Full wwPDB X-ray Structure Validation Report (i)

Mar 15, 2022 – 12:10 AM JST

PDB ID	:	7ERP
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 (i) symbol.

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

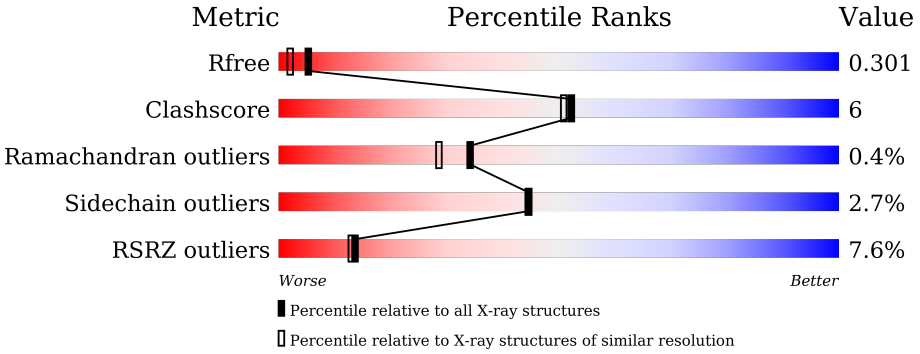
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.27
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 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}	130704	10434 (2.04-2.00)
Clashscore	141614	11643 (2.04-2.00)
Ramachandran outliers	138981	11493 (2.04-2.00)
Sidechain outliers	138945	11492 (2.04-2.00)
RSRZ outliers	127900	10220 (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 <=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	81% 13% 6%
1	B	208	6% 76% 19% •
1	C	208	% 85% 9% • 6%
1	D	208	21% 69% 16% • 12%

2 Entry composition (i)

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.

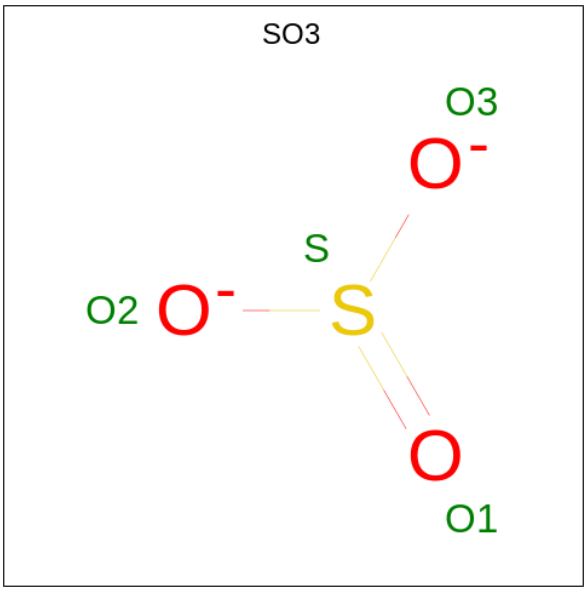
- Molecule 1 is a protein called LysR family transcriptional regulator.

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

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 (three-letter code: SO3) (formula: O_3S) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 3 is water.

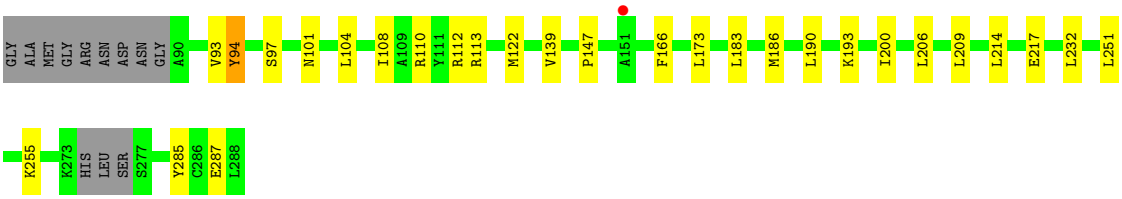
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	71	71	71	0	0
3	B	60	60	60	0	0
3	C	62	62	62	0	0
3	D	41	41	41	0	0

3 Residue-property plots (i)

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

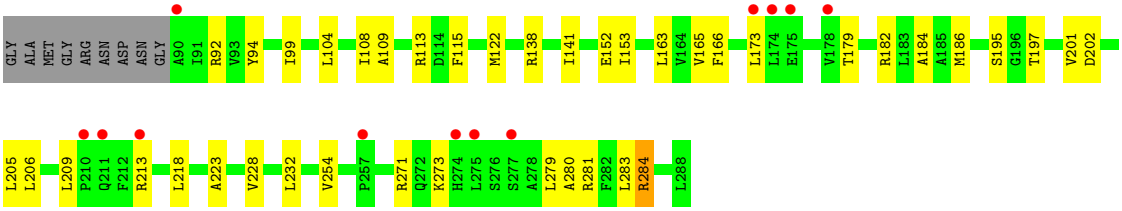
• Molecule 1: LysR family transcriptional regulator

Chain A:



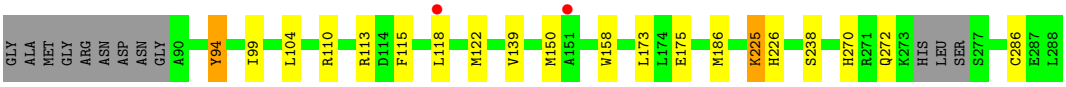
• Molecule 1: LysR family transcriptional regulator

Chain B:



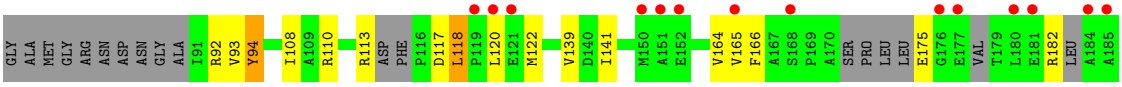
• Molecule 1: LysR family transcriptional regulator

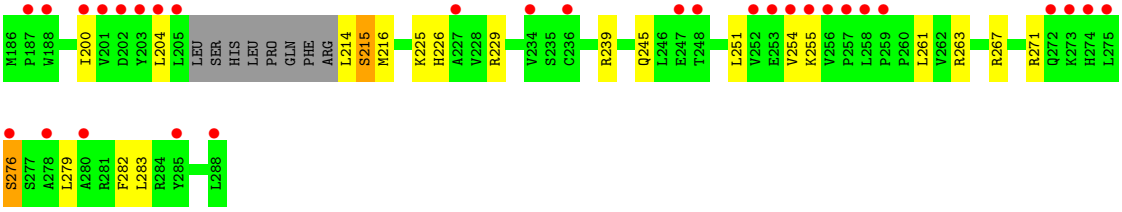
Chain C:



• Molecule 1: LysR family transcriptional regulator

Chain D:




M186
P187
W188
I200
V201
D202
Y203
L204
L205
LEU
SER
HIS
LEU
PRO
GLN
PHE
ARG
L214
S215
M216
K225
H226
A227
V228
R229
V234
S235
C236
R239
Q245
L246
E247
T248
L251
V252
E253
V254
K255
V256
P257
L258
P259
P260
L261
V262
R263
R267
R271
Q272
K273
H274
L275

S276
S277
A278
L279
A280
R281
F282
L283
R284
Y285
L288

4 Data and refinement statistics (i)

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) 86.7 (32.28-2.03)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.35 (at 2.03Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.268 , 0.297 0.271 , 0.301	Depositor DCC
R_{free} test set	2009 reflections (3.81%)	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)	0.33 , 46.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	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.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (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	0.25	0/1579	0.53	0/2143
1	B	0.26	0/1605	0.53	0/2180
1	C	0.26	0/1579	0.52	0/2143
1	D	0.27	0/1457	0.56	0/1968
All	All	0.26	0/6220	0.53	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	8	1
1	D	1434	0	1463	22	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	68	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 (68) 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:A:122:MET:HE3	1:B:218:LEU:HD21	1.91	0.52
1:B:92:ARG:HH11	1:B:92:ARG:HG3	1.74	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
1:B:165:VAL:HG12	1:B:254:VAL:HB	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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: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:C:225:LYS:HG3	1:C:226:HIS:N	2.33	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:A:112:ARG:HH11	1:A:112:ARG:HG2	1.84	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: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
1:D:117:ASP:O	1:D:118:LEU:HB2	2.21	0.41
1:D:214:LEU:O	1:D:215:SER:C	2.60	0.41
1:B:108:ILE:HD12	1:B:122:MET:HE2	2.04	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%)	8	3
All	All	751/832 (90%)	723 (96%)	25 (3%)	3 (0%)	34	28

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%)	166 (98%)	4 (2%)	49	49
1	B	173/178 (97%)	168 (97%)	5 (3%)	42	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	170/178 (96%)	165 (97%)	5 (3%)	42	41
1	D	157/178 (88%)	153 (98%)	4 (2%)	47	48
All	All	670/712 (94%)	652 (97%)	18 (3%)	44	44

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	94	TYR
1	A	97	SER
1	A	113	ARG
1	A	193	LYS
1	B	94	TYR
1	B	113	ARG
1	B	195	SER
1	B	213	ARG
1	B	284	ARG
1	C	94	TYR
1	C	122	MET
1	C	150	MET
1	C	225	LYS
1	C	238	SER
1	D	92	ARG
1	D	94	TYR
1	D	276	SER
1	D	282	PHE

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

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

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	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	C	301	-	1,3,3	0.59	0	0,3,3	-	-
2	SO3	A	301	-	1,3,3	0.59	0	0,3,3	-	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

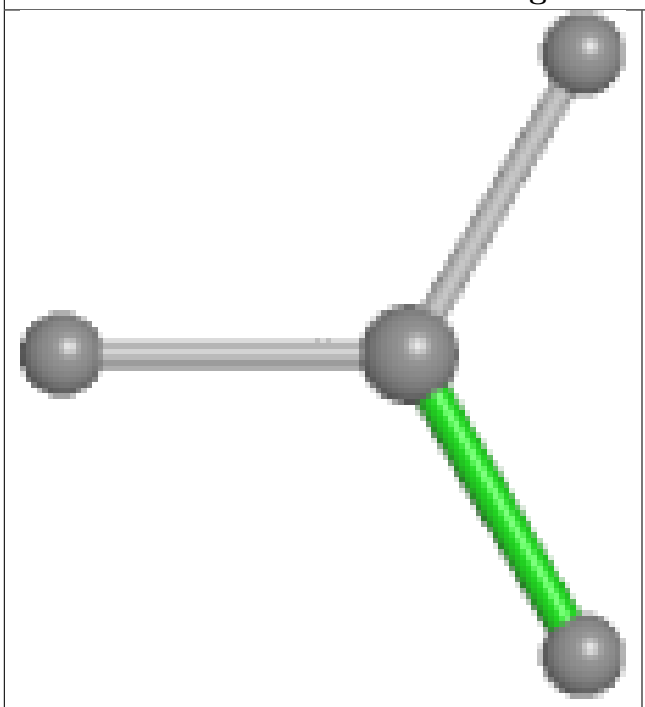
There are no torsion outliers.

There are no ring outliers.

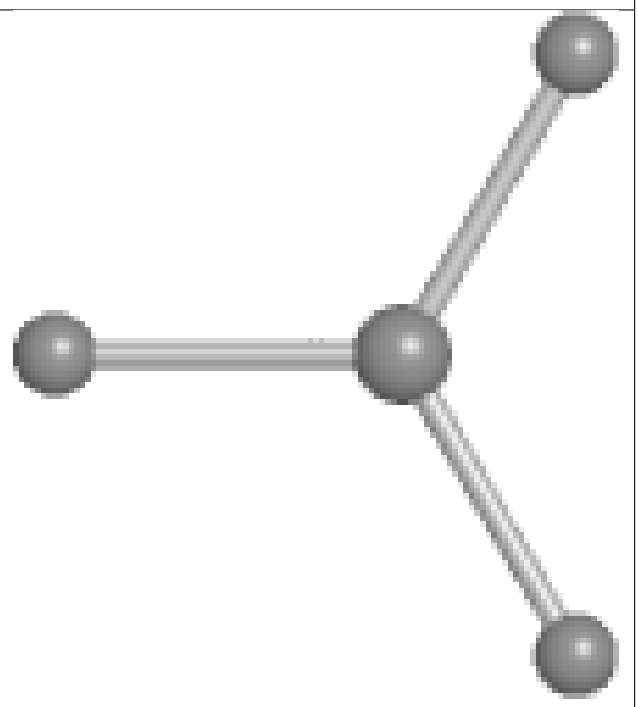
No monomer is involved in short contacts.

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

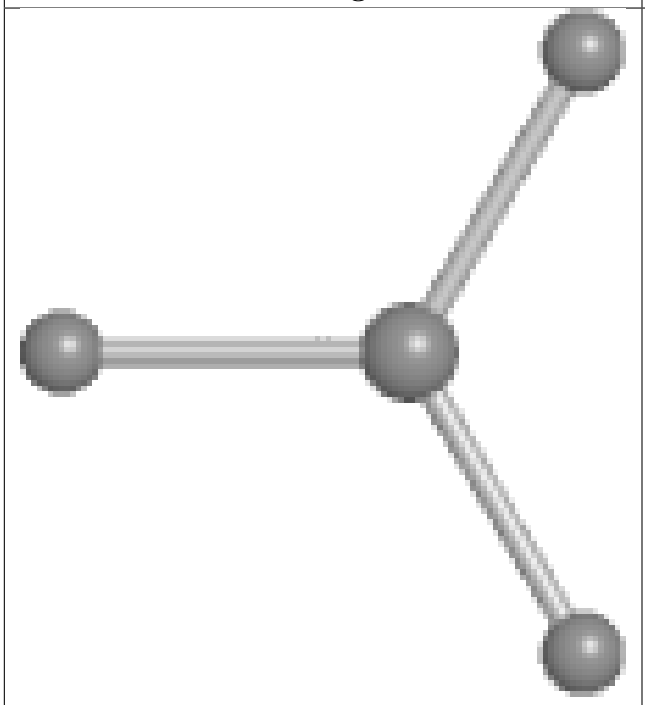
Ligand SO3 D 301



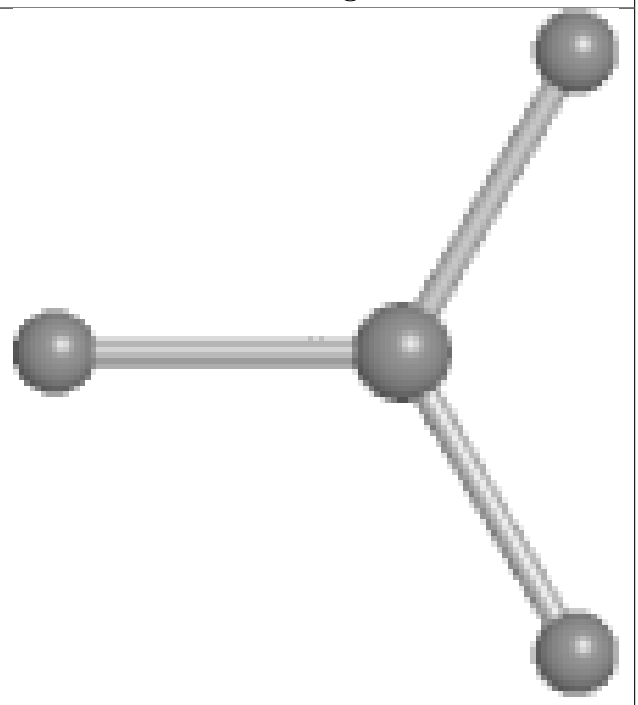
Bond lengths



Bond angles

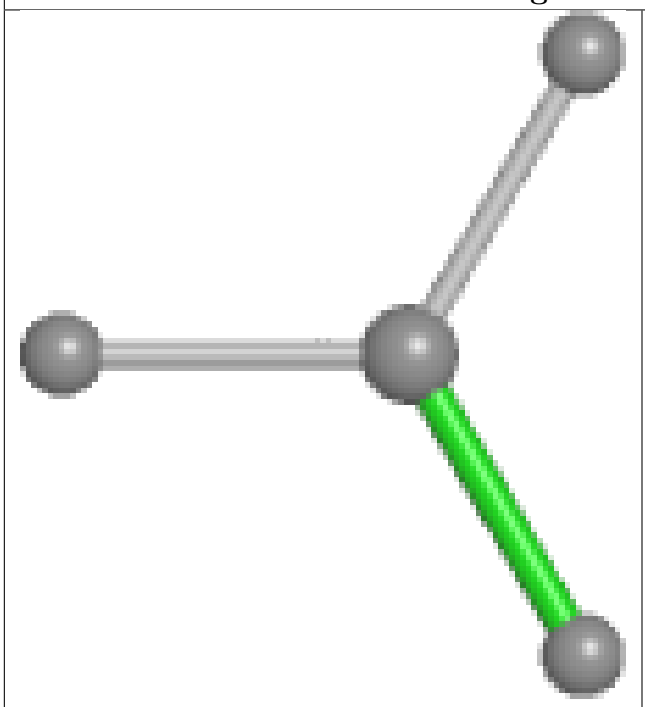


Torsions

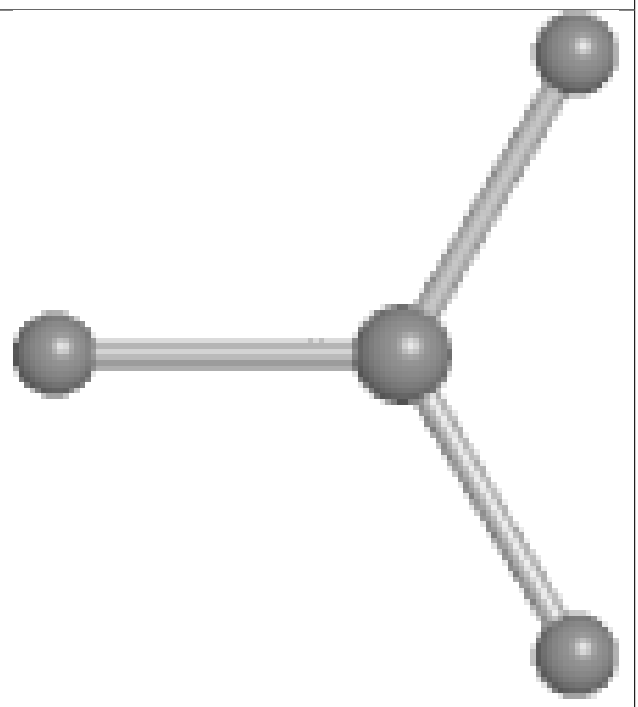


Rings

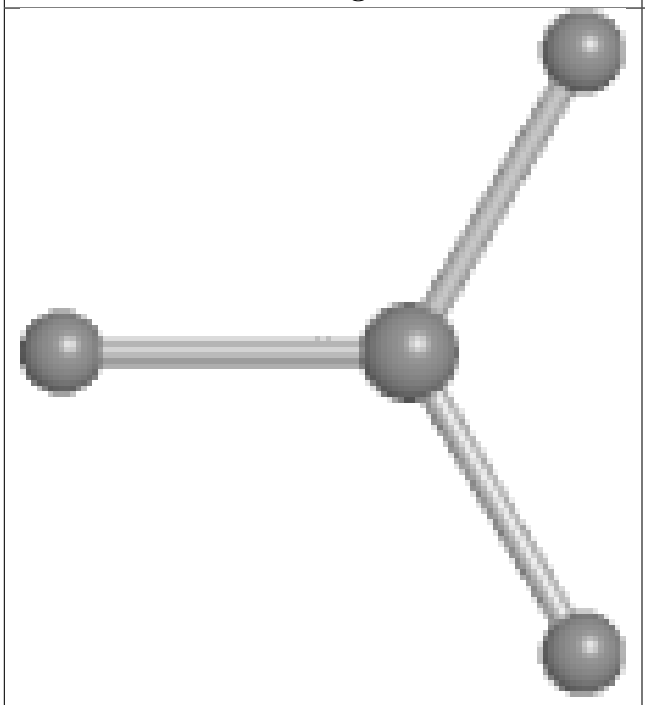
Ligand SO3 B 301



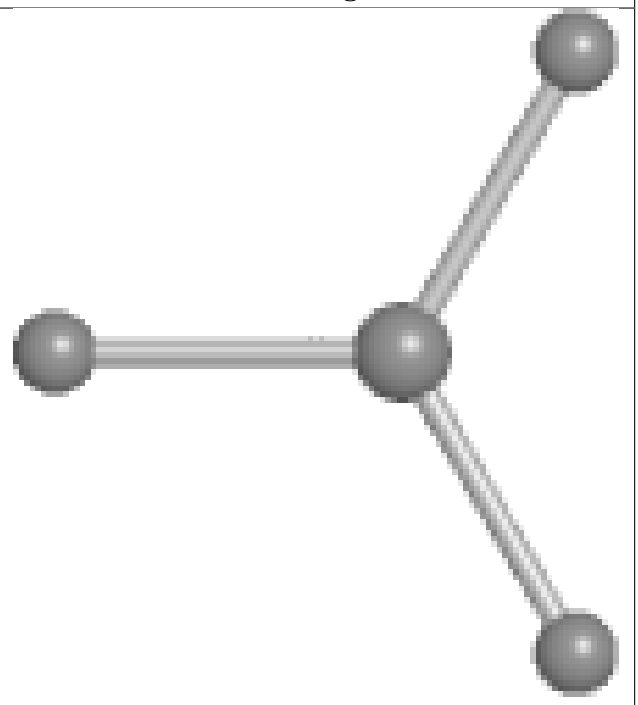
Bond lengths



Bond angles

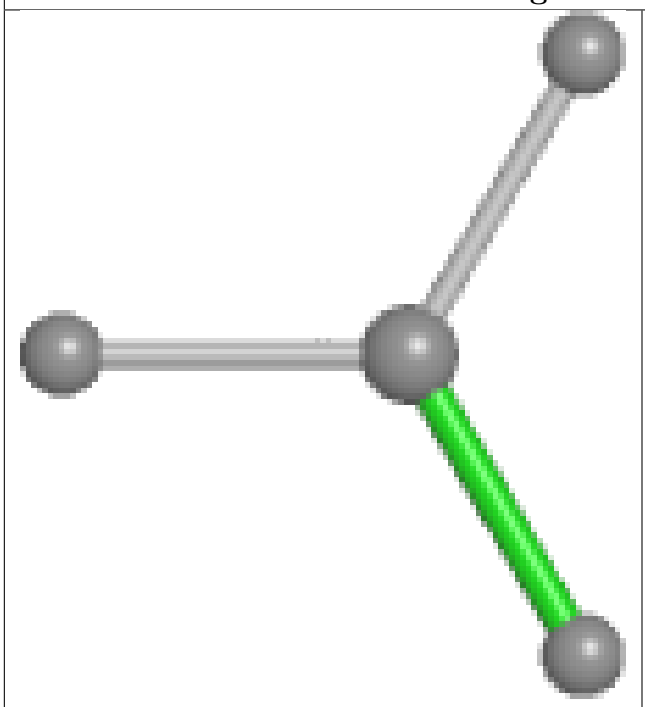


Torsions

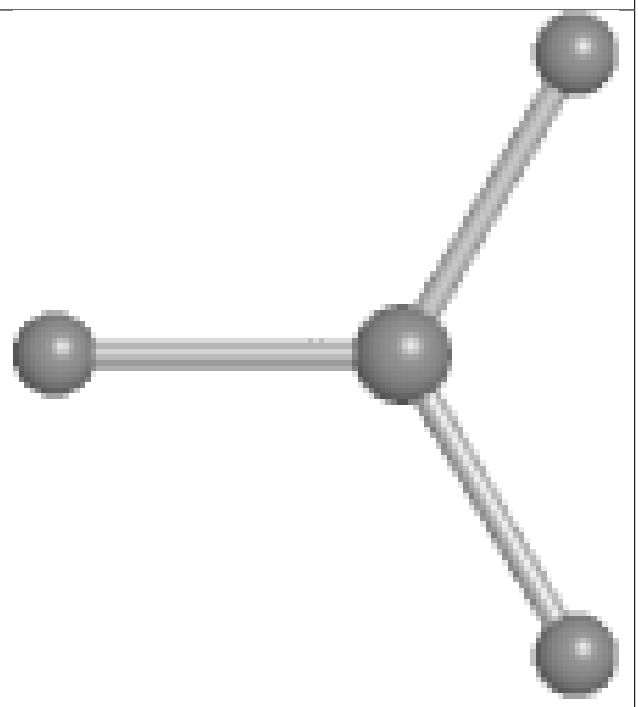


Rings

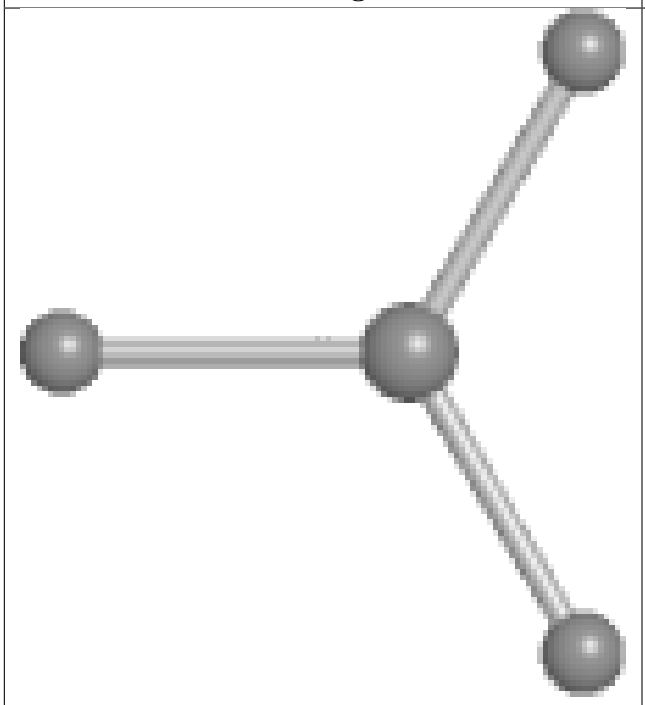
Ligand SO3 C 301



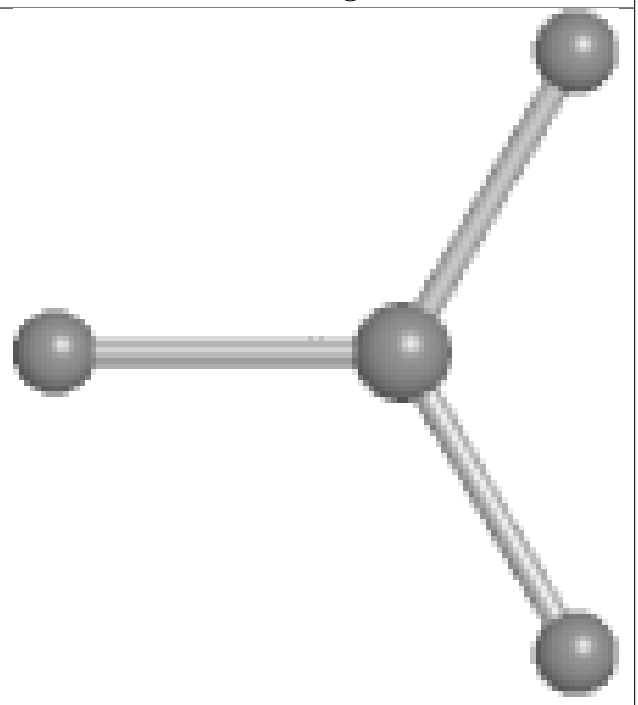
Bond lengths



Bond angles

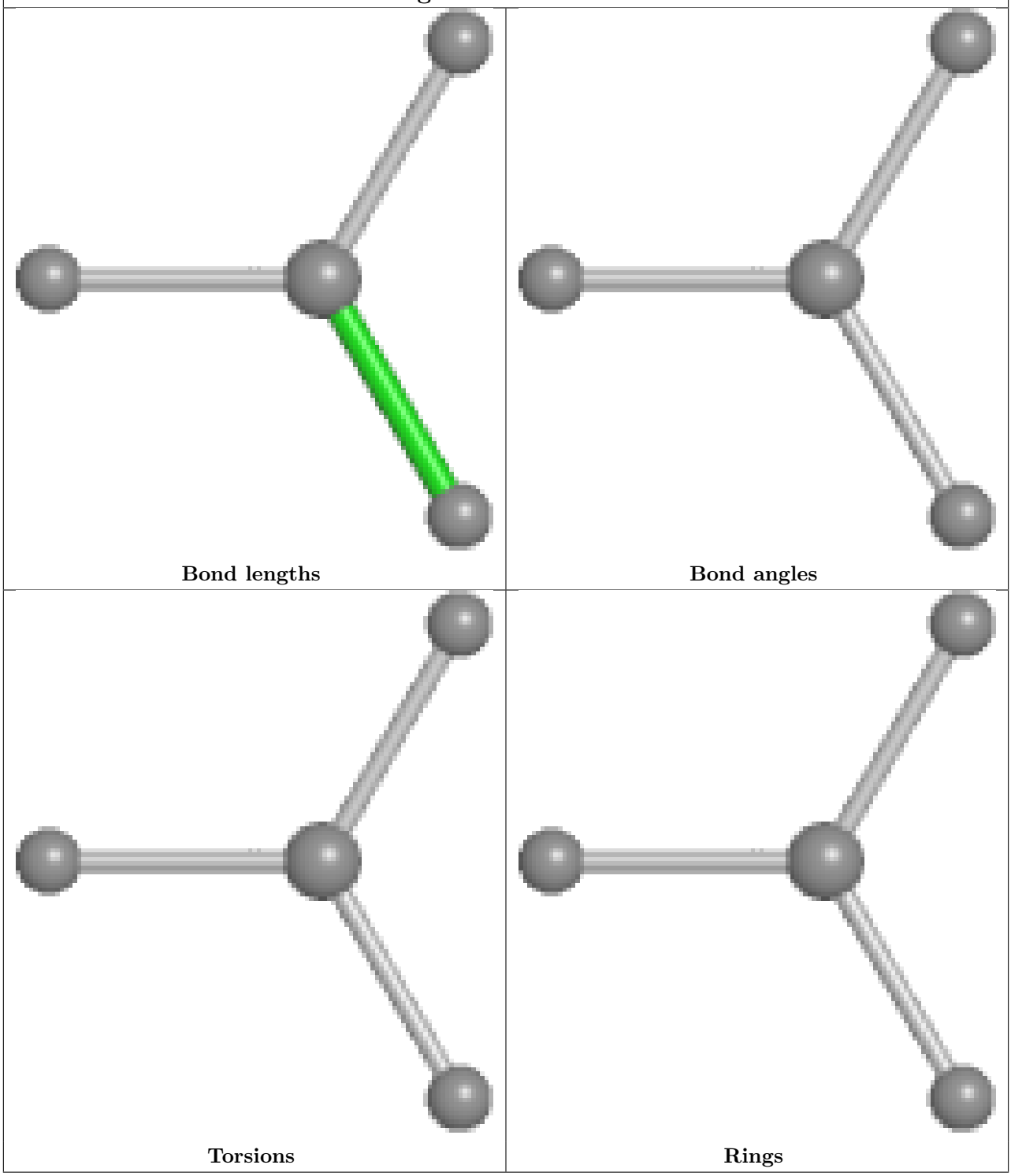


Torsions



Rings

Ligand SO3 A 301



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	196/208 (94%)	-0.01	1 (0%)	91	91	8, 22, 44, 63	0
1	B	199/208 (95%)	0.34	12 (6%)	21	21	8, 27, 48, 68	0
1	C	196/208 (94%)	0.05	2 (1%)	82	82	9, 21, 46, 58	0
1	D	182/208 (87%)	1.23	44 (24%)	0	0	10, 43, 65, 76	0
All	All	773/832 (92%)	0.39	59 (7%)	13	13	8, 26, 57, 76	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	201	VAL	5.1
1	D	275	LEU	4.9
1	D	151	ALA	4.8
1	D	188	TRP	4.8
1	D	165	VAL	4.4
1	D	119	PRO	4.2
1	D	247	GLU	4.1
1	D	181	GLU	4.0
1	B	277	SER	3.9
1	D	257	PRO	3.7
1	D	274	HIS	3.6
1	D	120	LEU	3.4
1	D	276	SER	3.3
1	C	151	ALA	3.3
1	B	211	GLN	3.2
1	D	176	GLY	3.2
1	D	248	THR	3.1
1	D	204	LEU	3.0
1	D	259	PRO	3.0
1	B	257	PRO	3.0
1	D	177	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	180	LEU	2.9
1	B	173	LEU	2.9
1	B	210	PRO	2.9
1	D	288	LEU	2.8
1	D	203	TYR	2.7
1	D	150	MET	2.7
1	B	274	HIS	2.6
1	D	236	CYS	2.5
1	D	234	VAL	2.5
1	D	254	VAL	2.5
1	B	174	LEU	2.5
1	D	205	LEU	2.4
1	D	272	GLN	2.4
1	D	200	ILE	2.4
1	D	255	LYS	2.4
1	D	227	ALA	2.3
1	D	121	GLU	2.3
1	D	256	VAL	2.3
1	B	213	ARG	2.3
1	D	278	ALA	2.3
1	B	90	ALA	2.3
1	D	280	ALA	2.3
1	D	285	TYR	2.2
1	B	175	GLU	2.2
1	D	187	PRO	2.2
1	D	202	ASP	2.2
1	D	168	SER	2.1
1	D	152	GLU	2.1
1	D	273	LYS	2.1
1	C	118	LEU	2.1
1	D	258	LEU	2.1
1	B	178	VAL	2.1
1	A	151	ALA	2.1
1	B	275	LEU	2.0
1	D	252	VAL	2.0
1	D	253	GLU	2.0
1	D	184	ALA	2.0
1	D	185	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 monosaccharides in this entry.

6.4 Ligands (i)

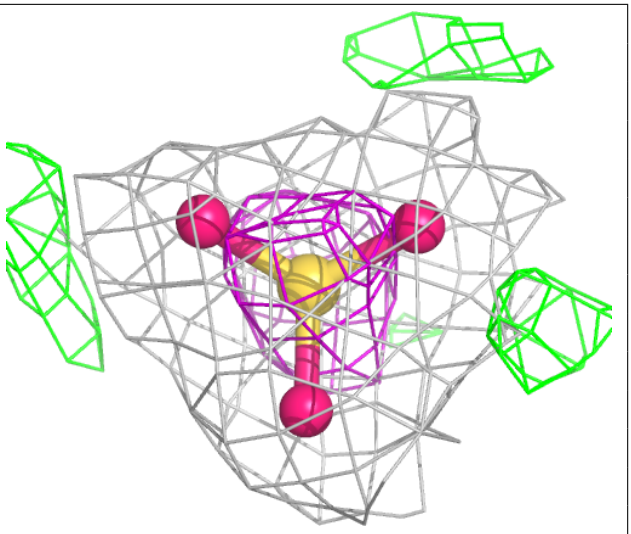
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

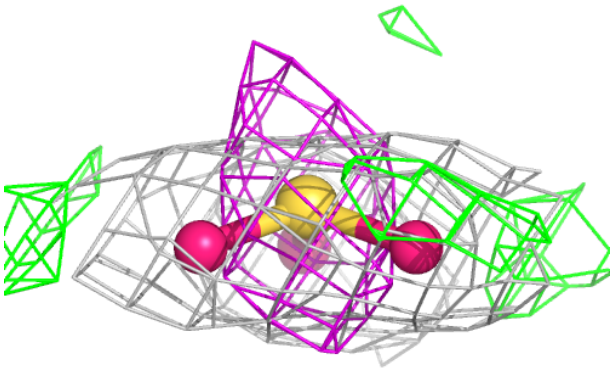
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	SO3	D	301	4/4	0.82	0.13	25,28,28,49	0
2	SO3	B	301	4/4	0.90	0.18	23,24,34,46	0
2	SO3	C	301	4/4	0.92	0.10	20,23,24,39	0
2	SO3	A	301	4/4	0.96	0.09	14,15,16,34	0

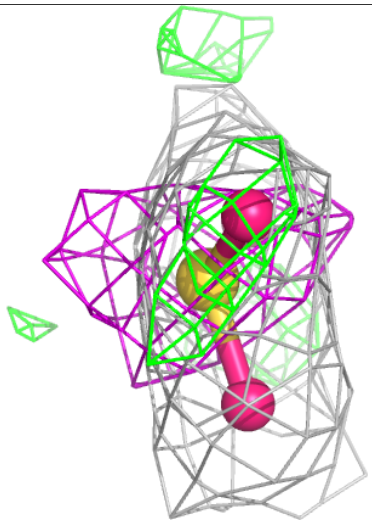
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

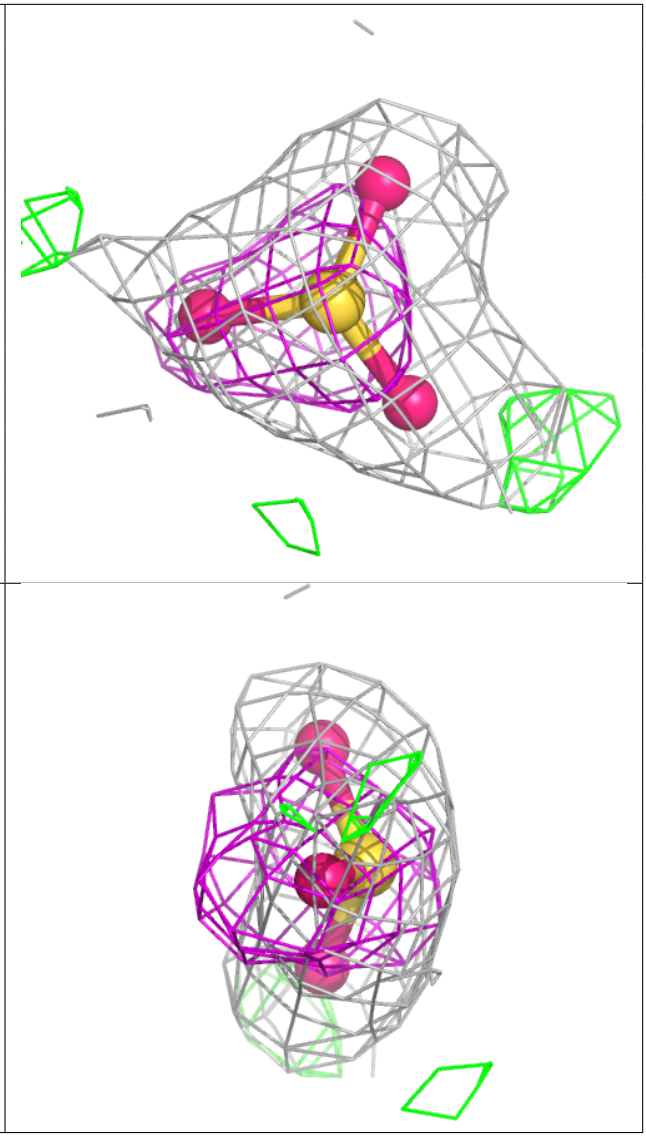






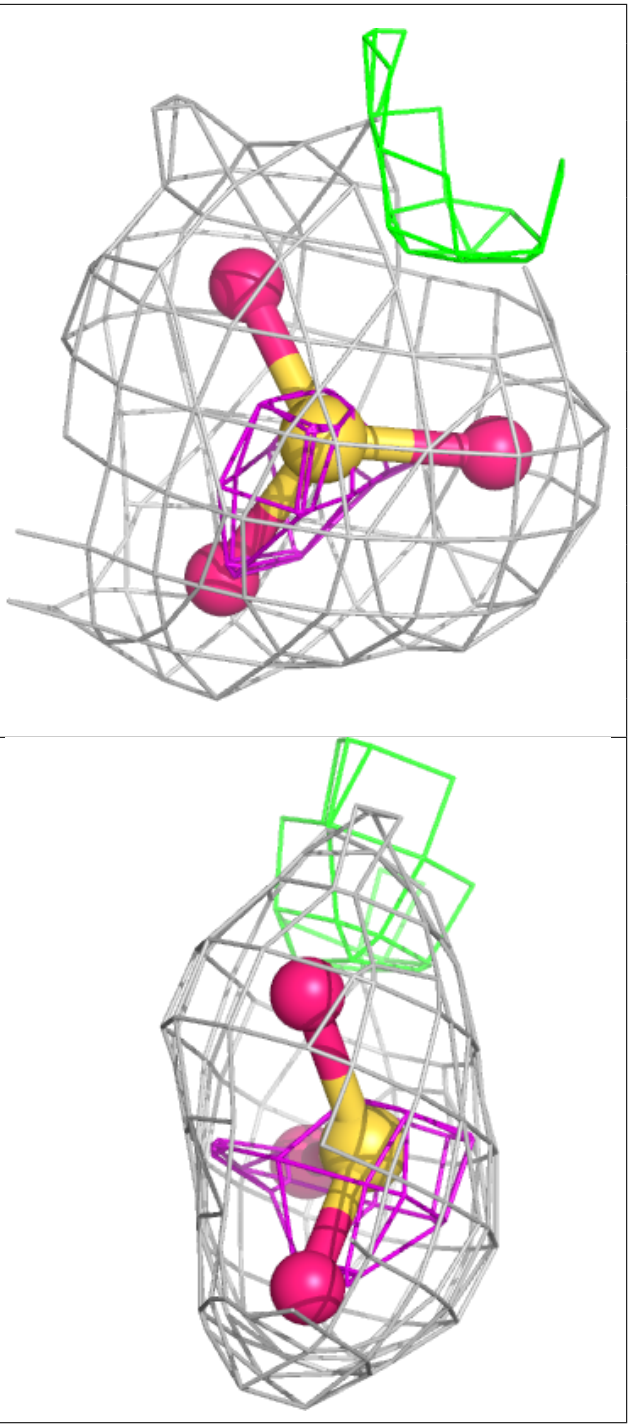
Electron density around SO3 B 301:

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



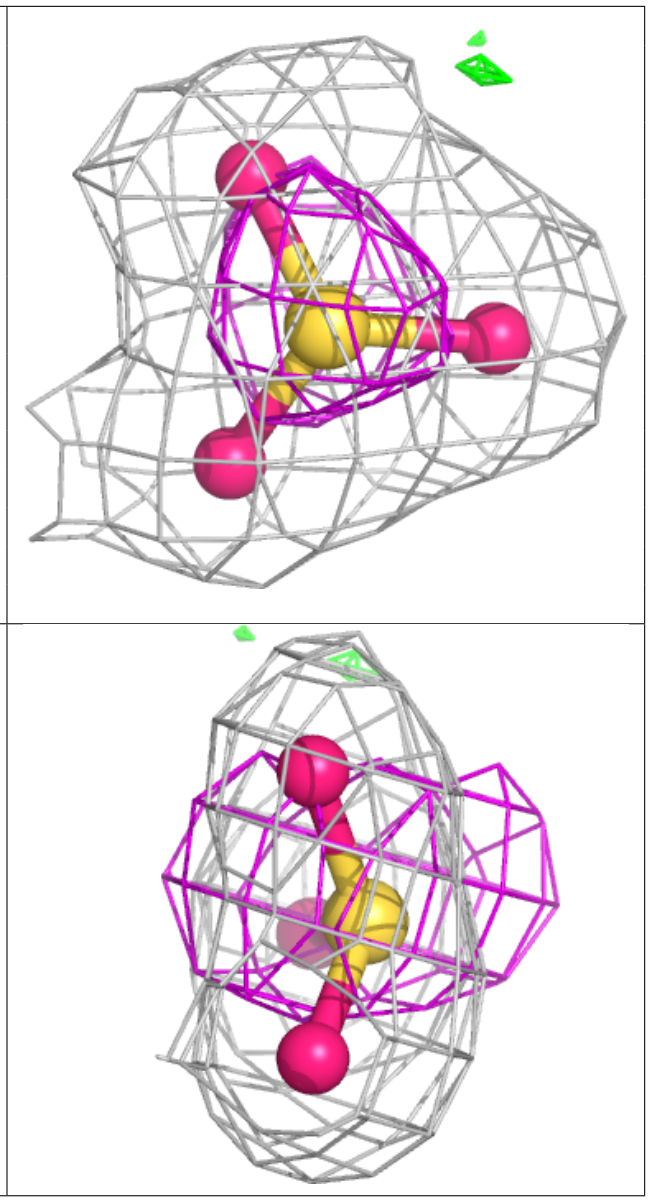
Electron density around SO3 C 301:

$2mF_o$-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.