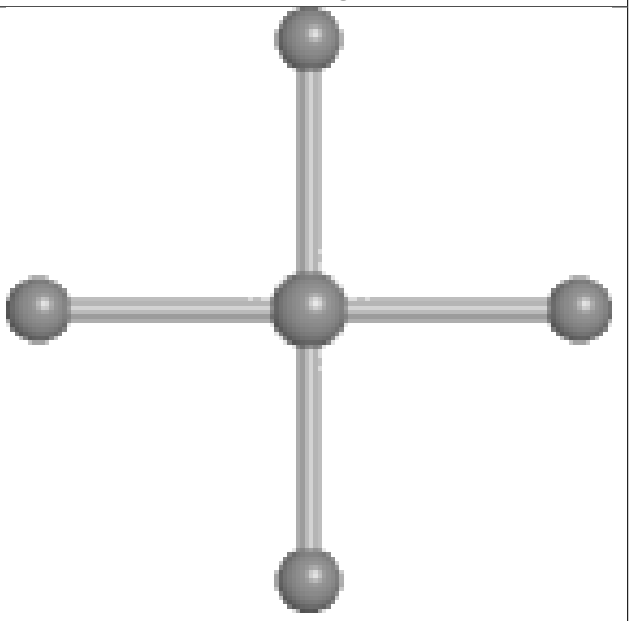
Bond lengths



Bond angles

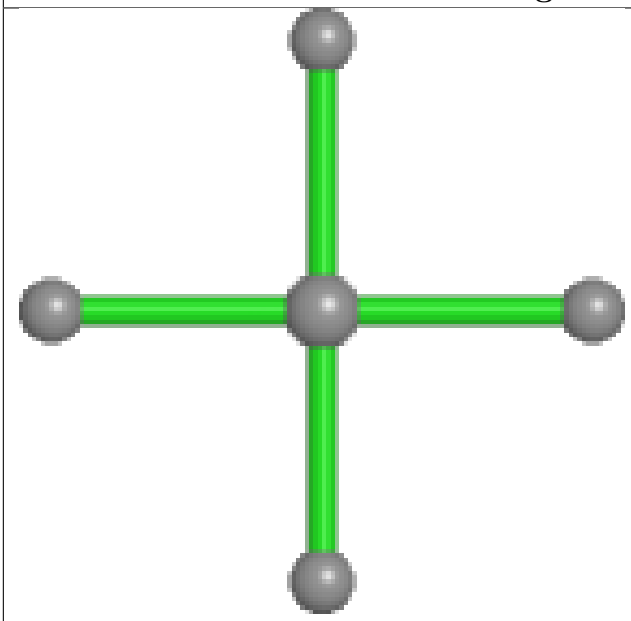


Torsions



Rings

Ligand SO4 I 208



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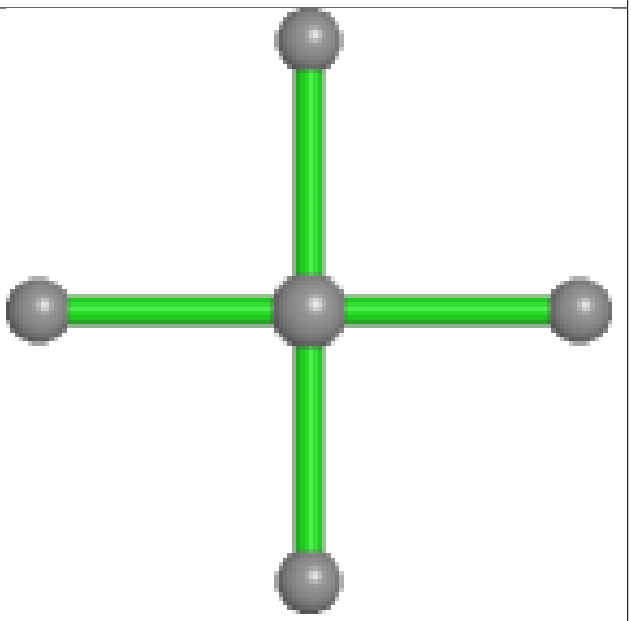

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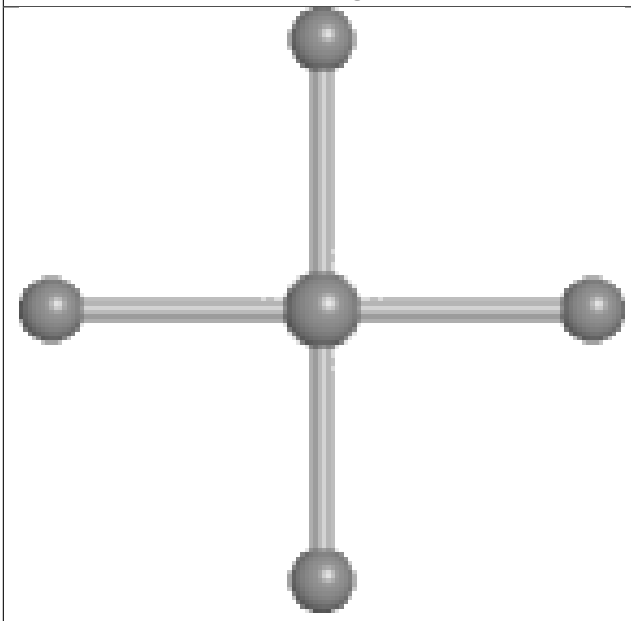

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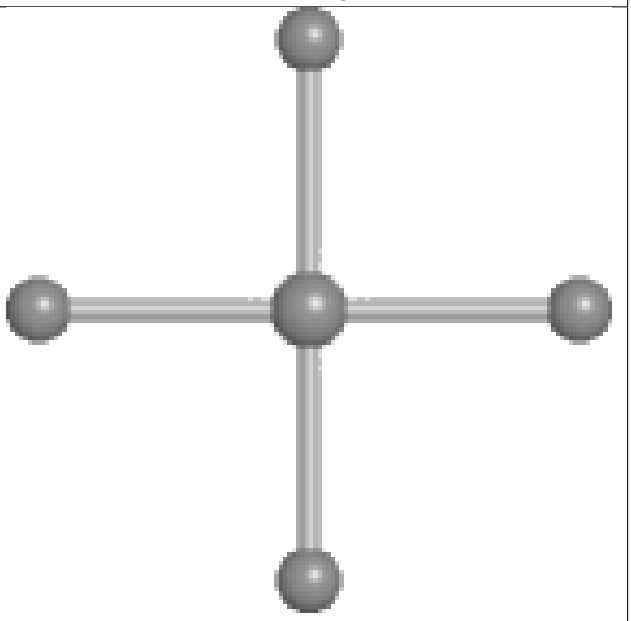
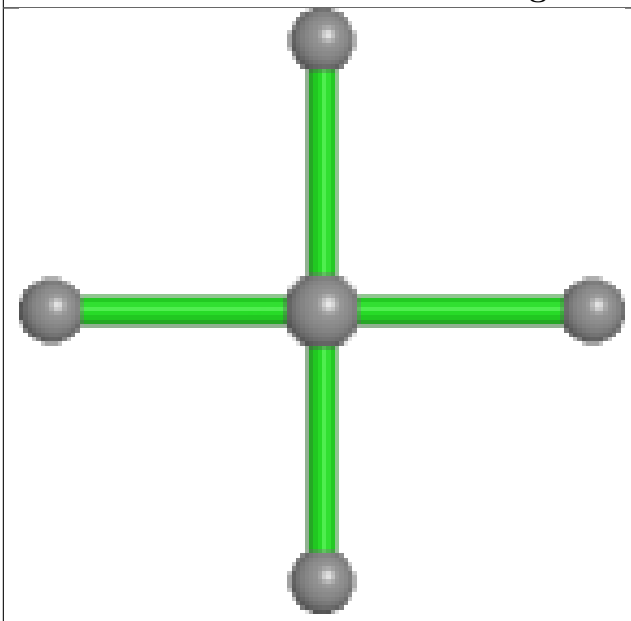


Rings

Ligand SO4 B 209



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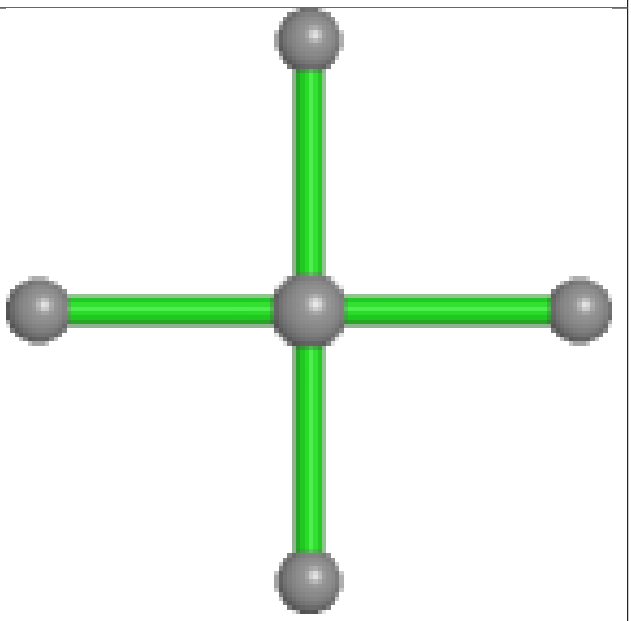
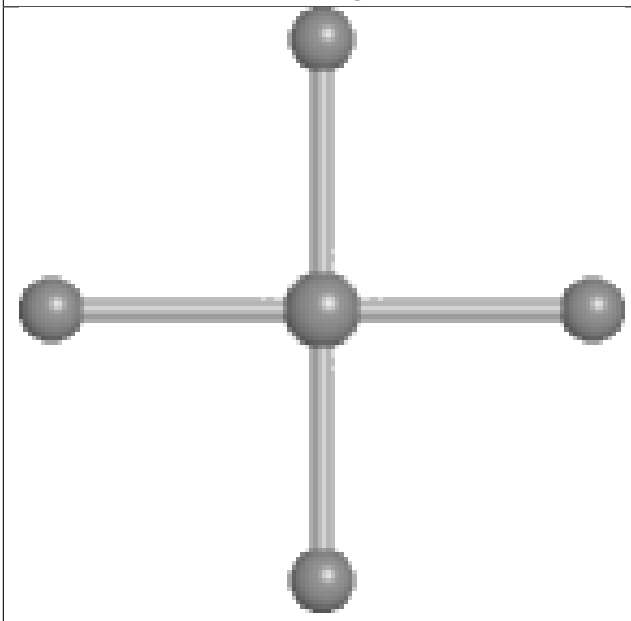


Bond angles



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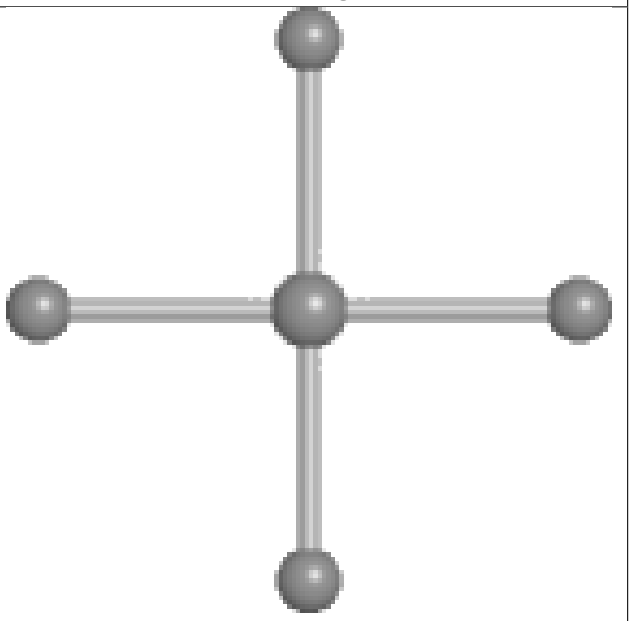
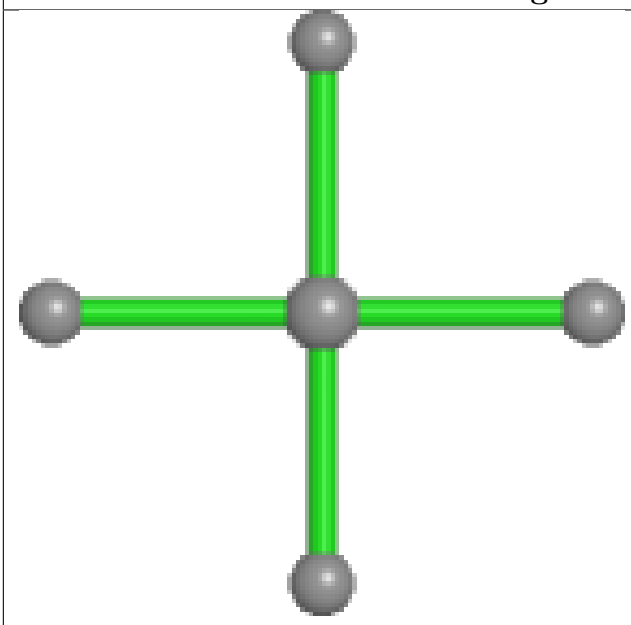


Rings

Ligand SO4 F 209



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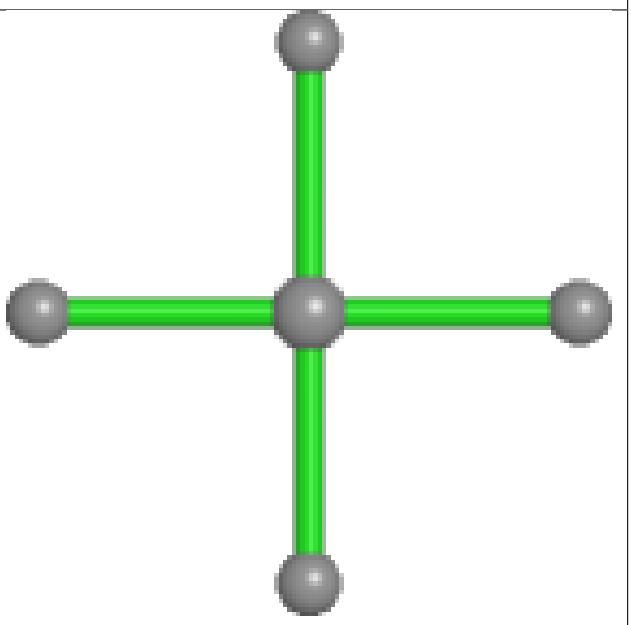
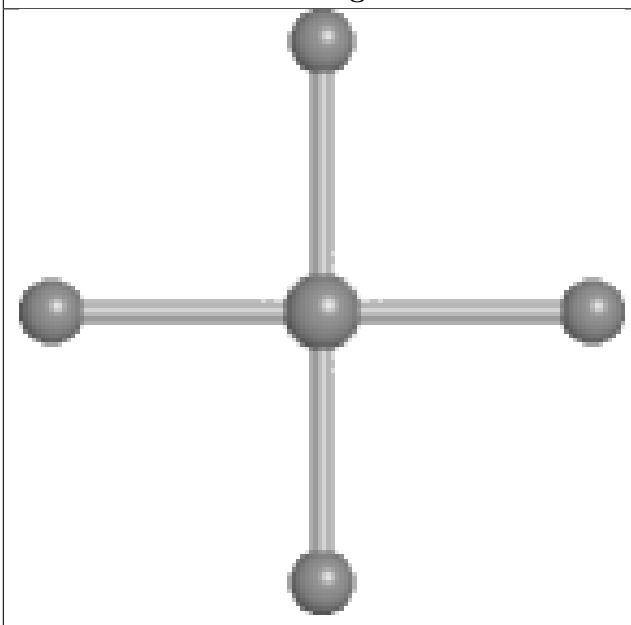


Bond angles



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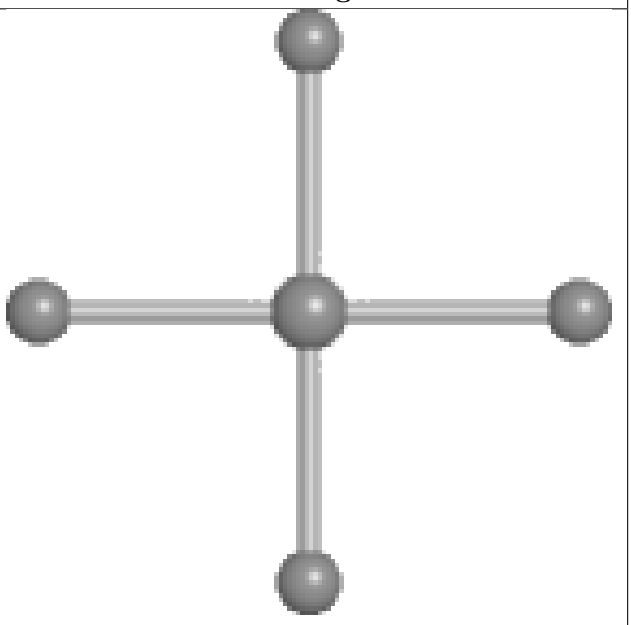
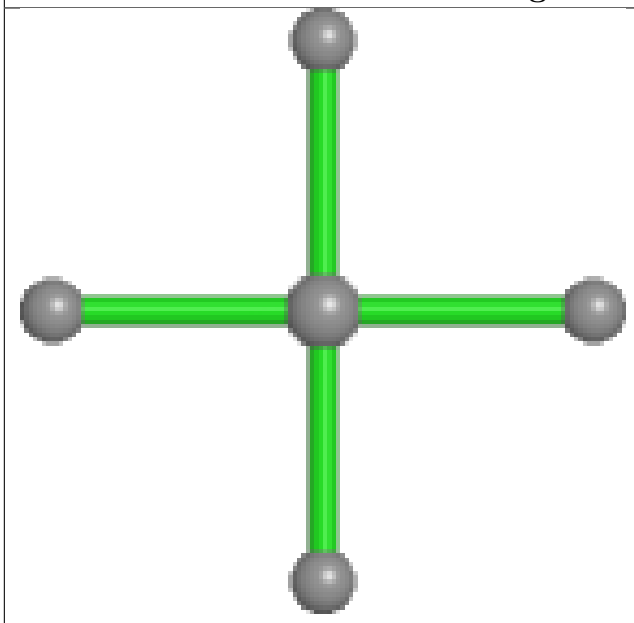


Rings

Ligand SO4 H 206



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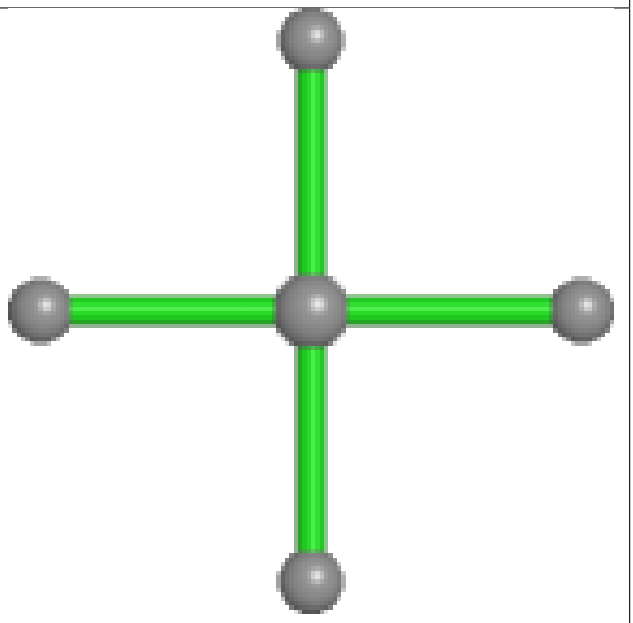
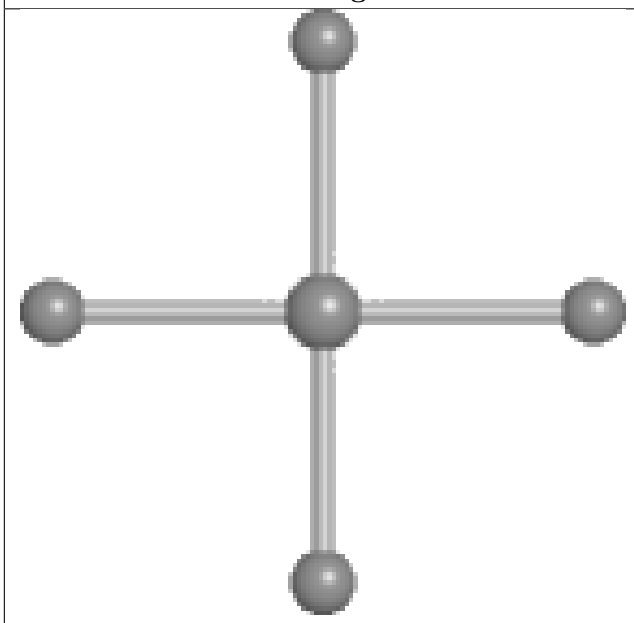


Bond angles



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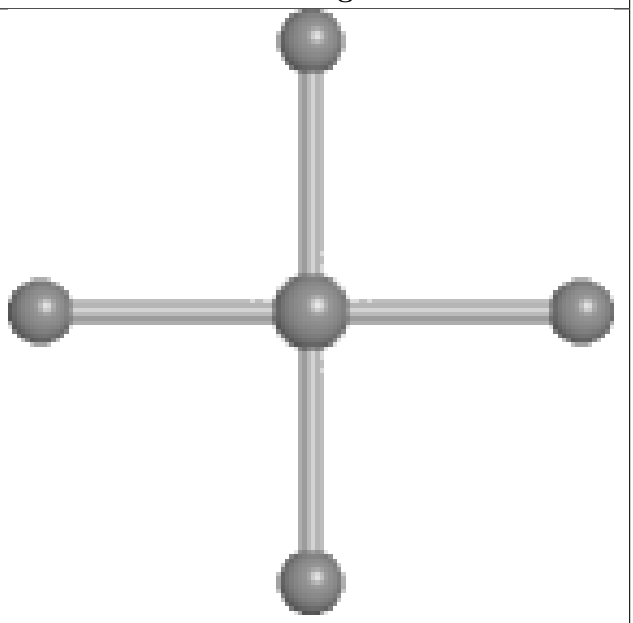
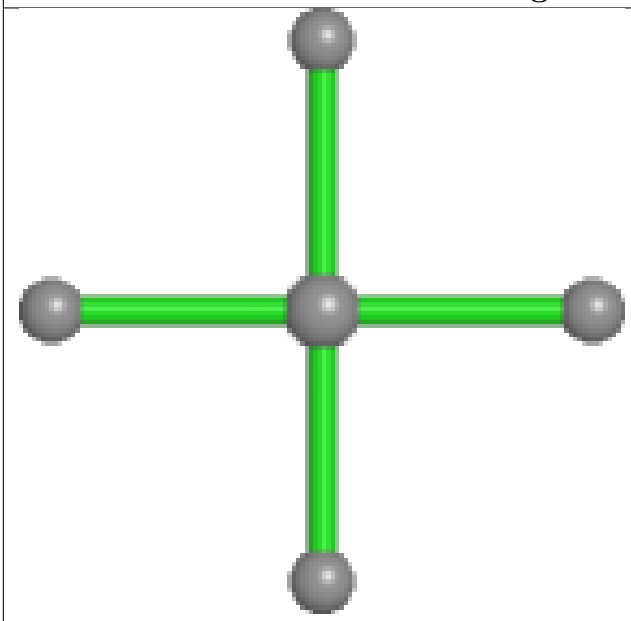


Rings

Ligand SO4 F 204



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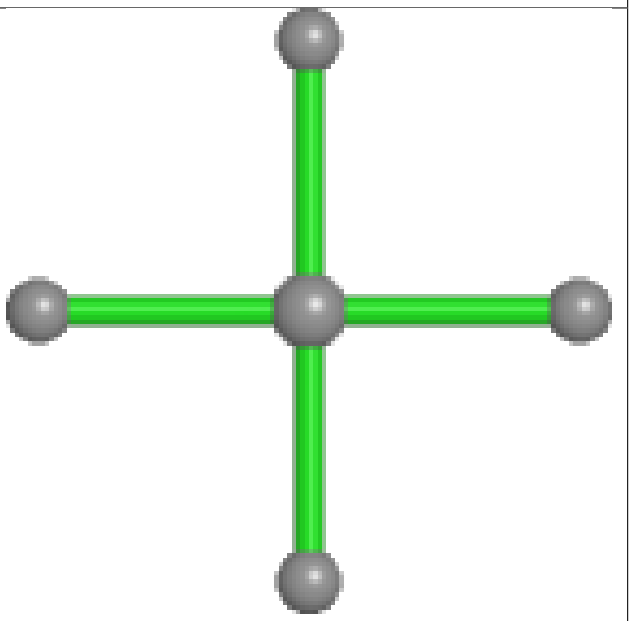
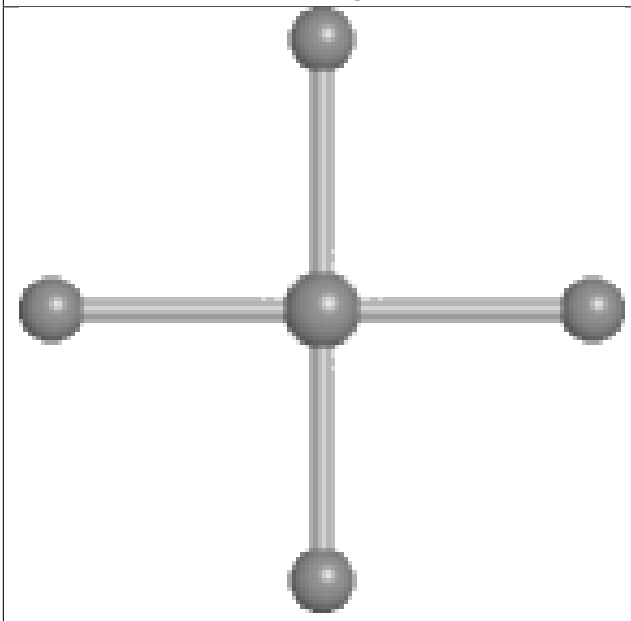


Bond angles



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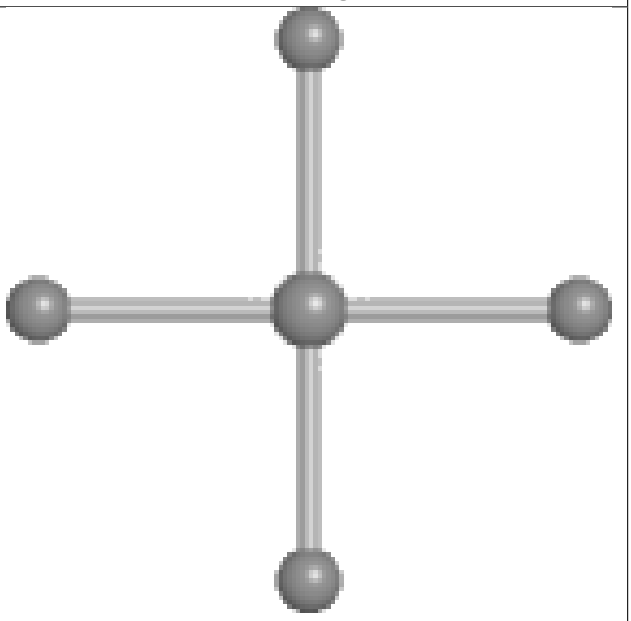
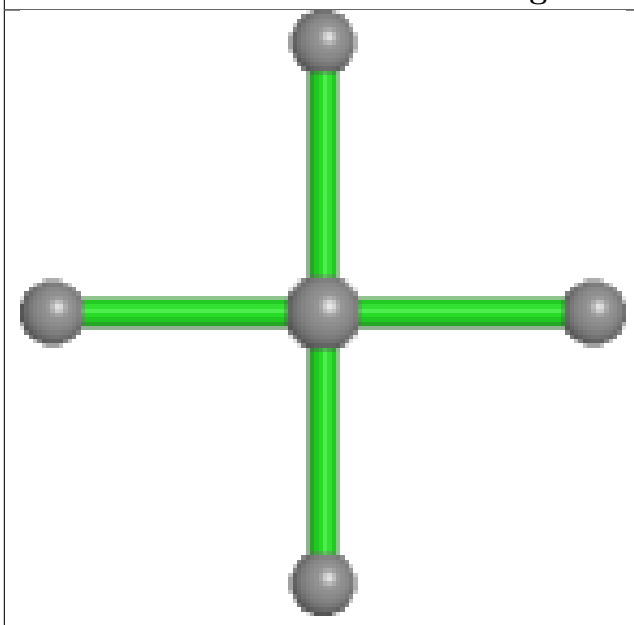


Rings

Ligand SO4 A 203



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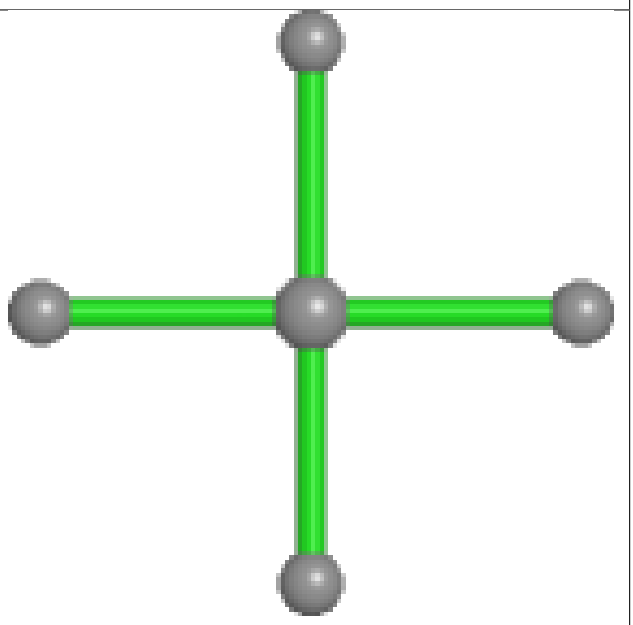
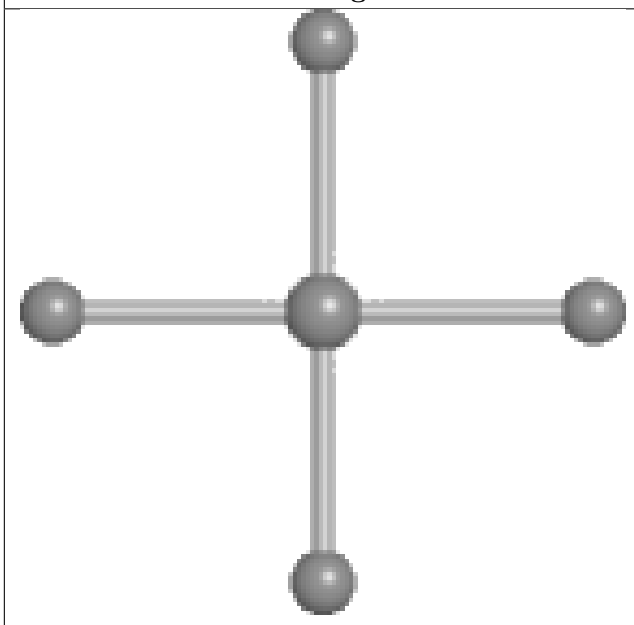


Bond angles



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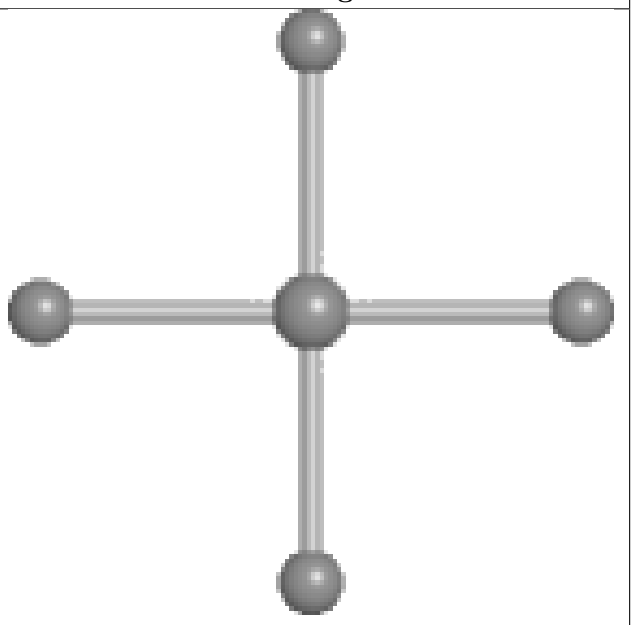
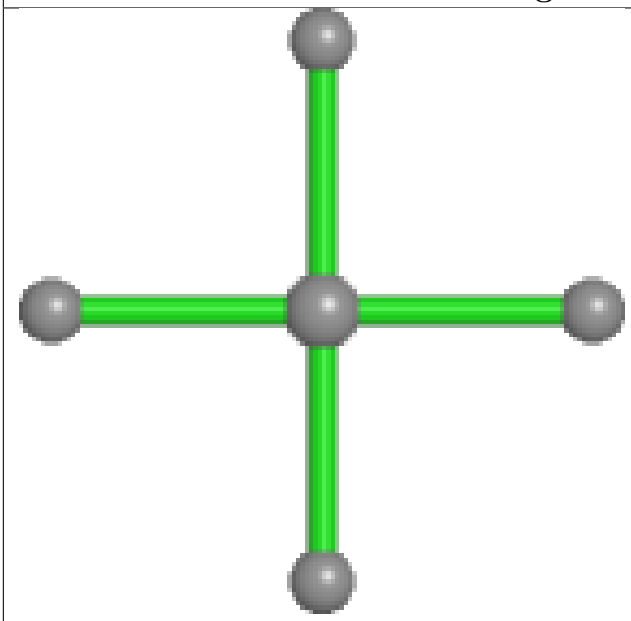


Rings

Ligand SO4 I 206



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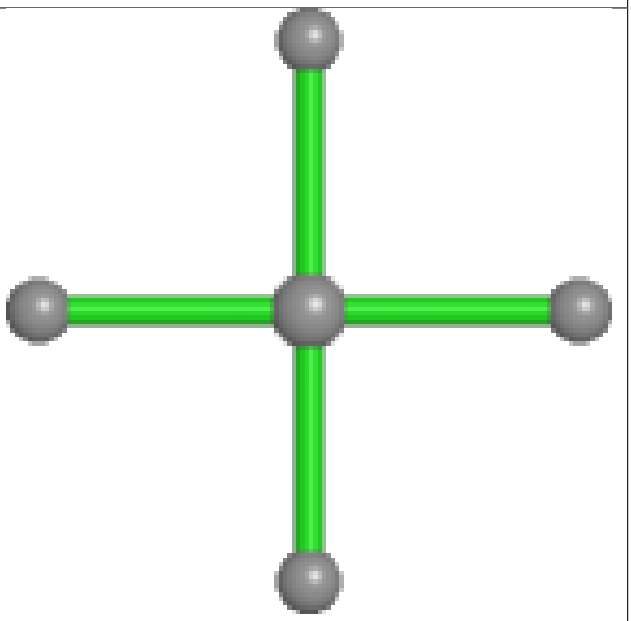
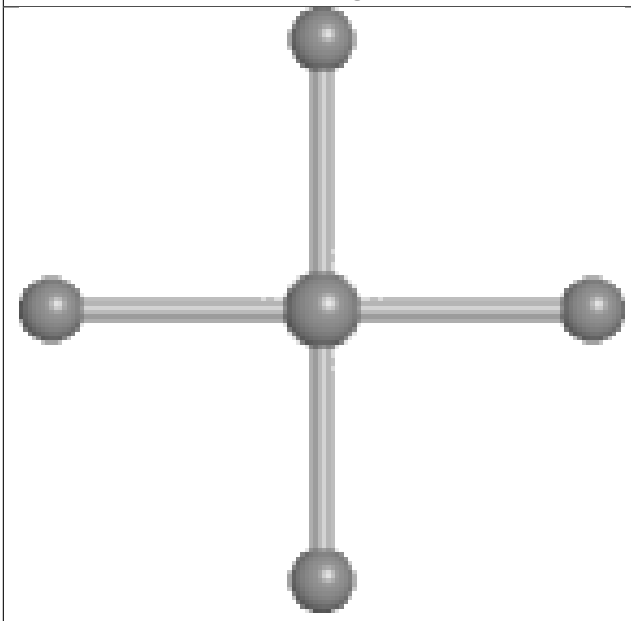


Bond angles



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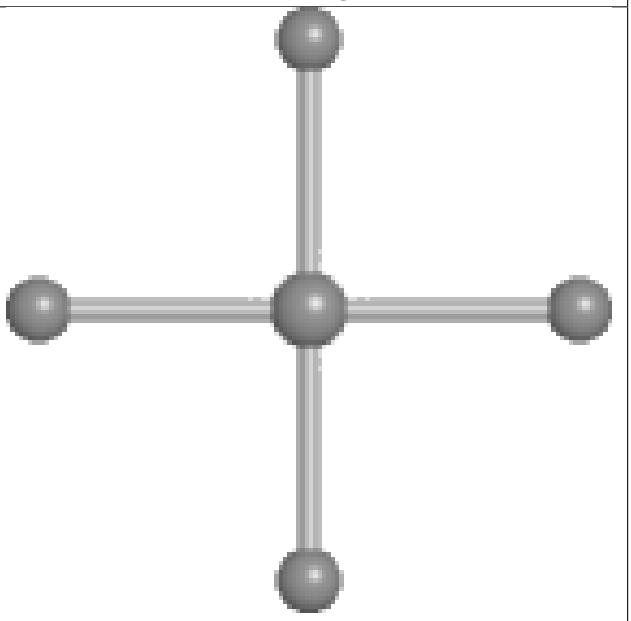
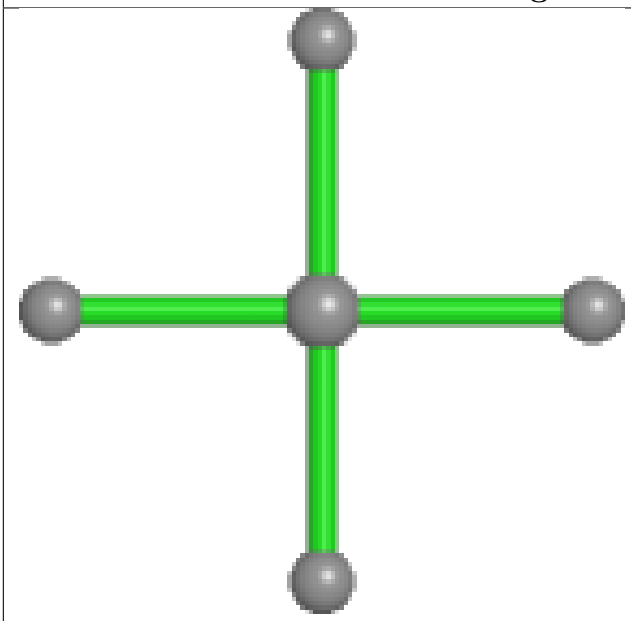


Rings

Ligand SO4 E 205



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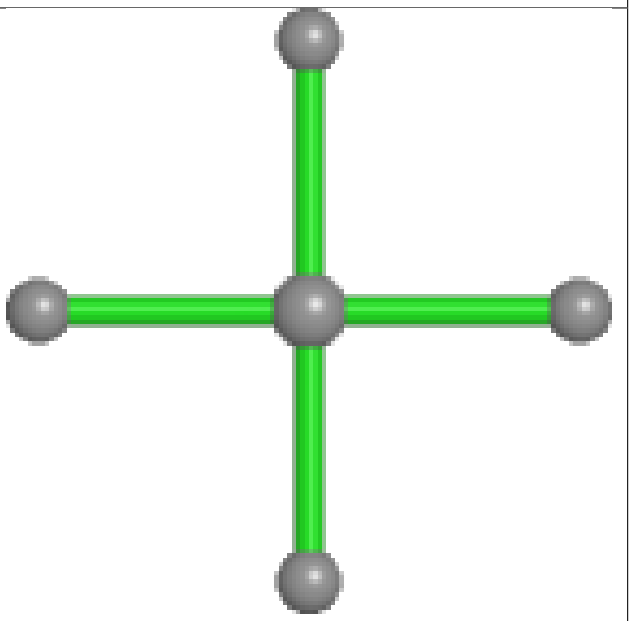
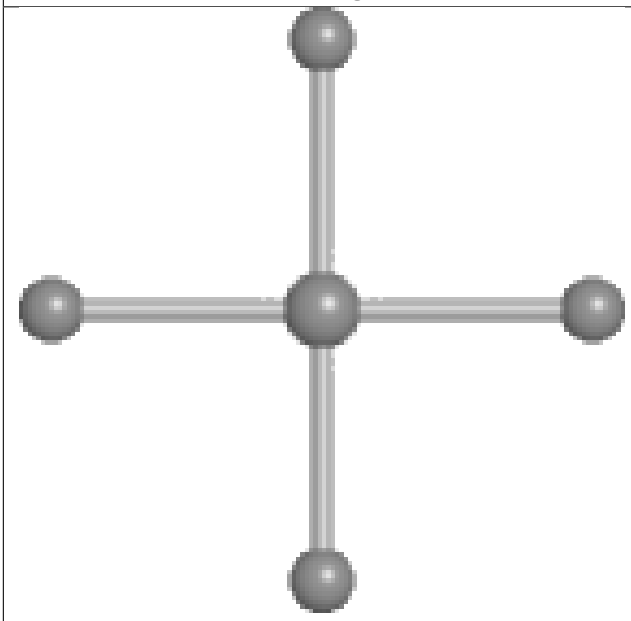


Bond angles



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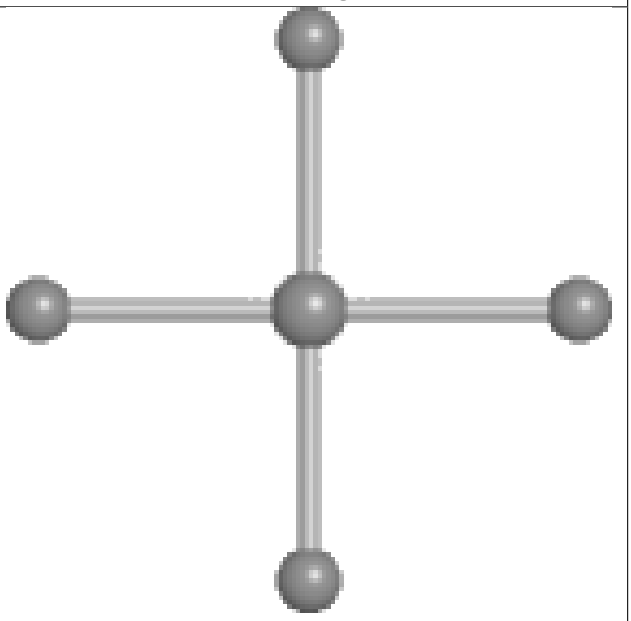
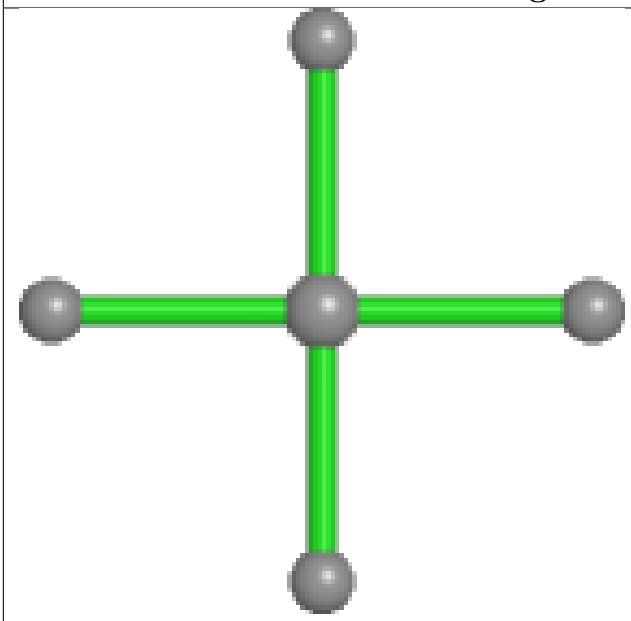
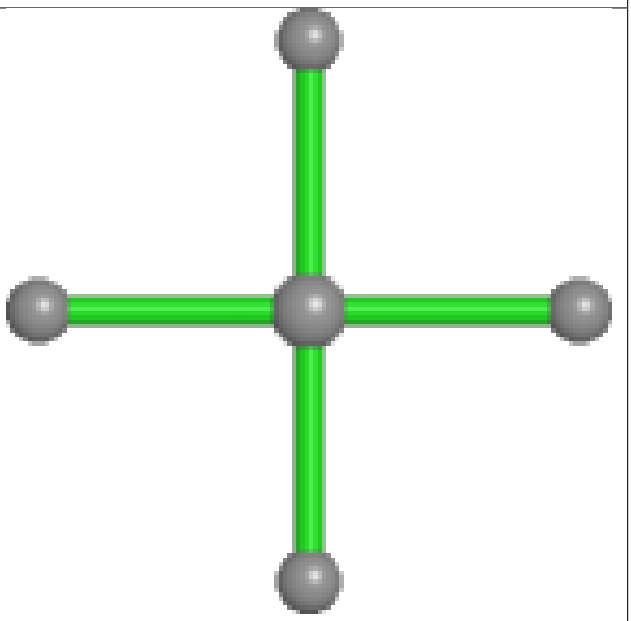


Rings

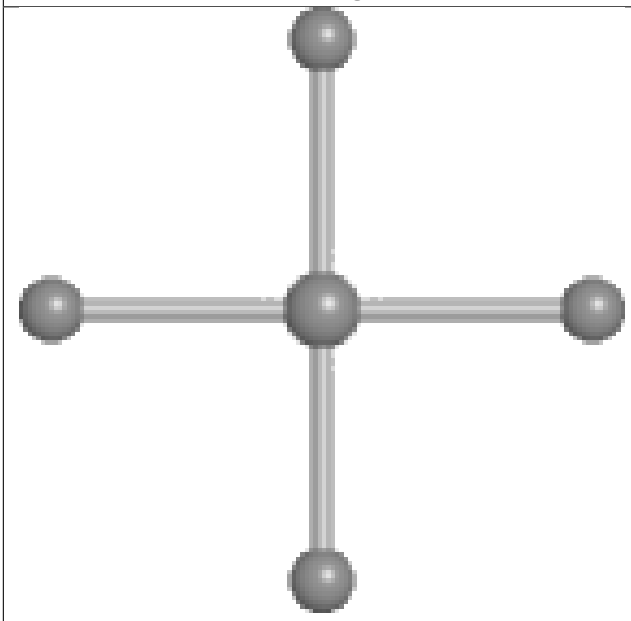
Ligand SO4 B 210



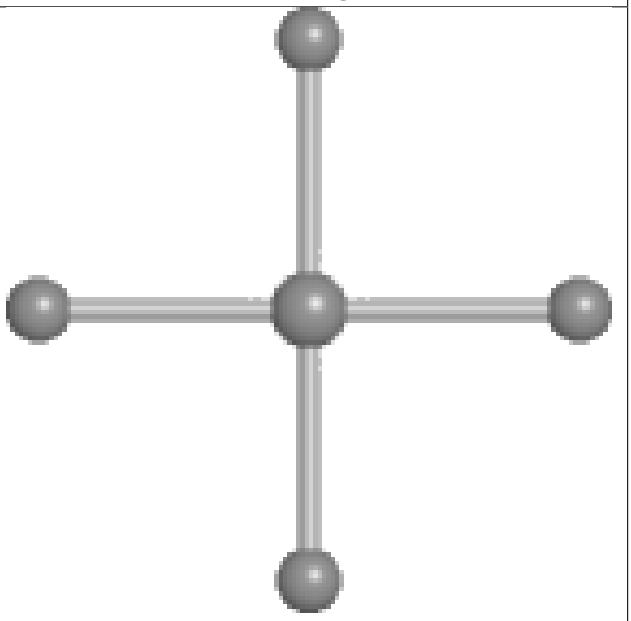
Bond lengths



Bond angles

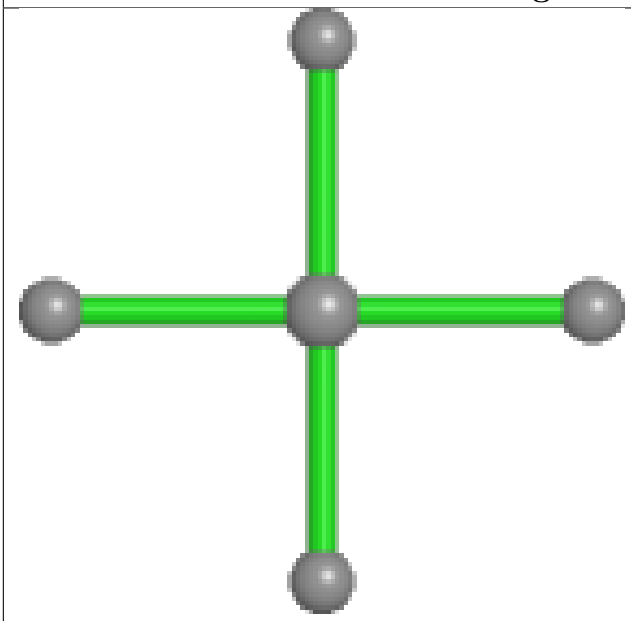


Torsions

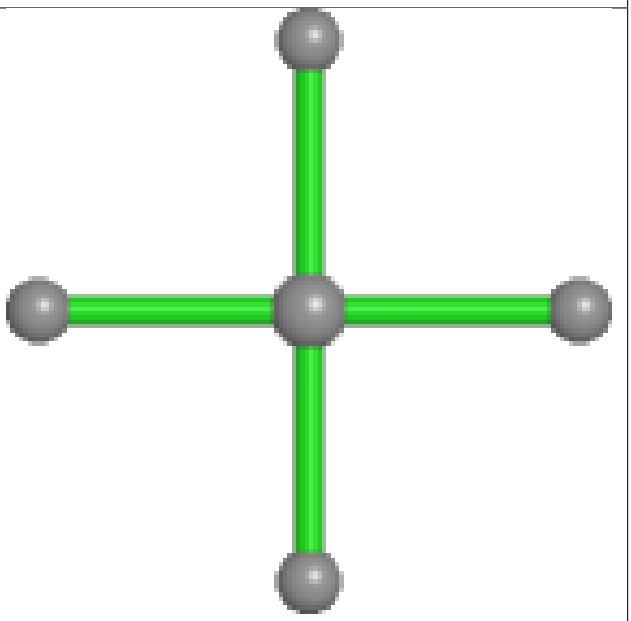


Rings

Ligand SO4 J 208



Bond lengths



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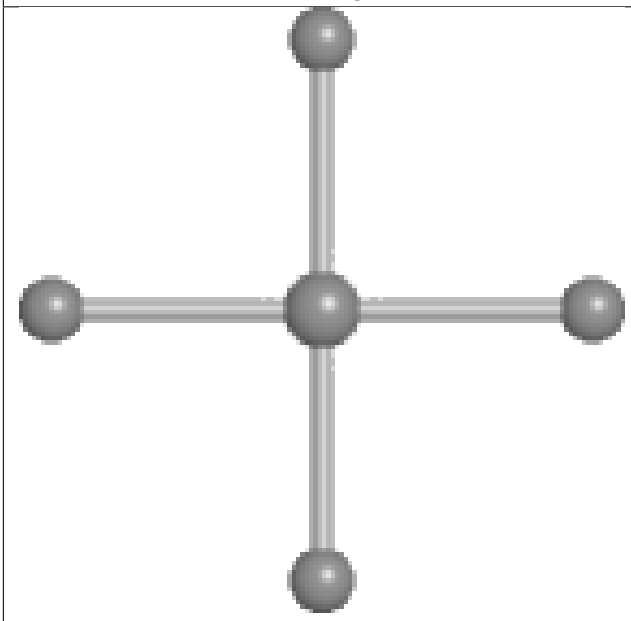

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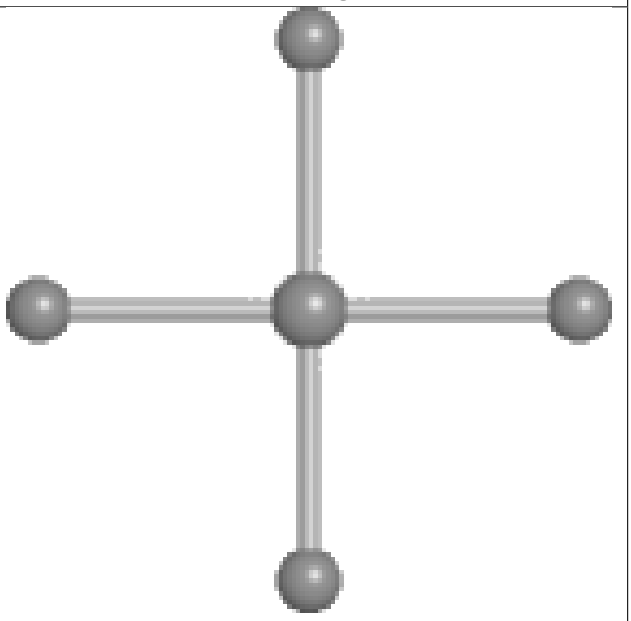
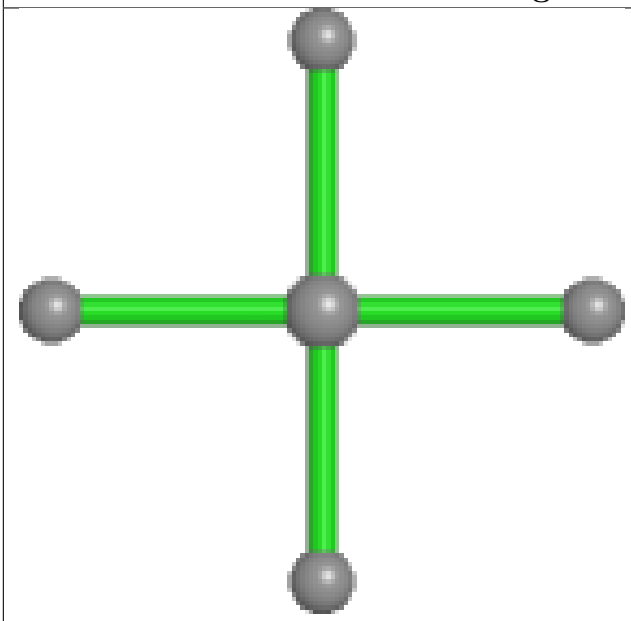
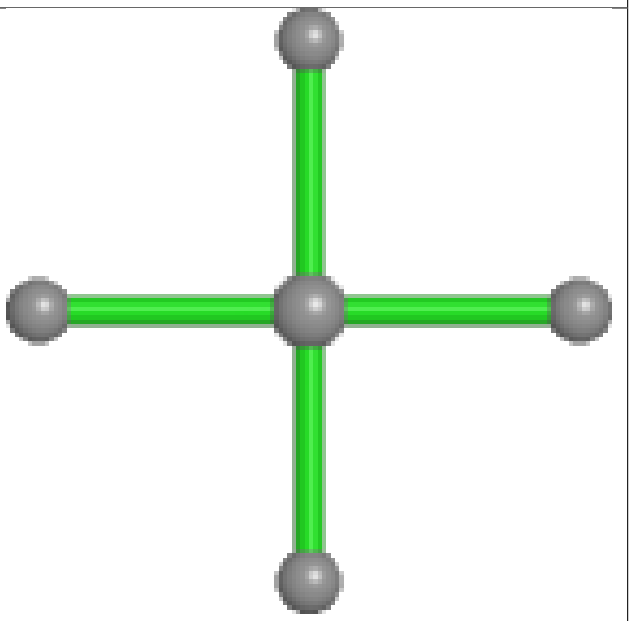


Rings

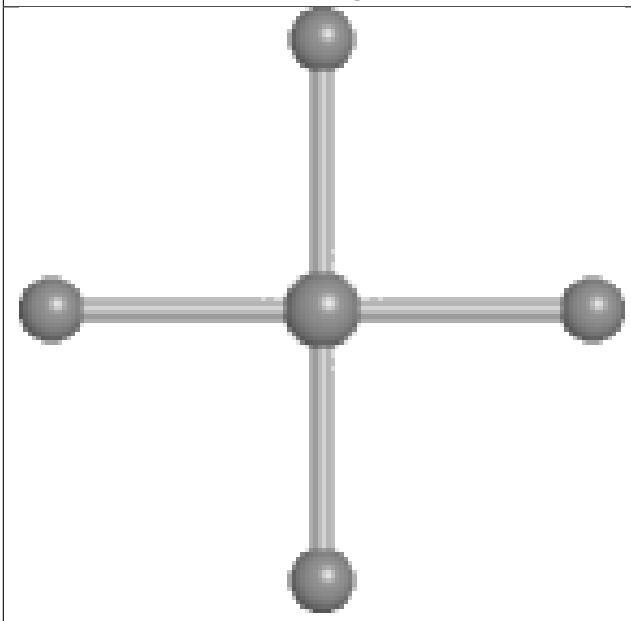
Ligand SO4 J 203



Bond lengths



Bond angles



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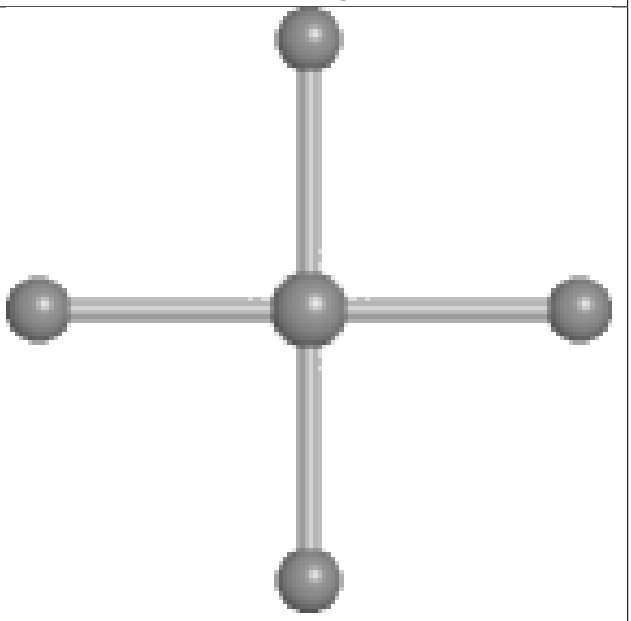
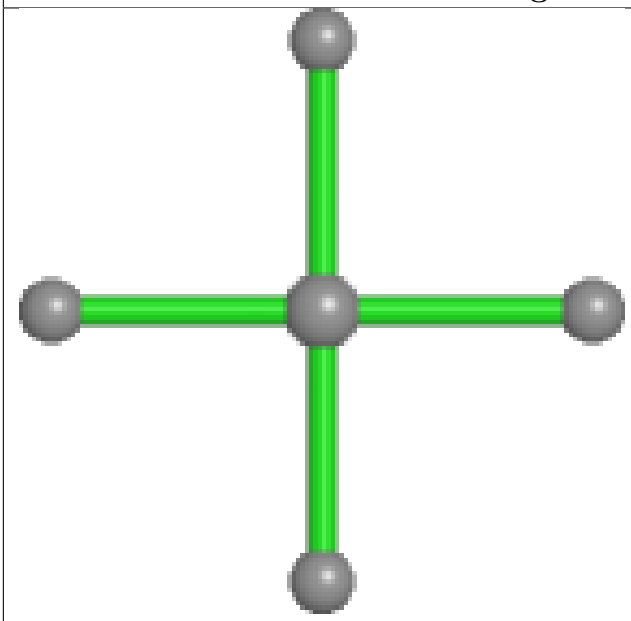


Rings

Ligand SO4 E 208



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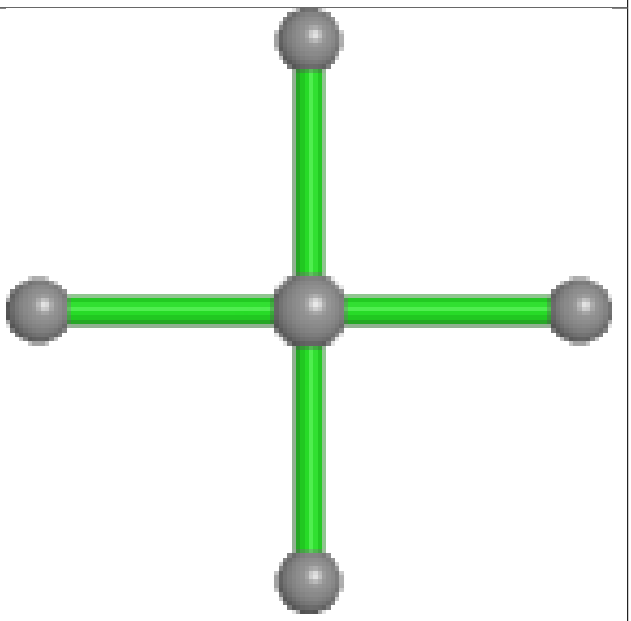
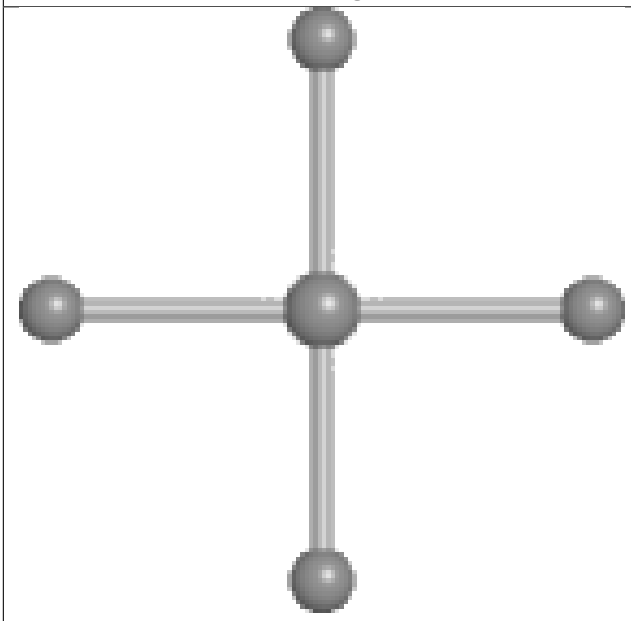


Bond angles



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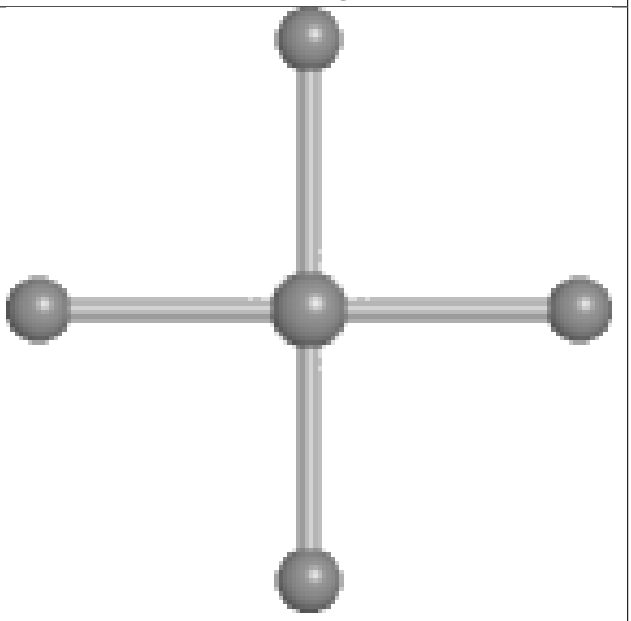
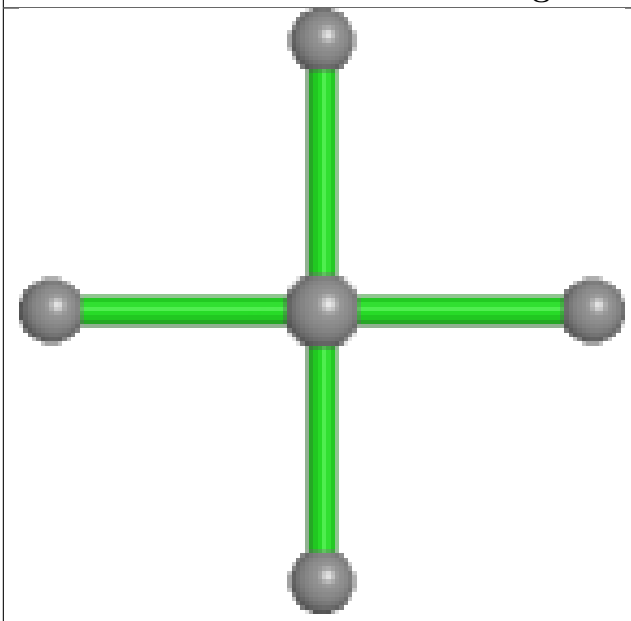
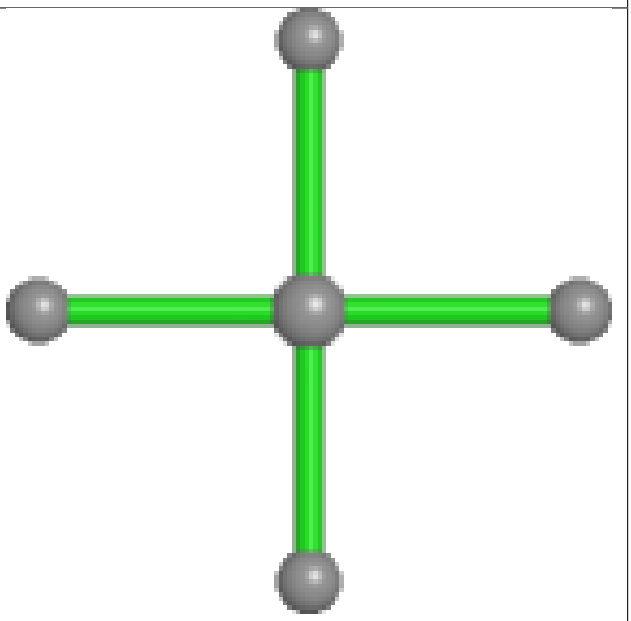


Rings

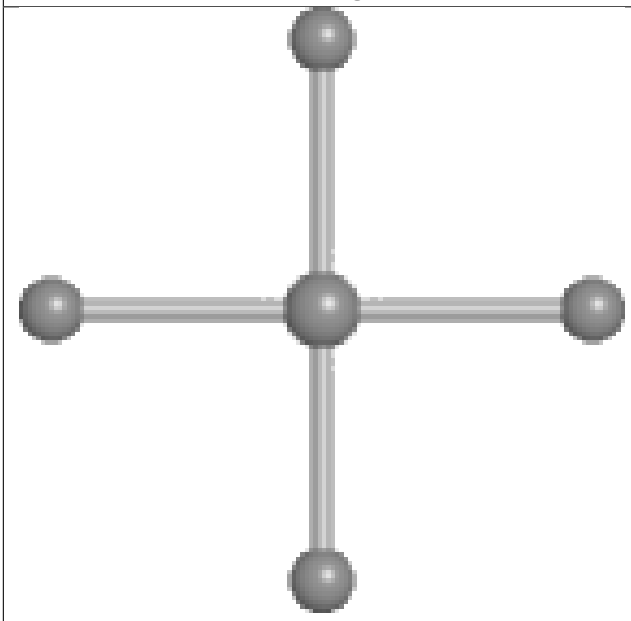
Ligand SO4 J 205



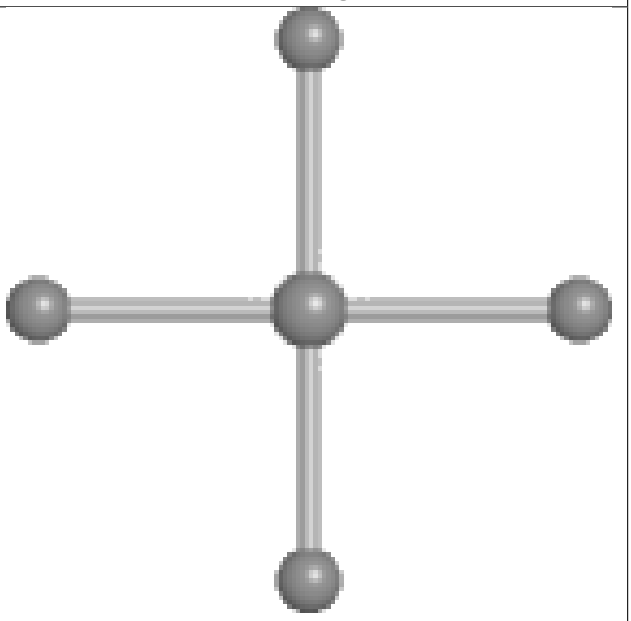
Bond lengths



Bond angles

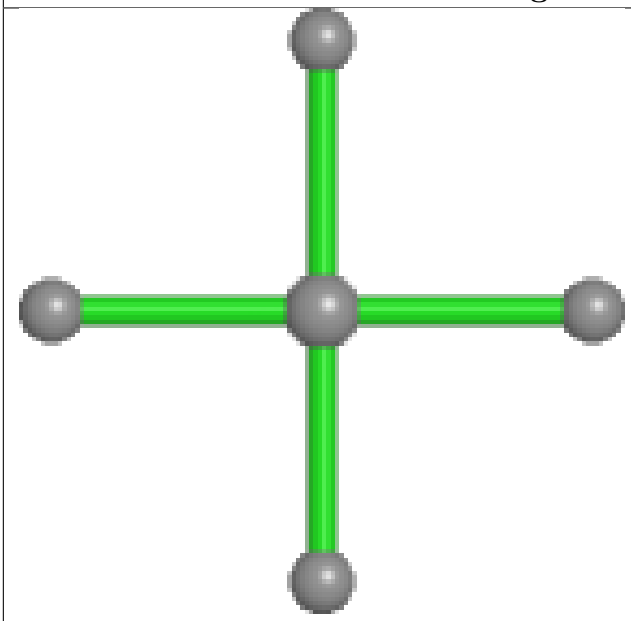


Torsions



Rings

Ligand SO4 E 209



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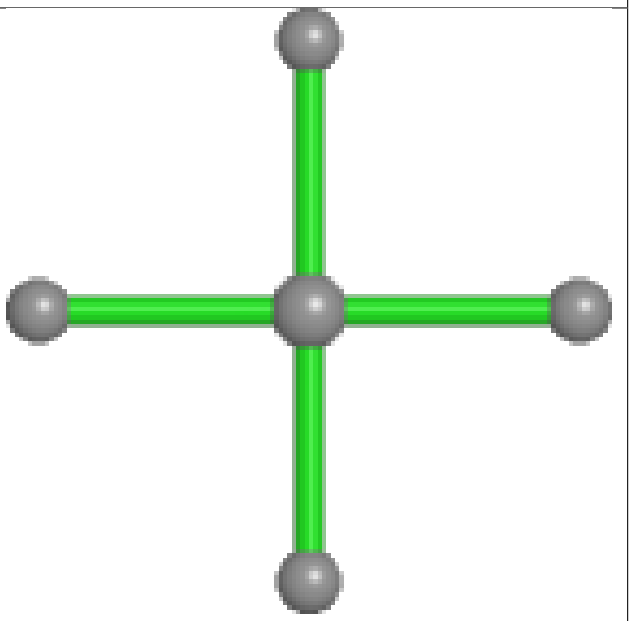
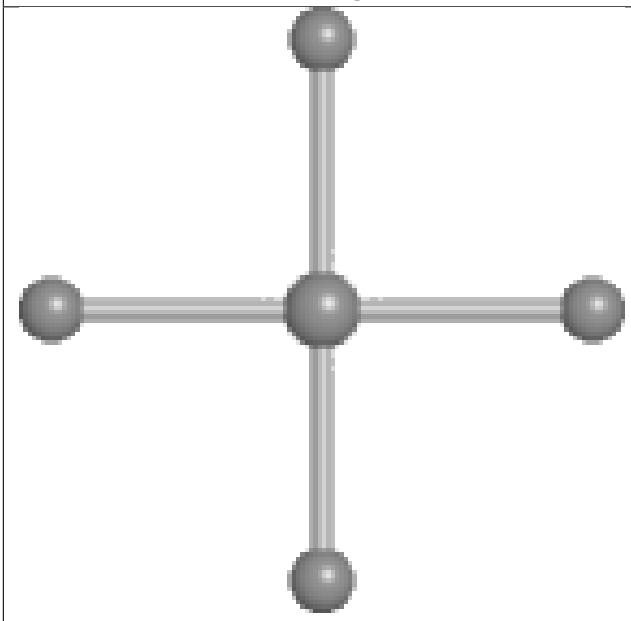
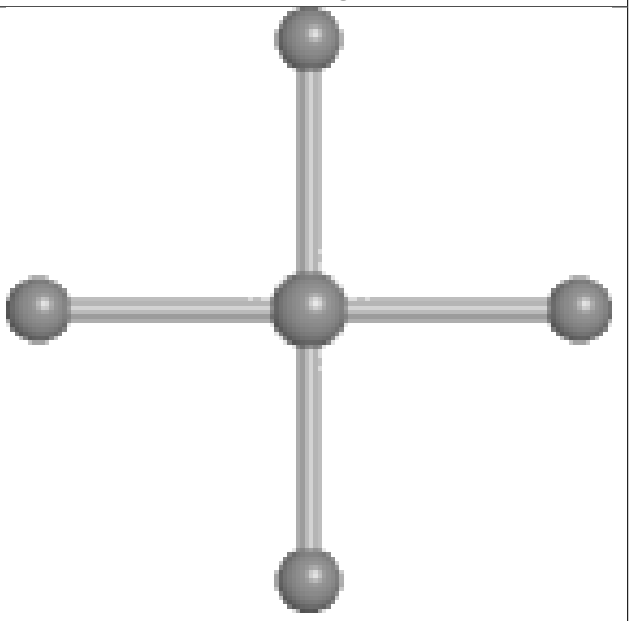


Bond angles

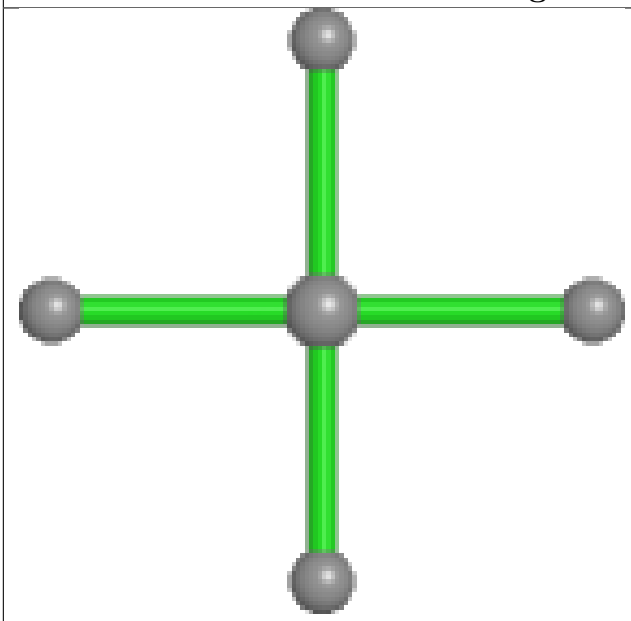


Torsions



Rings

Ligand SO4 C 206



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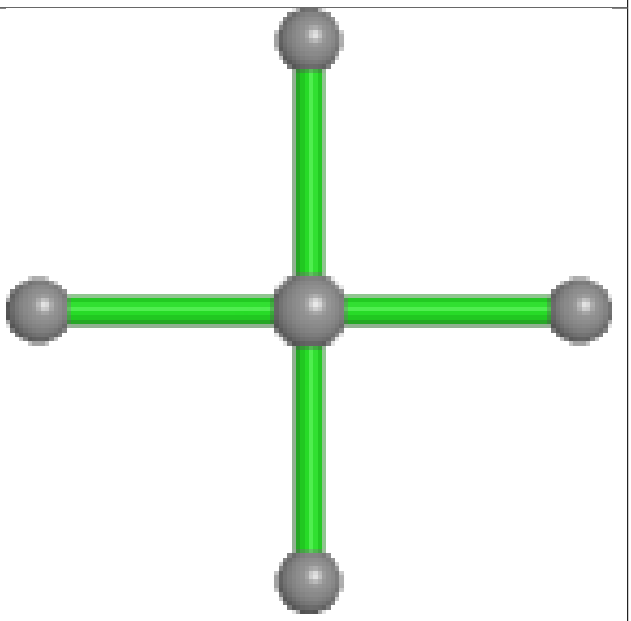
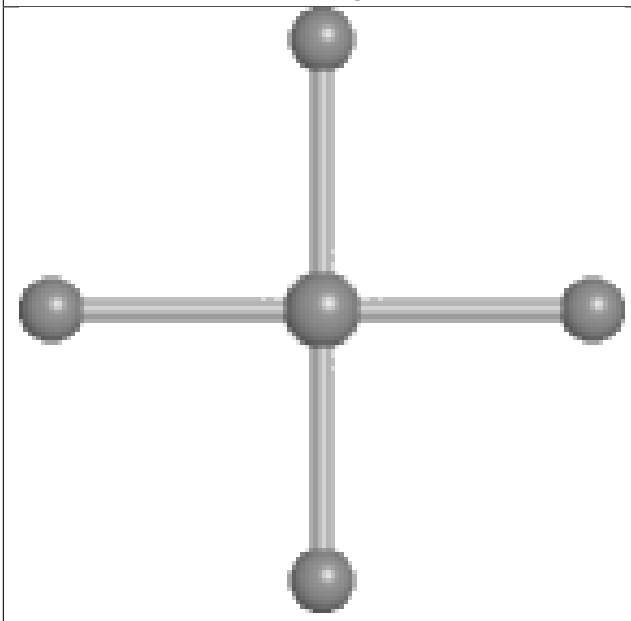
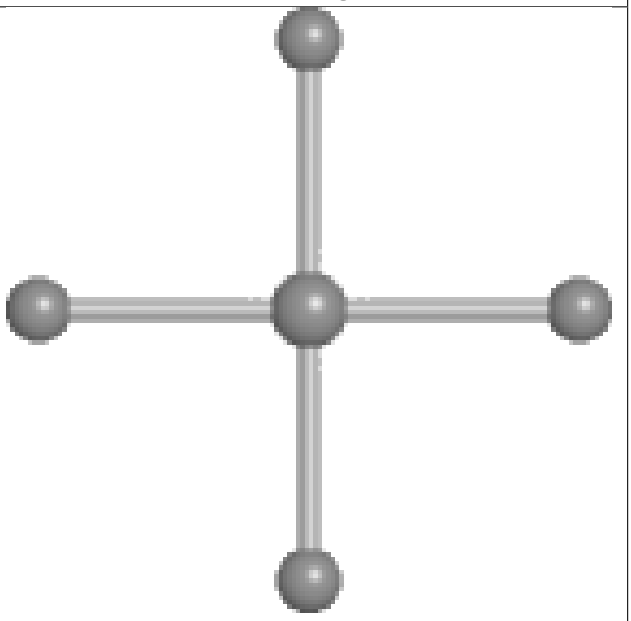


Bond angles

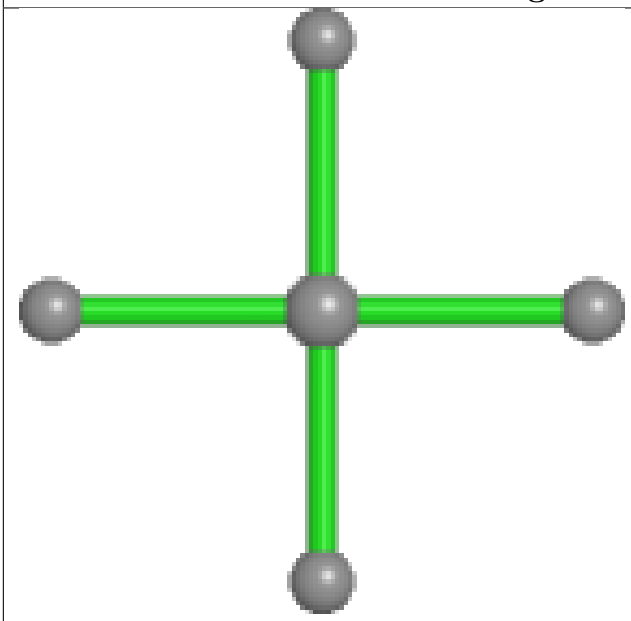


Torsions



Rings

Ligand SO4 G 205



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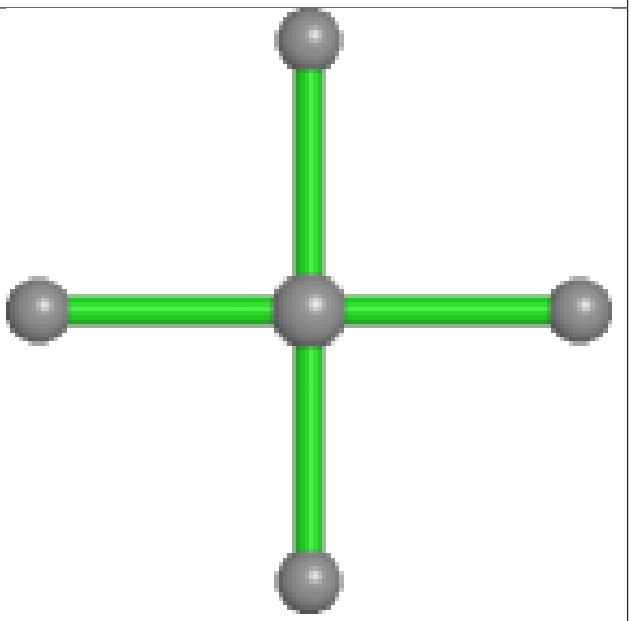

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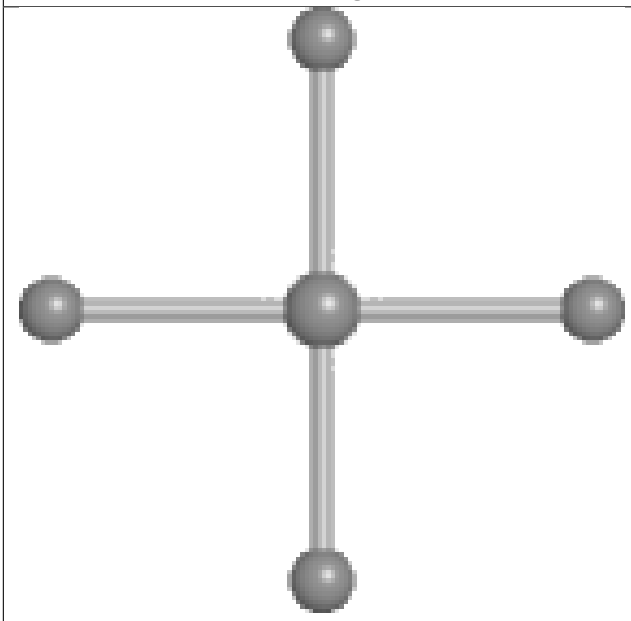

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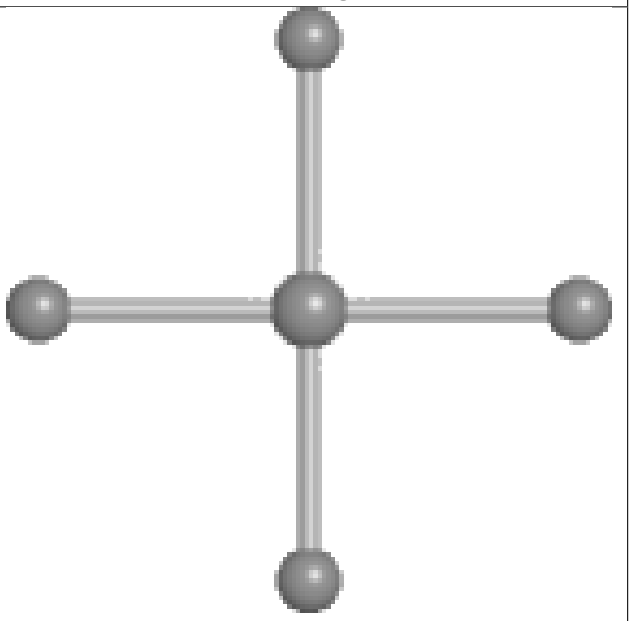
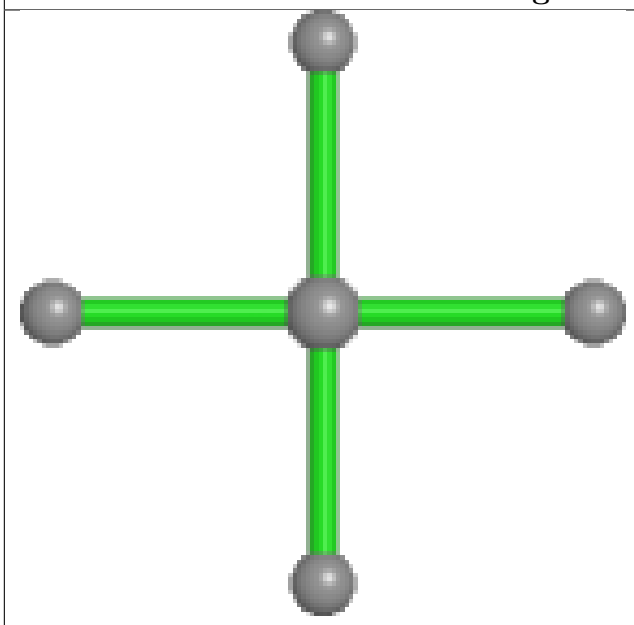


Rings

Ligand SO4 L 205



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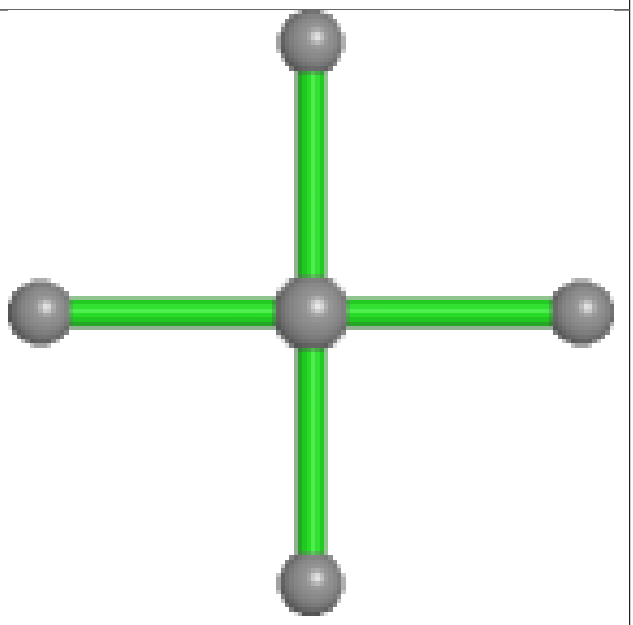
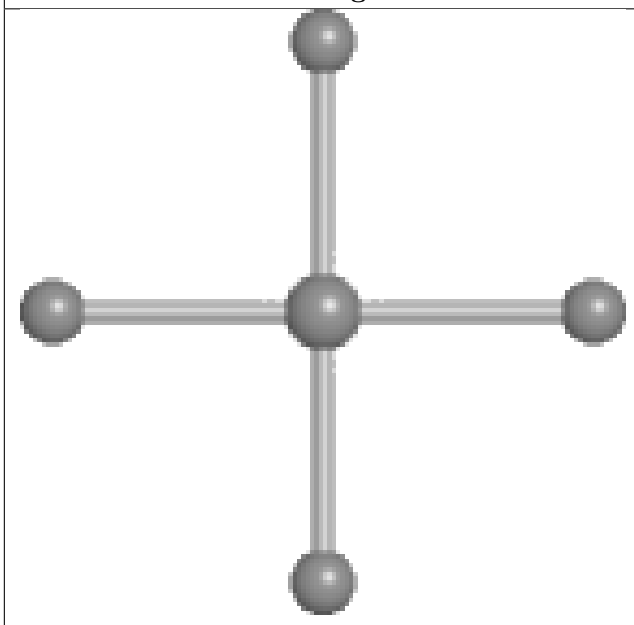
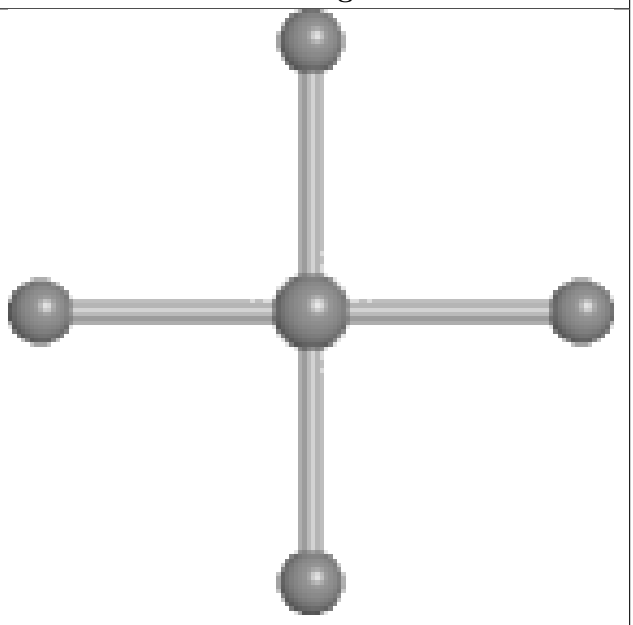


Bond angles

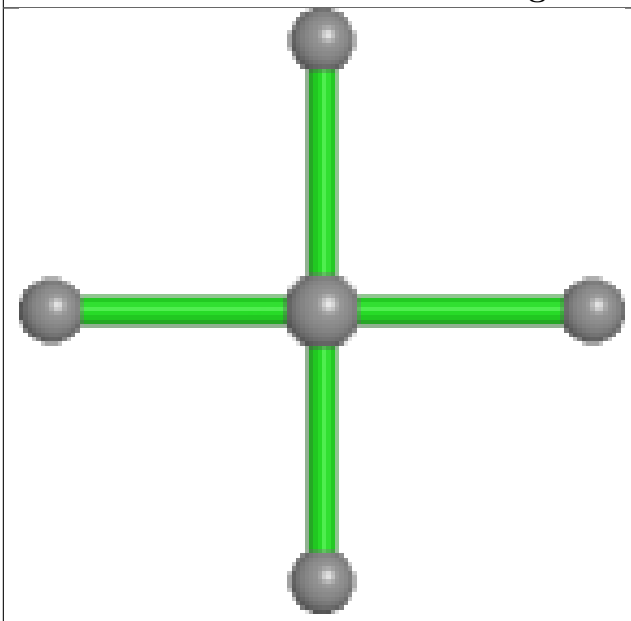


Torsions



Rings

Ligand SO4 A 207



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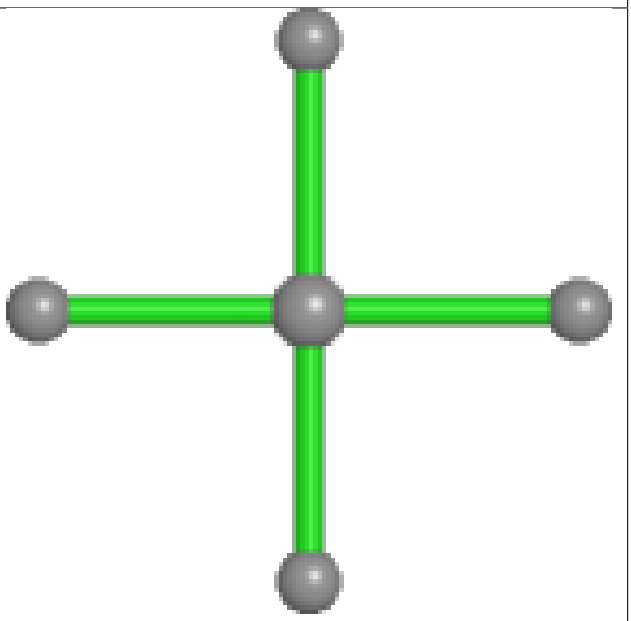
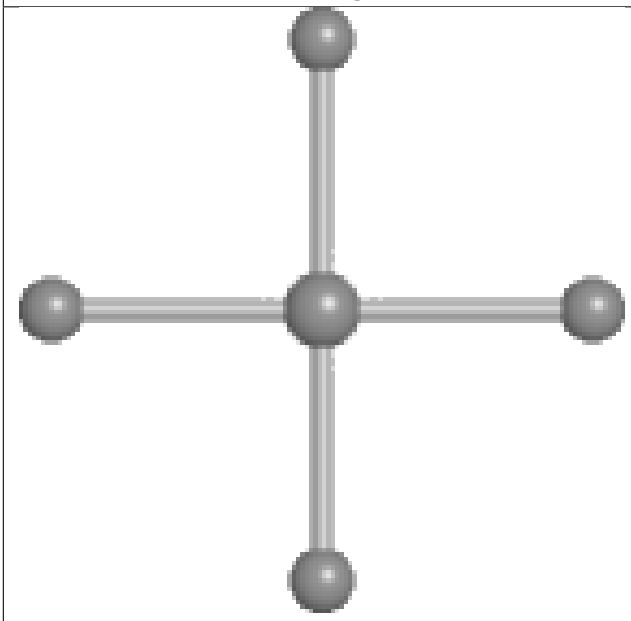


Bond angles



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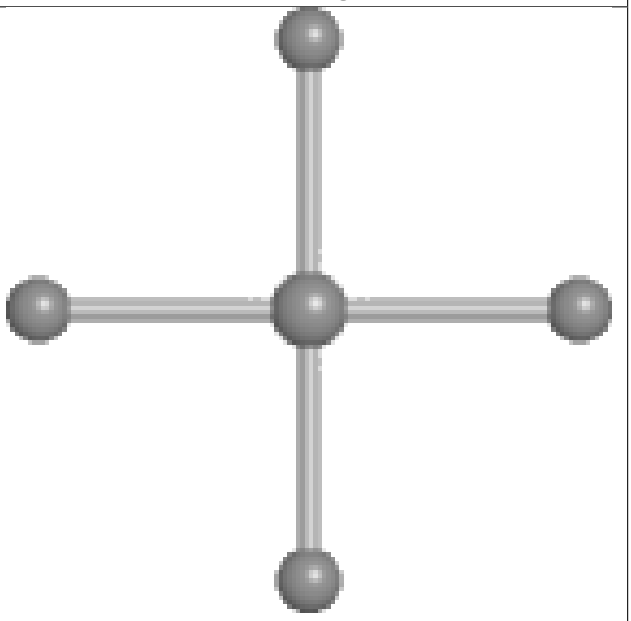
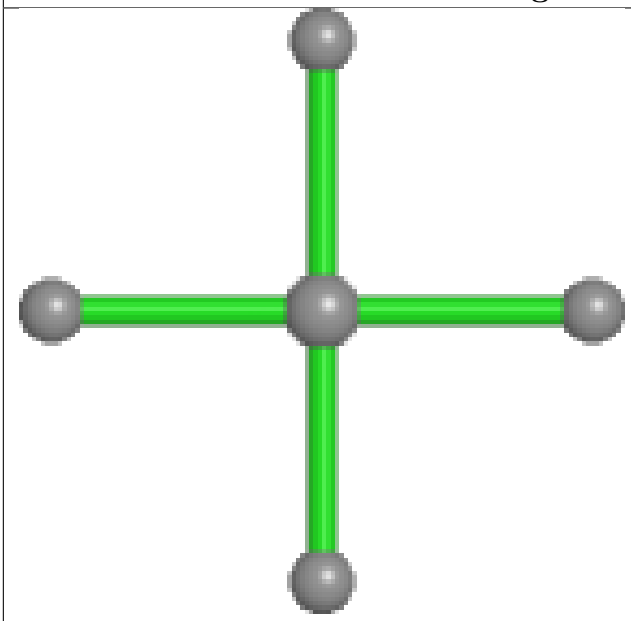


Rings

Ligand SO4 L 204



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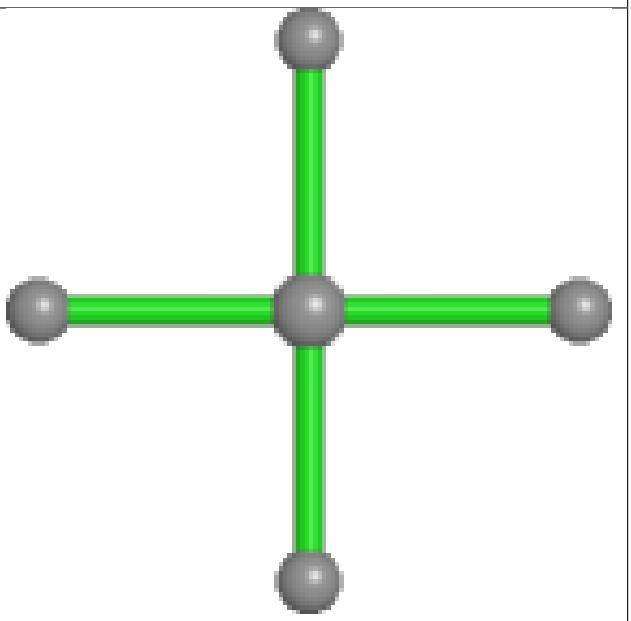
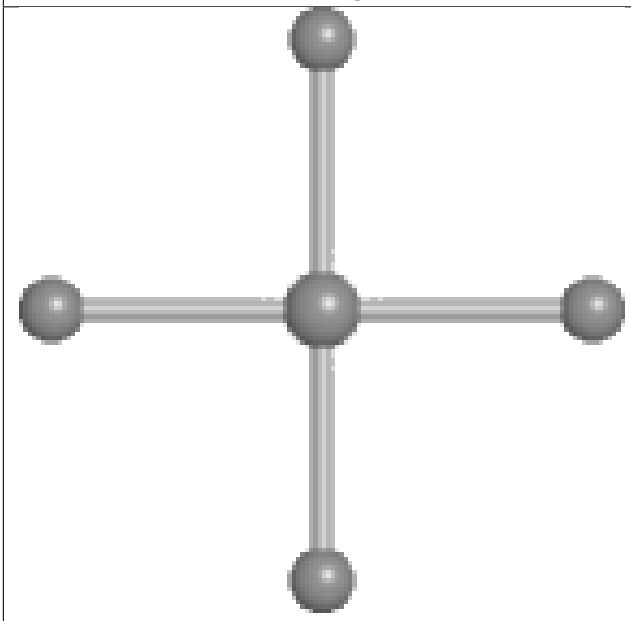
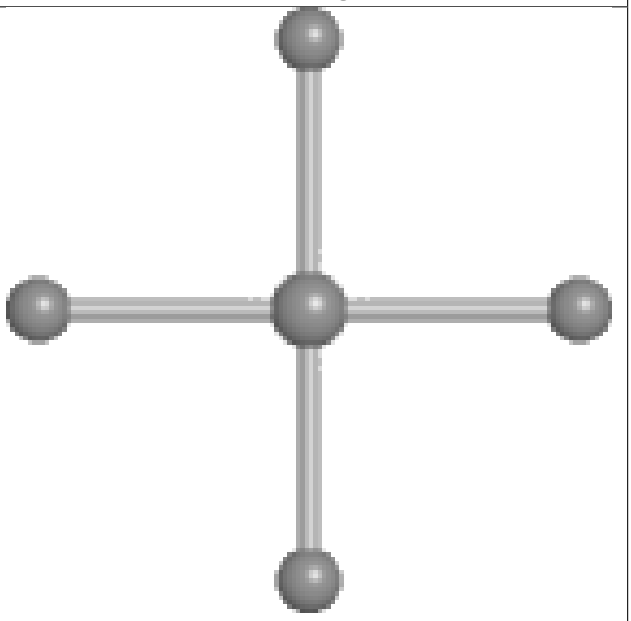


Bond angles

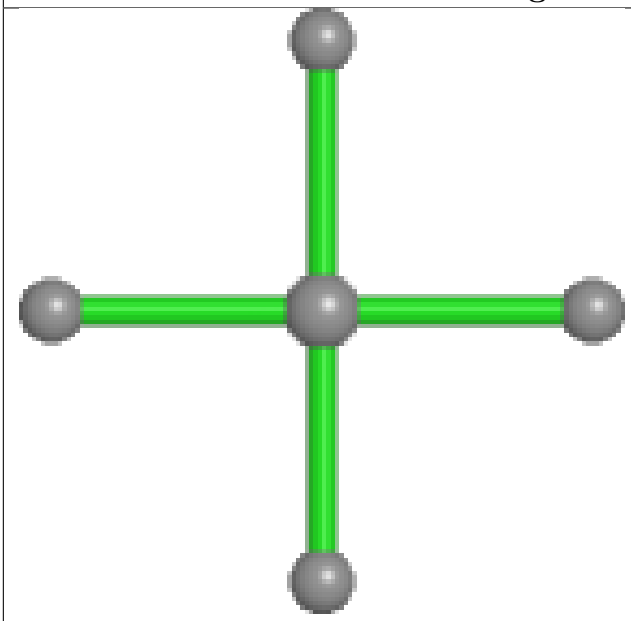


Torsions



Rings

Ligand SO4 A 208



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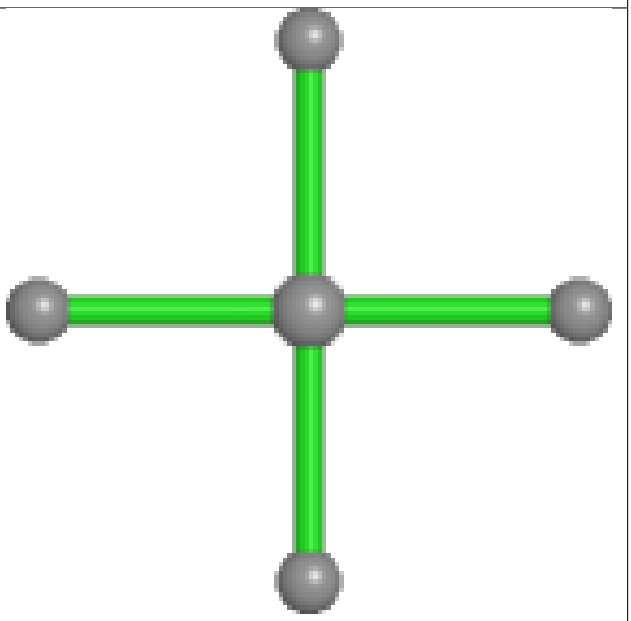
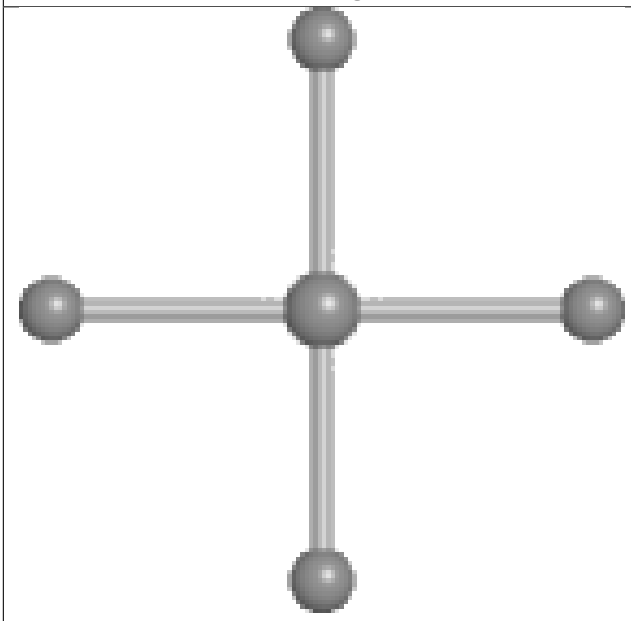


Bond angles



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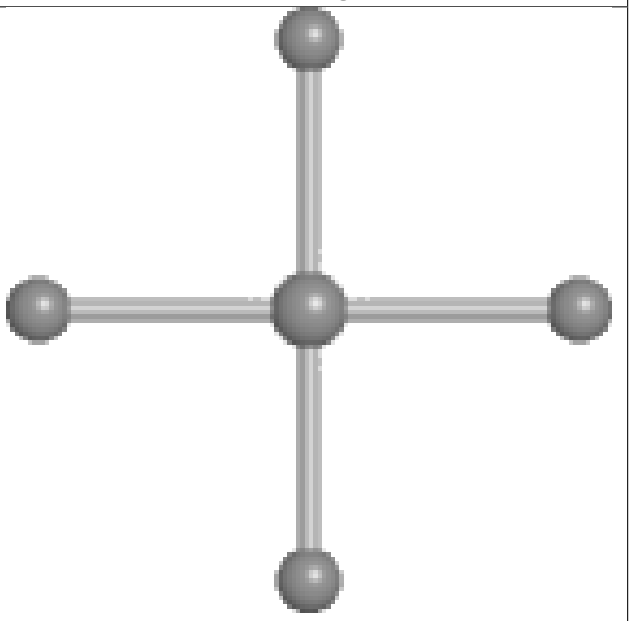
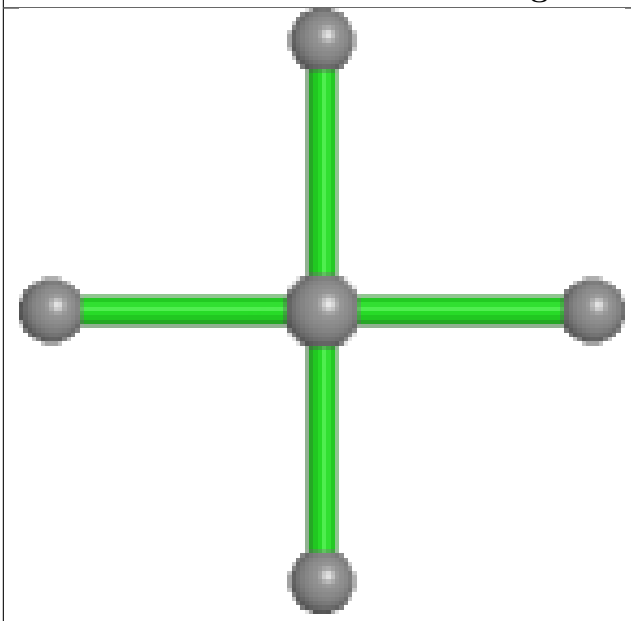


Rings

Ligand SO4 F 207



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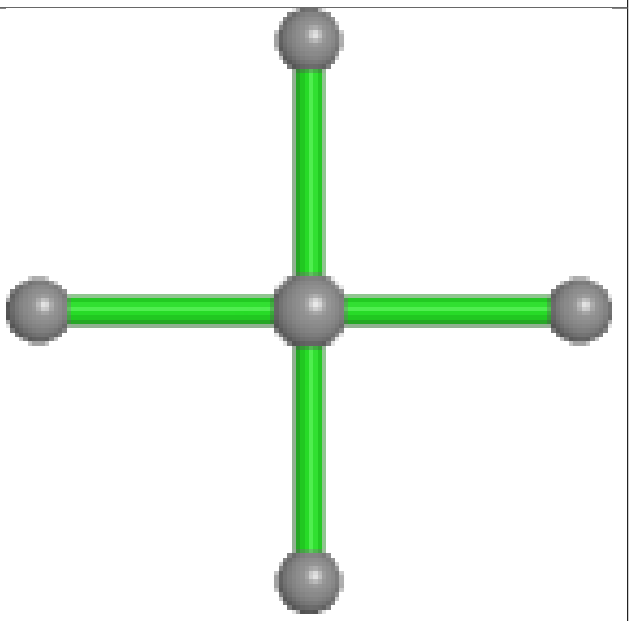
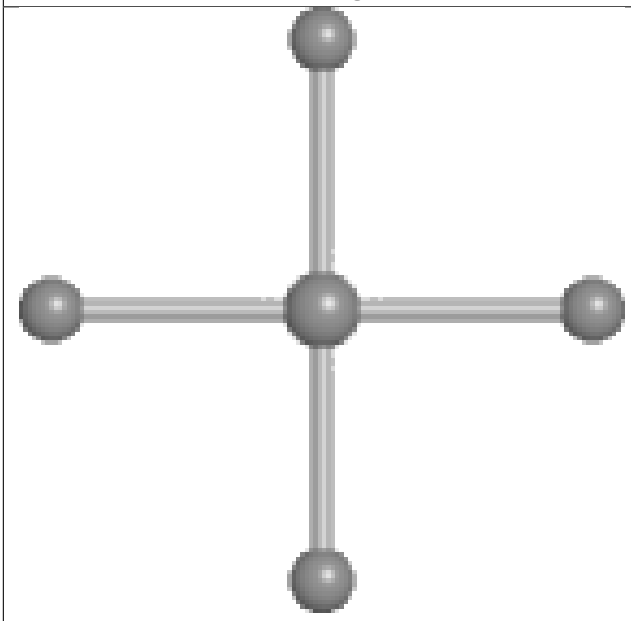


Bond angles



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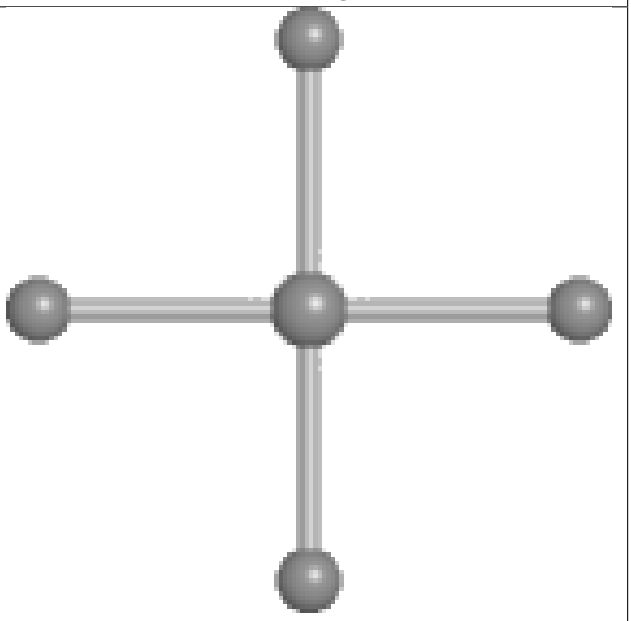
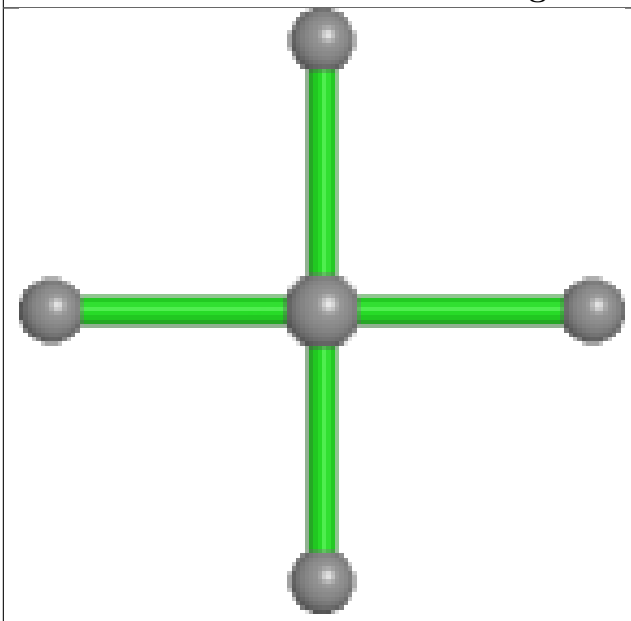


Rings

Ligand SO4 C 209



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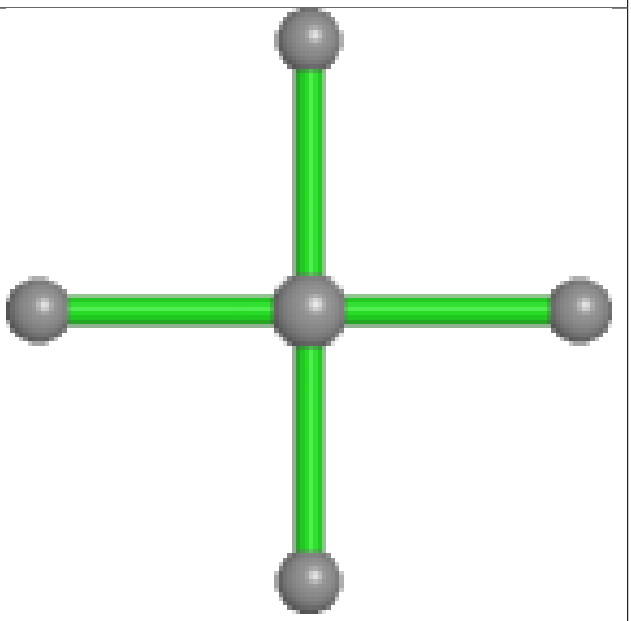
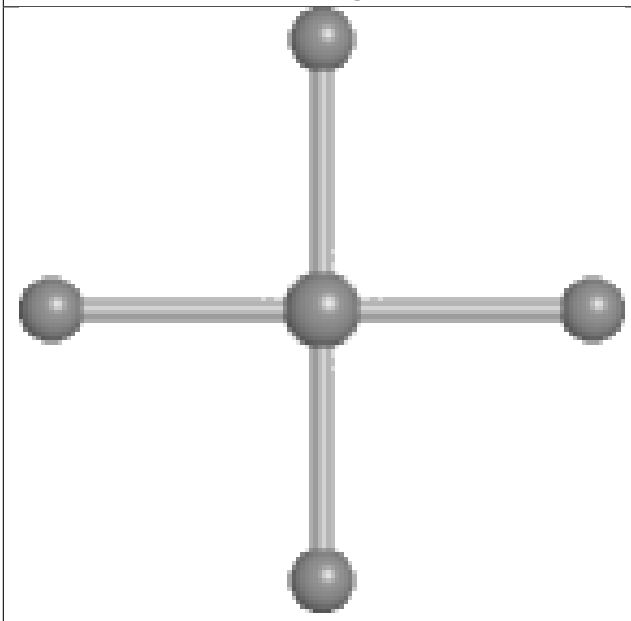


Bond angles



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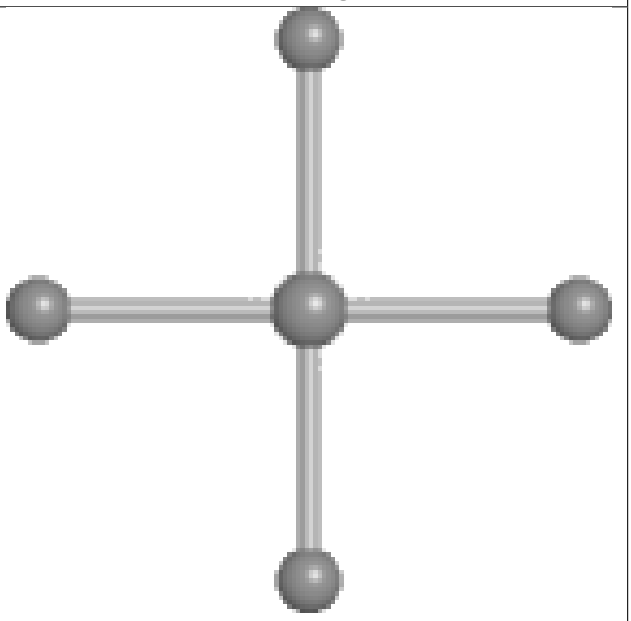
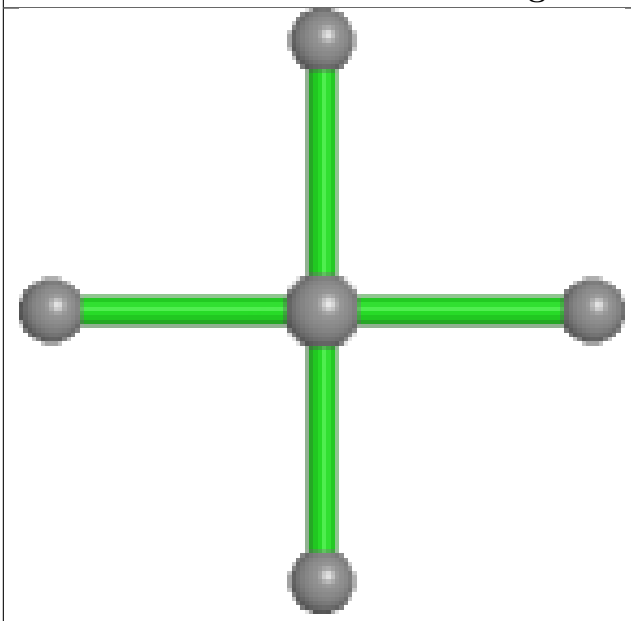
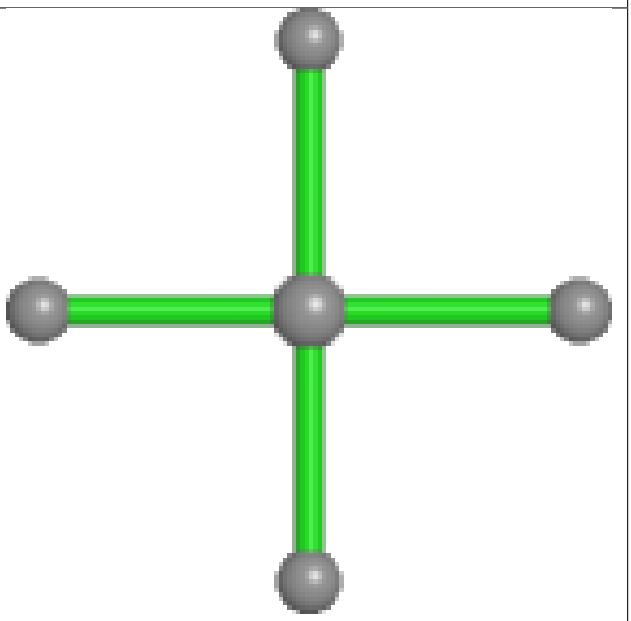


Rings

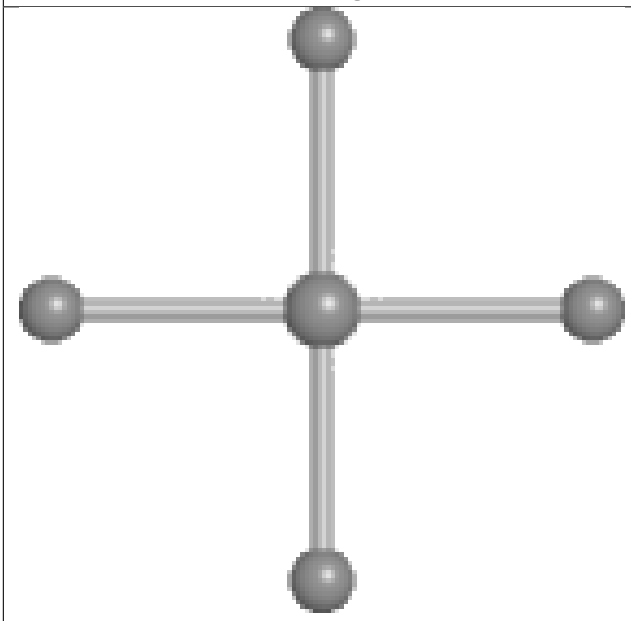
Ligand SO4 D 210



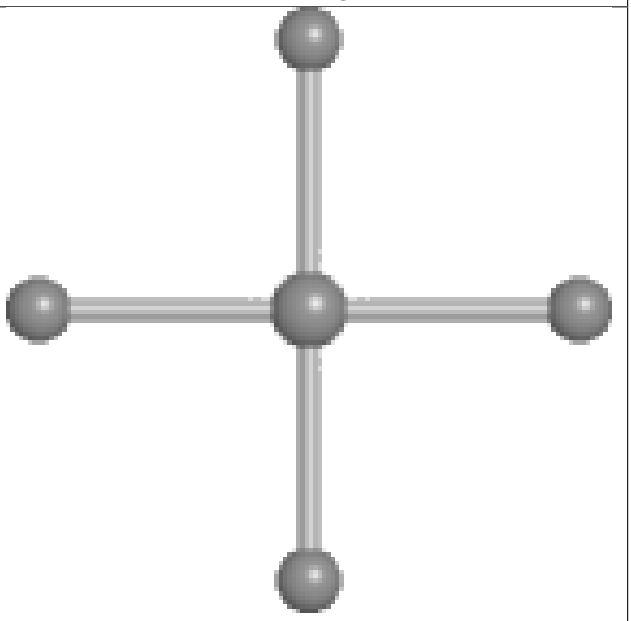
Bond lengths



Bond angles

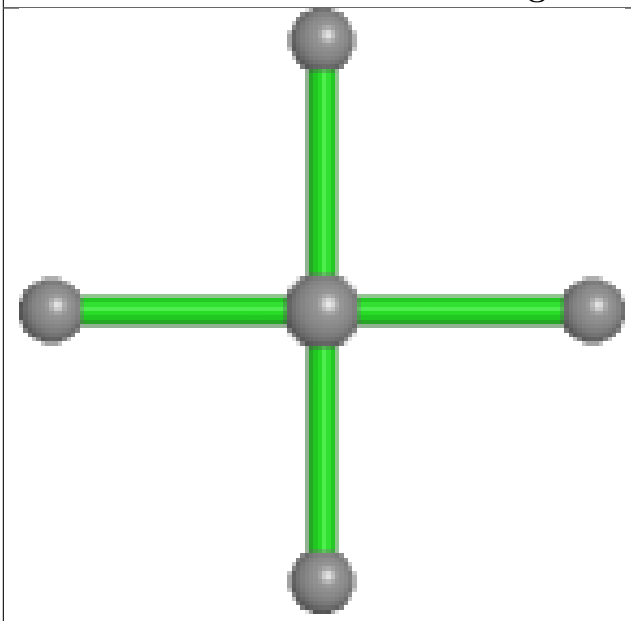


Torsions



Rings

Ligand SO4 D 209



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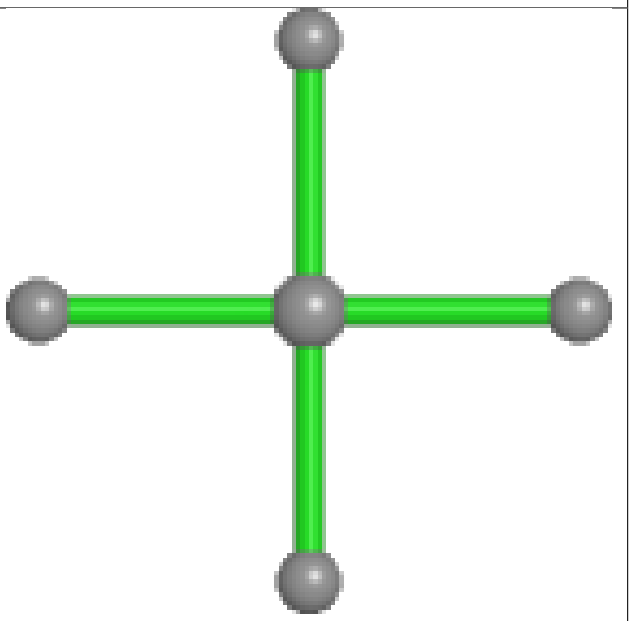
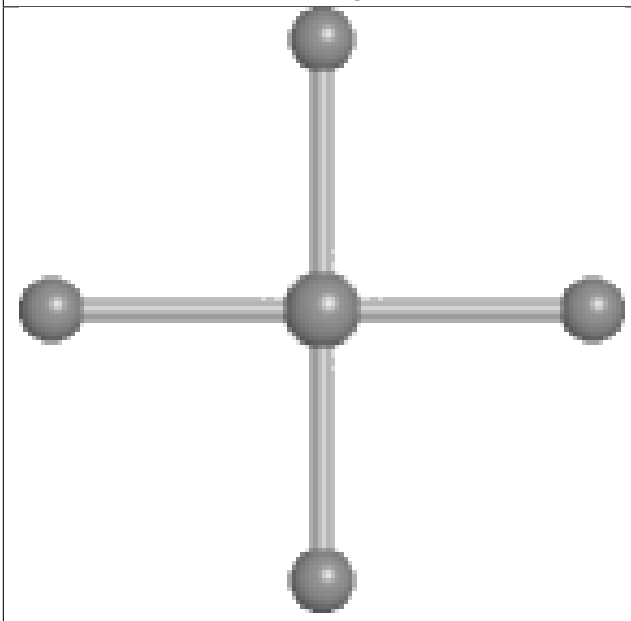
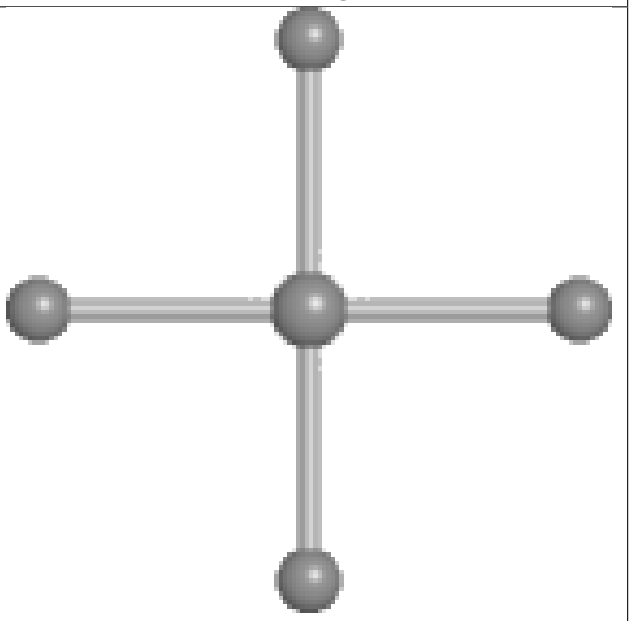


Bond angles

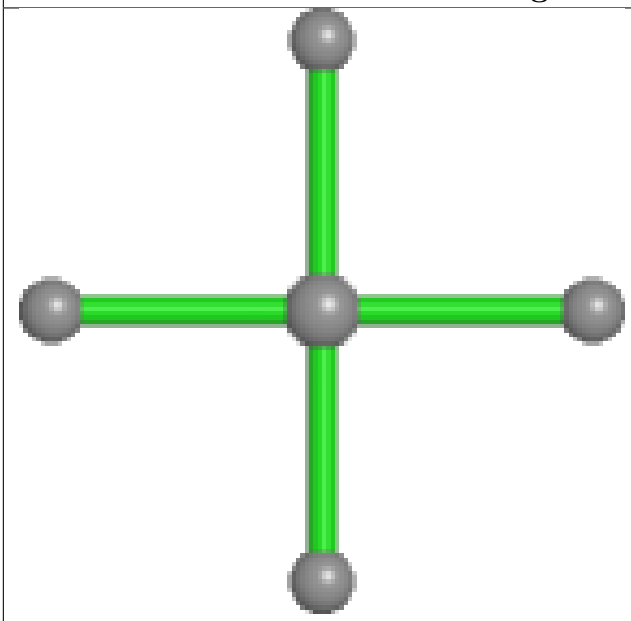


Torsions

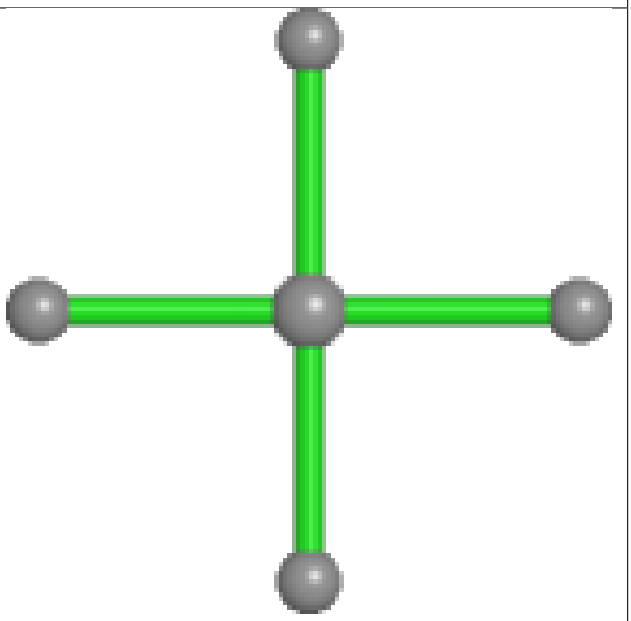


Rings

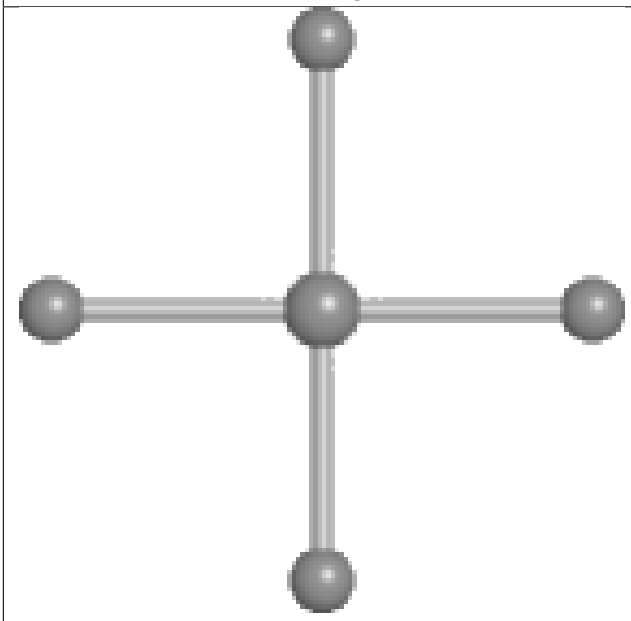
Ligand SO4 F 203



Bond lengths



Bond angles



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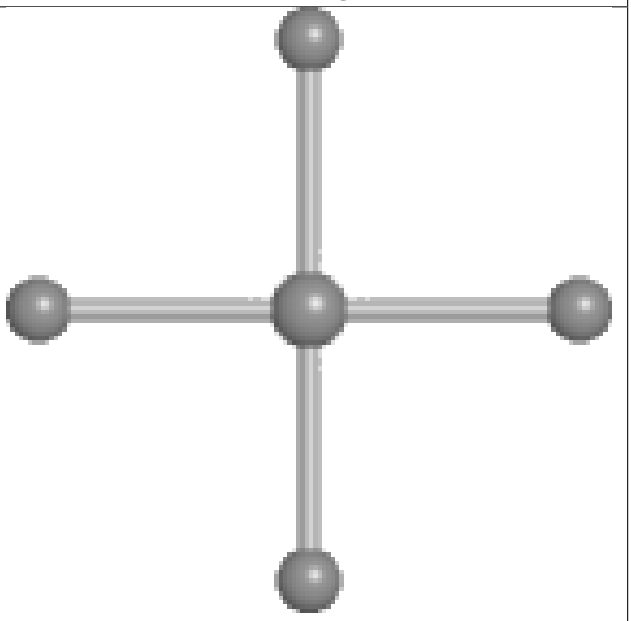
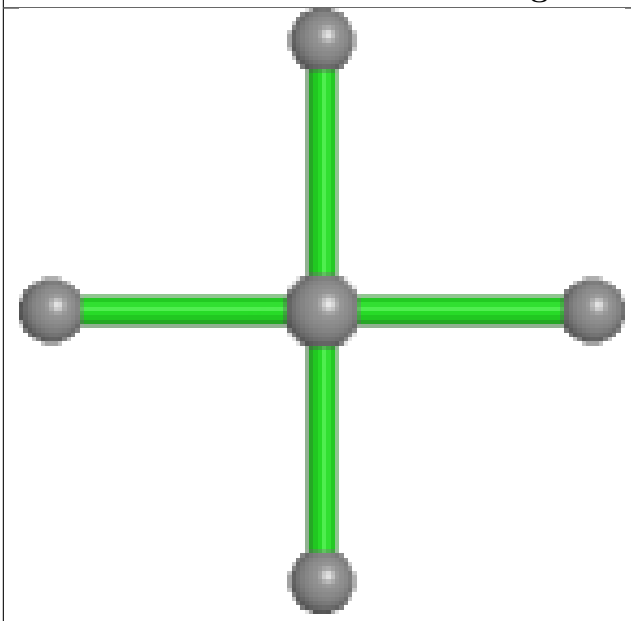
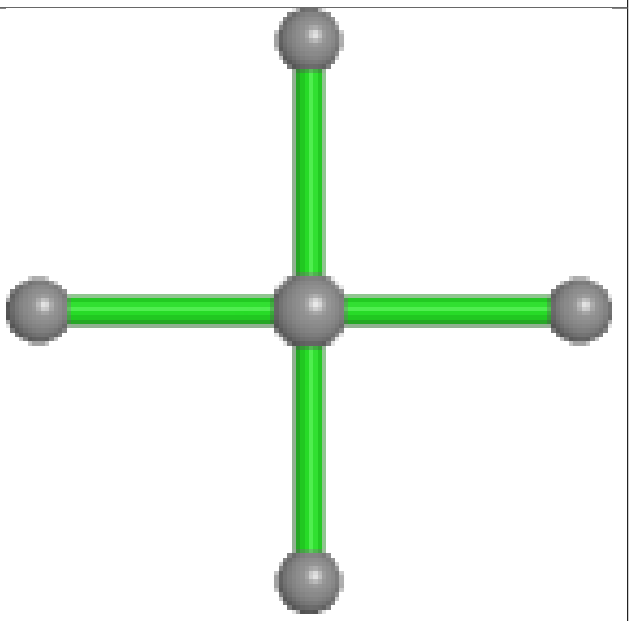


Rings

Ligand SO4 F 208



Bond lengths



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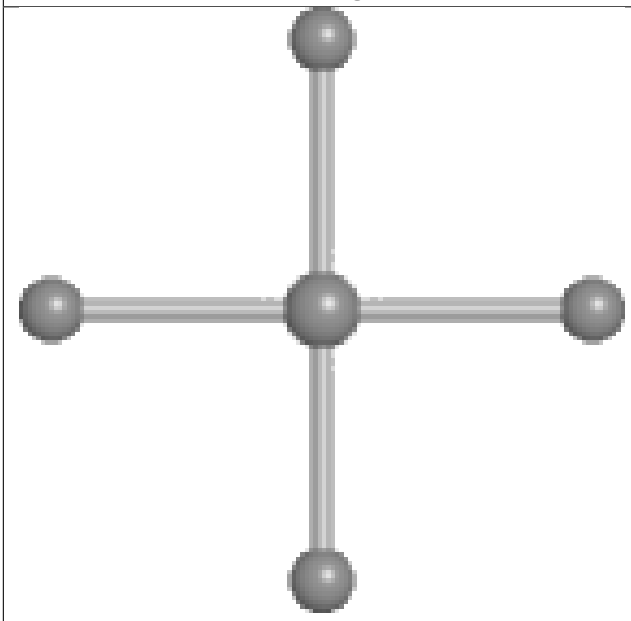

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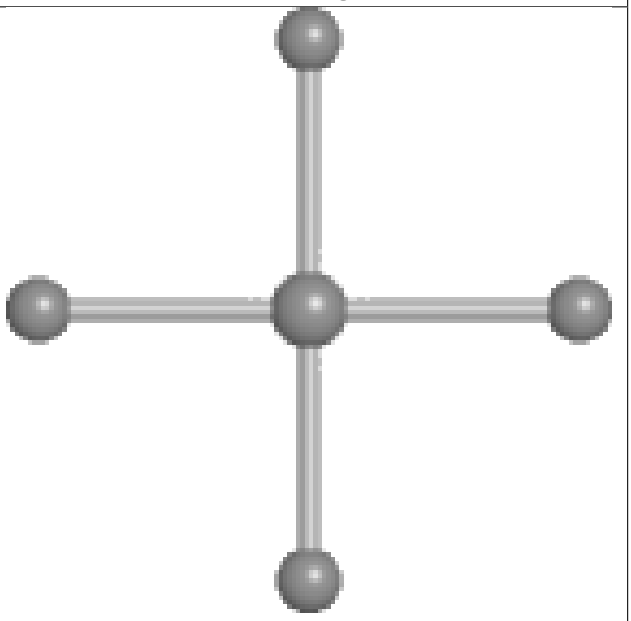
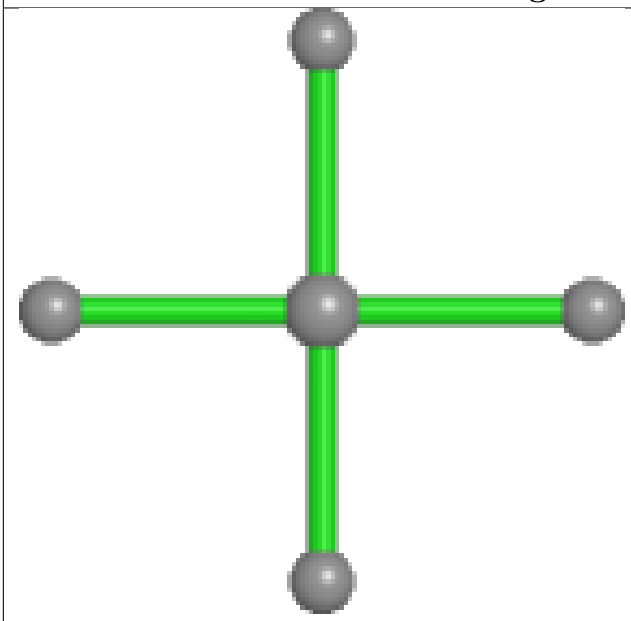
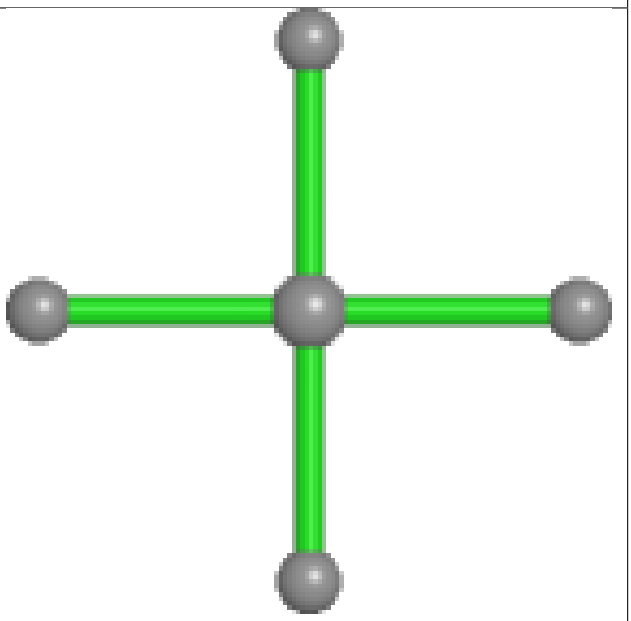


Rings

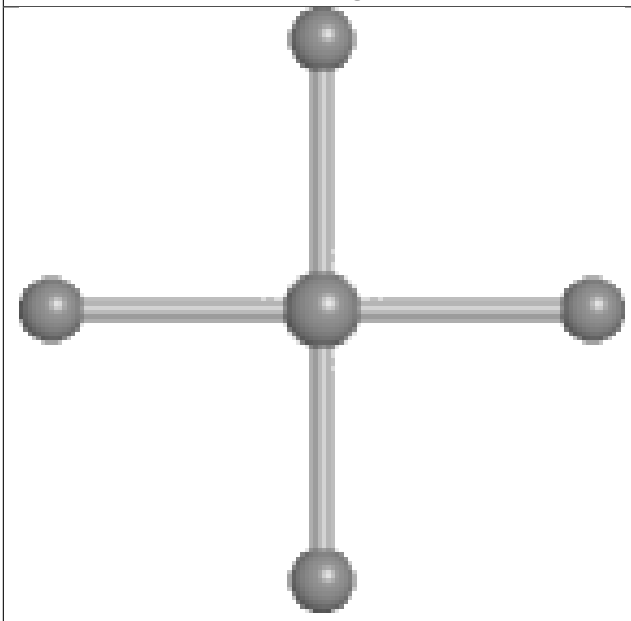
Ligand SO4 C 208



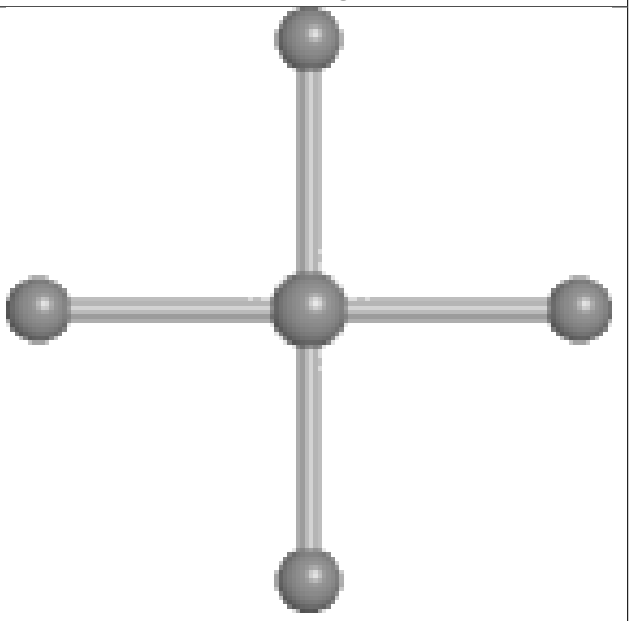
Bond lengths



Bond angles

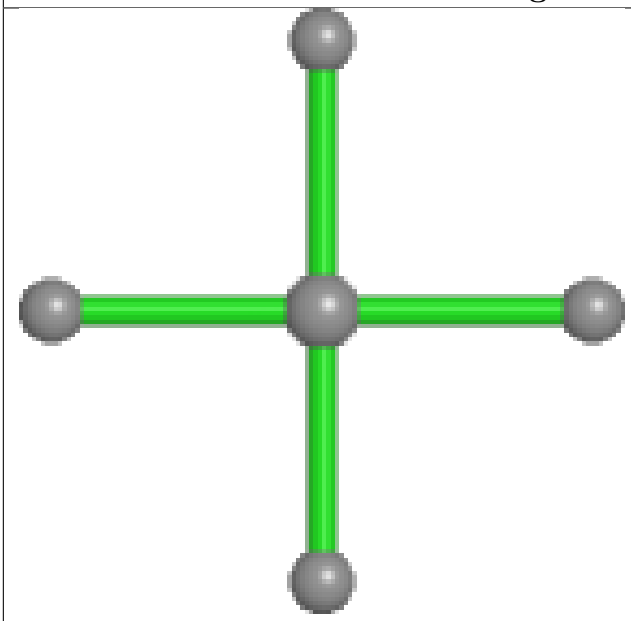


Torsions

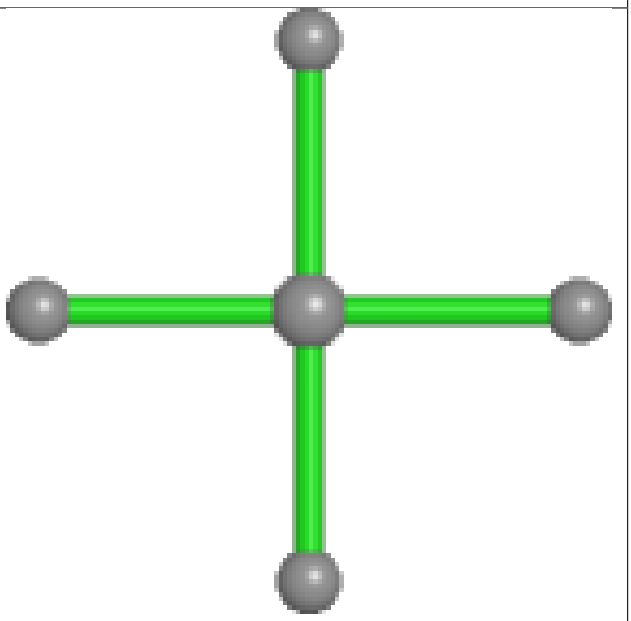


Rings

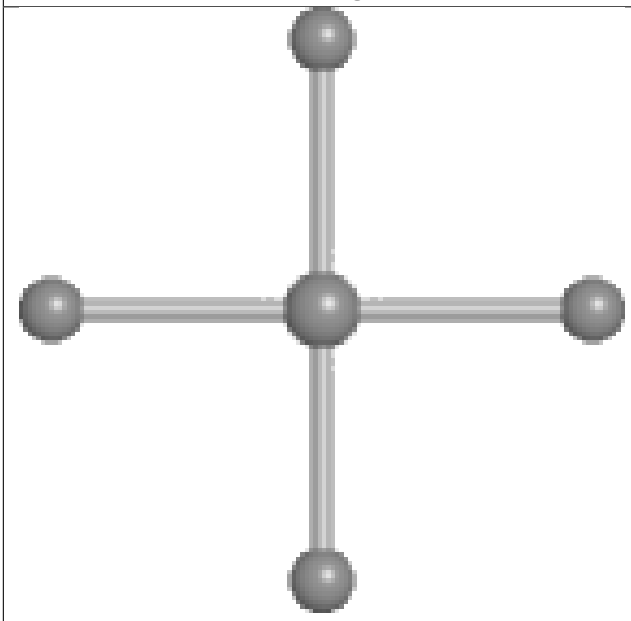
Ligand SO4 B 208



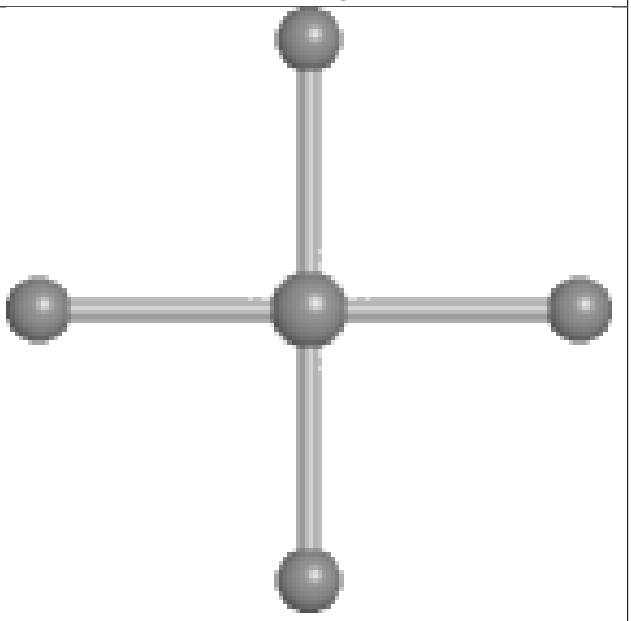
Bond lengths



Bond angles

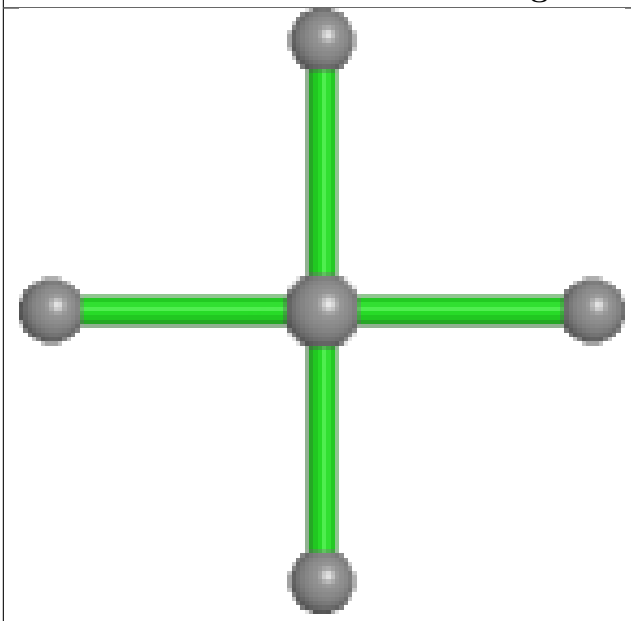


Torsions

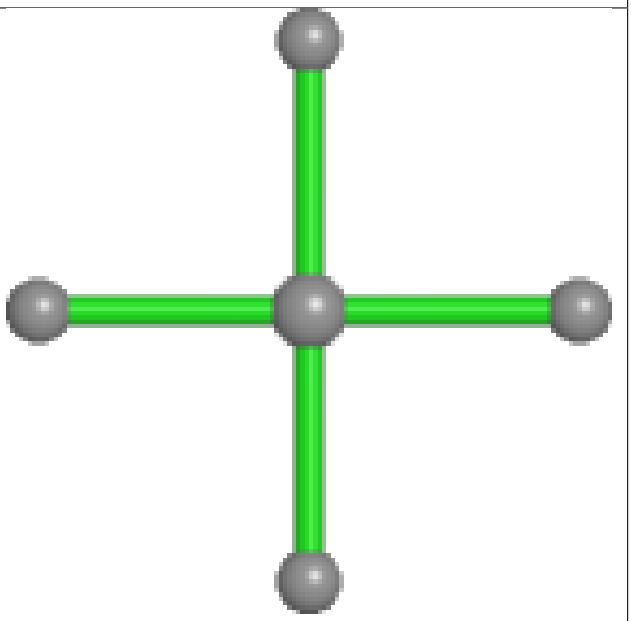


Rings

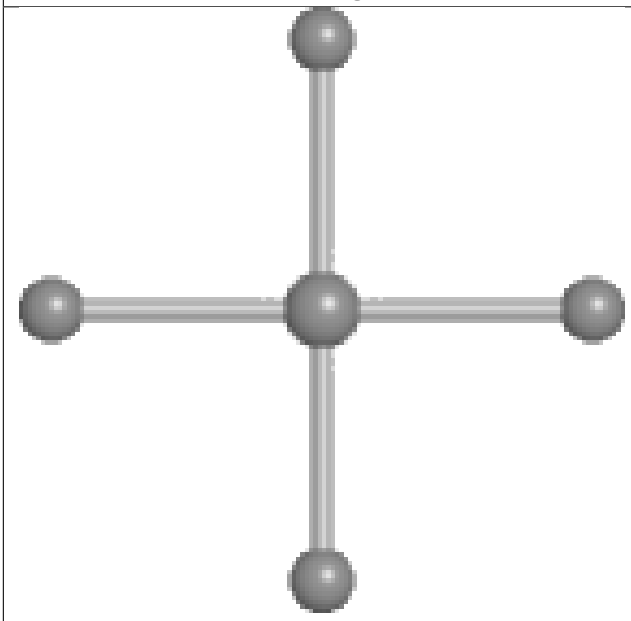
Ligand SO4 F 205



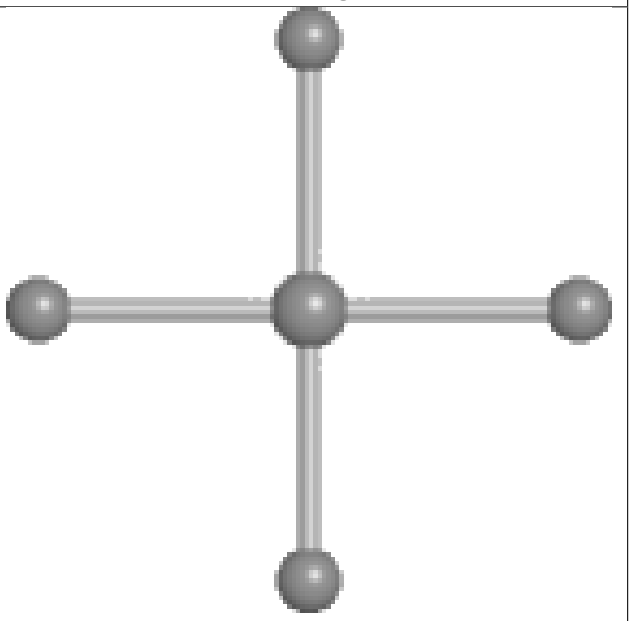
Bond lengths



Bond angles

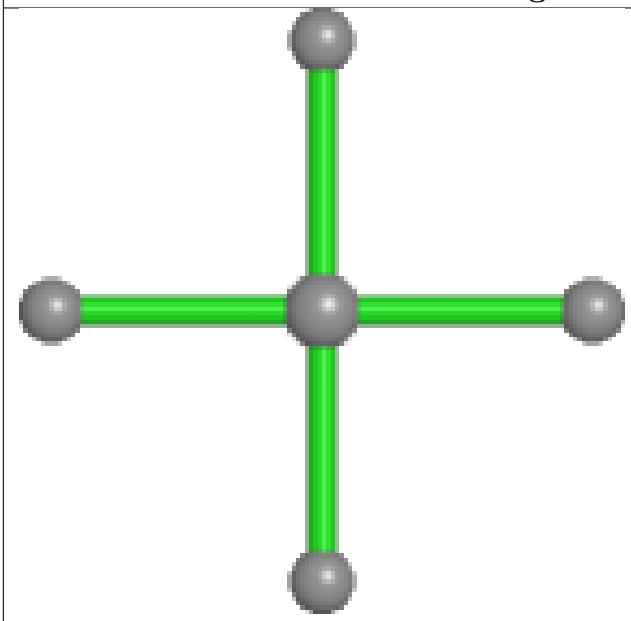


Torsions

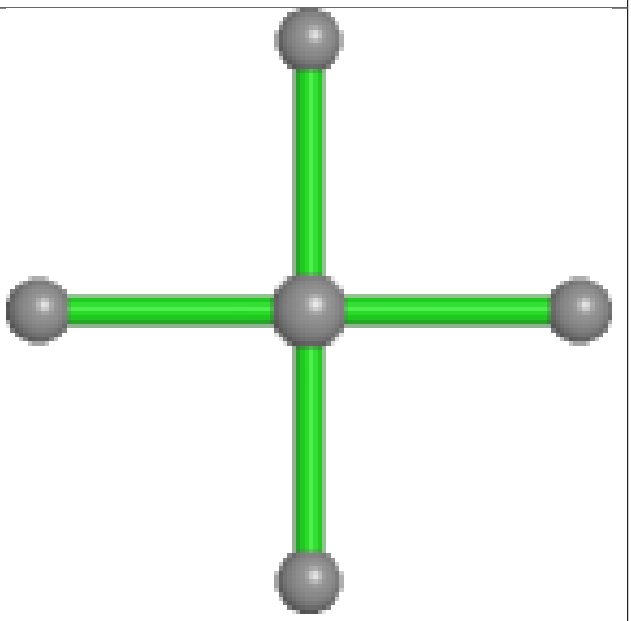


Rings

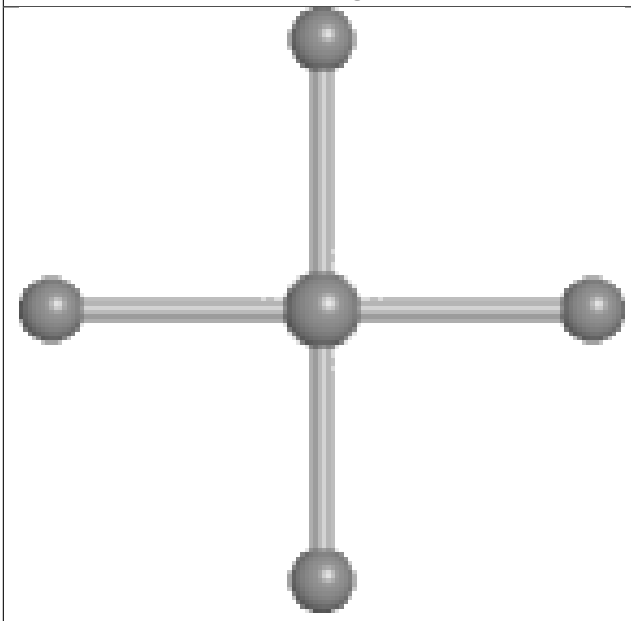
Ligand SO4 A 209



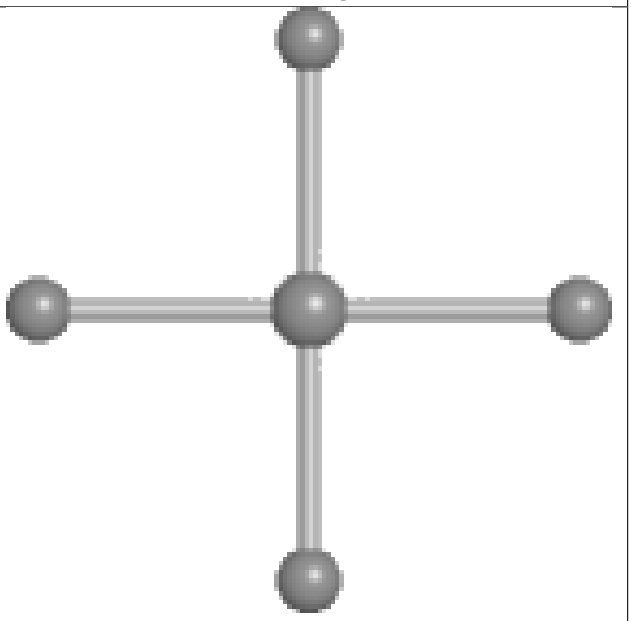
Bond lengths



Bond angles

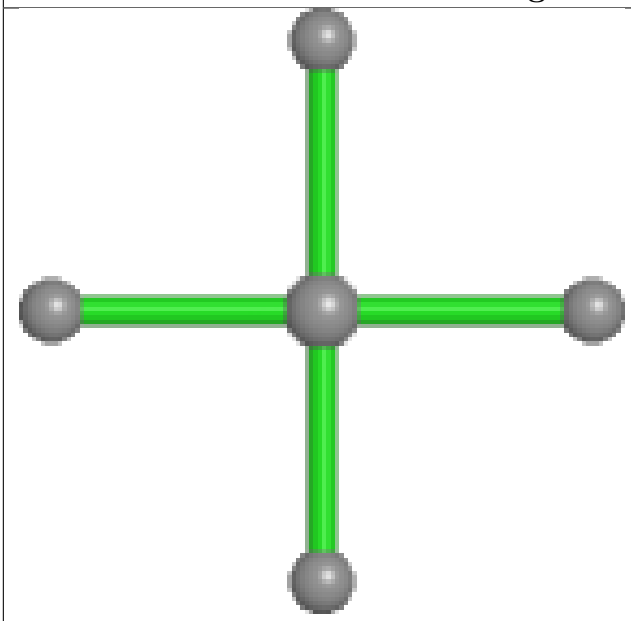


Torsions

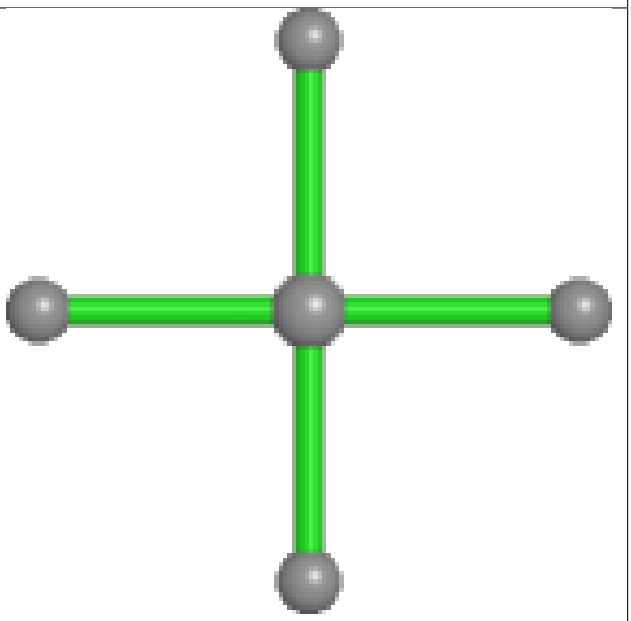


Rings

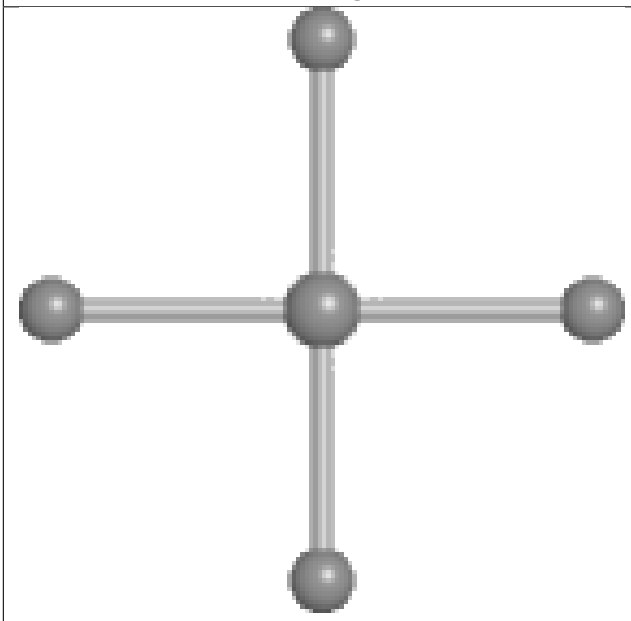
Ligand SO4 H 203



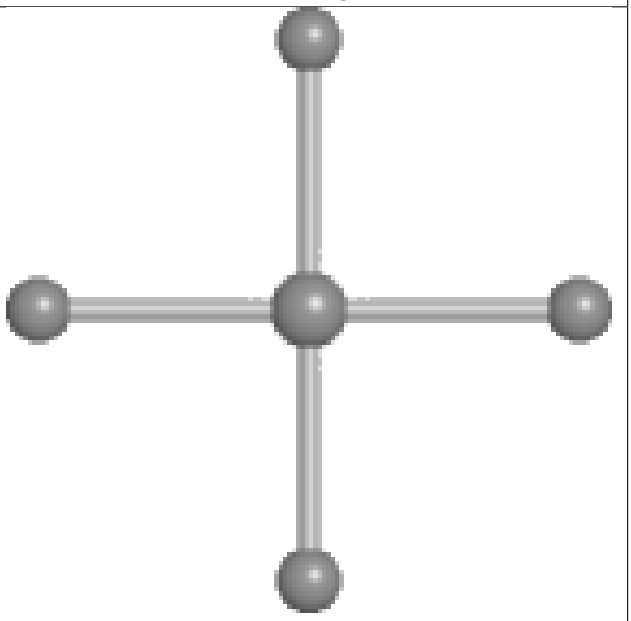
Bond lengths



Bond angles

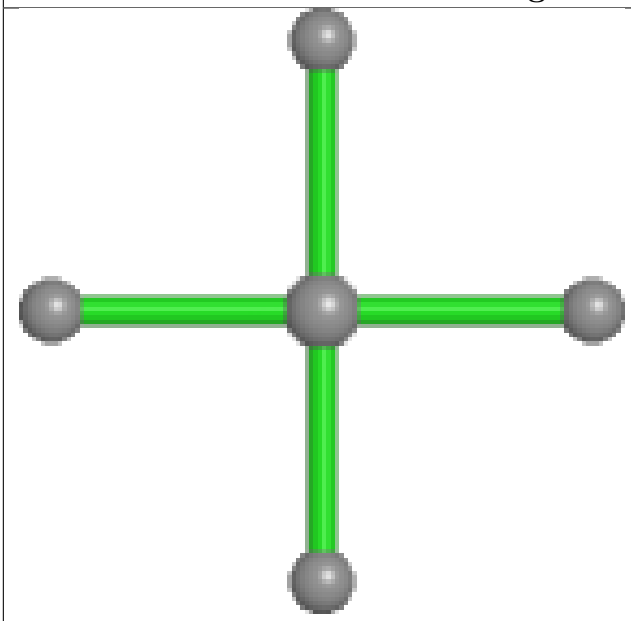


Torsions

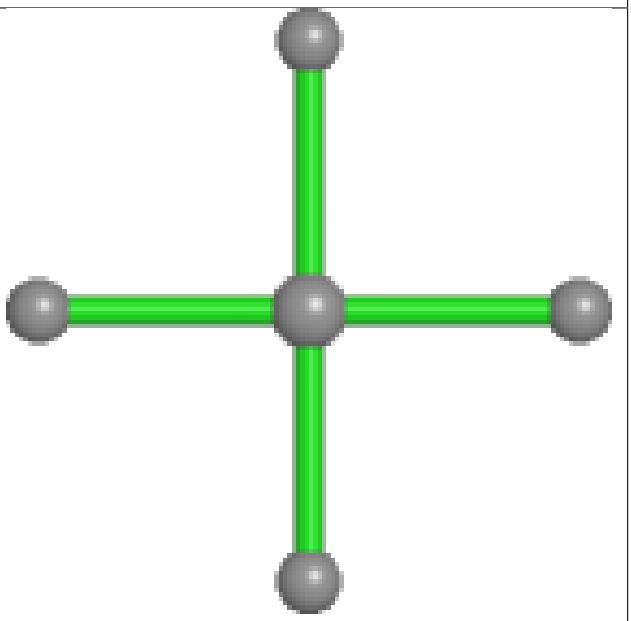


Rings

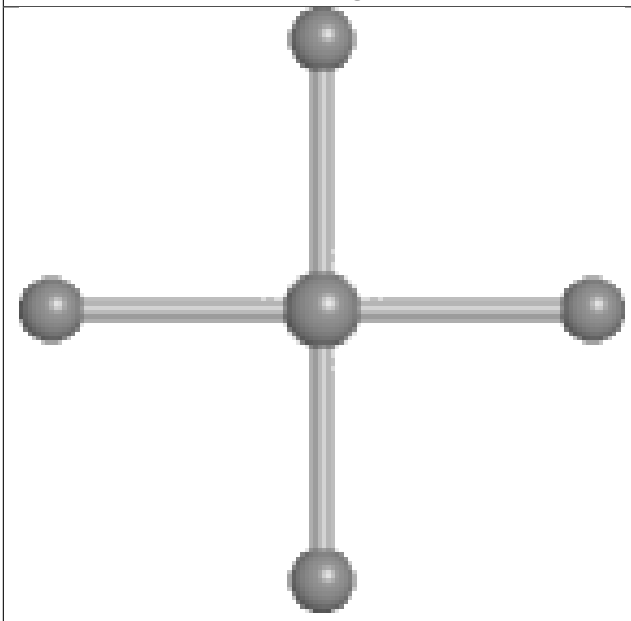
Ligand SO4 G 211



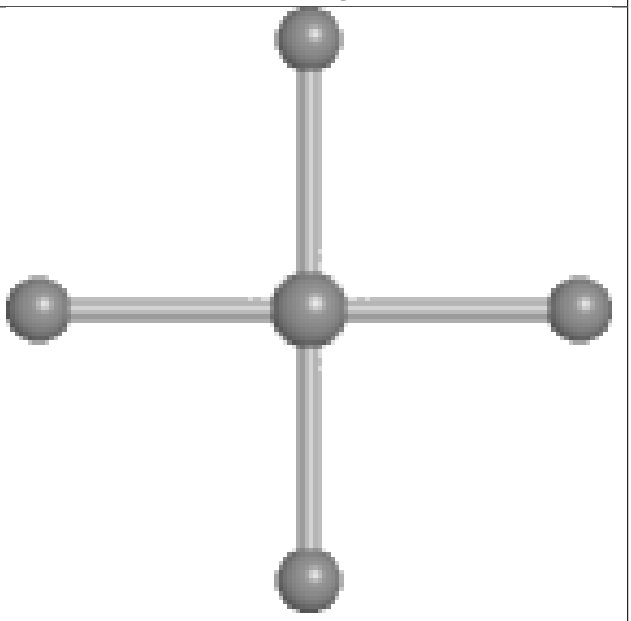
Bond lengths



Bond angles

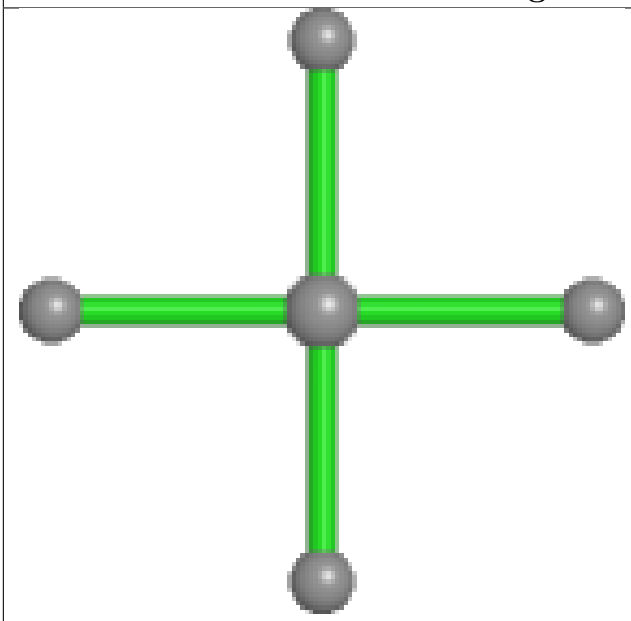


Torsions

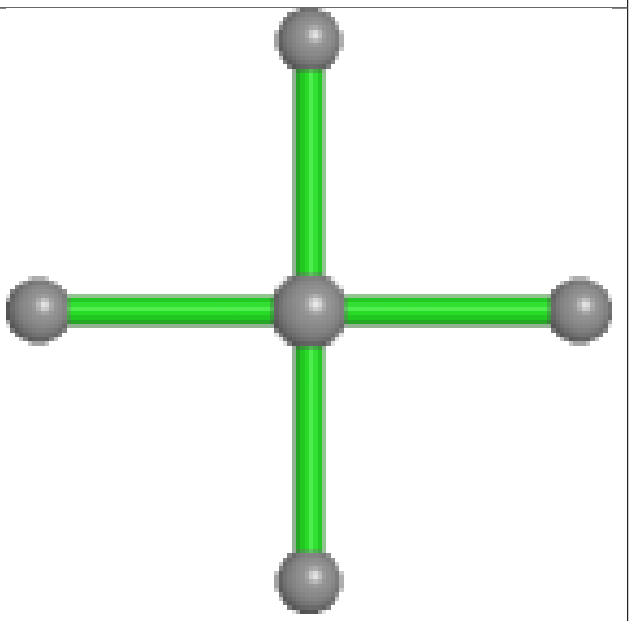


Rings

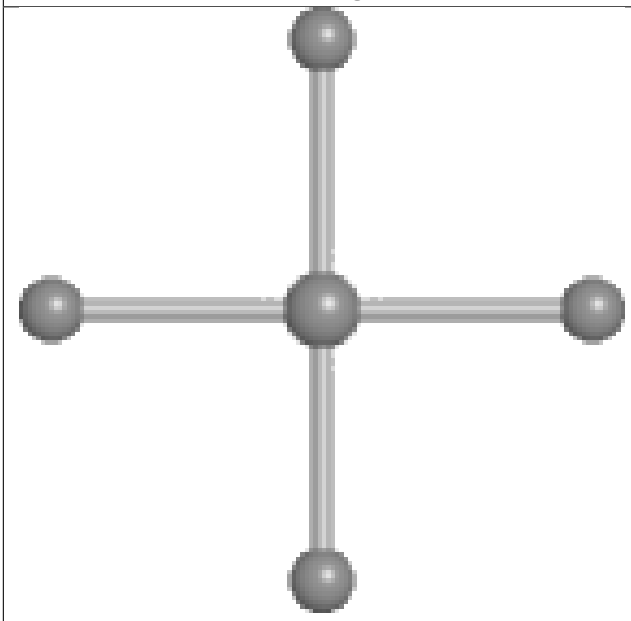
Ligand SO4 D 205



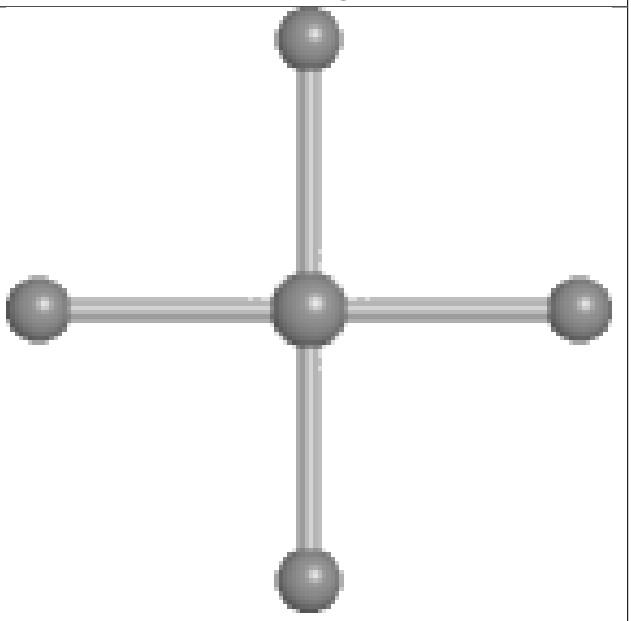
Bond lengths



Bond angles

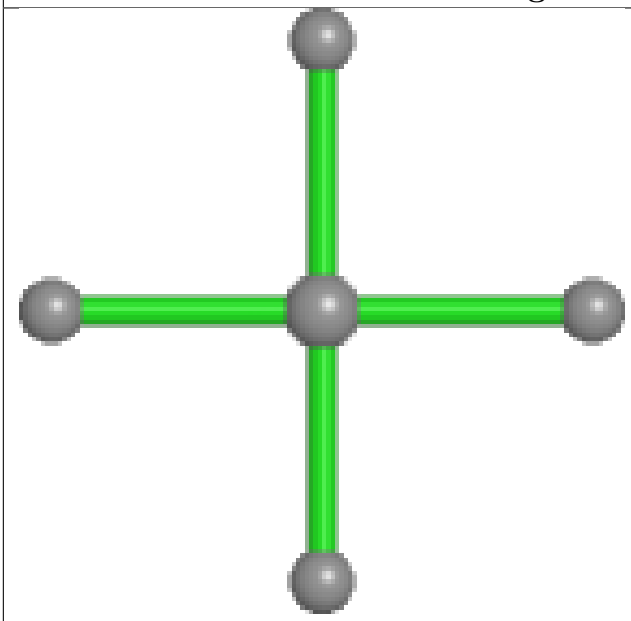


Torsions

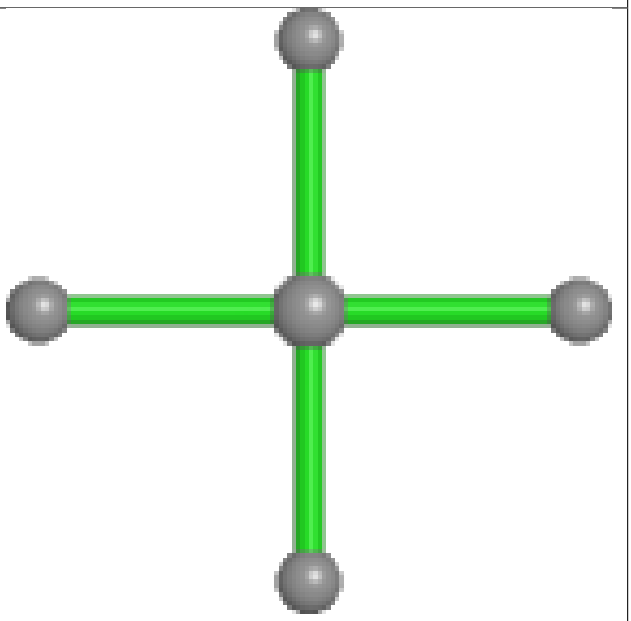


Rings

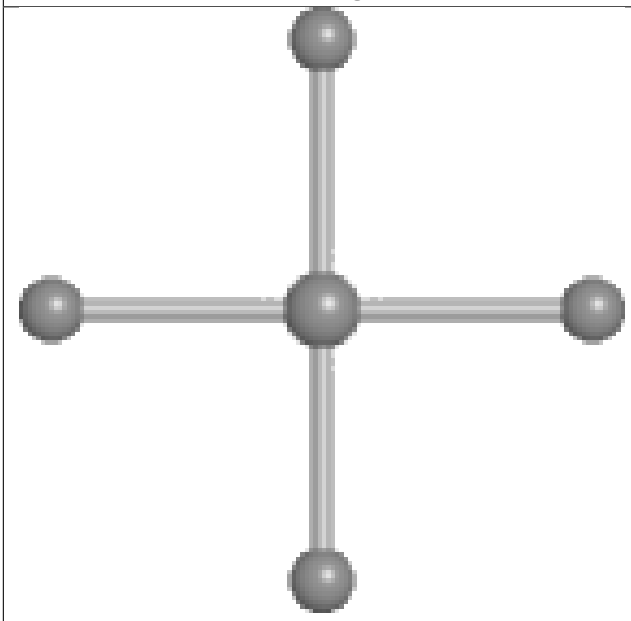
Ligand SO4 K 207



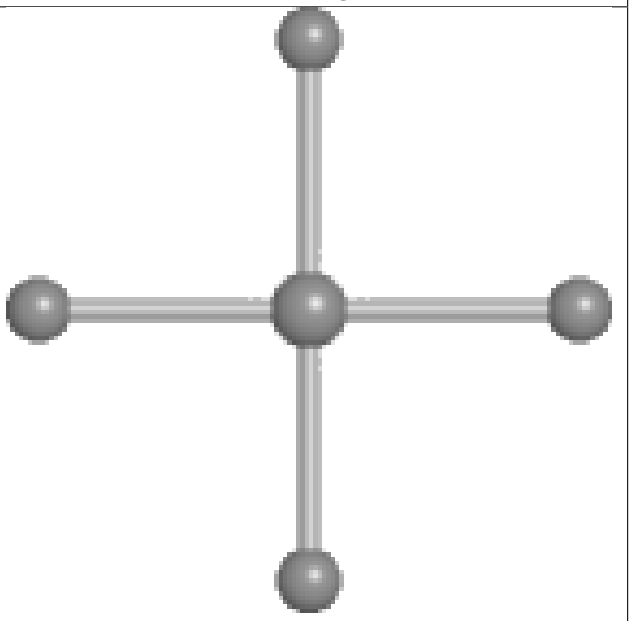
Bond lengths



Bond angles

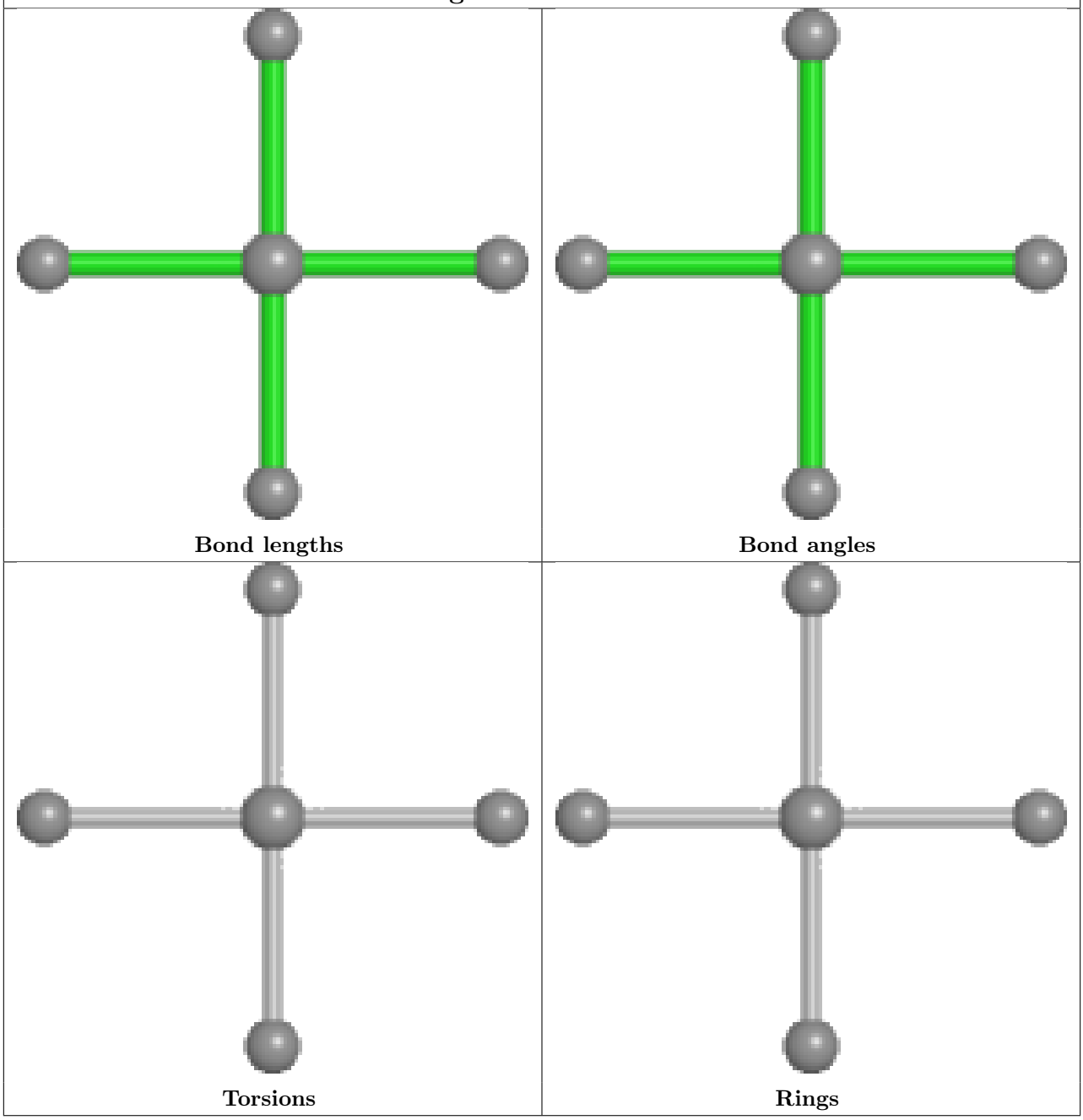


Torsions



Rings

Ligand SO4 L 203



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, 95^{th} 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	155/156 (99%)	-0.50	1 (0%)	89	91	17, 21, 34, 50	0
1	B	156/156 (100%)	-0.38	1 (0%)	89	91	15, 19, 28, 50	0
1	C	156/156 (100%)	-0.39	4 (2%)	56	60	16, 21, 35, 61	0
1	D	155/156 (99%)	-0.33	0	100	100	16, 20, 30, 40	0
1	E	155/156 (99%)	-0.41	0	100	100	16, 20, 32, 42	0
1	F	156/156 (100%)	-0.27	5 (3%)	47	52	17, 22, 41, 61	0
1	G	155/156 (99%)	-0.32	4 (2%)	56	60	17, 22, 36, 57	0
1	H	156/156 (100%)	-0.48	1 (0%)	89	91	14, 20, 33, 54	0
1	I	156/156 (100%)	-0.06	1 (0%)	89	91	16, 21, 31, 56	0
1	J	155/156 (99%)	-0.39	4 (2%)	56	60	17, 22, 36, 59	0
1	K	156/156 (100%)	-0.17	1 (0%)	89	91	14, 19, 30, 58	0
1	L	155/156 (99%)	-0.54	1 (0%)	89	91	16, 20, 31, 55	0
All	All	1866/1872 (99%)	-0.35	23 (1%)	79	82	14, 21, 34, 61	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	156	SER	5.6
1	F	156	SER	4.9
1	L	156	SER	4.5
1	C	156	SER	4.4
1	I	156	SER	4.2

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 (i)

There are no monosaccharides 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, 95^{th} 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	SO4	K	210	5/5	0.81	0.24	44,48,59,73	0
3	SO4	A	210	5/5	0.83	0.32	42,60,77,83	0
3	SO4	J	209	5/5	0.84	0.28	40,64,93,93	0
3	SO4	L	206	5/5	0.84	0.23	50,60,79,86	0
3	SO4	L	207	5/5	0.84	0.26	38,61,84,89	0
3	SO4	D	211	5/5	0.86	0.32	49,55,82,82	0
3	SO4	F	209	5/5	0.86	0.34	44,56,75,80	0
3	SO4	K	209	5/5	0.87	0.31	37,56,66,79	0
3	SO4	H	208	5/5	0.87	0.22	37,62,83,95	0
3	SO4	D	210	5/5	0.88	0.13	37,52,65,66	0
3	SO4	G	208	5/5	0.88	0.29	43,54,72,72	0
4	NA	E	202	1/1	0.88	0.26	43,43,43,43	0
3	SO4	E	208	5/5	0.89	0.20	42,61,77,89	0
3	SO4	B	213	5/5	0.89	0.23	37,60,78,80	0
3	SO4	H	205	5/5	0.90	0.21	36,49,59,67	0
3	SO4	B	212	5/5	0.90	0.12	41,52,67,72	0
3	SO4	I	209	5/5	0.90	0.20	52,64,95,95	0
3	SO4	G	211	5/5	0.91	0.28	55,61,84,94	0
3	SO4	J	206	5/5	0.91	0.28	47,55,70,80	0
3	SO4	C	208	5/5	0.91	0.28	37,58,77,84	0
2	CL	B	204	1/1	0.91	0.07	28,28,28,28	0
3	SO4	G	210	5/5	0.92	0.27	37,61,79,87	0
3	SO4	D	212	5/5	0.92	0.21	28,36,59,60	0
3	SO4	D	208	5/5	0.92	0.24	43,54,67,69	0
3	SO4	B	209	5/5	0.93	0.18	40,46,63,64	0
3	SO4	D	213	5/5	0.94	0.33	49,54,72,81	0
3	SO4	J	208	5/5	0.94	0.35	37,58,79,85	0
3	SO4	F	205	5/5	0.94	0.27	53,57,65,65	0
3	SO4	F	206	5/5	0.94	0.21	55,57,65,75	0
3	SO4	F	207	5/5	0.94	0.33	40,58,74,79	0
3	SO4	F	208	5/5	0.94	0.25	46,60,69,75	0
3	SO4	I	208	5/5	0.94	0.27	35,50,62,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	SO4	E	206	5/5	0.94	0.17	45,51,57,61	0
4	NA	K	202	1/1	0.94	0.06	32,32,32,32	0
3	SO4	K	208	5/5	0.95	0.12	29,47,59,60	0
3	SO4	C	209	5/5	0.95	0.25	59,59,64,73	0
3	SO4	B	211	5/5	0.95	0.10	31,42,60,63	0
3	SO4	E	207	5/5	0.95	0.22	41,49,68,71	0
3	SO4	D	209	5/5	0.95	0.28	66,68,75,75	0
4	NA	D	201	1/1	0.95	0.13	34,34,34,34	0
3	SO4	E	209	5/5	0.95	0.20	59,67,73,84	0
4	NA	K	201	1/1	0.95	0.26	36,36,36,36	0
3	SO4	K	206	5/5	0.95	0.11	46,49,57,63	0
3	SO4	J	205	5/5	0.96	0.24	47,56,59,62	0
3	SO4	G	204	5/5	0.96	0.20	42,47,51,51	0
3	SO4	G	207	5/5	0.96	0.30	51,51,65,70	0
3	SO4	C	207	5/5	0.96	0.29	43,47,61,76	0
3	SO4	G	209	5/5	0.96	0.23	58,59,61,66	0
3	SO4	F	203	5/5	0.96	0.17	42,45,51,56	0
3	SO4	B	210	5/5	0.96	0.12	52,55,62,64	0
3	SO4	A	209	5/5	0.96	0.25	56,58,63,66	0
3	SO4	L	203	5/5	0.96	0.28	40,40,48,55	0
3	SO4	H	207	5/5	0.96	0.28	54,56,61,62	0
2	CL	K	204	1/1	0.96	0.12	32,32,32,32	0
4	NA	B	201	1/1	0.96	0.12	34,34,34,34	0
4	NA	B	202	1/1	0.96	0.20	37,37,37,37	0
4	NA	C	201	1/1	0.96	0.17	33,33,33,33	0
3	SO4	I	205	5/5	0.96	0.24	42,54,64,67	0
4	NA	E	201	1/1	0.96	0.06	26,26,26,26	0
3	SO4	I	206	5/5	0.96	0.27	45,45,52,66	0
4	NA	I	201	1/1	0.96	0.07	34,34,34,34	0
3	SO4	A	207	5/5	0.96	0.24	39,47,59,63	0
3	SO4	C	206	5/5	0.96	0.25	50,55,64,68	0
3	SO4	H	206	5/5	0.97	0.17	29,40,41,43	0
2	CL	C	204	1/1	0.97	0.07	30,30,30,30	0
3	SO4	K	207	5/5	0.97	0.12	52,54,57,62	0
3	SO4	I	207	5/5	0.97	0.08	60,61,64,65	0
3	SO4	J	207	5/5	0.97	0.20	49,54,56,57	0
2	CL	J	201	1/1	0.97	0.17	35,35,35,35	0
3	SO4	A	205	5/5	0.98	0.16	32,38,44,51	0
3	SO4	D	205	5/5	0.98	0.18	42,46,52,55	0
3	SO4	D	206	5/5	0.98	0.20	43,43,54,62	0
3	SO4	G	206	5/5	0.98	0.11	28,30,34,53	0
3	SO4	D	207	5/5	0.98	0.19	34,35,48,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	SO4	L	204	5/5	0.98	0.16	32,34,42,58	0
3	SO4	L	205	5/5	0.98	0.27	56,57,60,61	0
3	SO4	B	206	5/5	0.98	0.15	38,45,55,56	0
3	SO4	B	207	5/5	0.98	0.13	33,36,47,48	0
3	SO4	J	203	5/5	0.98	0.15	43,45,58,58	0
3	SO4	J	204	5/5	0.98	0.18	34,36,44,52	0
3	SO4	F	204	5/5	0.98	0.22	40,42,48,53	0
4	NA	C	202	1/1	0.98	0.11	33,33,33,33	0
3	SO4	B	208	5/5	0.98	0.12	27,29,33,51	0
4	NA	D	202	1/1	0.98	0.10	36,36,36,36	0
3	SO4	H	203	5/5	0.98	0.17	43,43,47,48	0
3	SO4	H	204	5/5	0.98	0.18	29,33,46,46	0
4	NA	G	201	1/1	0.98	0.14	39,39,39,39	0
3	SO4	A	208	5/5	0.98	0.21	35,41,49,49	0
3	SO4	K	205	5/5	0.98	0.15	35,39,53,56	0
3	SO4	A	206	5/5	0.98	0.17	33,33,38,55	0
3	SO4	E	205	5/5	0.99	0.20	37,40,51,54	0
2	CL	I	203	1/1	0.99	0.08	28,28,28,28	0
2	CL	A	201	1/1	0.99	0.21	35,35,35,35	0
2	CL	K	203	1/1	0.99	0.10	33,33,33,33	0
2	CL	C	203	1/1	0.99	0.12	33,33,33,33	0
3	SO4	C	205	5/5	0.99	0.18	31,41,46,53	0
3	SO4	I	204	5/5	0.99	0.21	37,38,50,50	0
3	SO4	A	203	5/5	0.99	0.19	43,44,53,54	0
3	SO4	A	204	5/5	0.99	0.12	34,35,41,49	0
2	CL	B	203	1/1	0.99	0.12	30,30,30,30	0
2	CL	D	204	1/1	0.99	0.05	29,29,29,29	0
2	CL	E	203	1/1	0.99	0.16	34,34,34,34	0
2	CL	E	204	1/1	0.99	0.03	28,28,28,28	0
2	CL	F	201	1/1	0.99	0.14	37,37,37,37	0
3	SO4	G	205	5/5	0.99	0.25	37,39,49,51	0
2	CL	F	202	1/1	0.99	0.04	27,27,27,27	0
3	SO4	B	205	5/5	0.99	0.13	31,34,40,41	0
2	CL	G	202	1/1	0.99	0.18	36,36,36,36	0
2	CL	G	203	1/1	0.99	0.03	26,26,26,26	0
2	CL	H	201	1/1	0.99	0.13	31,31,31,31	0
2	CL	I	202	1/1	0.99	0.17	32,32,32,32	0
2	CL	D	203	1/1	1.00	0.13	32,32,32,32	0
2	CL	L	201	1/1	1.00	0.21	32,32,32,32	0
2	CL	L	202	1/1	1.00	0.04	23,23,23,23	0
2	CL	H	202	1/1	1.00	0.04	23,23,23,23	0
2	CL	J	202	1/1	1.00	0.03	24,24,24,24	0

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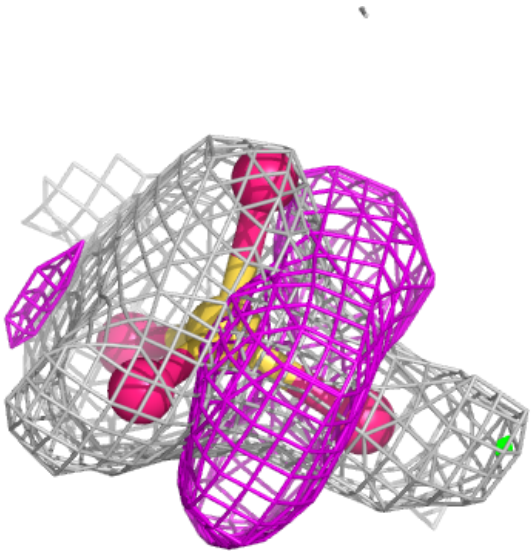
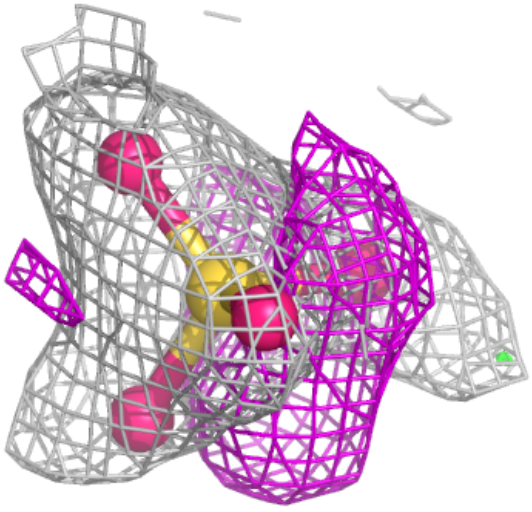
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	CL	A	202	1/1	1.00	0.04	25,25,25,25	0

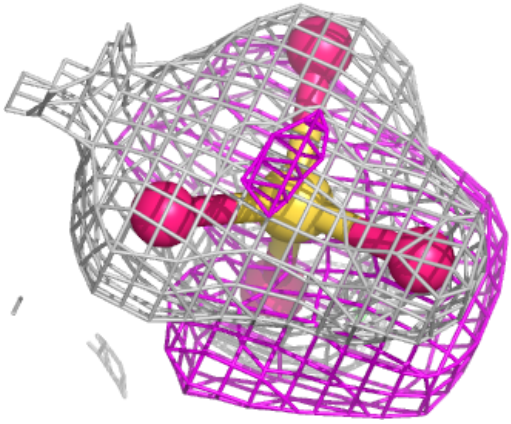
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around SO4 K 210:

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

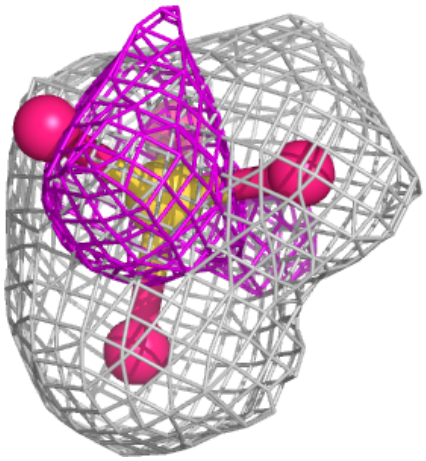


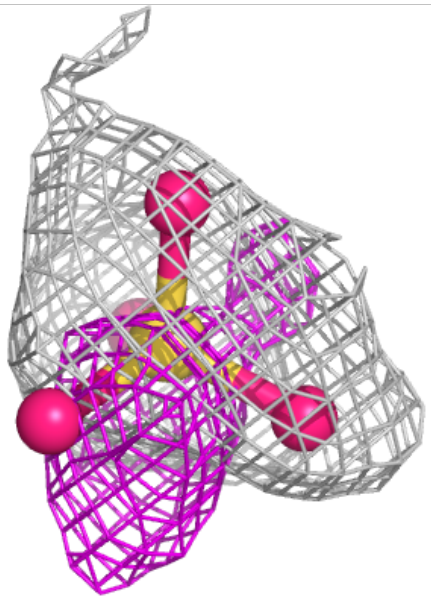


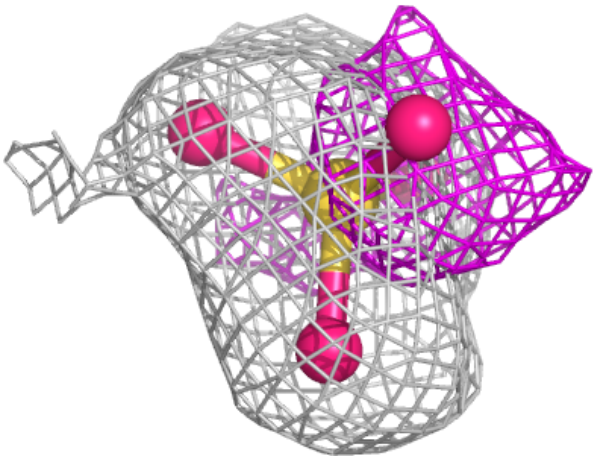


Electron density around SO4 A 210:

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

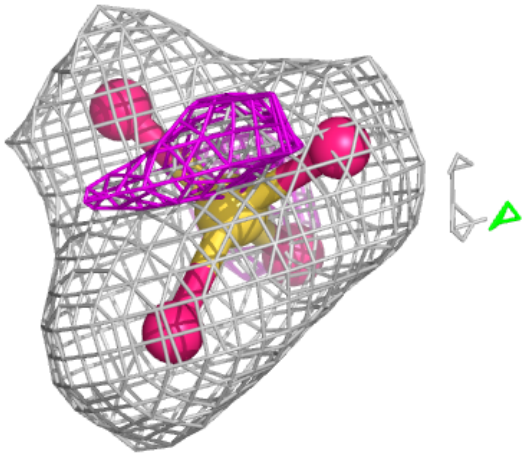


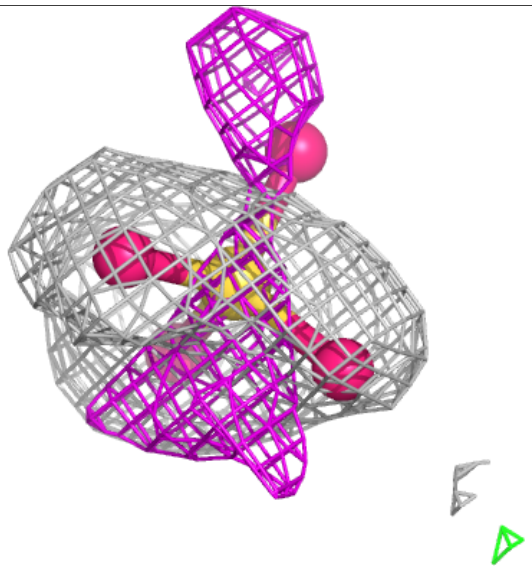


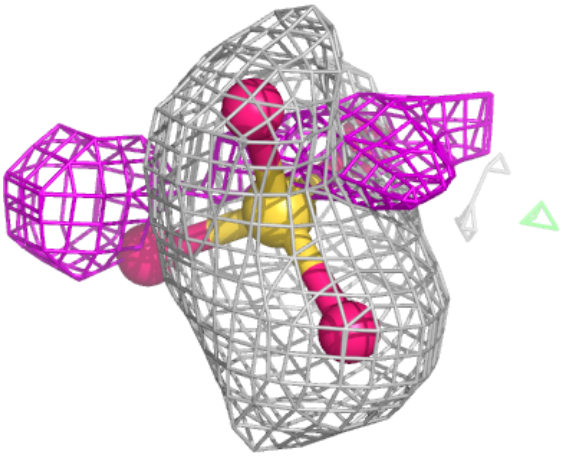


Electron density around SO4 J 209:

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

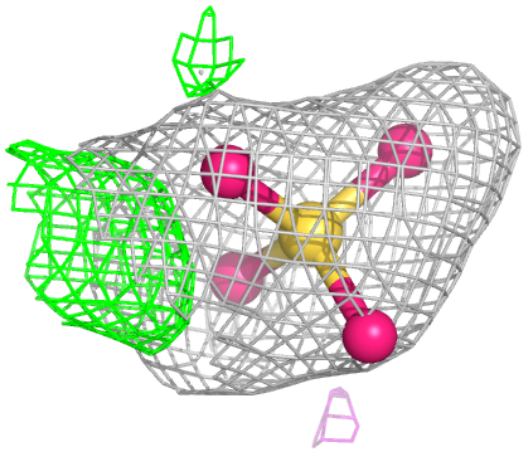


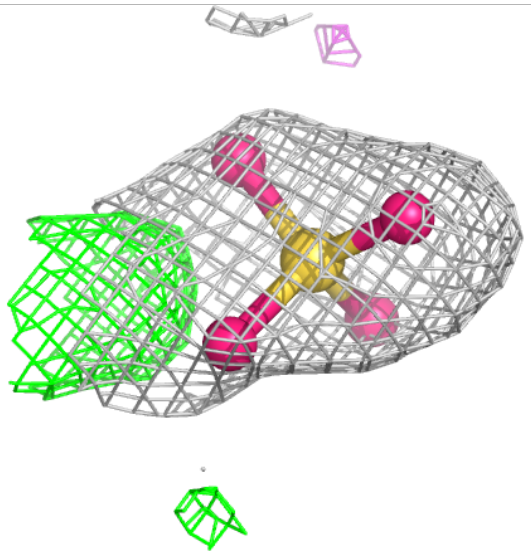


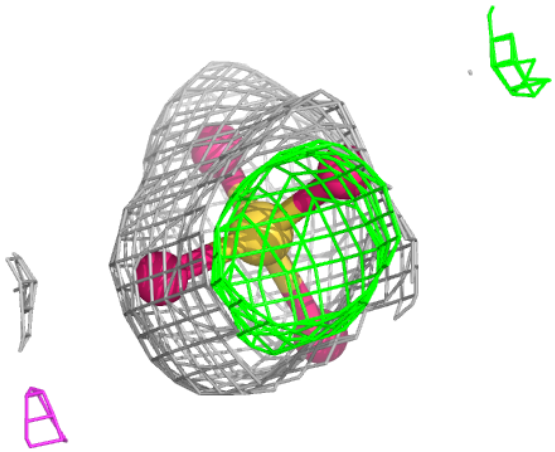


Electron density around SO4 L 206:

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

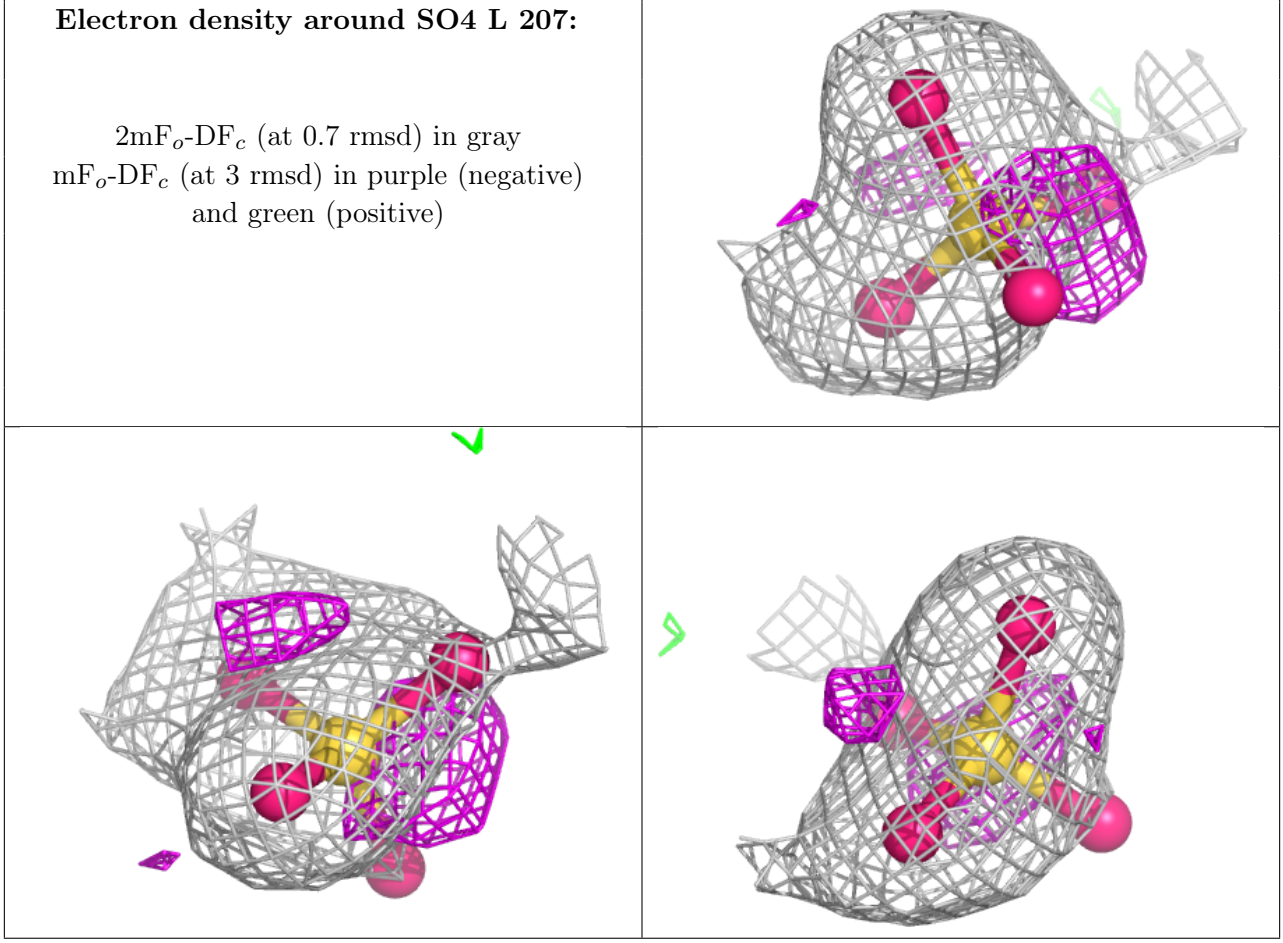






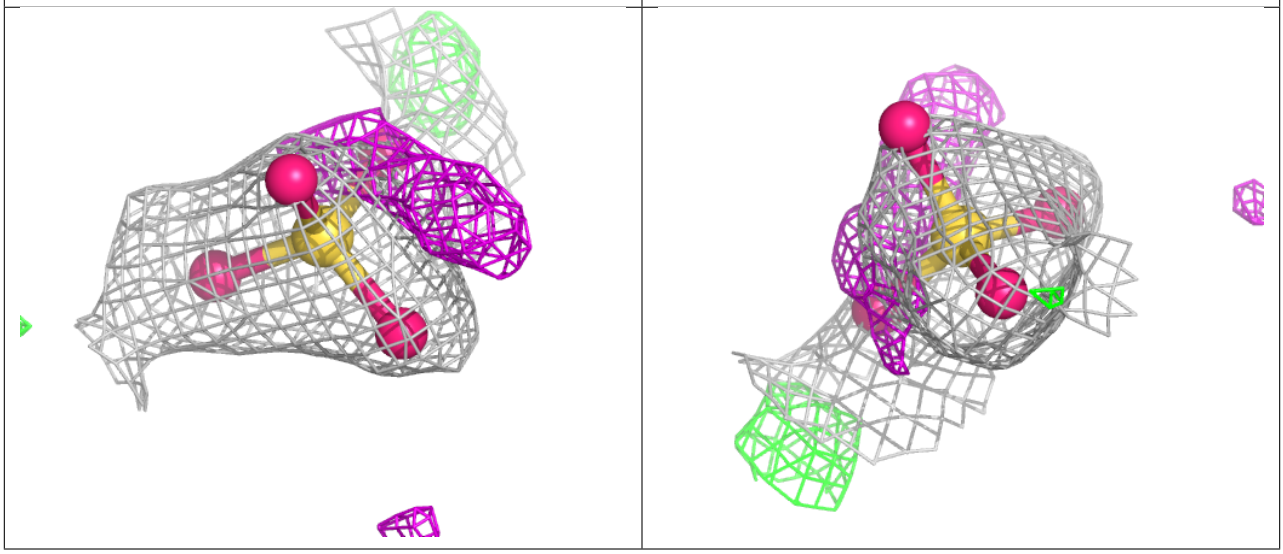
Electron density around SO4 L 207:

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



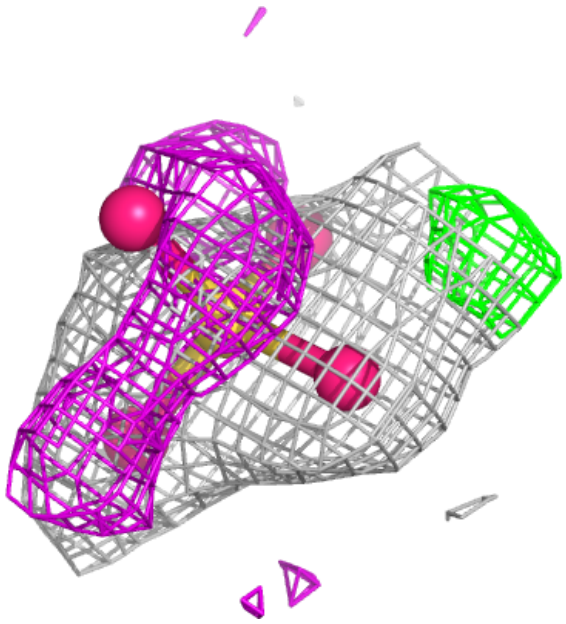
Electron density around SO4 D 211:

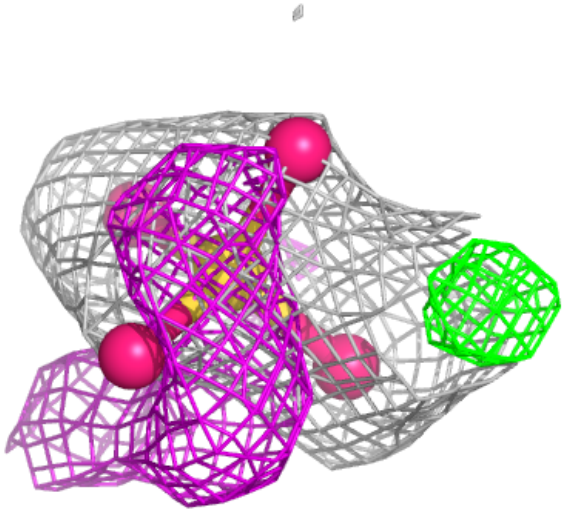
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

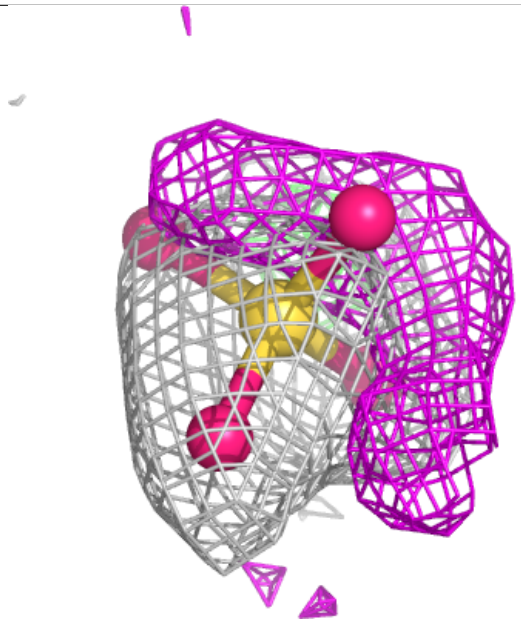


Electron density around SO4 F 209:

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

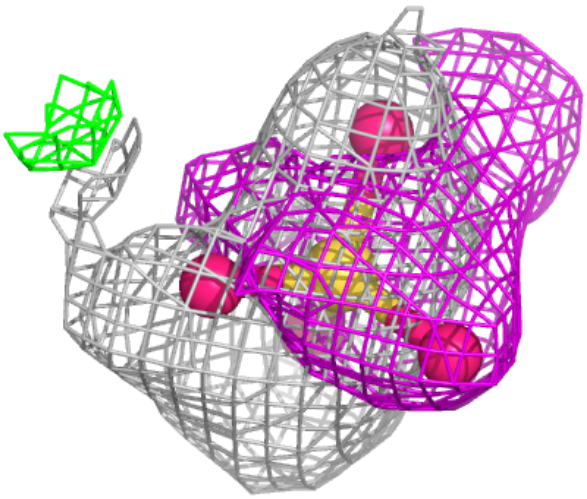


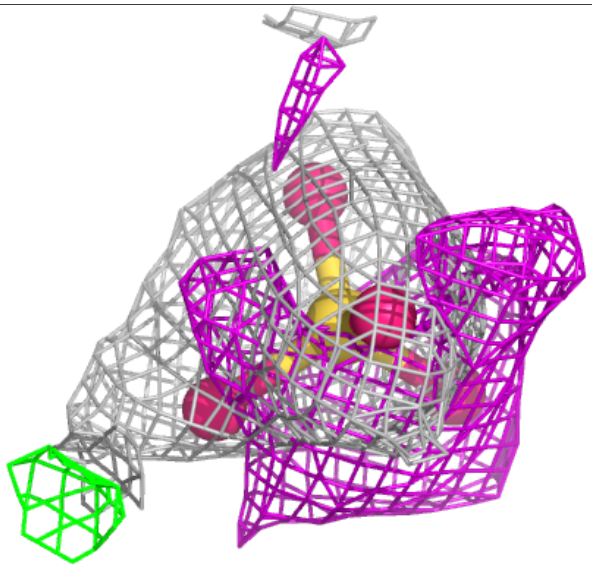


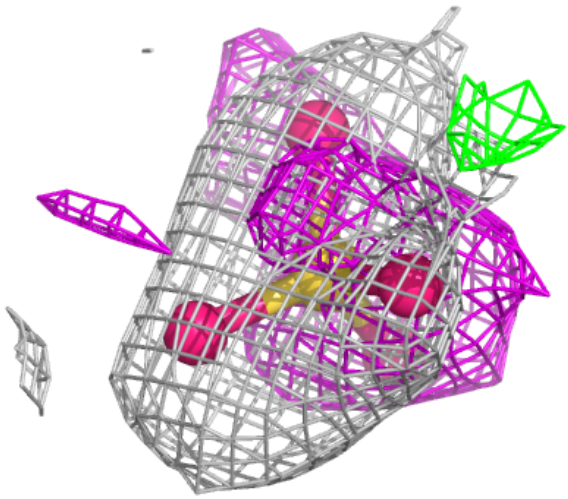


Electron density around SO4 K 209:

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

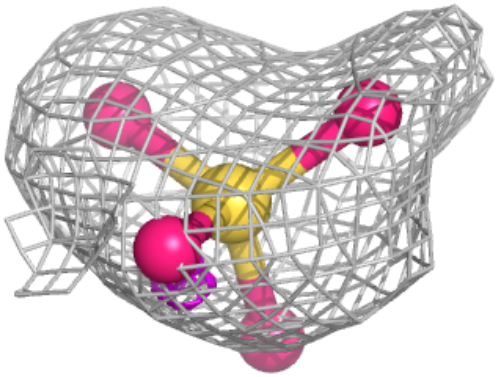


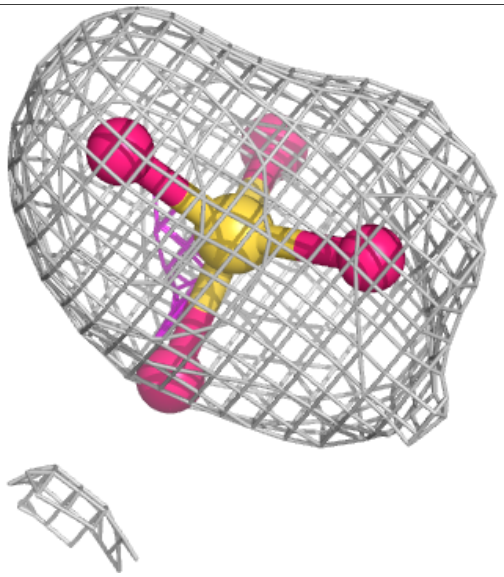


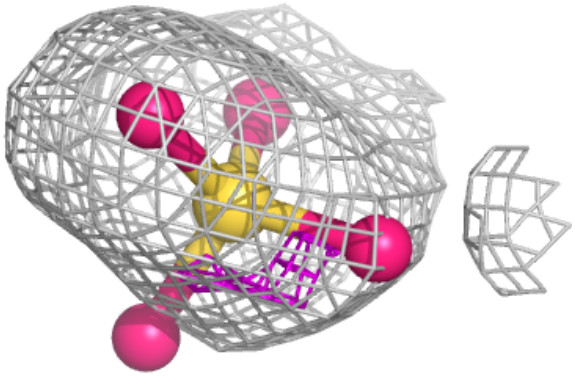


Electron density around SO4 H 208:

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

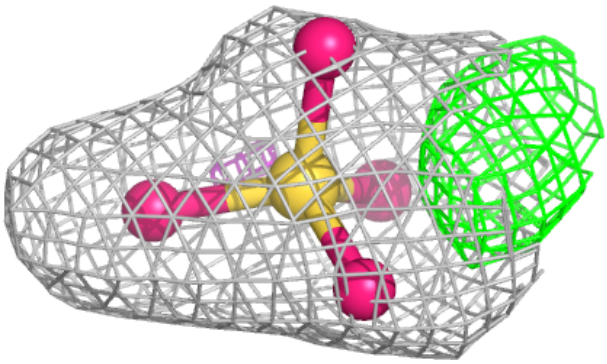


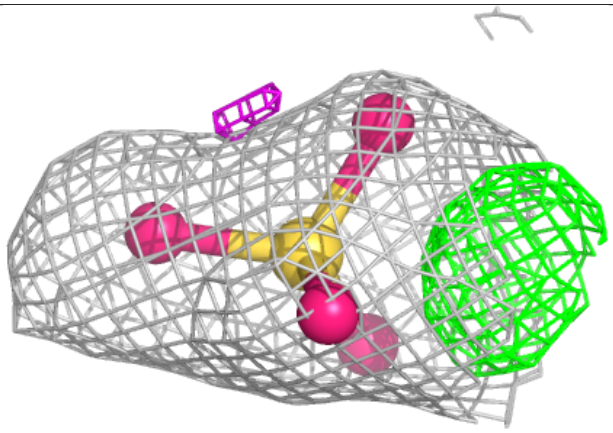


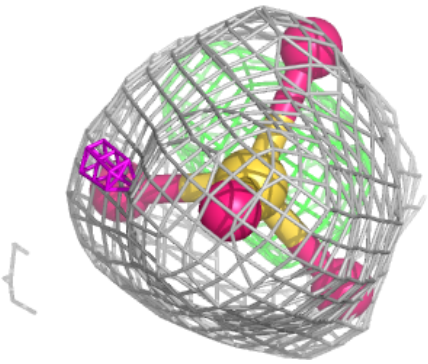


Electron density around SO4 D 210:

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

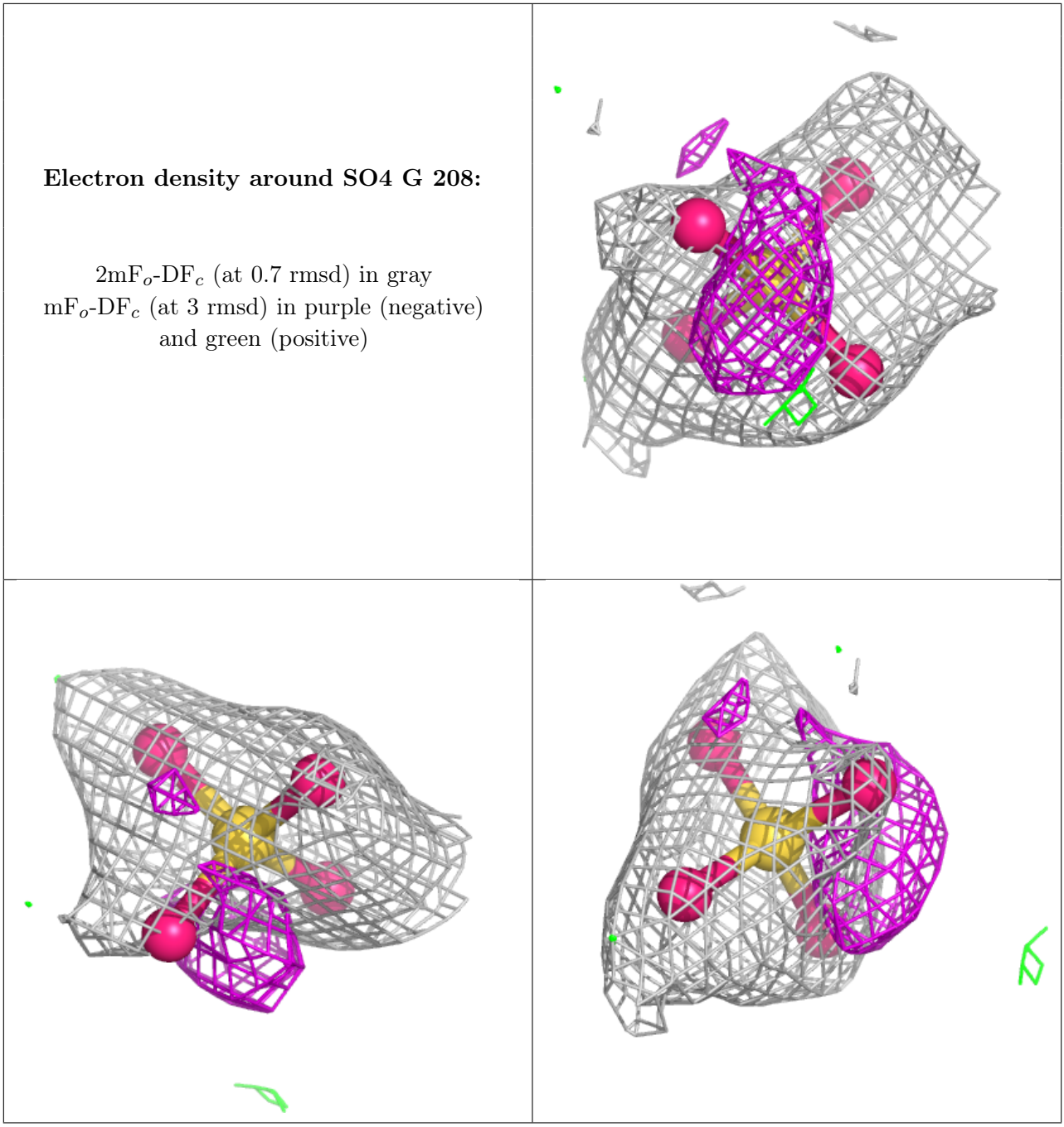






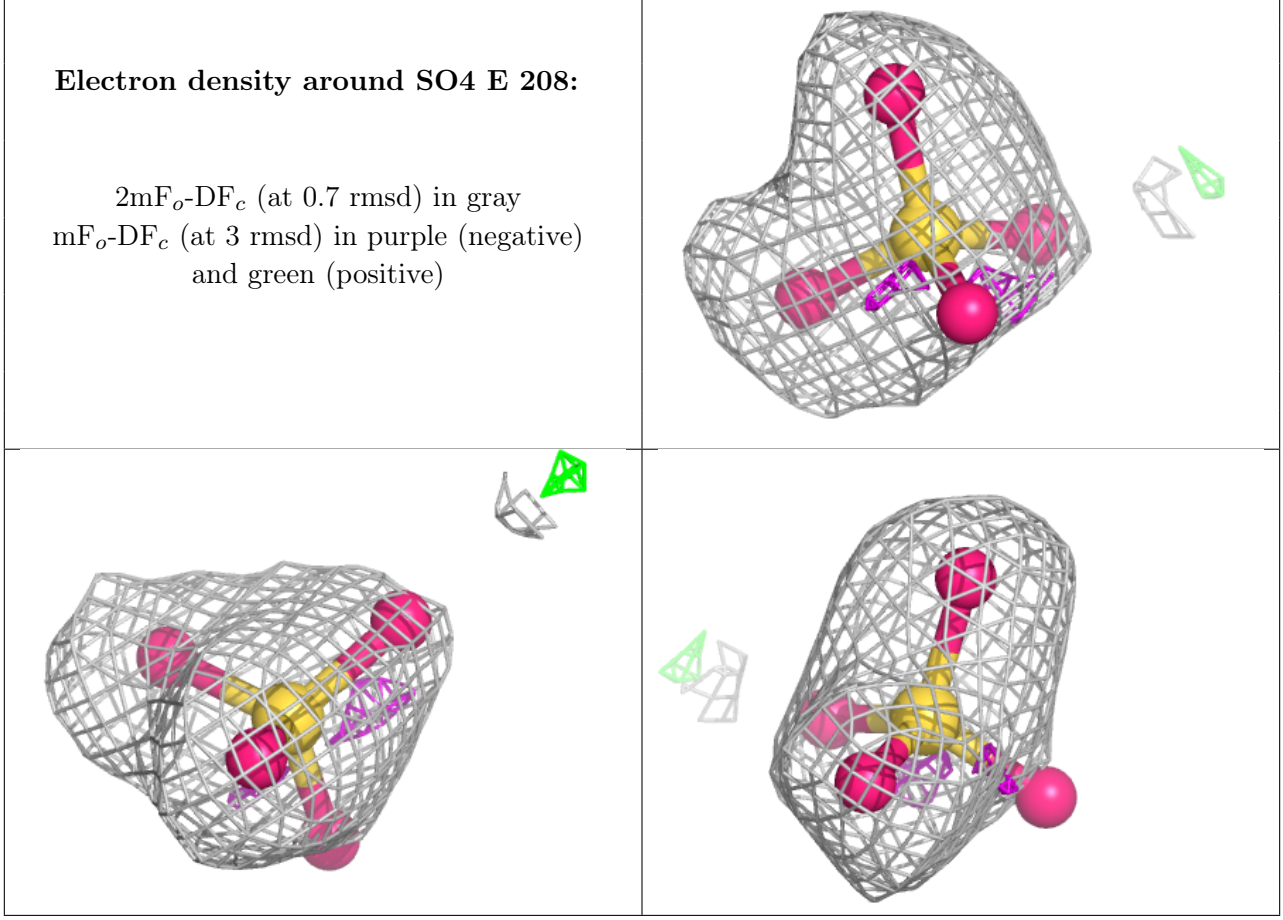
Electron density around SO4 G 208:

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



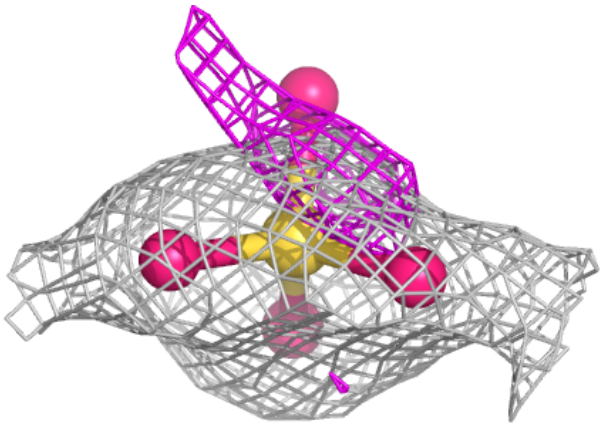
Electron density around SO4 E 208:

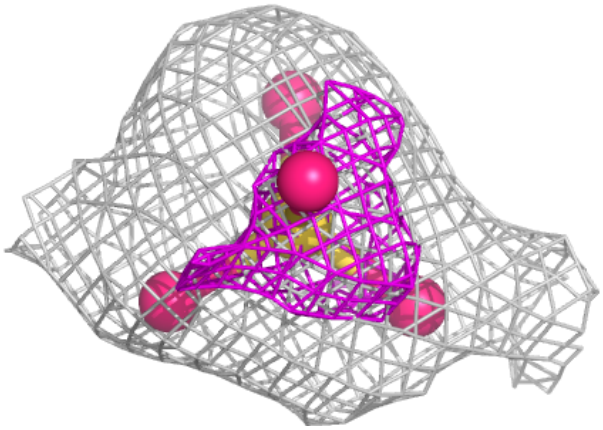
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

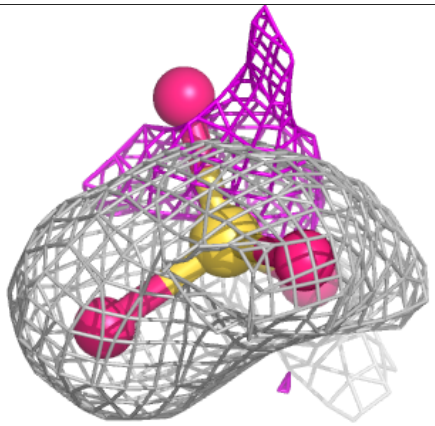


Electron density around SO4 B 213:

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

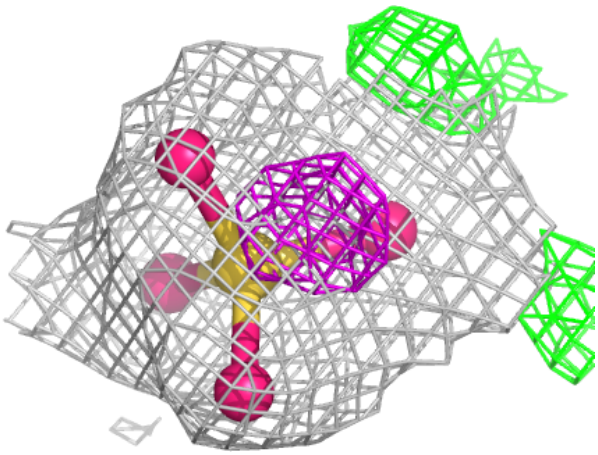


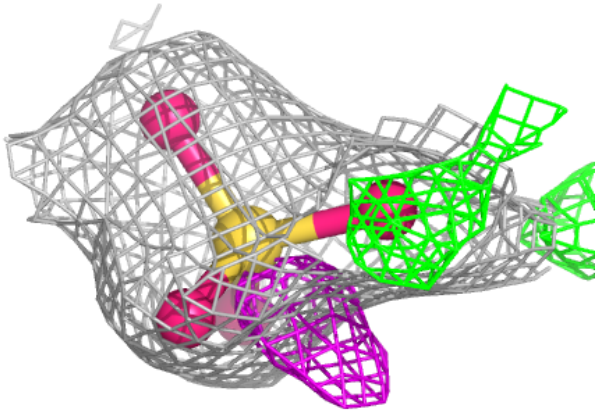


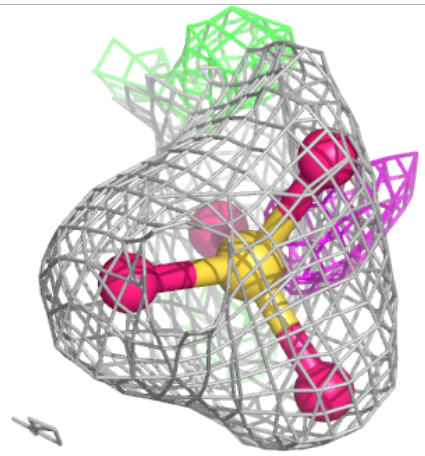


Electron density around SO4 H 205:

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

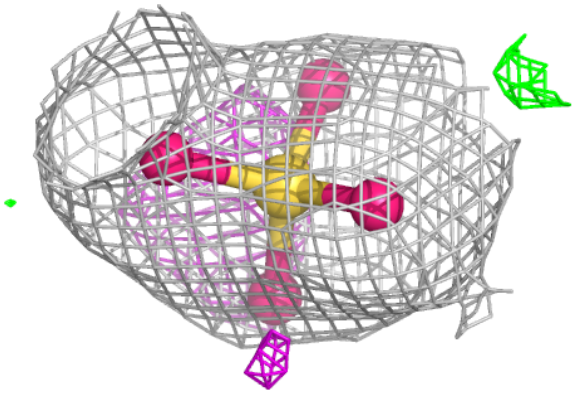


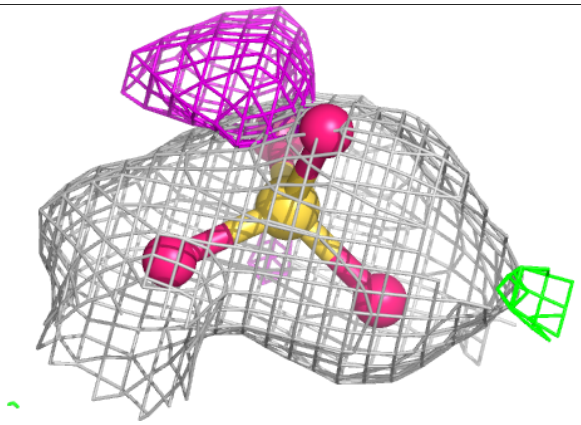


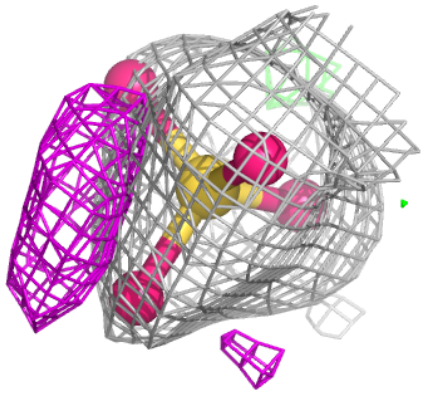


Electron density around SO4 B 212:

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

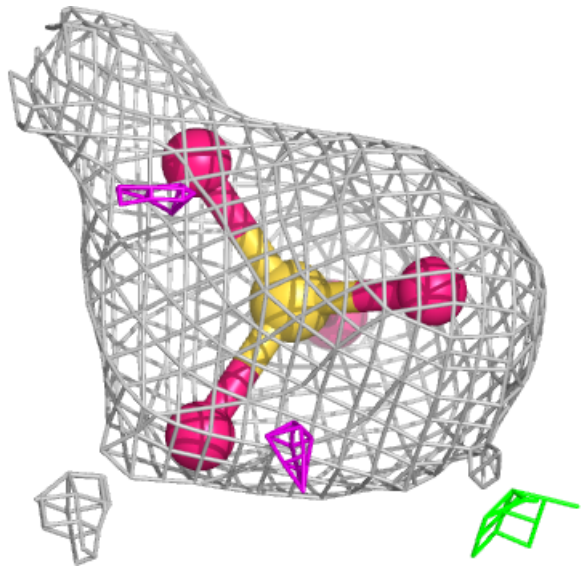


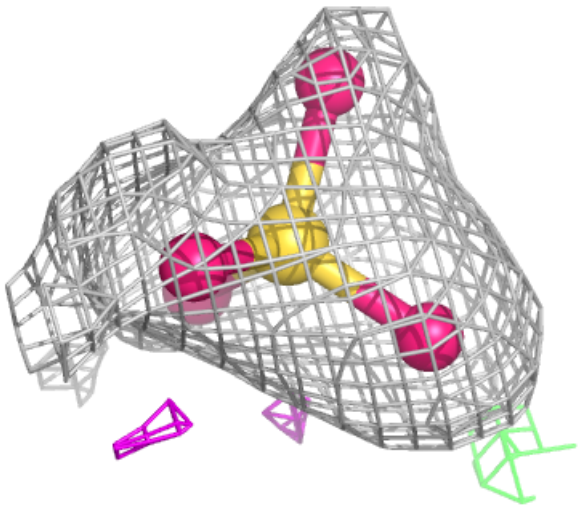


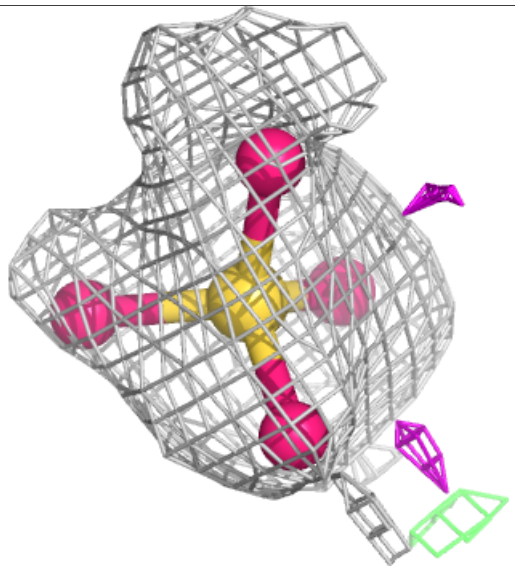


Electron density around SO4 I 209:

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

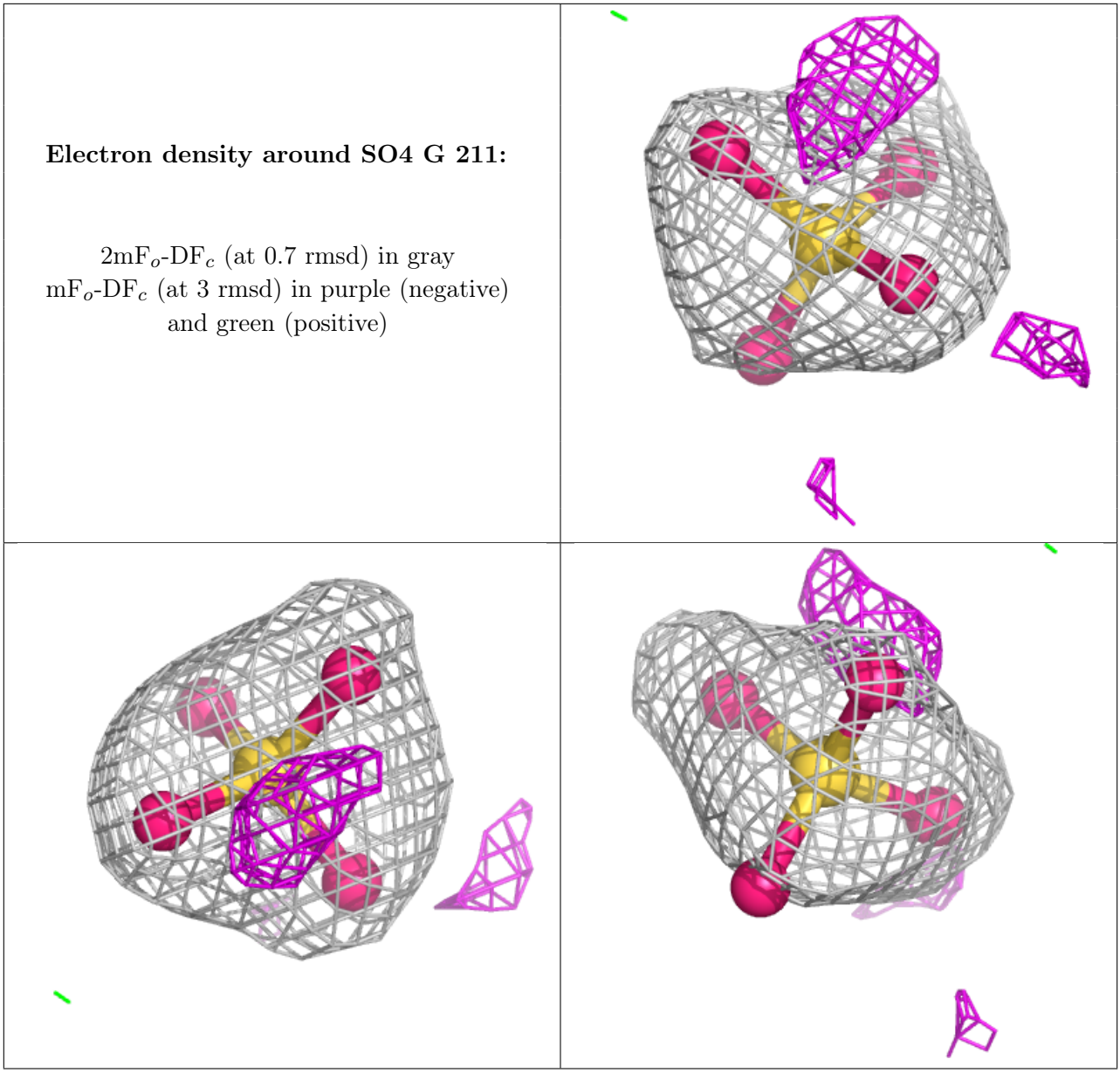






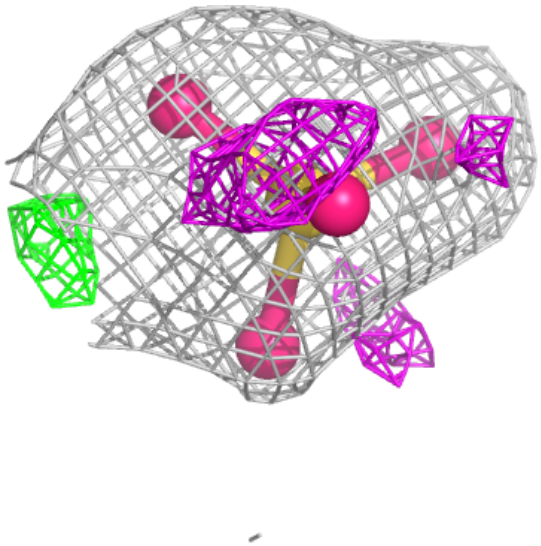
Electron density around SO4 G 211:

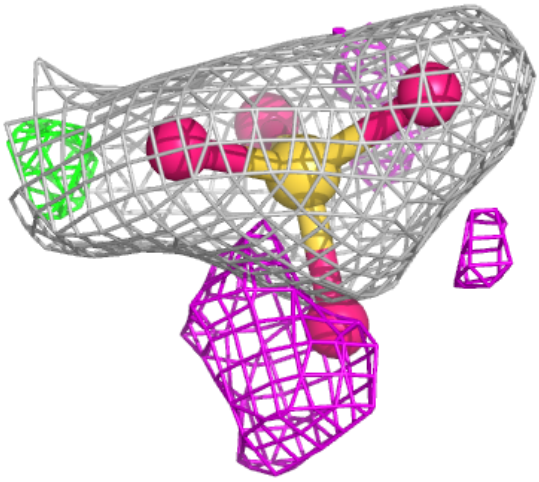
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

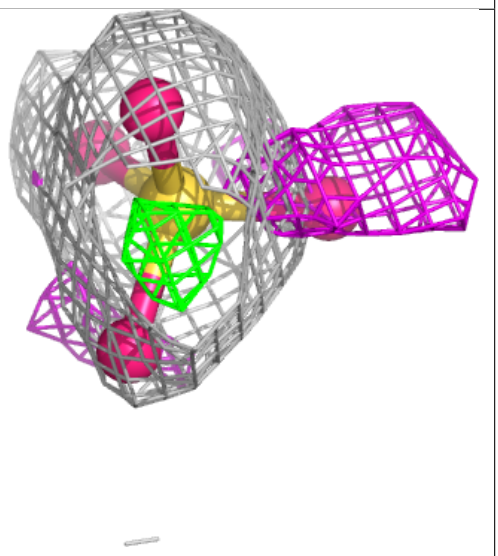


Electron density around SO4 J 206:

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

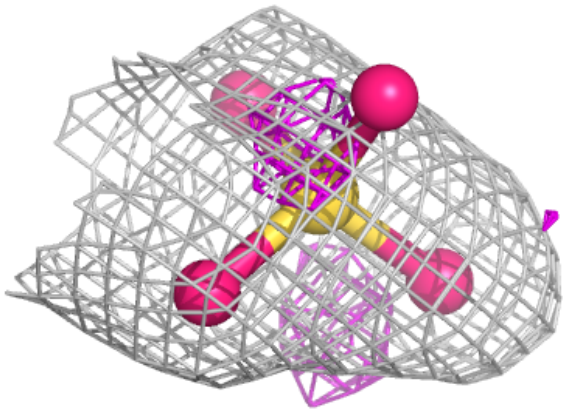


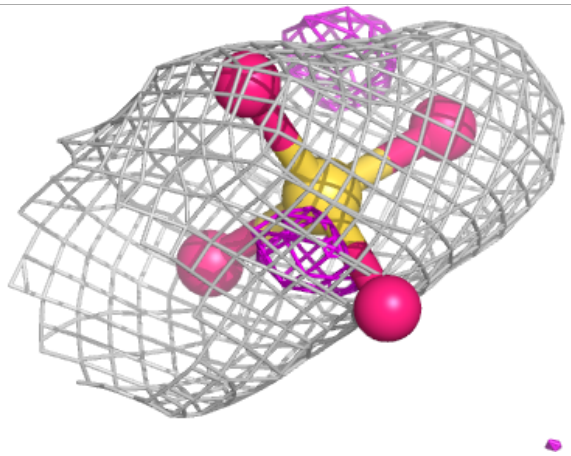


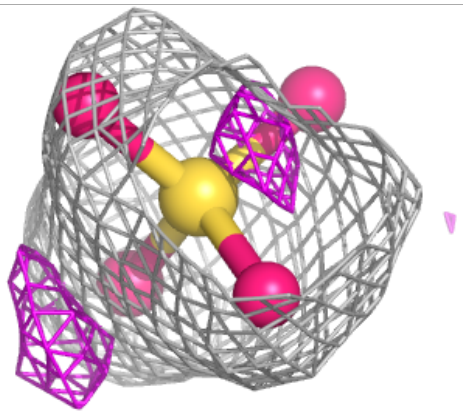


Electron density around SO4 C 208:

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

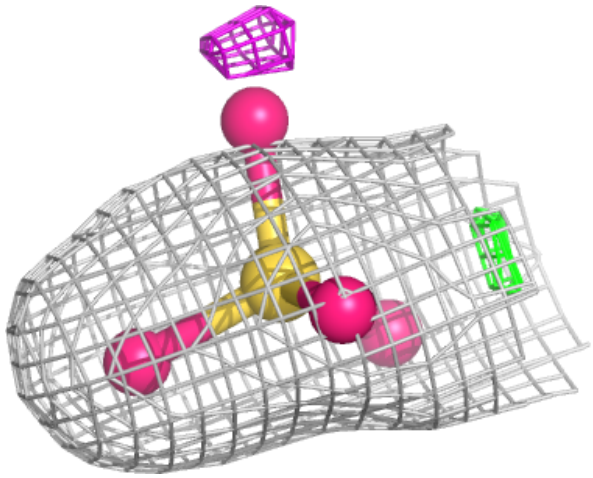


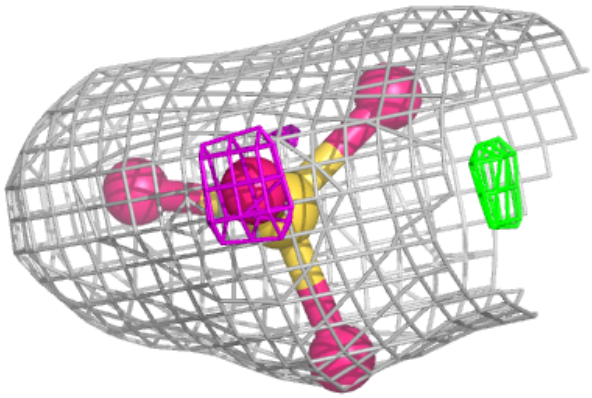


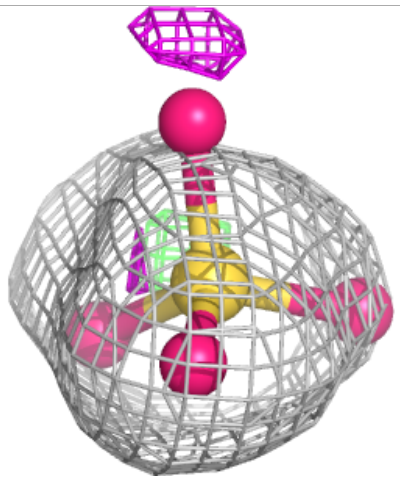


Electron density around SO4 G 210:

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

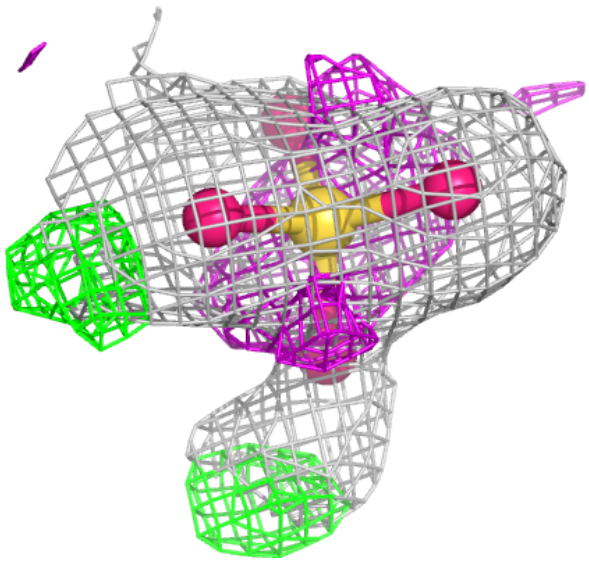


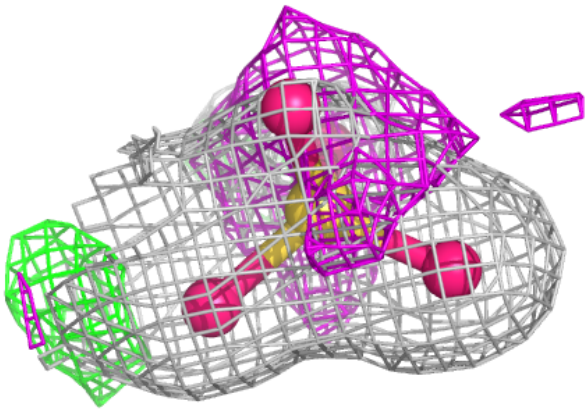


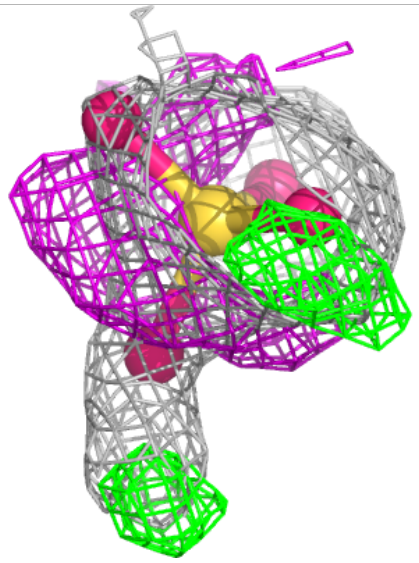


Electron density around SO4 D 212:

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

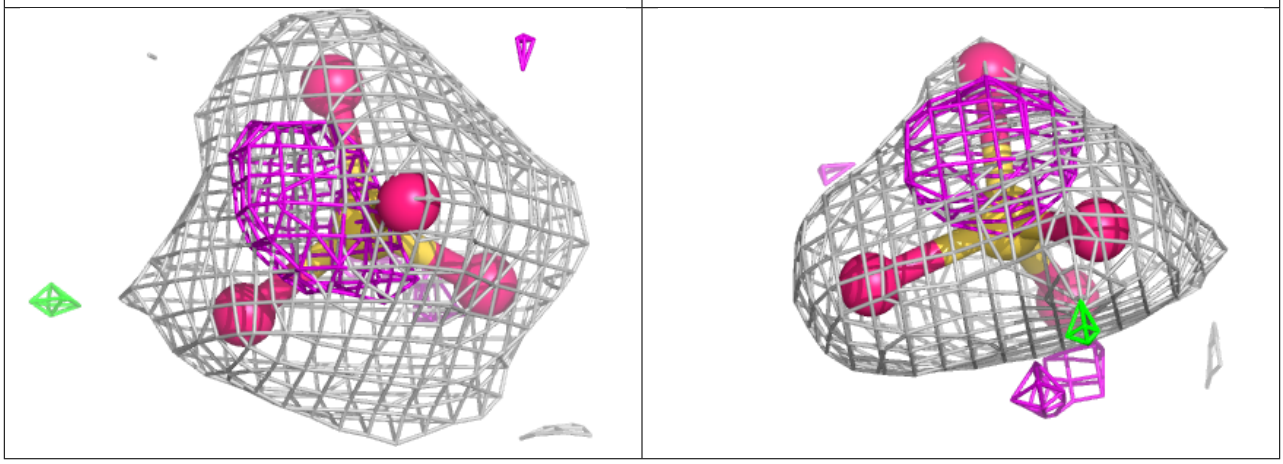






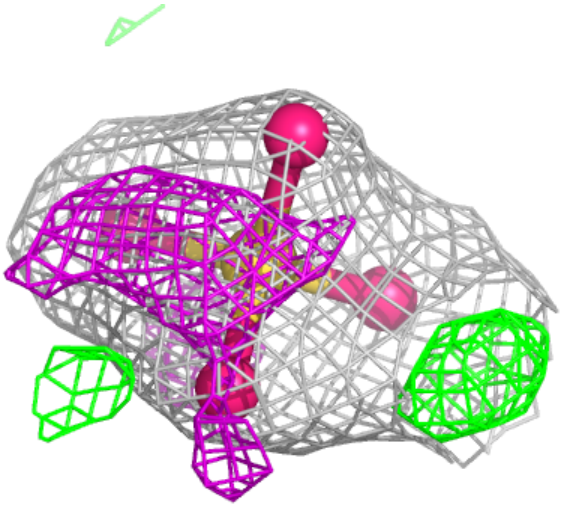
Electron density around SO4 D 208:

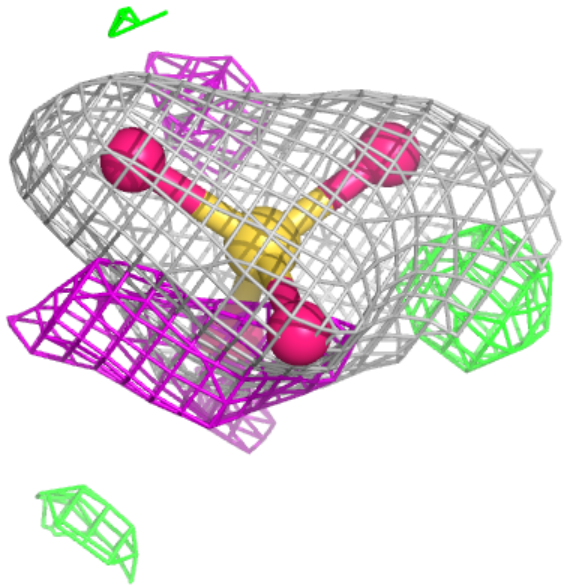
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

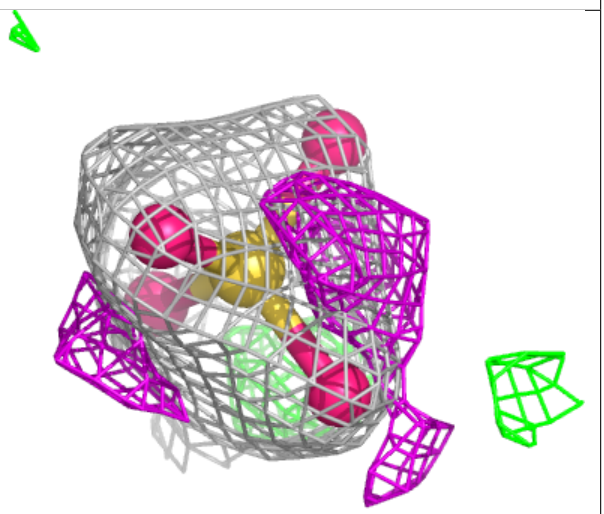


Electron density around SO4 B 209:

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

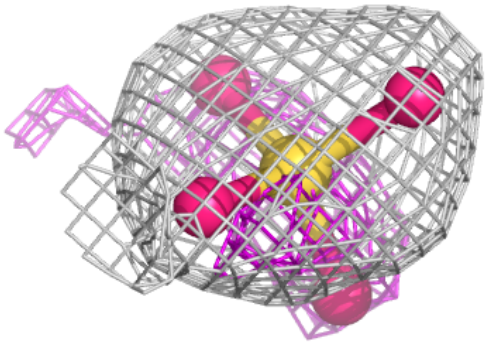


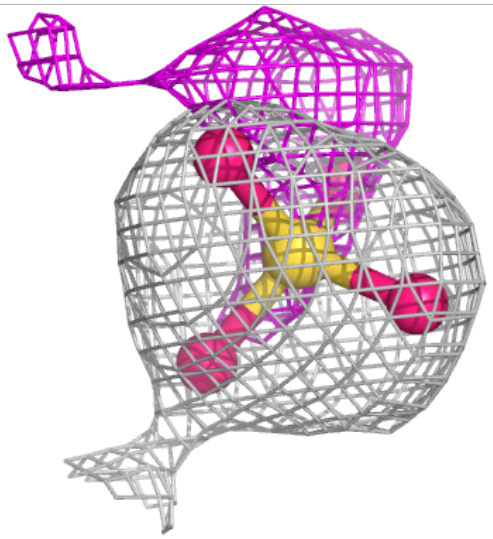


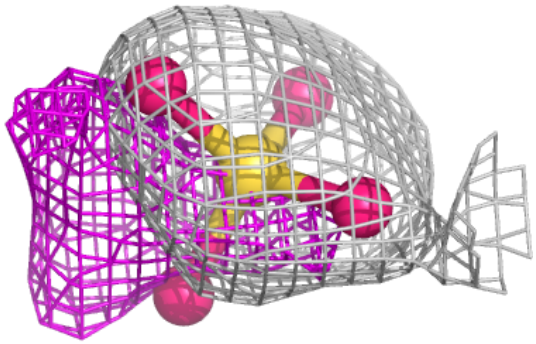


Electron density around SO4 D 213:

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

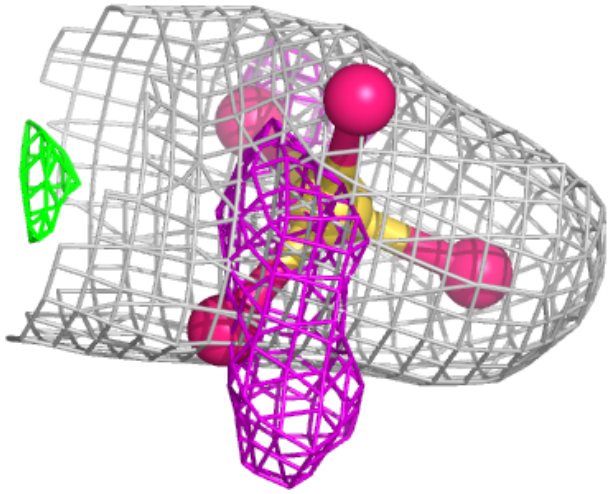


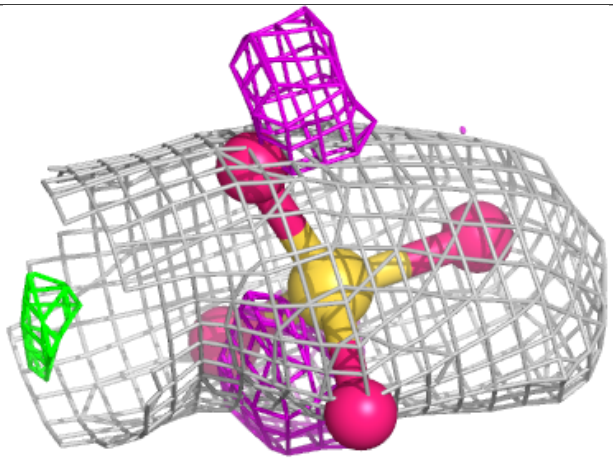


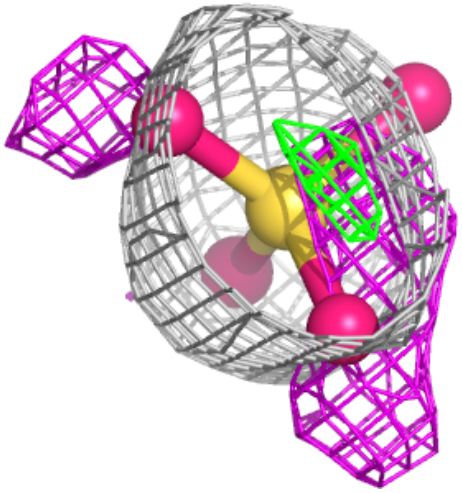


Electron density around SO4 J 208:

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

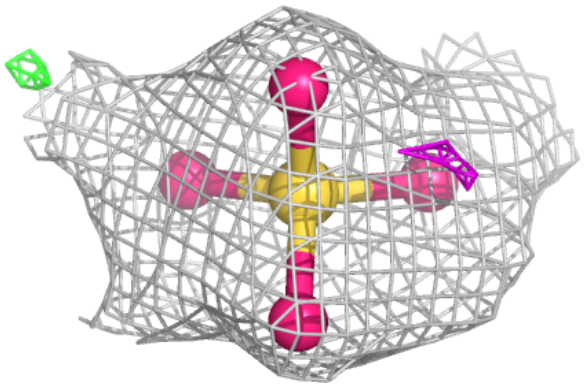


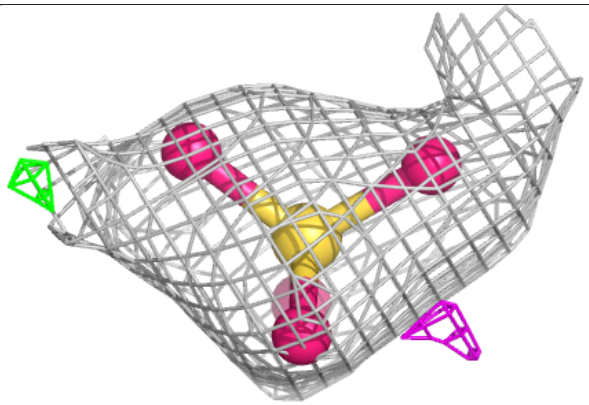


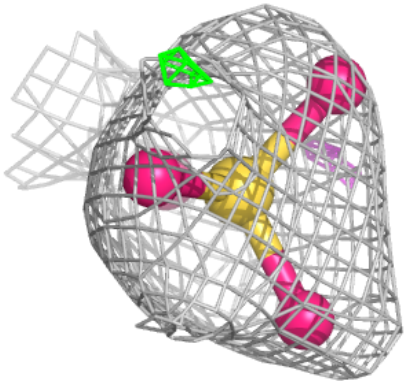


Electron density around SO4 F 205:

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

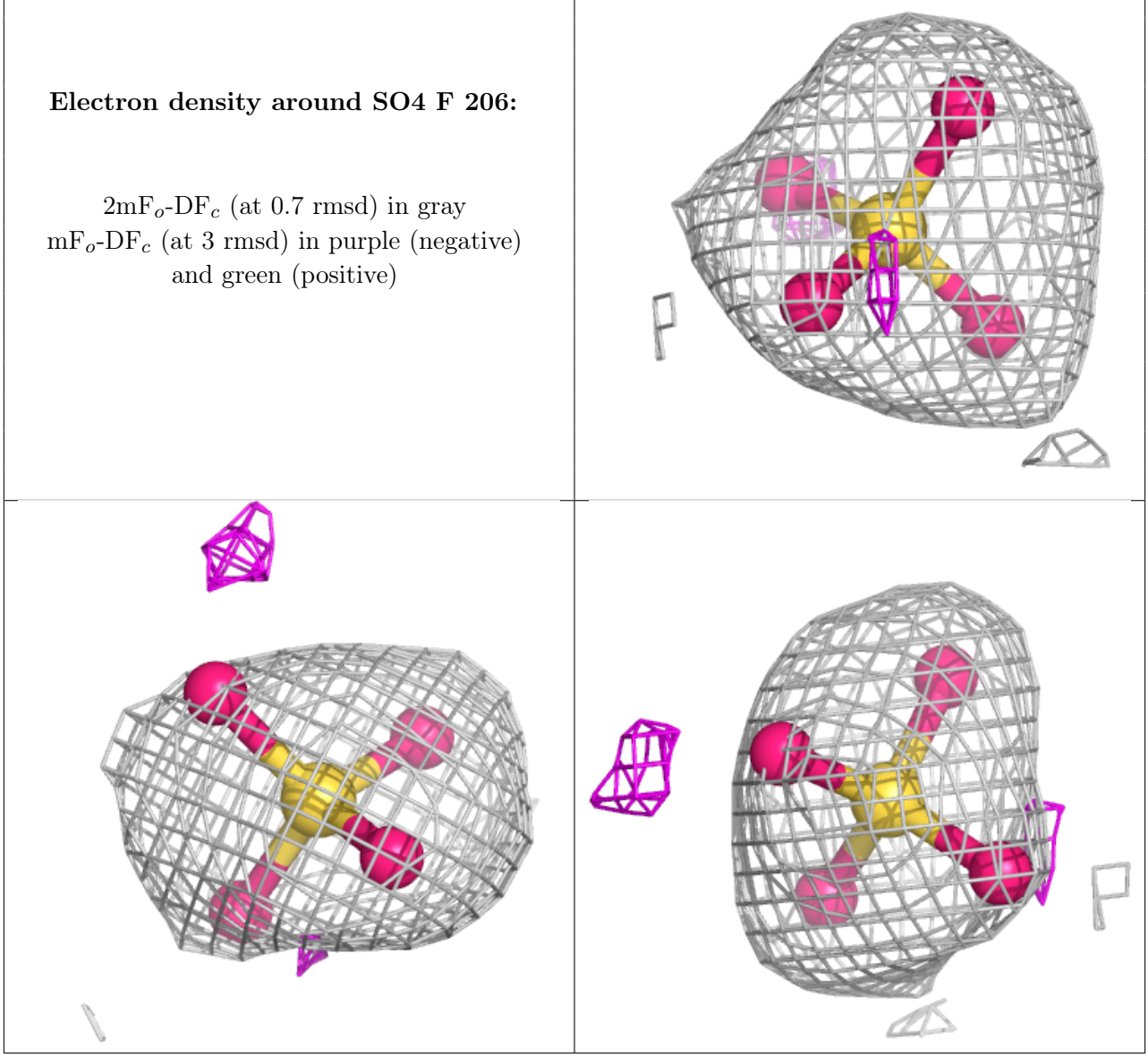






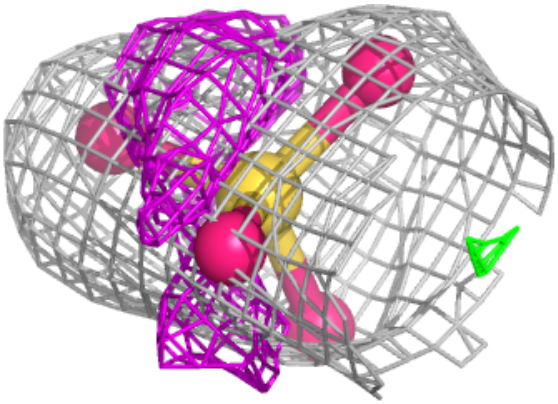
Electron density around SO4 F 206:

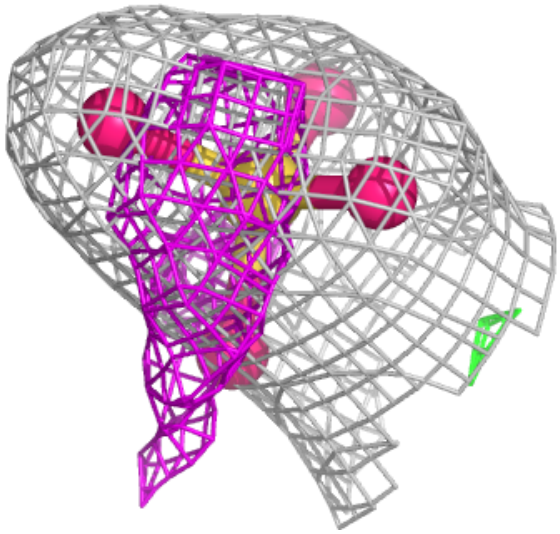
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

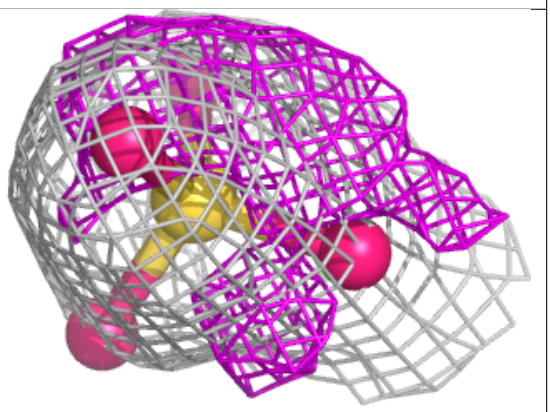


Electron density around SO4 F 207:

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

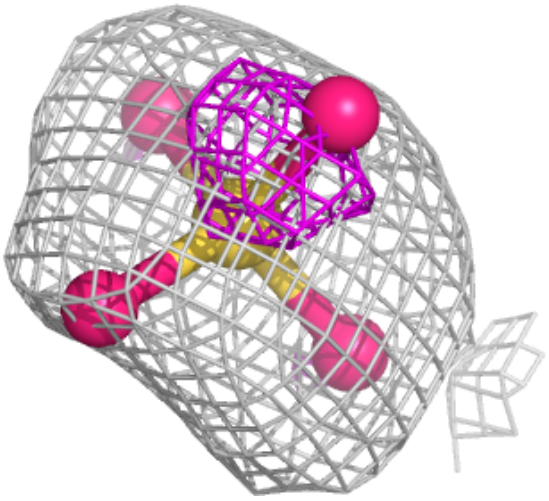


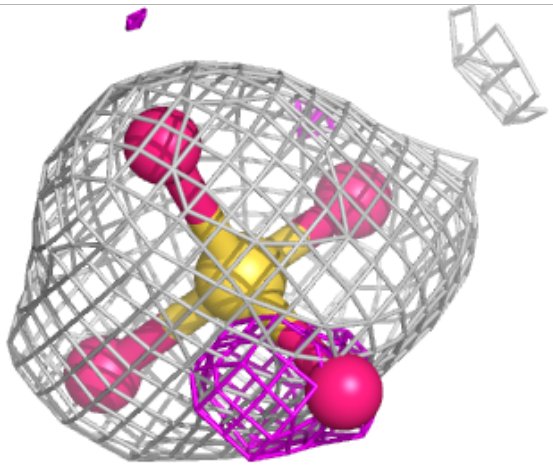


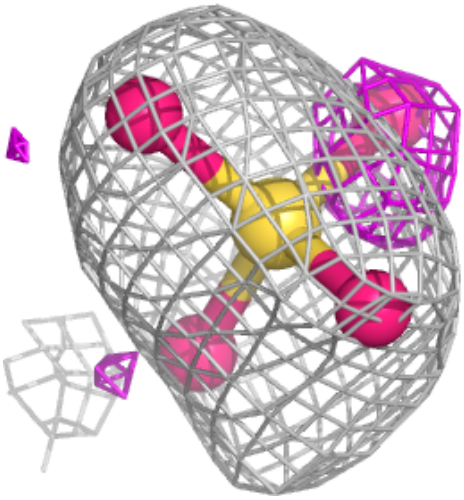


Electron density around SO4 F 208:

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

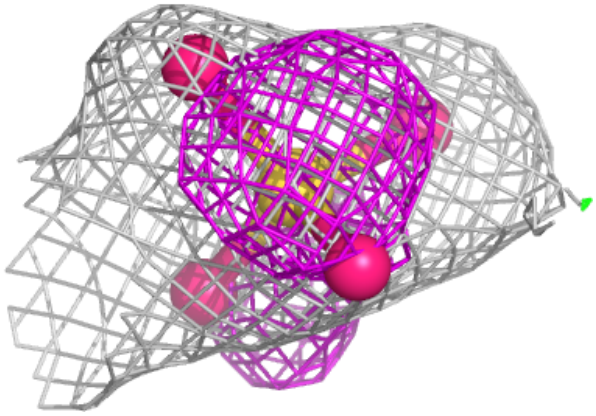


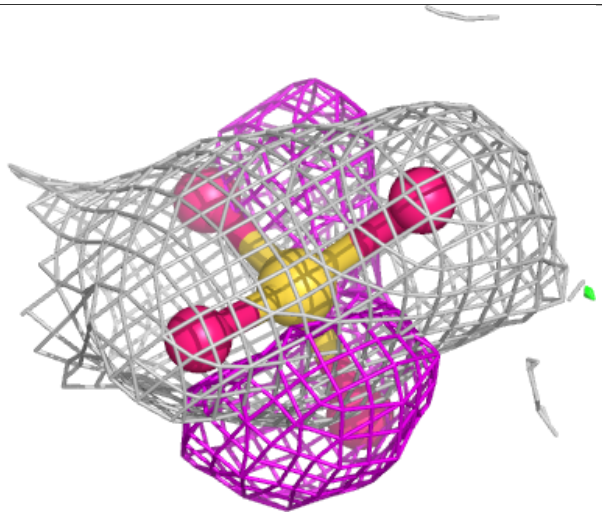


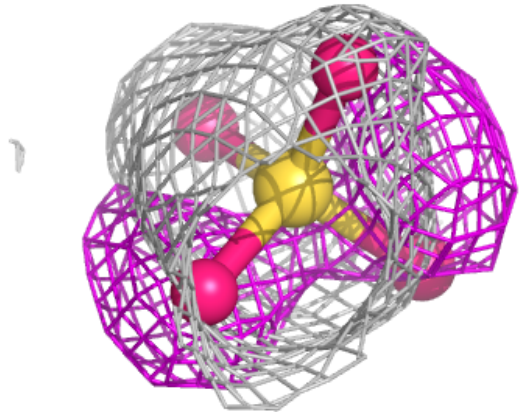


Electron density around SO4 I 208:

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

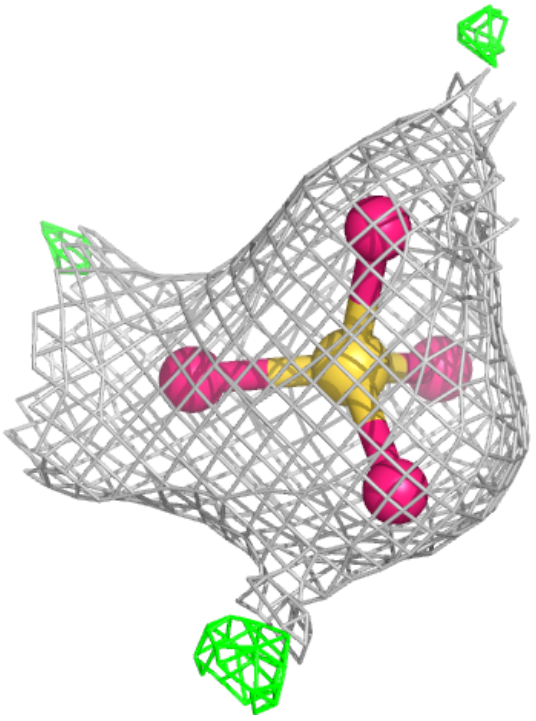


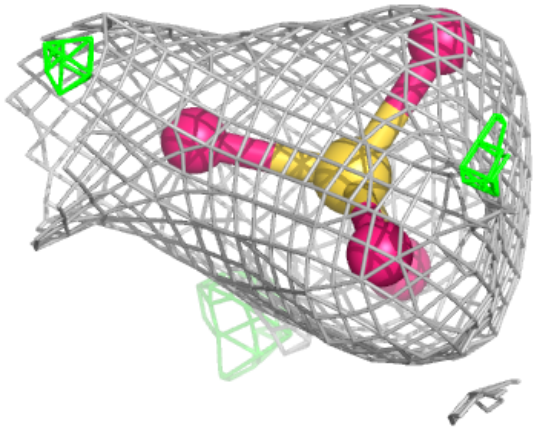


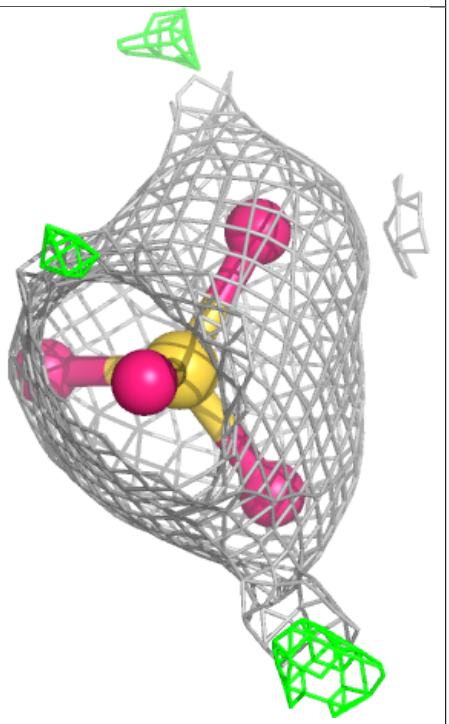


Electron density around SO4 E 206:

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

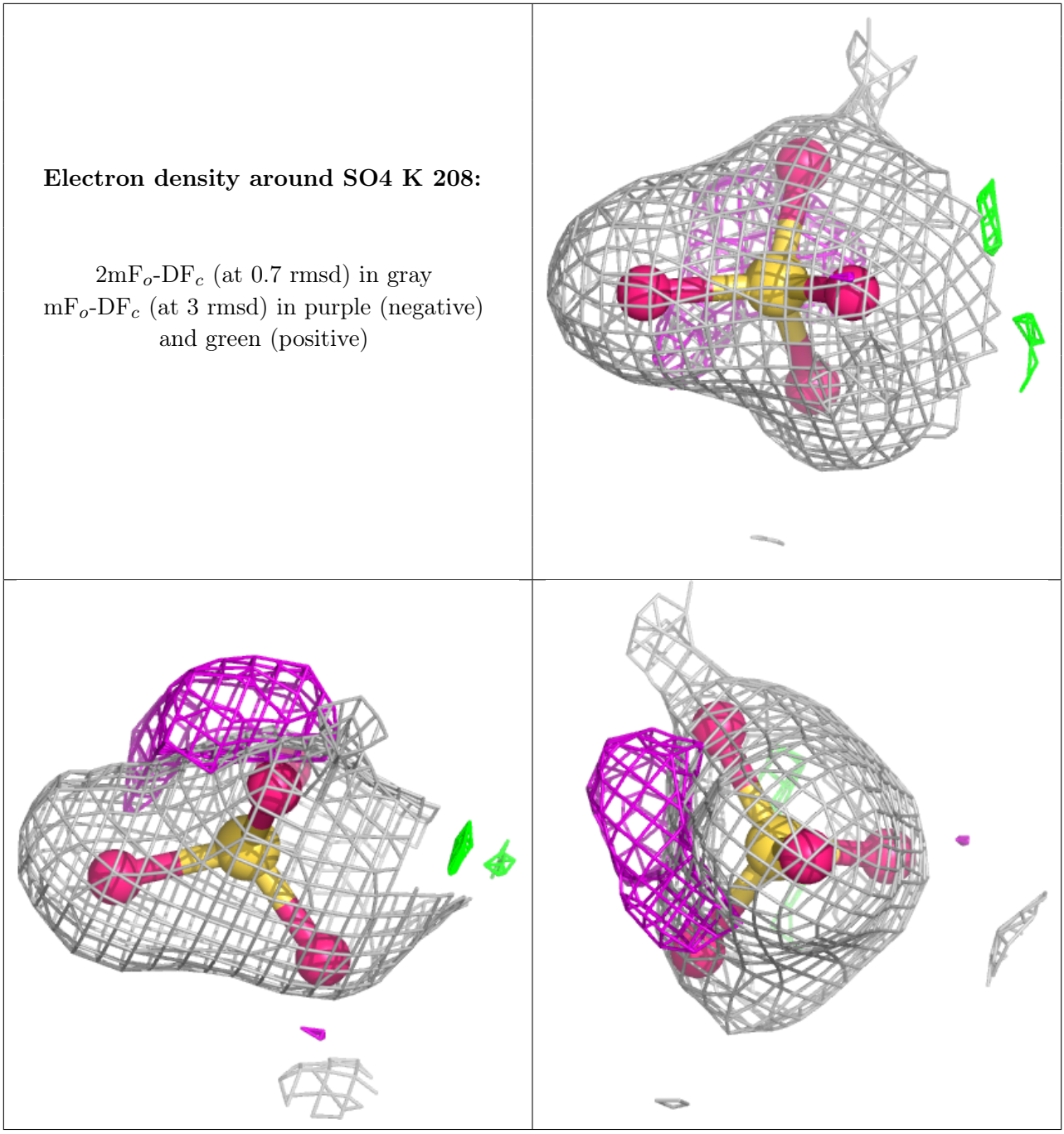






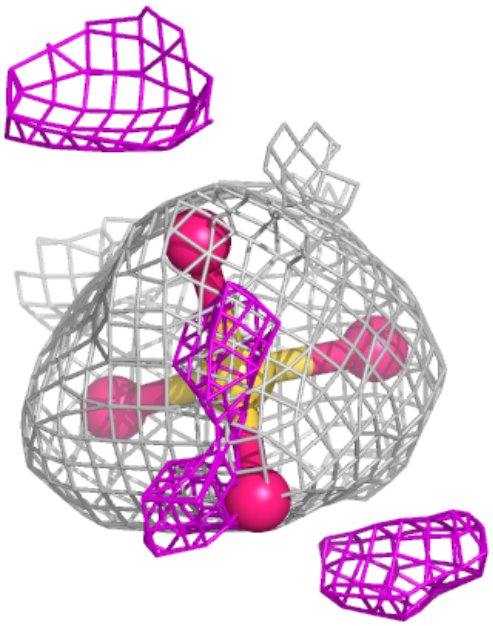
Electron density around SO4 K 208:

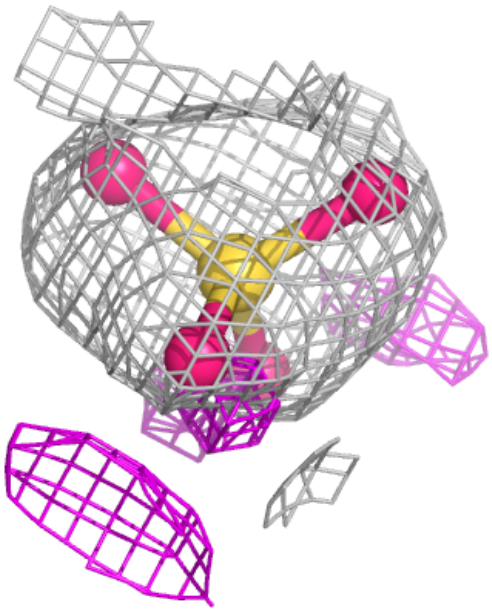
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

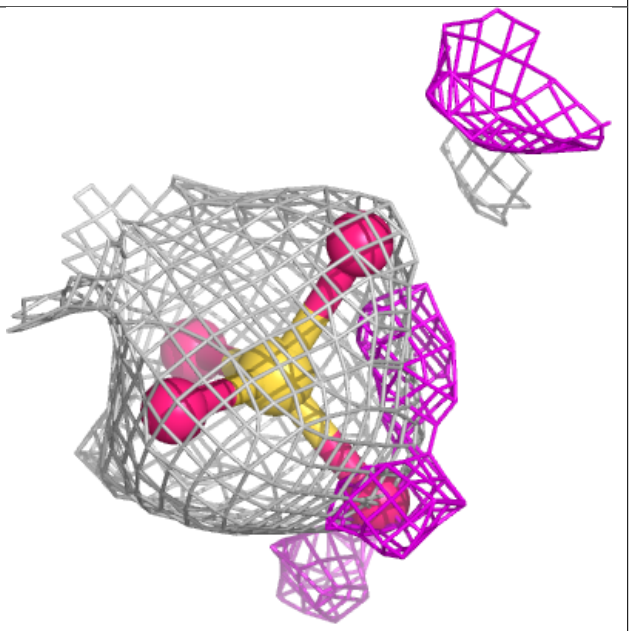


Electron density around SO4 C 209:

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

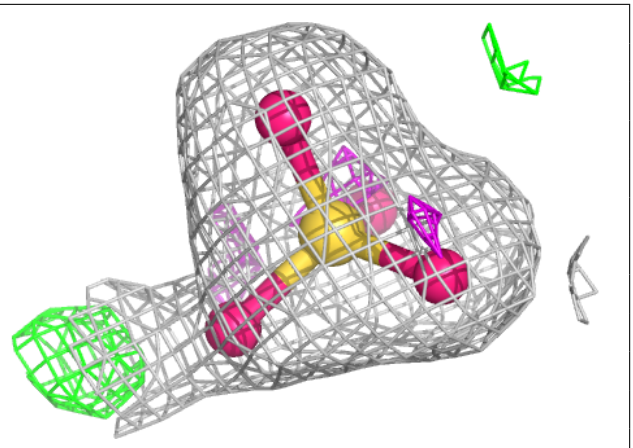


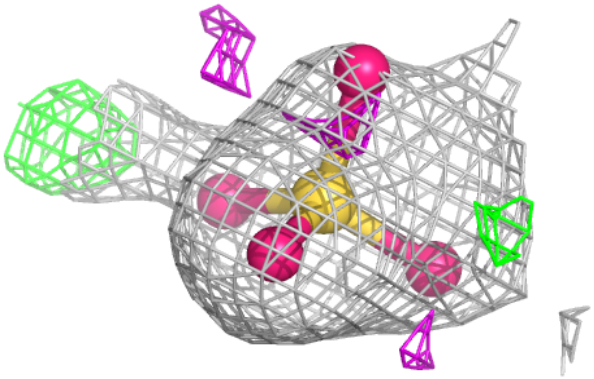


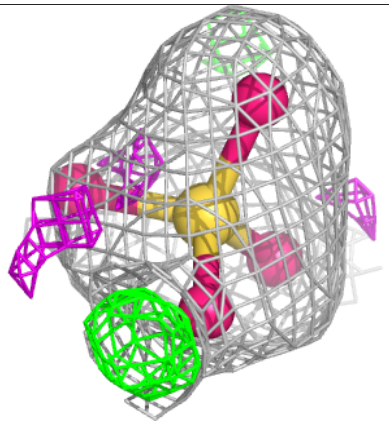


Electron density around SO4 B 211:

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

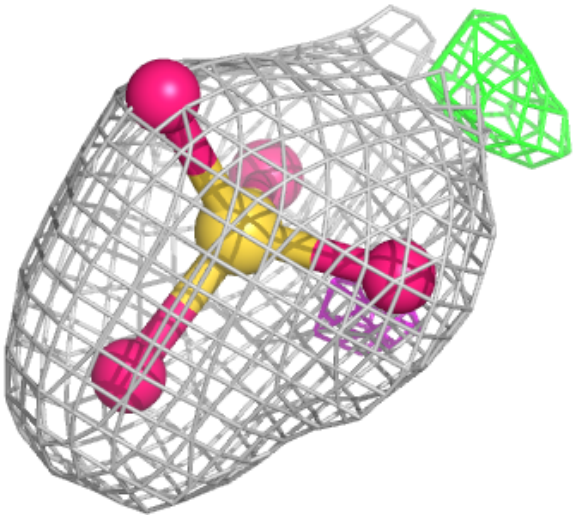


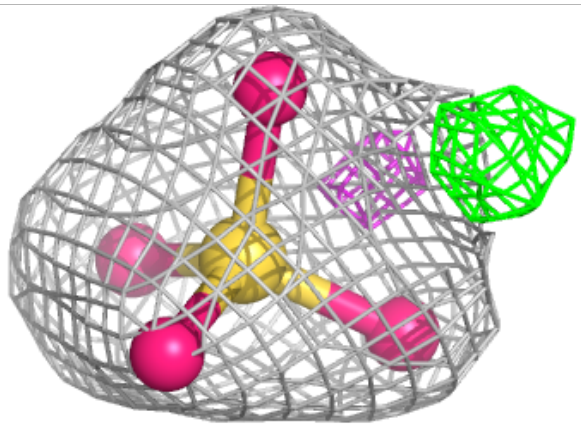


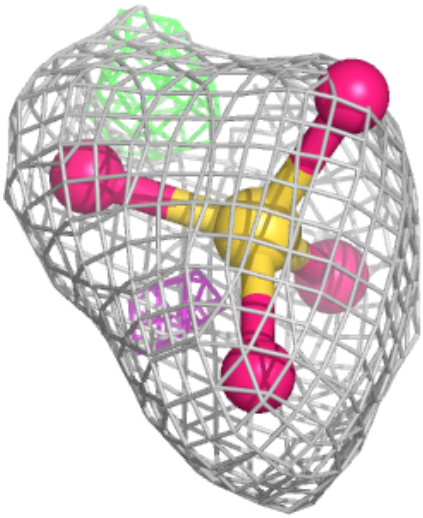


Electron density around SO4 E 207:

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

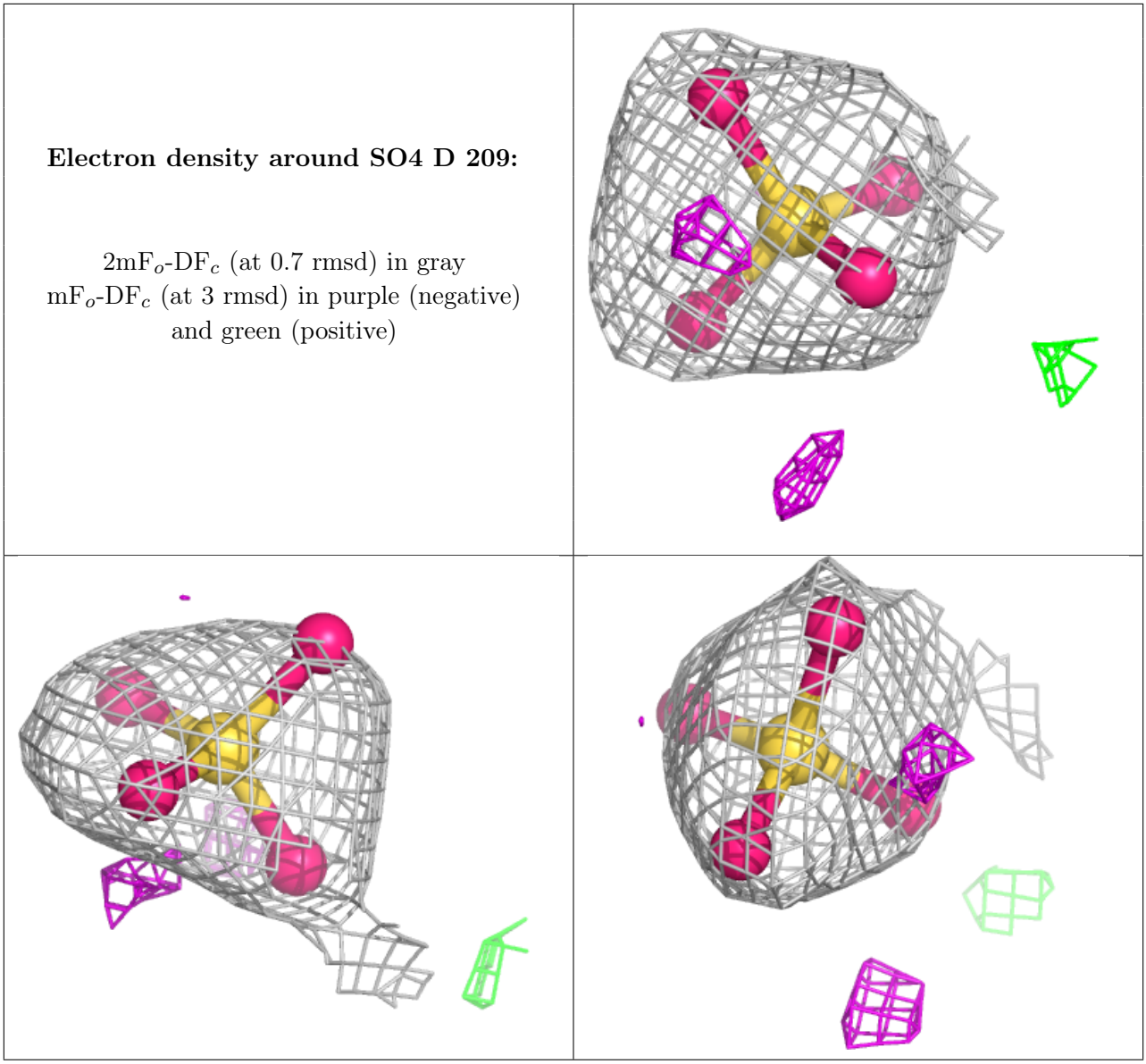






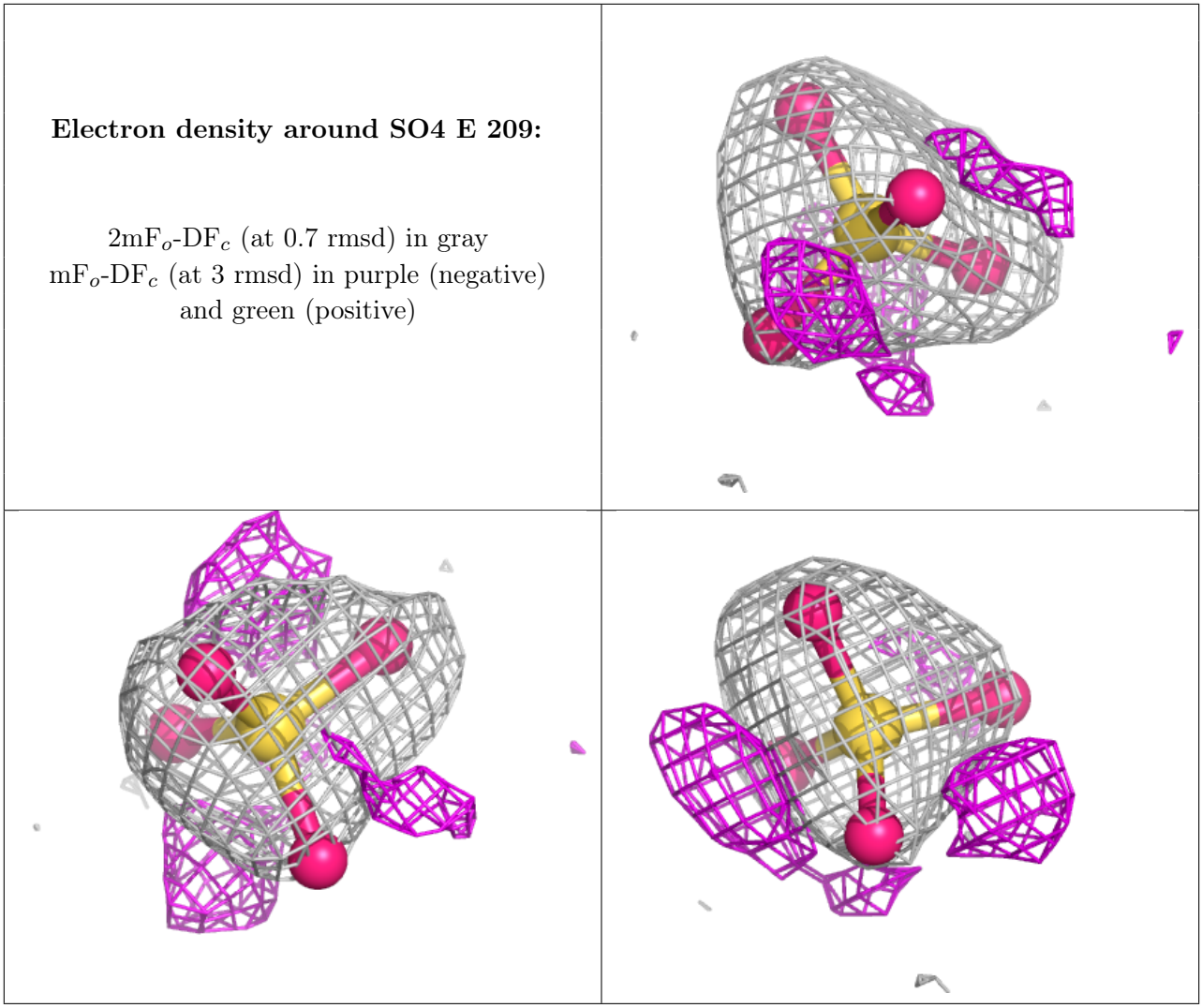
Electron density around SO4 D 209:

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



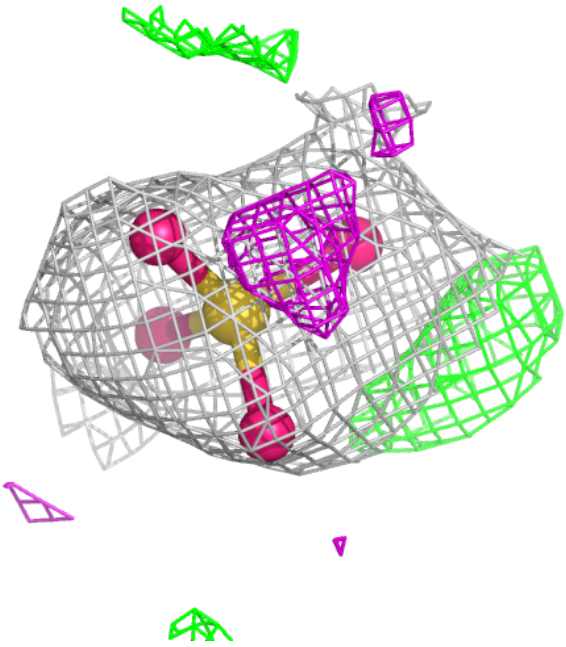
Electron density around SO4 E 209:

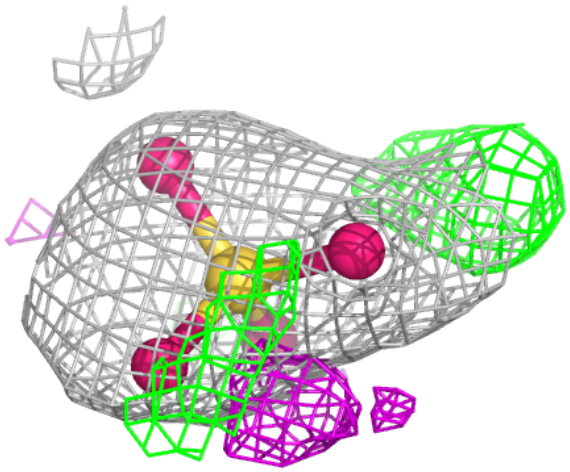
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

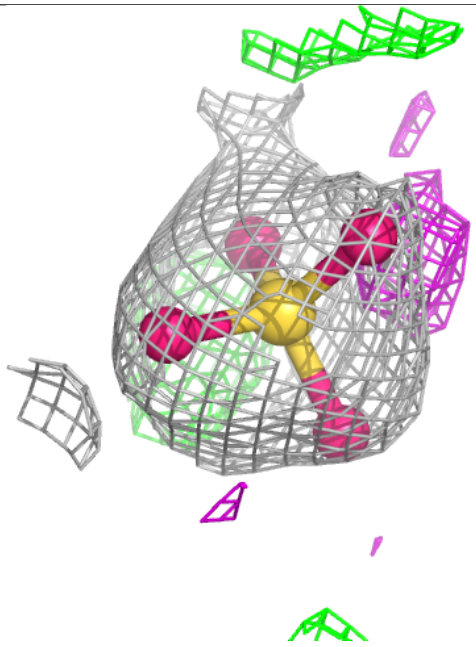


Electron density around SO4 K 206:

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

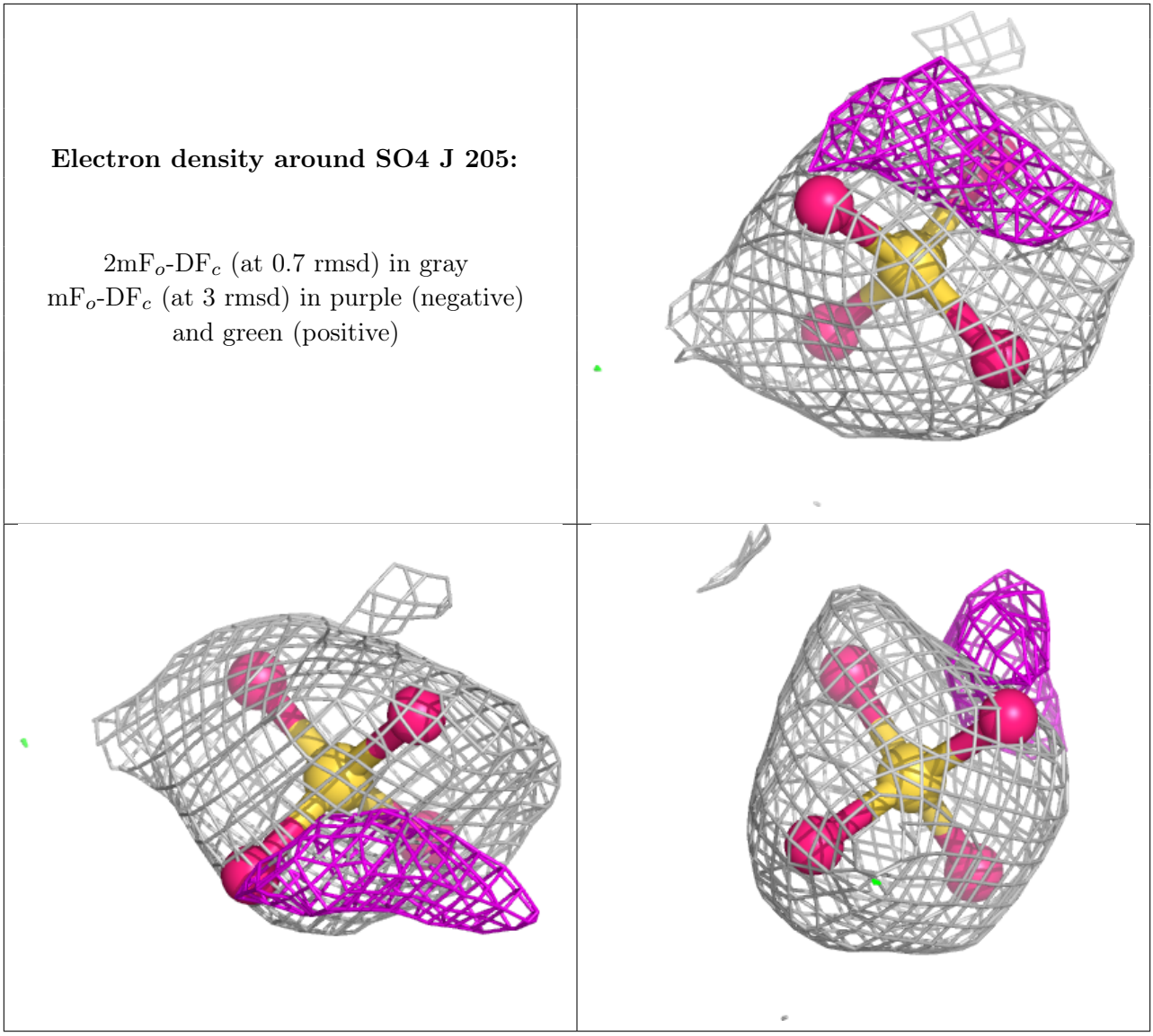






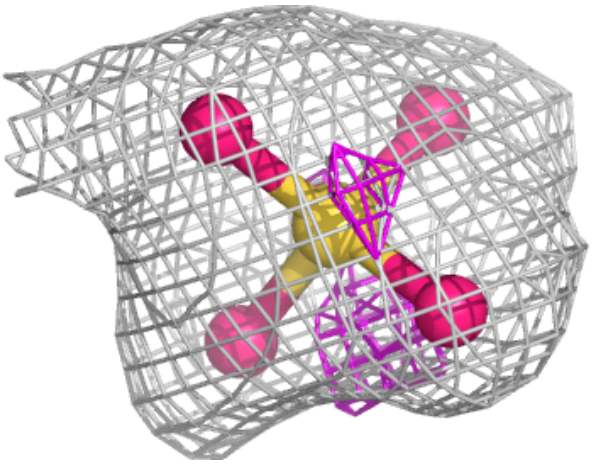
Electron density around SO4 J 205:

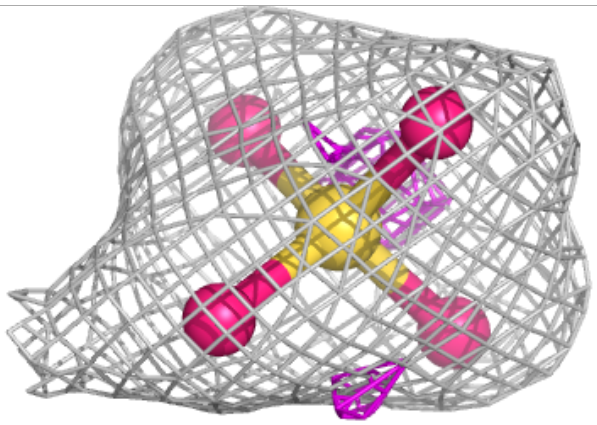
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

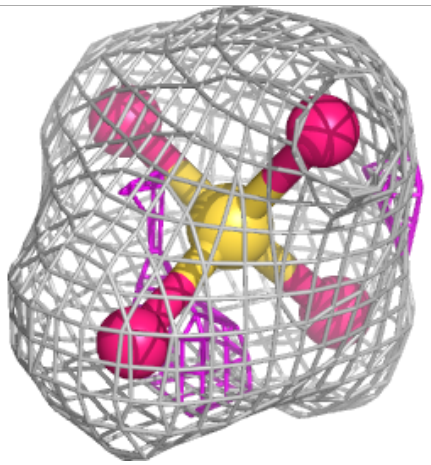


Electron density around SO4 G 204:

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

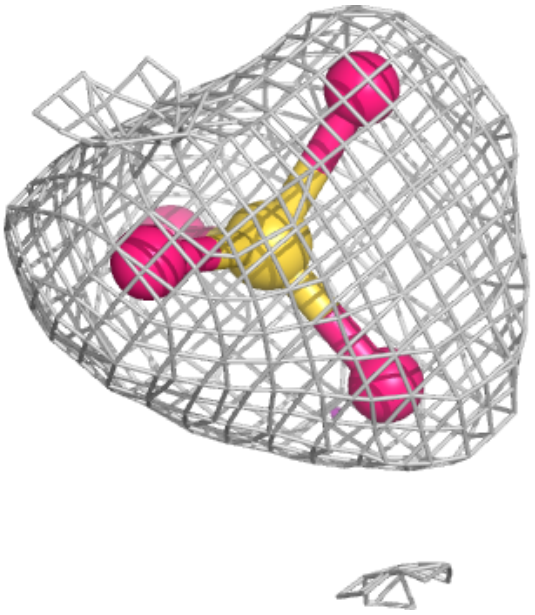


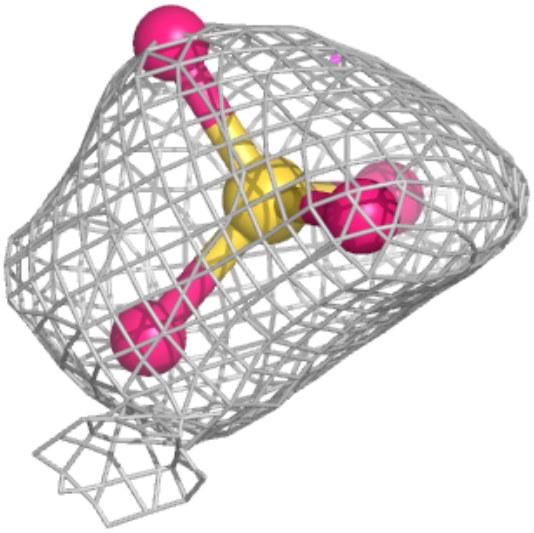


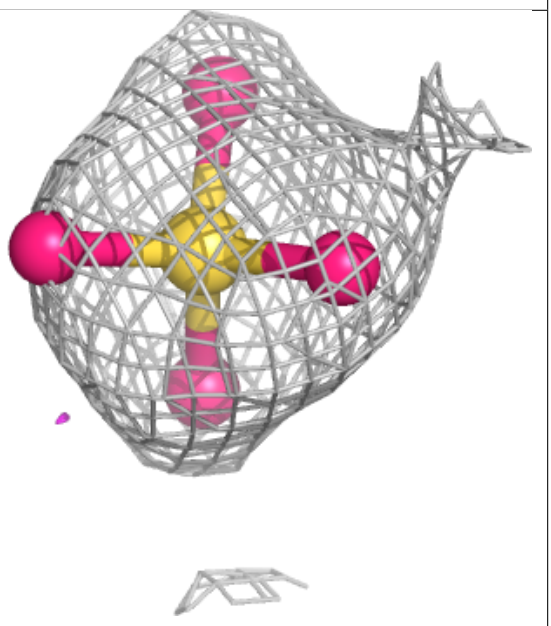


Electron density around SO4 G 207:

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

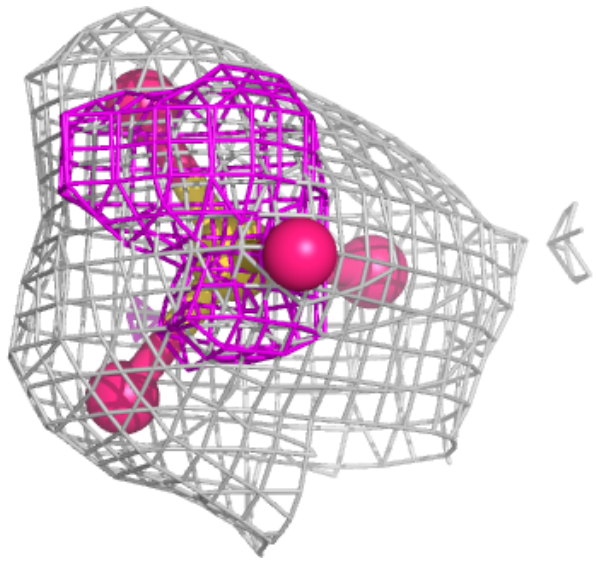


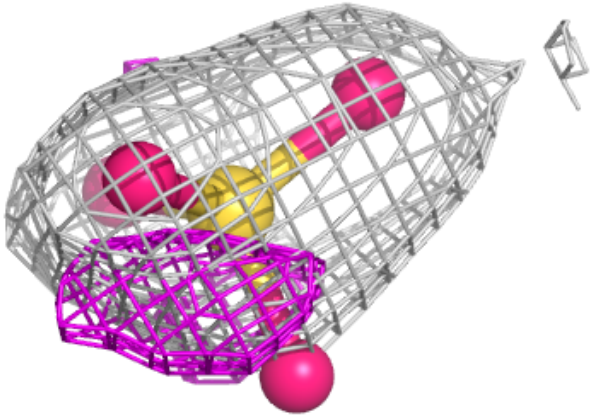


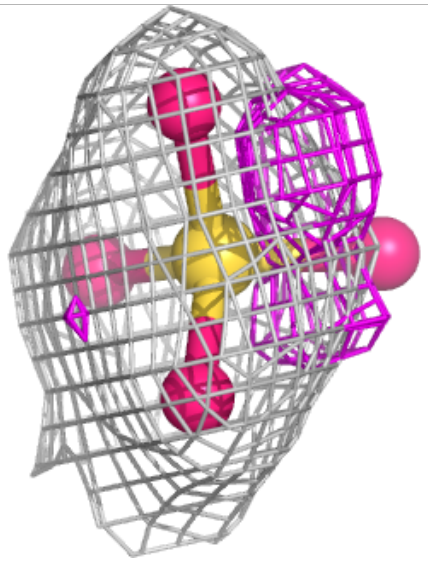


Electron density around SO4 C 207:

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

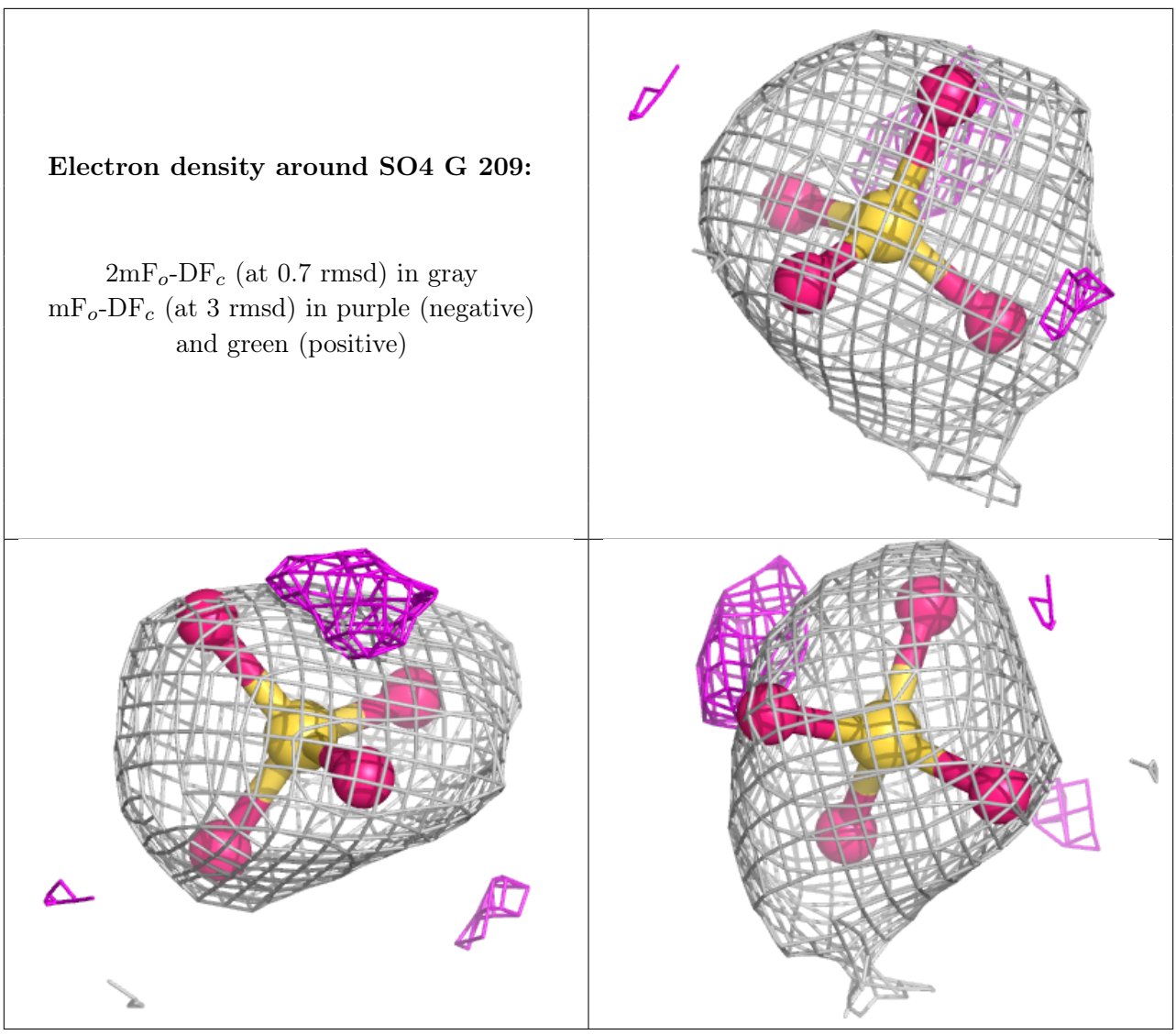






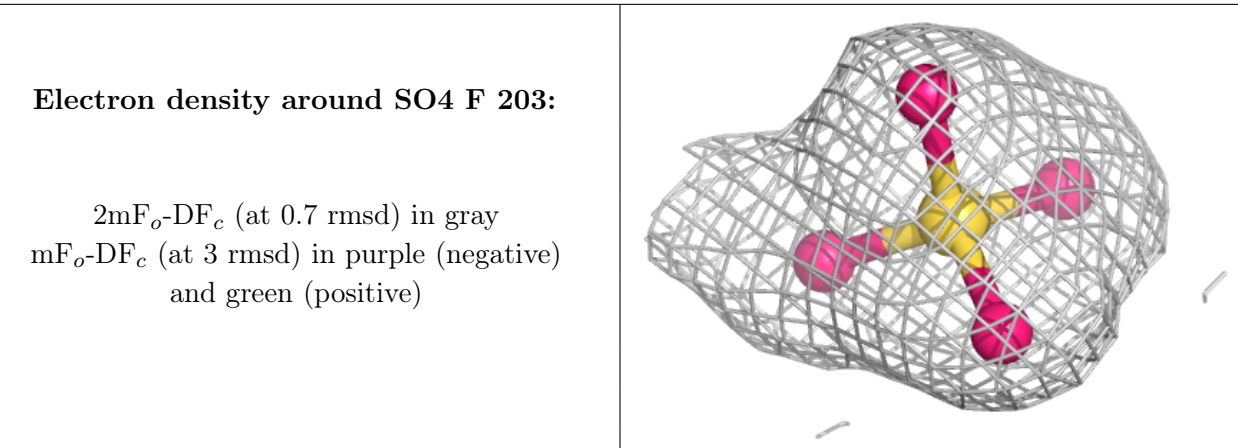
Electron density around SO4 G 209:

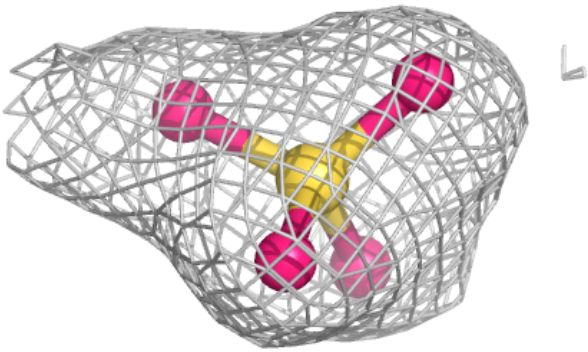
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

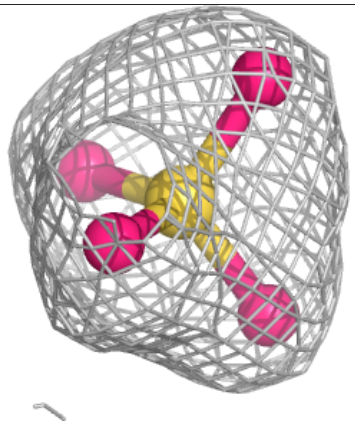


Electron density around SO4 F 203:

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

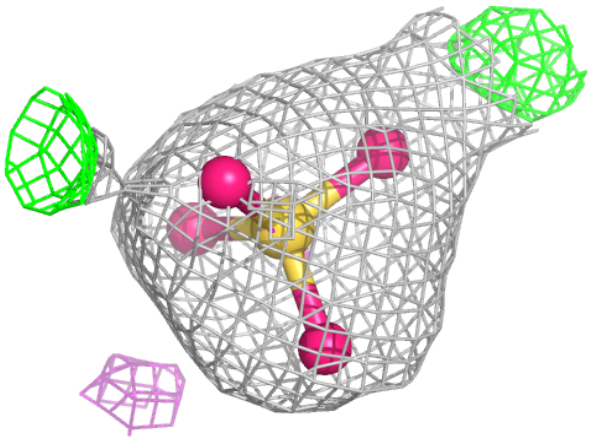


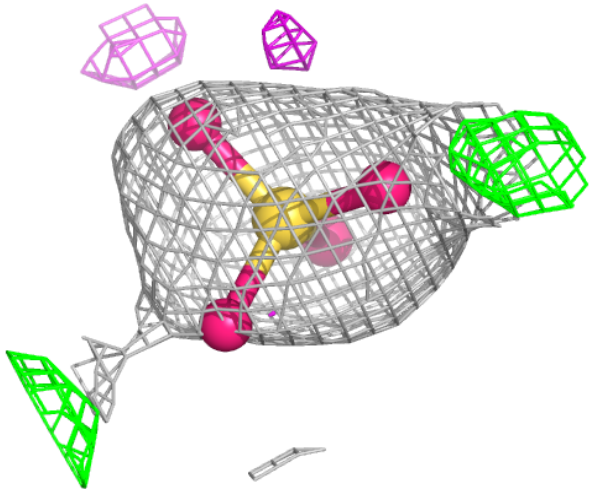


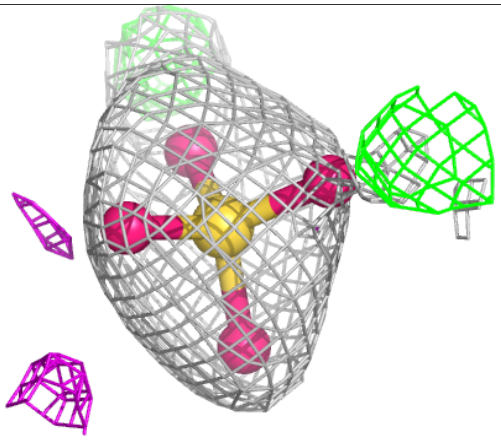


Electron density around SO4 B 210:

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

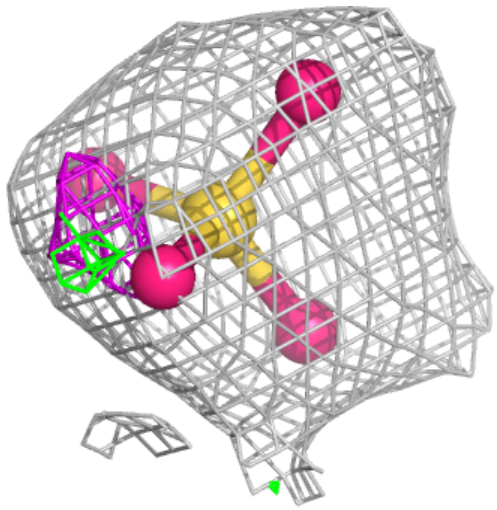


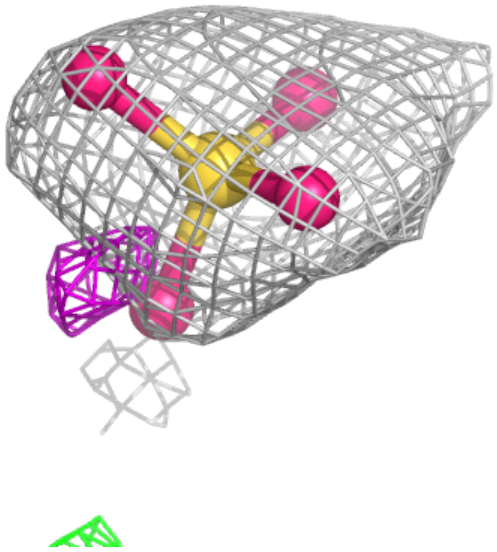


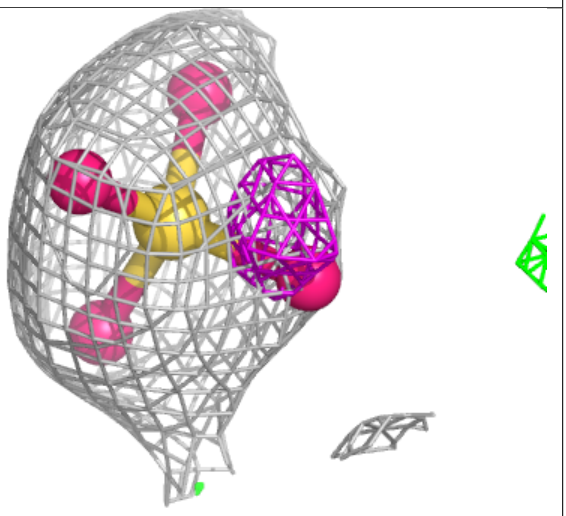


Electron density around SO4 A 209:

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

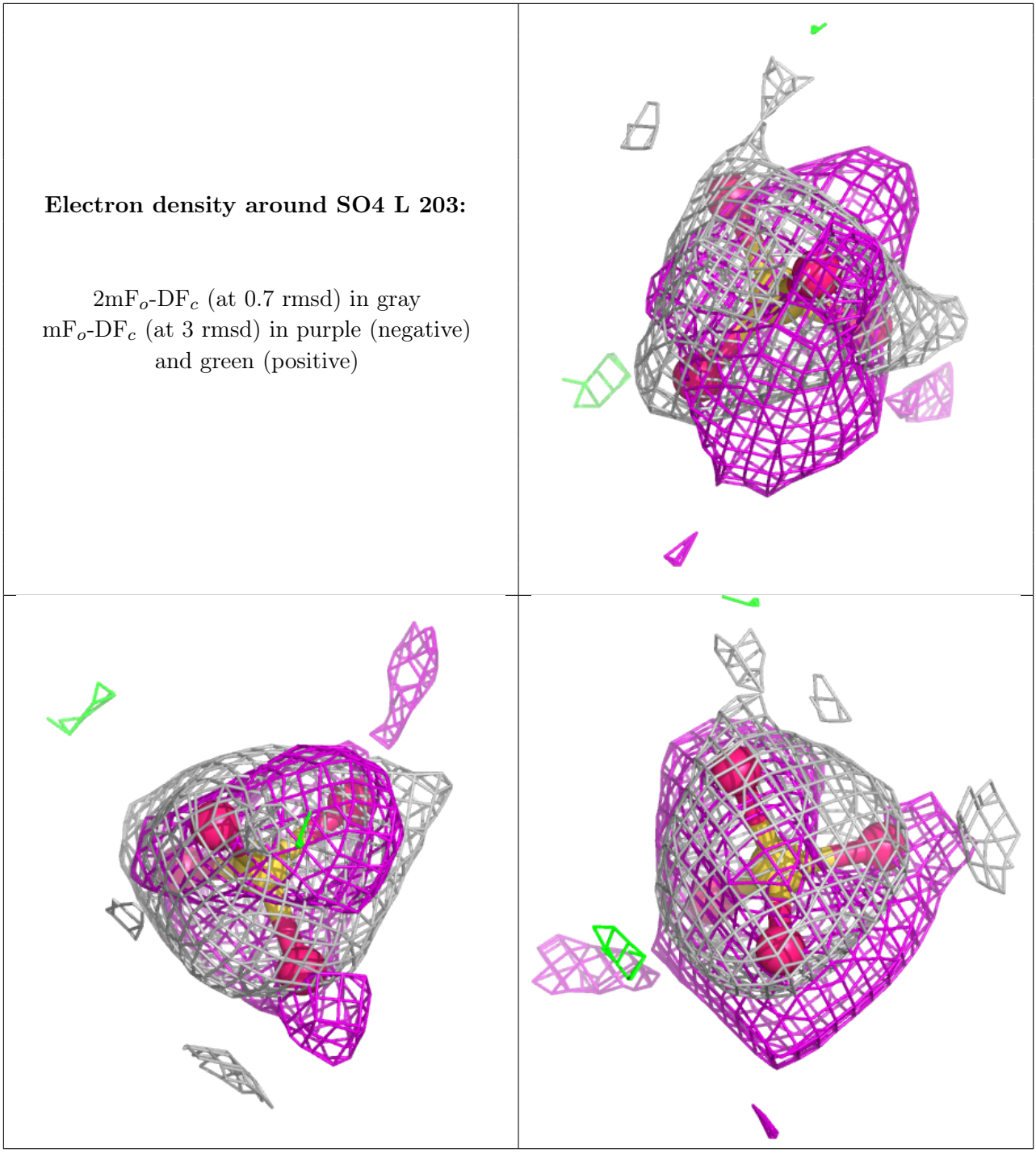






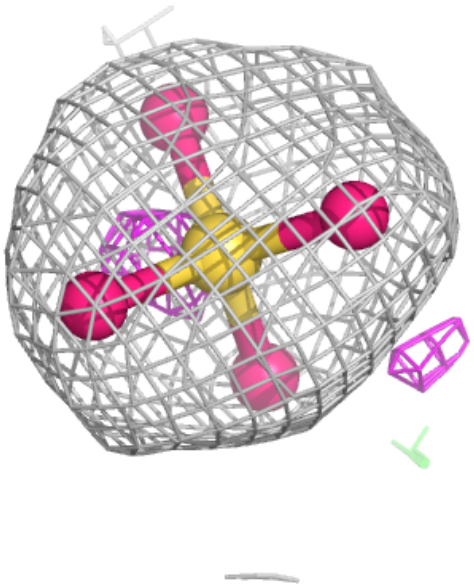
Electron density around SO4 L 203:

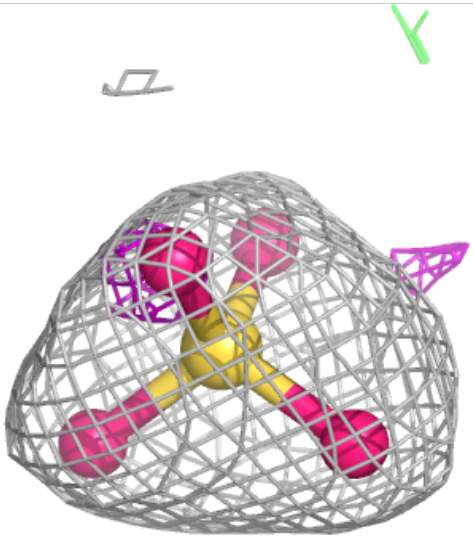
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

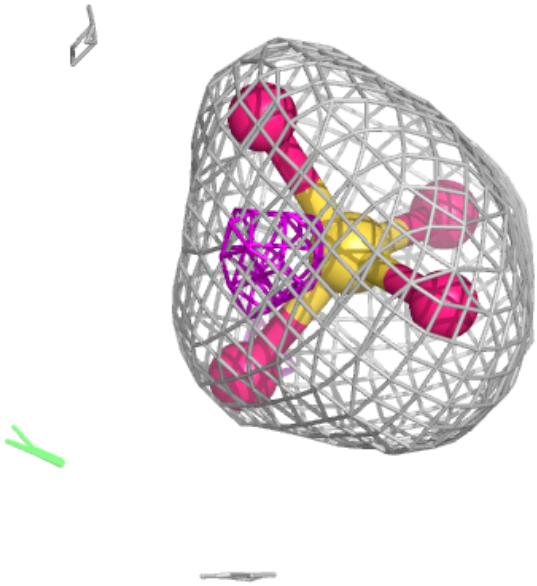


Electron density around SO4 H 207:

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

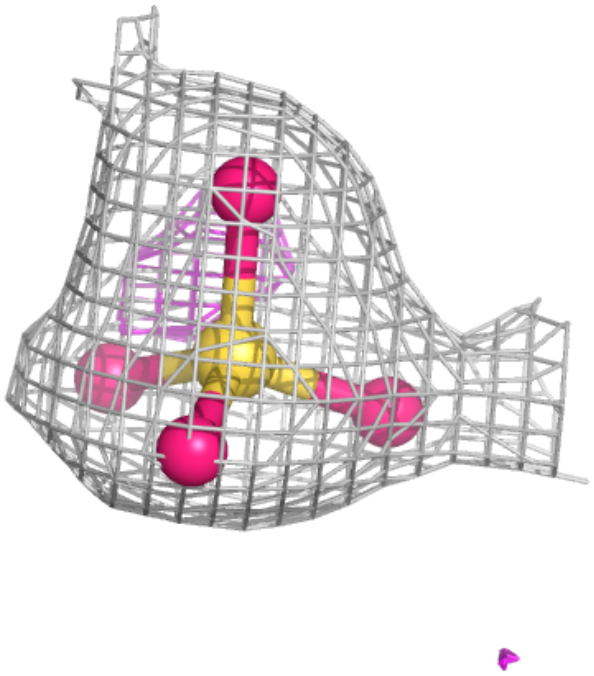


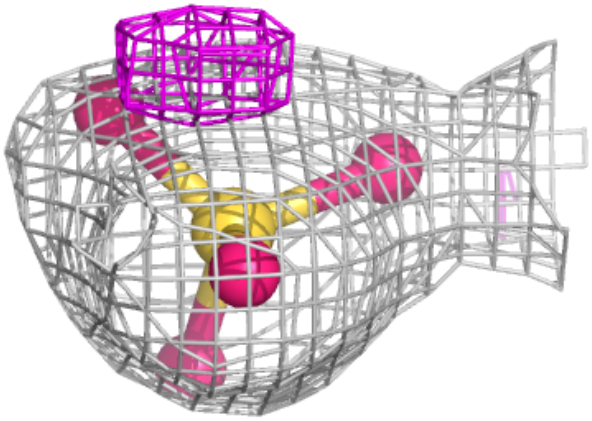


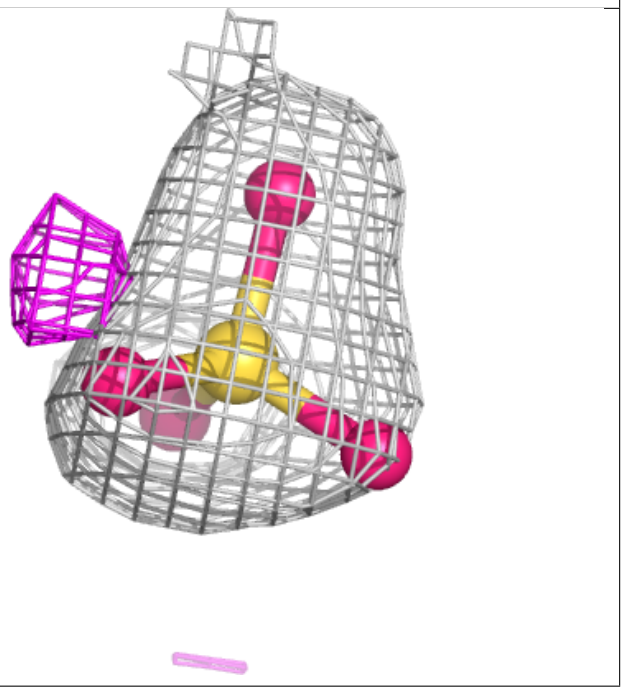


Electron density around SO4 I 205:

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

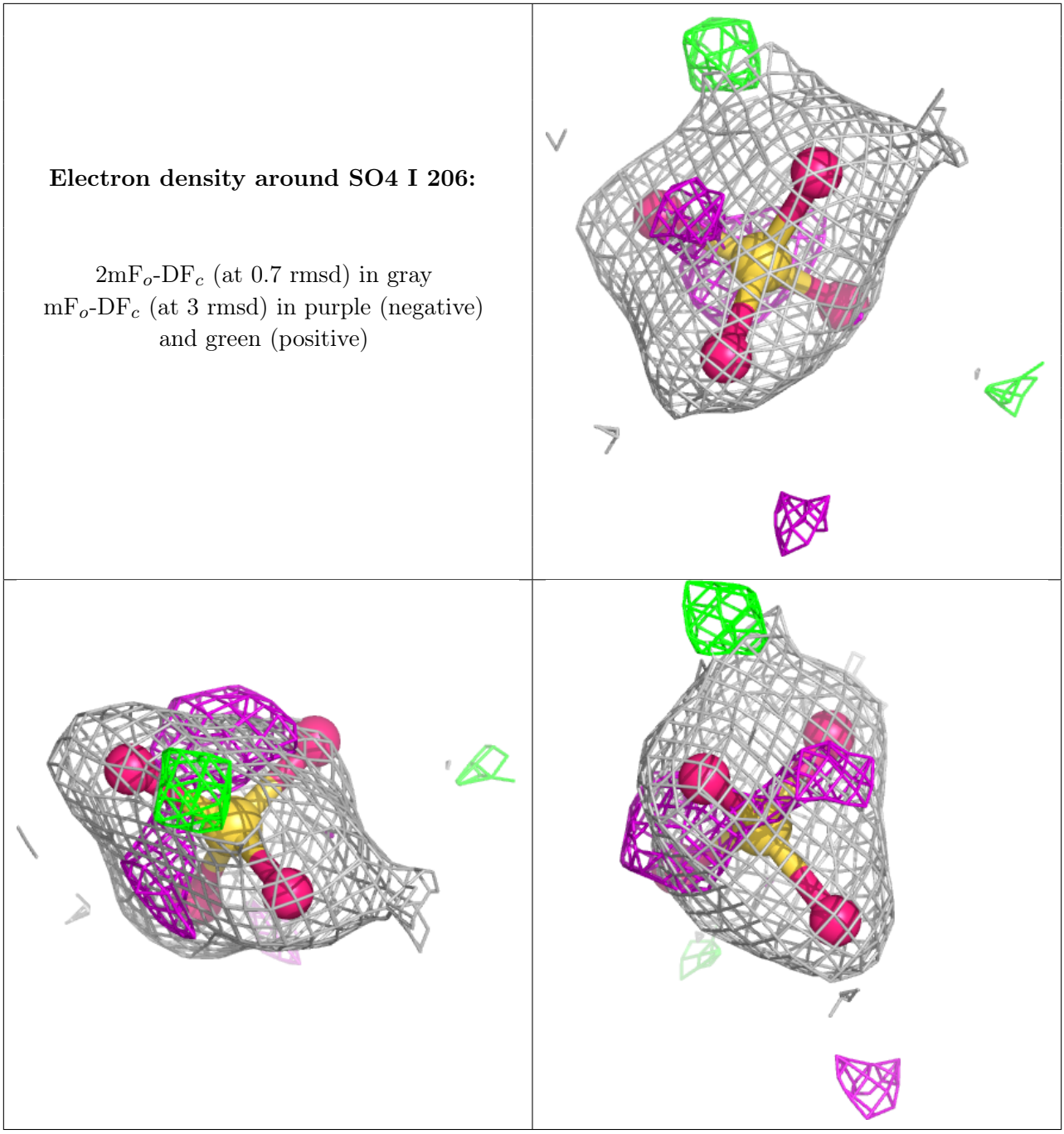






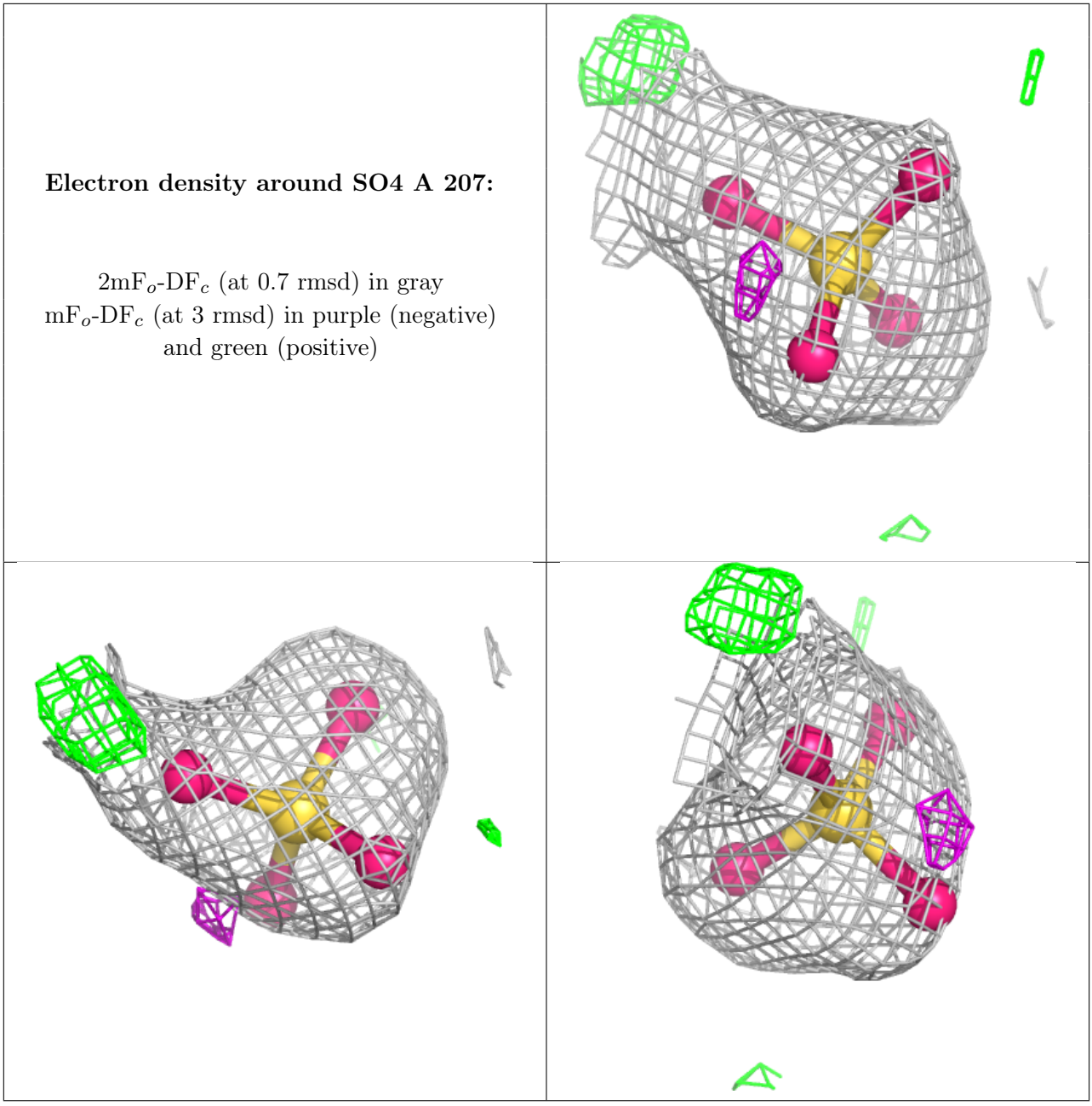
Electron density around SO4 I 206:

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



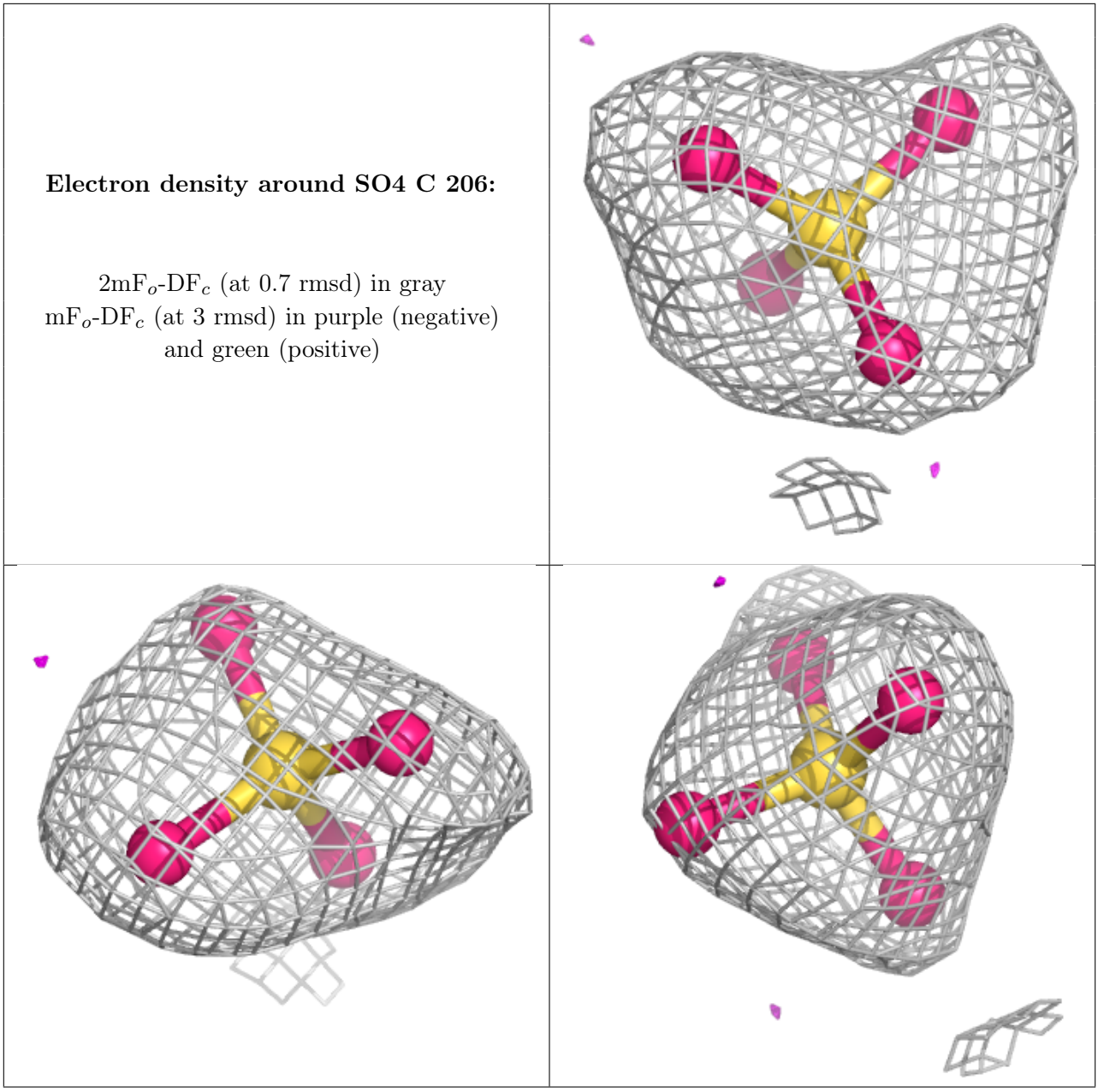
Electron density around SO4 A 207:

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



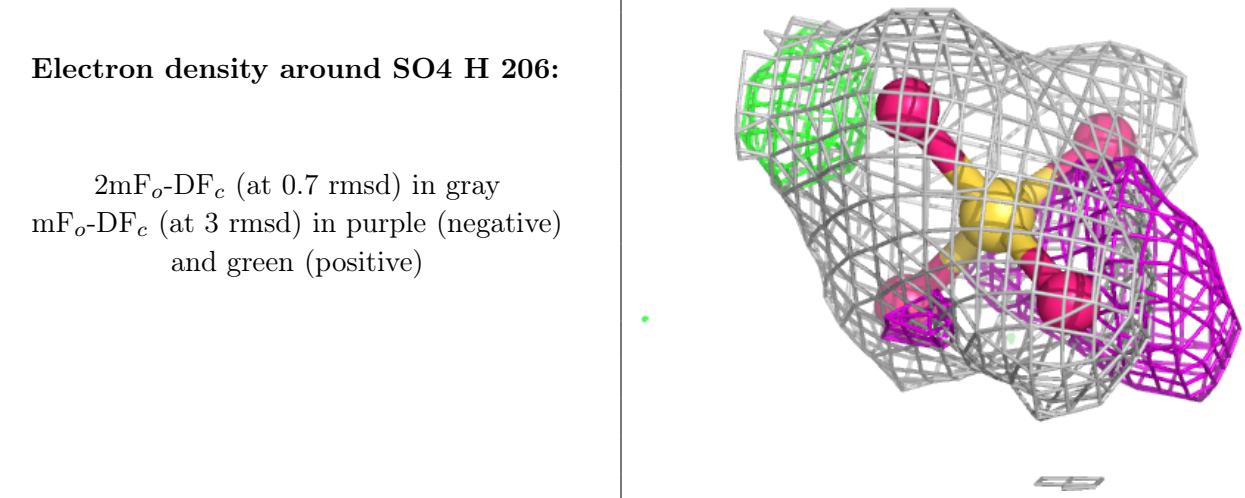
Electron density around SO4 C 206:

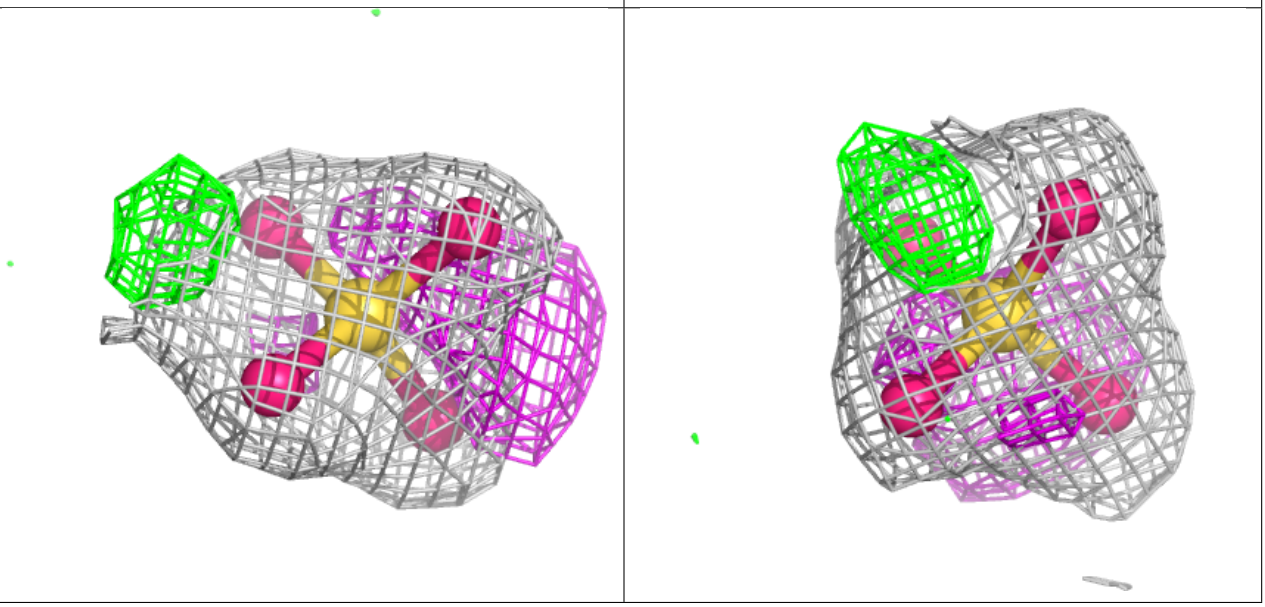
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around SO4 H 206:

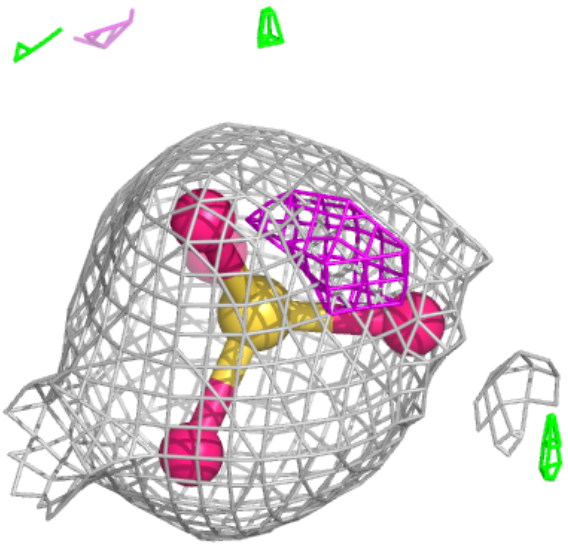
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

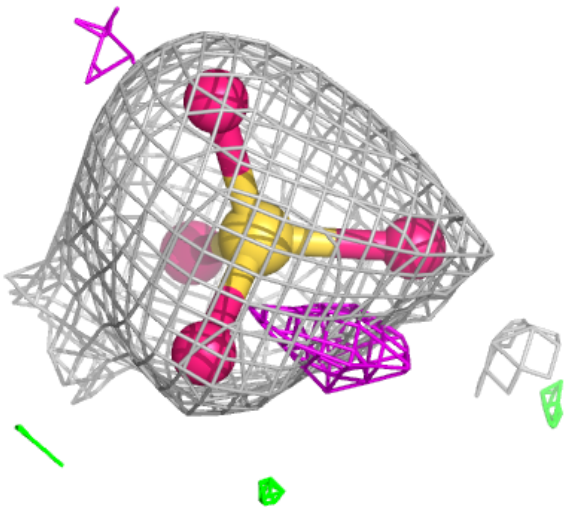


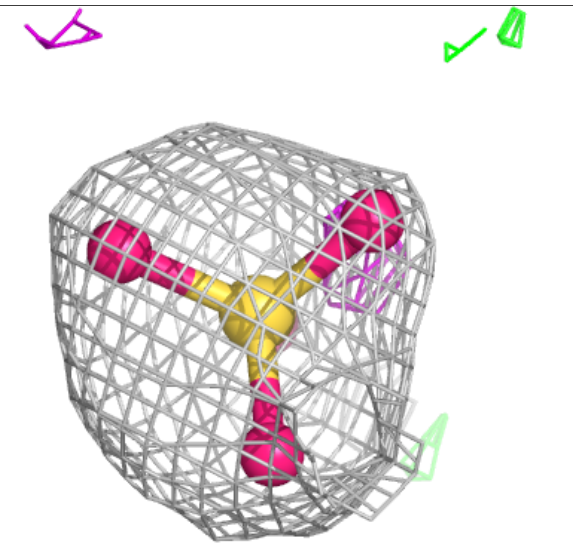


Electron density around SO4 K 207:

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

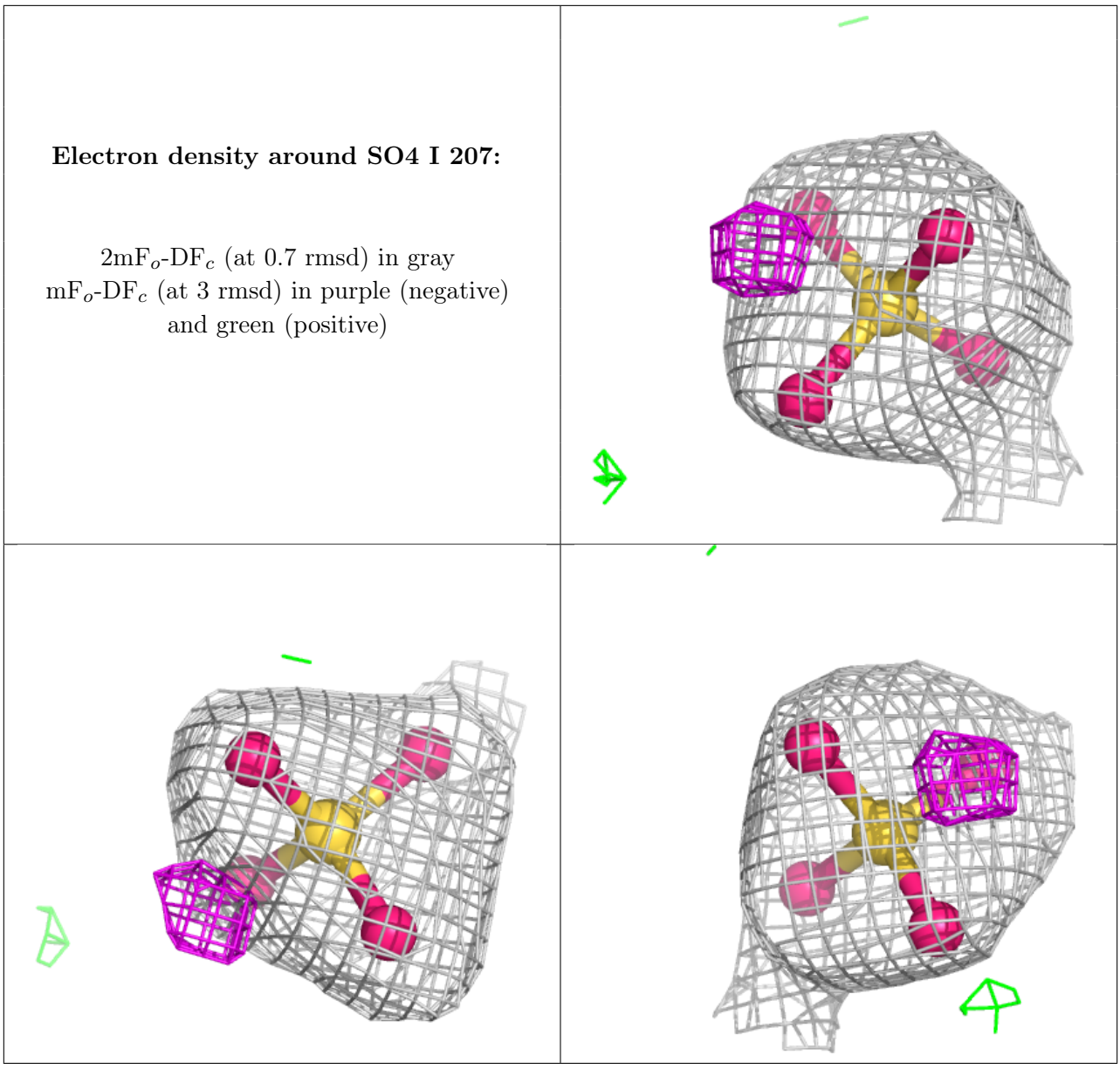






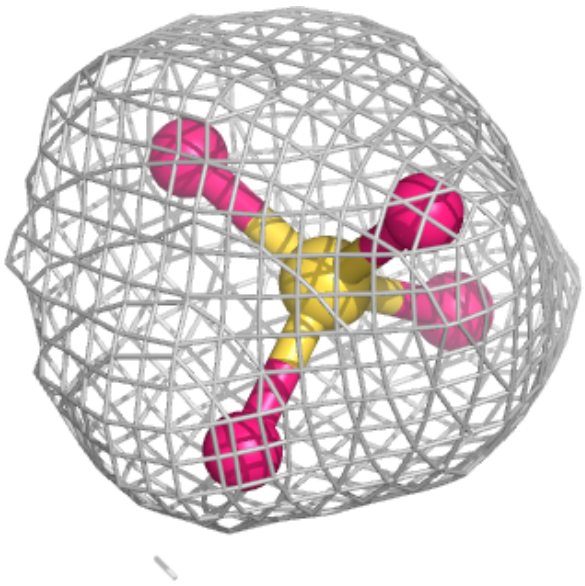
Electron density around SO4 I 207:

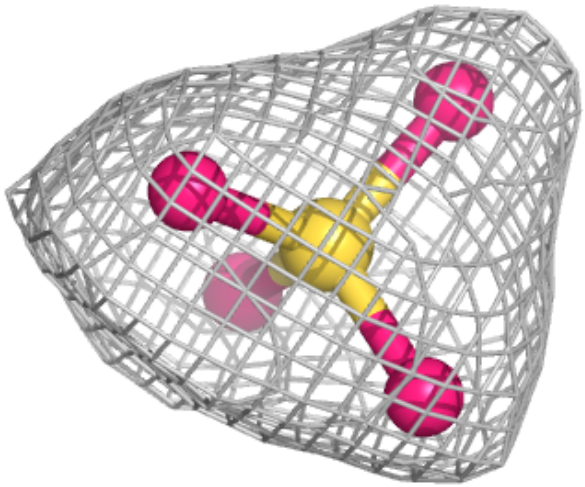
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

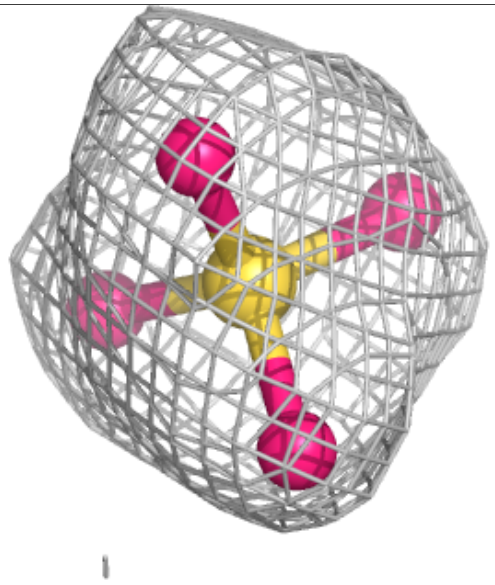


Electron density around SO4 J 207:

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

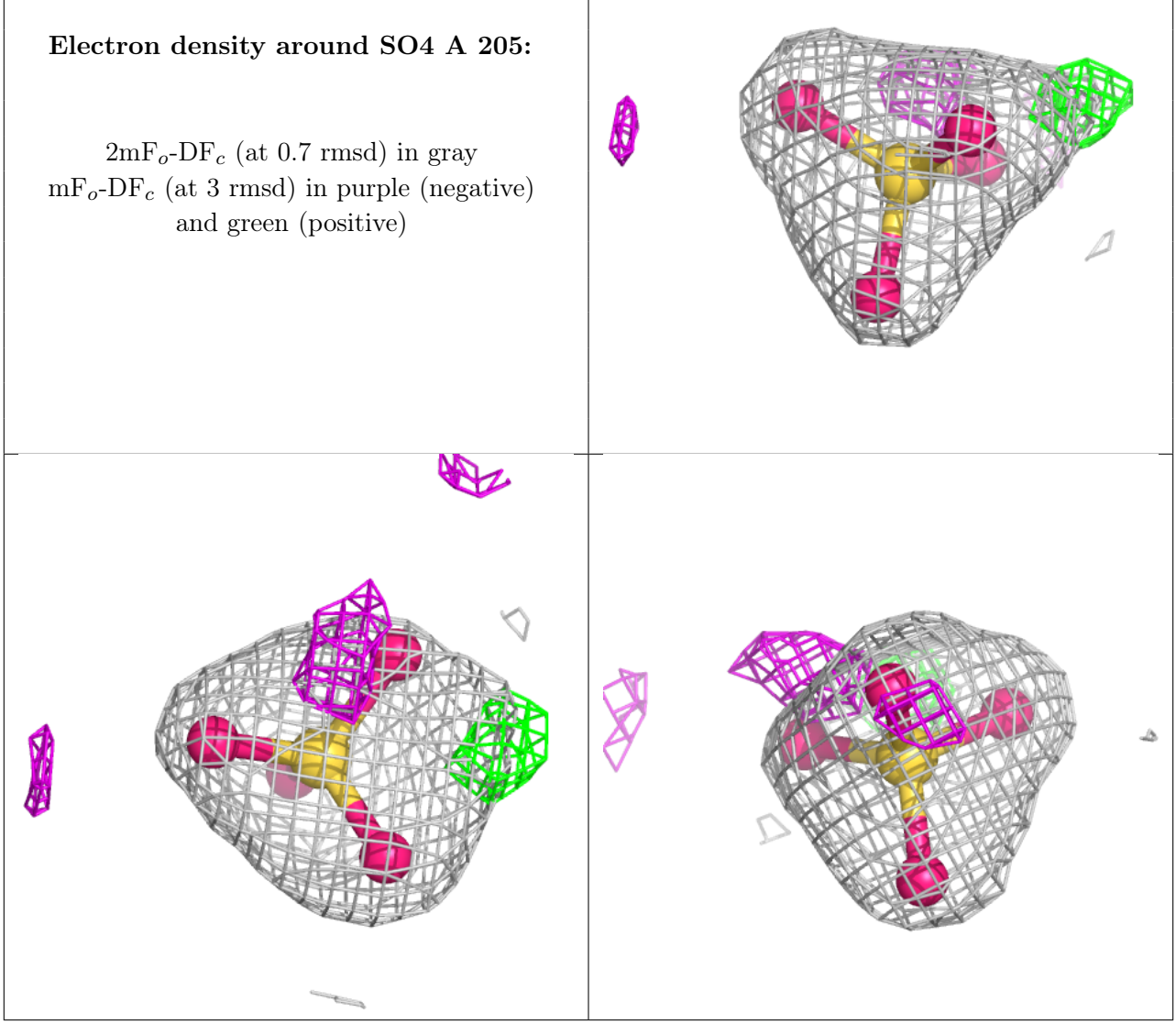






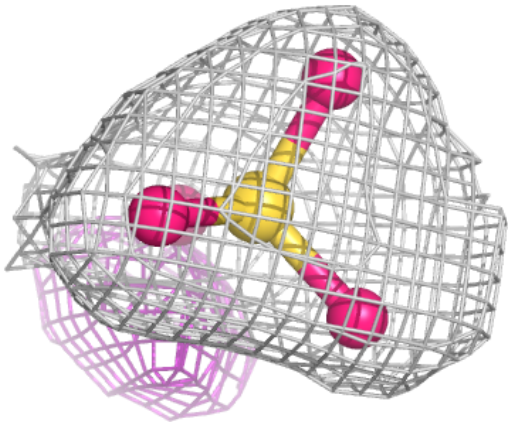
Electron density around SO4 A 205:

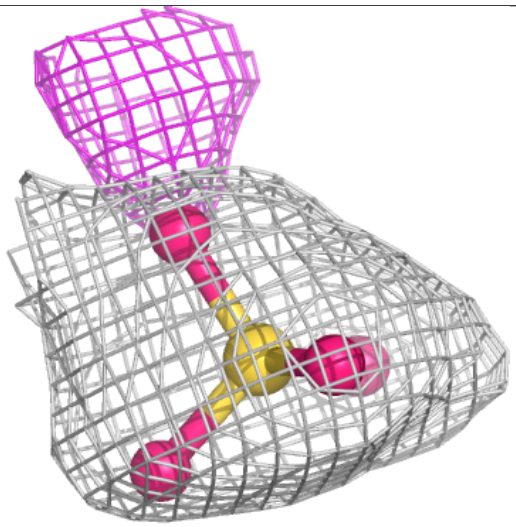
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

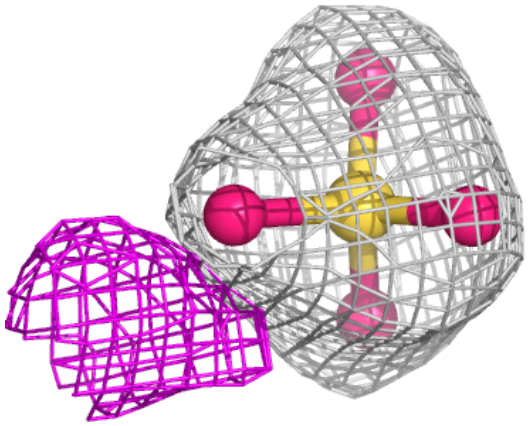


Electron density around SO4 D 205:

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

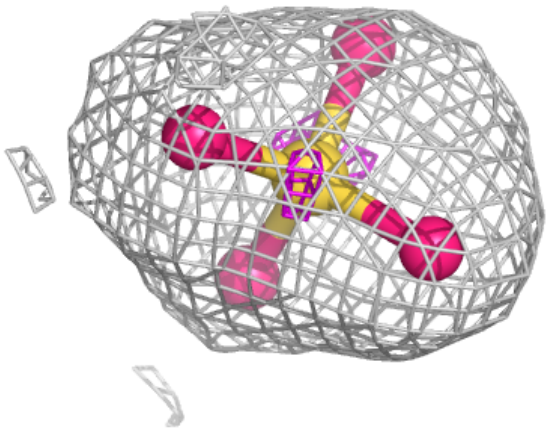


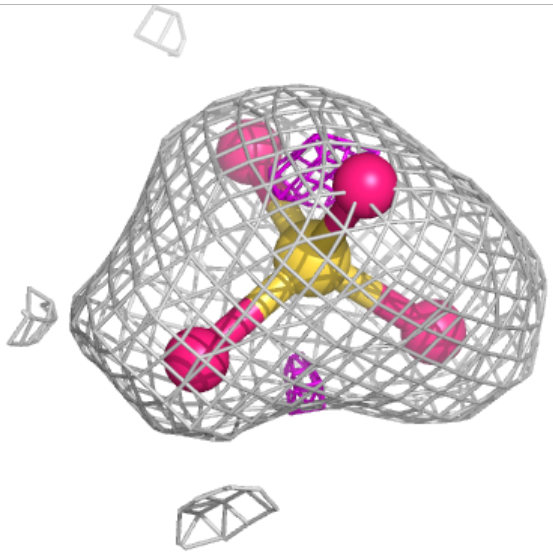


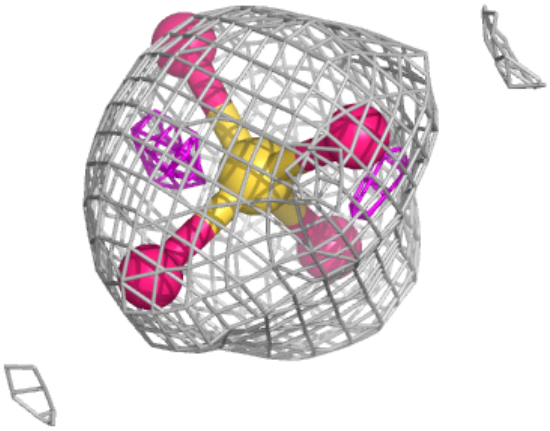


Electron density around SO4 D 206:

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

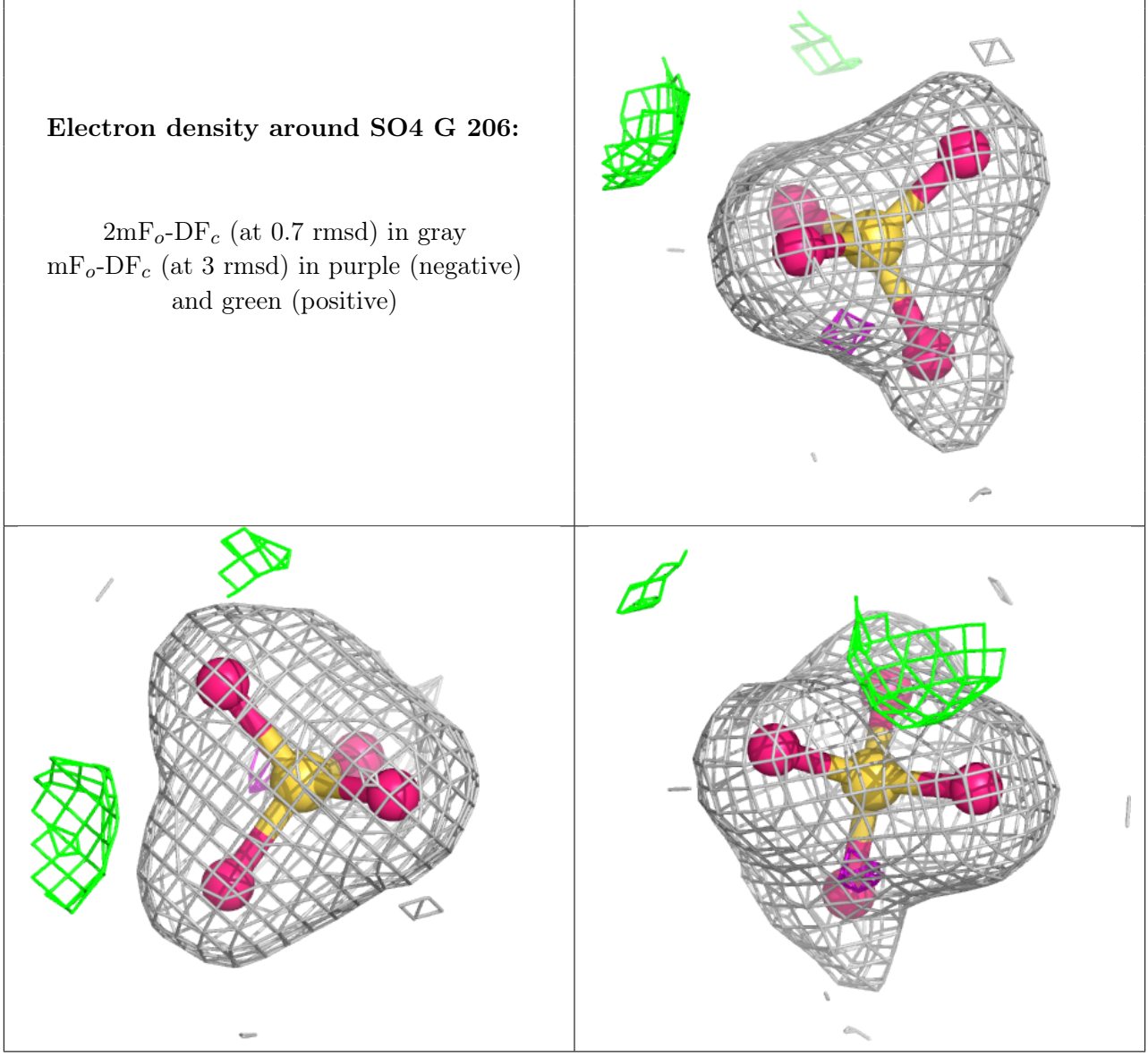






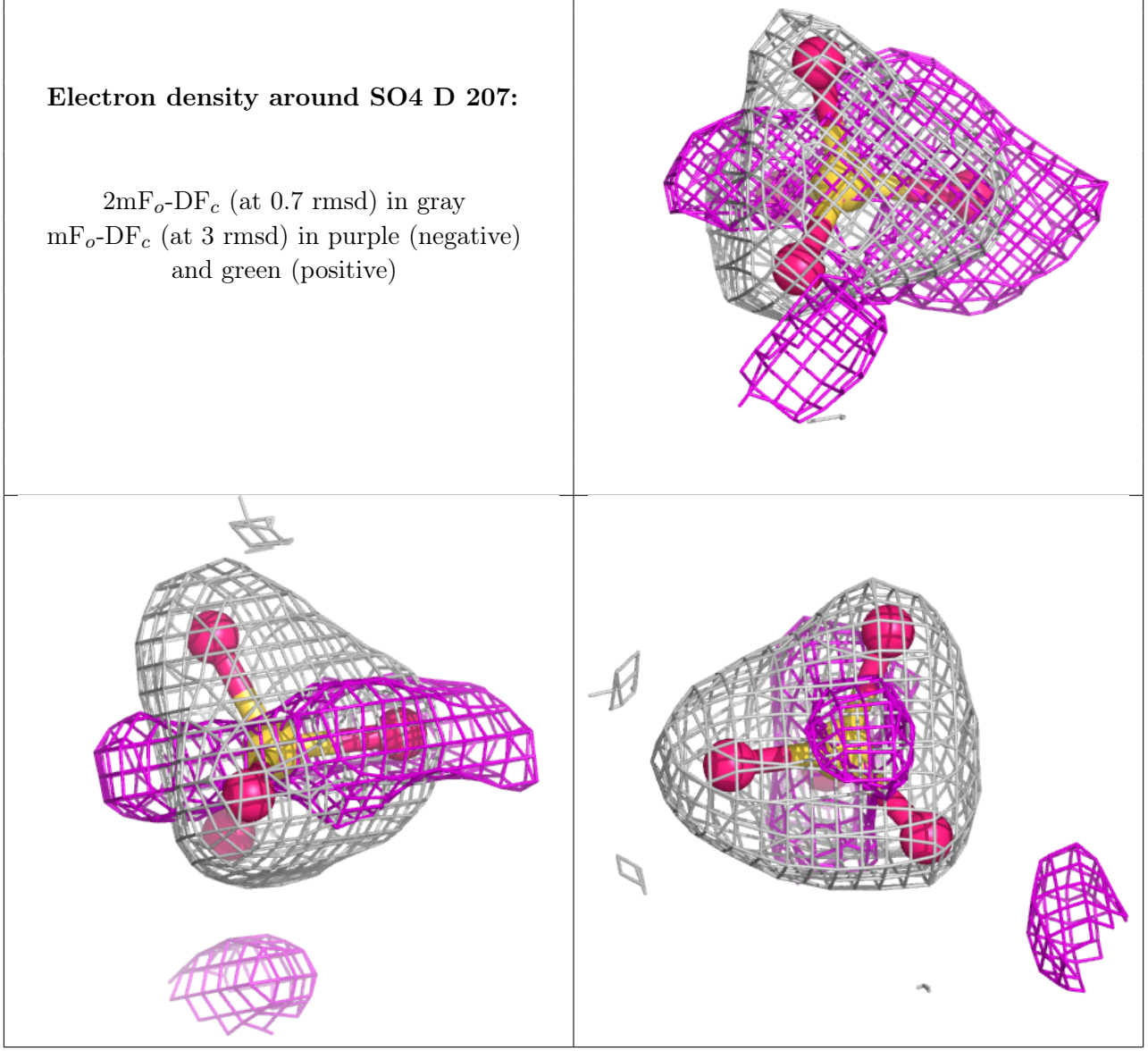
Electron density around SO4 G 206:

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



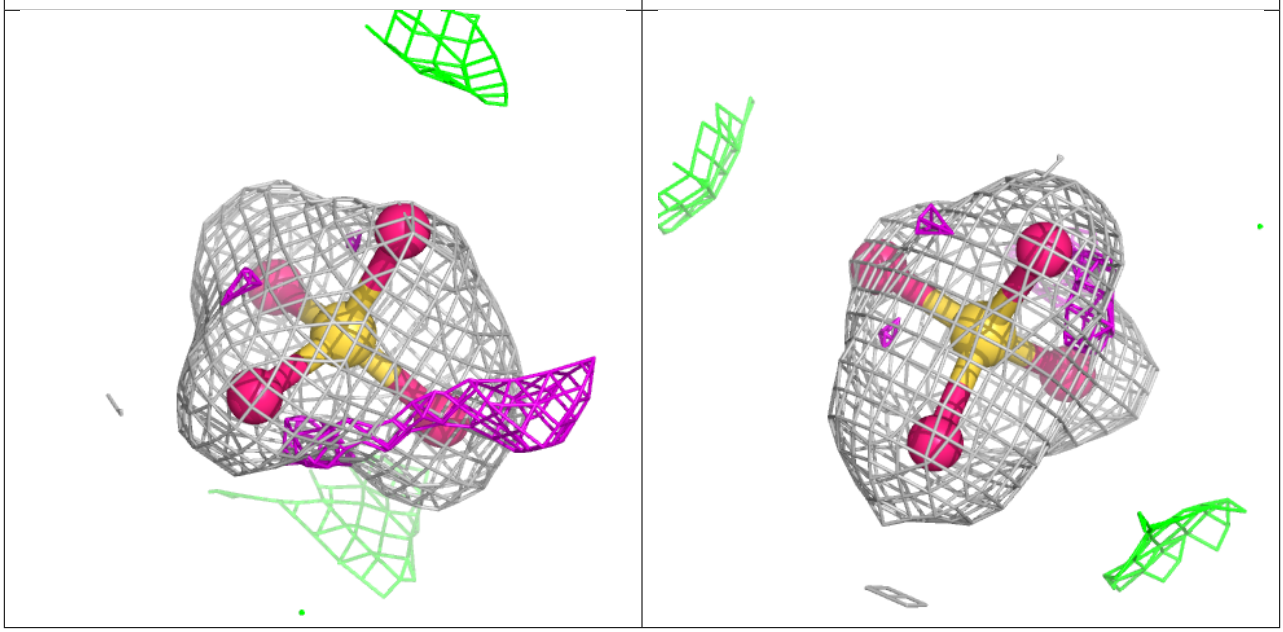
Electron density around SO4 D 207:

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



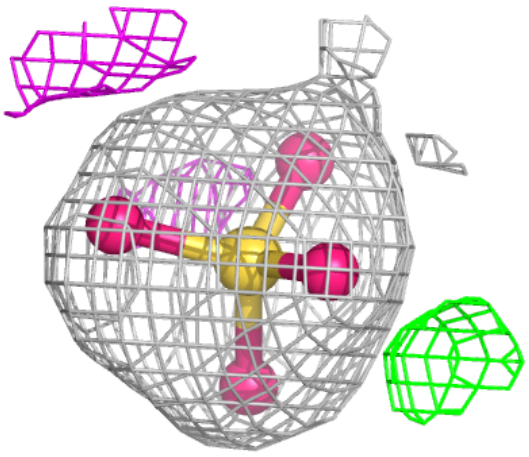
Electron density around SO4 L 204:

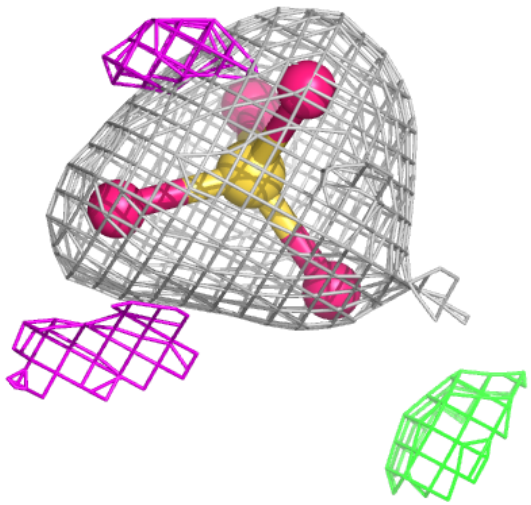
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

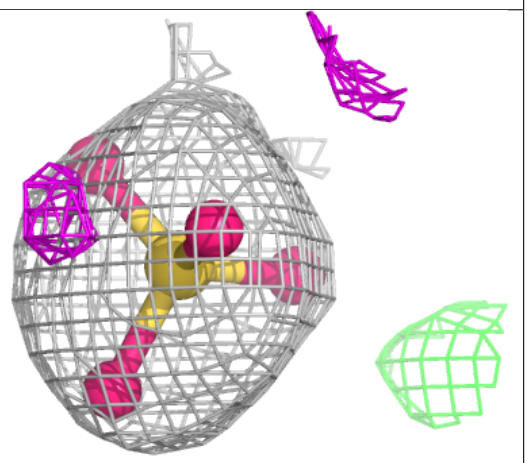


Electron density around SO4 L 205:

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

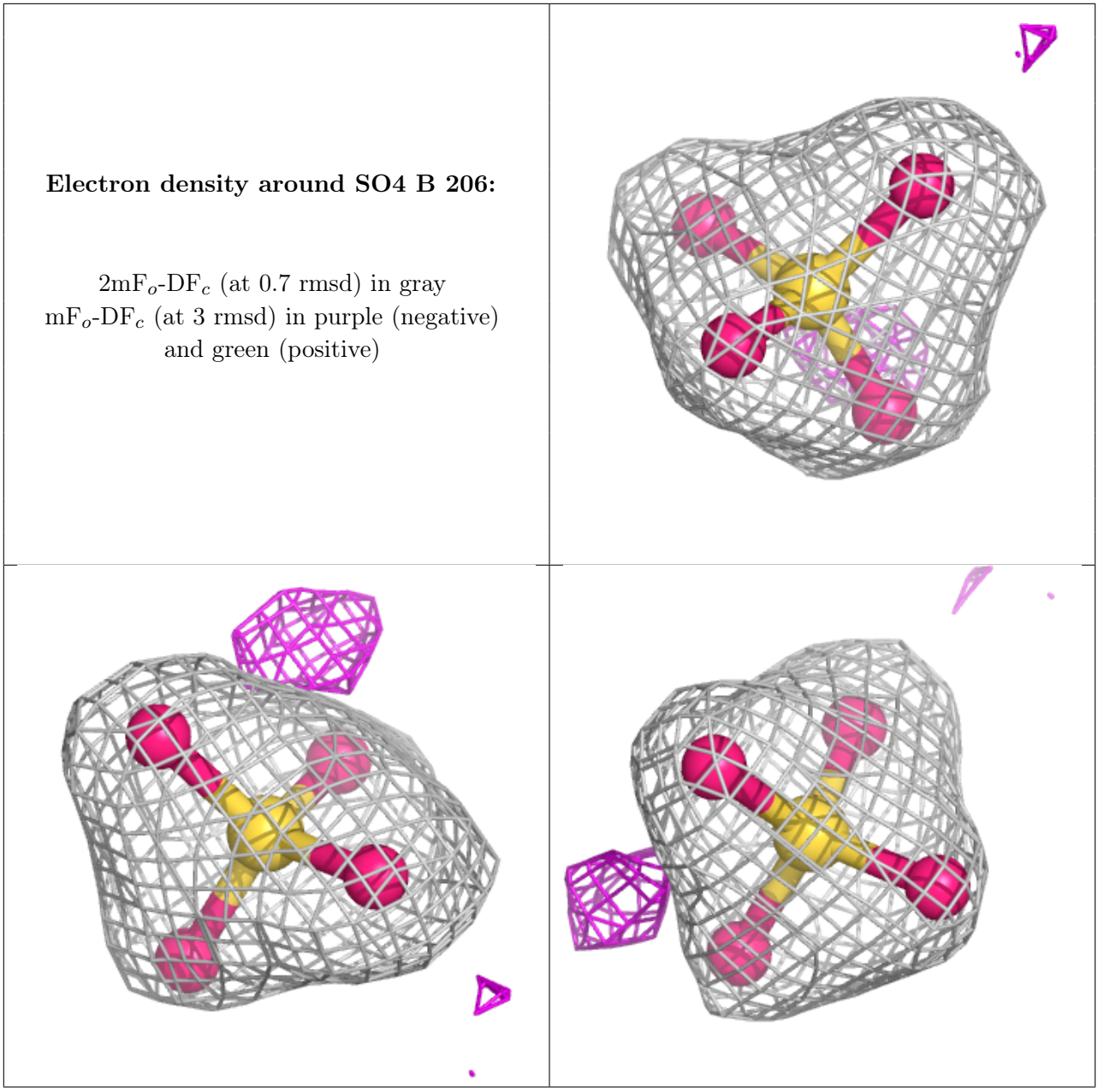






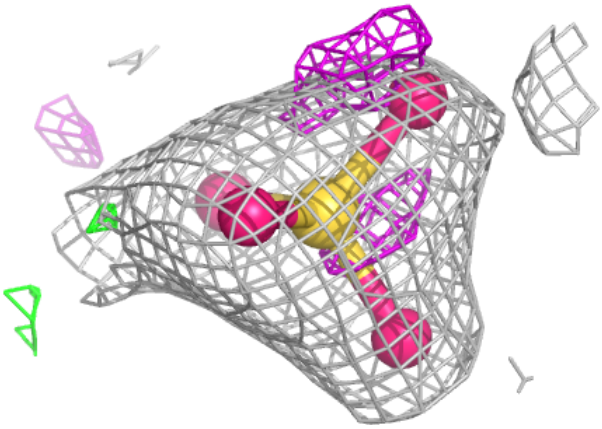
Electron density around SO4 B 206:

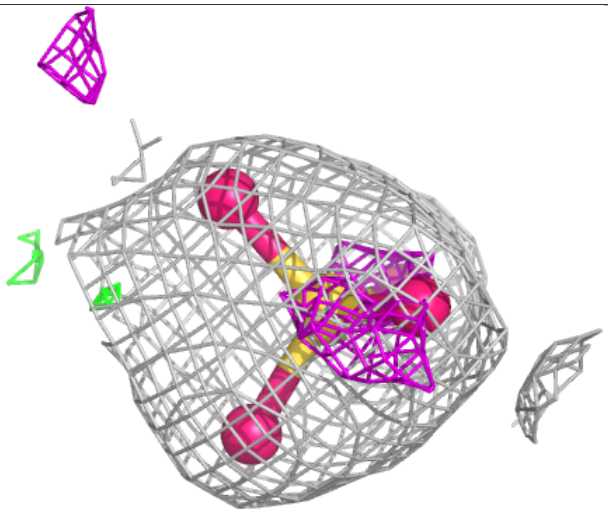
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

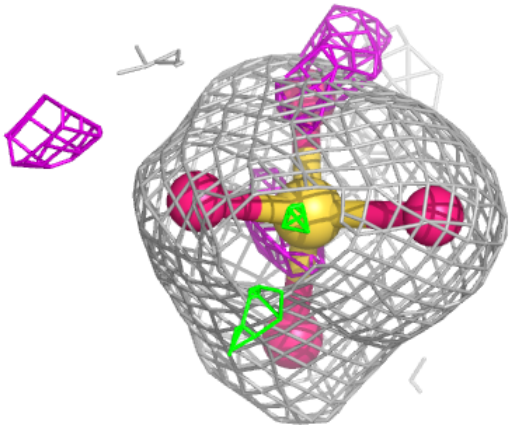


Electron density around SO4 B 207:

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

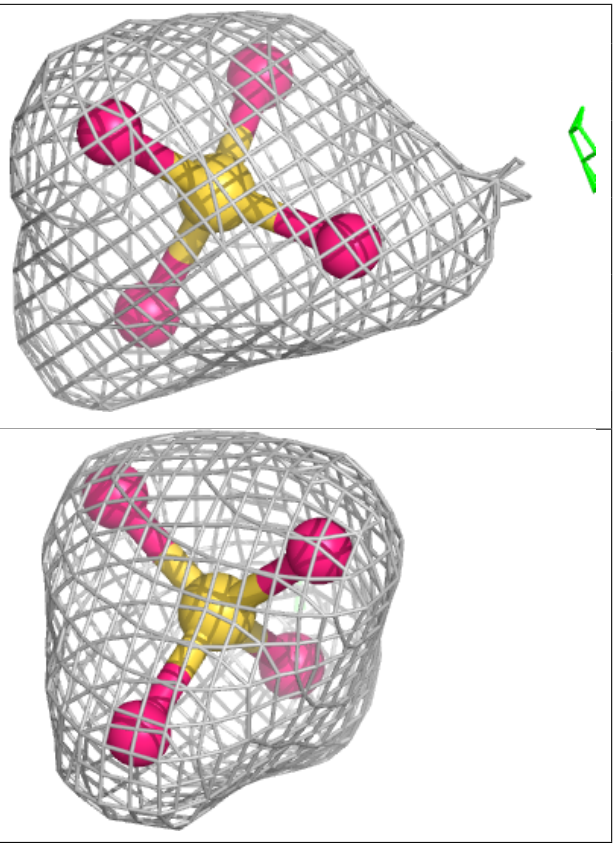


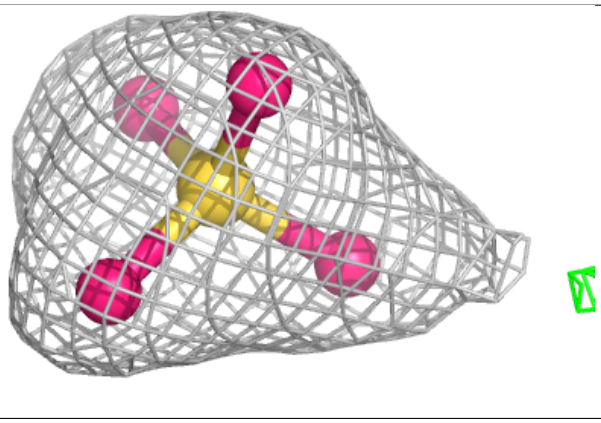




Electron density around SO4 J 203:

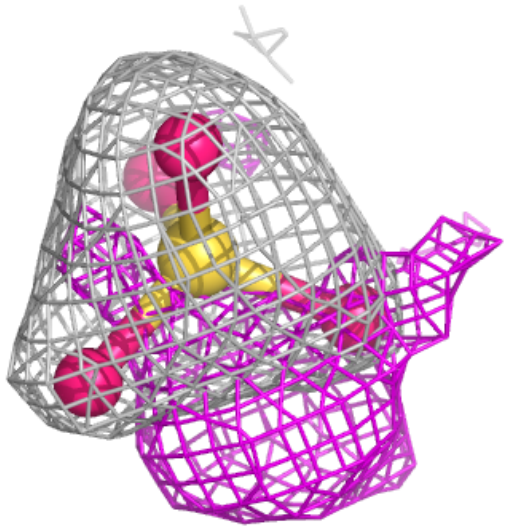
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

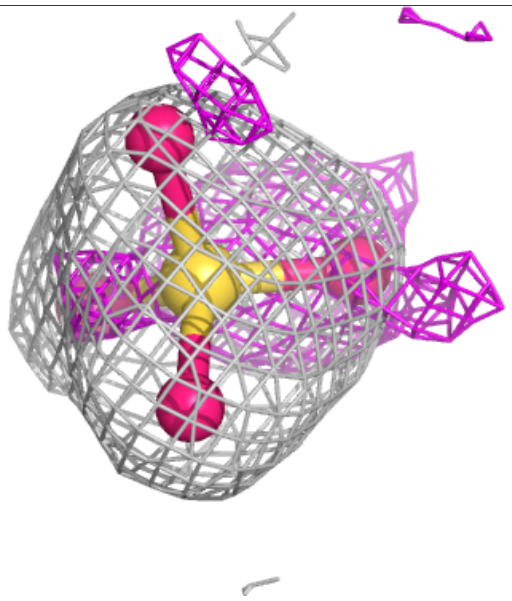


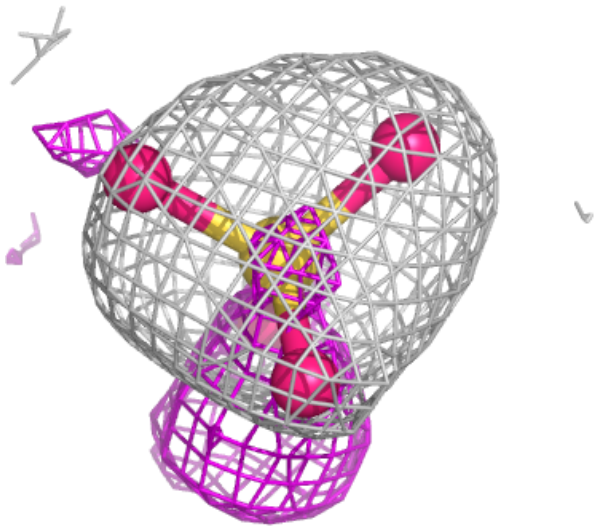


Electron density around SO4 J 204:

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

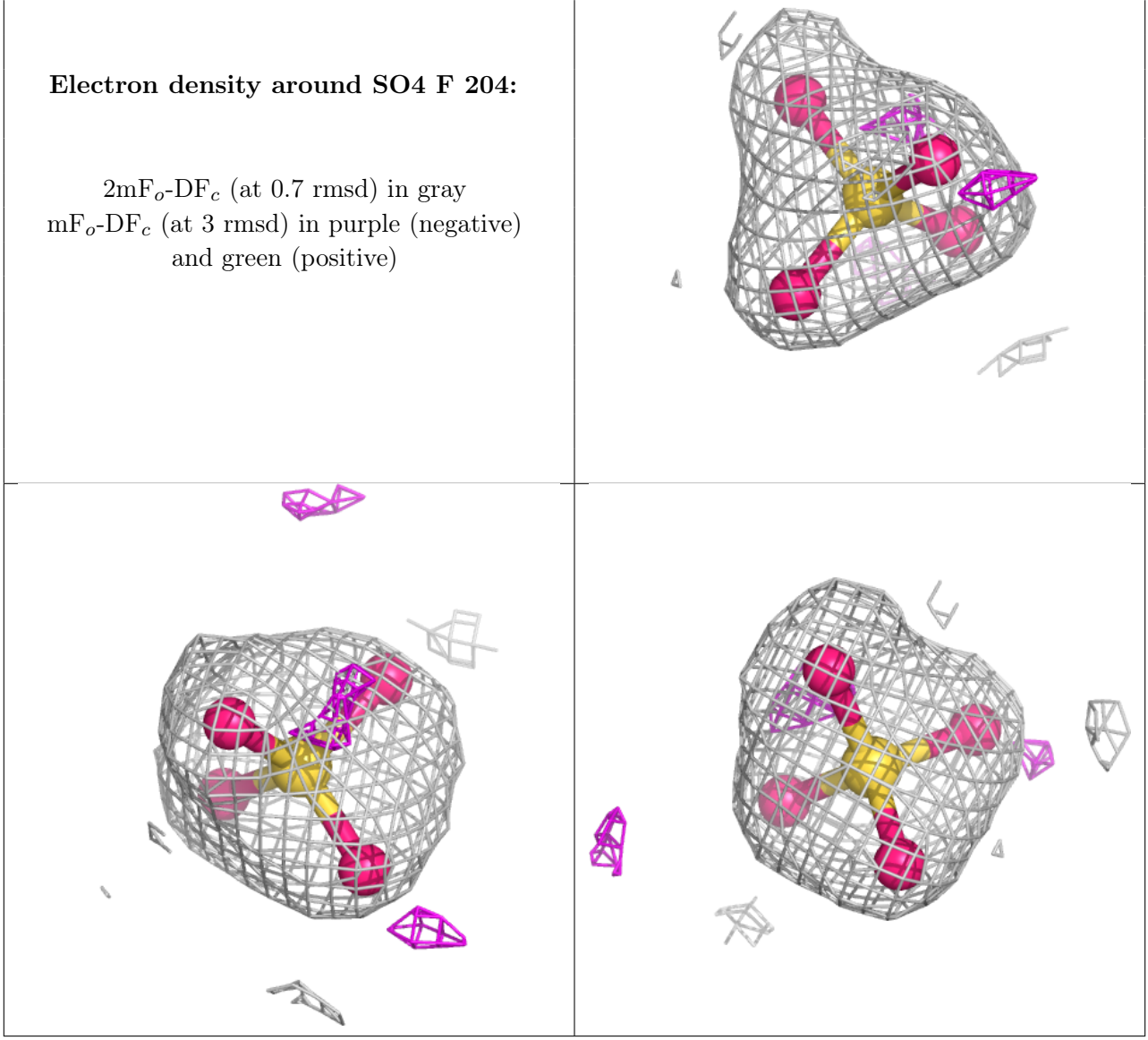






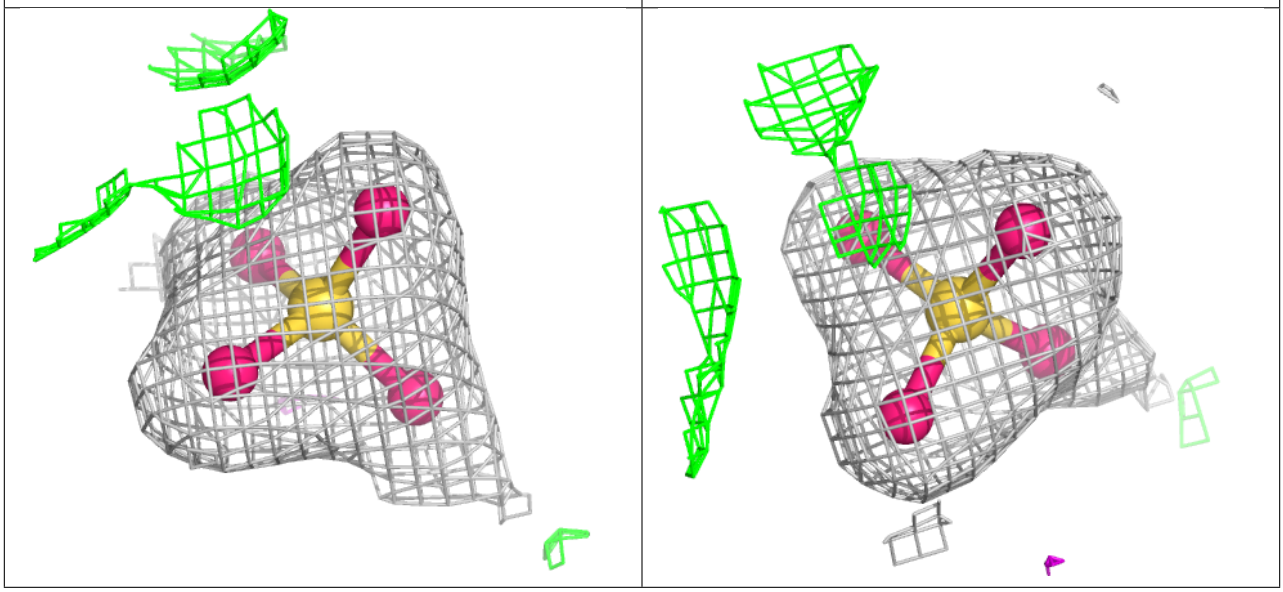
Electron density around SO4 F 204:

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



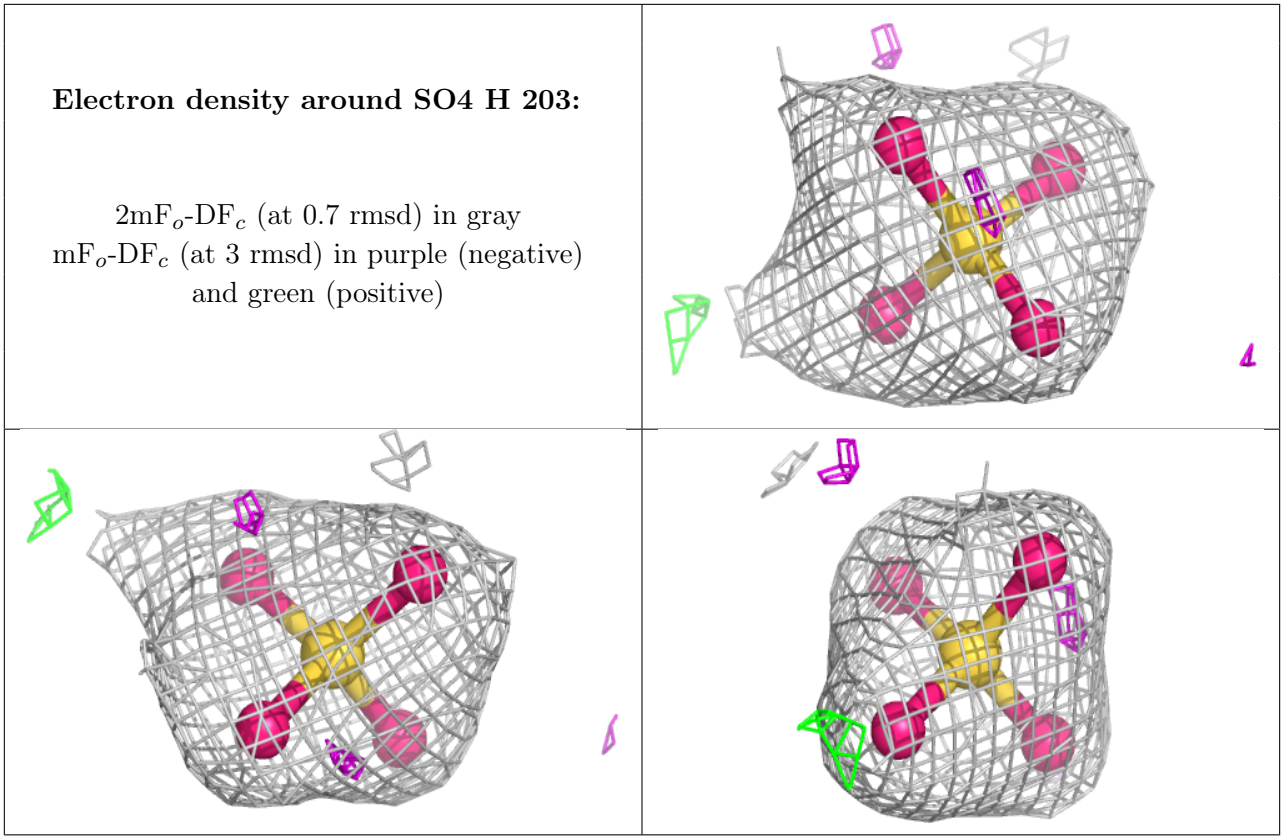
Electron density around SO4 B 208:

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



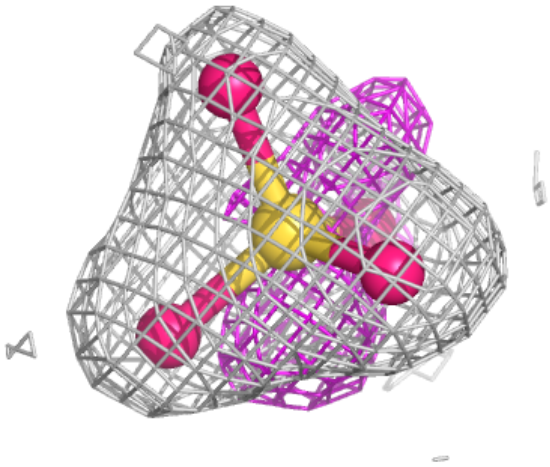
Electron density around SO4 H 203:

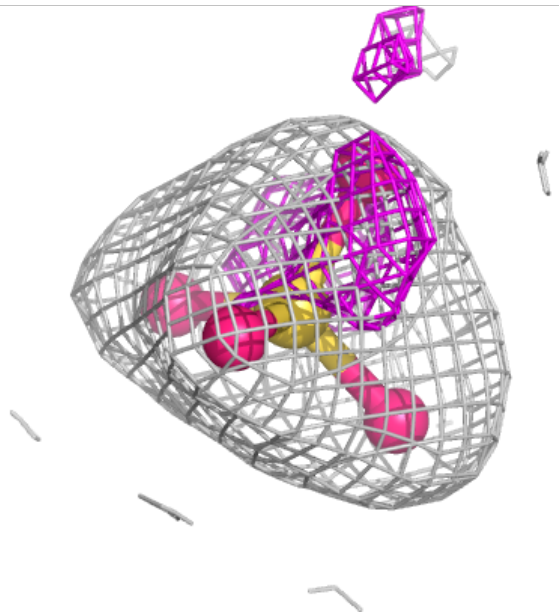
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

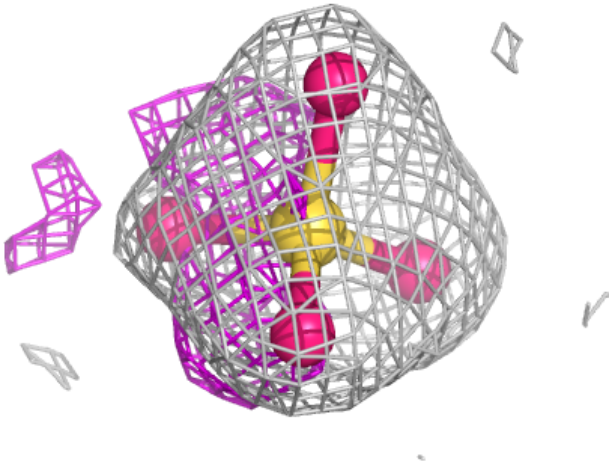


Electron density around SO4 H 204:

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

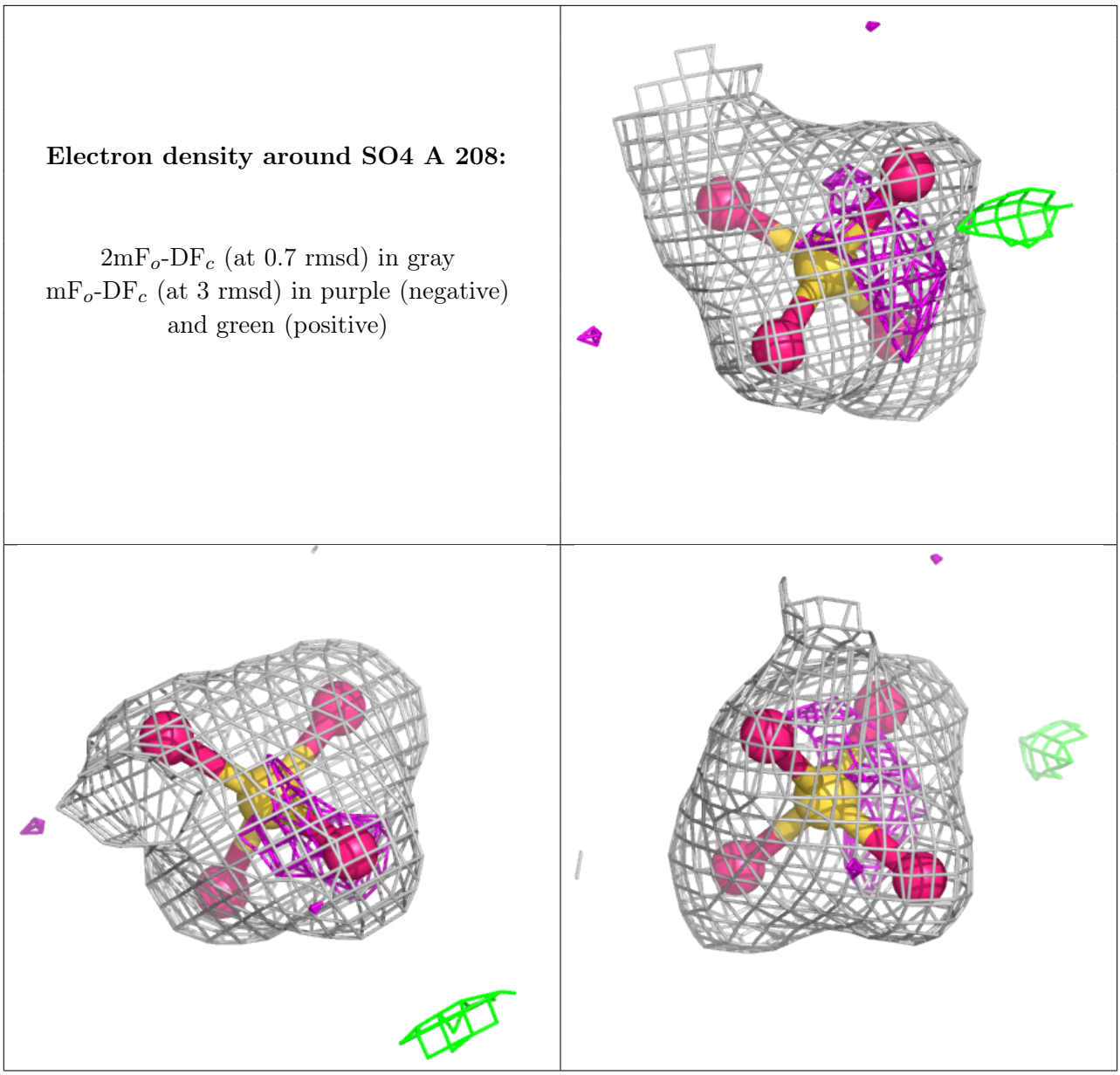






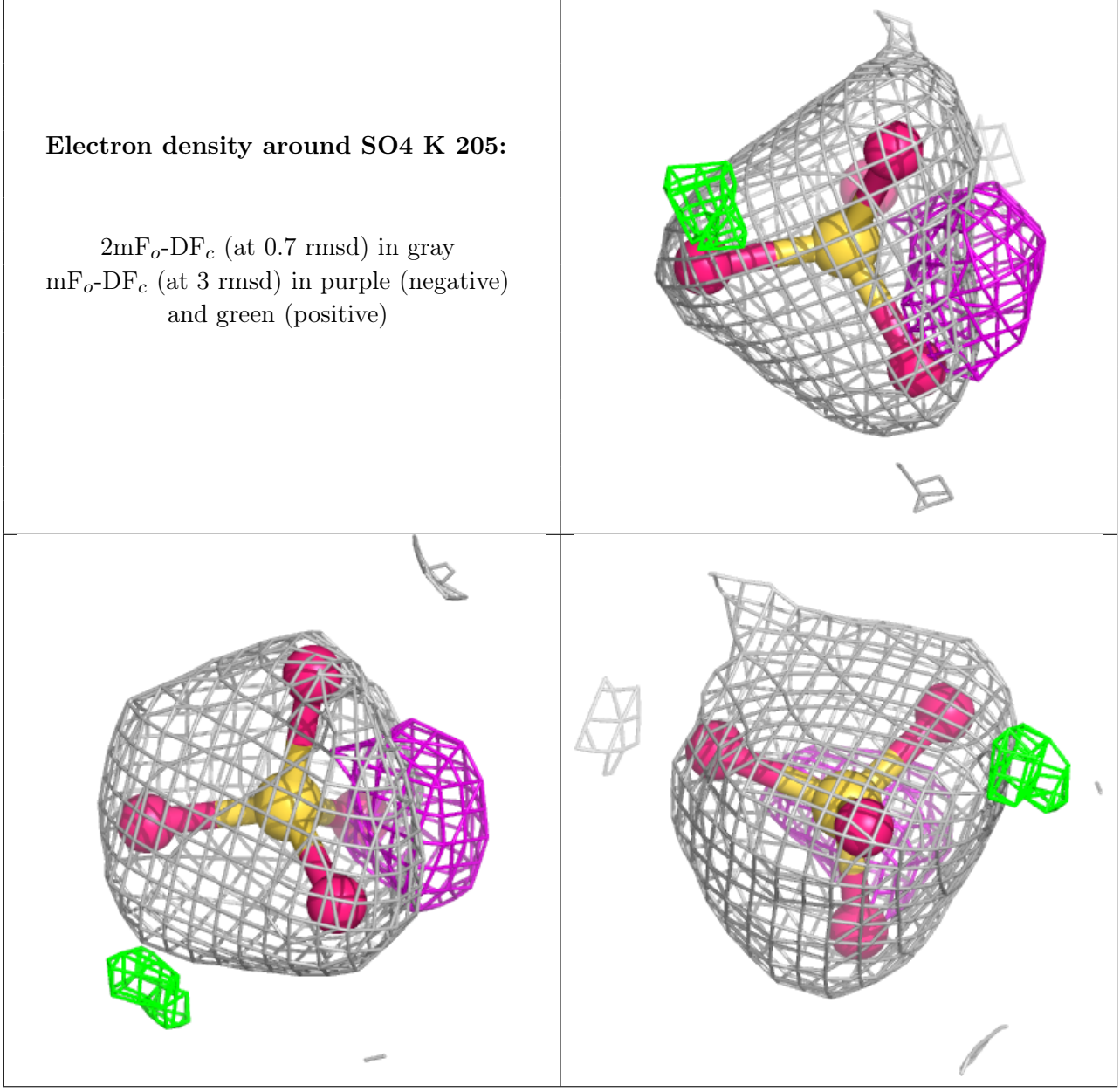
Electron density around SO4 A 208:

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



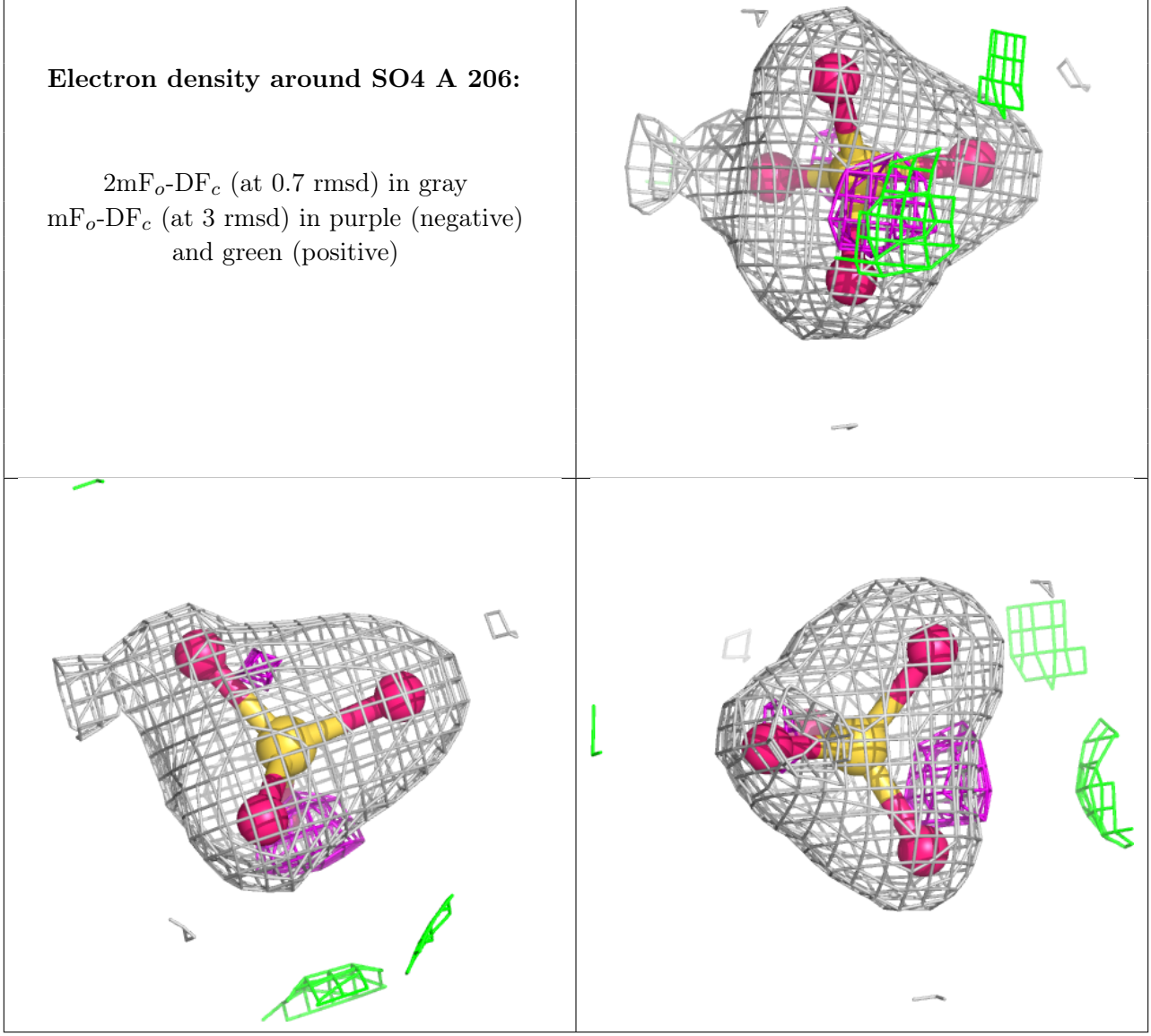
Electron density around SO4 K 205:

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



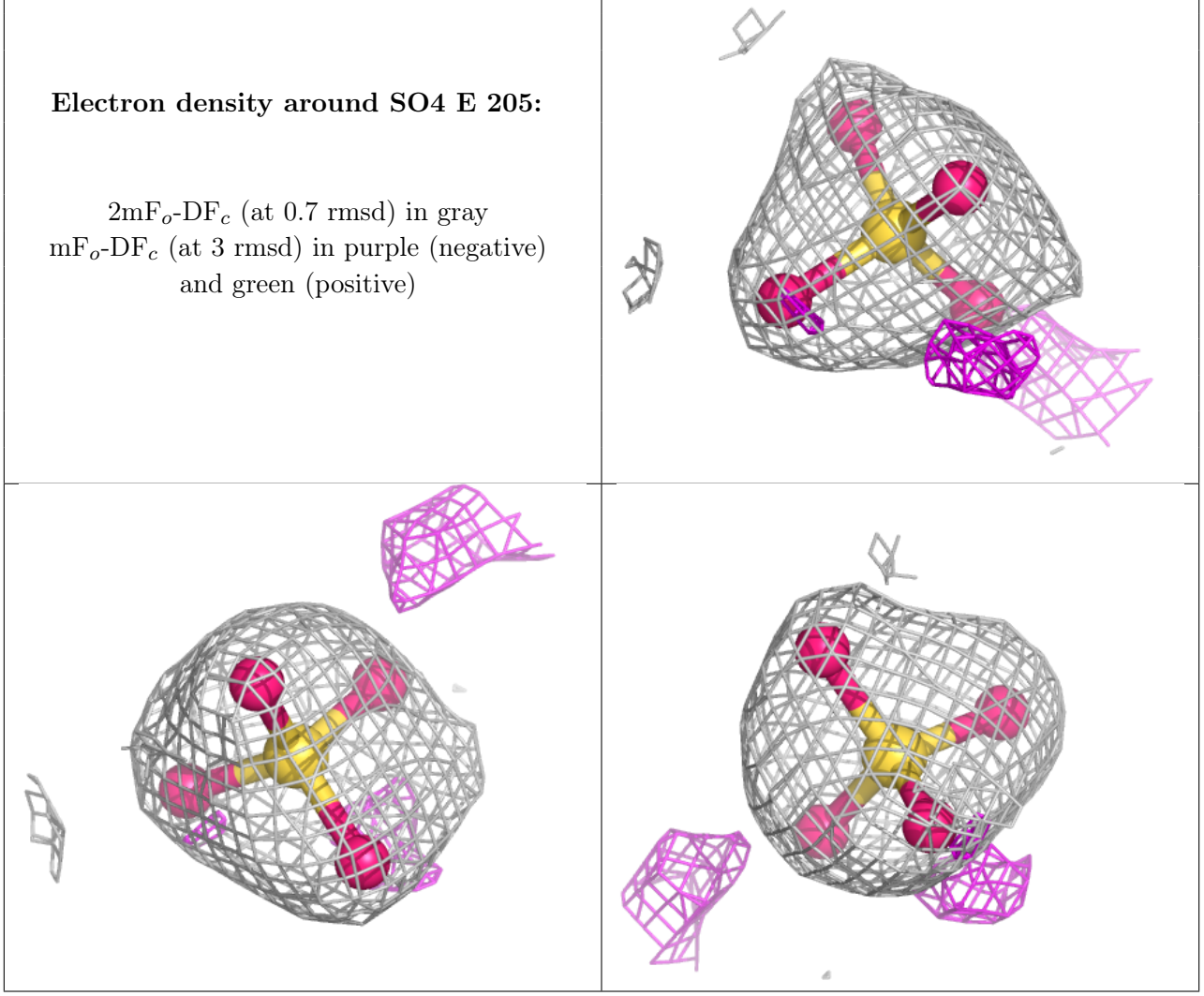
Electron density around SO4 A 206:

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



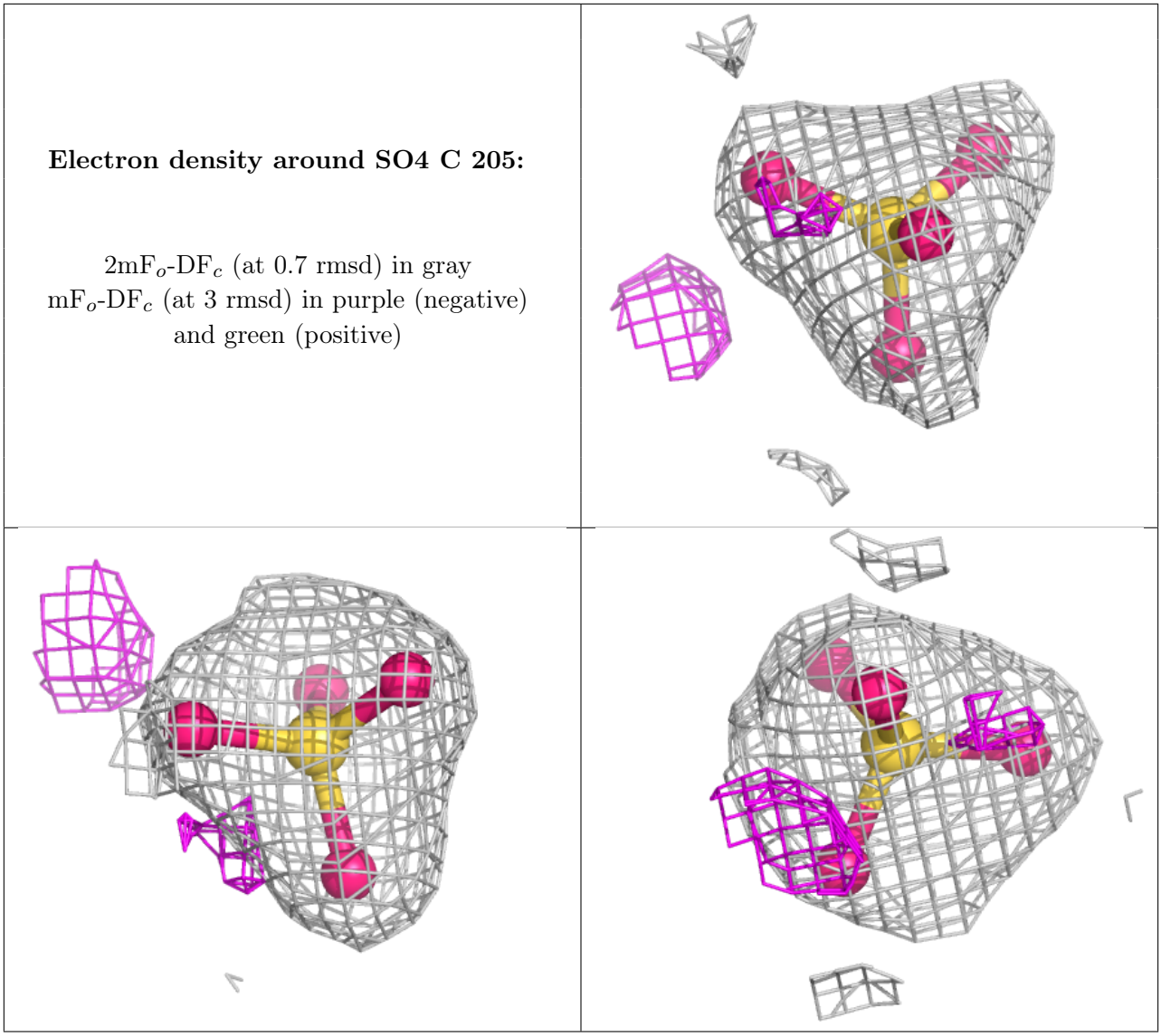
Electron density around SO4 E 205:

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



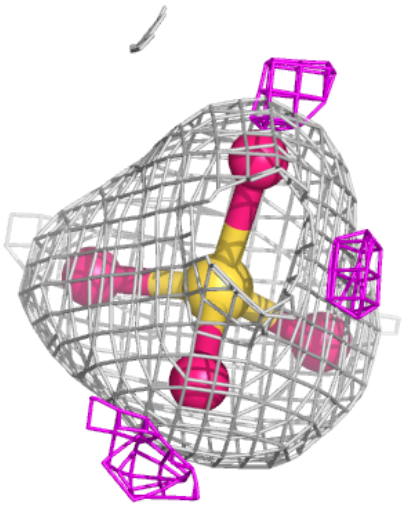
Electron density around SO4 C 205:

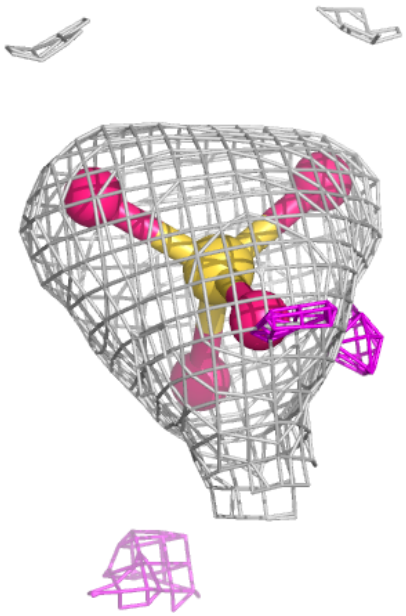
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

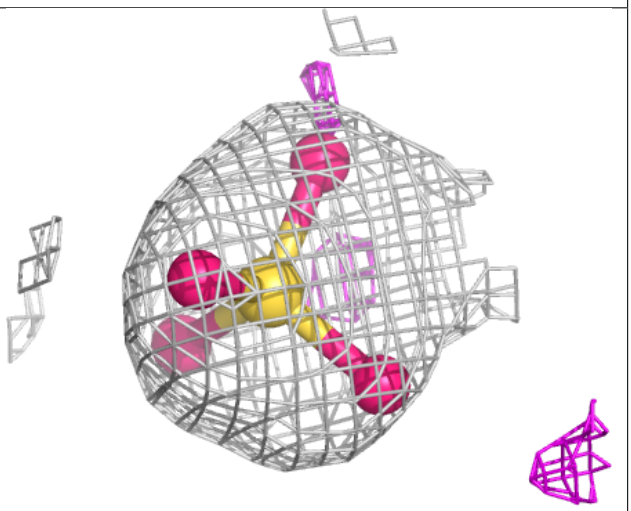


Electron density around SO4 I 204:

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

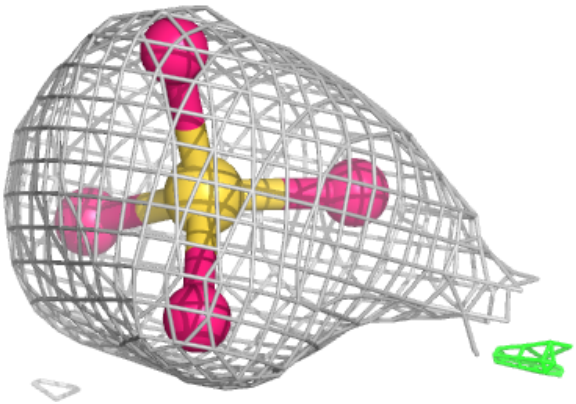


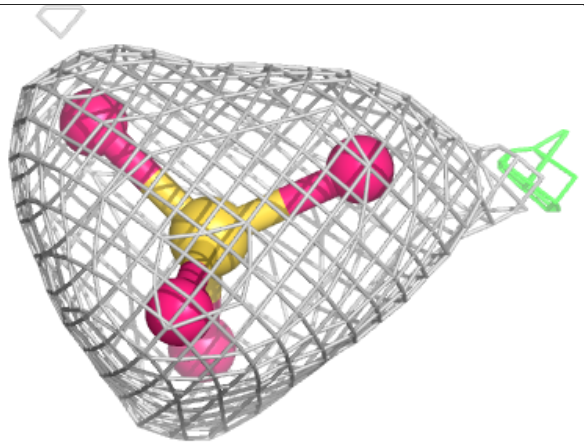


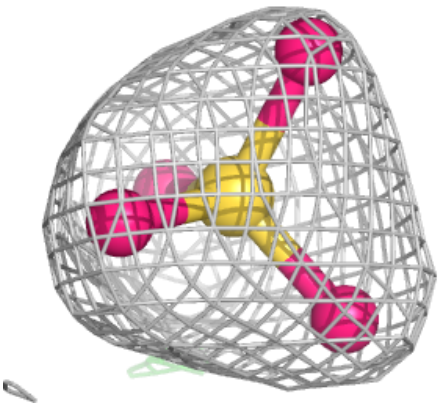


Electron density around SO4 A 203:

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

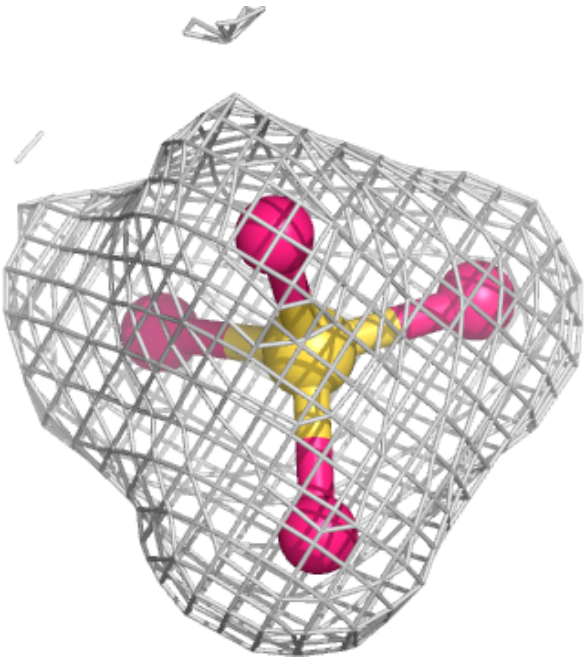


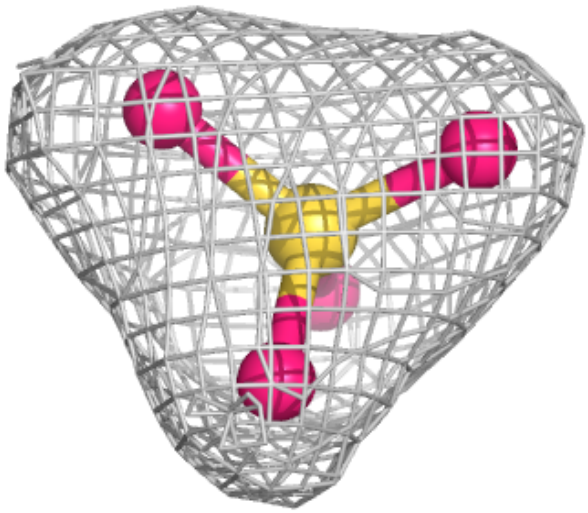


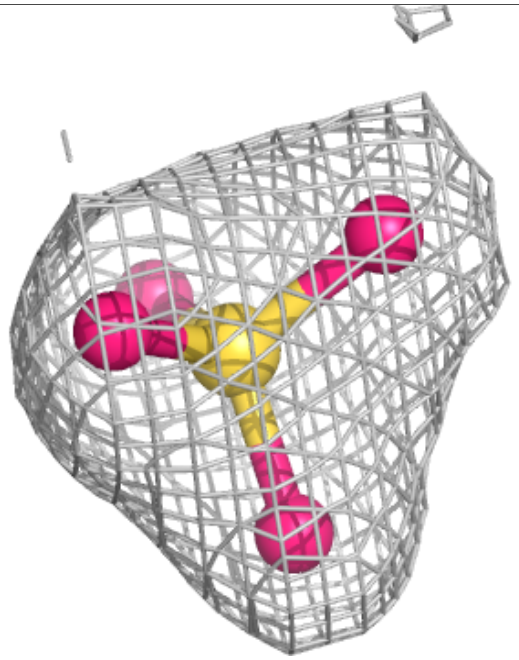


Electron density around SO4 A 204:

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

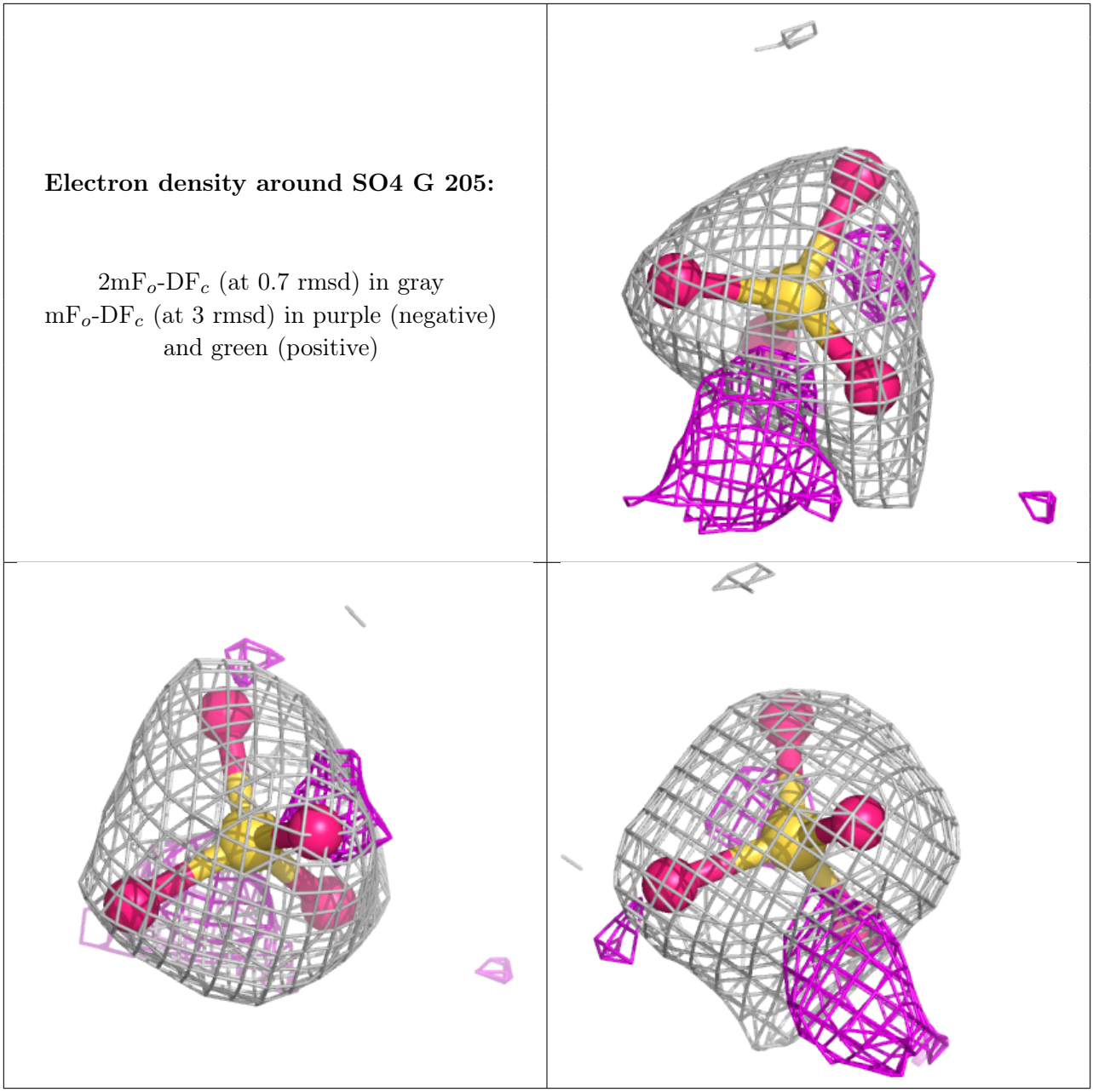






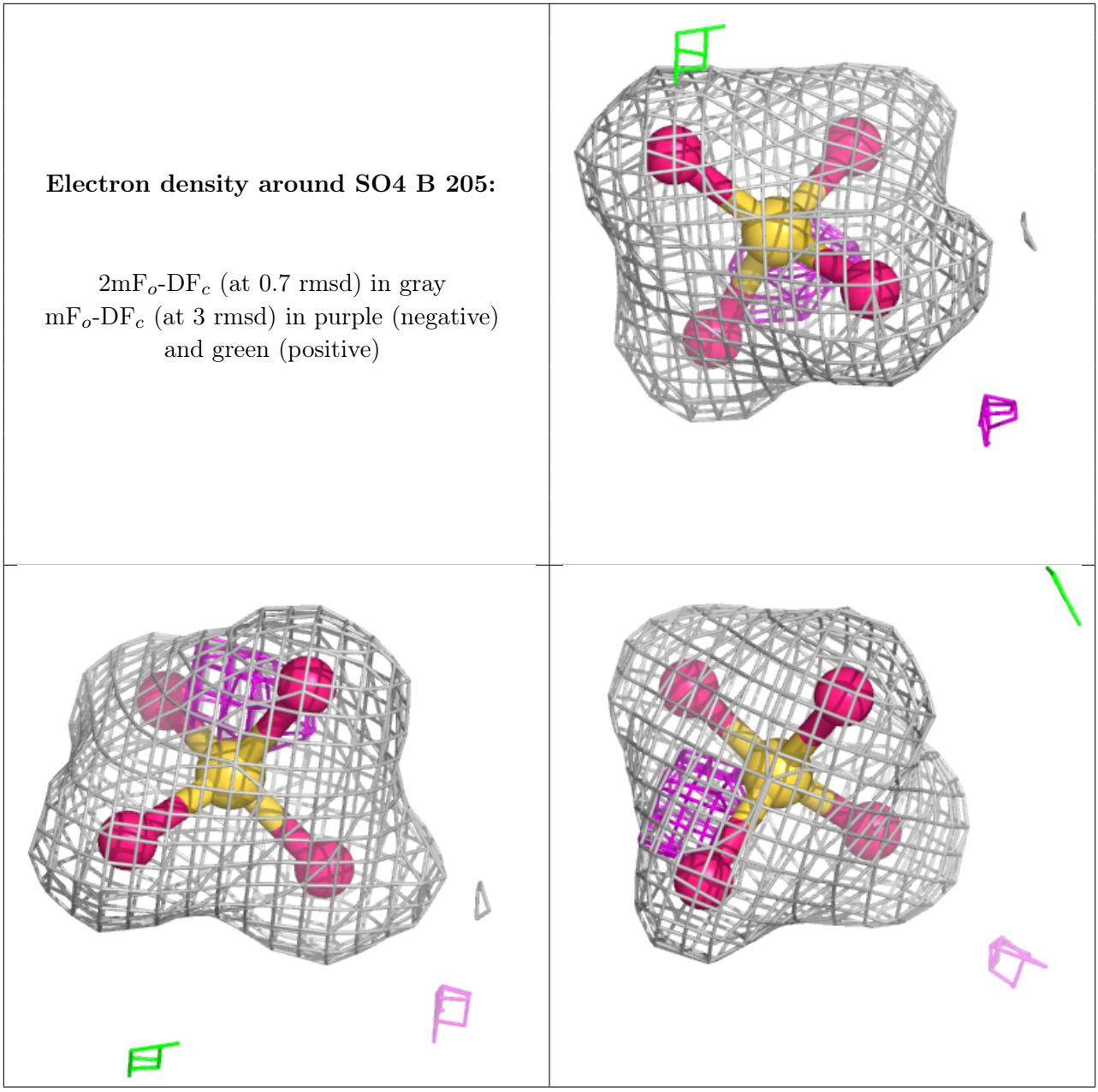
Electron density around SO4 G 205:

$2mF_o$-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 205:

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



6.5 Other polymers

There are no such residues in this entry.