



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:09 PM UTC

PDB ID : 8OFN / pdb_00008ofn
Title : Structure of the yellow fever virus (Asibi strain) dimeric envelope protein
Authors : Covernton, E.; Vaney, M.C.; Barba-Spaeth, G.; Rey, F.A.
Deposited on : 2023-03-16
Resolution : 3.48 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

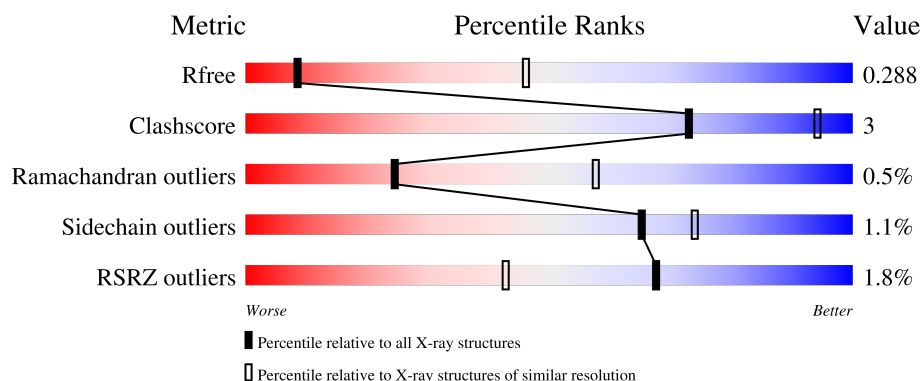
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

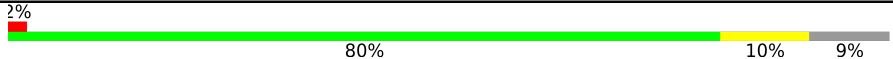
The reported resolution of this entry is 3.48 Å.

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	1083 (3.52-3.44)
Clashscore	190562	1139 (3.52-3.44)
Ramachandran outliers	187476	1111 (3.52-3.44)
Sidechain outliers	187428	1112 (3.52-3.44)
RSRZ outliers	180081	1082 (3.52-3.44)

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	428	
1	B	428	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5964 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 Envelope glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	389	Total	C	N	O	S	0	0	0
			2967	1859	512	576	20			
1	B	389	Total	C	N	O	S	0	0	0
			2967	1859	512	576	20			

There are 70 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	394	LEU	-	expression tag	UNP D0VF48
A	395	VAL	-	expression tag	UNP D0VF48
A	396	PRO	-	expression tag	UNP D0VF48
A	397	ARG	-	expression tag	UNP D0VF48
A	398	GLY	-	expression tag	UNP D0VF48
A	399	SER	-	expression tag	UNP D0VF48
A	400	SER	-	expression tag	UNP D0VF48
A	401	ALA	-	expression tag	UNP D0VF48
A	402	TRP	-	expression tag	UNP D0VF48
A	403	SER	-	expression tag	UNP D0VF48
A	404	HIS	-	expression tag	UNP D0VF48
A	405	PRO	-	expression tag	UNP D0VF48
A	406	GLN	-	expression tag	UNP D0VF48
A	407	PHE	-	expression tag	UNP D0VF48
A	408	GLU	-	expression tag	UNP D0VF48
A	409	LYS	-	expression tag	UNP D0VF48
A	410	GLY	-	expression tag	UNP D0VF48
A	411	GLY	-	expression tag	UNP D0VF48
A	412	SER	-	expression tag	UNP D0VF48
A	413	GLY	-	expression tag	UNP D0VF48
A	414	GLY	-	expression tag	UNP D0VF48
A	415	GLY	-	expression tag	UNP D0VF48
A	416	SER	-	expression tag	UNP D0VF48
A	417	GLY	-	expression tag	UNP D0VF48
A	418	GLY	-	expression tag	UNP D0VF48

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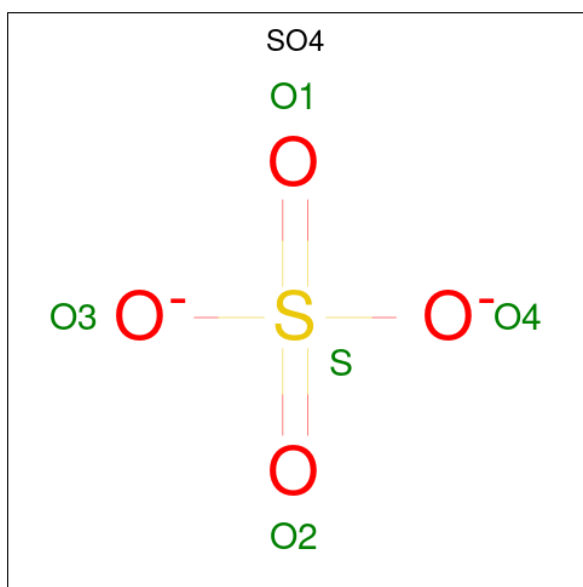
Chain	Residue	Modelled	Actual	Comment	Reference
A	419	SER	-	expression tag	UNP D0VF48
A	420	ALA	-	expression tag	UNP D0VF48
A	421	TRP	-	expression tag	UNP D0VF48
A	422	SER	-	expression tag	UNP D0VF48
A	423	HIS	-	expression tag	UNP D0VF48
A	424	PRO	-	expression tag	UNP D0VF48
A	425	GLN	-	expression tag	UNP D0VF48
A	426	PHE	-	expression tag	UNP D0VF48
A	427	GLU	-	expression tag	UNP D0VF48
A	428	LYS	-	expression tag	UNP D0VF48
B	394	LEU	-	expression tag	UNP D0VF48
B	395	VAL	-	expression tag	UNP D0VF48
B	396	PRO	-	expression tag	UNP D0VF48
B	397	ARG	-	expression tag	UNP D0VF48
B	398	GLY	-	expression tag	UNP D0VF48
B	399	SER	-	expression tag	UNP D0VF48
B	400	SER	-	expression tag	UNP D0VF48
B	401	ALA	-	expression tag	UNP D0VF48
B	402	TRP	-	expression tag	UNP D0VF48
B	403	SER	-	expression tag	UNP D0VF48
B	404	HIS	-	expression tag	UNP D0VF48
B	405	PRO	-	expression tag	UNP D0VF48
B	406	GLN	-	expression tag	UNP D0VF48
B	407	PHE	-	expression tag	UNP D0VF48
B	408	GLU	-	expression tag	UNP D0VF48
B	409	LYS	-	expression tag	UNP D0VF48
B	410	GLY	-	expression tag	UNP D0VF48
B	411	GLY	-	expression tag	UNP D0VF48
B	412	SER	-	expression tag	UNP D0VF48
B	413	GLY	-	expression tag	UNP D0VF48
B	414	GLY	-	expression tag	UNP D0VF48
B	415	GLY	-	expression tag	UNP D0VF48
B	416	SER	-	expression tag	UNP D0VF48
B	417	GLY	-	expression tag	UNP D0VF48
B	418	GLY	-	expression tag	UNP D0VF48
B	419	SER	-	expression tag	UNP D0VF48
B	420	ALA	-	expression tag	UNP D0VF48
B	421	TRP	-	expression tag	UNP D0VF48
B	422	SER	-	expression tag	UNP D0VF48
B	423	HIS	-	expression tag	UNP D0VF48
B	424	PRO	-	expression tag	UNP D0VF48
B	425	GLN	-	expression tag	UNP D0VF48

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Chain	Residue	Modelled	Actual	Comment	Reference
B	426	PHE	-	expression tag	UNP D0VF48
B	427	GLU	-	expression tag	UNP D0VF48
B	428	LYS	-	expression tag	UNP D0VF48

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

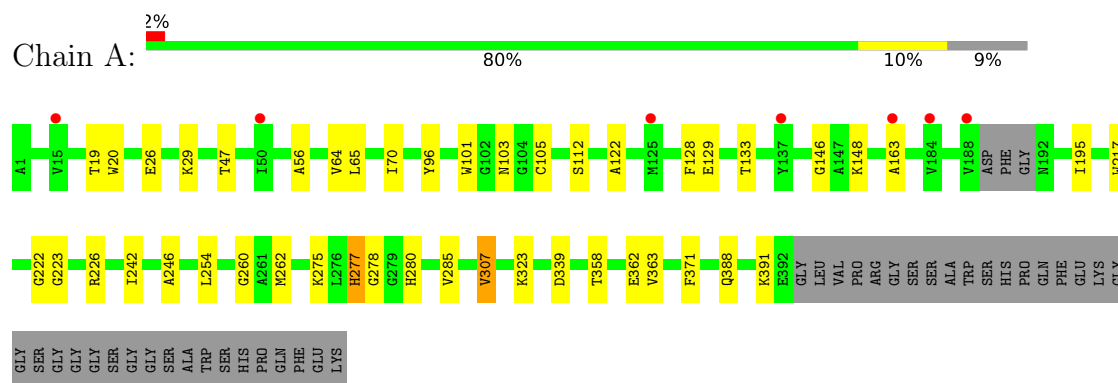


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

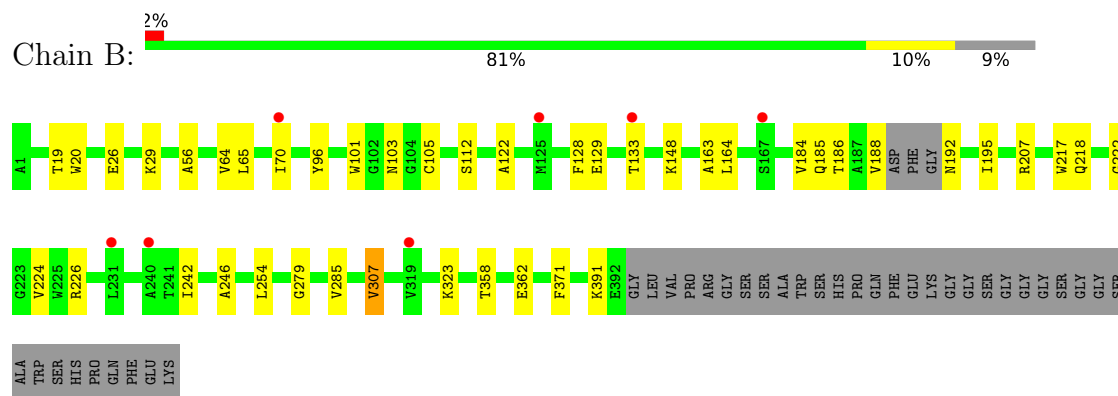
3 Residue-property plots [i](#)

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: Envelope glycoprotein



- Molecule 1: Envelope glycoprotein



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	92.54Å 92.54Å 308.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.48 30.00 – 3.48	Depositor EDS
% Data completeness (in resolution range)	64.3 (30.00-3.48) 64.2 (30.00-3.48)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 3.47Å)	Xtriage
Refinement program	BUSTER	Depositor
R, R_{free}	0.255 , 0.273 0.274 , 0.288	Depositor DCC
R_{free} test set	983 reflections (8.46%)	wwPDB-VP
Wilson B-factor (Å ²)	135.0	Xtriage
Anisotropy	0.095	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 135.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5964	wwPDB-VP
Average B, all atoms (Å ²)	169.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.53	0/3025	0.93	4/4104 (0.1%)
1	B	0.51	0/3025	0.94	4/4104 (0.1%)
All	All	0.52	0/6050	0.94	8/8208 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	184	VAL	CA-C-N	-6.51	114.12	122.77
1	B	184	VAL	C-N-CA	-6.51	114.12	122.77
1	B	307	VAL	N-CA-C	-5.64	105.23	110.53
1	A	339	ASP	CA-CB-CG	5.63	118.23	112.60
1	A	277	HIS	CA-CB-CG	5.61	119.41	113.80
1	A	307	VAL	N-CA-C	-5.57	105.30	110.53
1	B	285	VAL	N-CA-C	5.26	115.54	108.17
1	A	285	VAL	N-CA-C	5.01	115.18	108.17

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2967	0	2914	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2967	0	2914	20	0
2	A	15	0	0	0	0
2	B	15	0	0	0	0
All	All	5964	0	5828	38	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 3.

All (38) 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:A:262:MET:HE3	1:A:277:HIS:H	1.57	0.69
1:A:260:GLY:HA3	1:B:185:GLN:HG3	1.73	0.69
1:A:148:LYS:HE2	1:A:362:GLU:HB2	1.79	0.65
1:A:56:ALA:HB2	1:A:129:GLU:HG2	1.81	0.63
1:B:148:LYS:HE2	1:B:362:GLU:HB2	1.82	0.61
1:B:56:ALA:HB2	1:B:129:GLU:HG2	1.83	0.60
1:A:19:THR:HG1	1:A:20:TRP:CD1	2.22	0.57
1:B:96:TYR:HD1	1:B:112:SER:HA	1.70	0.56
1:B:70:ILE:HD13	1:B:242:ILE:H	1.71	0.56
1:A:371:PHE:HA	1:A:391:LYS:HB3	1.88	0.55
1:A:47:THR:HG21	1:A:275:LYS:HD3	1.86	0.55
1:B:371:PHE:HA	1:B:391:LYS:HB3	1.90	0.54
1:A:70:ILE:HD13	1:A:242:ILE:H	1.72	0.54
1:A:96:TYR:HD1	1:A:112:SER:HA	1.72	0.53
1:B:26:GLU:HB2	1:B:29:LYS:HD2	1.91	0.52
1:A:133:THR:HA	1:A:163:ALA:HB3	1.92	0.51
1:A:26:GLU:HB2	1:A:29:LYS:HD2	1.93	0.50
1:B:19:THR:HG1	1:B:20:TRP:CD1	2.29	0.50
1:B:218:GLN:HG2	1:B:222:GLY:HA2	1.93	0.49
1:B:307:VAL:HG23	1:B:323:LYS:HB2	1.93	0.49
1:A:307:VAL:HG23	1:A:323:LYS:HB2	1.95	0.48
1:A:101:TRP:HD1	1:A:105:CYS:O	1.96	0.48
1:A:64:VAL:HG23	1:A:122:ALA:HB2	1.96	0.47
1:A:254:LEU:HD12	1:A:254:LEU:HA	1.83	0.46
1:B:64:VAL:HG23	1:B:122:ALA:HB2	1.98	0.46
1:B:133:THR:HA	1:B:163:ALA:HB3	1.98	0.45
1:A:65:LEU:HG	1:A:246:ALA:HB2	1.99	0.44
1:A:128:PHE:HB2	1:A:195:ILE:HB	2.00	0.44
1:A:217:TRP:CZ2	1:A:226:ARG:HD3	2.52	0.44
1:B:254:LEU:HD12	1:B:254:LEU:HA	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:218:GLN:HG3	1:B:224:VAL:O	2.19	0.43
1:B:65:LEU:HG	1:B:246:ALA:HB2	2.00	0.43
1:B:188:VAL:HG21	1:B:279:GLY:HA2	2.01	0.43
1:B:128:PHE:HB2	1:B:195:ILE:HB	2.01	0.42
1:B:101:TRP:HD1	1:B:105:CYS:O	2.03	0.42
1:B:217:TRP:CZ2	1:B:226:ARG:HD3	2.55	0.42
1:A:146:GLY:HA3	1:A:363:VAL:HG13	2.01	0.41
1:B:192:ASN:HA	1:B:207:ARG:HD3	2.02	0.41

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	385/428 (90%)	375 (97%)	7 (2%)	3 (1%)	16	49
1	B	385/428 (90%)	375 (97%)	9 (2%)	1 (0%)	36	67
All	All	770/856 (90%)	750 (97%)	16 (2%)	4 (0%)	24	58

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	222	GLY
1	A	278	GLY
1	A	223	GLY
1	B	186	THR

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	323/351 (92%)	319 (99%)	4 (1%)	63	73
1	B	323/351 (92%)	320 (99%)	3 (1%)	70	75
All	All	646/702 (92%)	639 (99%)	7 (1%)	65	74

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	103	ASN
1	A	280	HIS
1	A	358	THR
1	A	388	GLN
1	B	103	ASN
1	B	164	LEU
1	B	358	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	81	HIS
1	A	90	ASN
1	A	132	GLN
1	A	277	HIS
1	A	388	GLN
1	B	16	HIS
1	B	81	HIS
1	B	90	ASN
1	B	136	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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](#)

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SO4	A	503	-	4,4,4	0.27	0	6,6,6	0.16	0
2	SO4	A	502	-	4,4,4	0.29	0	6,6,6	0.11	0
2	SO4	B	502	-	4,4,4	0.23	0	6,6,6	0.16	0
2	SO4	B	501	-	4,4,4	0.41	0	6,6,6	0.08	0
2	SO4	B	503	-	4,4,4	0.24	0	6,6,6	0.09	0
2	SO4	A	501	-	4,4,4	0.25	0	6,6,6	0.15	0

There are no bond length outliers.

There are no bond angle outliers.

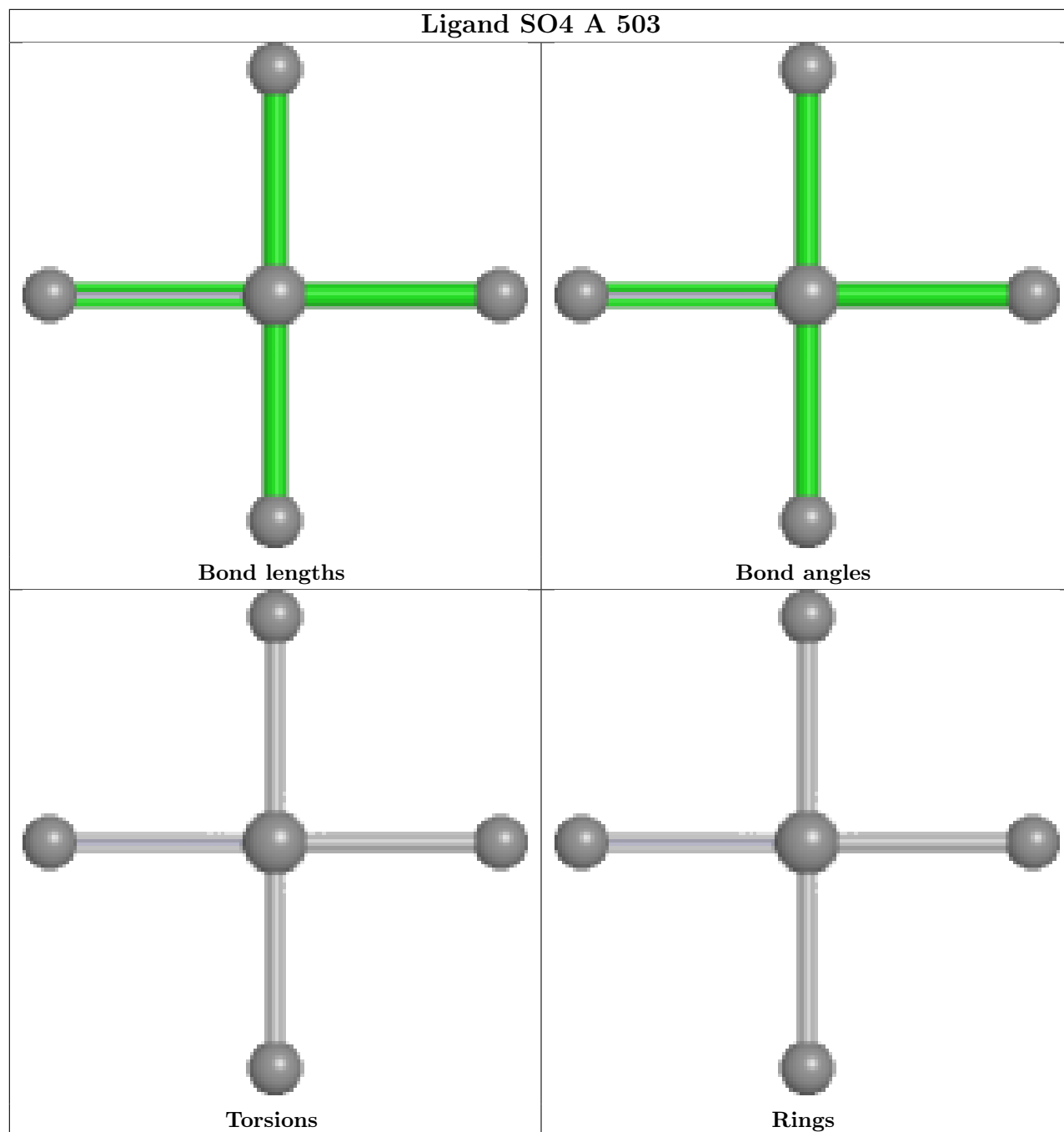
There are no chirality outliers.

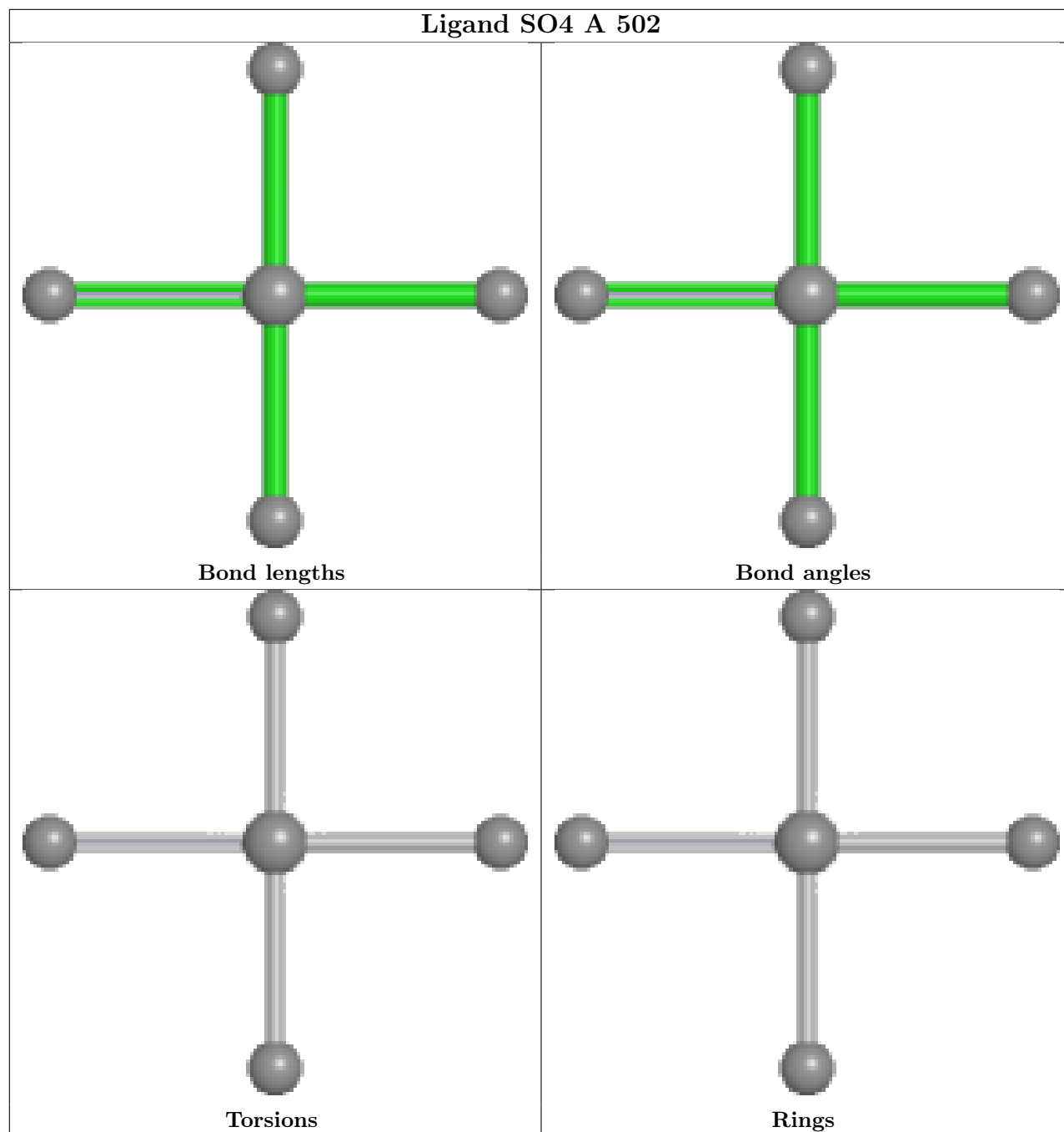
There are no torsion outliers.

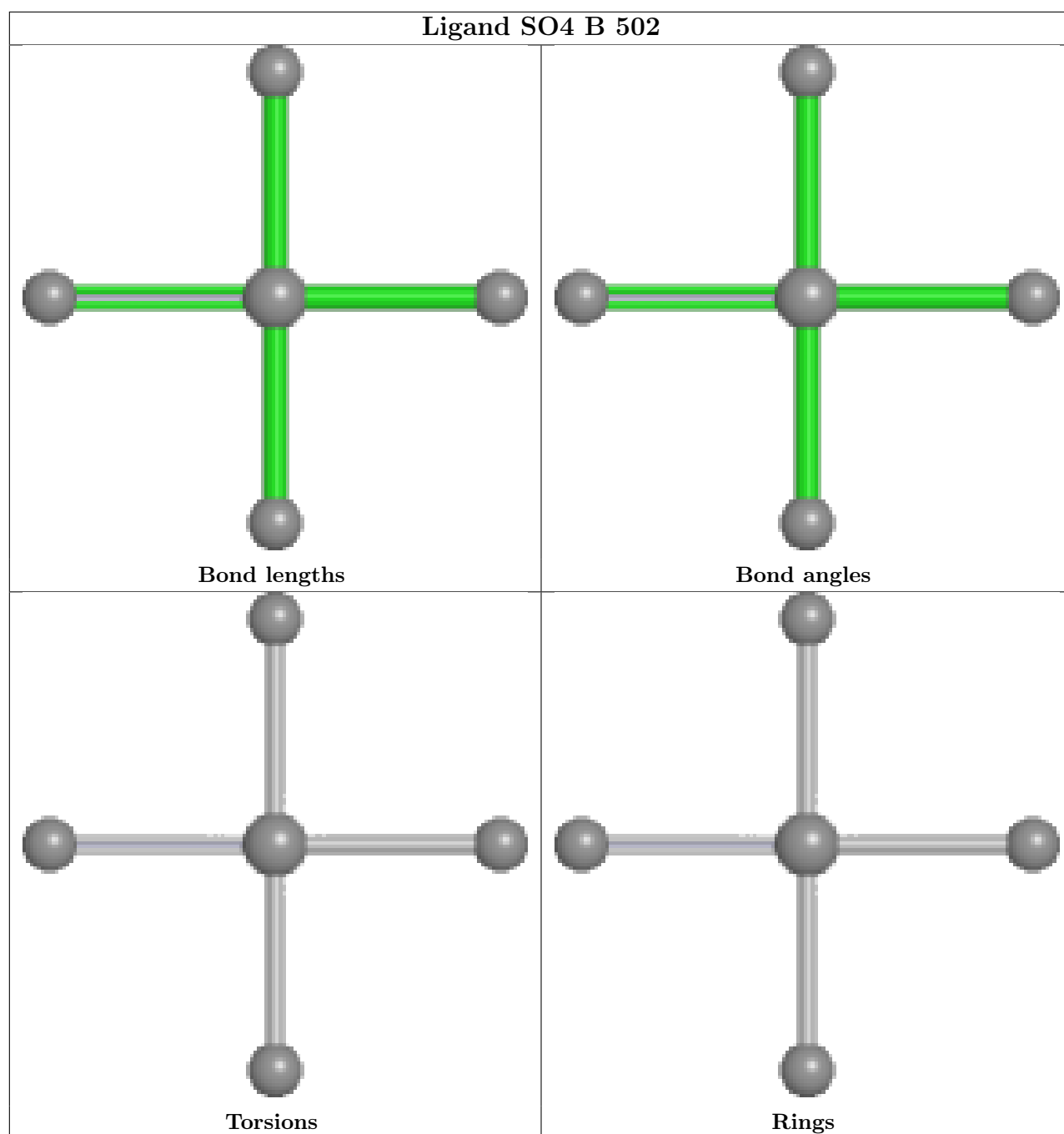
There are no ring outliers.

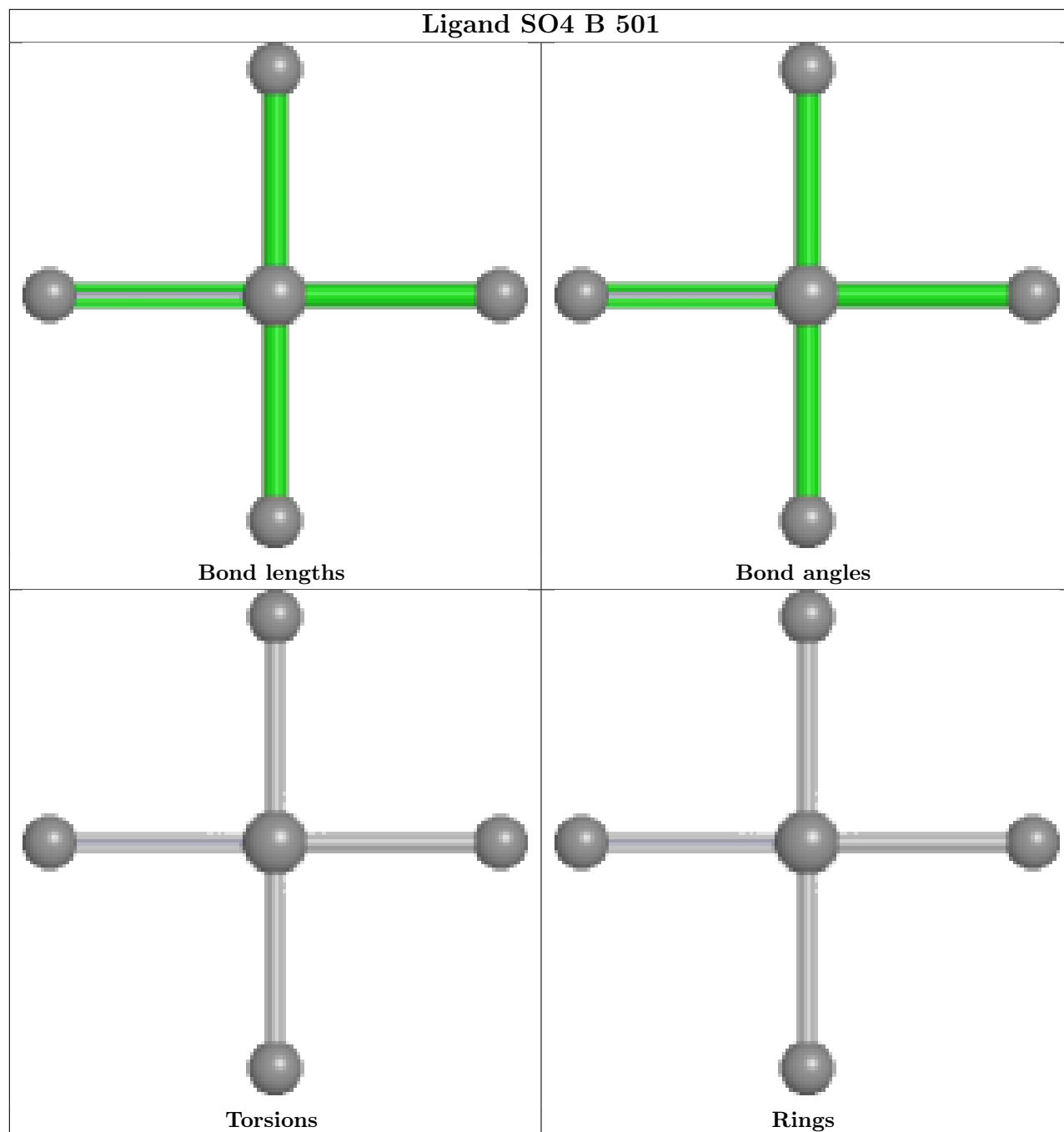
No monomer is involved in short contacts.

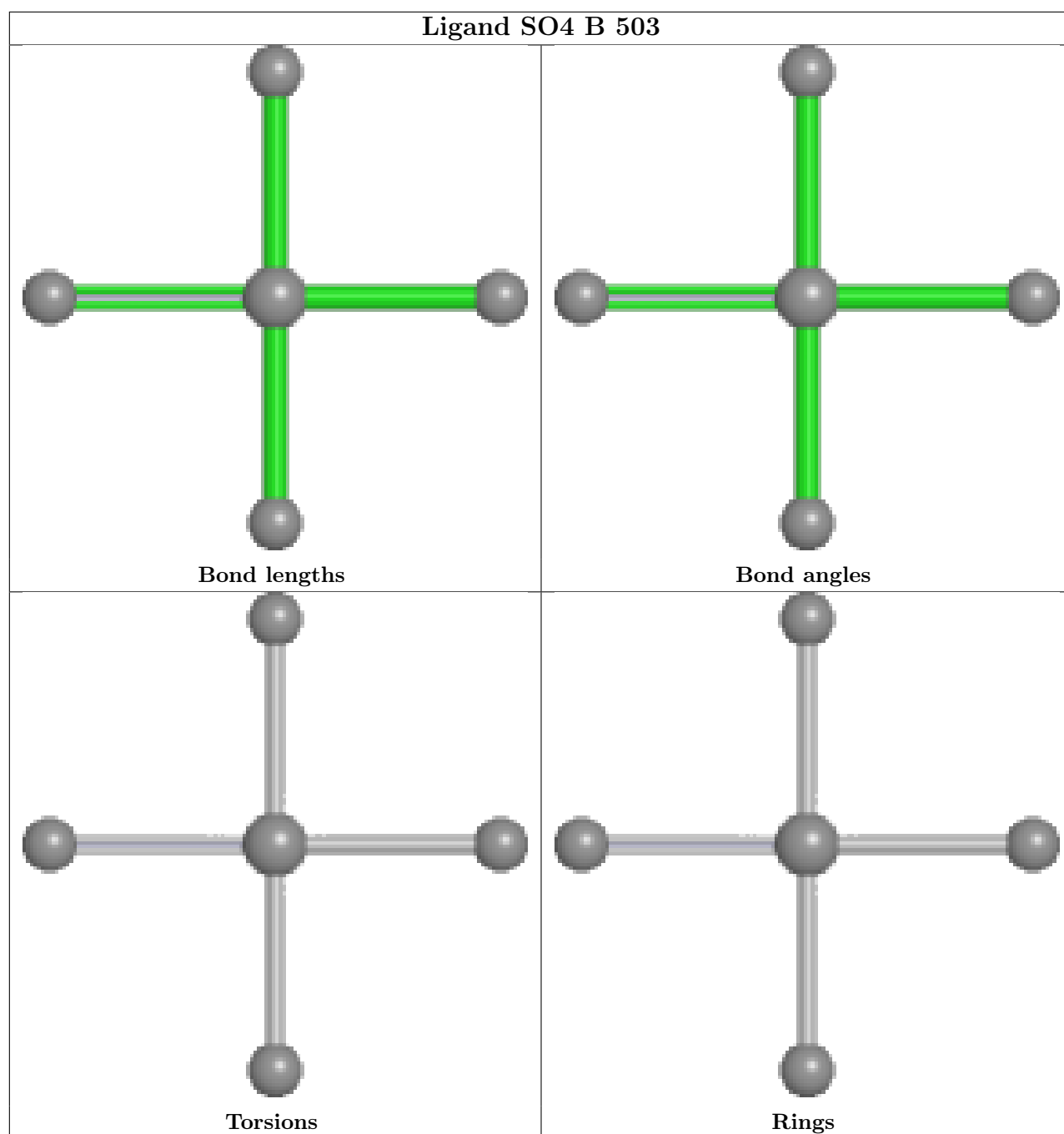
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

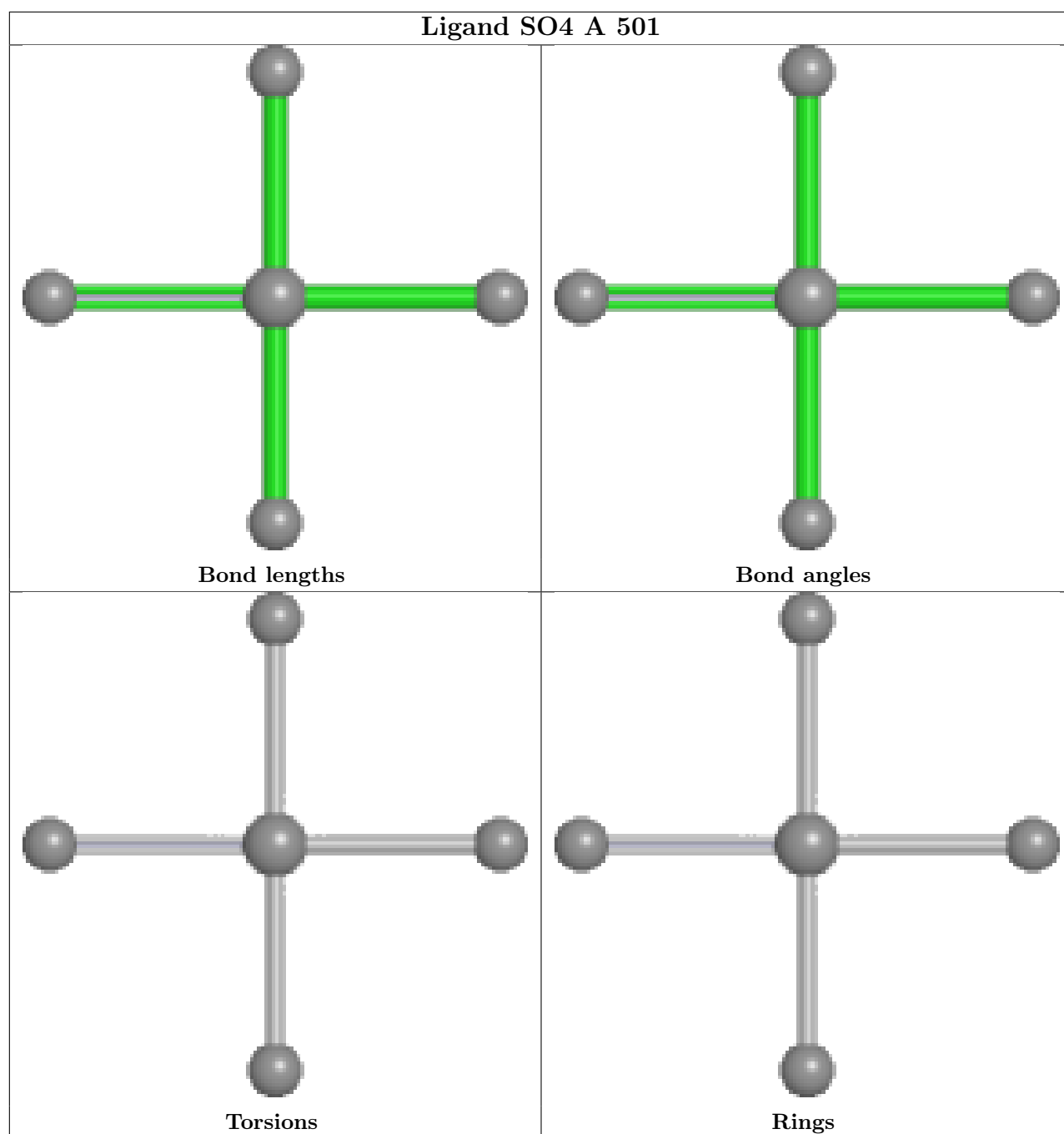












5.7 Other polymers [i](#)

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	389/428 (90%)	-0.03	7 (1%) 67 43	115, 159, 208, 234	0
1	B	389/428 (90%)	0.08	7 (1%) 67 43	127, 172, 218, 244	0
All	All	778/856 (90%)	0.02	14 (1%) 67 43	115, 166, 211, 244	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	188	VAL	2.8
1	A	163	ALA	2.7
1	A	184	VAL	2.7
1	B	125	MET	2.6
1	B	231	LEU	2.6
1	B	70	ILE	2.5
1	B	167	SER	2.4
1	A	137	TYR	2.4
1	B	319	VAL	2.3
1	B	133	THR	2.2
1	A	15	VAL	2.2
1	A	50	ILE	2.2
1	A	125	MET	2.1
1	B	240	ALA	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

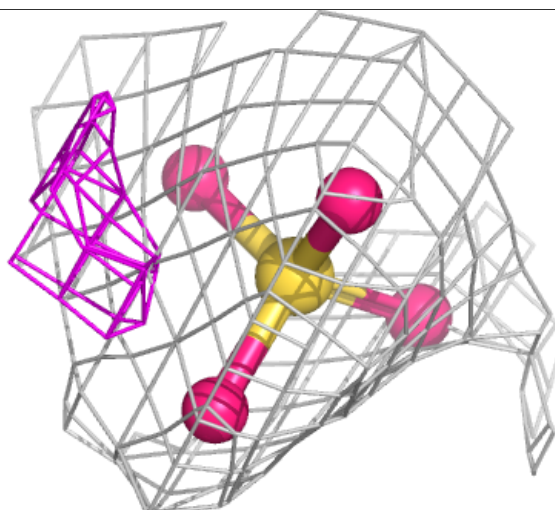
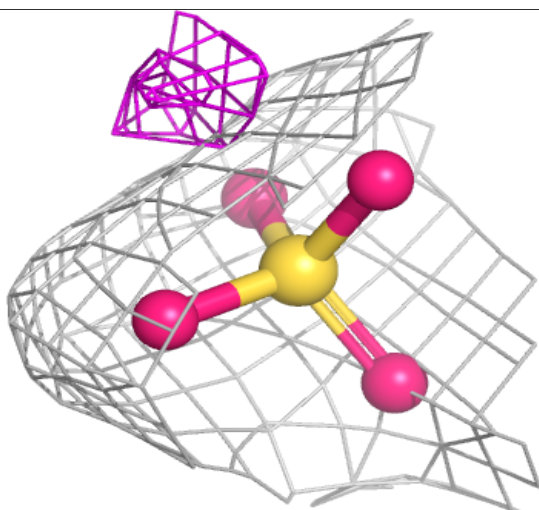
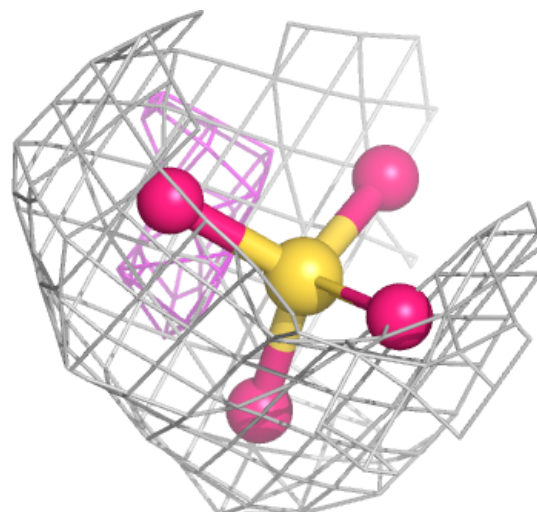
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	SO4	A	502	5/5	0.40	0.11	228,228,228,228	0
2	SO4	B	503	5/5	0.42	0.19	213,214,214,214	0
2	SO4	A	501	5/5	0.54	0.13	198,198,198,199	0
2	SO4	B	501	5/5	0.61	0.14	202,202,203,203	0
2	SO4	B	502	5/5	0.71	0.06	200,201,201,201	0
2	SO4	A	503	5/5	0.84	0.12	196,196,196,196	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.

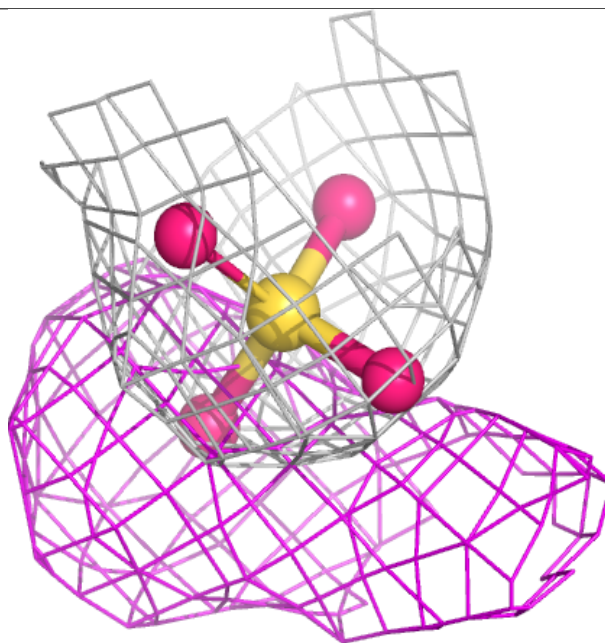
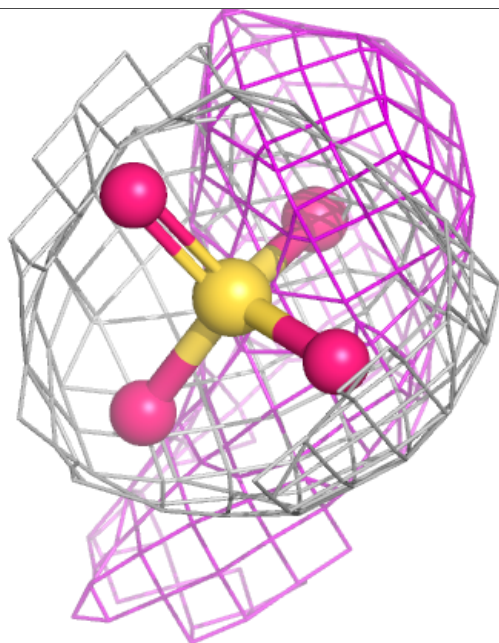
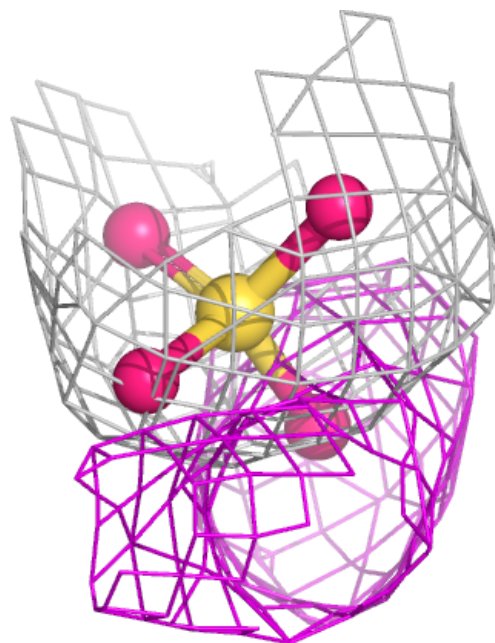
Electron density around SO4 A 502:

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



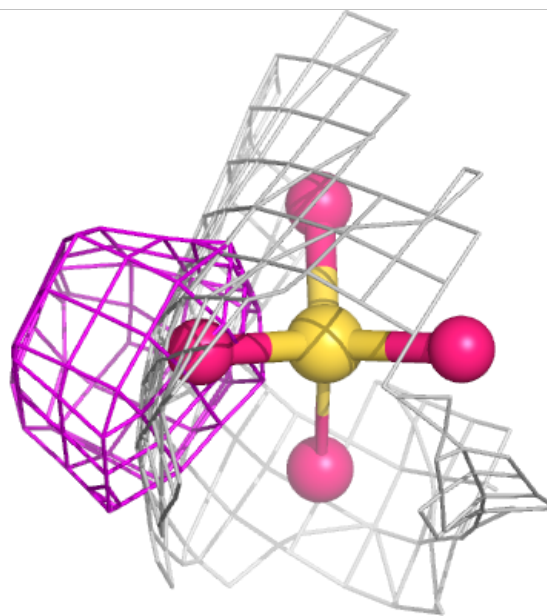
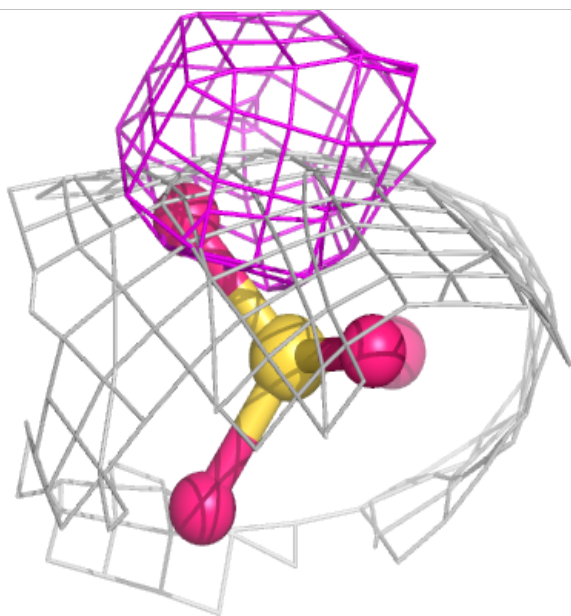
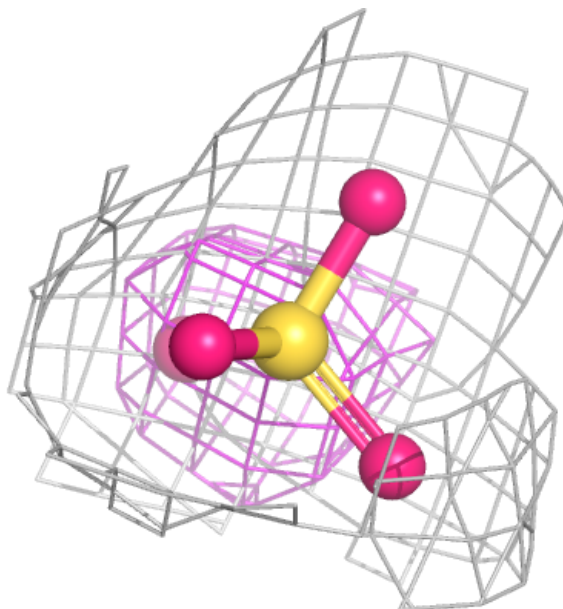
Electron density around SO4 B 503:

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



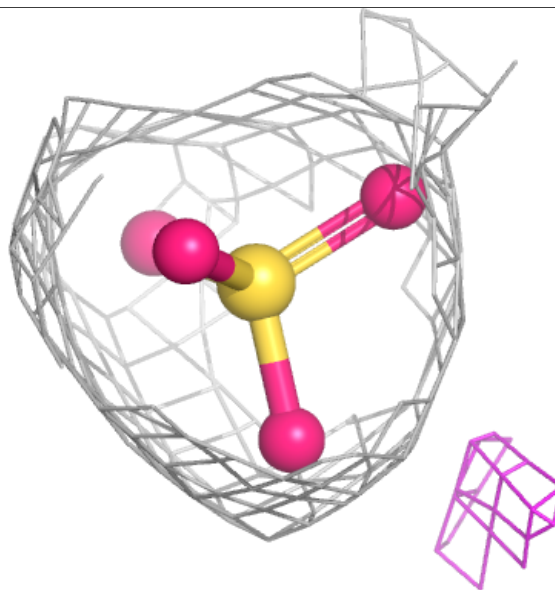
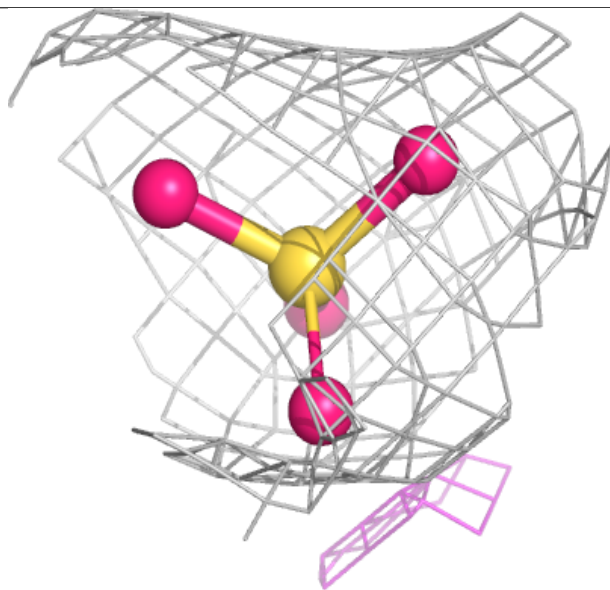
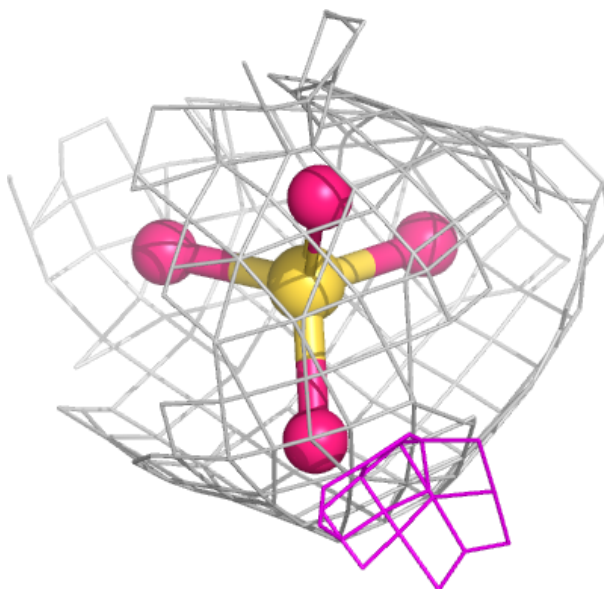
Electron density around SO4 A 501:

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



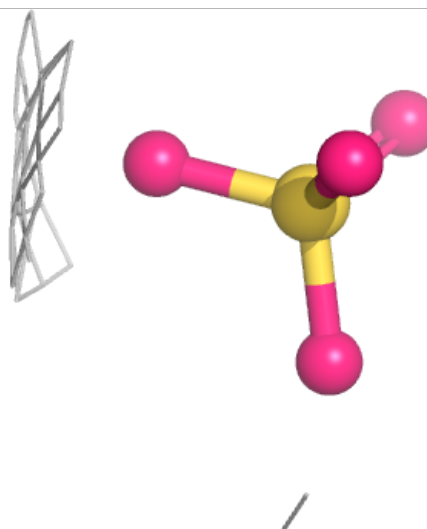
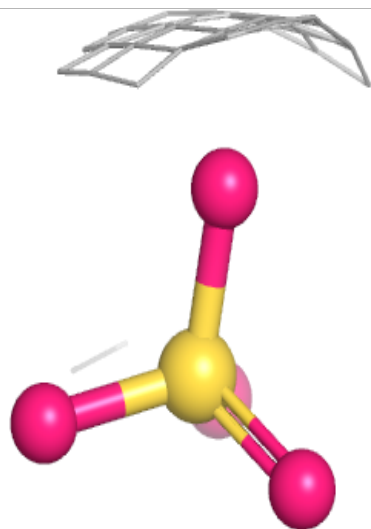
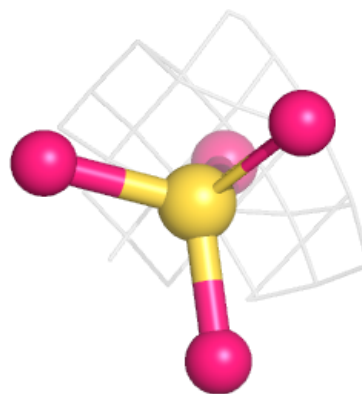
Electron density around SO4 B 501:

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



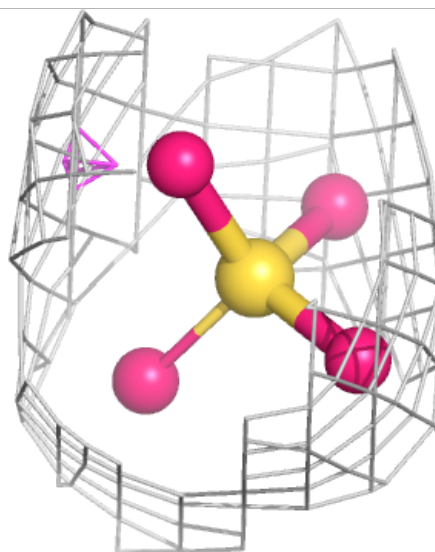
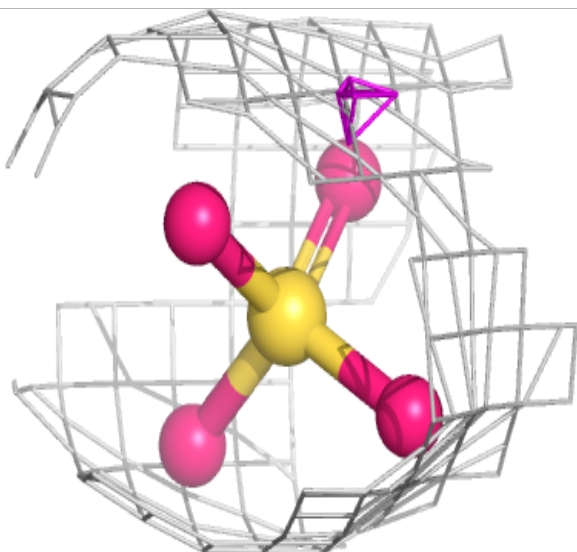
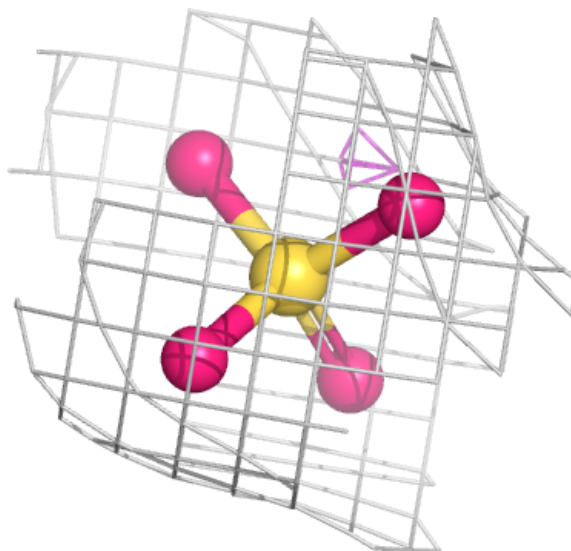
Electron density around SO4 B 502:

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



Electron density around SO4 A 503:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.