



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 16, 2024 – 06:55 AM EDT

PDB ID : 5B46  
Title : 2-Oxoacid:Ferredoxin Oxidoreductase 2 from Sulfolobus tokodai - ligand free form  
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Deposited on : 2016-04-01  
Resolution : 2.10 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](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	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
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)	:	2.37.1

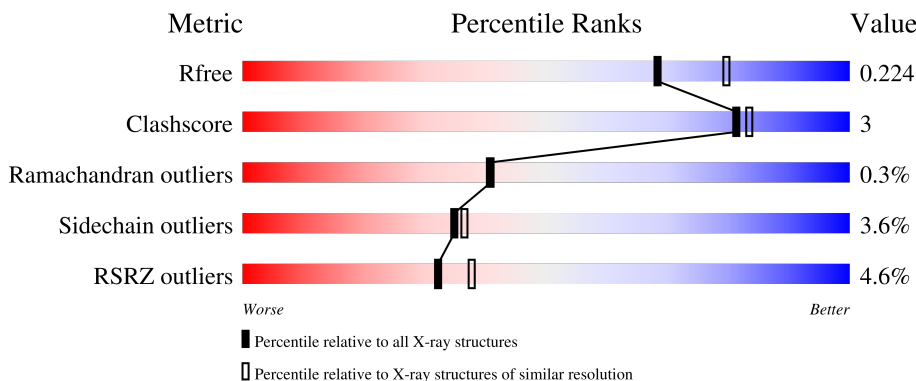
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	628	<div> <div>2%</div> <div>90%</div> <div>8%</div> <div>.</div> </div>
2	B	304	<div> <div>10%</div> <div>88%</div> <div>10%</div> <div>..</div> </div>

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 7592 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.

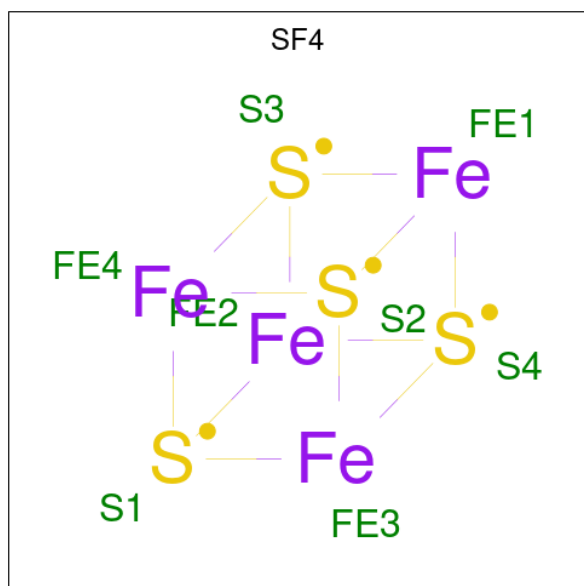
- Molecule 1 is a protein called 2-oxoacid--ferredoxin oxidoreductase alpha subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	627	4937	3159	822	937	19	0	0	0

- Molecule 2 is a protein called 2-oxoacid--ferredoxin oxidoreductase beta subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	301	2357	1513	409	425	10	0	0	0

- Molecule 3 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe<sub>4</sub>S<sub>4</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	S		
3	B	1	8	4	4	0	0

- Molecule 4 is THIAMINE DIPHOSPHATE (three-letter code: TPP) (formula: C<sub>12</sub>H<sub>19</sub>N<sub>4</sub>O<sub>7</sub>P<sub>2</sub>S).



- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

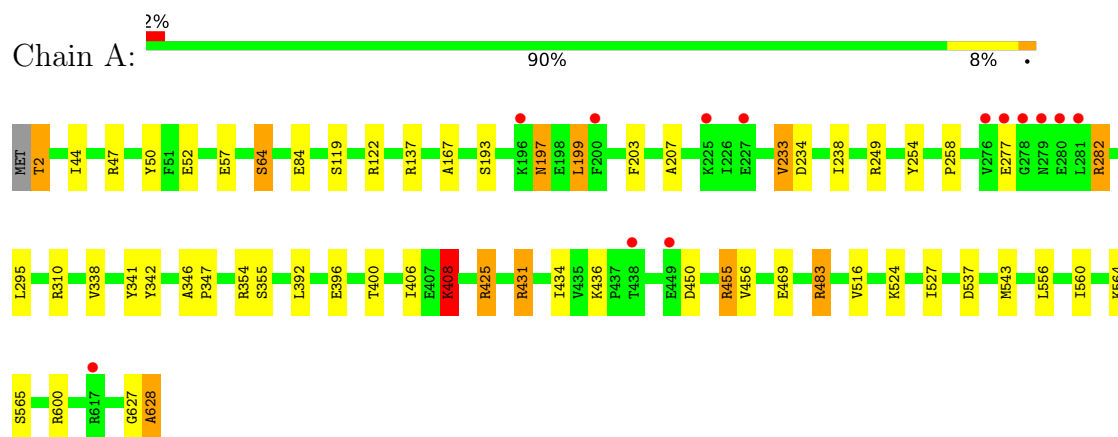
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	192	Total O 192 192	0	0
6	B	71	Total O 71 71	0	0

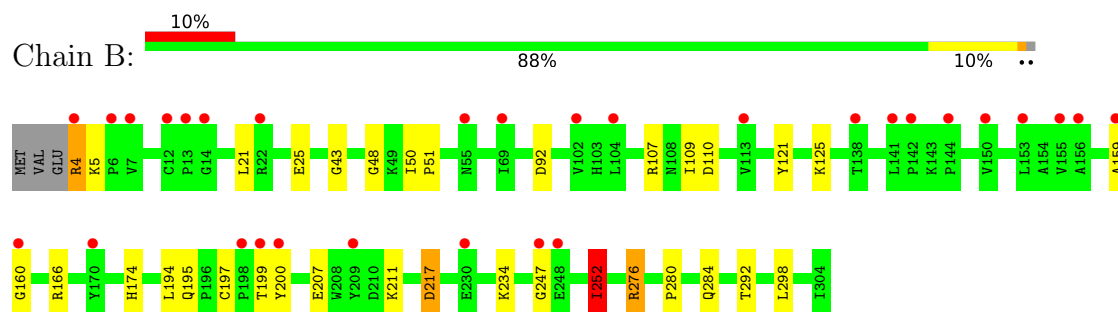
### 3 Residue-property plots

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: 2-oxoacid--ferredoxin oxidoreductase alpha subunit



- Molecule 2: 2-oxoacid--ferredoxin oxidoreductase beta subunit



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.89Å 205.05Å 126.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.93 – 2.10 33.93 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.7 (33.93-2.10) 98.7 (33.93-2.10)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.34 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.175 , 0.219 0.182 , 0.224	Depositor DCC
$R_{free}$ test set	3866 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	35.4	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 31.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7592	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.21% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SF4, MG, TPP

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	1.04	4/5031 (0.1%)	1.05	22/6797 (0.3%)
2	B	1.03	2/2412 (0.1%)	1.00	14/3267 (0.4%)
All	All	1.03	6/7443 (0.1%)	1.03	36/10064 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	160	GLY	N-CA	-8.91	1.32	1.46
1	A	64	SER	CB-OG	7.83	1.52	1.42
1	A	84	GLU	CD-OE1	5.68	1.31	1.25
2	B	217	ASP	CB-CG	5.58	1.63	1.51
1	A	119	SER	CB-OG	-5.50	1.35	1.42
1	A	52	GLU	CD-OE2	5.33	1.31	1.25

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	455	ARG	NE-CZ-NH1	13.38	126.99	120.30
1	A	431	ARG	NE-CZ-NH2	-12.81	113.90	120.30
1	A	234	ASP	CB-CG-OD1	11.59	128.73	118.30
1	A	122	ARG	NE-CZ-NH2	-11.39	114.61	120.30
1	A	455	ARG	NE-CZ-NH2	-10.15	115.22	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	122	ARG	NE-CZ-NH1	8.74	124.67	120.30
1	A	431	ARG	NE-CZ-NH1	8.03	124.31	120.30
2	B	217	ASP	CB-CG-OD1	7.91	125.42	118.30
2	B	159	ALA	CA-C-N	7.80	131.80	116.20
2	B	166	ARG	NE-CZ-NH1	7.72	124.16	120.30
2	B	166	ARG	NE-CZ-NH2	-7.69	116.45	120.30
1	A	425	ARG	NE-CZ-NH2	-7.59	116.51	120.30
1	A	249	ARG	NE-CZ-NH1	7.03	123.81	120.30
2	B	159	ALA	O-C-N	-6.77	111.69	123.20
1	A	408	LYS	CD-CE-NZ	6.46	126.55	111.70
2	B	107	ARG	NE-CZ-NH2	-6.45	117.08	120.30
1	A	483	ARG	NE-CZ-NH2	-6.42	117.09	120.30
1	A	47	ARG	NE-CZ-NH1	6.39	123.50	120.30
2	B	4	ARG	NE-CZ-NH1	6.29	123.45	120.30
1	A	628	ALA	CB-CA-C	-6.05	101.02	110.10
2	B	159	ALA	N-CA-C	5.92	126.97	111.00
2	B	159	ALA	C-N-CA	5.83	134.53	122.30
1	A	295	LEU	CA-CB-CG	5.75	128.53	115.30
2	B	92	ASP	CB-CG-OD1	5.73	123.46	118.30
2	B	276	ARG	NE-CZ-NH1	-5.66	117.47	120.30
2	B	92	ASP	CB-CG-OD2	-5.60	113.26	118.30
2	B	252	ILE	CA-CB-CG2	5.56	122.02	110.90
1	A	310	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	A	282	ARG	NE-CZ-NH1	5.53	123.06	120.30
1	A	137	ARG	NE-CZ-NH1	5.47	123.03	120.30
1	A	455	ARG	CD-NE-CZ	5.38	131.13	123.60
1	A	450	ASP	CB-CG-OD1	5.34	123.11	118.30
1	A	354	ARG	NE-CZ-NH2	-5.22	117.69	120.30
2	B	276	ARG	NE-CZ-NH2	5.20	122.90	120.30
1	A	137	ARG	NE-CZ-NH2	-5.17	117.72	120.30
1	A	483	ARG	NE-CZ-NH1	5.10	122.85	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	627	GLY	Peptide



## 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	4937	0	4964	29	0
2	B	2357	0	2391	10	0
3	B	8	0	0	0	0
4	B	26	0	16	2	0
5	B	1	0	0	0	0
6	A	192	0	0	1	0
6	B	71	0	0	0	0
All	All	7592	0	7371	38	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 3.

All (38) 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)
2:B:284:GLN:O	2:B:292:THR:HG21	1.86	0.75
1:A:50:TYR:OH	1:A:628:ALA:HB2	1.90	0.71
1:A:258:PRO:HG3	1:A:408:LYS:HB2	1.74	0.69
1:A:556:LEU:O	1:A:560:ILE:HG13	1.94	0.67
2:B:197:CYS:O	2:B:200:TYR:O	2.16	0.63
2:B:174:HIS:CE1	2:B:252:ILE:HG23	2.34	0.62
1:A:600:ARG:HE	1:A:628:ALA:HB3	1.65	0.61
1:A:396:GLU:OE1	1:A:431:ARG:HD2	2.04	0.57
1:A:197:ASN:OD1	1:A:197:ASN:C	2.44	0.56
1:A:2:THR:N	1:A:57:GLU:OE1	2.39	0.55
1:A:254:TYR:CE2	4:B:402:TPP:HM42	2.43	0.54
1:A:455:ARG:HD2	6:A:864:HOH:O	2.06	0.54
1:A:338:VAL:HG13	1:A:392:LEU:HD23	1.93	0.51
1:A:600:ARG:HE	1:A:628:ALA:CB	2.24	0.51
1:A:524:LYS:O	1:A:543:MET:HE1	2.11	0.50
1:A:527:ILE:HG22	1:A:543:MET:HE3	1.93	0.50
2:B:43:GLY:O	2:B:48:GLY:HA3	2.12	0.49
1:A:167:ALA:HB1	1:A:207:ALA:HB2	1.93	0.49
1:A:527:ILE:HB	1:A:543:MET:CE	2.42	0.49
1:A:516:VAL:HG23	1:A:564:LYS:HG2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:TYR:HA	1:A:406:ILE:O	2.15	0.46
1:A:431:ARG:HB3	1:A:434:ILE:HD12	1.97	0.46
2:B:21:LEU:HA	2:B:50:ILE:HD11	1.98	0.46
1:A:516:VAL:CG2	1:A:564:LYS:HG2	2.47	0.45
1:A:600:ARG:NE	1:A:628:ALA:HB3	2.29	0.44
1:A:527:ILE:CG2	1:A:543:MET:CE	2.97	0.43
1:A:355:SER:HB2	1:A:408:LYS:HG3	2.00	0.43
1:A:233:VAL:HB	1:A:238:ILE:HD11	2.01	0.43
1:A:346:ALA:HB1	1:A:347:PRO:HA	2.00	0.42
1:A:44:ILE:HG21	2:B:199:THR:HG21	2.00	0.42
1:A:469:GLU:HG2	1:A:483:ARG:HD3	2.01	0.42
1:A:527:ILE:CG2	1:A:543:MET:HE3	2.49	0.42
2:B:50:ILE:HG23	2:B:51:PRO:HD3	2.02	0.42
2:B:109:ILE:HG22	2:B:110:ASP:N	2.35	0.42
2:B:121:TYR:HB3	4:B:402:TPP:H62	2.01	0.41
1:A:197:ASN:OD1	1:A:199:LEU:N	2.53	0.41
1:A:396:GLU:OE2	1:A:455:ARG:NH2	2.54	0.40
2:B:194:LEU:HD12	2:B:252:ILE:HD11	2.02	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	625/628 (100%)	608 (97%)	16 (3%)	1 (0%)	47	49
2	B	299/304 (98%)	289 (97%)	8 (3%)	2 (1%)	22	18
All	All	924/932 (99%)	897 (97%)	24 (3%)	3 (0%)	41	41

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	247	GLY
2	B	125	LYS
1	A	277	GLU

### 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	527/528 (100%)	511 (97%)	16 (3%)	41	44
2	B	254/257 (99%)	242 (95%)	12 (5%)	26	25
All	All	781/785 (100%)	753 (96%)	28 (4%)	35	36

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	64	SER
1	A	193	SER
1	A	197	ASN
1	A	199	LEU
1	A	203	PHE
1	A	233	VAL
1	A	282	ARG
1	A	341	TYR
1	A	400	THR
1	A	408	LYS
1	A	425	ARG
1	A	436	LYS
1	A	456	VAL
1	A	537	ASP
1	A	565	SER
2	B	4	ARG
2	B	5	LYS
2	B	25	GLU
2	B	195	GLN
2	B	207	GLU

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Mol	Chain	Res	Type
2	B	211	LYS
2	B	217	ASP
2	B	234	LYS
2	B	252	ILE
2	B	276	ARG
2	B	280	PRO
2	B	298	LEU

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](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	TPP	B	402	5	22,27,27	1.47	3 (13%)	29,40,40	2.11	11 (37%)
3	SF4	B	401	2	0,12,12	-	-	-		

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	TPP	B	402	5	-	3/16/17/17	0/2/2/2
3	SF4	B	401	2	-	-	0/6/5/5

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	402	TPP	C5'-C4'	5.11	1.51	1.42
4	B	402	TPP	PB-O1B	2.14	1.57	1.50
4	B	402	TPP	C6-C5	2.13	1.51	1.50

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	402	TPP	CM4-C4-N3	4.68	128.50	122.53
4	B	402	TPP	CM4-C4-C5	-4.27	118.27	127.60
4	B	402	TPP	C6'-N1'-C2'	3.14	121.31	115.96
4	B	402	TPP	PA-O3A-PB	-2.98	122.61	132.83
4	B	402	TPP	C2'-N3'-C4'	2.96	122.69	118.08
4	B	402	TPP	N1'-C2'-N3'	-2.92	120.51	125.54
4	B	402	TPP	C5-C4-N3	2.82	113.20	107.57
4	B	402	TPP	O3B-PB-O3A	2.67	113.58	104.64
4	B	402	TPP	C5'-C4'-N3'	-2.45	117.39	121.24
4	B	402	TPP	CM2-C2'-N3'	2.25	120.66	117.15
4	B	402	TPP	O2A-PA-O1A	2.07	122.47	112.24

There are no chirality outliers.

All (3) torsion outliers are listed below:

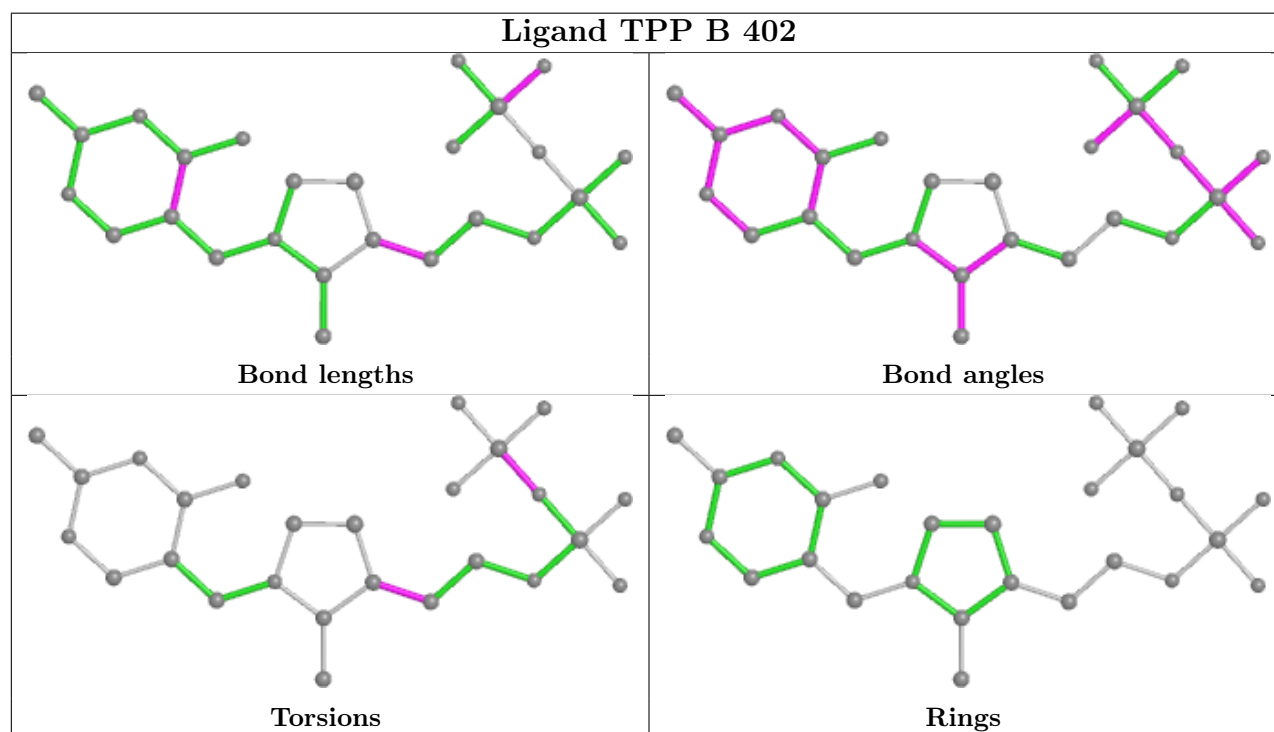
Mol	Chain	Res	Type	Atoms
4	B	402	TPP	PA-O3A-PB-O2B
4	B	402	TPP	PA-O3A-PB-O3B
4	B	402	TPP	C4-C5-C6-C7

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	402	TPP	2	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

### 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, 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	627/628 (99%)	-0.23	13 (2%) 63 68	23, 38, 63, 101	0
2	B	301/304 (99%)	0.28	30 (9%) 7 9	25, 44, 70, 120	0
All	All	928/932 (99%)	-0.06	43 (4%) 32 38	23, 39, 66, 120	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	277	GLU	5.7
2	B	4	ARG	5.5
1	A	278	GLY	5.3
1	A	280	GLU	4.4
1	A	196	LYS	4.2
1	A	279	ASN	3.9
2	B	14	GLY	3.7
2	B	247	GLY	3.7
2	B	209	TYR	3.6
2	B	12	CYS	3.4
1	A	276	VAL	3.2
2	B	138	THR	3.0
1	A	449	GLU	2.8
2	B	230	GLU	2.8
2	B	142	PRO	2.7
2	B	150	VAL	2.7
1	A	438	THR	2.7
2	B	200	TYR	2.7
2	B	13	PRO	2.6
2	B	6	PRO	2.6
1	A	200	PHE	2.5
2	B	144	PRO	2.5
1	A	617	ARG	2.5
2	B	170	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	227	GLU	2.5
2	B	22	ARG	2.4
2	B	102	VAL	2.4
2	B	155	VAL	2.3
2	B	69	ILE	2.3
2	B	156	ALA	2.3
2	B	159	ALA	2.2
2	B	7	VAL	2.2
2	B	55	ASN	2.2
1	A	225	LYS	2.2
2	B	199	THR	2.1
1	A	281	LEU	2.1
2	B	198	PRO	2.1
2	B	248	GLU	2.0
2	B	104	LEU	2.0
2	B	153	LEU	2.0
2	B	113	VAL	2.0
2	B	141	LEU	2.0
2	B	160	GLY	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.

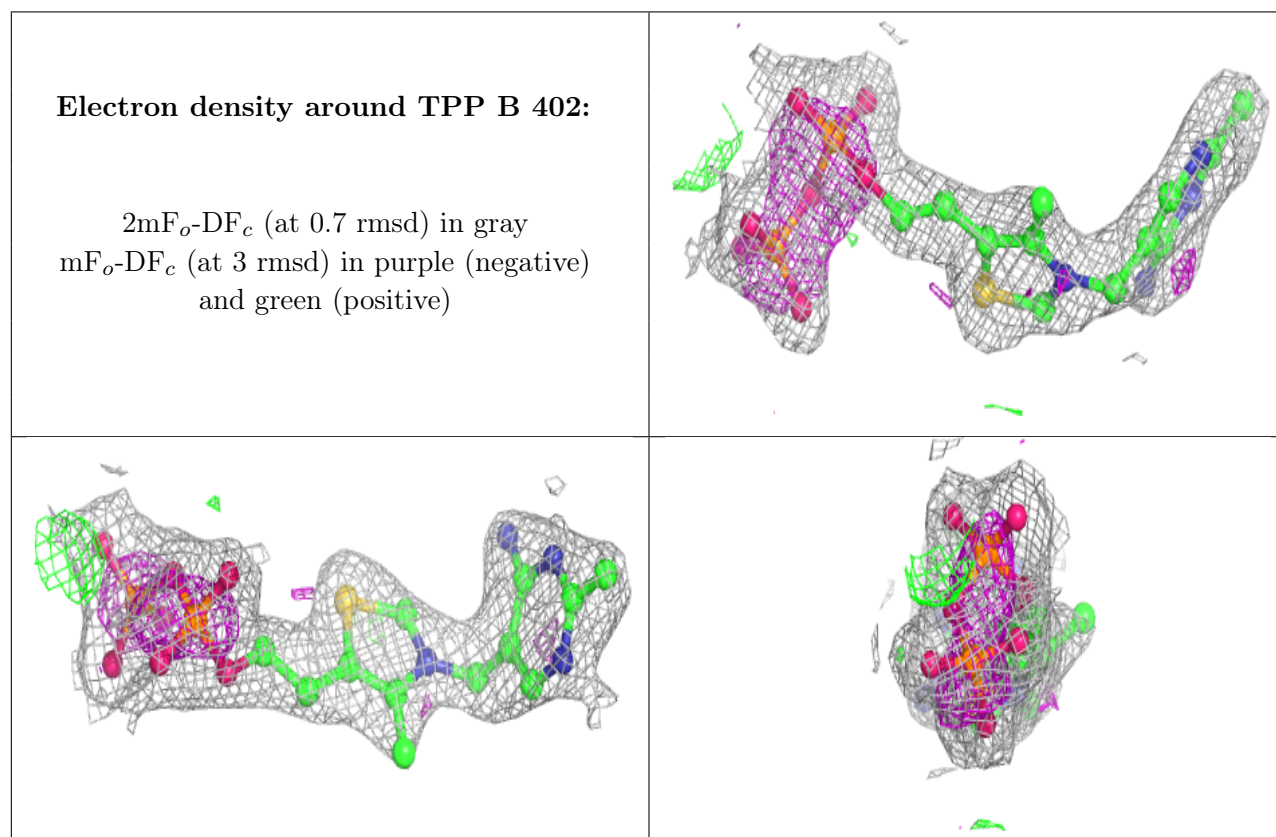
## 6.4 Ligands [i](#)

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, 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
5	MG	B	403	1/1	0.84	0.10	52,52,52,52	0
4	TPP	B	402	26/26	0.96	0.13	40,50,56,59	0
3	SF4	B	401	8/8	0.96	0.06	35,38,41,45	8



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.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.