



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 01:56 PM UTC

PDB ID : 8DOL / pdb\_00008dol  
Title : Mechanism of regulation of the Helicobacter pylori Cagbeta ATPase by CagZ  
Authors : Wu, X.; Zhao, Y.; Yang, W.; Sun, L.; Ye, X.; Jiang, M.; Wang, Q.; Wang, Q.;  
Zhang, X.; Wu, Y.  
Deposited on : 2022-07-13  
Resolution : 2.80 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](mailto: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>.

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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)  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

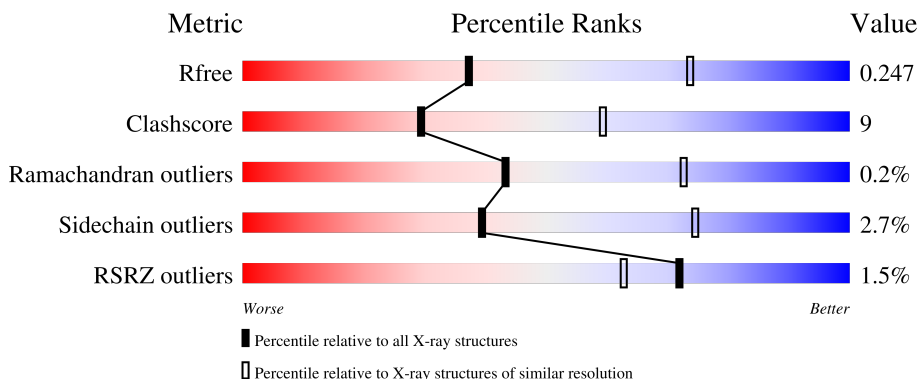
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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  $\geq 3$ , 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	593	 74% 16% • 9%
1	B	593	 64% 20% • 16%
1	C	593	 66% 19% • 14%
1	D	593	 72% 17% • 11%
1	E	593	 70% 20% • 9%

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Mol	Chain	Length	Quality of chain
1	F	593	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into four segments: a small red segment at the beginning labeled '2%', followed by a large green segment labeled '65%', a yellow segment labeled '23%', and a small grey segment at the end labeled '11%'.</p>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 24565 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 Cag pathogenicity island protein (Cag5).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	540	4301	2760	716	797	28	0	0	0
1	B	498	3861	2480	643	714	24	0	0	0
1	C	510	3741	2390	635	697	19	0	0	0
1	D	530	4186	2688	693	778	27	0	0	0
1	E	540	4273	2739	713	794	27	0	0	0
1	F	527	4120	2648	677	770	25	0	0	0

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	156	GLY	-	expression tag	UNP O25260
A	157	THR	-	expression tag	UNP O25260
A	158	SER	-	expression tag	UNP O25260
A	159	SER	-	expression tag	UNP O25260
A	160	MET	-	expression tag	UNP O25260
A	161	ALA	-	expression tag	UNP O25260
A	162	ASP	-	expression tag	UNP O25260
A	163	ILE	-	expression tag	UNP O25260
A	164	GLY	-	expression tag	UNP O25260
A	165	SER	-	expression tag	UNP O25260
B	156	GLY	-	expression tag	UNP O25260
B	157	THR	-	expression tag	UNP O25260
B	158	SER	-	expression tag	UNP O25260
B	159	SER	-	expression tag	UNP O25260
B	160	MET	-	expression tag	UNP O25260
B	161	ALA	-	expression tag	UNP O25260
B	162	ASP	-	expression tag	UNP O25260

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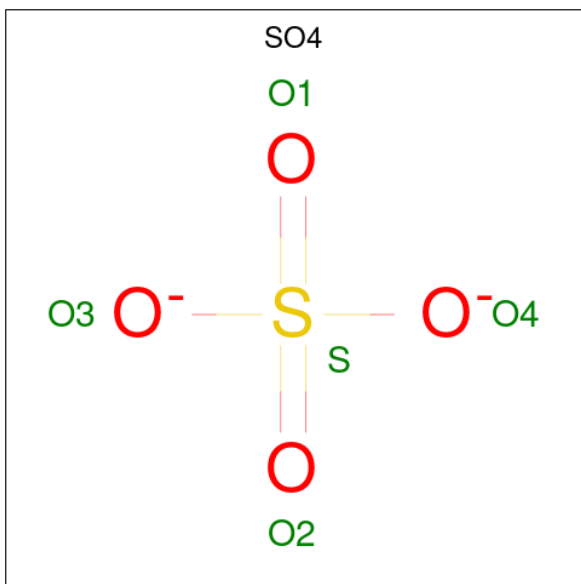
Chain	Residue	Modelled	Actual	Comment	Reference
B	163	ILE	-	expression tag	UNP O25260
B	164	GLY	-	expression tag	UNP O25260
B	165	SER	-	expression tag	UNP O25260
C	156	GLY	-	expression tag	UNP O25260
C	157	THR	-	expression tag	UNP O25260
C	158	SER	-	expression tag	UNP O25260
C	159	SER	-	expression tag	UNP O25260
C	160	MET	-	expression tag	UNP O25260
C	161	ALA	-	expression tag	UNP O25260
C	162	ASP	-	expression tag	UNP O25260
C	163	ILE	-	expression tag	UNP O25260
C	164	GLY	-	expression tag	UNP O25260
C	165	SER	-	expression tag	UNP O25260
D	156	GLY	-	expression tag	UNP O25260
D	157	THR	-	expression tag	UNP O25260
D	158	SER	-	expression tag	UNP O25260
D	159	SER	-	expression tag	UNP O25260
D	160	MET	-	expression tag	UNP O25260
D	161	ALA	-	expression tag	UNP O25260
D	162	ASP	-	expression tag	UNP O25260
D	163	ILE	-	expression tag	UNP O25260
D	164	GLY	-	expression tag	UNP O25260
D	165	SER	-	expression tag	UNP O25260
E	156	GLY	-	expression tag	UNP O25260
E	157	THR	-	expression tag	UNP O25260
E	158	SER	-	expression tag	UNP O25260
E	159	SER	-	expression tag	UNP O25260
E	160	MET	-	expression tag	UNP O25260
E	161	ALA	-	expression tag	UNP O25260
E	162	ASP	-	expression tag	UNP O25260
E	163	ILE	-	expression tag	UNP O25260
E	164	GLY	-	expression tag	UNP O25260
E	165	SER	-	expression tag	UNP O25260
F	156	GLY	-	expression tag	UNP O25260
F	157	THR	-	expression tag	UNP O25260
F	158	SER	-	expression tag	UNP O25260
F	159	SER	-	expression tag	UNP O25260
F	160	MET	-	expression tag	UNP O25260
F	161	ALA	-	expression tag	UNP O25260
F	162	ASP	-	expression tag	UNP O25260
F	163	ILE	-	expression tag	UNP O25260
F	164	GLY	-	expression tag	UNP O25260

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Chain	Residue	Modelled	Actual	Comment	Reference
F	165	SER	-	expression tag	UNP O25260

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O<sub>4</sub>S) (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	B	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	E	1	Total O S 5 4 1	0	0
2	F	1	Total O S 5 4 1	0	0

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).

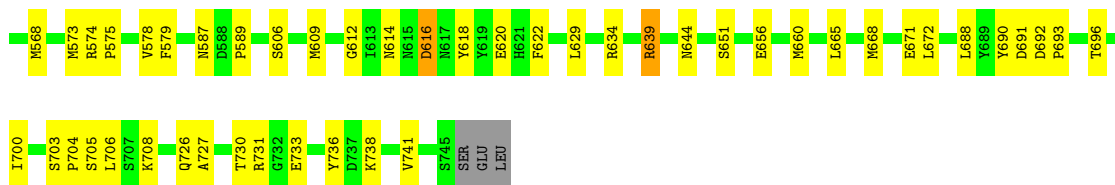


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 7 4 3	0	0
3	B	1	Total C O 7 4 3	0	0
3	C	1	Total C O 7 4 3	0	0
3	D	1	Total C O 7 4 3	0	0
3	E	1	Total C O 7 4 3	0	0
3	F	1	Total C O 7 4 3	0	0

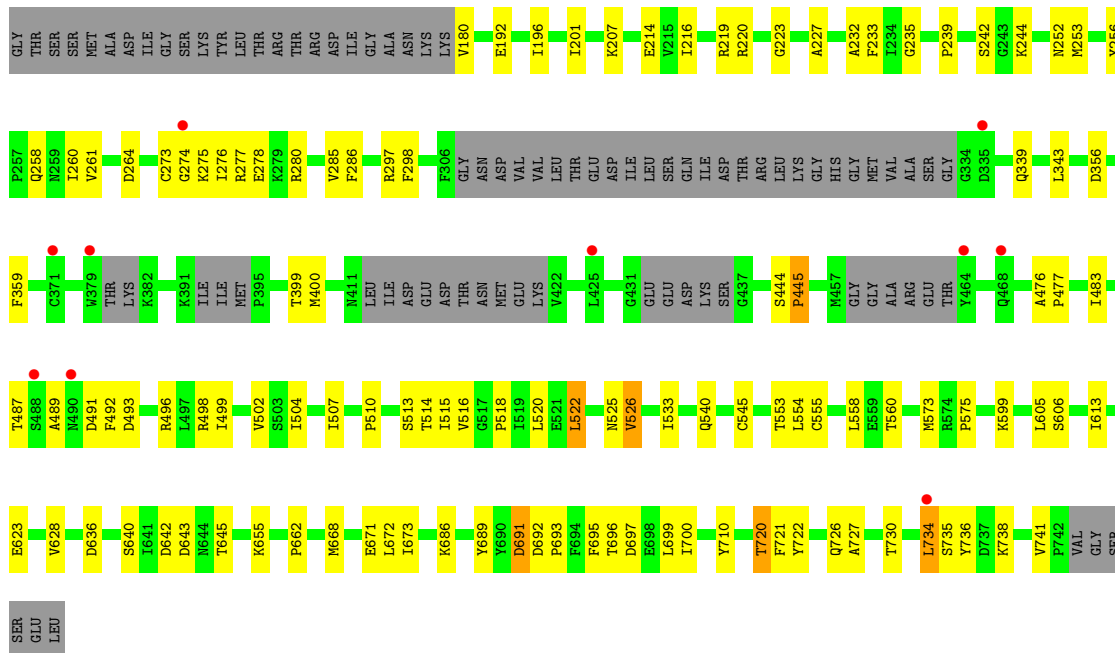
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	3	Total O 3 3	0	0
4	B	2	Total O 2 2	0	0
4	C	1	Total O 1 1	0	0
4	D	1	Total O 1 1	0	0
4	E	3	Total O 3 3	0	0
4	F	1	Total O 1 1	0	0

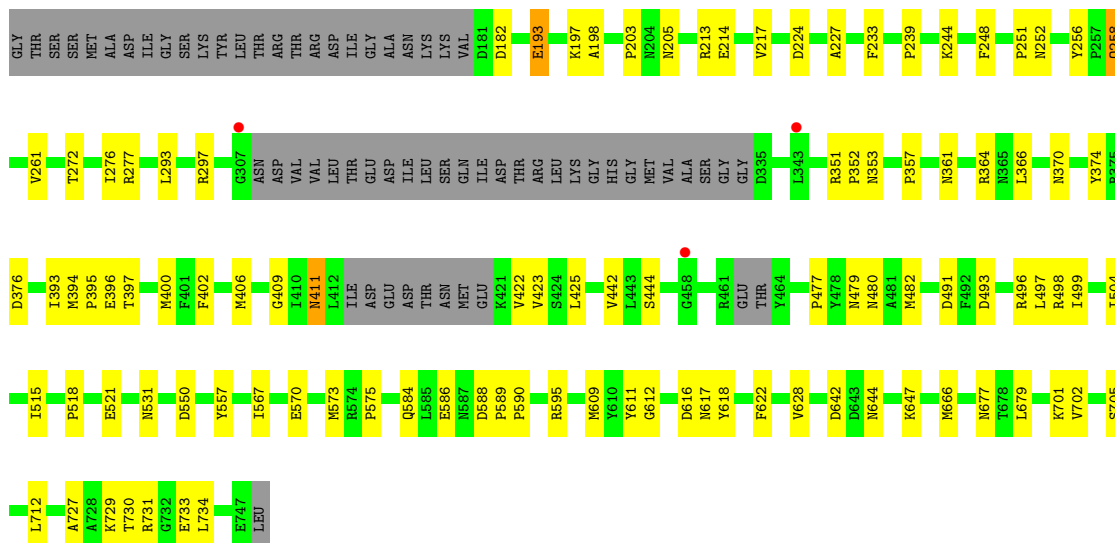




• Molecule 1: Cag pathogenicity island protein (Cag5)

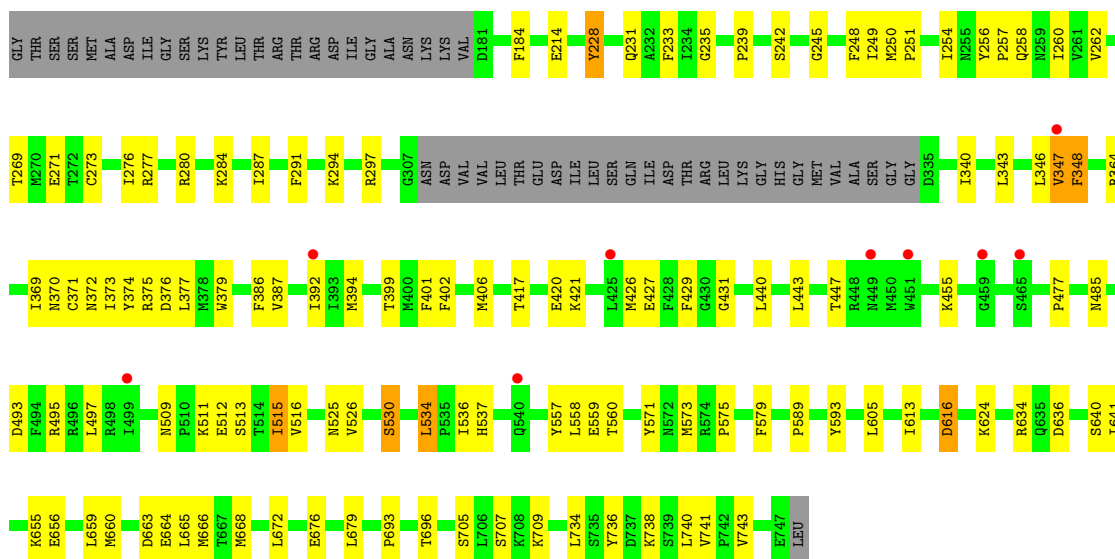


• Molecule 1: Cag pathogenicity island protein (Cag5)



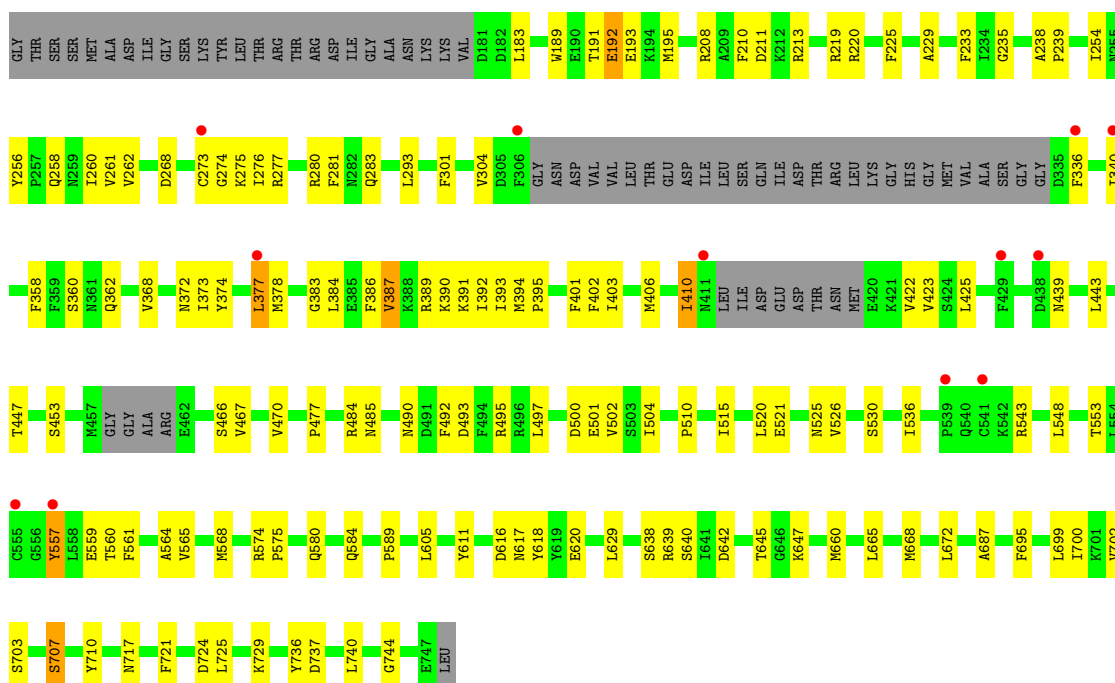
- Molecule 1: Cag pathogenicity island protein (Cag5)

Chain E: 70% 20% 9%



- Molecule 1: Cag pathogenicity island protein (Cag5)

Chain F: 65% 23% 11%



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	112.11Å 163.28Å 112.22Å 90.00° 93.33° 90.00°	Depositor
Resolution (Å)	40.79 – 2.80 40.79 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.2 (40.79-2.80) 99.3 (40.79-2.80)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.88 (at 2.81Å)	Xtrriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, $R_{free}$	0.197 , 0.247 0.198 , 0.247	Depositor DCC
$R_{free}$ test set	1988 reflections (2.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	77.4	Xtrriage
Anisotropy	0.058	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 91.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.015 for l,-k,h	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	24565	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	99.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.67% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: PEG, 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	0.12	0/4397	0.30	0/5932
1	B	0.13	0/3946	0.34	2/5334 (0.0%)
1	C	0.14	0/3814	0.33	0/5170
1	D	0.13	0/4280	0.30	0/5780
1	E	0.12	0/4368	0.30	0/5898
1	F	0.12	0/4211	0.30	0/5695
All	All	0.13	0/25016	0.31	2/33809 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	445	PRO	N-CA-CB	6.40	110.31	103.52
1	B	378	MET	CB-CG-SD	5.17	128.20	112.70

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	4301	0	4260	59	0
1	B	3861	0	3707	74	0
1	C	3741	0	3439	68	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	4186	0	4097	62	0
1	E	4273	0	4199	77	0
1	F	4120	0	4009	92	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	1	0
2	D	5	0	0	0	0
2	E	5	0	0	0	0
2	F	5	0	0	0	0
3	A	7	0	10	0	0
3	B	7	0	10	0	0
3	C	7	0	10	0	0
3	D	7	0	10	0	0
3	E	7	0	10	0	0
3	F	7	0	10	1	0
4	A	3	0	0	2	0
4	B	2	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	1	0
4	E	3	0	0	1	0
4	F	1	0	0	0	0
All	All	24565	0	23771	416	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 9.

The worst 5 of 416 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:356:ASP:OD1	1:C:359:PHE:N	2.10	0.84
1:F:192:GLU:OE2	1:F:220:ARG:NH1	2.13	0.80
1:D:611:TYR:O	4:D:901:HOH:O	2.02	0.78
1:E:493:ASP:OD1	1:E:495:ARG:HG3	1.86	0.75
1:A:596:ASN:OD1	1:B:587:ASN:ND2	2.19	0.74

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	536/593 (90%)	508 (95%)	28 (5%)	0	100	100
1	B	490/593 (83%)	465 (95%)	24 (5%)	1 (0%)	43	72
1	C	496/593 (84%)	469 (95%)	26 (5%)	1 (0%)	43	72
1	D	522/593 (88%)	500 (96%)	19 (4%)	3 (1%)	21	51
1	E	536/593 (90%)	516 (96%)	19 (4%)	1 (0%)	43	72
1	F	519/593 (88%)	501 (96%)	18 (4%)	0	100	100
All	All	3099/3558 (87%)	2959 (96%)	134 (4%)	6 (0%)	43	72

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	445	PRO
1	B	456	THR
1	E	347	VAL
1	D	193	GLU
1	D	213	ARG

### 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	469/520 (90%)	460 (98%)	9 (2%)	50	81
1	B	399/520 (77%)	390 (98%)	9 (2%)	44	78
1	C	354/520 (68%)	342 (97%)	12 (3%)	32	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	452/520 (87%)	442 (98%)	10 (2%)	45	78
1	E	461/520 (89%)	447 (97%)	14 (3%)	36	72
1	F	442/520 (85%)	426 (96%)	16 (4%)	31	66
All	All	2577/3120 (83%)	2507 (97%)	70 (3%)	39	74

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	377	LEU
1	F	387	VAL
1	F	557	TYR
1	C	553	THR
1	C	526	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	296	HIS
1	F	635	GLN
1	D	644	ASN
1	F	718	GLN
1	F	485	ASN

### 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

12 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	C	801	-	4,4,4	0.24	0	6,6,6	0.15	0
3	PEG	C	802	-	6,6,6	0.12	0	5,5,5	0.09	0
2	SO4	A	801	-	4,4,4	0.25	0	6,6,6	0.08	0
2	SO4	F	801	-	4,4,4	0.23	0	6,6,6	0.15	0
2	SO4	E	801	-	4,4,4	0.22	0	6,6,6	0.13	0
3	PEG	A	802	-	6,6,6	0.13	0	5,5,5	0.06	0
2	SO4	D	801	-	4,4,4	0.24	0	6,6,6	0.08	0
2	SO4	B	801	-	4,4,4	0.23	0	6,6,6	0.12	0
3	PEG	D	802	-	6,6,6	0.12	0	5,5,5	0.10	0
3	PEG	B	802	-	6,6,6	0.10	0	5,5,5	0.10	0
3	PEG	E	802	-	6,6,6	0.14	0	5,5,5	0.06	0
3	PEG	F	802	-	6,6,6	0.14	0	5,5,5	0.11	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	PEG	C	802	-	-	2/4/4/4	-
3	PEG	A	802	-	-	2/4/4/4	-
3	PEG	E	802	-	-	2/4/4/4	-
3	PEG	D	802	-	-	1/4/4/4	-
3	PEG	B	802	-	-	1/4/4/4	-
3	PEG	F	802	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

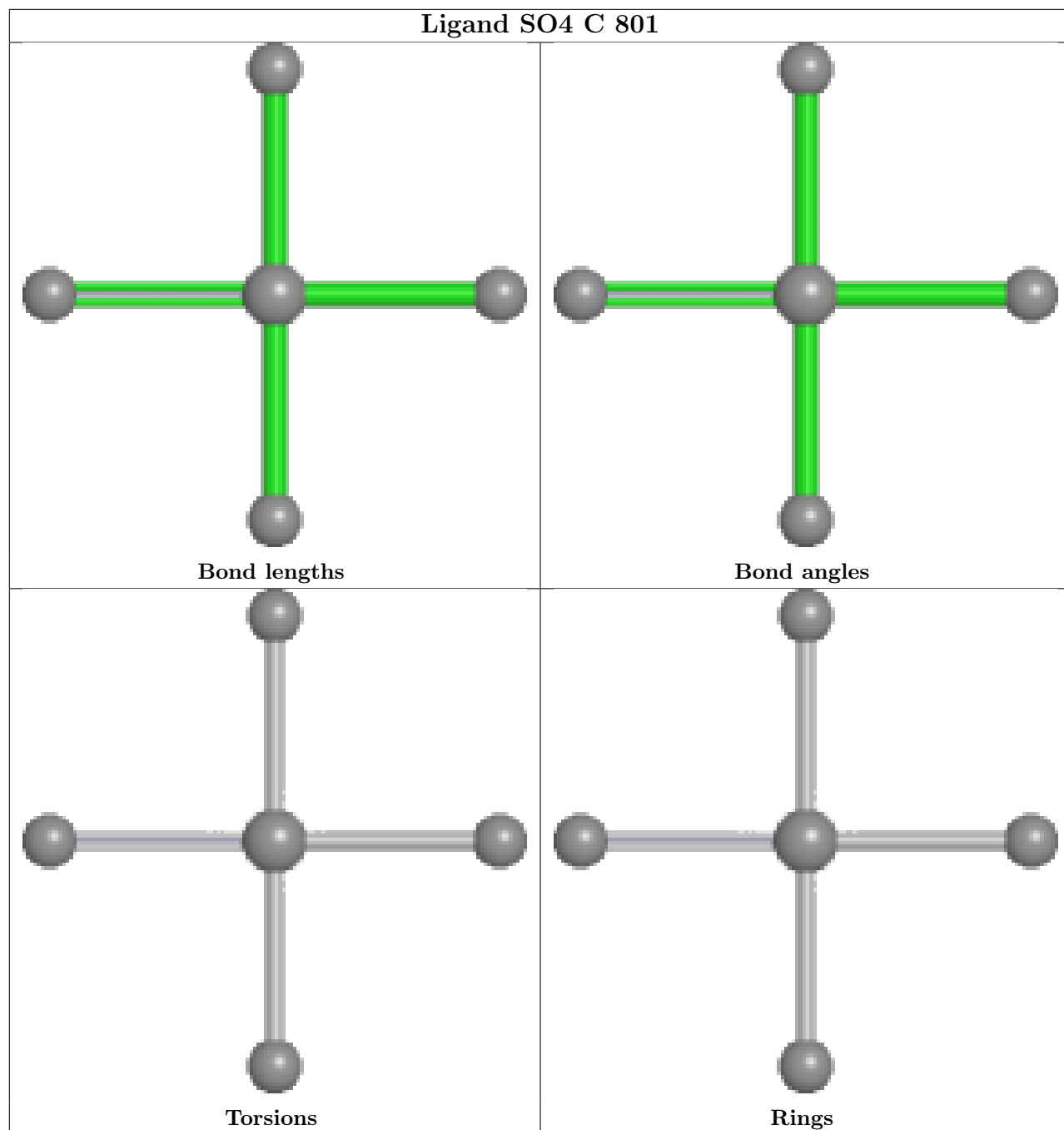
Mol	Chain	Res	Type	Atoms
3	A	802	PEG	O1-C1-C2-O2
3	F	802	PEG	O2-C3-C4-O4
3	C	802	PEG	O1-C1-C2-O2
3	E	802	PEG	O1-C1-C2-O2
3	F	802	PEG	O1-C1-C2-O2

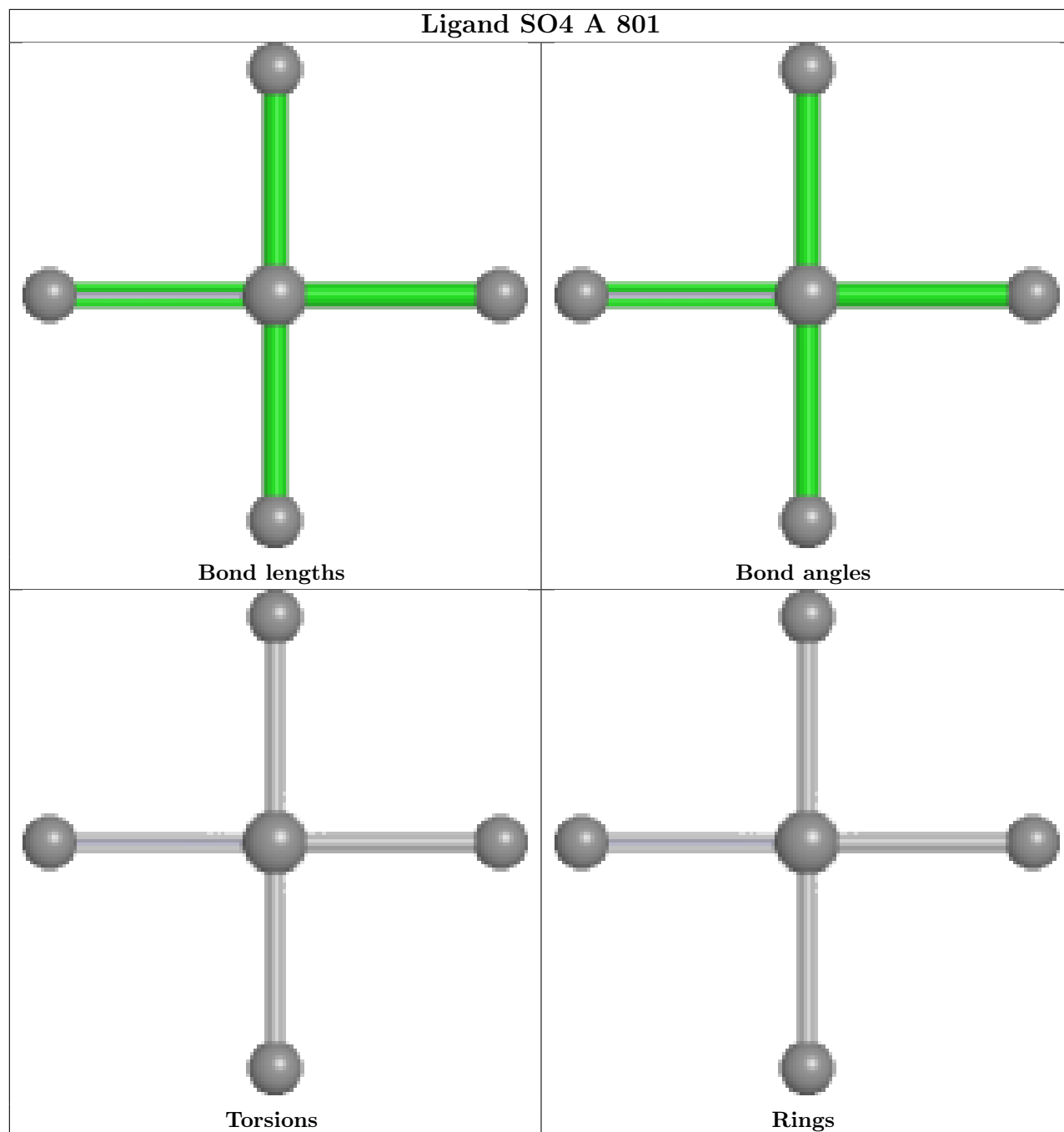
There are no ring outliers.

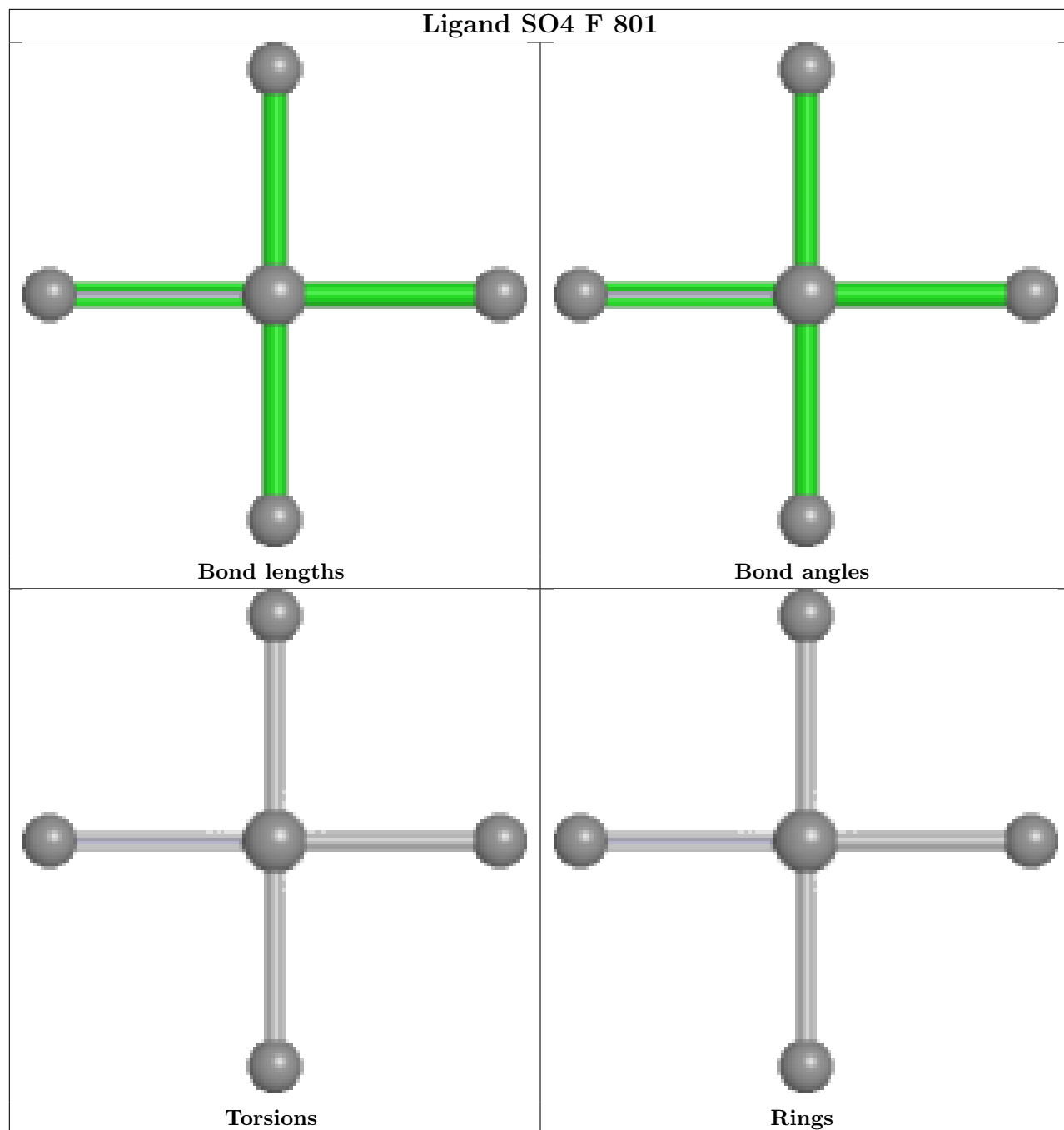
2 monomers are involved in 2 short contacts:

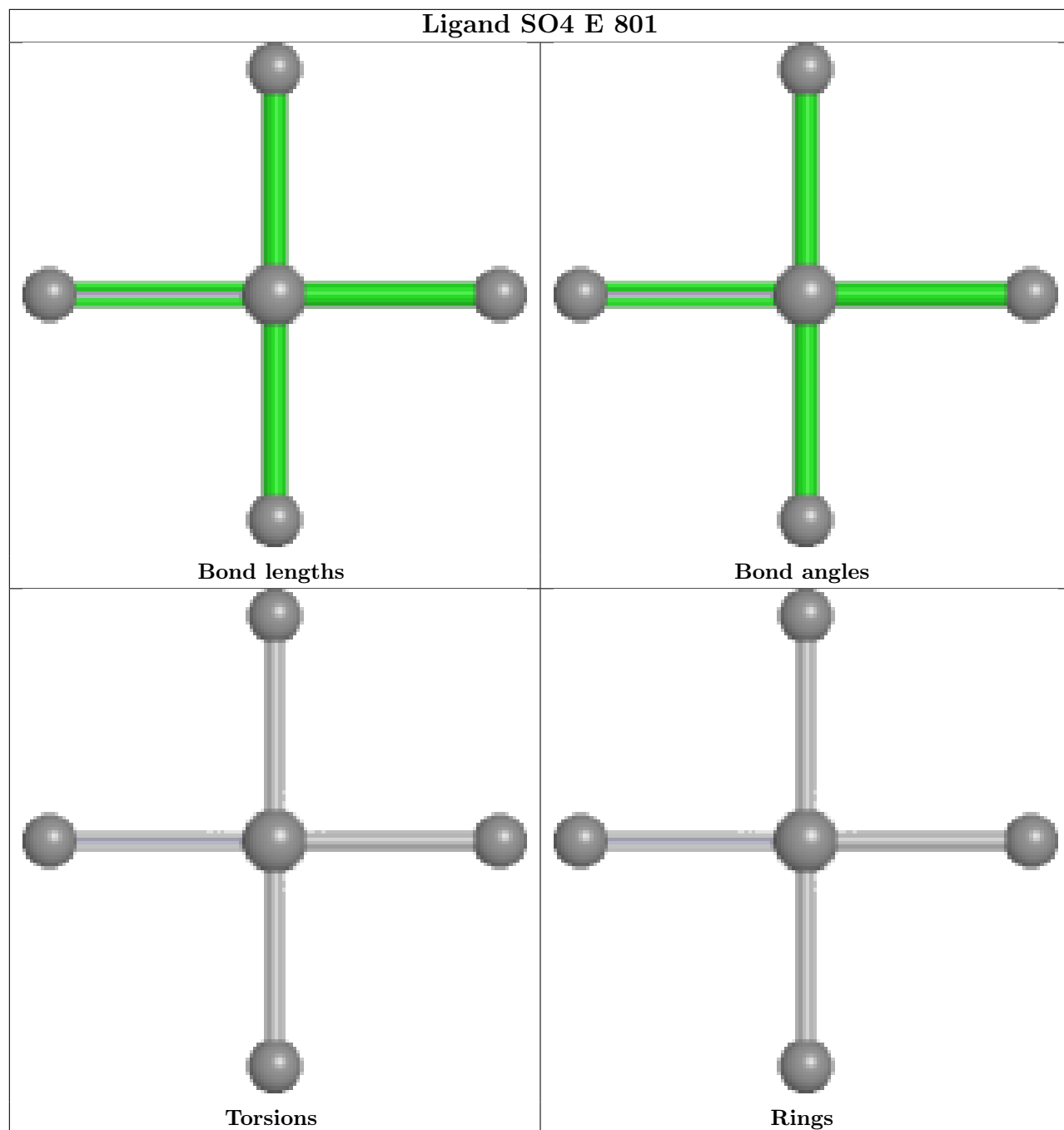
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	801	SO4	1	0
3	F	802	PEG	1	0

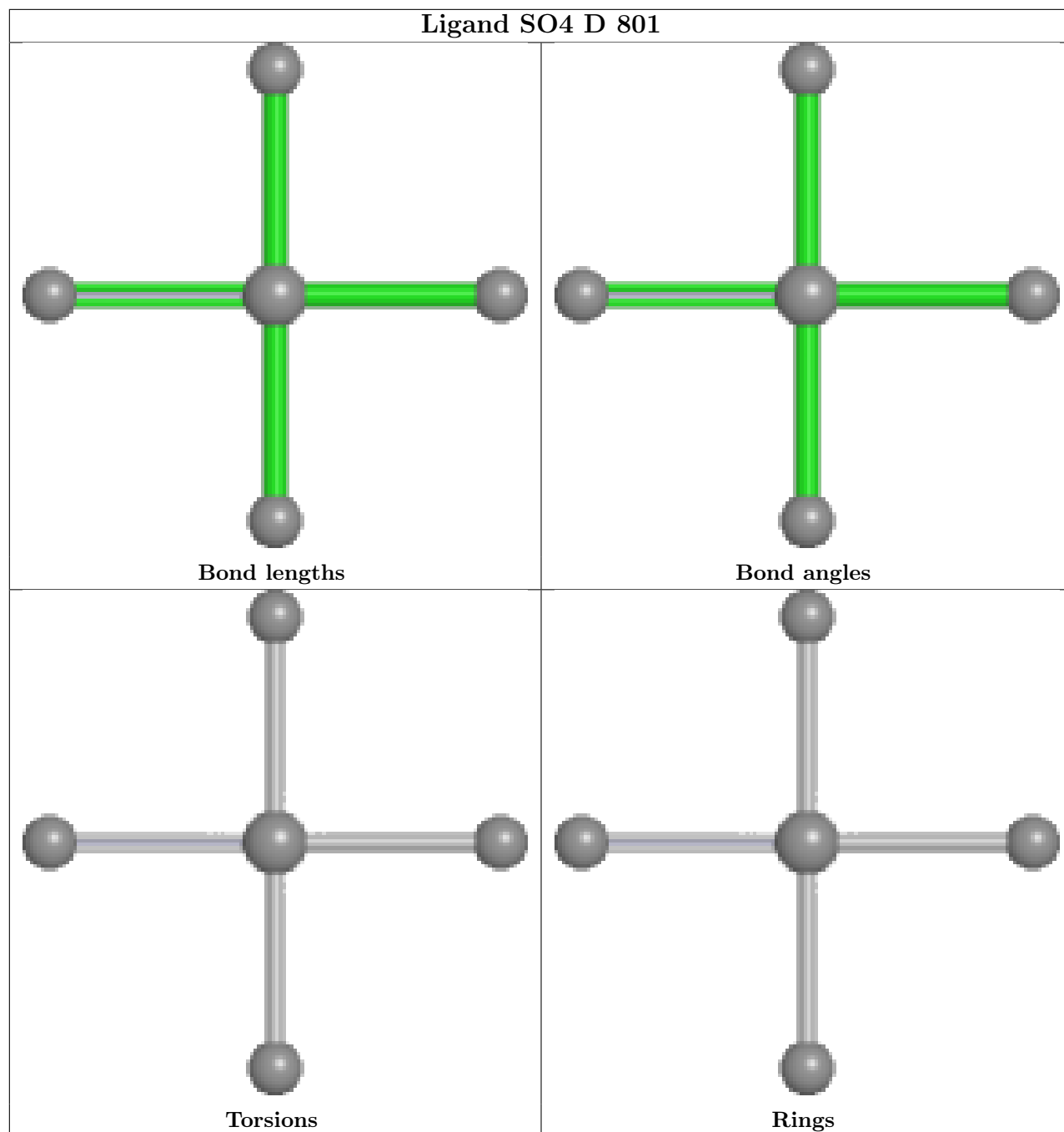
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

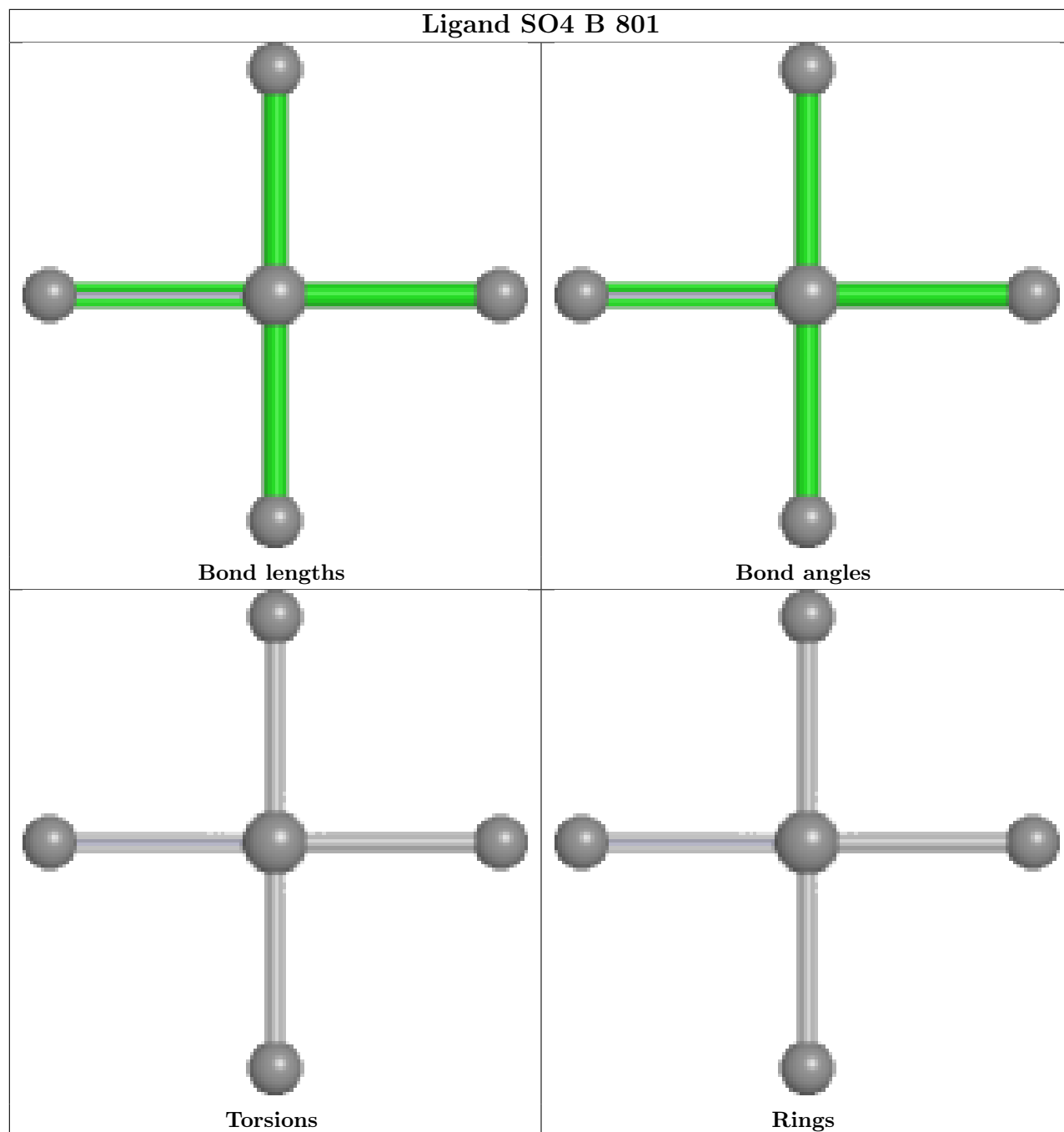












## 5.7 Other polymers [i](#)

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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	540/593 (91%)	-0.33	5 (0%) 81 74	44, 74, 113, 185	0
1	B	498/593 (83%)	-0.03	8 (1%) 70 61	45, 85, 197, 250	0
1	C	510/593 (86%)	0.24	10 (1%) 65 56	47, 109, 216, 272	0
1	D	530/593 (89%)	-0.07	3 (0%) 85 80	45, 96, 172, 230	0
1	E	540/593 (91%)	-0.06	9 (1%) 69 60	44, 80, 175, 214	0
1	F	527/593 (88%)	0.03	12 (2%) 61 51	47, 101, 215, 273	0
All	All	3145/3558 (88%)	-0.04	47 (1%) 72 63	44, 89, 198, 273	0

The worst 5 of 47 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	451	TRP	3.9
1	C	488	SER	3.9
1	C	734	LEU	3.4
1	B	472	THR	3.4
1	F	377	LEU	3.3

### 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

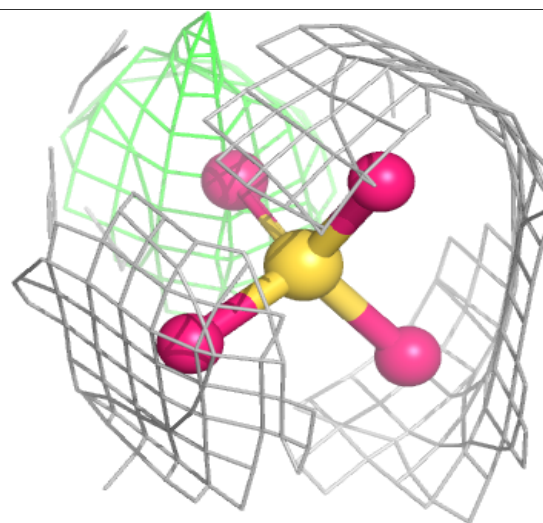
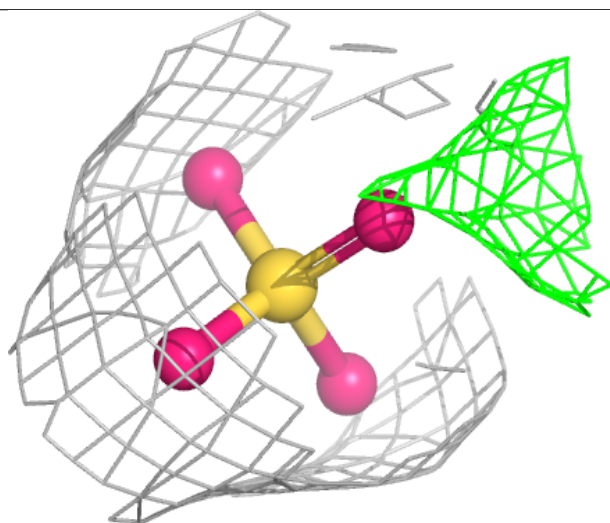
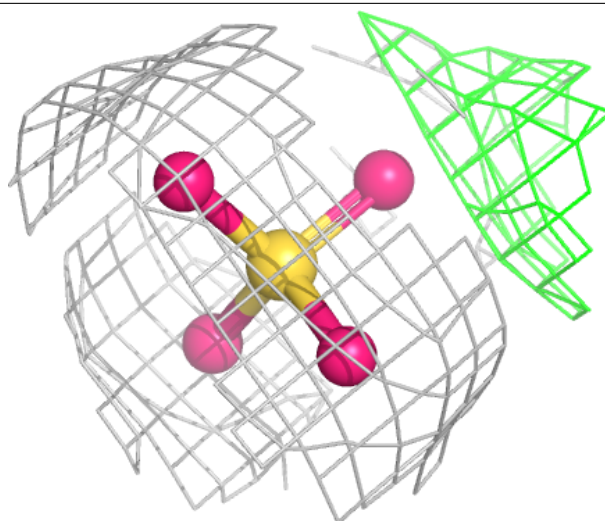
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	SO4	C	801	5/5	0.79	0.10	74,98,106,107	0
3	PEG	E	802	7/7	0.80	0.13	80,100,103,108	0
2	SO4	E	801	5/5	0.82	0.14	63,70,81,306	0
3	PEG	A	802	7/7	0.85	0.11	71,82,97,101	0
2	SO4	F	801	5/5	0.89	0.11	63,72,85,234	0
3	PEG	C	802	7/7	0.90	0.14	72,81,92,92	0
2	SO4	A	801	5/5	0.90	0.08	65,75,80,90	0
3	PEG	F	802	7/7	0.90	0.12	81,89,94,94	0
3	PEG	D	802	7/7	0.91	0.11	74,81,94,99	0
3	PEG	B	802	7/7	0.91	0.10	71,80,89,108	0
2	SO4	D	801	5/5	0.91	0.06	66,66,73,77	0
2	SO4	B	801	5/5	0.94	0.06	72,78,79,83	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.

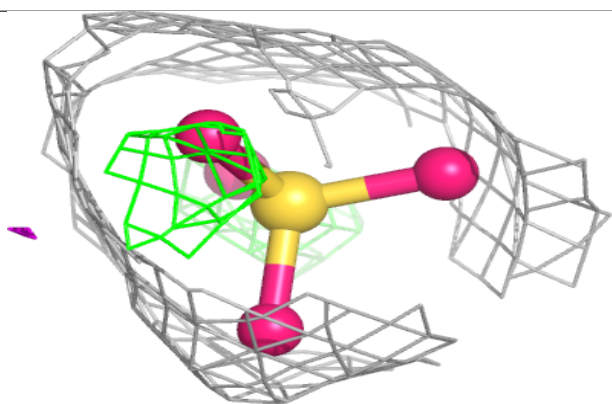
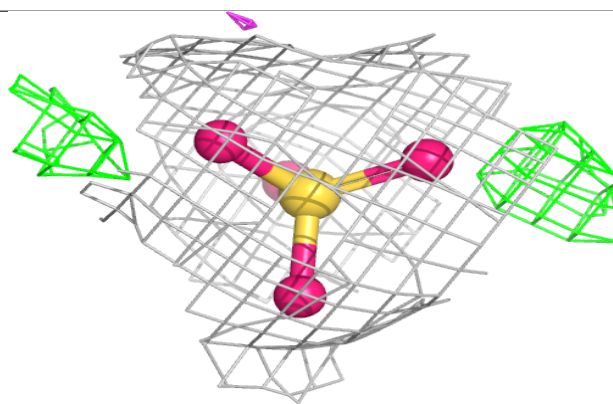
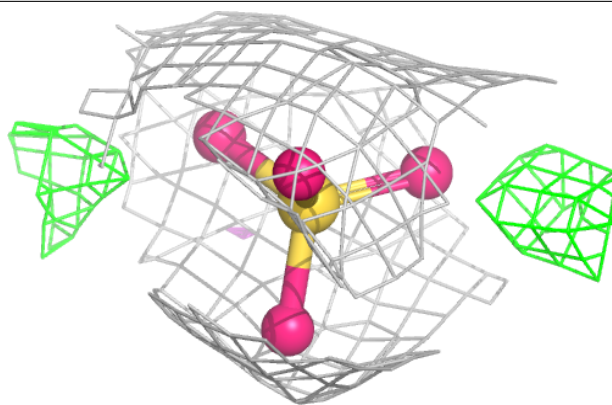
**Electron density around SO4 C 801:**

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



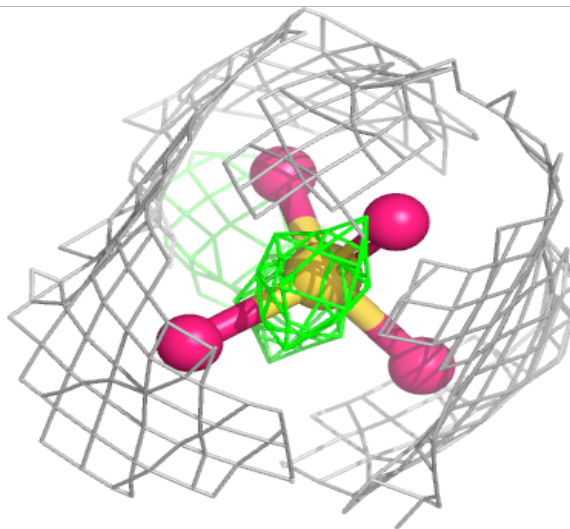
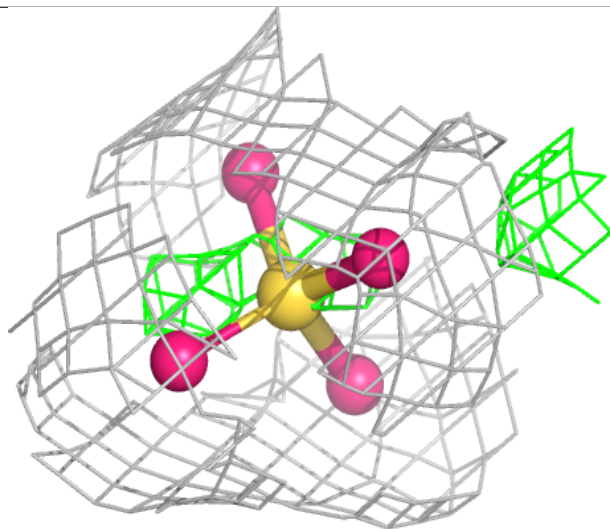
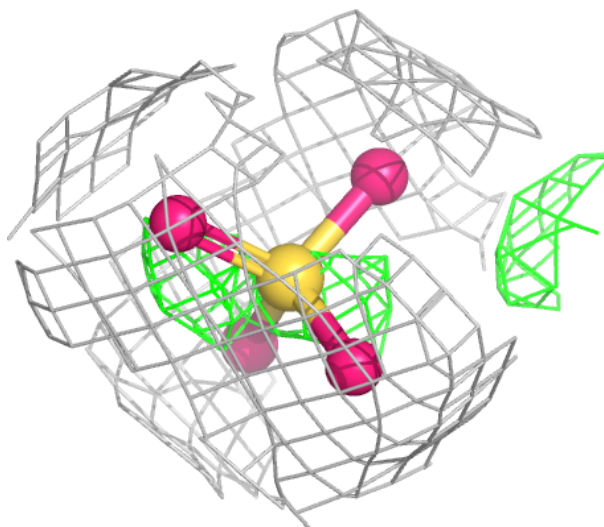
**Electron density around SO4 E 801:**

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



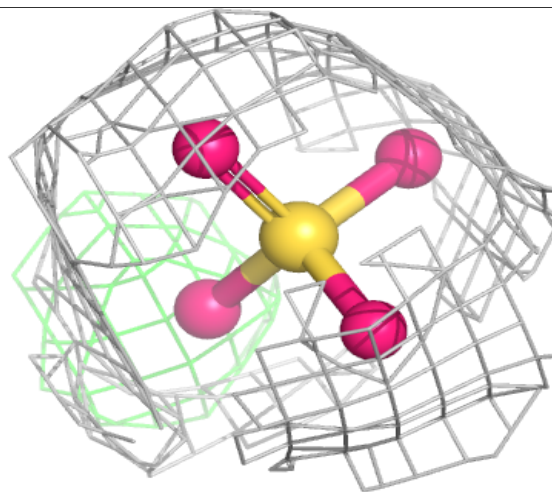
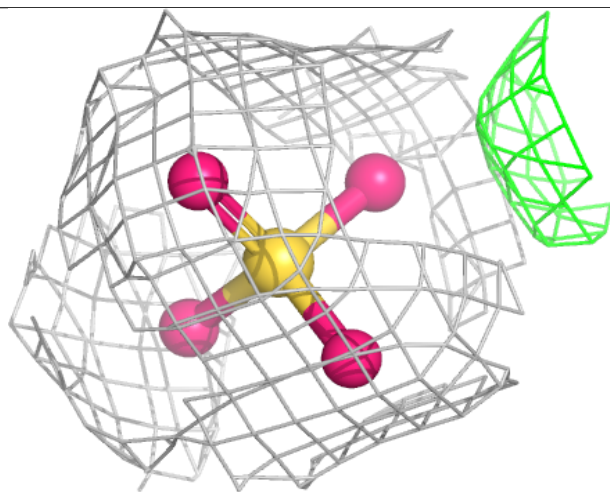
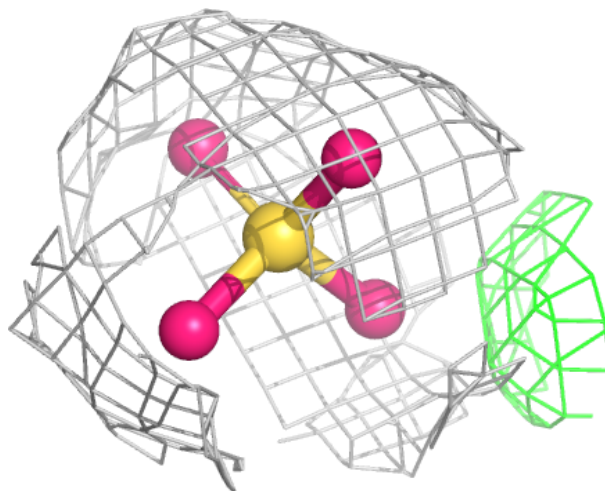
**Electron density around SO4 F 801:**

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



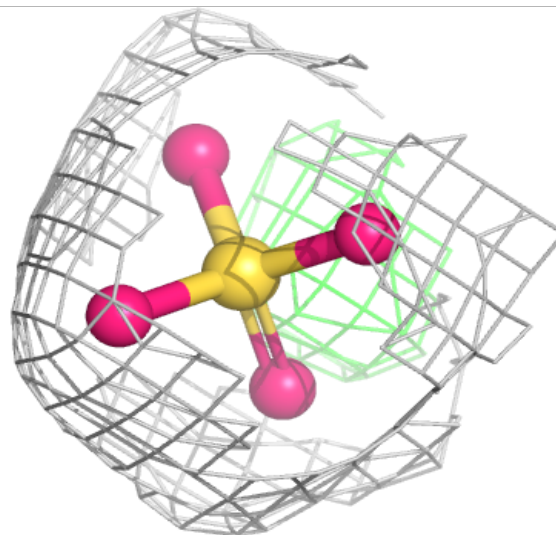
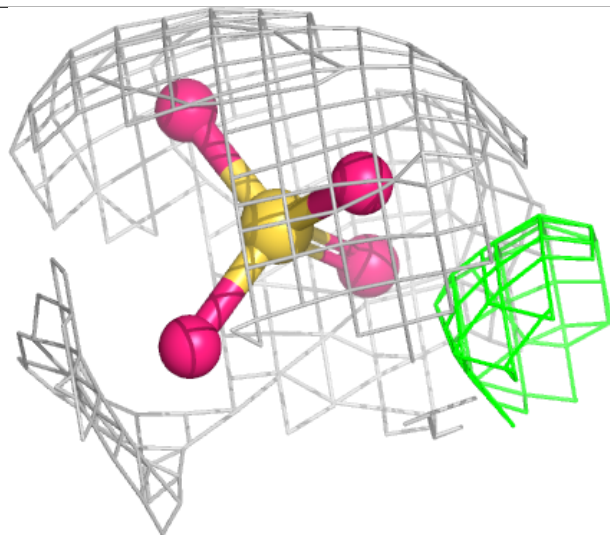
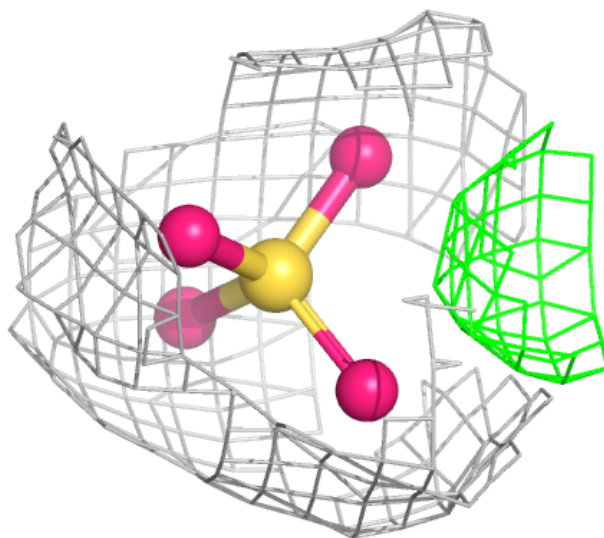
**Electron density around SO4 A 801:**

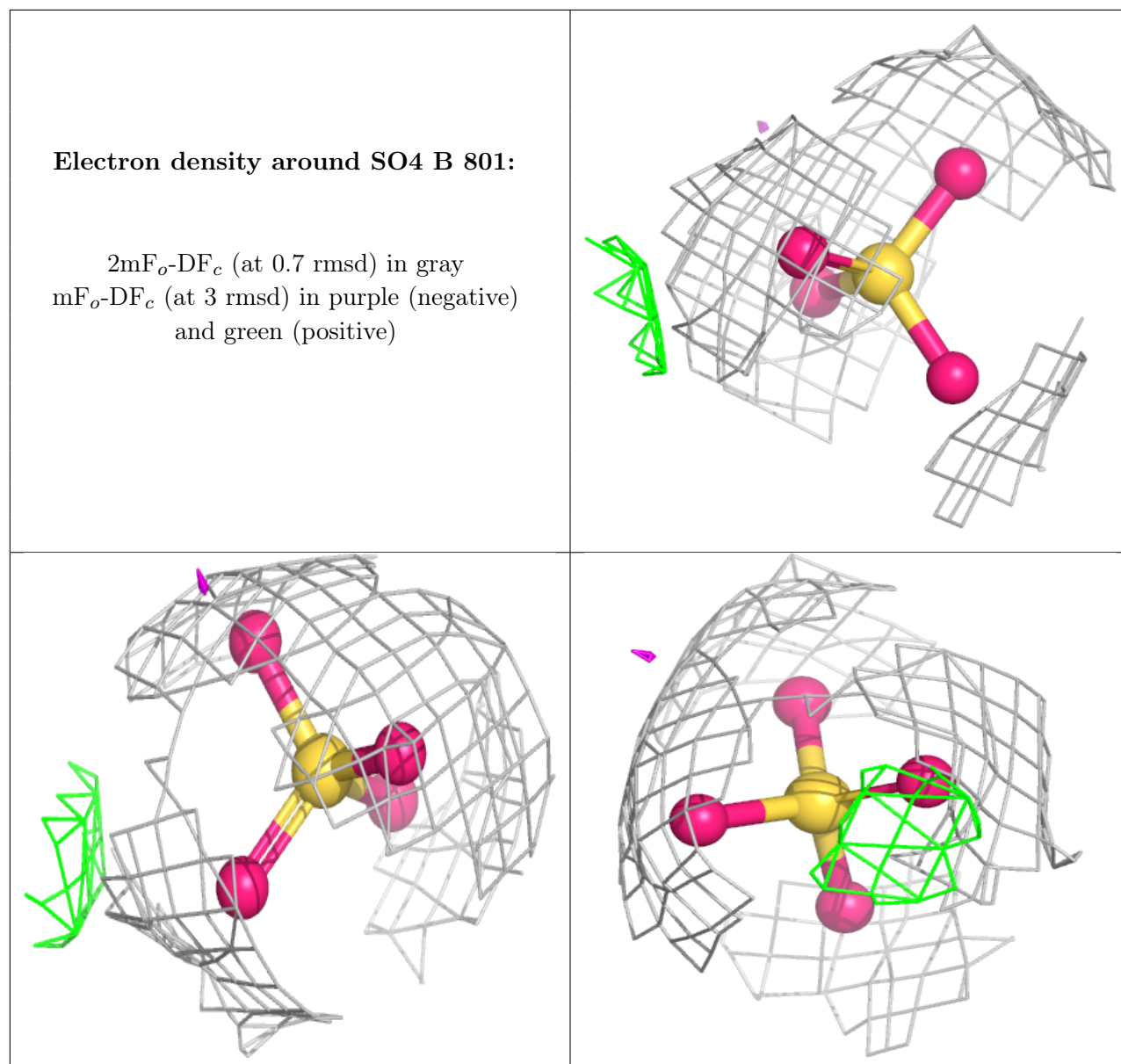
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around SO4 D 801:**

$2mF_o-DF_c$  (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.