Full wwPDB X-ray Structure Validation Report (i)

Nov 7, 2023 – 01:44 PM JST

PDB ID	:	5B47
Title	:	2-Oxoacid:Ferredoxin Oxidoreductase 2 from Sulfolobus tokodai - pyruvate complex
Authors	:	Yan, Z.; Maruyama, A.; Arakawa, T.; Fushinobu, S.; Wakagi, T.
Deposited on	:	2016-04-01
Resolution	:	2.20 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 (i)) were used in the production of this report:

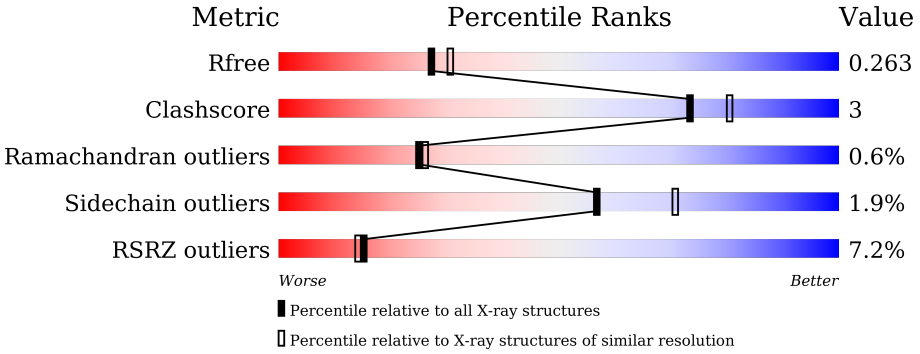
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	628	2%, 89%, 10% •
2	B	304	17%, 81%, 9% • 10%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 7310 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.

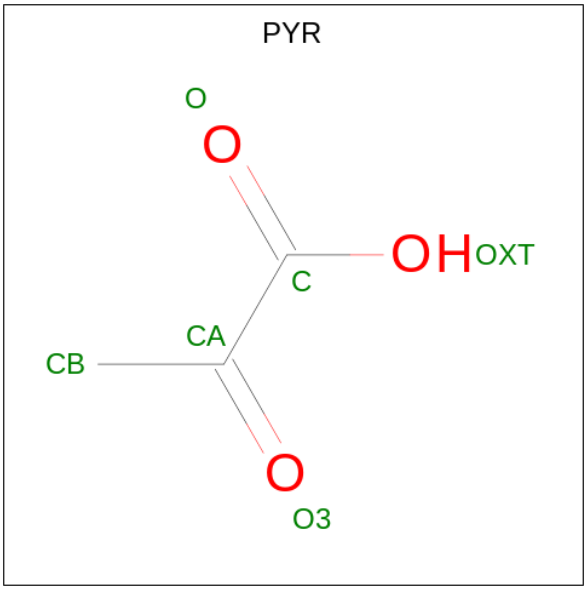
- Molecule 1 is a protein called 2-oxoacid--ferredoxin oxidoreductase alpha subunit.

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.

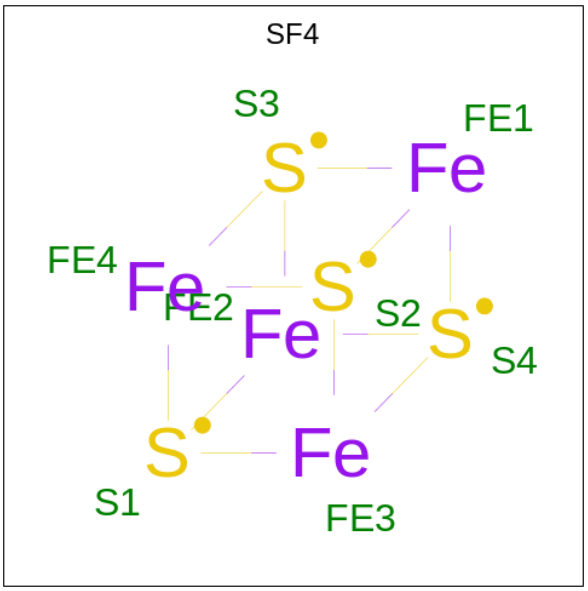
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	275	2141	1375	370	386	10	0	0	0

- Molecule 3 is PYRUVIC ACID (three-letter code: PYR) (formula: $C_3H_4O_3$).



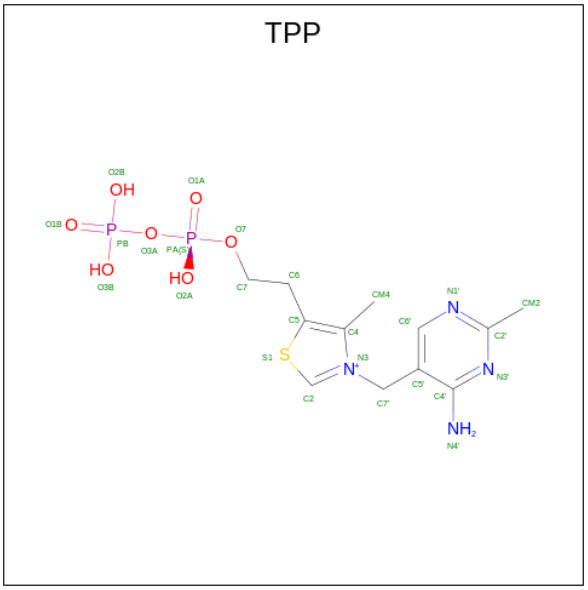
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	6	3	3	0	0

- Molecule 4 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).



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

- Molecule 5 is THIAMINE DIPHOSPHATE (three-letter code: TPP) (formula: $C_{12}H_{19}N_4O_7P_2S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
5	B	1	26	12	4	7	2	1	0	0

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
6	B	1	1	1	0	0

- Molecule 7 is water.

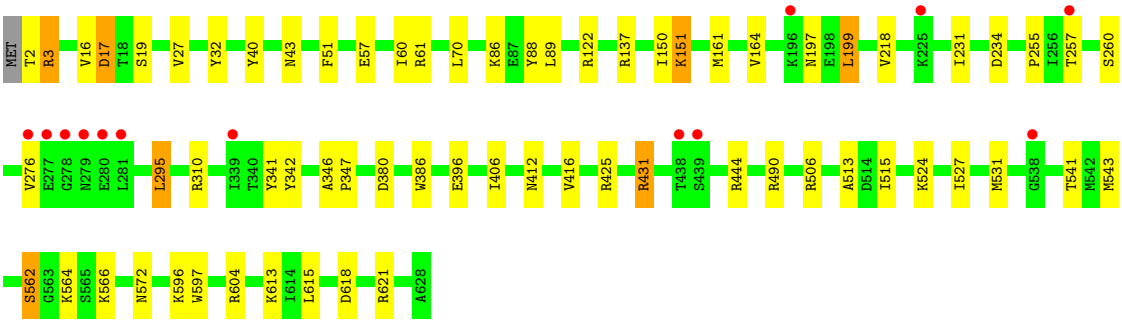
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	159	159	159	0	0
			Total	O		
7	B	32	32	32	0	0

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.

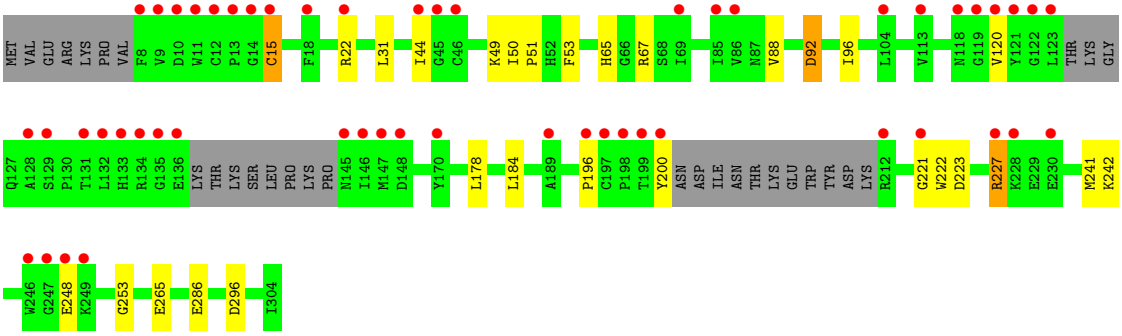
- Molecule 1: 2-oxoacid--ferredoxin oxidoreductase alpha subunit

Chain A:



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

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	100.67Å 203.66Å 126.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.17 – 2.20 36.17 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.0 (36.17-2.20) 98.1 (36.17-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.83 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.205 , 0.259 0.212 , 0.263	Depositor DCC
R_{free} test set	3263 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	42.7	Xtriage
Anisotropy	0.073	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 40.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	7310	wwPDB-VP
Average B, all atoms (Å^2)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% 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 (i)

5.1 Standard geometry (i)

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

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	0.95	1/5031 (0.0%)	1.00	17/6797 (0.3%)
2	B	0.89	0/2187	0.95	3/2959 (0.1%)
All	All	0.93	1/7218 (0.0%)	0.98	20/9756 (0.2%)

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
2	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	597	TRP	CZ3-CH2	5.27	1.48	1.40

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	621	ARG	NE-CZ-NH2	-10.38	115.11	120.30
1	A	122	ARG	NE-CZ-NH2	-8.28	116.16	120.30
1	A	310	ARG	NE-CZ-NH2	-7.61	116.49	120.30
1	A	310	ARG	NE-CZ-NH1	7.49	124.04	120.30
1	A	295	LEU	CA-CB-CG	7.45	132.44	115.30
1	A	506	ARG	NE-CZ-NH2	-6.74	116.93	120.30
1	A	431	ARG	NE-CZ-NH2	-6.64	116.98	120.30
1	A	604	ARG	NE-CZ-NH2	-6.35	117.13	120.30
1	A	621	ARG	NE-CZ-NH1	6.18	123.39	120.30
1	A	234	ASP	CB-CG-OD1	6.15	123.84	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	380	ASP	CB-CG-OD1	6.10	123.79	118.30
1	A	137	ARG	NE-CZ-NH1	6.04	123.32	120.30
2	B	227	ARG	NE-CZ-NH1	5.76	123.18	120.30
1	A	604	ARG	NE-CZ-NH1	5.72	123.16	120.30
1	A	490	ARG	NE-CZ-NH2	-5.66	117.47	120.30
1	A	3	ARG	NE-CZ-NH1	5.49	123.04	120.30
1	A	40	TYR	CA-CB-CG	5.40	123.66	113.40
2	B	67	ARG	NE-CZ-NH2	-5.18	117.71	120.30
1	A	444	ARG	NE-CZ-NH1	5.04	122.82	120.30
2	B	22	ARG	NE-CZ-NH1	5.01	122.81	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	221	GLY	Peptide

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	4937	0	4964	30	0
2	B	2141	0	2158	14	0
3	A	6	0	0	3	0
4	B	8	0	0	0	0
5	B	26	0	16	5	0
6	B	1	0	0	0	0
7	A	159	0	0	2	0
7	B	32	0	0	0	0
All	All	7310	0	7138	47	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 (47) 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:386:TRP:CH2	1:A:425:ARG:HG3	2.09	0.87
3:A:701:PYR:CA	5:B:402:TPP:H2	2.24	0.68
1:A:527:ILE:HG22	1:A:543:MET:HE3	1.76	0.66
1:A:396:GLU:OE1	1:A:431:ARG:HD2	1.96	0.65
2:B:50:ILE:HG23	2:B:51:PRO:HD3	1.79	0.65
1:A:17:ASP:HB2	1:A:51:PHE:CE1	2.32	0.64
2:B:223:ASP:OD1	2:B:227:ARG:NH2	2.33	0.62
1:A:527:ILE:CG2	1:A:543:MET:HE3	2.31	0.60
1:A:88:TYR:OH	1:A:218:VAL:HG11	2.01	0.60
1:A:527:ILE:HB	1:A:543:MET:CE	2.34	0.58
1:A:531:MET:HG2	1:A:541:THR:OG1	2.05	0.56
1:A:524:LYS:O	1:A:543:MET:HE1	2.08	0.54
2:B:222:TRP:CH2	2:B:242:LYS:HG3	2.43	0.54
1:A:255:PRO:O	5:B:402:TPP:HM43	2.07	0.54
1:A:527:ILE:CG2	1:A:543:MET:CE	2.86	0.54
2:B:15:CYS:O	2:B:196:PRO:O	2.26	0.53
1:A:566:LYS:NZ	1:A:618:ASP:OD1	2.44	0.51
2:B:222:TRP:CZ3	2:B:242:LYS:HG3	2.47	0.50
1:A:61:ARG:HD3	7:A:952:HOH:O	2.12	0.49
2:B:178:LEU:HD21	2:B:253:GLY:HA2	1.94	0.49
1:A:513:ALA:O	1:A:564:LYS:NZ	2.39	0.49
3:A:701:PYR:O3	5:B:402:TPP:H2	2.13	0.48
1:A:70:LEU:HD23	1:A:89:LEU:HD13	1.95	0.47
2:B:88:VAL:CG2	2:B:92:ASP:OD1	2.63	0.47
1:A:16:VAL:O	1:A:19:SER:HB2	2.15	0.47
1:A:88:TYR:CZ	1:A:218:VAL:HG11	2.50	0.47
1:A:346:ALA:HB1	1:A:347:PRO:HA	1.96	0.47
2:B:44:ILE:HG22	5:B:402:TPP:S1	2.54	0.47
2:B:49:LYS:HB3	2:B:53:PHE:CZ	2.50	0.46
1:A:412:ASN:HB2	7:A:871:HOH:O	2.14	0.46
1:A:197:ASN:OD1	1:A:199:LEU:N	2.45	0.46
1:A:342:TYR:HA	1:A:406:ILE:O	2.15	0.46
2:B:50:ILE:HG23	2:B:51:PRO:CD	2.47	0.44
1:A:151:LYS:HB2	1:A:161:MET:HE2	1.99	0.44
3:A:701:PYR:CA	5:B:402:TPP:C2	2.94	0.43
2:B:120:VAL:HG21	2:B:200:TYR:HB2	1.98	0.43
2:B:31:LEU:HD22	2:B:184:LEU:HD11	2.00	0.43
1:A:27:VAL:HG12	1:A:32:TYR:HB2	2.00	0.43
1:A:572:ASN:HA	1:A:596:LYS:O	2.18	0.43
1:A:3:ARG:NH1	1:A:60:ILE:HD11	2.34	0.43
1:A:515:ILE:HD13	1:A:615:LEU:HD21	2.02	0.42
1:A:150:ILE:HG23	1:A:164:VAL:HG23	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:65:HIS:CD2	2:B:96:ILE:HG21	2.55	0.41
1:A:231:ILE:O	1:A:416:VAL:HA	2.19	0.41
1:A:151:LYS:HB2	1:A:161:MET:CE	2.51	0.41
2:B:265:GLU:OE1	2:B:265:GLU:N	2.49	0.41
1:A:2:THR:N	1:A:57:GLU:OE1	2.54	0.40

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	625/628 (100%)	602 (96%)	21 (3%)	2 (0%)	41	46
2	B	267/304 (88%)	249 (93%)	15 (6%)	3 (1%)	14	12
All	All	892/932 (96%)	851 (95%)	36 (4%)	5 (1%)	25	26

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	562	SER
2	B	15	CYS
2	B	248	GLU
2	B	92	ASP
1	A	43	ASN

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%)	516 (98%)	11 (2%)	53 67
2	B	229/257 (89%)	226 (99%)	3 (1%)	69 81
All	All	756/785 (96%)	742 (98%)	14 (2%)	57 71

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ASP
1	A	86	LYS
1	A	151	LYS
1	A	199	LEU
1	A	257	THR
1	A	260	SER
1	A	276	VAL
1	A	295	LEU
1	A	341	TYR
1	A	562	SER
1	A	613	LYS
2	B	241	MET
2	B	286	GLU
2	B	296	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	505	GLN
2	B	87	ASN

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 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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	$\#\|Z\| > 2$
3	PYR	A	701	-	5,5,5	1.60	1 (20%)	3,6,6	1.61	1 (33%)
4	SF4	B	401	2	0,12,12	-	-	-		
5	TPP	B	402	6	22,27,27	1.61	3 (13%)	29,40,40	2.51	10 (34%)

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	PYR	A	701	-	-	0/4/4/4	-
4	SF4	B	401	2	-	-	0/6/5/5
5	TPP	B	402	6	-	2/16/17/17	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	402	TPP	C5'-C4'	4.79	1.51	1.42
5	B	402	TPP	C4-N3	-3.99	1.36	1.39
3	A	701	PYR	O-C	2.79	1.30	1.22
5	B	402	TPP	C6'-C5'	2.21	1.42	1.37

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	402	TPP	C6-C5-C4	8.70	134.42	127.43
5	B	402	TPP	C5'-C7'-N3	4.72	121.14	113.28
5	B	402	TPP	CM4-C4-N3	3.78	127.34	122.53
5	B	402	TPP	C5'-C4'-N3'	-3.41	115.89	121.24
5	B	402	TPP	CM4-C4-C5	-3.11	120.80	127.60
5	B	402	TPP	C2'-N3'-C4'	2.87	122.56	118.08
5	B	402	TPP	O3B-PB-O2B	2.26	116.28	107.64
3	A	701	PYR	OXT-C-O	-2.17	118.65	123.61
5	B	402	TPP	C5-C4-N3	2.14	111.85	107.57
5	B	402	TPP	C7'-N3-C2	-2.10	121.55	125.35
5	B	402	TPP	C5'-C4'-N4'	2.09	125.15	122.19

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	402	TPP	PA-O3A-PB-O3B
5	B	402	TPP	PA-O3A-PB-O2B

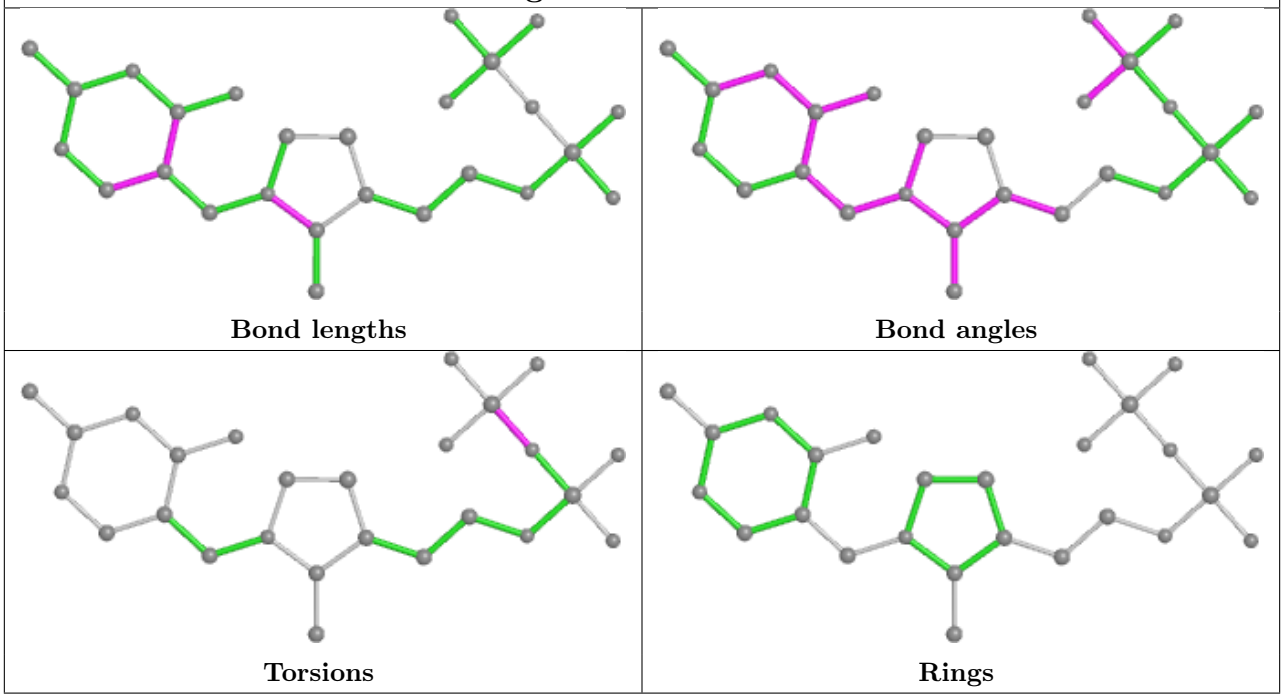
There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	701	PYR	3	0
5	B	402	TPP	5	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 TPP B 402



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	627/628 (99%)	-0.13	13 (2%) 63 61	29, 44, 75, 97	0
2	B	275/304 (90%)	0.84	52 (18%) 1 1	33, 60, 104, 122	0
All	All	902/932 (96%)	0.17	65 (7%) 15 14	29, 47, 90, 122	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	197	CYS	6.3
2	B	198	PRO	6.0
2	B	14	GLY	5.8
2	B	15	CYS	5.8
2	B	13	PRO	5.7
2	B	200	TYR	5.4
2	B	199	THR	5.4
2	B	136	GLU	5.2
2	B	196	PRO	5.2
2	B	135	GLY	4.9
2	B	121	TYR	4.8
2	B	46	CYS	4.8
2	B	119	GLY	4.8
2	B	132	LEU	4.6
2	B	146	ILE	4.5
2	B	12	CYS	4.5
2	B	133	HIS	4.3
2	B	120	VAL	4.2
2	B	247	GLY	4.2
2	B	134	ARG	3.9
1	A	438	THR	3.9
2	B	170	TYR	3.9
2	B	145	ASN	3.8
2	B	147	MET	3.6

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Mol	Chain	Res	Type	RSRZ
2	B	11	TRP	3.6
2	B	9	VAL	3.5
2	B	10	ASP	3.4
2	B	128	ALA	3.4
2	B	118	ASN	3.3
2	B	131	THR	3.3
1	A	257	THR	3.3
1	A	279	ASN	3.2
1	A	278	GLY	3.2
1	A	280	GLU	3.2
2	B	230	GLU	3.1
2	B	246	TRP	3.1
1	A	538	GLY	3.1
1	A	439	SER	3.0
2	B	249	LYS	2.9
1	A	277	GLU	2.9
2	B	122	GLY	2.9
2	B	248	GLU	2.8
2	B	8	PHE	2.7
2	B	113	VAL	2.7
1	A	339	ILE	2.5
2	B	221	GLY	2.5
1	A	281	LEU	2.4
1	A	276	VAL	2.4
1	A	196	LYS	2.3
2	B	148	ASP	2.3
2	B	104	LEU	2.3
2	B	44	ILE	2.3
2	B	228	LYS	2.2
2	B	123	LEU	2.2
2	B	129	SER	2.2
2	B	212	ARG	2.2
2	B	18	PHE	2.1
2	B	45	GLY	2.1
1	A	225	LYS	2.1
2	B	22	ARG	2.1
2	B	85	ILE	2.1
2	B	69	ILE	2.1
2	B	227	ARG	2.1
2	B	189	ALA	2.1
2	B	86	VAL	2.1

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)

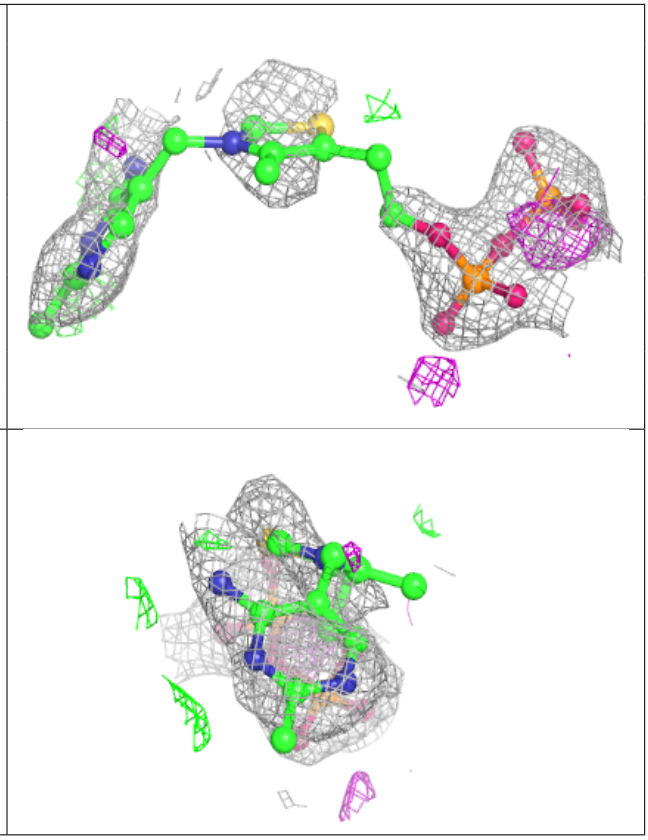
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	PYR	A	701	6/6	0.72	0.32	58,82,85,85	0
5	TPP	B	402	26/26	0.86	0.28	62,99,135,151	0
6	MG	B	403	1/1	0.87	0.21	69,69,69,69	0
4	SF4	B	401	8/8	0.90	0.21	62,65,72,76	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.

Electron density around TPP B 402:

$2mF_o$-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.