wwPDB X-ray Structure Validation Summary Report (i)

May 23, 2022 – 02:16 PM JST

PDB ID	:	7VOS
Title	:	High-resolution neutron and X-ray joint refined structure of high-potential iron-sulfur protein in the oxidized state
Authors	:	Hanazono, Y.; Hirano, Y.; Takeda, K.; Kusaka, K.; Tamada, T.; Miki, K.
Deposited on	:	2021-10-14
Resolution	:	0.66 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*
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 (1)) were used in the production of this report:

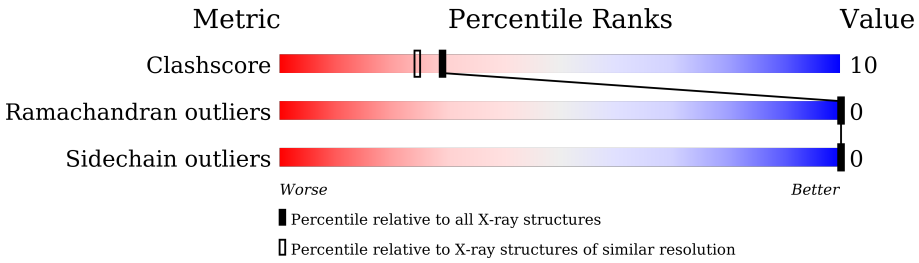
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.28.1

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 0.66 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))
Clashscore	141614	1000 (1.02-0.48)
Ramachandran outliers	138981	1074 (1.04-0.48)
Sidechain outliers	138945	1075 (1.04-0.48)

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	83	89% 10% •

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	A	104[B]	-	-	X	-

2 Entry composition

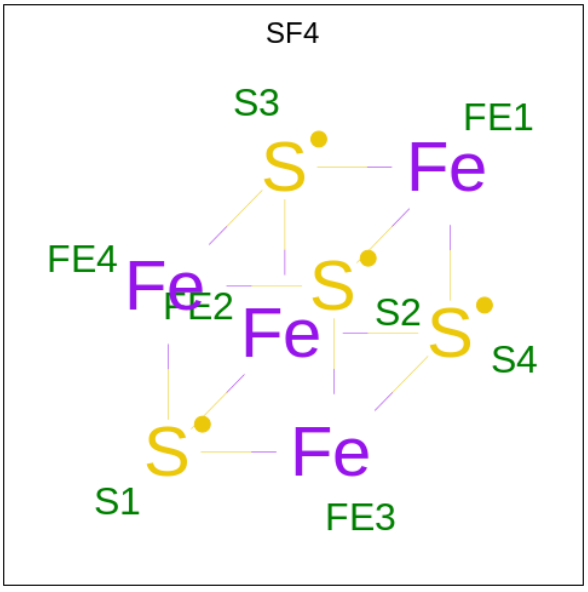
There are 7 unique types of molecules in this entry. The entry contains 2034 atoms, of which 647 are hydrogens and 428 are deuteriums.

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 High-potential iron-sulfur protein.

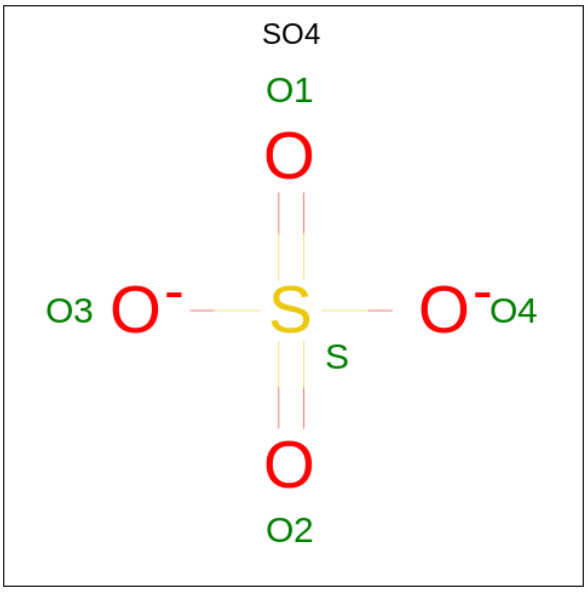
Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
			Total	C	D	H	N	O	S			
1	A	83	1534	455	160	647	129	137	6	0	79	0

- Molecule 2 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4) (labeled as "Ligand of Interest" by depositor).



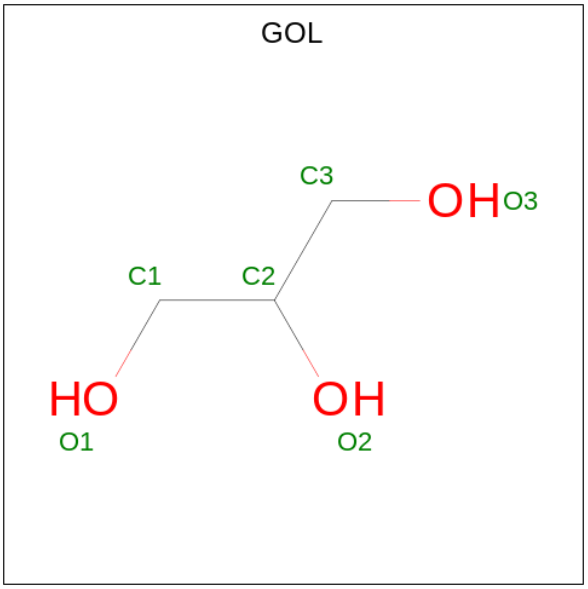
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	S		
2	A	1	8	4	4	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



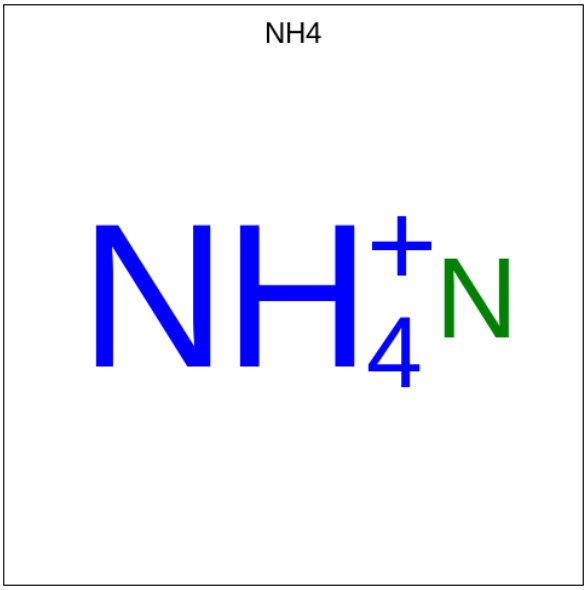
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 15 12 3	0	1
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 10 8 2	0	1
3	A	1	Total O S 10 8 2	0	1
3	A	1	Total O S 5 4 1	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



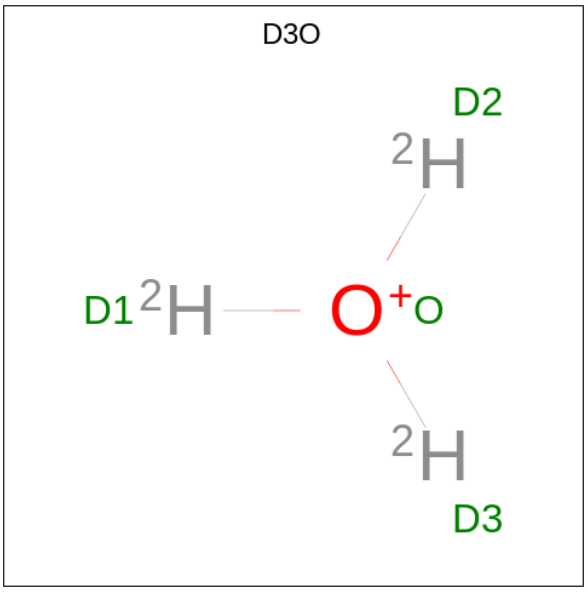
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C D O 28 6 16 6	0	1
4	A	1	Total C D O 14 3 8 3	0	0
4	A	1	Total C D O 14 3 8 3	0	0
4	A	1	Total C D O 14 3 8 3	0	0
4	A	1	Total C D O 14 3 8 3	0	0

- Molecule 5 is AMMONIUM ION (three-letter code: NH4) (formula: H_4N).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total D N 5 4 1	0	0
5	A	1	Total D N 5 4 1	0	0
5	A	1	Total D N 5 4 1	0	0
5	A	1	Total D N 5 4 1	0	0

- Molecule 6 is trideuteriooxidanium (three-letter code: D3O) (formula: D_3O).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total D O 4 3 1	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	129	Total D O 339 201 138	0	12

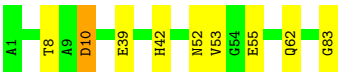
3 Residue-property plots (i)

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: High-potential iron-sulfur protein

Chain A:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	46.33Å 58.85Å 23.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.41 – 0.66	Depositor
% Data completeness (in resolution range)	96.3 (36.41-0.66)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.03 (at 0.66Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.074 , 0.082	Depositor
Wilson B-factor (Å^2)	3.8	Xtriage
Anisotropy	0.076	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2034	wwPDB-VP
Average B, all atoms (Å^2)	6.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.23% of the height of the origin peak. No significant pseudotranslation is detected.*

[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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: D3O, DOD, SF4, GOL, SO4, NH4

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	0.82	6/1181 (0.5%)	1.15	12/1606 (0.7%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	39[A]	GLU	CD-OE2	7.18	1.33	1.25
1	A	39[B]	GLU	CD-OE2	7.18	1.33	1.25
1	A	55[A]	GLU	CD-OE2	5.55	1.31	1.25
1	A	55[B]	GLU	CD-OE2	5.55	1.31	1.25
1	A	39[A]	GLU	CD-OE1	-5.05	1.20	1.25

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	53[A]	VAL	CA-CB-CG1	10.07	126.00	110.90
1	A	53[B]	VAL	CA-CB-CG1	10.07	126.00	110.90
1	A	10[A]	ASP	O-C-N	-9.17	108.03	122.70
1	A	10[B]	ASP	O-C-N	-9.17	108.03	122.70
1	A	10[A]	ASP	C-N-CA	7.05	139.33	121.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	887	647	296	11	0
2	A	8	0	0	0	0
3	A	45	0	0	4	0
4	A	84	0	45	3	0
5	A	20	0	0	1	0
6	A	4	0	0	0	0
7	A	339	0	0	10	0
All	All	1387	647	341	15	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 10.

The worst 5 of 15 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10[A]:ASP:HB2	7:A:206:DOD:O	1.36	1.19
1:A:10[A]:ASP:OD2	7:A:205:DOD:O	1.64	1.13
1:A:62[B]:GLN:CD	4:A:109:GOL:O2	2.13	0.85
1:A:62[B]:GLN:NE2	4:A:109:GOL:O2	2.10	0.84
1:A:10[A]:ASP:CB	7:A:206:DOD:O	2.10	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	151/83 (182%)	149 (99%)	2 (1%)	0	100 100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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	113/61 (185%)	113 (100%)	0	100 100

There are no protein residues with a non-rotameric sidechain to report.

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

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 21 ligands modelled in this entry, 5 are modelled with single atom - leaving 16 for Mogul analysis.

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	$\#\|Z\|>2$
4	GOL	A	107[A]	-	5,5,5	0.29	0	5,5,5	0.95	0
4	GOL	A	108	-	5,5,5	0.96	0	5,5,5	1.00	0
3	SO4	A	102[C]	-	4,4,4	0.30	0	6,6,6	0.42	0
3	SO4	A	106	-	4,4,4	0.45	0	6,6,6	0.23	0
4	GOL	A	111	-	5,5,5	1.63	2 (40%)	5,5,5	1.89	1 (20%)
3	SO4	A	104[B]	-	4,4,4	0.35	0	6,6,6	0.77	0
3	SO4	A	105[A]	-	4,4,4	0.11	0	6,6,6	0.50	0
4	GOL	A	107[B]	-	5,5,5	1.00	0	5,5,5	1.28	1 (20%)
4	GOL	A	110	-	5,5,5	0.84	0	5,5,5	1.39	1 (20%)
2	SF4	A	101	1	0,12,12	-	-	-		
3	SO4	A	103	-	4,4,4	0.26	0	6,6,6	0.17	0
3	SO4	A	105[B]	-	4,4,4	0.19	0	6,6,6	1.20	0
4	GOL	A	109	-	5,5,5	1.28	0	5,5,5	1.25	1 (20%)
3	SO4	A	102[A]	-	4,4,4	0.39	0	6,6,6	0.50	0
3	SO4	A	104[A]	-	4,4,4	0.42	0	6,6,6	0.18	0
3	SO4	A	102[B]	-	4,4,4	0.21	0	6,6,6	0.28	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
4	GOL	A	107[A]	-	-	0/4/4/4	-
4	GOL	A	108	-	-	0/4/4/4	-
4	GOL	A	111	-	-	2/4/4/4	-
4	GOL	A	107[B]	-	-	0/4/4/4	-
4	GOL	A	110	-	-	0/4/4/4	-
4	GOL	A	109	-	-	1/4/4/4	-
2	SF4	A	101	1	-	-	0/6/5/5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	111	GOL	O1-C1	-2.40	1.32	1.42
4	A	111	GOL	O3-C3	2.35	1.52	1.42

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	111	GOL	O2-C2-C1	-2.36	98.72	109.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	107[B]	GOL	O3-C3-C2	-2.28	99.27	110.20
4	A	110	GOL	O2-C2-C3	-2.26	99.18	109.12
4	A	109	GOL	O2-C2-C3	2.26	119.06	109.12

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	111	GOL	O1-C1-C2-C3
4	A	111	GOL	O1-C1-C2-O2
4	A	109	GOL	O1-C1-C2-O2

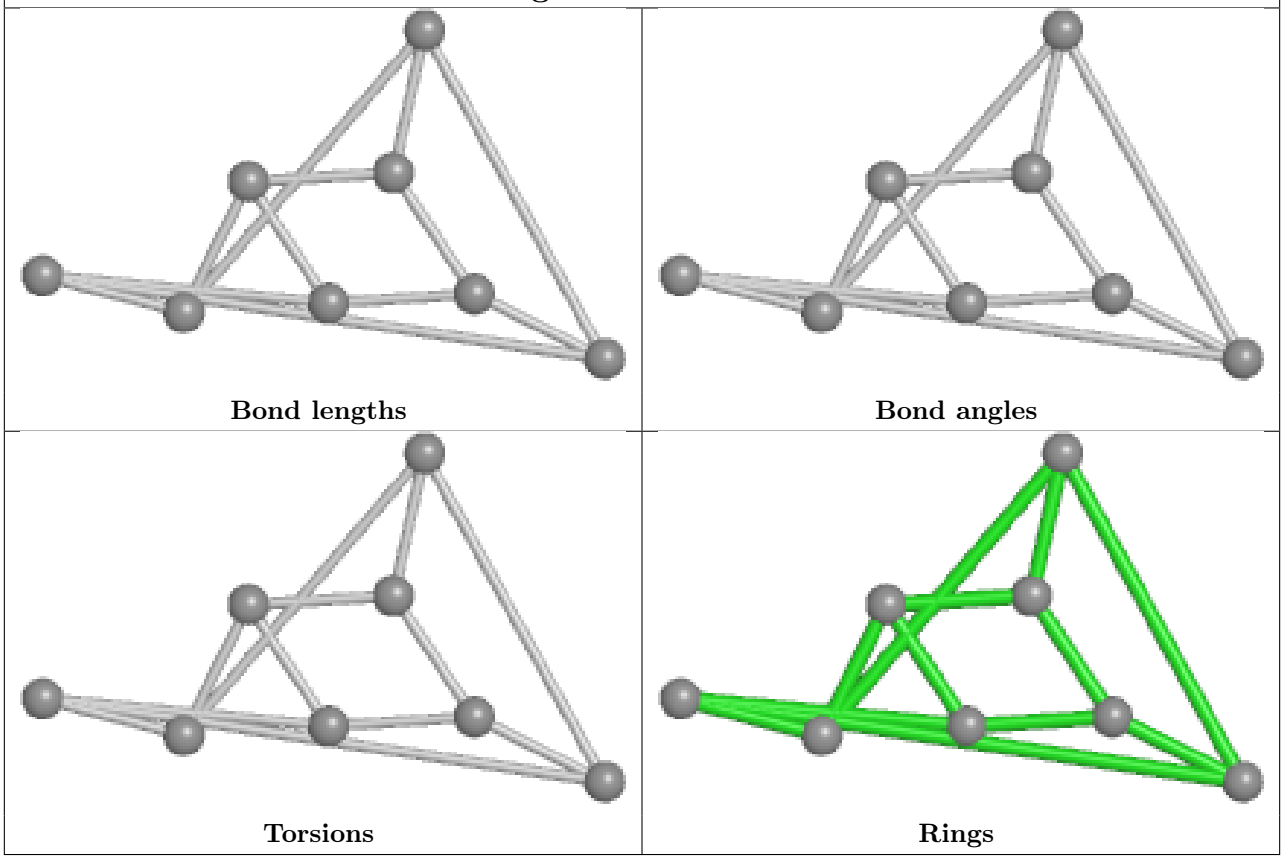
There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	104[B]	SO4	2	0
4	A	109	GOL	3	0
3	A	104[A]	SO4	1	0
3	A	102[B]	SO4	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 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 SF4 A 101



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

6.1 Protein, DNA and RNA chains

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

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

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

6.4 Ligands

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

6.5 Other polymers

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