

# Full wwPDB X-ray Structure Validation Report (i)

#### Nov 5, 2023 – 06:20 PM EST

PDB ID : 8SUI

Title: Joint X-ray/neutron structure of Thermus thermophilus serine hydroxymeth

yltransferase (TthSHMT) in internal aldimine state with L-Ser bound in a

pre-Michalis complex

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Deposited on : 2023-05-12

Resolution : 2.30 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) 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 : FAILED

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

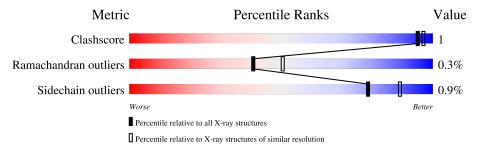
Validation Pipeline (wwPDB-VP) : 2.36

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.30 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}(\AA))$
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)

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%

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain	
1	A	405	97%	•
1	В	405	98%	



# 2 Entry composition (i)

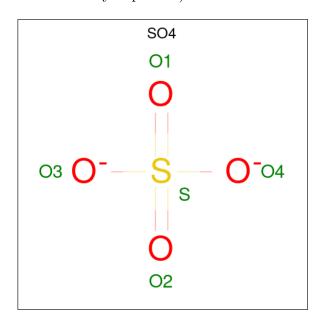
There are 4 unique types of molecules in this entry. The entry contains 14982 atoms, of which 6233 are hydrogens and 2086 are deuteriums.

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 Serine hydroxymethyltransferase.

Mol	Chain	Residues			A	Atoms					ZeroOcc	AltConf	Trace
1	Λ	402	Total	С	D	Н	N	О	Р	S	0	338	0
1	A	402	6888	1984	644	3119	556	575	1	9	0	550	U
1	D	402	Total	С	D	Н	N	О	Р	S	0	337	0
1	D	402	6882	1984	643	3114	556	575	1	9		99 <i>1</i>	U

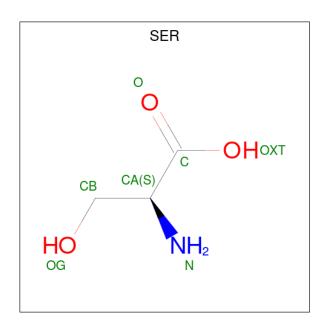
• Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S) (labeled as "Ligand of Interest" by depositor).



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

• Molecule 3 is SERINE (three-letter code: SER) (formula: C<sub>3</sub>H<sub>7</sub>NO<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
9	D	1	Total	С	D	N	О	0	0
3	Б	1	14	3	7	1	3	U	0

#### • Molecule 4 is water.

Mol	Chain	Residues	${f Atoms}$			ZeroOcc	AltConf
4	A	200	Total 5 600 4		O 200	0	0
4	В	196	Total 588 3		O 196	0	0

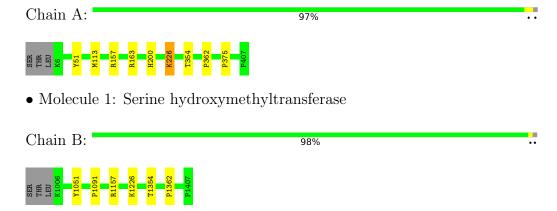


# 3 Residue-property plots (i)

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. 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. 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.

Note EDS failed to run properly.

• Molecule 1: Serine hydroxymethyltransferase





# 4 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	58.81Å 83.33Å 95.57Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $91.68^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	40.00 - 2.30	Depositor
% Data completeness	97.0 (40.00-2.30)	Depositor
(in resolution range)		1
$R_{merge}$	0.23	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	0.00  (at  2.00Å)	Xtriage
Refinement program	nCNS 1.0.8	Depositor
$R, R_{free}$	0.204 , $0.221$	Depositor
Wilson B-factor $(Å^2)$	3.6	Xtriage
Anisotropy	0.265	Xtriage
L-test for twinning <sup>2</sup>	$< L > = 0.39, < L^2> = 0.21$	Xtriage
Estimated twinning fraction	0.067 for h,-k,-l	Xtriage
Total number of atoms	14982	wwPDB-VP
Average B, all atoms $(\mathring{A}^2)$	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.67% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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, DOD, LLP

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		
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.34	0/5858	0.58	0/7924	
1	В	0.35	0/5836	0.58	0/7895	
All	All	0.35	0/11694	0.58	0/15819	

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	3769	3119	480	4	0
1	В	3768	3114	493	2	0
2	A	5	0	0	0	0
2	В	5	0	0	0	0
3	В	14	0	4	0	0
4	A	600	0	0	0	0
4	В	588	0	0	1	0
All	All	8749	6233	977	7	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 1.



All (7) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A + 0 mg 1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${\rm distance} \ (\mathring{\rm A})$	overlap (Å)

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	Percer	ntiles
1	A	736/405 (182%)	717 (97%)	17 (2%)	2 (0%)	41	50
1	В	735/405 (182%)	713 (97%)	20 (3%)	2 (0%)	41	50
All	All	1471/810 (182%)	1430 (97%)	37 (2%)	4 (0%)	41	50

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	1354[A]	THR
1	В	1354[B]	THR
1	A	354[A]	THR
1	A	354[B]	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.

$\mathbf{Mol}$	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	585/322~(182%)	577 (99%)	8 (1%)	67 81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles			
1	В	582/322 (181%)	578 (99%)	4 (1%)	84 92			
All	All	1167/644 (181%)	1155 (99%)	12 (1%)	78 87			

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51[A]	TYR
1	A	51[B]	TYR
1	A	157[A]	ARG
1	A	157[B]	ARG
1	A	163[A]	ARG
1	A	163[B]	ARG
1	A	200[A]	HIS
1	A	200[B]	HIS
1	В	1051[A]	TYR
1	В	1051[B]	TYR
1	В	1157[A]	ARG
1	В	1157[B]	ARG

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)

2 non-standard protein/DNA/RNA residues 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	Chain	Chain	Chain	Res	Link	Bo	ond leng	hs	В	ond ang	gles
			nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2			
	1	LLP	В	1226	1	23,24,25	1.90	5 (21%)	25,32,34	2.57	10 (40%)		



	Mol	Type	Type	Chain	Chain	Chain	Chain	Chain	Res	Link	Bo	ond leng	hs	В	ond ang	gles
			Chain	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2					
	1	LLP	A	226	1	23,24,25	2.07	6 (26%)	25,32,34	2.53	10 (40%)					

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
1	LLP	В	1226	1	-	5/16/17/19	0/1/1/1
1	LLP	A	226	1	-	8/16/17/19	0/1/1/1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	$Ideal(\AA)$
1	A	226	LLP	C4-C5	5.00	1.48	1.42
1	В	1226	LLP	C4-C3	4.67	1.47	1.40
1	A	226	LLP	C4-C3	4.41	1.47	1.40
1	A	226	LLP	C3-C2	4.32	1.45	1.40
1	В	1226	LLP	C4-C5	3.92	1.46	1.42
1	В	1226	LLP	C3-C2	3.87	1.44	1.40
1	A	226	LLP	CB-CA	3.14	1.57	1.53
1	В	1226	LLP	CB-CA	2.91	1.57	1.53
1	A	226	LLP	OP4-C5'	-2.51	1.35	1.45
1	В	1226	LLP	OP4-C5'	-2.20	1.36	1.45
1	A	226	LLP	CD-CE	2.10	1.58	1.51

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$Ideal(^{o})$
1	В	1226	LLP	OP4-C5'-C5	7.79	124.20	109.35
1	A	226	LLP	OP4-C5'-C5	7.11	122.91	109.35
1	A	226	LLP	C6-N1-C2	5.26	128.92	119.17
1	В	1226	LLP	C6-N1-C2	5.17	128.74	119.17
1	A	226	LLP	CE-NZ-C4'	3.39	129.32	118.90
1	В	1226	LLP	C3-C2-N1	-3.27	116.54	120.77
1	В	1226	LLP	C2'-C2-C3	3.18	124.82	120.89
1	A	226	LLP	C3-C2-N1	-3.15	116.70	120.77
1	В	1226	LLP	C5-C4-C4'	3.07	126.61	121.56
1	В	1226	LLP	CE-NZ-C4'	2.92	127.86	118.90
1	A	226	LLP	C5-C4-C4'	2.91	126.34	121.56
1	A	226	LLP	C5-C6-N1	-2.88	119.01	123.82

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Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	226	LLP	C2'-C2-C3	2.84	124.40	120.89
1	В	1226	LLP	C3-C4-C5	-2.66	116.22	118.26
1	A	226	LLP	CD-CE-NZ	-2.64	104.46	110.93
1	В	1226	LLP	C5-C6-N1	-2.59	119.51	123.82
1	A	226	LLP	C3-C4-C5	-2.46	116.37	118.26
1	A	226	LLP	C4-C3-C2	-2.27	118.78	120.19
1	В	1226	LLP	CD-CE-NZ	-2.26	105.38	110.93
1	В	1226	LLP	C4-C3-C2	-2.01	118.94	120.19

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	226	LLP	C4-C5-C5'-OP4
1	A	226	LLP	O-C-CA-CB
1	В	1226	LLP	O-C-CA-CB
1	В	1226	LLP	CG-CD-CE-NZ
1	A	226	LLP	C6-C5-C5'-OP4
1	В	1226	LLP	C4-C5-C5'-OP4
1	A	226	LLP	CG-CD-CE-NZ
1	A	226	LLP	CD-CE-NZ-C4'
1	A	226	LLP	C5'-OP4-P-OP1
1	В	1226	LLP	CD-CE-NZ-C4'
1	A	226	LLP	C3-C4-C4'-NZ
1	A	226	LLP	C5'-OP4-P-OP2
1	В	1226	LLP	C3-C4-C4'-NZ

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	226	LLP	1	0

## 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

# 5.6 Ligand geometry (i)

3 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	В	ond leng	$_{ m gths}$	В	ond ang	gles
MIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	SER	В	1502	-	5,6,6	0.99	0	5,7,7	1.52	1 (20%)
2	SO4	A	2001	-	4,4,4	0.25	0	6,6,6	0.12	0
2	SO4	В	1501	-	4,4,4	0.14	0	6,6,6	0.16	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	SER	В	1502	_	-	4/6/6/6	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
3	В	1502	SER	OXT-C-O	-2.77	117.79	124.09

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	В	1502	SER	O-C-CA-N
3	В	1502	SER	O-C-CA-CB
3	В	1502	SER	OXT-C-CA-CB
3	В	1502	SER	OXT-C-CA-N

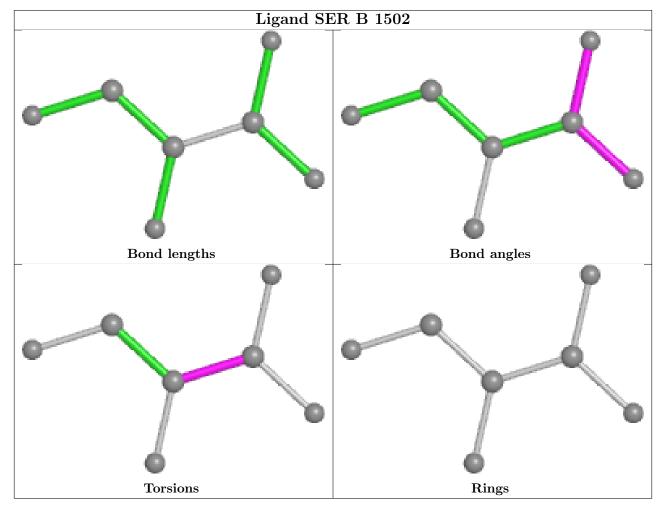
There are no ring outliers.

No monomer is involved in short contacts.

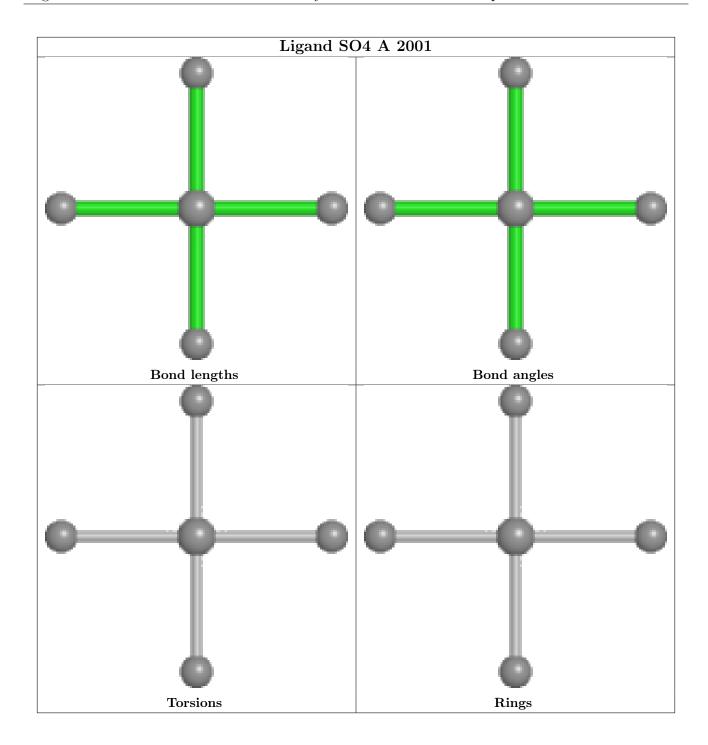
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will



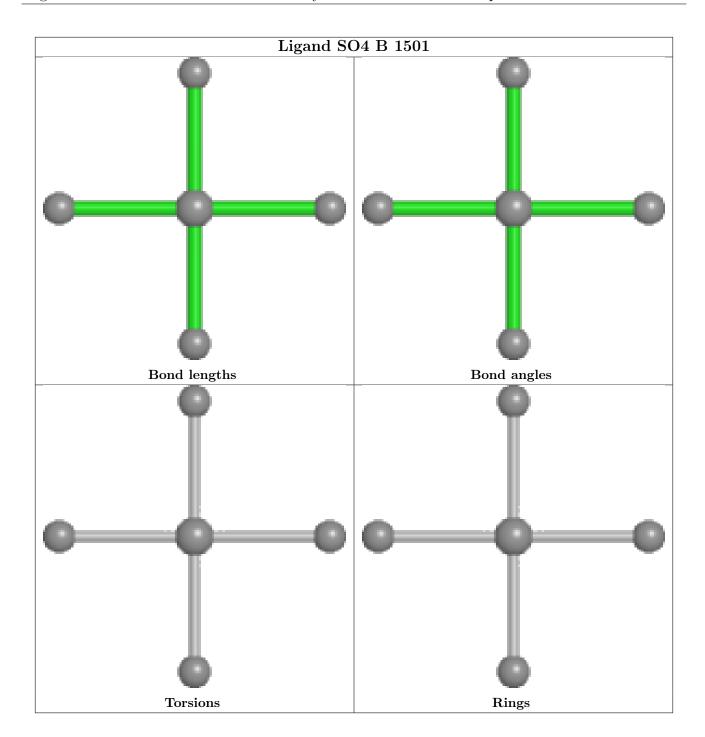
also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted 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.











# 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)

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

## 6.3 Carbohydrates (i)

EDS failed to run properly - this section is therefore empty.

## 6.4 Ligands (i)

EDS failed to run properly - this section is therefore empty.

## 6.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.

