



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 12:03 PM UTC

PDB ID : 8R2V / pdb_00008r2v
Title : Crystal structure of hydroxyquinol-1,2-dioxygenase from *Gelatoporia subvermispora* (GsHDX1)
Authors : Zahn, M.; Kuatsjah, E.; Salvachua, D.
Deposited on : 2023-11-07
Resolution : 1.78 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

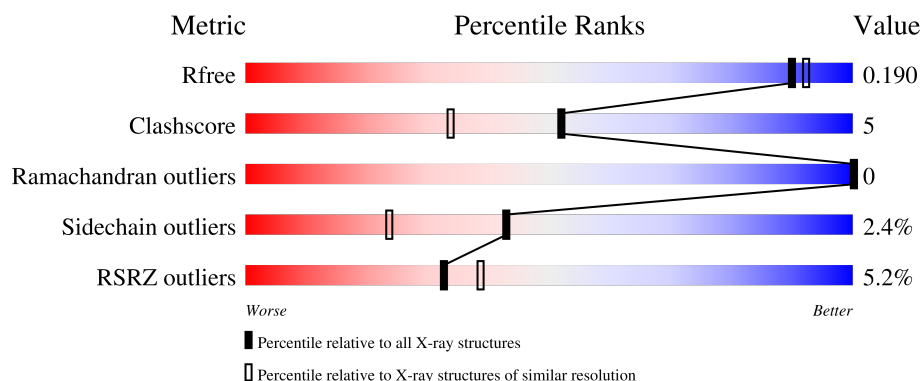
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.78 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1365 (1.78-1.78)
Clashscore	190562	1395 (1.78-1.78)
Ramachandran outliers	187476	1382 (1.78-1.78)
Sidechain outliers	187428	1382 (1.78-1.78)
RSRZ outliers	180081	1365 (1.78-1.78)

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

Mol	Chain	Length	Quality of chain
1	A	348	5% 84% 7% 8%
1	B	348	4% 85% 5% 8%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	403	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5661 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 Intradiol ring-cleavage dioxygenases domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	319	Total	C	N	O	S	0	1	0
			2491	1572	424	488	7			
1	B	319	Total	C	N	O	S	0	3	0
			2500	1578	424	491	7			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	331	ALA	-	expression tag	UNP M2PH20
A	332	GLU	-	expression tag	UNP M2PH20
A	333	ASN	-	expression tag	UNP M2PH20
A	334	LEU	-	expression tag	UNP M2PH20
A	335	TYR	-	expression tag	UNP M2PH20
A	336	PHE	-	expression tag	UNP M2PH20
A	337	GLN	-	expression tag	UNP M2PH20
A	338	GLY	-	expression tag	UNP M2PH20
A	339	HIS	-	expression tag	UNP M2PH20
A	340	HIS	-	expression tag	UNP M2PH20
A	341	HIS	-	expression tag	UNP M2PH20
A	342	HIS	-	expression tag	UNP M2PH20
A	343	HIS	-	expression tag	UNP M2PH20
A	344	HIS	-	expression tag	UNP M2PH20
A	345	HIS	-	expression tag	UNP M2PH20
A	346	HIS	-	expression tag	UNP M2PH20
A	347	HIS	-	expression tag	UNP M2PH20
A	348	HIS	-	expression tag	UNP M2PH20
B	331	ALA	-	expression tag	UNP M2PH20
B	332	GLU	-	expression tag	UNP M2PH20
B	333	ASN	-	expression tag	UNP M2PH20
B	334	LEU	-	expression tag	UNP M2PH20
B	335	TYR	-	expression tag	UNP M2PH20
B	336	PHE	-	expression tag	UNP M2PH20
B	337	GLN	-	expression tag	UNP M2PH20

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Chain	Residue	Modelled	Actual	Comment	Reference
B	338	GLY	-	expression tag	UNP M2PH20
B	339	HIS	-	expression tag	UNP M2PH20
B	340	HIS	-	expression tag	UNP M2PH20
B	341	HIS	-	expression tag	UNP M2PH20
B	342	HIS	-	expression tag	UNP M2PH20
B	343	HIS	-	expression tag	UNP M2PH20
B	344	HIS	-	expression tag	UNP M2PH20
B	345	HIS	-	expression tag	UNP M2PH20
B	346	HIS	-	expression tag	UNP M2PH20
B	347	HIS	-	expression tag	UNP M2PH20
B	348	HIS	-	expression tag	UNP M2PH20

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S) (labeled as "Ligand of Interest" by depositor).



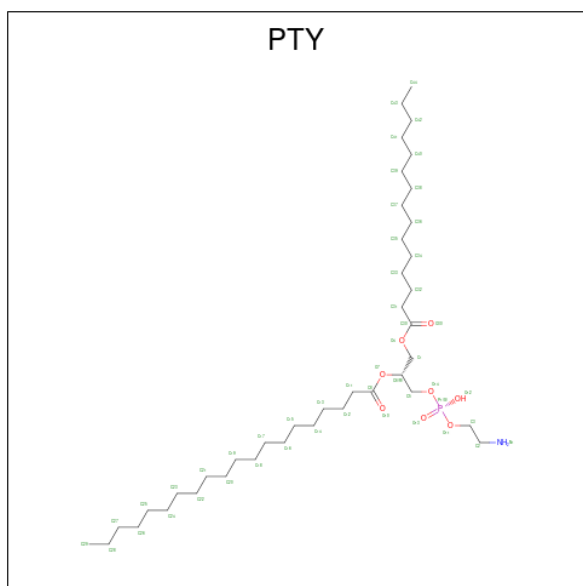
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0

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

- Molecule 3 is PHOSPHATIDYLETHANOLAMINE (CCD ID: PTY) (formula: $C_{40}H_{80}NO_8P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			50	40	1	8	1		
3	B	1	Total	C	N	O	P	0	0
			50	40	1	8	1		

- Molecule 4 is FE (III) ION (CCD ID: FE) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Fe	0	0
			1	1		
4	B	1	Total	Fe	0	0
			1	1		

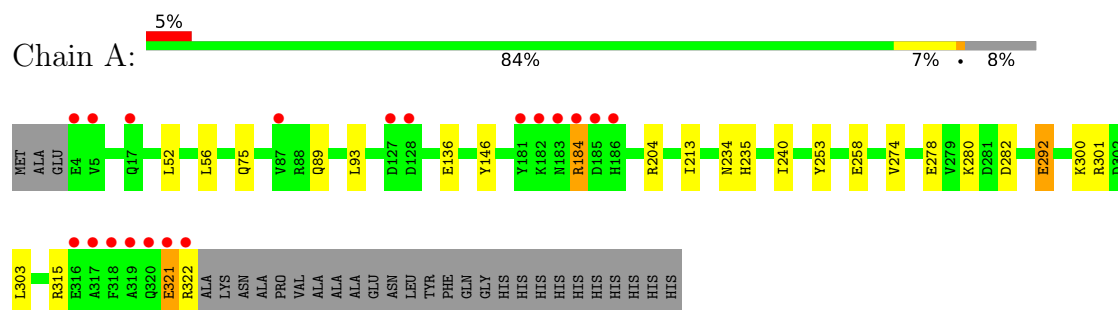
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	250	Total 250	O 250	0	0
5	B	273	Total 273	O 273	0	0

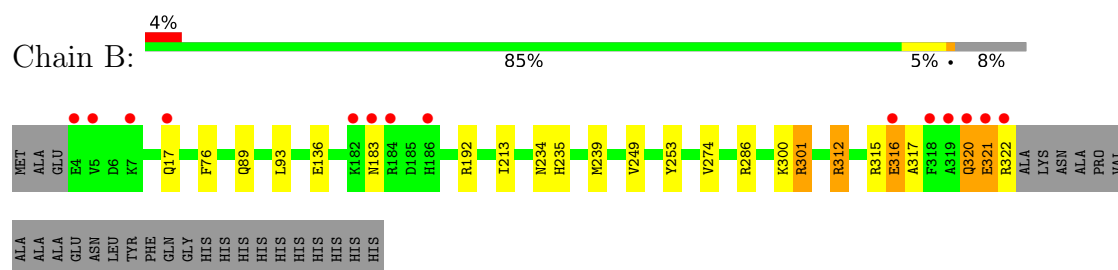
3 Residue-property plots

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

- Molecule 1: Intradiol ring-cleavage dioxygenases domain-containing protein



- Molecule 1: Intradiol ring-cleavage dioxygenases domain-containing protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	48.43Å 148.66Å 157.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	108.19 – 1.78 108.19 – 1.78	Depositor EDS
% Data completeness (in resolution range)	71.8 (108.19-1.78) 71.8 (108.19-1.78)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.85 (at 1.77Å)	Xtriage
Refinement program	REFMAC 5.8.0411	Depositor
R, R_{free}	0.173 , 0.197 (Not available) , 0.190	Depositor DCC
R_{free} test set	3939 reflections (3.56%)	wwPDB-VP
Wilson B-factor (Å ²)	23.9	Xtriage
Anisotropy	0.005	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 35.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5661	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.69% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PTY, SO4, FE

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.69	0/2552	0.97	1/3474 (0.0%)
1	B	0.68	0/2567	0.96	0/3494
All	All	0.69	0/5119	0.97	1/6968 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	3
All	All	0	5

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	282	ASP	CA-CB-CG	5.30	117.90	112.60

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	315	ARG	Sidechain
1	A	322	ARG	Sidechain
1	B	286	ARG	Sidechain
1	B	312	ARG	Sidechain
1	B	315	ARG	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2491	0	2436	16	0
1	B	2500	0	2447	22	0
2	A	25	0	0	2	0
2	B	20	0	0	1	0
3	A	50	0	79	10	0
3	B	50	0	79	17	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	250	0	0	4	0
5	B	273	0	0	5	0
All	All	5661	0	5041	52	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 5.

All (52) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:136[B]:GLU:OE1	5:B:501:HOH:O	1.79	0.97
3:A:404:PTY:H211	3:B:401:PTY:H292	1.59	0.85
2:B:403:SO4:O2	5:B:502:HOH:O	1.96	0.81
1:A:184:ARG:HB2	5:A:510:HOH:O	1.83	0.76
3:B:401:PTY:HC11	3:B:401:PTY:P1	2.28	0.73
1:A:136:GLU:HG2	2:A:403:SO4:O1	1.89	0.72
3:A:404:PTY:H211	3:B:401:PTY:C29	2.19	0.71
1:B:17[B]:GLN:NE2	5:B:504:HOH:O	2.27	0.67
1:B:76:PHE:CD2	3:B:401:PTY:H171	2.31	0.66
1:B:322:ARG:HG3	1:B:322:ARG:HH11	1.59	0.65
1:B:312:ARG:O	1:B:316:GLU:HG3	2.00	0.61
1:A:75:GLN:OE1	5:A:501:HOH:O	2.17	0.59
3:A:404:PTY:H442	3:B:401:PTY:H421	1.84	0.59
1:B:312:ARG:HD3	5:B:507:HOH:O	2.05	0.57
1:B:322:ARG:HG3	1:B:322:ARG:NH1	2.23	0.53
1:A:93:LEU:HD11	1:A:213:ILE:HD12	1.91	0.52
1:B:76:PHE:CD1	3:B:401:PTY:H151	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:146:TYR:OH	1:A:292:GLU:HG2	2.10	0.52
1:A:301:ARG:NH1	5:A:506:HOH:O	2.43	0.51
1:B:320:GLN:N	1:B:320:GLN:HE21	2.07	0.51
3:A:404:PTY:C44	3:B:401:PTY:H421	2.40	0.51
3:B:401:PTY:HC12	3:B:401:PTY:H141	1.93	0.51
1:B:274:VAL:HG12	1:B:301:ARG:CZ	2.41	0.50
1:B:317:ALA:O	1:B:320:GLN:HB2	2.12	0.50
1:B:320:GLN:NE2	1:B:320:GLN:CA	2.74	0.49
1:B:301:ARG:CG	1:B:301:ARG:HH11	2.26	0.49
3:A:404:PTY:C21	3:B:401:PTY:H292	2.35	0.48
3:A:404:PTY:H441	3:B:401:PTY:H401	1.96	0.47
3:B:401:PTY:HC11	3:B:401:PTY:O11	2.15	0.47
1:A:56:LEU:HD12	3:A:404:PTY:H251	1.96	0.46
1:A:204:ARG:NH2	2:A:403:SO4:O2	2.43	0.46
1:B:320:GLN:NE2	1:B:320:GLN:HA	2.31	0.46
3:B:401:PTY:P1	3:B:401:PTY:C1	3.02	0.46
1:A:274:VAL:HG12	1:A:301:ARG:NH2	2.31	0.46
1:B:93:LEU:HD11	1:B:213:ILE:HD12	1.98	0.45
1:A:52:LEU:HD22	3:B:401:PTY:H362	1.97	0.45
1:B:274:VAL:HG12	1:B:301:ARG:NH2	2.33	0.45
1:A:278:GLU:OE1	1:A:280:LYS:HE2	2.17	0.44
1:B:183:ASN:C	1:B:183:ASN:OD1	2.60	0.44
1:B:192:ARG:HD2	5:B:703:HOH:O	2.18	0.44
3:A:404:PTY:H293	3:B:401:PTY:H431	2.01	0.43
3:A:404:PTY:C44	3:B:401:PTY:C42	2.97	0.42
1:B:321:GLU:N	1:B:321:GLU:OE2	2.52	0.42
1:A:274:VAL:HG12	1:A:301:ARG:CZ	2.49	0.42
1:A:235:HIS:HB3	1:A:253:TYR:CD2	2.54	0.42
1:B:239:MET:HE2	1:B:249:VAL:HG22	2.00	0.42
1:B:76:PHE:CD1	3:B:401:PTY:H121	2.55	0.42
3:A:404:PTY:H442	3:B:401:PTY:C42	2.49	0.41
1:A:321:GLU:N	1:A:321:GLU:OE2	2.54	0.41
1:B:235:HIS:HB3	1:B:253:TYR:CD2	2.55	0.41
1:A:240:ILE:HG12	1:A:303:LEU:HD13	2.03	0.40
1:A:258:GLU:HG2	5:A:674:HOH:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	318/348 (91%)	311 (98%)	7 (2%)	0	100	100
1	B	320/348 (92%)	313 (98%)	7 (2%)	0	100	100
All	All	638/696 (92%)	624 (98%)	14 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	275/296 (93%)	269 (98%)	6 (2%)	45	26
1	B	277/296 (94%)	270 (98%)	7 (2%)	42	22
All	All	552/592 (93%)	539 (98%)	13 (2%)	43	24

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	89	GLN
1	A	184	ARG
1	A	234	ASN
1	A	292	GLU
1	A	300	LYS
1	A	321	GLU
1	B	89	GLN
1	B	234	ASN

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Mol	Chain	Res	Type
1	B	300	LYS
1	B	301	ARG
1	B	316	GLU
1	B	320	GLN
1	B	321	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	225	GLN
1	B	246	ASN
1	B	320	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 2 are monoatomic - leaving 11 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	$\# Z > 2$
2	SO4	B	404	-	4,4,4	0.27	0	6,6,6	0.07	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	B	405	-	4,4,4	0.31	0	6,6,6	0.15	0
2	SO4	A	402	-	4,4,4	0.34	0	6,6,6	0.13	0
2	SO4	A	405	-	4,4,4	0.28	0	6,6,6	0.14	0
3	PTY	B	401	-	49,49,49	0.42	0	52,54,54	0.77	2 (3%)
2	SO4	B	402	-	4,4,4	0.29	0	6,6,6	0.13	0
2	SO4	A	401	-	4,4,4	0.34	0	6,6,6	0.22	0
2	SO4	A	403	-	4,4,4	0.28	0	6,6,6	0.20	0
3	PTY	A	404	-	49,49,49	0.44	0	52,54,54	0.58	0
2	SO4	A	406	-	4,4,4	0.47	0	6,6,6	0.48	0
2	SO4	B	403	-	4,4,4	0.32	0	6,6,6	0.15	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PTY	A	404	-	-	30/53/53/53	-
3	PTY	B	401	-	-	22/53/53/53	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	401	PTY	O7-C8-C11	-3.19	104.58	111.48
3	B	401	PTY	O4-C1-C6	2.31	115.07	108.40

There are no chirality outliers.

All (52) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	404	PTY	N1-C2-C3-O11
3	A	404	PTY	C5-O14-P1-O11
3	A	404	PTY	C5-O14-P1-O12
3	A	404	PTY	C5-O14-P1-O13
3	B	401	PTY	N1-C2-C3-O11
3	B	401	PTY	C5-O14-P1-O11
3	B	401	PTY	C5-O14-P1-O13
3	A	404	PTY	C23-C24-C25-C26
3	A	404	PTY	C21-C22-C23-C24

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Mol	Chain	Res	Type	Atoms
3	A	404	PTY	C38-C39-C40-C41
3	A	404	PTY	C12-C13-C14-C15
3	A	404	PTY	C34-C35-C36-C37
3	B	401	PTY	C40-C41-C42-C43
3	A	404	PTY	C25-C26-C27-C28
3	A	404	PTY	C15-C16-C17-C18
3	B	401	PTY	C11-C8-O7-C6
3	A	404	PTY	C16-C17-C18-C19
3	A	404	PTY	C33-C34-C35-C36
3	B	401	PTY	O4-C1-C6-C5
3	A	404	PTY	C39-C40-C41-C42
3	A	404	PTY	C41-C42-C43-C44
3	B	401	PTY	C23-C24-C25-C26
3	B	401	PTY	C15-C16-C17-C18
3	B	401	PTY	C30-C31-C32-C33
3	A	404	PTY	C32-C33-C34-C35
3	A	404	PTY	C8-C11-C12-C13
3	B	401	PTY	C6-C5-O14-P1
3	A	404	PTY	C2-C3-O11-P1
3	B	401	PTY	O10-C8-O7-C6
3	A	404	PTY	C18-C19-C20-C21
3	A	404	PTY	C17-C18-C19-C20
3	B	401	PTY	O4-C1-C6-O7
3	B	401	PTY	C3-O11-P1-O13
3	B	401	PTY	C5-O14-P1-O12
3	A	404	PTY	C6-C5-O14-P1
3	B	401	PTY	C31-C32-C33-C34
3	B	401	PTY	C35-C36-C37-C38
3	A	404	PTY	O14-C5-C6-O7
3	B	401	PTY	C12-C11-C8-O7
3	A	404	PTY	O4-C1-C6-O7
3	A	404	PTY	C40-C41-C42-C43
3	A	404	PTY	C35-C36-C37-C38
3	B	401	PTY	C13-C14-C15-C16
3	B	401	PTY	C20-C21-C22-C23
3	A	404	PTY	O4-C1-C6-C5
3	B	401	PTY	C17-C18-C19-C20
3	A	404	PTY	C20-C21-C22-C23
3	B	401	PTY	C37-C38-C39-C40
3	A	404	PTY	C22-C23-C24-C25
3	B	401	PTY	C33-C34-C35-C36
3	A	404	PTY	C24-C25-C26-C27

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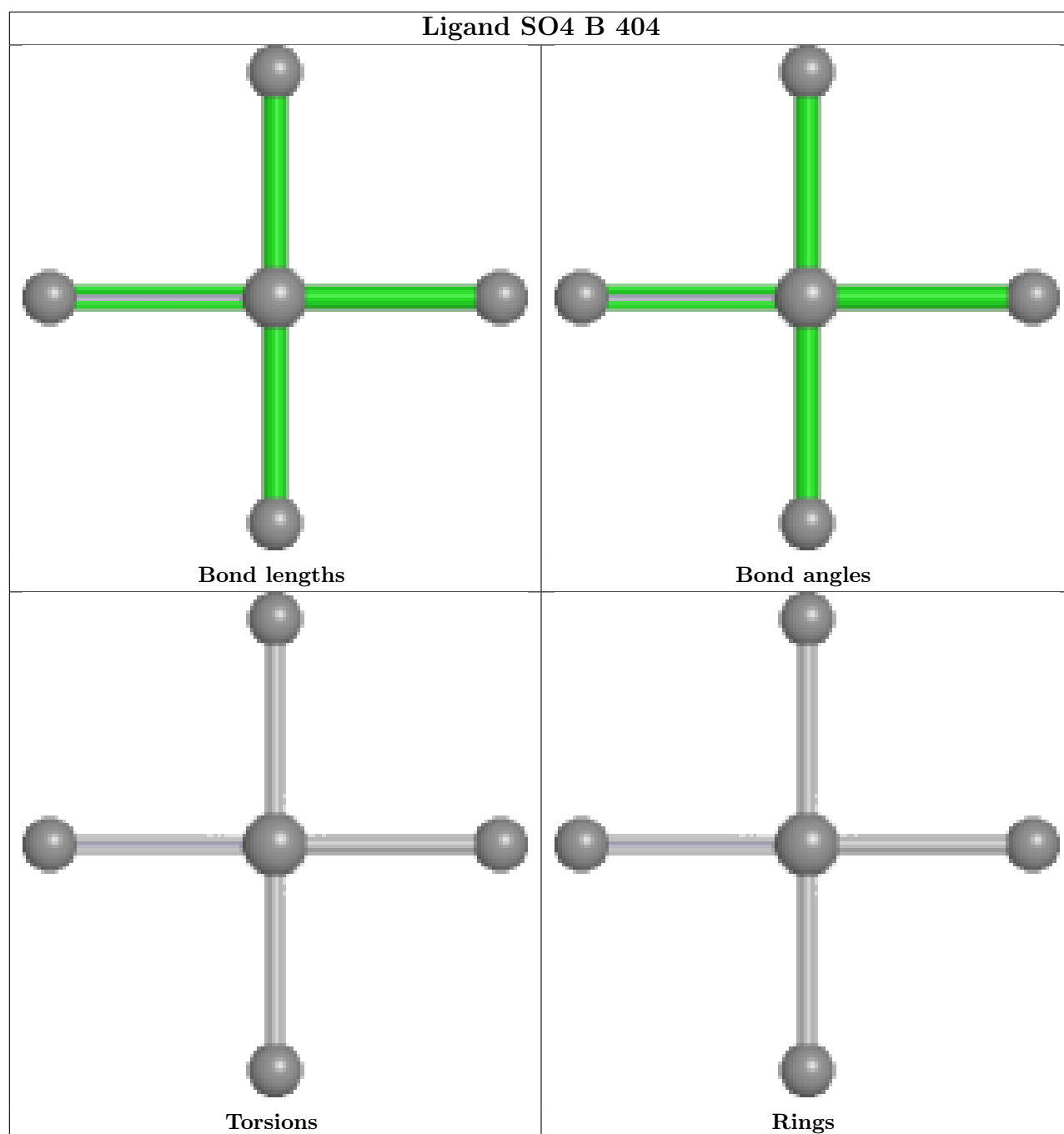
Mol	Chain	Res	Type	Atoms
3	A	404	PTY	O14-C5-C6-C1

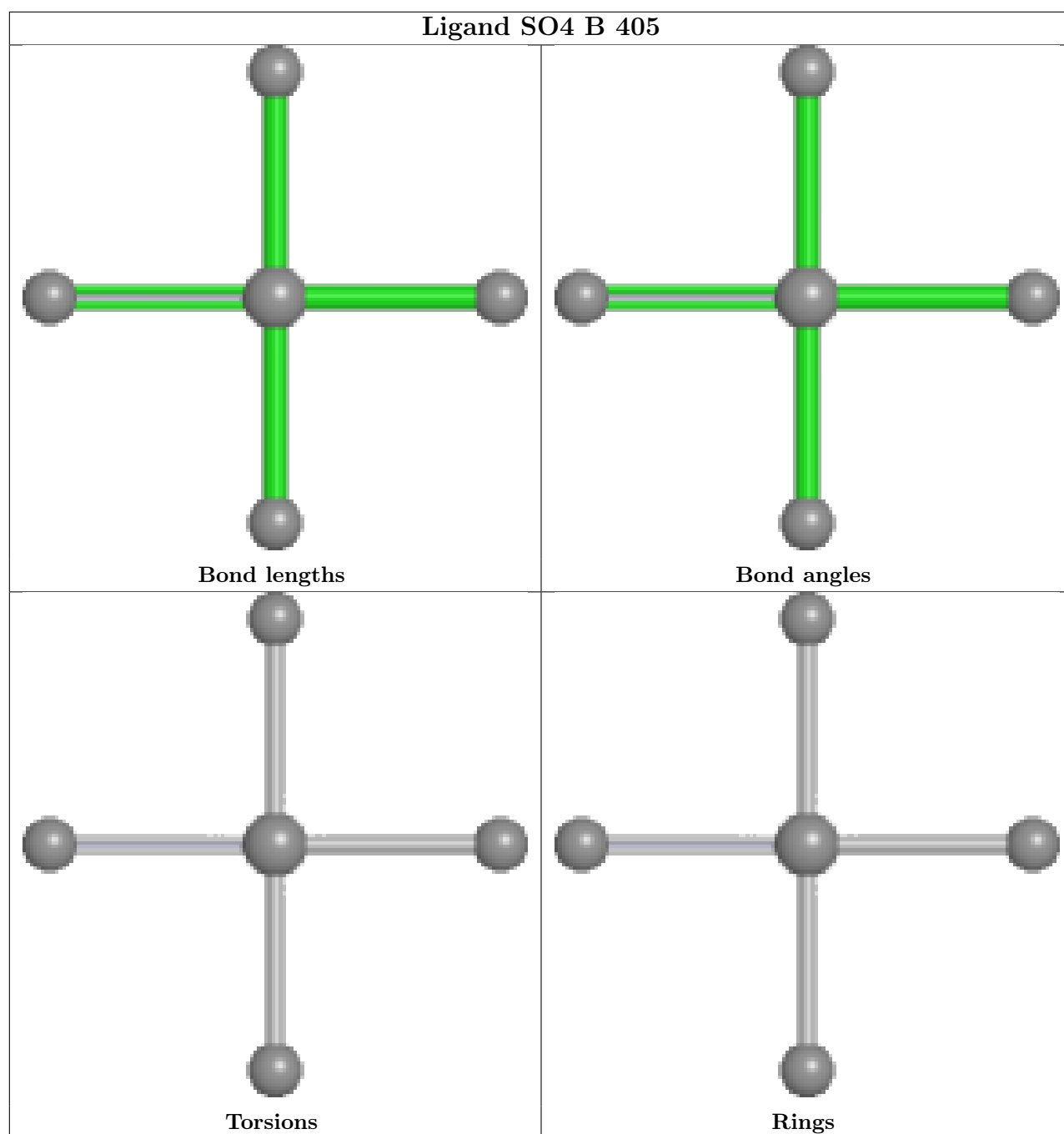
There are no ring outliers.

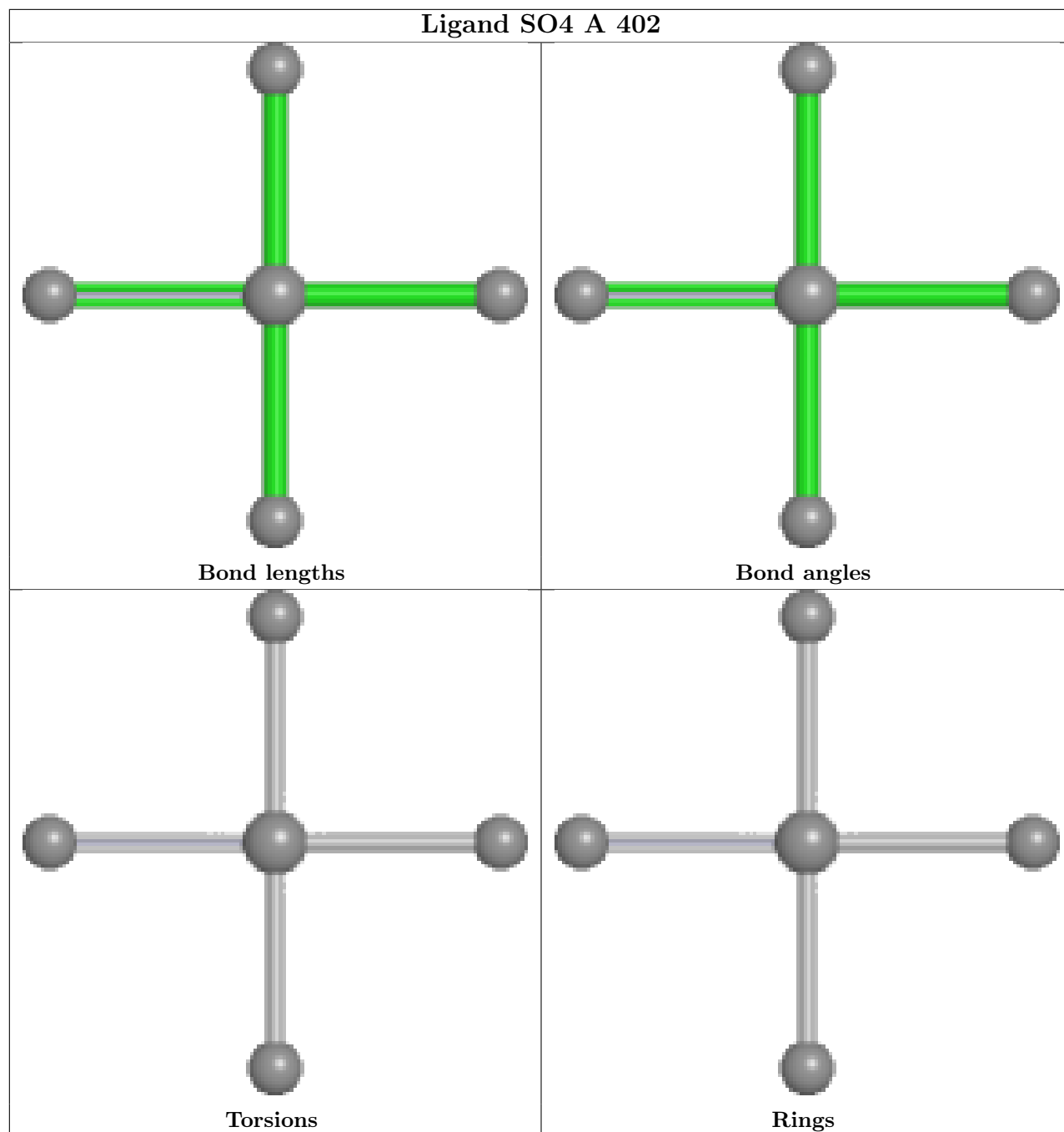
4 monomers are involved in 21 short contacts:

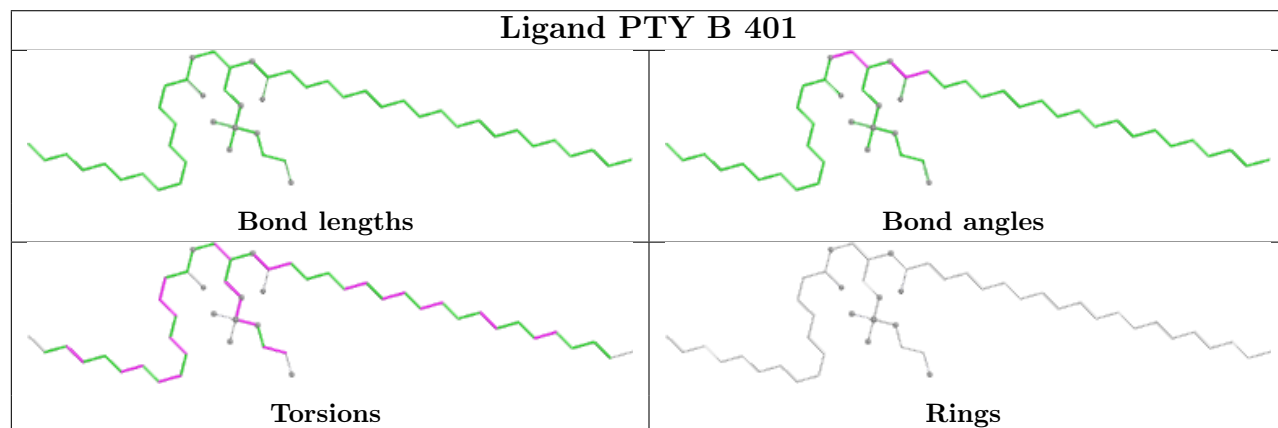
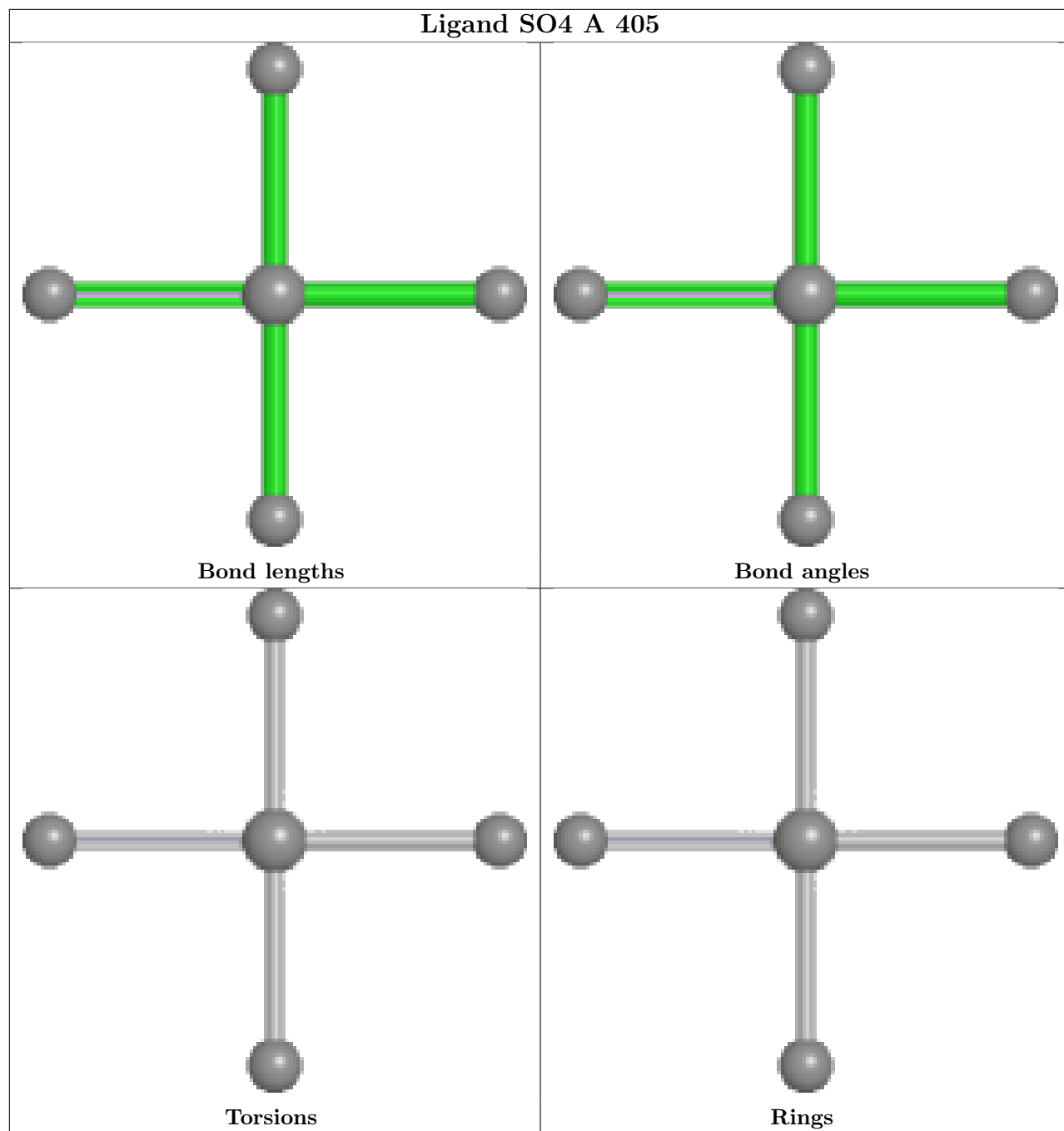
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	401	PTY	17	0
2	A	403	SO4	2	0
3	A	404	PTY	10	0
2	B	403	SO4	1	0

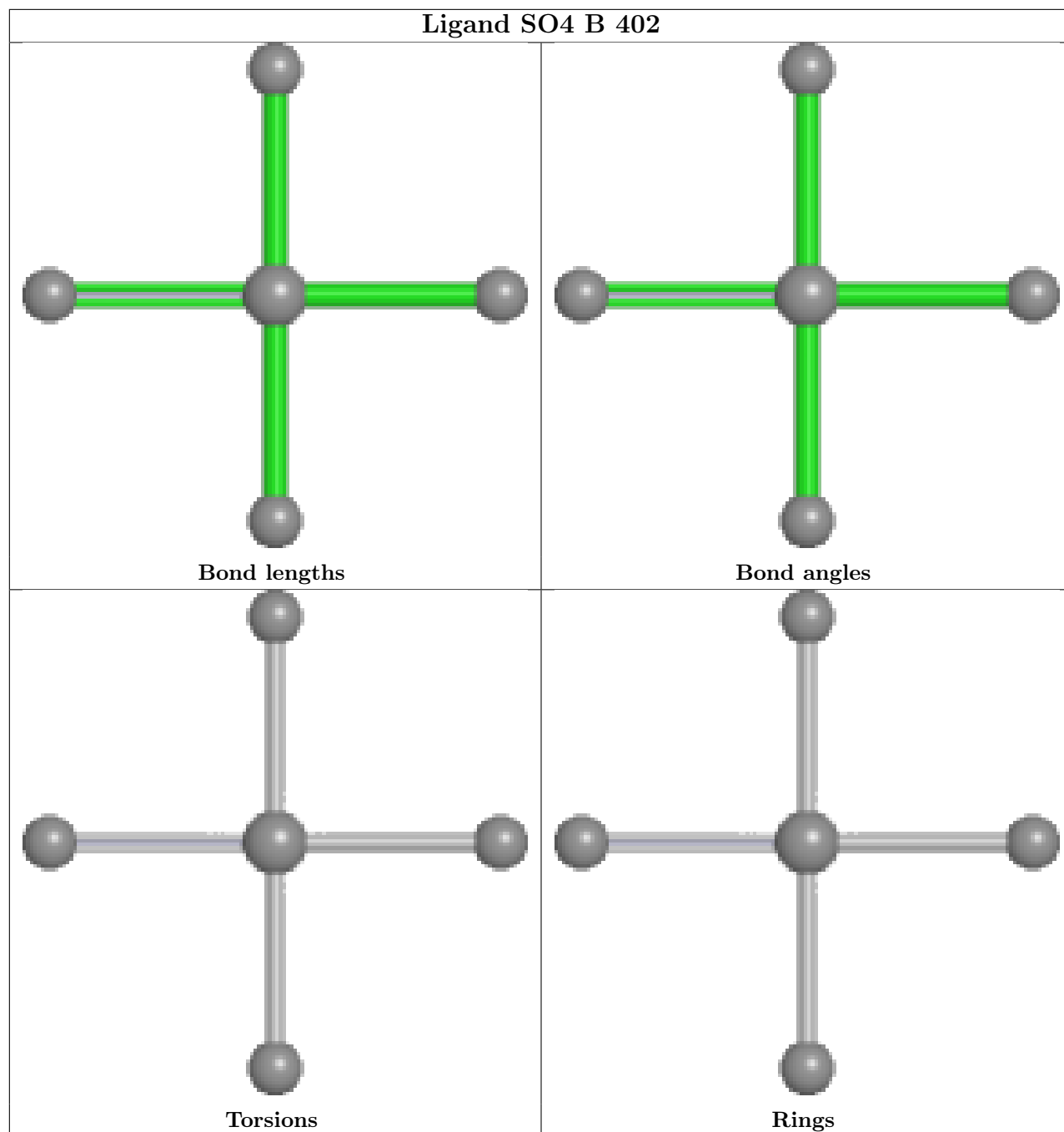
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

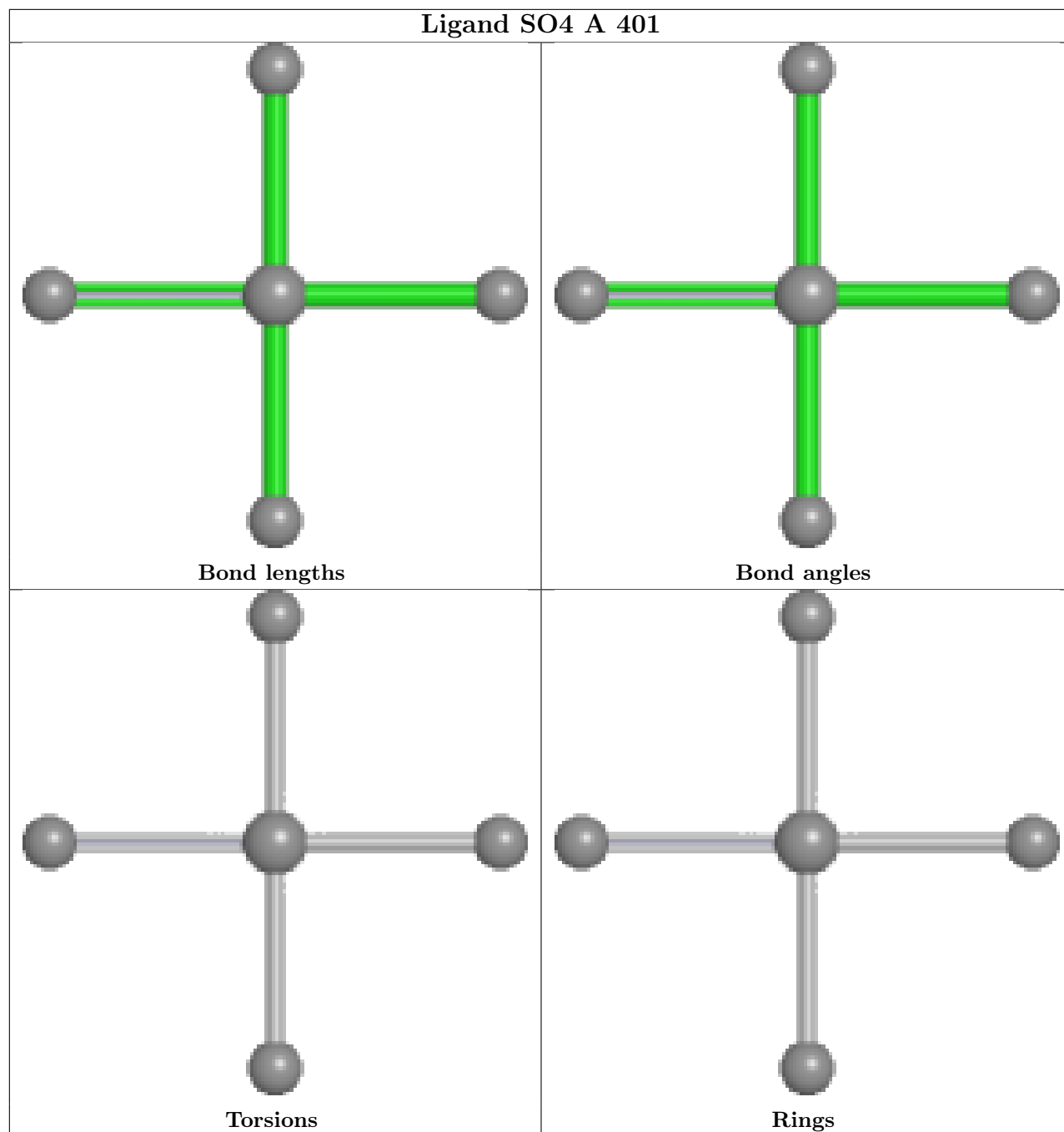


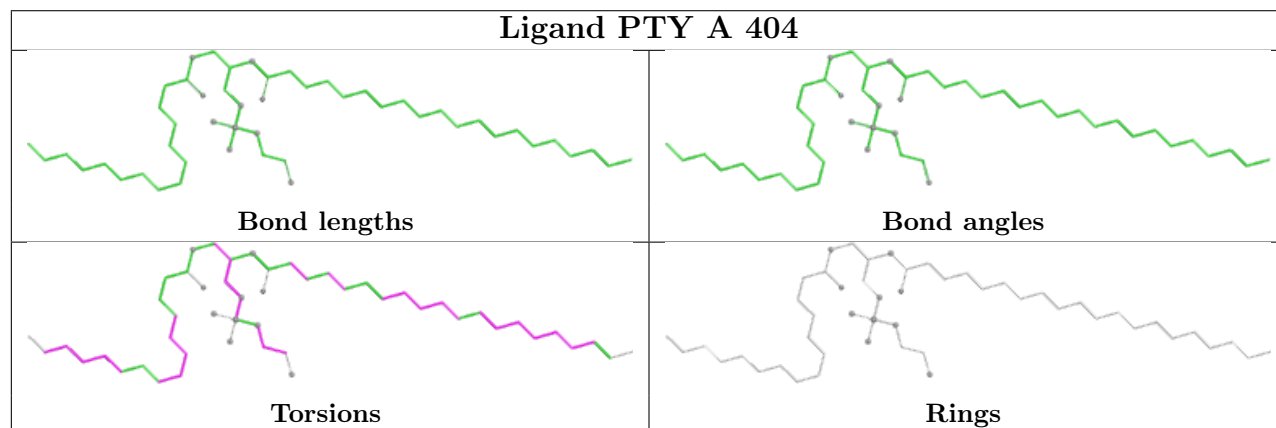
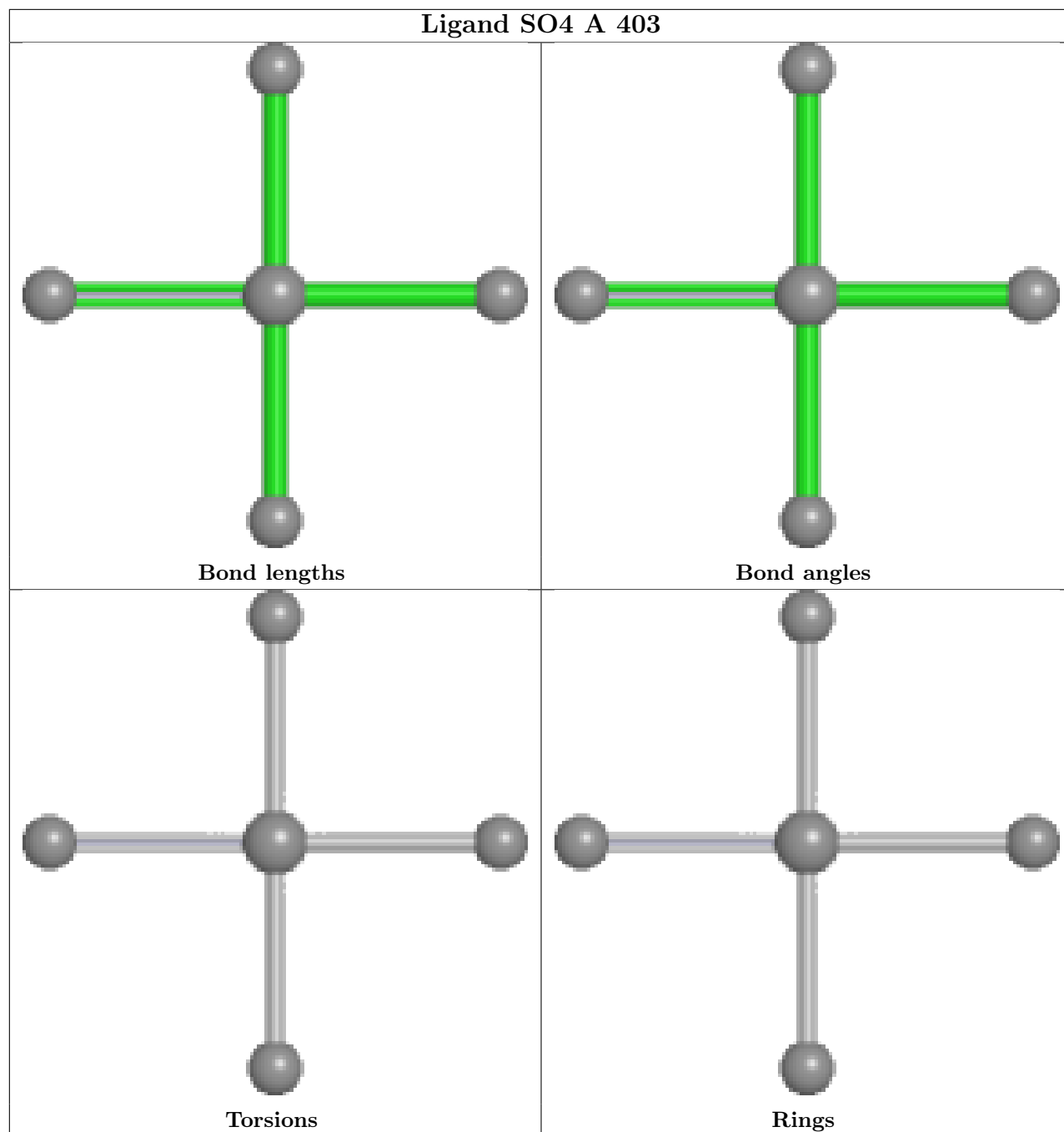


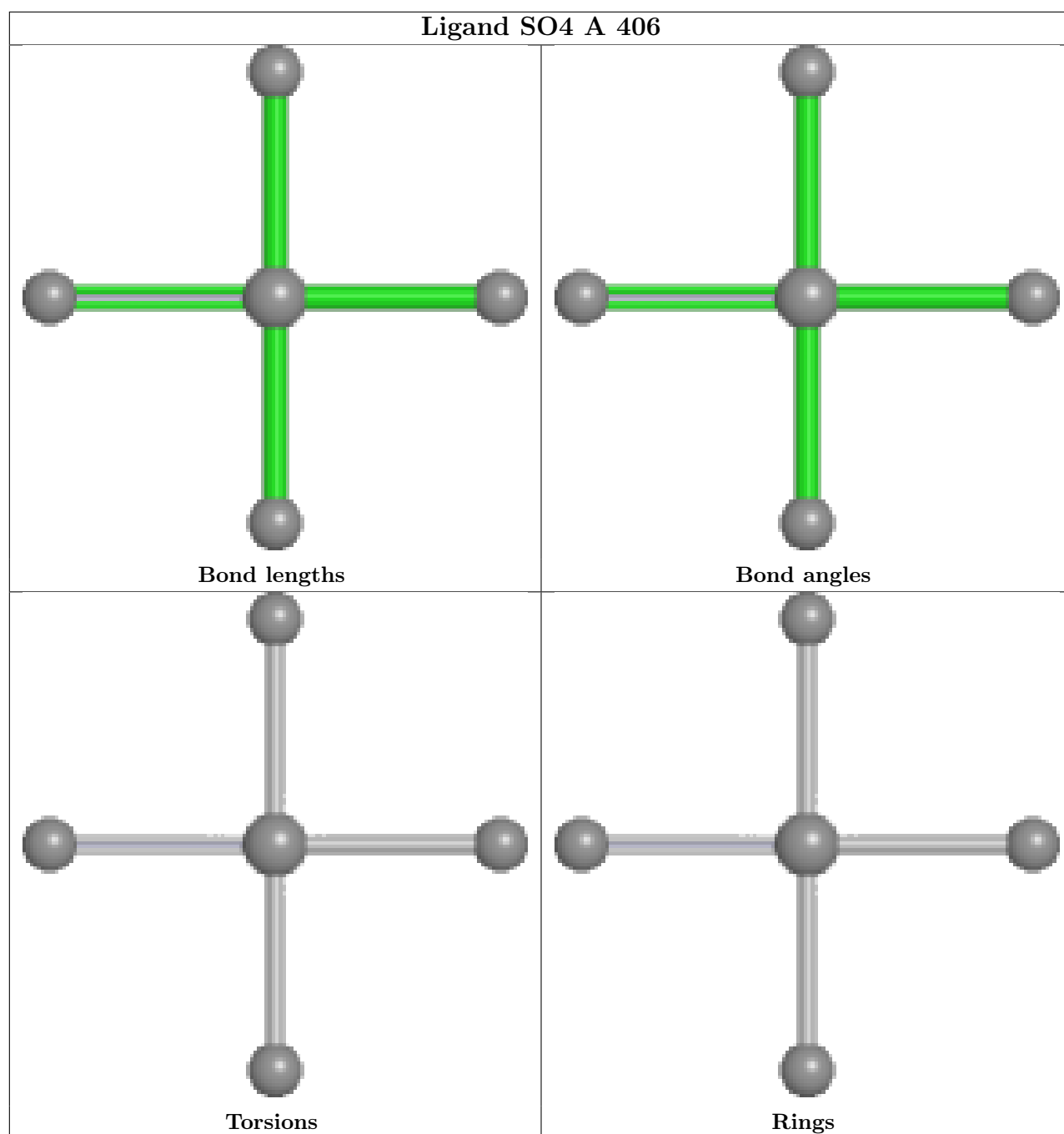


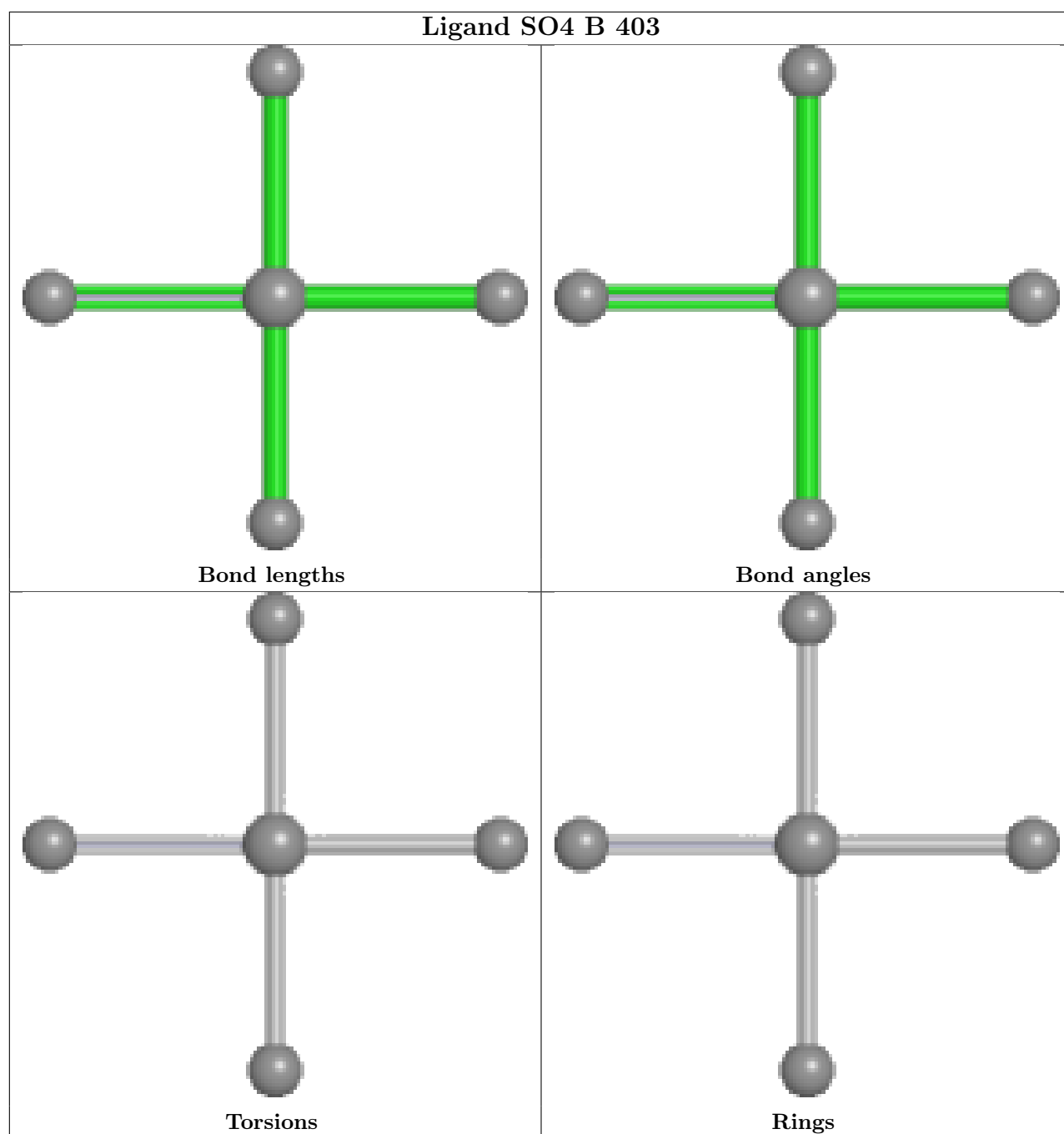












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å ²)	Q < 0.9
1	A	319/348 (91%)	0.14	19 (5%)	27 33	18, 27, 54, 90	1 (0%)
1	B	319/348 (91%)	0.08	14 (4%)	39 44	13, 27, 53, 105	3 (0%)
All	All	638/696 (91%)	0.11	33 (5%)	33 39	13, 27, 54, 105	4 (0%)

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	322	ARG	5.1
1	B	5	VAL	5.0
1	A	319	ALA	4.8
1	A	5	VAL	4.8
1	B	319	ALA	4.7
1	A	186	HIS	4.4
1	B	318	PHE	4.1
1	A	316	GLU	4.0
1	A	322	ARG	3.9
1	A	320	GLN	3.8
1	A	182	LYS	3.5
1	B	186	HIS	3.5
1	B	17[A]	GLN	3.4
1	B	321	GLU	3.4
1	A	321	GLU	3.2
1	A	17[A]	GLN	3.2
1	B	182	LYS	3.2
1	B	4	GLU	3.1
1	B	184	ARG	3.1
1	A	87	VAL	3.0
1	B	320	GLN	3.0
1	A	184	ARG	3.0
1	A	183	ASN	3.0
1	B	316	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	318	PHE	2.8
1	A	185	ASP	2.4
1	A	4	GLU	2.3
1	B	183	ASN	2.3
1	A	317	ALA	2.3
1	B	7	LYS	2.2
1	A	181	TYR	2.2
1	A	128	ASP	2.1
1	A	127	ASP	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

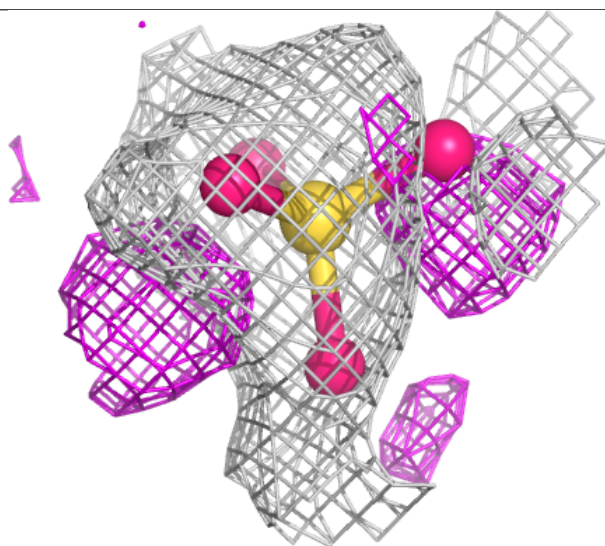
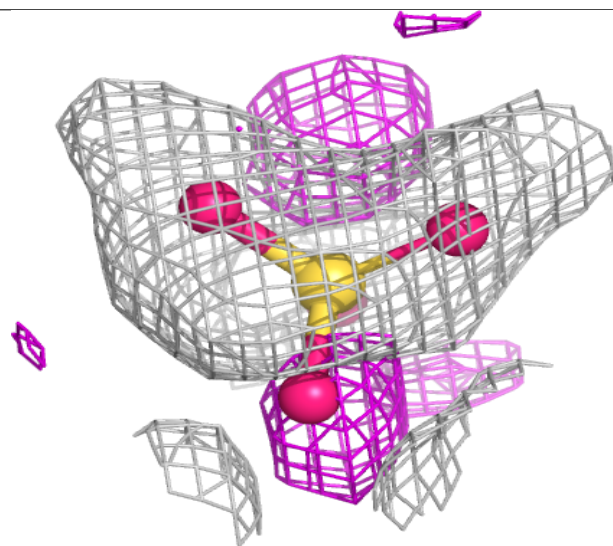
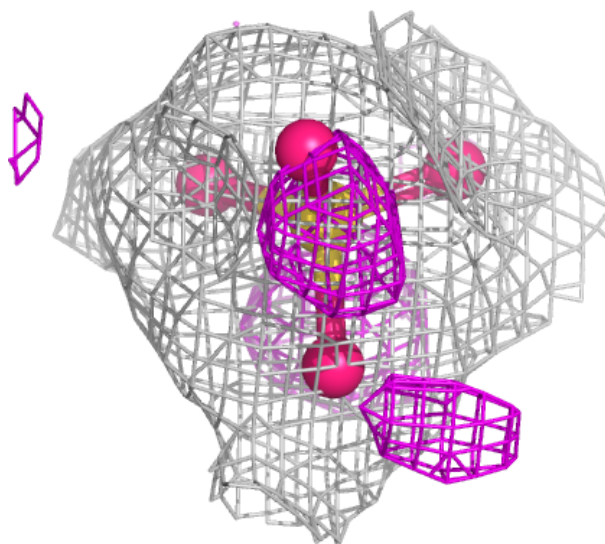
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	SO4	A	403	5/5	0.74	0.16	90,100,110,117	0
2	SO4	A	405	5/5	0.77	0.14	89,92,106,108	0
2	SO4	B	405	5/5	0.77	0.14	77,83,100,105	0
2	SO4	B	404	5/5	0.79	0.12	84,86,98,100	0
2	SO4	B	403	5/5	0.82	0.16	72,85,104,105	0
3	PTY	B	401	50/50	0.83	0.27	46,65,108,133	0
2	SO4	A	402	5/5	0.85	0.11	59,79,82,86	0
2	SO4	A	406	5/5	0.86	0.22	41,47,94,100	0
3	PTY	A	404	50/50	0.87	0.26	48,63,103,139	0
2	SO4	A	401	5/5	0.90	0.10	52,69,79,93	0
2	SO4	B	402	5/5	0.92	0.09	54,62,66,73	0
4	FE	A	407	1/1	1.00	0.02	23,23,23,23	0
4	FE	B	406	1/1	1.00	0.01	22,22,22,22	0

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

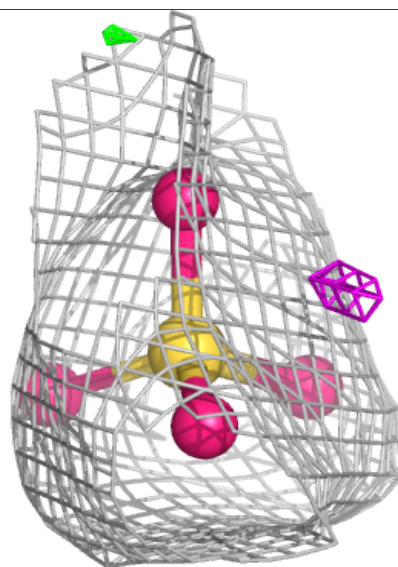
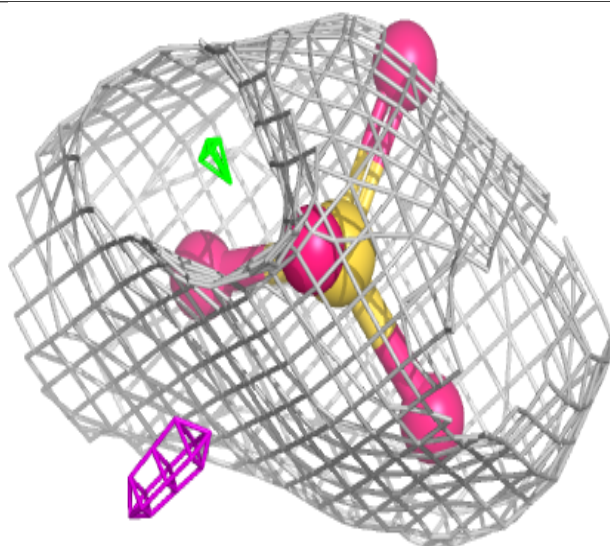
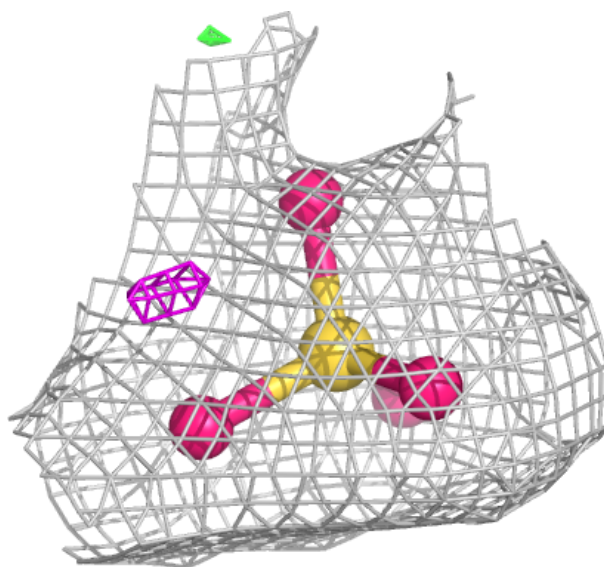
Electron density around SO4 A 403:

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



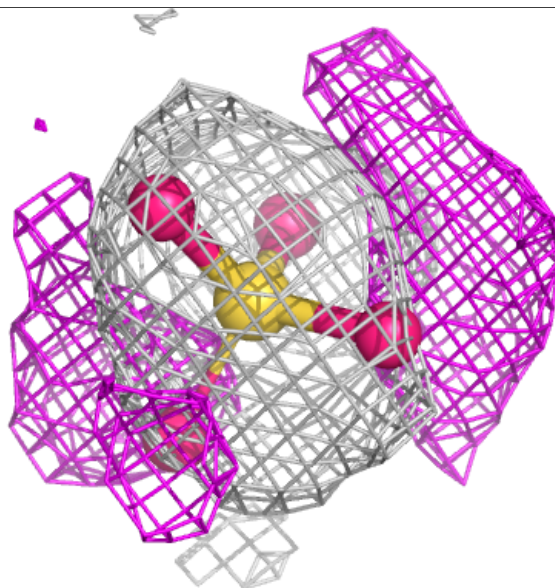
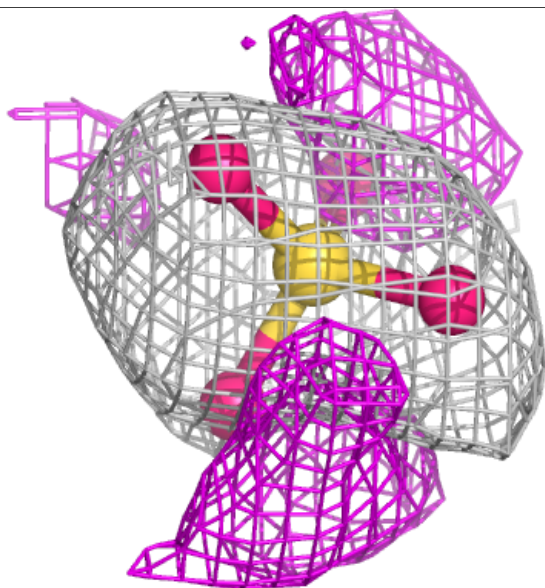
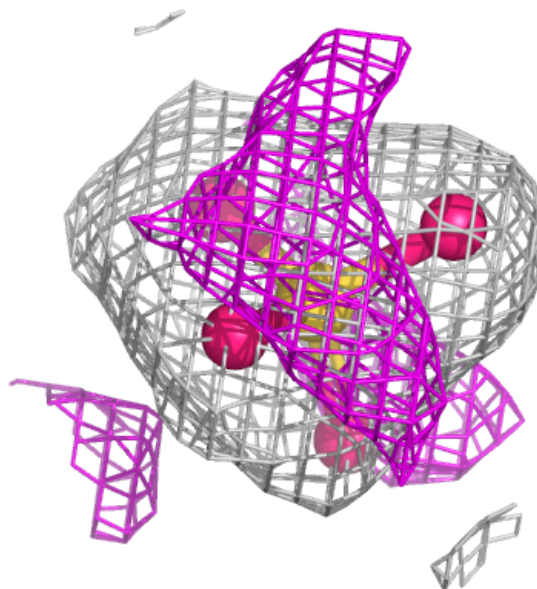
Electron density around SO4 A 405:

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



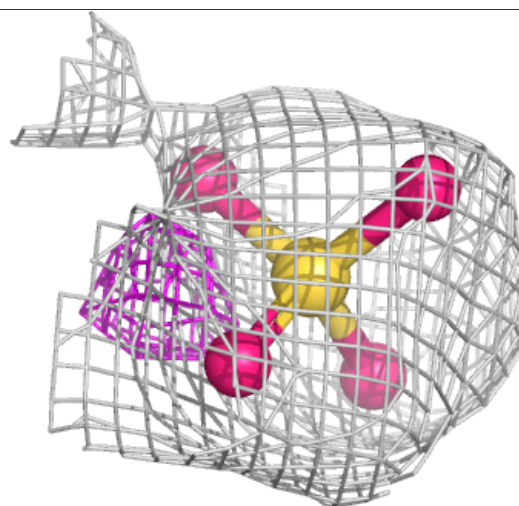
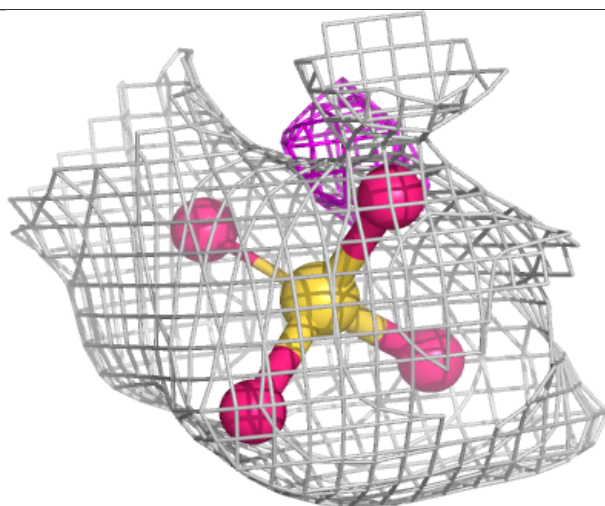
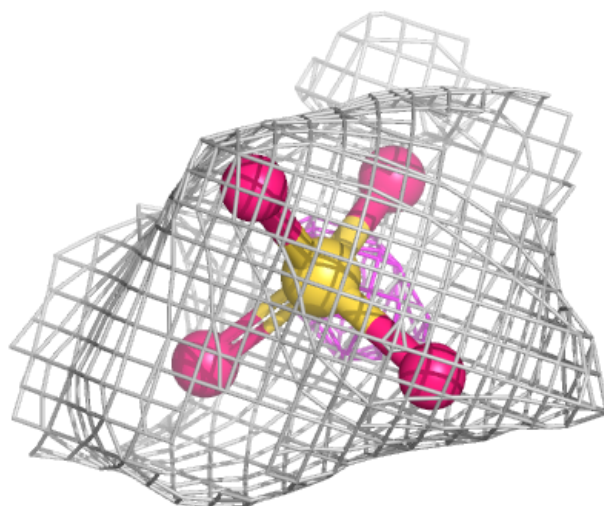
Electron density around SO4 B 405:

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



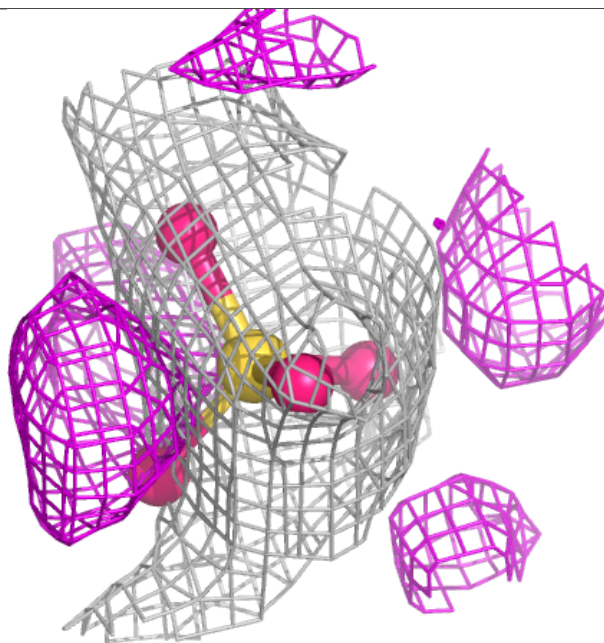
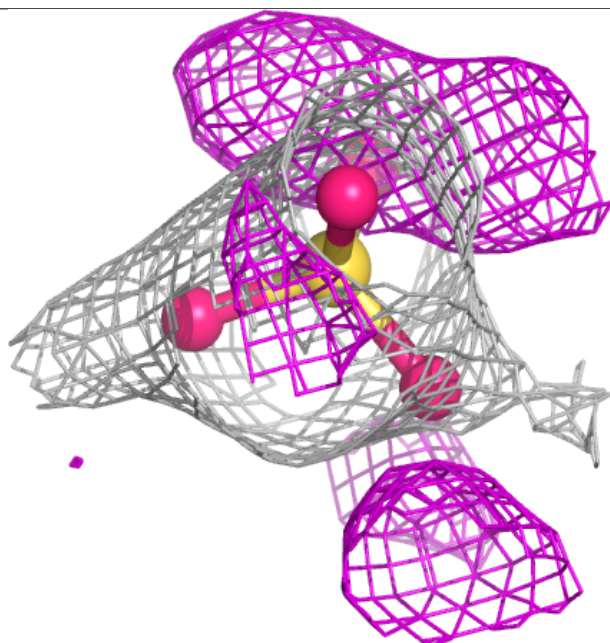
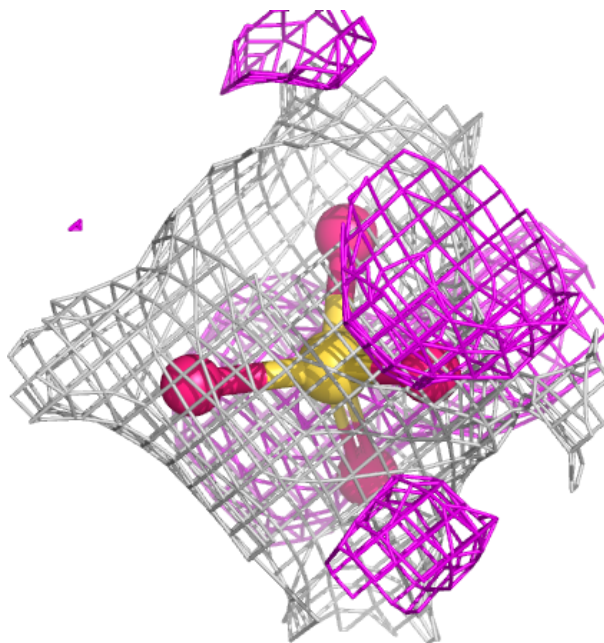
Electron density around SO4 B 404:

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



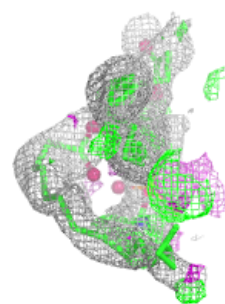
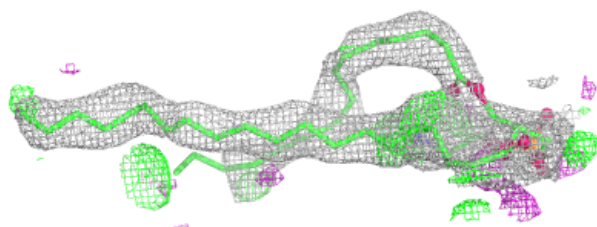
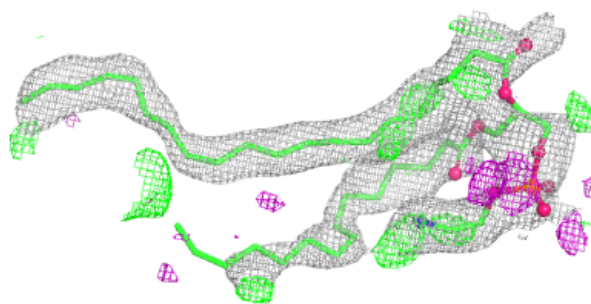
Electron density around SO4 B 403:

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



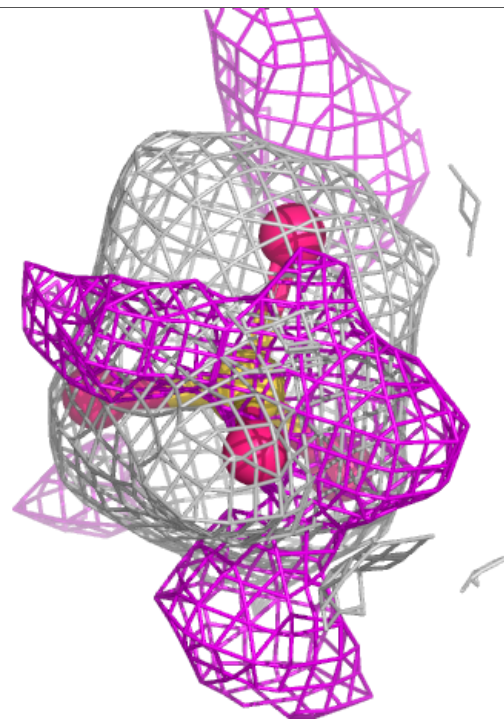
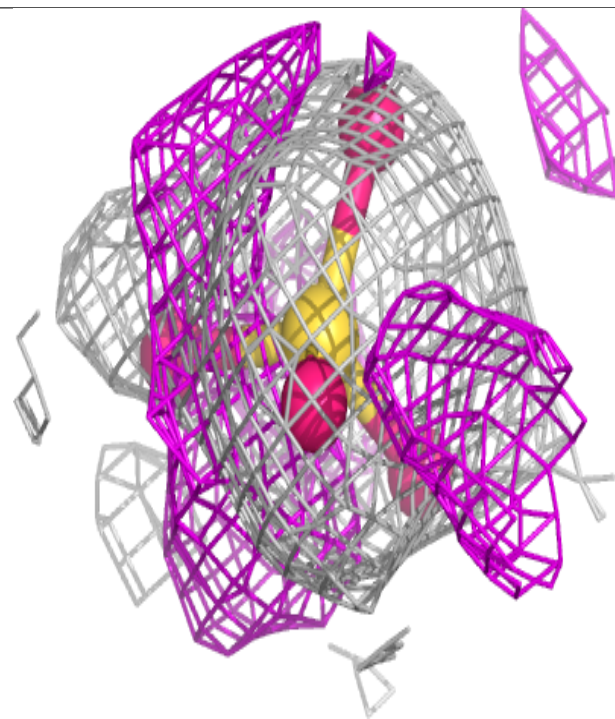
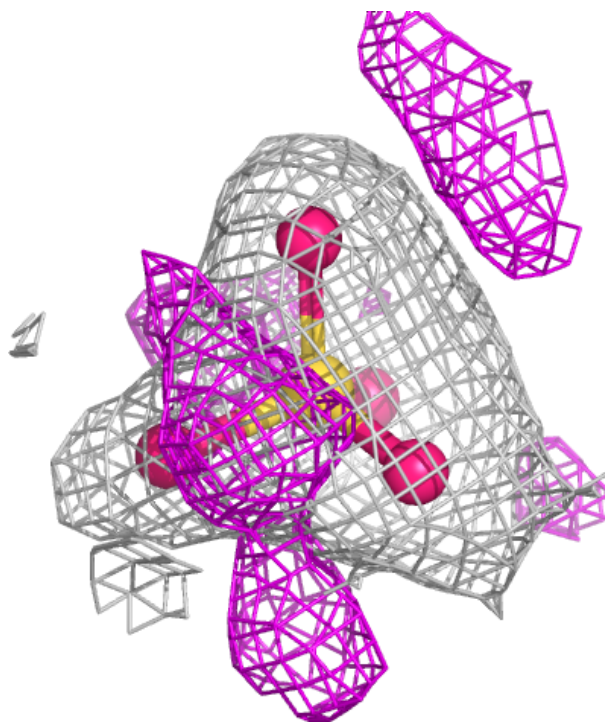
Electron density around PTY B 401:

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



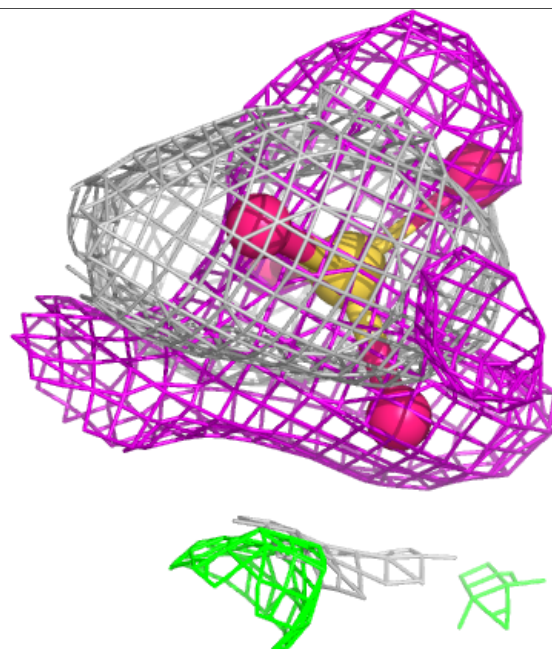
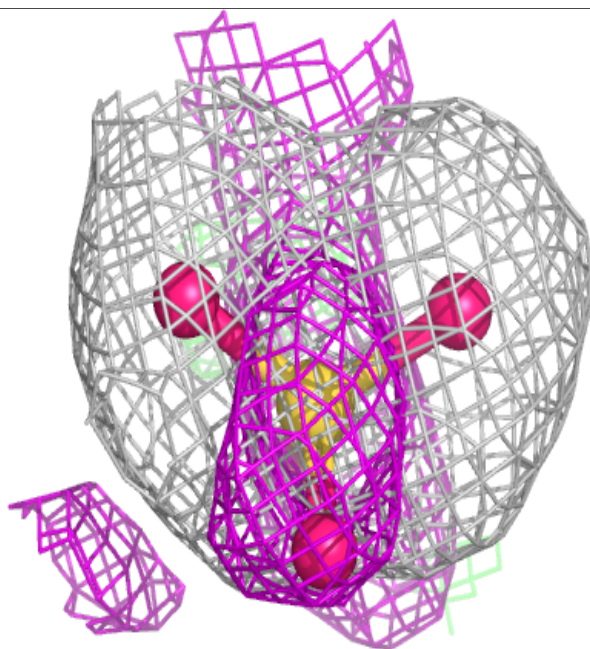
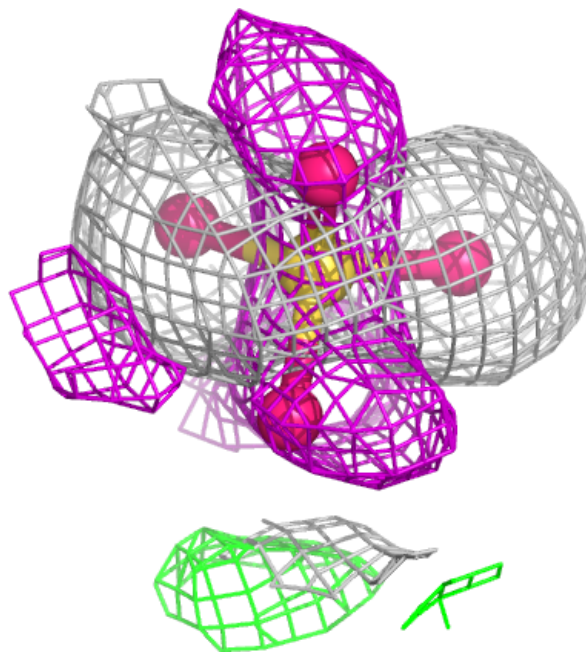
Electron density around SO4 A 402:

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and green (positive)



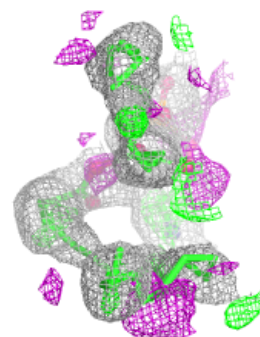
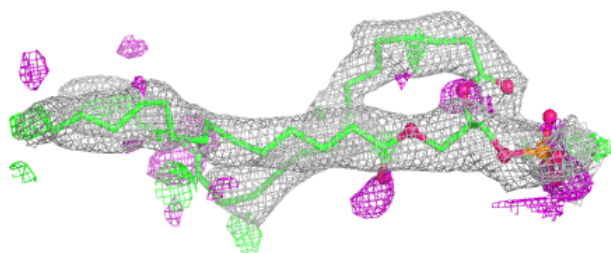
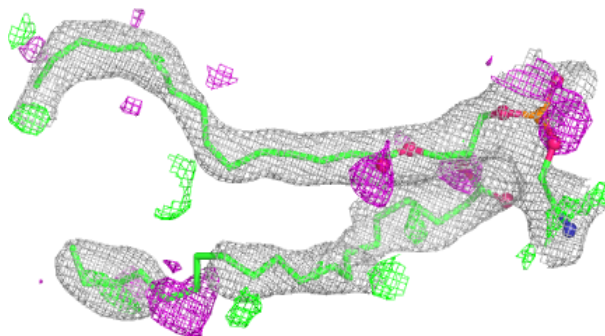
Electron density around SO4 A 406:

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



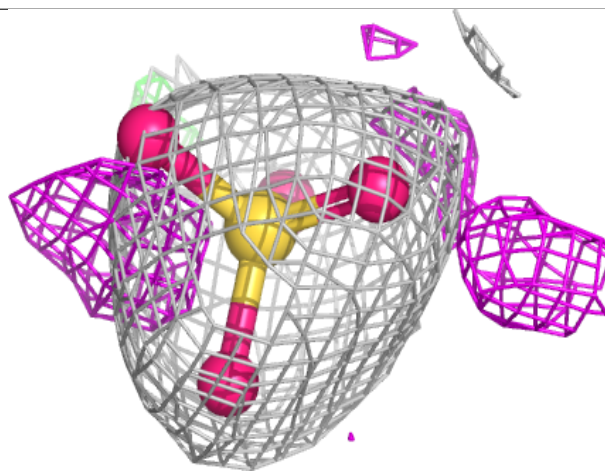
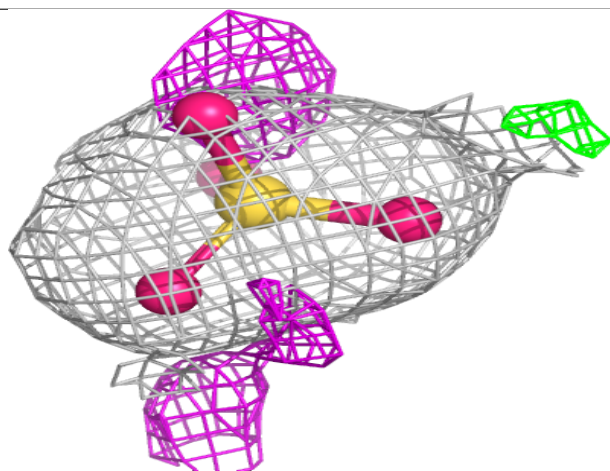
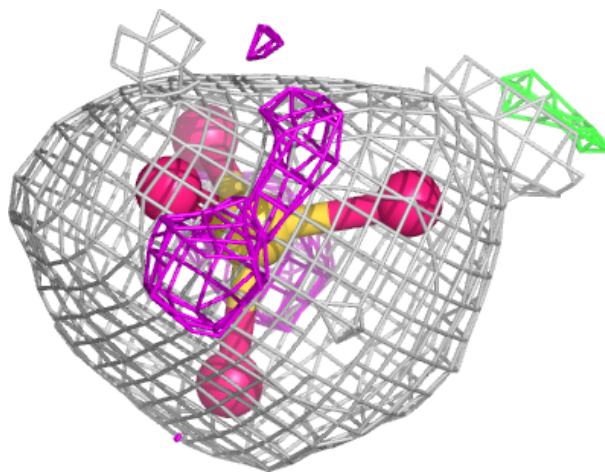
Electron density around PTY A 404:

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



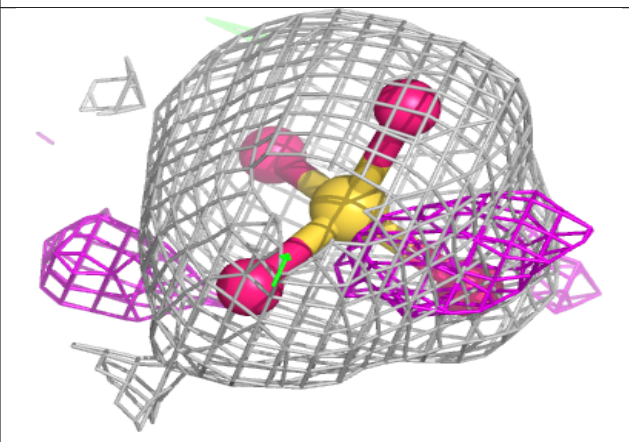
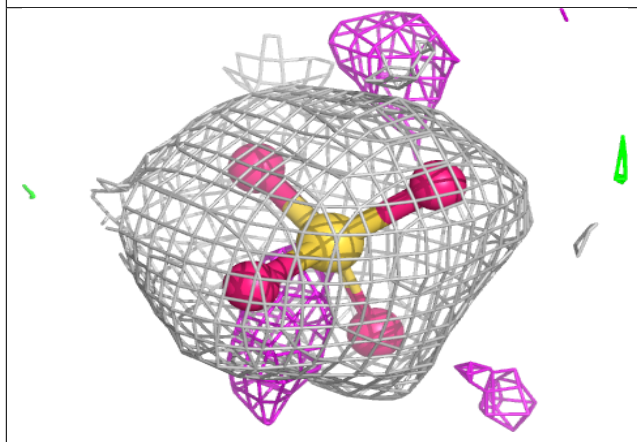
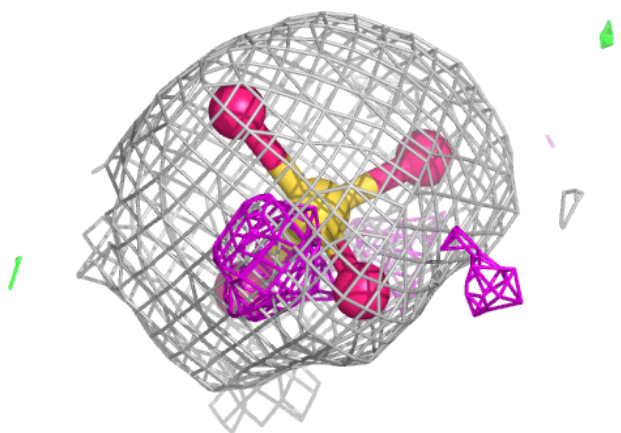
Electron density around SO4 A 401:

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



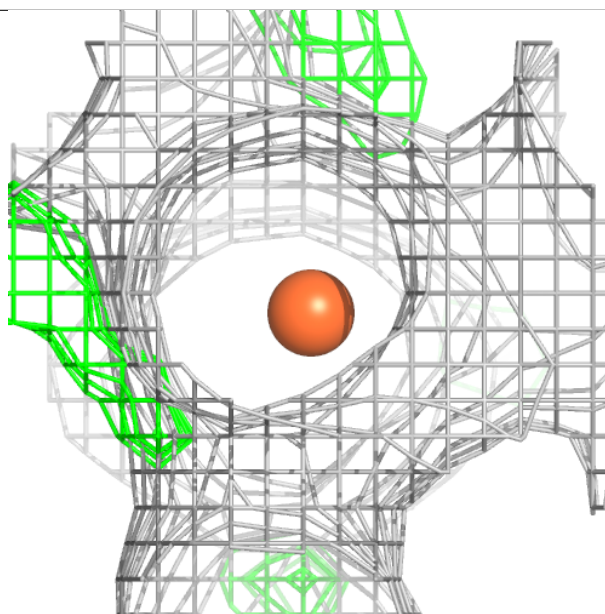
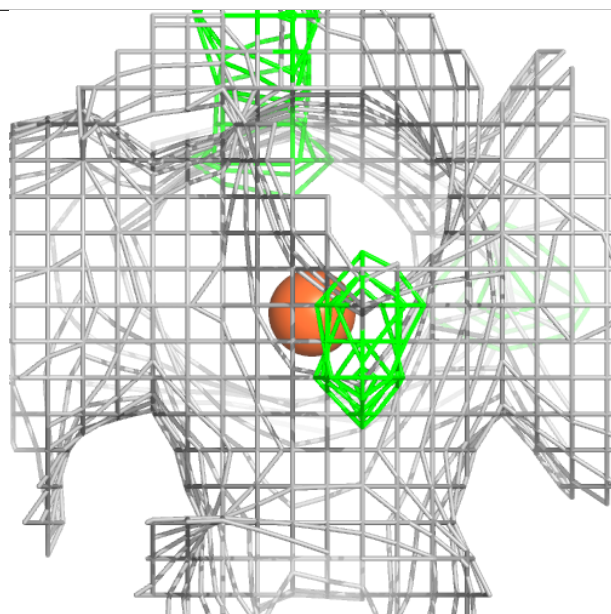
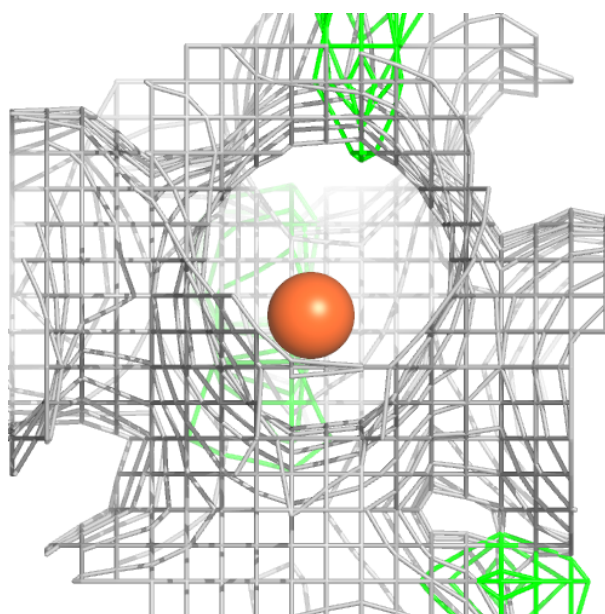
Electron density around SO4 B 402:

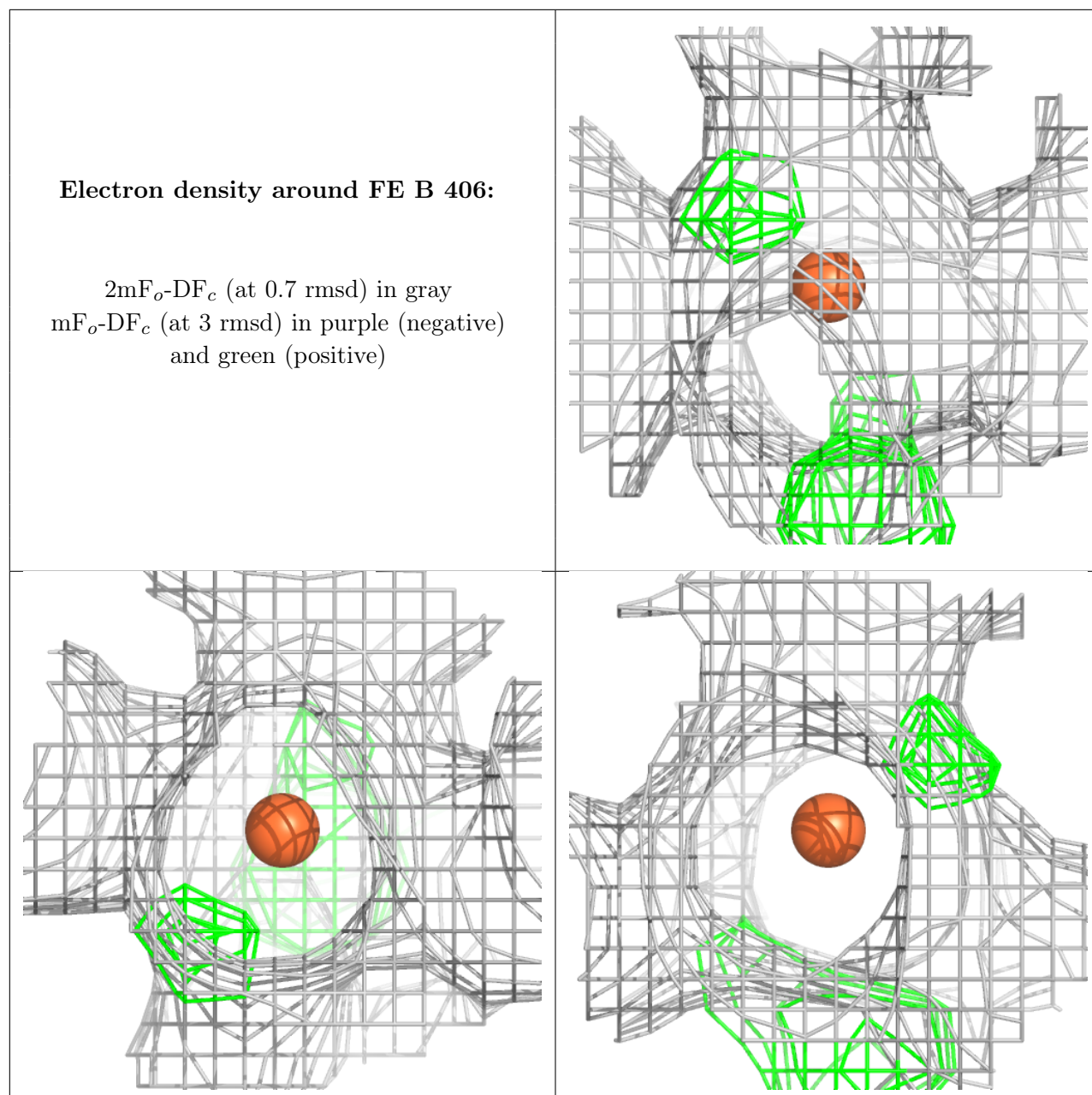
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around FE A 407:

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





6.5 Other polymers ⓘ

There are no such residues in this entry.