



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:21 PM UTC

PDB ID : 7ERP / pdb_00007erp
Title : The regulatory domain of YeiE, a sulfite sensing LysR-type transcriptional regulator from Cronobacter sakazakii (sulfite-bound form)
Authors : Hong, S.; Ha, N.-C.
Deposited on : 2021-05-06
Resolution : 2.03 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

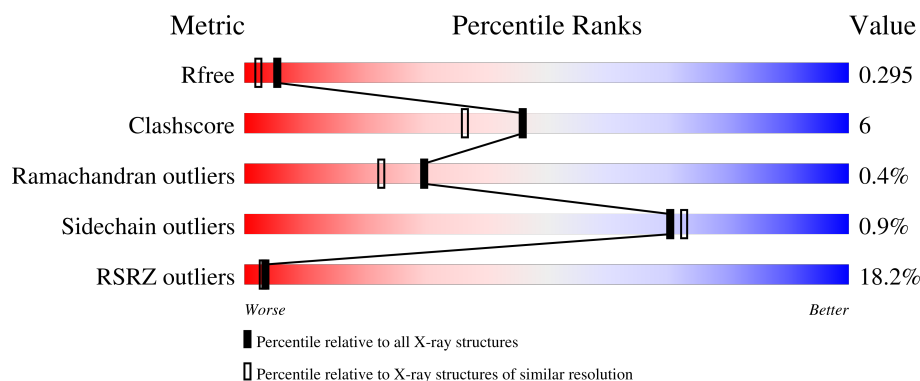
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.03 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	13299 (2.04-2.00)
Clashscore	190562	1022 (2.02-2.02)
Ramachandran outliers	187476	1014 (2.02-2.02)
Sidechain outliers	187428	1014 (2.02-2.02)
RSRZ outliers	180081	13314 (2.04-2.00)

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	208	
1	B	208	
1	C	208	
1	D	208	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6352 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.

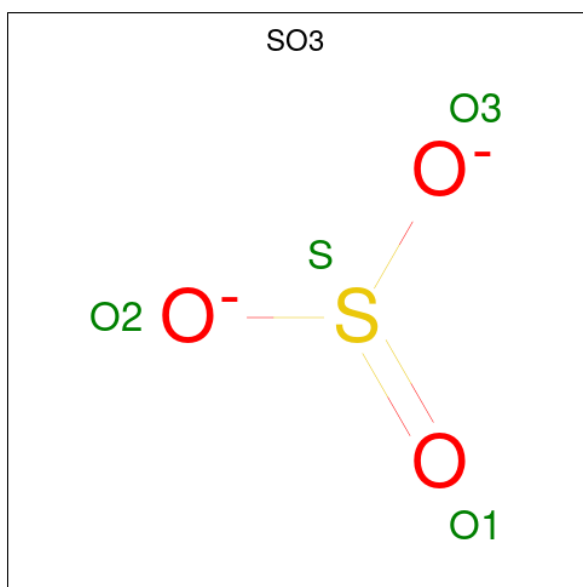
- Molecule 1 is a protein called LysR family transcriptional regulator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	196	Total	C	N	O	S	0	0	0
			1548	990	273	277	8			
1	B	199	Total	C	N	O	S	0	0	0
			1572	1005	278	281	8			
1	C	196	Total	C	N	O	S	0	0	0
			1548	990	273	277	8			
1	D	182	Total	C	N	O	S	0	0	0
			1434	912	255	259	8			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	81	GLY	-	expression tag	UNP H9BVC9
A	82	ALA	-	expression tag	UNP H9BVC9
A	83	MET	-	expression tag	UNP H9BVC9
A	84	GLY	-	expression tag	UNP H9BVC9
B	81	GLY	-	expression tag	UNP H9BVC9
B	82	ALA	-	expression tag	UNP H9BVC9
B	83	MET	-	expression tag	UNP H9BVC9
B	84	GLY	-	expression tag	UNP H9BVC9
C	81	GLY	-	expression tag	UNP H9BVC9
C	82	ALA	-	expression tag	UNP H9BVC9
C	83	MET	-	expression tag	UNP H9BVC9
C	84	GLY	-	expression tag	UNP H9BVC9
D	81	GLY	-	expression tag	UNP H9BVC9
D	82	ALA	-	expression tag	UNP H9BVC9
D	83	MET	-	expression tag	UNP H9BVC9
D	84	GLY	-	expression tag	UNP H9BVC9

- Molecule 2 is SULFITE ION (CCD ID: SO3) (formula: O₃S) (labeled as "Ligand of Interest" by depositor).



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

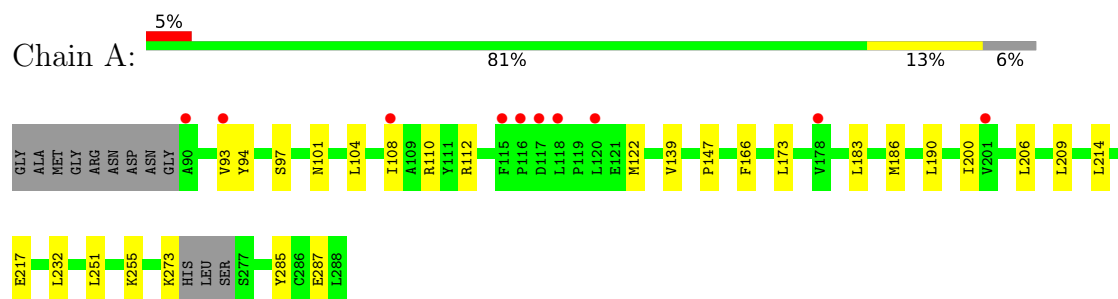
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	71	Total	O	0	0
			71	71		
3	B	60	Total	O	0	0
			60	60		
3	C	62	Total	O	0	0
			62	62		
3	D	41	Total	O	0	0
			41	41		

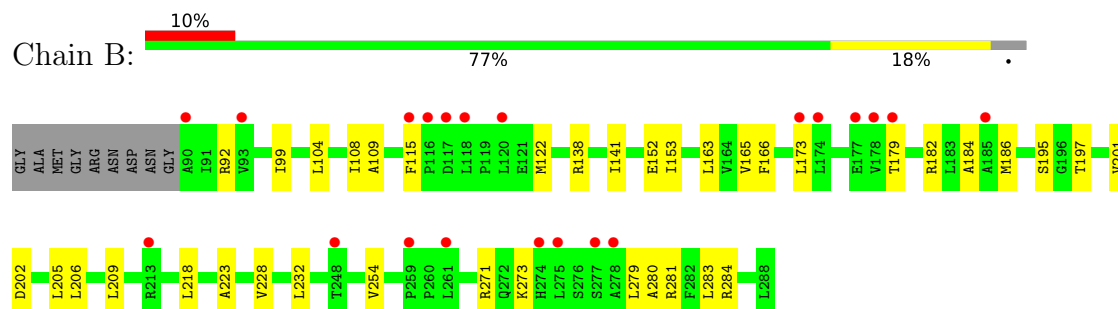
3 Residue-property plots

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.

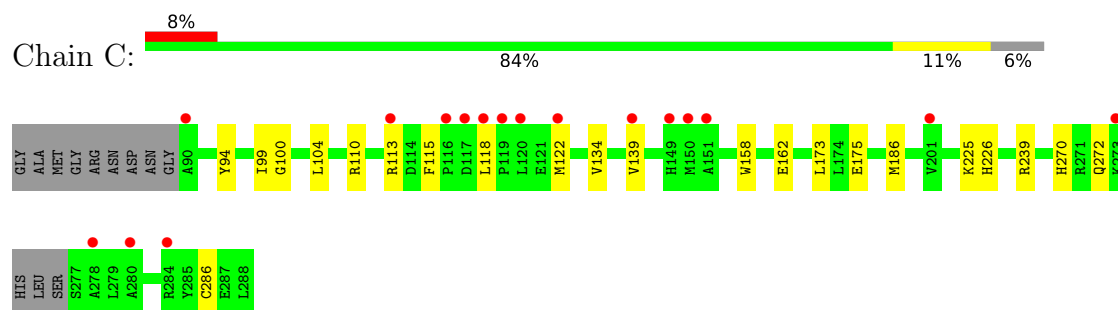
- Molecule 1: LysR family transcriptional regulator



- Molecule 1: LysR family transcriptional regulator

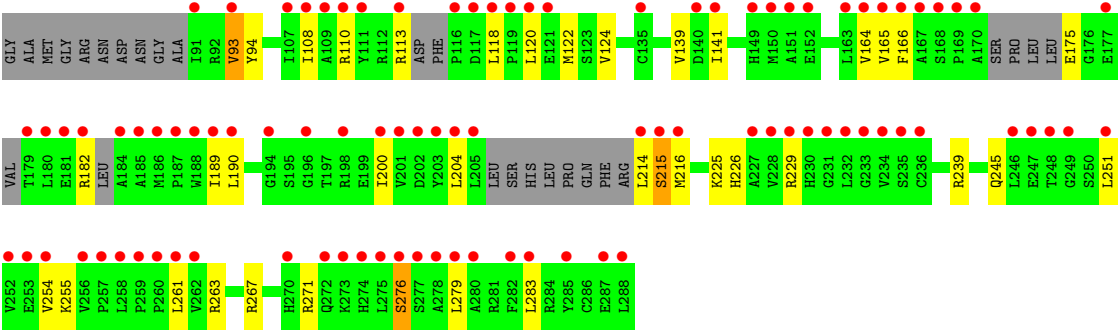


- Molecule 1: LysR family transcriptional regulator



- Molecule 1: LysR family transcriptional regulator





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	83.36Å 101.33Å 109.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.28 – 2.03 32.28 – 2.03	Depositor EDS
% Data completeness (in resolution range)	86.7 (32.28-2.03) 86.9 (32.28-2.03)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.35 (at 2.03Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.268 , 0.297 (Not available) , 0.295	Depositor DCC
R_{free} test set	2010 reflections (3.30%)	wwPDB-VP
Wilson B-factor (Å ²)	20.3	Xtriage
Anisotropy	0.064	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 38.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6352	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 46.96 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.0621e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: SO3

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	0.14	0/1579	0.30	0/2143
1	B	0.16	0/1605	0.32	0/2180
1	C	0.13	0/1579	0.32	0/2143
1	D	0.17	0/1457	0.37	0/1968
All	All	0.15	0/6220	0.33	0/8434

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 [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	1548	0	1586	18	1
1	B	1572	0	1610	24	2
1	C	1548	0	1586	11	1
1	D	1434	0	1463	23	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
2	C	4	0	0	0	0
2	D	4	0	0	0	0
3	A	71	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	60	0	0	2	0
3	C	62	0	0	0	0
3	D	41	0	0	0	0
All	All	6352	0	6245	72	2

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 6.

All (72) 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:D:245:GLN:HB3	1:D:251:LEU:HB2	1.59	0.84
1:B:202:ASP:HA	1:B:206:LEU:HB2	1.70	0.73
1:B:280:ALA:HA	1:B:283:LEU:HD12	1.71	0.72
1:C:115:PHE:HB3	1:C:118:LEU:HD23	1.71	0.71
1:A:110:ARG:NH1	3:A:402:HOH:O	2.30	0.64
1:C:94:TYR:HB2	1:C:139:VAL:HG11	1.79	0.64
1:A:110:ARG:NH2	1:A:285:TYR:O	2.32	0.62
1:A:94:TYR:HB2	1:A:139:VAL:HG11	1.82	0.61
1:D:204:LEU:HB3	1:D:261:LEU:HD12	1.83	0.60
1:C:99:ILE:HG22	1:C:104:LEU:HD13	1.83	0.60
1:D:166:PHE:HB2	1:D:251:LEU:HD12	1.86	0.58
1:B:166:PHE:CE2	1:B:228:VAL:HG21	2.39	0.57
1:B:141:ILE:HG21	1:B:279:LEU:HD11	1.85	0.56
1:D:245:GLN:HG2	1:D:251:LEU:HD23	1.87	0.56
1:B:99:ILE:HG22	1:B:104:LEU:HD13	1.88	0.55
1:B:138:ARG:NH2	3:B:404:HOH:O	2.40	0.55
1:D:225:LYS:HD3	1:D:245:GLN:NE2	2.21	0.55
1:A:173:LEU:HD21	1:A:183:LEU:HD23	1.89	0.54
1:B:184:ALA:HB2	1:B:209:LEU:HB3	1.87	0.54
1:B:173:LEU:HD11	1:B:186:MET:HG3	1.89	0.54
1:B:179:THR:HG23	1:B:182:ARG:H	1.73	0.53
1:A:206:LEU:HD23	1:A:209:LEU:HD12	1.90	0.53
1:D:93:VAL:HG22	1:D:122:MET:HA	1.90	0.53
1:B:92:ARG:HH11	1:B:92:ARG:HG3	1.74	0.52
1:C:104:LEU:HD22	1:C:122:MET:HE3	1.90	0.52
1:A:122:MET:HE3	1:B:218:LEU:HD21	1.92	0.52
1:C:173:LEU:HD22	1:C:186:MET:HG3	1.90	0.52
1:B:197:THR:O	1:B:201:VAL:HG23	2.11	0.50
1:D:226:HIS:HA	1:D:229:ARG:HG2	1.92	0.50
1:D:200:ILE:HG21	1:D:263:ARG:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:165:VAL:HG12	1:B:254:VAL:HB	1.94	0.49
1:A:147:PRO:HD3	1:A:200:ILE:HD11	1.94	0.49
1:B:115:PHE:CZ	1:B:281:ARG:HD3	2.48	0.49
1:C:110:ARG:HG2	1:C:113:ARG:NH2	2.28	0.48
1:D:175:GLU:O	1:D:182:ARG:NH2	2.47	0.48
1:D:165:VAL:HG12	1:D:254:VAL:HB	1.94	0.48
1:D:141:ILE:HD11	1:D:267:ARG:HG3	1.96	0.46
1:B:108:ILE:HD12	1:B:122:MET:HE2	1.97	0.45
1:C:100:GLY:HA2	1:C:122:MET:HE1	1.99	0.45
1:D:214:LEU:O	1:D:216:MET:N	2.49	0.45
1:A:104:LEU:HG	1:A:108:ILE:HD11	1.98	0.45
1:A:190:LEU:HD21	1:A:206:LEU:HD13	2.00	0.44
1:D:214:LEU:O	1:D:215:SER:C	2.60	0.44
1:C:158:TRP:HE1	1:C:286:CYS:HB3	1.82	0.44
1:B:104:LEU:HD23	1:B:122:MET:HG3	1.99	0.44
1:B:152:GLU:HG3	1:B:271:ARG:HB3	2.00	0.43
1:D:271:ARG:NH1	1:D:271:ARG:HG3	2.33	0.43
1:D:164:VAL:HG21	1:D:239:ARG:HE	1.83	0.43
1:C:270:HIS:ND1	1:C:272:GLN:HG2	2.33	0.43
1:C:225:LYS:HG3	1:C:226:HIS:N	2.33	0.43
1:A:112:ARG:HH11	1:A:112:ARG:HG2	1.84	0.43
1:D:189:ILE:C	1:D:190:LEU:HD23	2.44	0.43
1:B:153:ILE:O	3:B:401:HOH:O	2.21	0.43
1:A:101:ASN:OD1	1:B:223:ALA:HB2	2.19	0.42
1:A:173:LEU:HD22	1:A:186:MET:HG3	2.01	0.42
1:A:166:PHE:HD2	1:A:251:LEU:HD22	1.84	0.42
1:D:94:TYR:HB2	1:D:139:VAL:HG11	2.02	0.42
1:A:232:LEU:HD21	1:B:109:ALA:HA	2.02	0.42
1:B:205:LEU:HG	1:B:209:LEU:HD21	2.02	0.42
1:D:279:LEU:O	1:D:283:LEU:HG	2.19	0.42
1:D:108:ILE:HG23	1:D:120:LEU:HD22	2.01	0.42
1:A:108:ILE:HG22	1:B:232:LEU:HD11	2.02	0.41
1:D:214:LEU:O	1:D:214:LEU:HD23	2.20	0.41
1:D:110:ARG:HA	1:D:113:ARG:HB2	2.01	0.41
1:D:122:MET:HE3	1:D:124:VAL:CG2	2.51	0.41
1:B:163:LEU:HD13	1:B:201:VAL:HG22	2.03	0.41
1:A:214:LEU:HD21	1:A:217:GLU:HG3	2.02	0.41
1:A:255:LYS:HA	1:A:255:LYS:HD2	1.80	0.41
1:B:92:ARG:HG3	1:B:92:ARG:NH1	2.35	0.41
1:D:255:LYS:HE3	1:D:255:LYS:HB2	1.70	0.41
1:A:93:VAL:HG11	1:A:104:LEU:HD21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:162:GLU:CD	1:C:239:ARG:HH21	2.29	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:287:GLU:OE2	1:B:284:ARG:NH2[3_444]	2.07	0.13
1:B:273:LYS:NZ	1:C:175:GLU:OE2[3_554]	2.09	0.11

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	192/208 (92%)	184 (96%)	8 (4%)	0	100	100
1	B	197/208 (95%)	193 (98%)	4 (2%)	0	100	100
1	C	192/208 (92%)	185 (96%)	7 (4%)	0	100	100
1	D	170/208 (82%)	161 (95%)	6 (4%)	3 (2%)	6	2
All	All	751/832 (90%)	723 (96%)	25 (3%)	3 (0%)	30	22

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	276	SER
1	D	215	SER
1	D	118	LEU

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	170/178 (96%)	168 (99%)	2 (1%)	63	65
1	B	173/178 (97%)	172 (99%)	1 (1%)	78	79
1	C	170/178 (96%)	169 (99%)	1 (1%)	78	79
1	D	157/178 (88%)	155 (99%)	2 (1%)	61	63
All	All	670/712 (94%)	664 (99%)	6 (1%)	70	73

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

Mol	Chain	Res	Type
1	A	97	SER
1	A	273	LYS
1	B	195	SER
1	C	134	VAL
1	D	93	VAL
1	D	276	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	149	HIS

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

4 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	SO3	C	301	-	1,3,3	0.58	0	0,3,3	-	-
2	SO3	D	301	-	1,3,3	0.52	0	0,3,3	-	-
2	SO3	B	301	-	1,3,3	0.57	0	0,3,3	-	-
2	SO3	A	301	-	1,3,3	0.58	0	0,3,3	-	-

There are no bond length outliers.

There are no bond angle outliers.

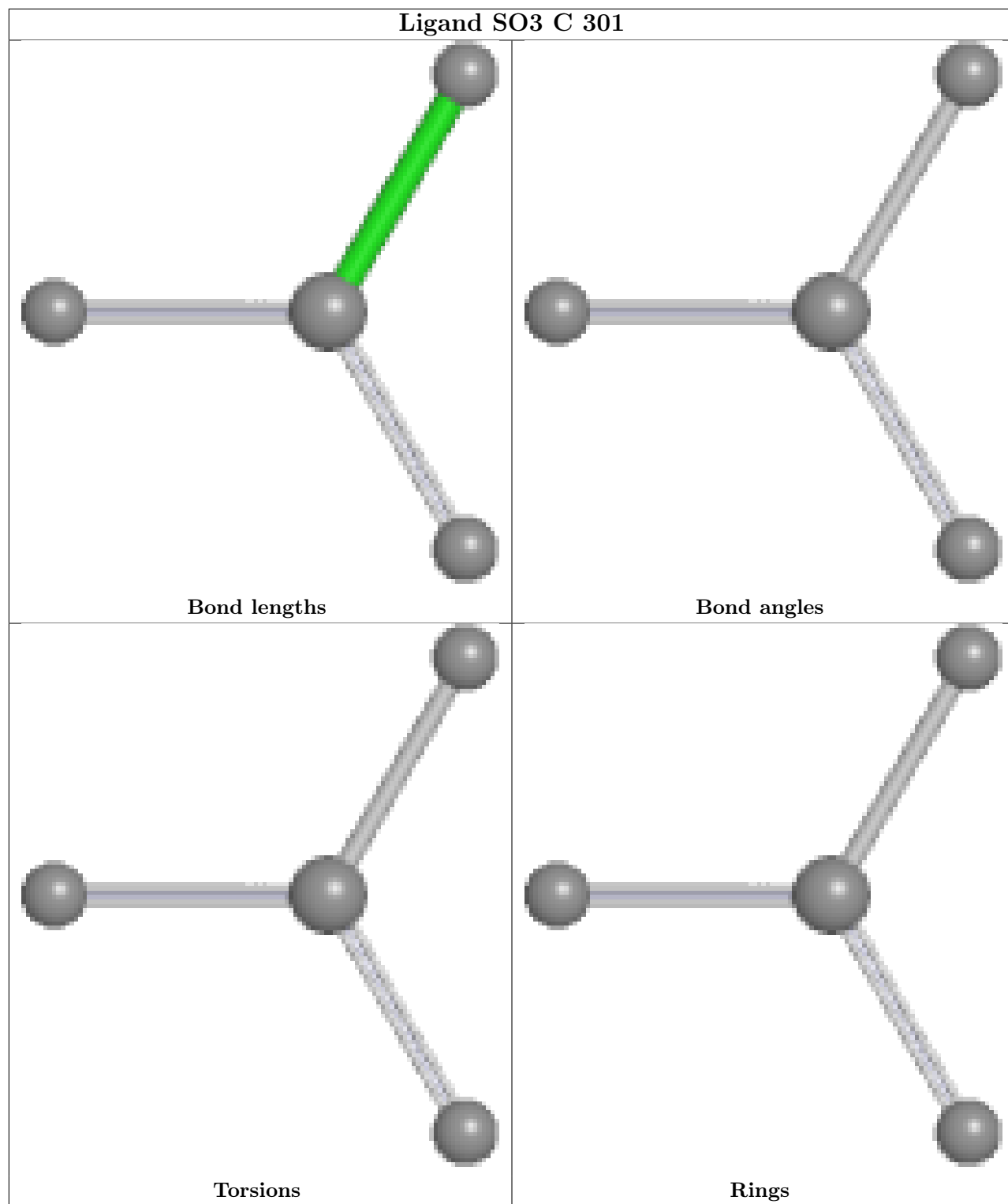
There are no chirality outliers.

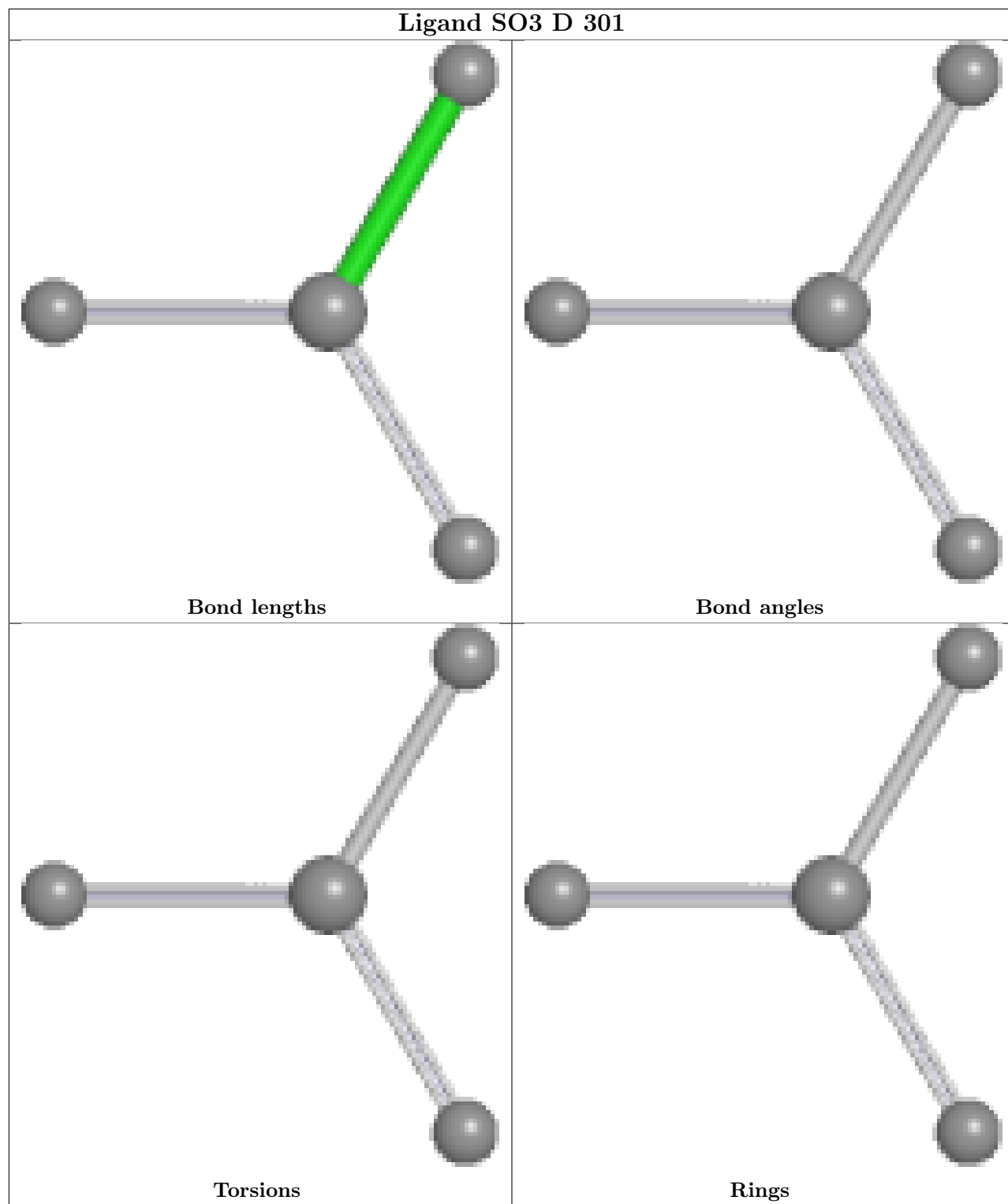
There are no torsion outliers.

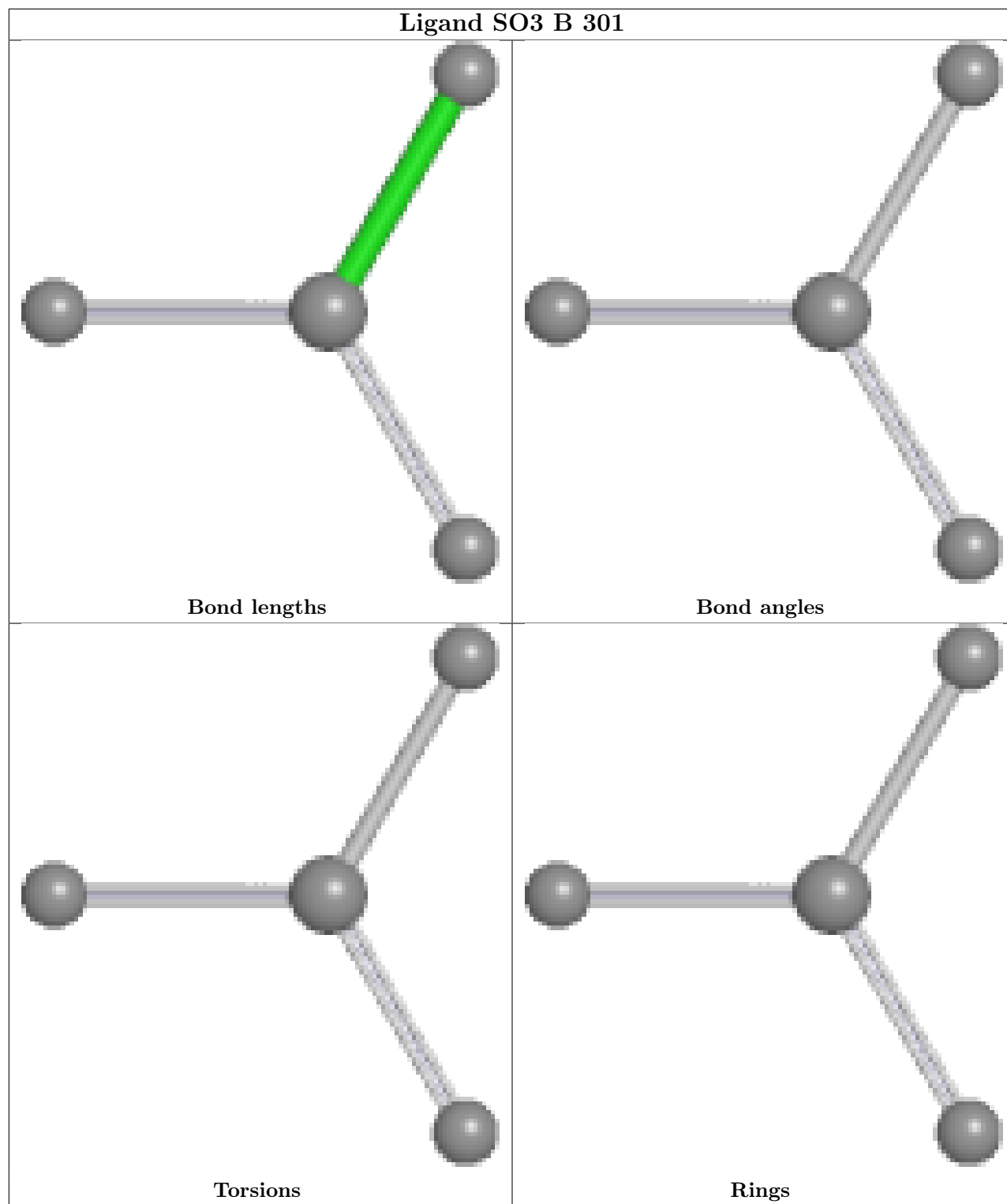
There are no ring outliers.

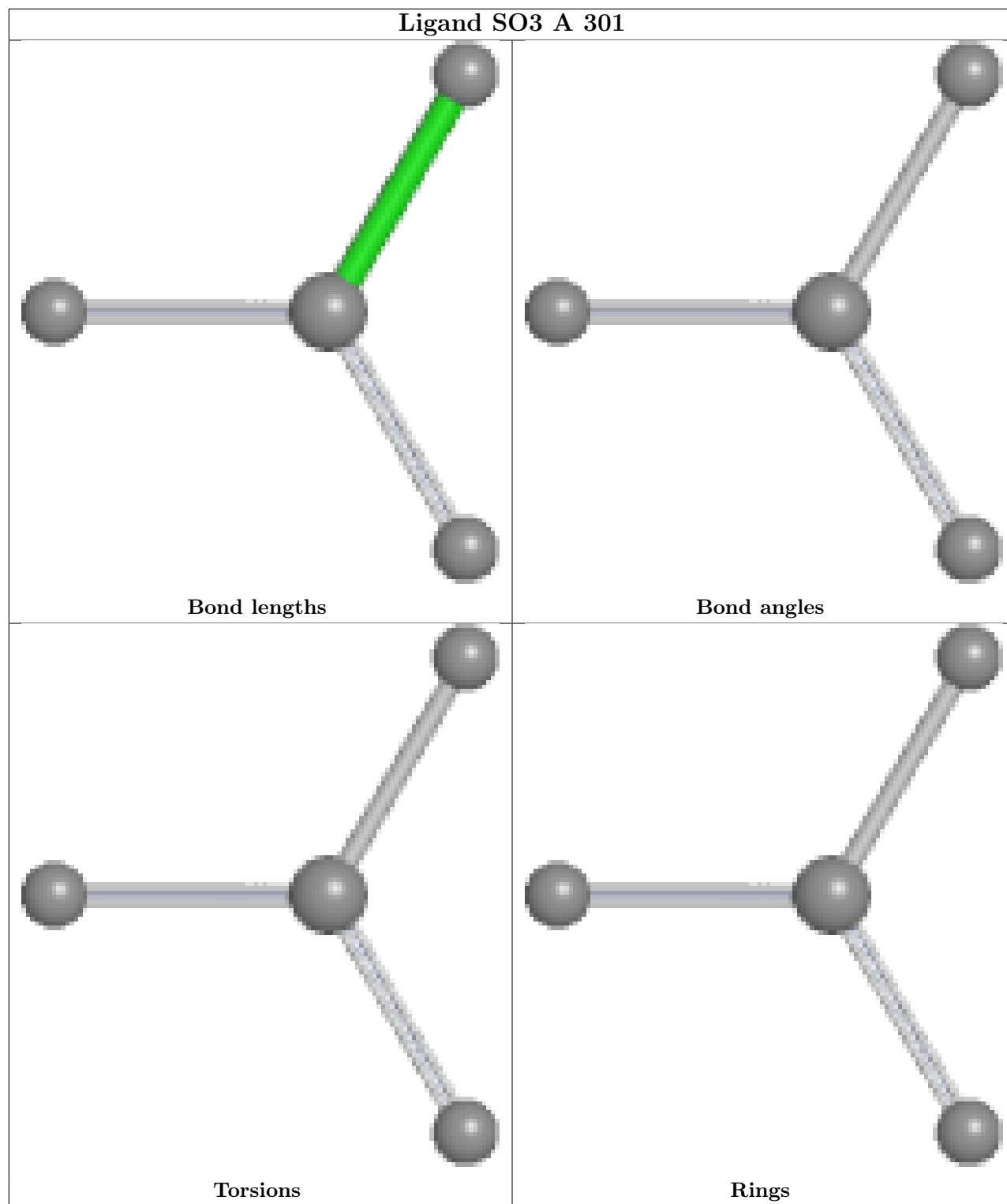
No monomer is involved in short contacts.

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 ⓘ

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	196/208 (94%)	0.48	10 (5%) 33 33	8, 22, 44, 63	0
1	B	199/208 (95%)	0.92	21 (10%) 11 10	8, 27, 48, 68	0
1	C	196/208 (94%)	0.56	17 (8%) 16 15	9, 21, 46, 58	0
1	D	182/208 (87%)	2.16	93 (51%) 0 0	10, 43, 65, 76	0
All	All	773/832 (92%)	1.01	141 (18%) 3 3	8, 26, 57, 76	0

All (141) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	201	VAL	6.6
1	D	180	LEU	6.5
1	D	188	TRP	6.2
1	D	184	ALA	5.7
1	D	236	CYS	5.6
1	D	116	PRO	5.6
1	D	275	LEU	5.5
1	D	234	VAL	5.5
1	D	165	VAL	5.2
1	D	187	PRO	5.2
1	C	120	LEU	5.2
1	D	120	LEU	5.2
1	D	276	SER	5.0
1	D	181	GLU	4.5
1	B	90	ALA	4.5
1	D	164	VAL	4.5
1	D	254	VAL	4.5
1	D	119	PRO	4.3
1	D	203	TYR	4.3
1	D	251	LEU	4.2
1	D	204	LEU	4.2

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Mol	Chain	Res	Type	RSRZ
1	D	200	ILE	4.1
1	D	259	PRO	3.9
1	B	277	SER	3.9
1	D	280	ALA	3.8
1	D	167	ALA	3.8
1	D	261	LEU	3.8
1	C	118	LEU	3.8
1	D	214	LEU	3.8
1	D	258	LEU	3.8
1	D	118	LEU	3.7
1	D	282	PHE	3.7
1	D	111	TYR	3.7
1	D	121	GLU	3.7
1	A	118	LEU	3.6
1	D	279	LEU	3.6
1	D	151	ALA	3.5
1	D	166	PHE	3.4
1	A	120	LEU	3.4
1	B	275	LEU	3.3
1	D	168	SER	3.3
1	A	116	PRO	3.3
1	D	252	VAL	3.3
1	D	91	ILE	3.3
1	D	278	ALA	3.3
1	D	288	LEU	3.3
1	D	179	THR	3.3
1	B	117	ASP	3.3
1	D	249	GLY	3.2
1	B	173	LEU	3.2
1	D	93	VAL	3.2
1	D	205	LEU	3.2
1	D	247	GLU	3.2
1	D	248	THR	3.2
1	D	109	ALA	3.1
1	D	274	HIS	3.1
1	D	117	ASP	3.1
1	D	256	VAL	3.1
1	C	117	ASP	3.1
1	D	185	ALA	3.1
1	D	285	TYR	3.0
1	D	257	PRO	3.0
1	D	227	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	228	VAL	3.0
1	D	108	ILE	3.0
1	D	113	ARG	3.0
1	D	170	ALA	3.0
1	D	189	ILE	3.0
1	A	115	PHE	3.0
1	D	202	ASP	2.9
1	D	177	GLU	2.9
1	B	278	ALA	2.9
1	D	194	GLY	2.9
1	D	260	PRO	2.9
1	C	278	ALA	2.9
1	C	280	ALA	2.9
1	D	215	SER	2.8
1	D	152	GLU	2.8
1	B	118	LEU	2.8
1	A	117	ASP	2.8
1	D	149	HIS	2.7
1	D	246	LEU	2.7
1	D	169	PRO	2.7
1	C	139	VAL	2.7
1	A	90	ALA	2.7
1	C	151	ALA	2.7
1	D	233	GLY	2.7
1	D	235	SER	2.7
1	D	182	ARG	2.7
1	B	274	HIS	2.6
1	B	213	ARG	2.6
1	D	229	ARG	2.6
1	D	277	SER	2.6
1	A	178	VAL	2.6
1	B	248	THR	2.5
1	B	174	LEU	2.5
1	D	190	LEU	2.5
1	C	113	ARG	2.5
1	D	163	LEU	2.5
1	B	93	VAL	2.4
1	C	116	PRO	2.4
1	D	196	GLY	2.4
1	D	287	GLU	2.4
1	C	201	VAL	2.4
1	D	216	MET	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	115	PHE	2.4
1	D	150	MET	2.4
1	D	198	ARG	2.4
1	C	119	PRO	2.4
1	B	120	LEU	2.3
1	D	107	ILE	2.3
1	D	231	GLY	2.3
1	C	122	MET	2.3
1	D	186	MET	2.3
1	C	90	ALA	2.3
1	C	273	LYS	2.3
1	D	110	ARG	2.2
1	D	140	ASP	2.2
1	B	177	GLU	2.2
1	C	284	ARG	2.2
1	D	141	ILE	2.2
1	B	178	VAL	2.2
1	A	93	VAL	2.2
1	B	185	ALA	2.2
1	D	283	LEU	2.2
1	A	201	VAL	2.1
1	C	149	HIS	2.1
1	D	273	LYS	2.1
1	A	108	ILE	2.1
1	B	179	THR	2.1
1	D	270	HIS	2.1
1	D	232	LEU	2.1
1	D	253	GLU	2.1
1	D	272	GLN	2.1
1	B	116	PRO	2.1
1	B	259	PRO	2.1
1	D	262	VAL	2.1
1	B	261	LEU	2.0
1	C	150	MET	2.0
1	D	135	CYS	2.0
1	D	230	HIS	2.0

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

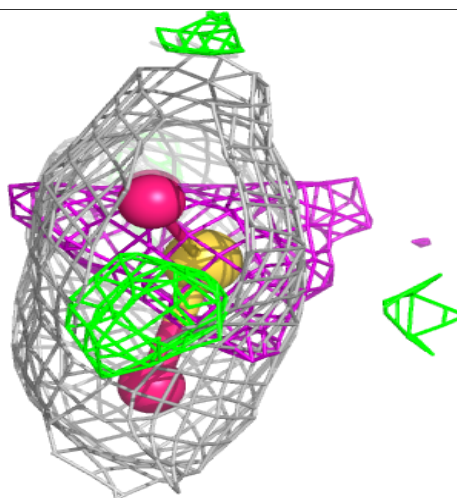
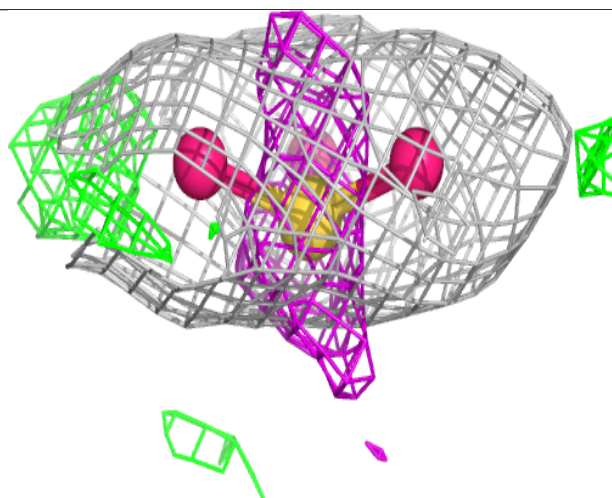
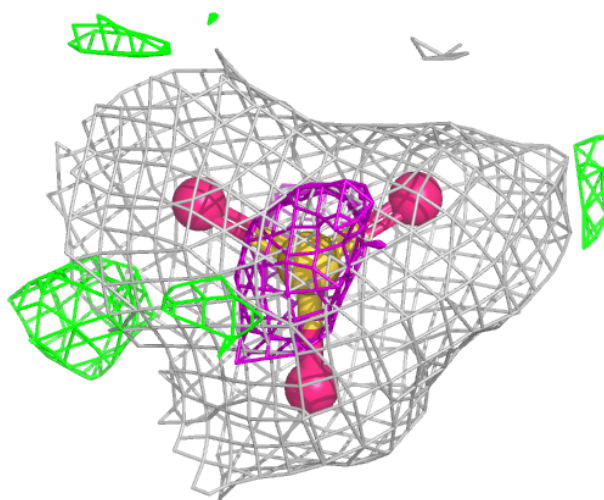
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	SO3	D	301	4/4	0.76	0.16	25,28,28,49	0
2	SO3	B	301	4/4	0.84	0.18	23,24,34,46	0
2	SO3	C	301	4/4	0.88	0.14	20,23,24,39	0
2	SO3	A	301	4/4	0.90	0.15	14,15,16,34	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.

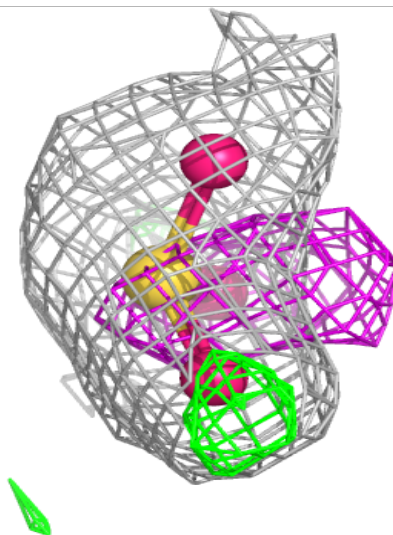
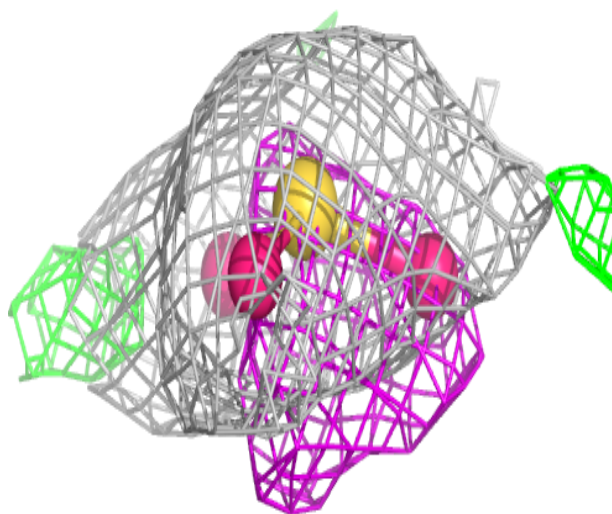
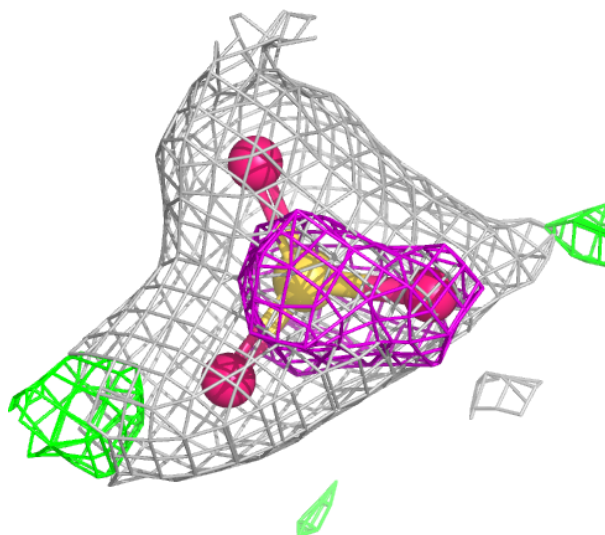
Electron density around SO3 D 301:

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



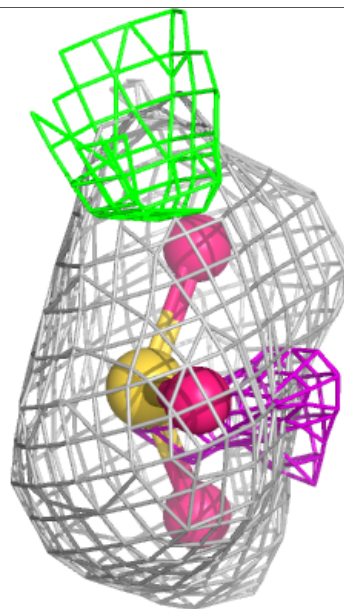
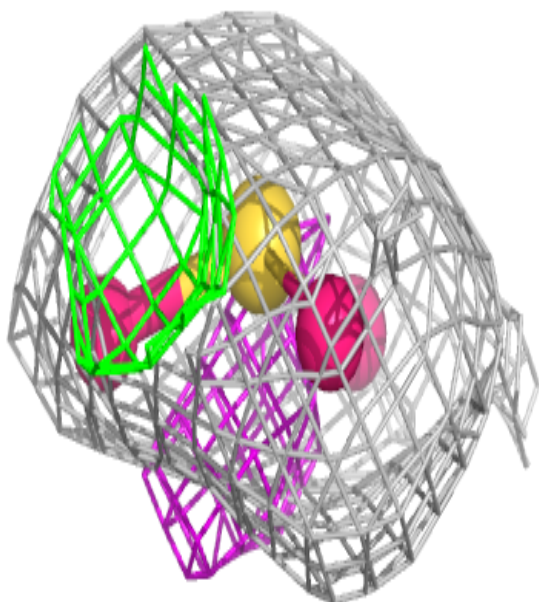
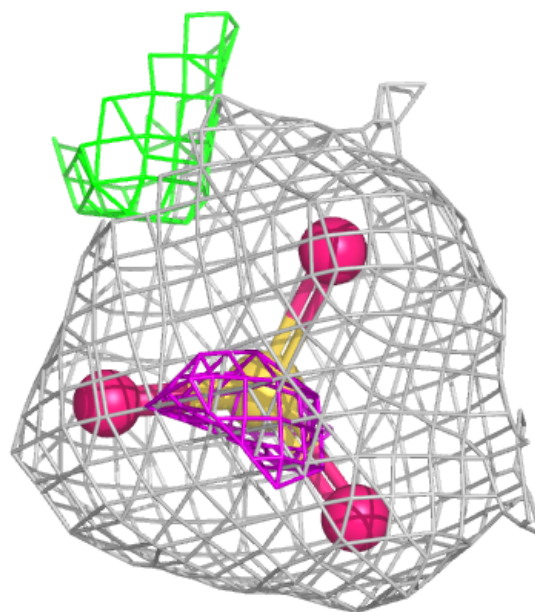
Electron density around SO3 B 301:

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



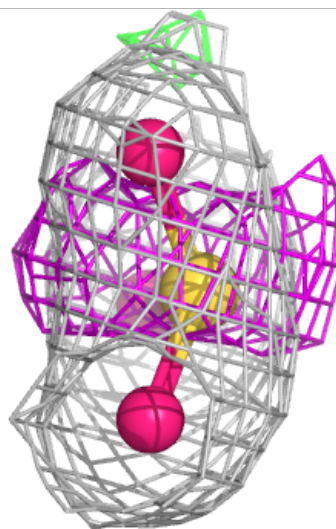
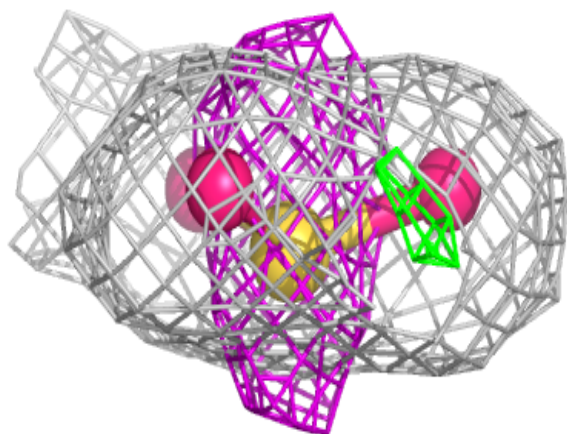
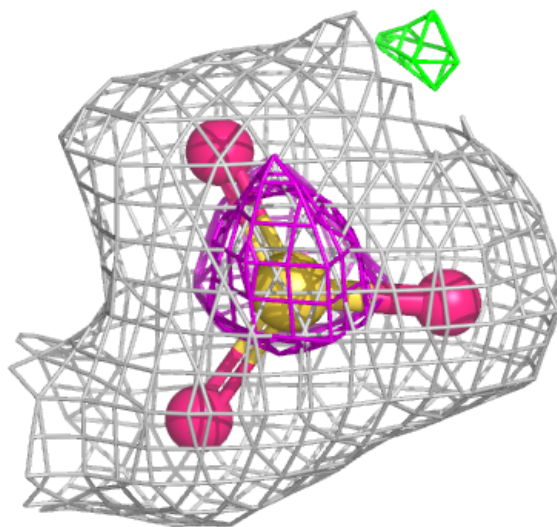
Electron density around SO3 C 301:

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



Electron density around SO3 A 301:

$2mF_o-DF_c$ (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.