



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 13, 2018 – 03:20 pm GMT

PDB ID : 1VBF  
Title : Crystal structure of protein L-isoaspartate O-methyltransferase homologue from *Sulfolobus tokodaii*  
Authors : Tanaka, Y.; Tsumoto, K.; Yasutake, Y.; Umetsu, M.; Yao, M.; Tanaka, I.; Fukada, H.; Kumagai, I.  
Deposited on : 2004-02-25  
Resolution : 2.80 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](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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	trunk31020
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk31020

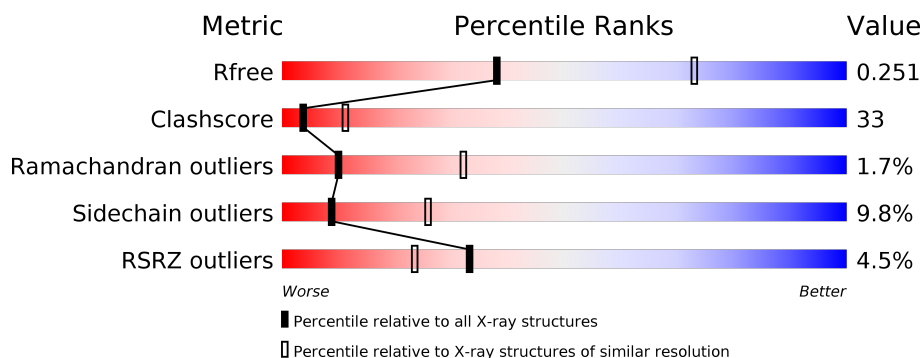
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
$R_{free}$	111664	2792 (2.80-2.80)
Clashscore	122126	3209 (2.80-2.80)
Ramachandran outliers	120053	3158 (2.80-2.80)
Sidechain outliers	120020	3160 (2.80-2.80)
RSRZ outliers	108989	2726 (2.80-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	231	<div> <div>3%</div> <div> <div></div> <div>56%</div> <div>35%</div> <div>6%</div> <div></div> </div> </div>
1	B	231	<div> <div>3%</div> <div> <div></div> <div>52%</div> <div>37%</div> <div>9%</div> <div></div> </div> </div>
1	C	231	<div> <div>6%</div> <div> <div></div> <div>48%</div> <div>39%</div> <div>8%</div> <div></div> </div> </div>
1	D	231	<div> <div>5%</div> <div> <div></div> <div>42%</div> <div>48%</div> <div>6%</div> <div></div> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7576 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 231aa long hypothetical protein-L-isoaspartate O-methyltransferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	224	Total	C	N	O	S	Se	0	0	0
			1788	1159	288	336	1	4			
1	B	226	Total	C	N	O	S	Se	0	0	0
			1804	1167	291	341	1	4			
1	C	224	Total	C	N	O	S	Se	0	0	0
			1788	1159	288	336	1	4			
1	D	224	Total	C	N	O	S	Se	0	0	0
			1788	1159	288	336	1	4			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	MET	SEE REMARK 999	UNP Q972K9
A	62	MSE	MET	MODIFIED RESIDUE	UNP Q972K9
A	104	MSE	MET	MODIFIED RESIDUE	UNP Q972K9
A	161	MSE	MET	MODIFIED RESIDUE	UNP Q972K9
A	192	MSE	MET	MODIFIED RESIDUE	UNP Q972K9
B	1	ALA	MET	SEE REMARK 999	UNP Q972K9
B	62	MSE	MET	MODIFIED RESIDUE	UNP Q972K9
B	104	MSE	MET	MODIFIED RESIDUE	UNP Q972K9
B	161	MSE	MET	MODIFIED RESIDUE	UNP Q972K9
B	192	MSE	MET	MODIFIED RESIDUE	UNP Q972K9
C	1	ALA	MET	SEE REMARK 999	UNP Q972K9
C	62	MSE	MET	MODIFIED RESIDUE	UNP Q972K9
C	104	MSE	MET	MODIFIED RESIDUE	UNP Q972K9
C	161	MSE	MET	MODIFIED RESIDUE	UNP Q972K9
C	192	MSE	MET	MODIFIED RESIDUE	UNP Q972K9
D	1	ALA	MET	SEE REMARK 999	UNP Q972K9
D	62	MSE	MET	MODIFIED RESIDUE	UNP Q972K9
D	104	MSE	MET	MODIFIED RESIDUE	UNP Q972K9
D	161	MSE	MET	MODIFIED RESIDUE	UNP Q972K9
D	192	MSE	MET	MODIFIED RESIDUE	UNP Q972K9

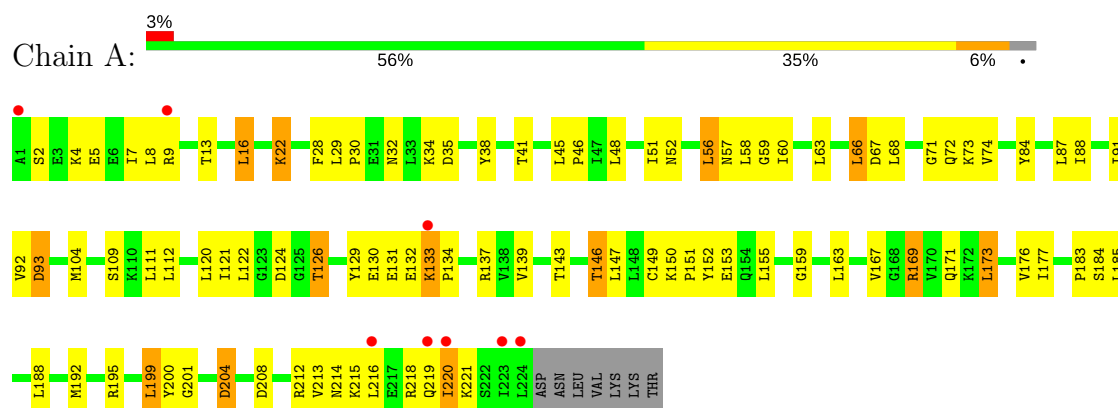
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	90	Total 90	O 90	0	0
2	B	140	Total 140	O 140	0	0
2	C	99	Total 99	O 99	0	0
2	D	79	Total 79	O 79	0	0

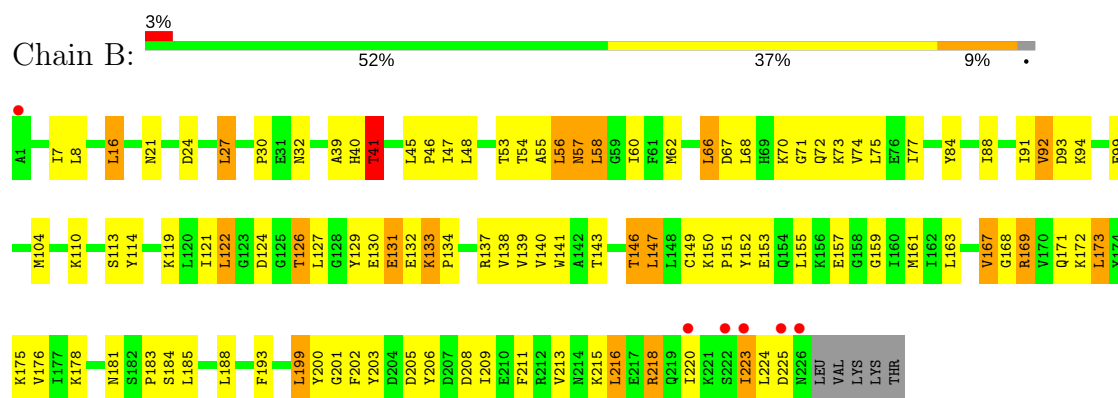
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

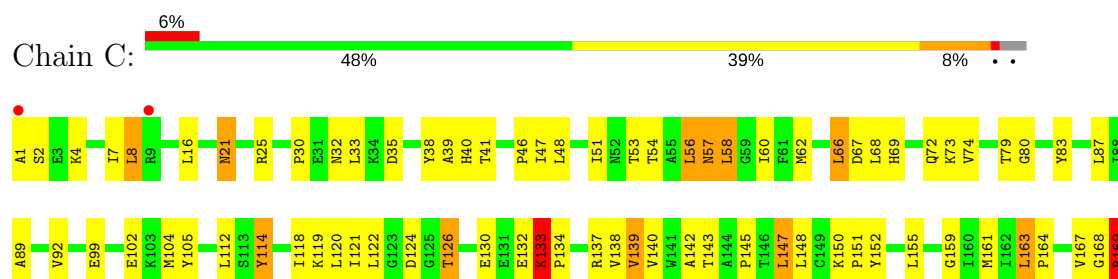
- Molecule 1: 231aa long hypothetical protein-L-isoaspartate O-methyltransferase

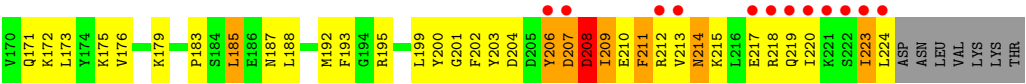


- Molecule 1: 231aa long hypothetical protein-L-isoaspartate O-methyltransferase

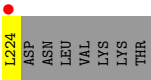
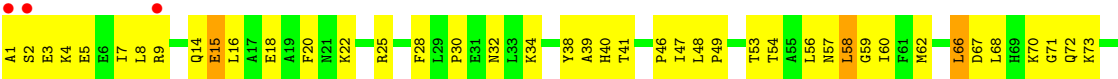


- Molecule 1: 231aa long hypothetical protein-L-isoaspartate O-methyltransferase





● Molecule 1: 231aa long hypothetical protein-L-isoaspartate O-methyltransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	F 2 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	277.80Å 277.80Å 277.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.80 37.12 – 2.81	Depositor EDS
% Data completeness (in resolution range)	99.3 (15.00-2.80) 100.0 (37.12-2.81)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	8.29 (at 2.81Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.205 , 0.255 0.204 , 0.251	Depositor DCC
$R_{free}$ test set	4310 reflections (9.96%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	54.0	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 57.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.028 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	7576	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.44% 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 [i](#)

### 5.1 Standard geometry [i](#)

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	0.46	0/1817	0.73	0/2447
1	B	0.52	0/1833	0.80	1/2469 (0.0%)
1	C	0.50	0/1817	0.83	5/2447 (0.2%)
1	D	0.48	0/1817	0.74	0/2447
All	All	0.49	0/7284	0.78	6/9810 (0.1%)

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	C	0	1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	208	ASP	N-CA-C	10.18	138.48	111.00
1	C	207	ASP	N-CA-C	7.70	131.78	111.00
1	B	167	VAL	N-CA-C	-5.44	96.32	111.00
1	C	207	ASP	C-N-CA	-5.44	108.11	121.70
1	C	208	ASP	CA-C-N	-5.38	105.36	117.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	114	TYR	Sidechain



## 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	1788	0	1830	90	0
1	B	1804	0	1840	125	0
1	C	1788	0	1830	131	0
1	D	1788	0	1830	154	0
2	A	90	0	0	4	0
2	B	140	0	0	8	0
2	C	99	0	0	7	0
2	D	79	0	0	11	0
All	All	7576	0	7330	478	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 33.

The worst 5 of 478 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:B:126:THR:HG21	1:B:200:TYR:H	1.17	1.06
1:C:215:LYS:HG2	1:C:218:ARG:HH21	1.17	1.06
1:A:130:GLU:OE1	1:A:133:LYS:HD2	1.56	1.05
1:C:126:THR:HG21	1:C:200:TYR:H	1.23	1.00
1:C:155:LEU:HD22	1:C:159:GLY:HA3	1.47	0.97

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	222/231 (96%)	206 (93%)	13 (6%)	3 (1%)	12	38
1	B	224/231 (97%)	208 (93%)	14 (6%)	2 (1%)	19	50
1	C	222/231 (96%)	201 (90%)	18 (8%)	3 (1%)	12	38
1	D	222/231 (96%)	204 (92%)	11 (5%)	7 (3%)	4	15
All	All	890/924 (96%)	819 (92%)	56 (6%)	15 (2%)	10	32

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	133	LYS
1	C	133	LYS
1	D	133	LYS
1	D	209	ILE
1	D	210	GLU

### 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	193/196 (98%)	176 (91%)	17 (9%)	11	31
1	B	195/196 (100%)	174 (89%)	21 (11%)	7	21
1	C	193/196 (98%)	172 (89%)	21 (11%)	7	21
1	D	193/196 (98%)	176 (91%)	17 (9%)	11	31
All	All	774/784 (99%)	698 (90%)	76 (10%)	9	26

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	199	LEU
1	C	57	ASN
1	D	155	LEU
1	B	216	LEU
1	C	8	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	21	ASN
1	C	42	HIS
1	D	14	GLN
1	B	214	ASN
1	C	181	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 carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 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, 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(Å²)	Q<0.9
1	A	220/231 (95%)	-0.11	8 (3%)	42	32	26, 47, 70, 99	0
1	B	222/231 (96%)	-0.26	6 (2%)	54	44	23, 38, 58, 100	0
1	C	220/231 (95%)	0.08	14 (6%)	19	12	28, 43, 97, 100	0
1	D	220/231 (95%)	0.01	12 (5%)	25	16	31, 51, 87, 100	0
All	All	882/924 (95%)	-0.07	40 (4%)	33	23	23, 45, 83, 100	0

The worst 5 of 40 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	226	ASN	6.8
1	C	220	ILE	6.2
1	C	207	ASP	5.8
1	A	224	LEU	5.3
1	B	1	ALA	4.7

### 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 carbohydrates in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.