



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 09:34 PM GMT

PDB ID : 5AVO  
Title : Crystal structure of the reduced form of homoserine dehydrogenase from *Sulfolobus tokodaii*.  
Authors : Goto, M.; Yoshimune, K.; Kaneko, R.  
Deposited on : 2015-06-25  
Resolution : 1.80 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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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 : unknown  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026982  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20026982

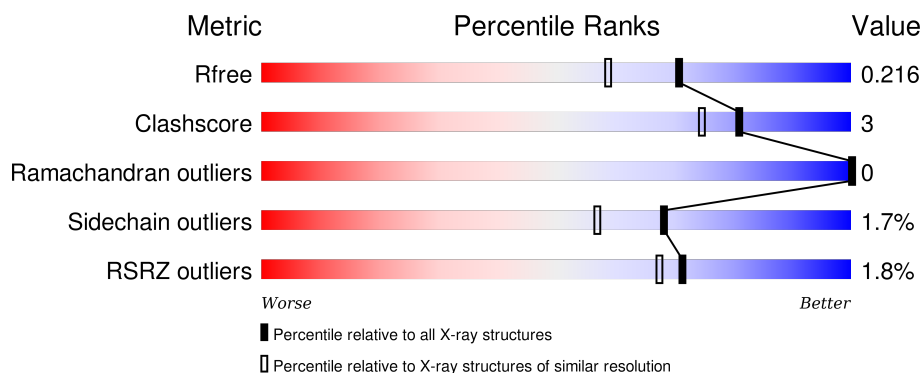
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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))
$R_{free}$	91344	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)

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	304	<div> <div>3%</div> <div>92%</div> <div>6%</div> </div>
1	B	304	<div> <div>%</div> <div>91%</div> <div>7%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4662 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 Homoserine dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	299	Total	C	N	O	S	0	0	0
			2250	1444	378	422	6			
1	B	300	Total	C	N	O	S	0	0	0
			2250	1446	376	422	6			

- Molecule 2 is water.

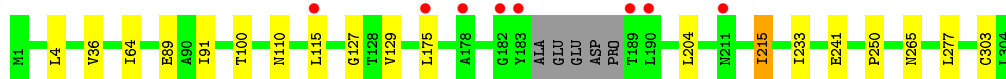
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	66	Total	O	0	0
			66	66		
2	B	96	Total	O	0	0
			96	96		

### 3 Residue-property plots [i](#)


These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Homoserine dehydrogenase

Chain A: 



- Molecule 1: Homoserine dehydrogenase

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.40Å 79.47Å 65.90Å 90.00° 107.16° 90.00°	Depositor
Resolution (Å)	50.00 – 1.80 30.90 – 1.80	Depositor EDS
% Data completeness (in resolution range)	90.3 (50.00-1.80) 90.3 (30.90-1.80)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.14 (at 1.79Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.211 , 0.247 0.220 , 0.216	Depositor DCC
$R_{free}$ test set	2338 reflections (5.18%)	DCC
Wilson B-factor (Å <sup>2</sup> )	27.6	Xtriage
Anisotropy	0.063	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 43.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	1 of 47580 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4662	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.14% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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	0.40	0/2285	0.62	0/3097
1	B	0.41	0/2285	0.61	0/3097
All	All	0.40	0/4570	0.61	0/6194

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

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	2250	0	2279	12	0
1	B	2250	0	2276	19	0
2	A	66	0	0	2	0
2	B	96	0	0	6	0
All	All	4662	0	4555	29	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 (29) 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:303:CYS:HG	1:B:303:CYS:HG	1.11	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:GLU:CB	2:A:438:HOH:O	2.26	0.83
1:B:281:PRO:HA	2:B:403:HOH:O	1.80	0.80
1:A:91:ILE:HG21	1:A:115:LEU:HG	1.63	0.80
1:B:211:ASN:CB	2:B:477:HOH:O	2.42	0.67
1:B:161:ILE:HG22	1:B:165:MET:CE	2.25	0.67
1:B:281:PRO:CA	2:B:403:HOH:O	2.39	0.66
1:B:142:LEU:HD11	1:B:276:ILE:HD11	1.80	0.63
1:A:265:ASN:HB2	2:A:428:HOH:O	1.98	0.62
1:B:285:PRO:HB3	2:B:482:HOH:O	2.01	0.61
1:A:215:ILE:HD13	1:A:215:ILE:O	2.02	0.59
1:B:161:ILE:HG22	1:B:165:MET:HE2	1.83	0.59
1:B:43:LEU:HD11	1:B:53:LEU:HD11	1.85	0.59
1:B:161:ILE:HG22	1:B:165:MET:HE3	1.91	0.51
1:A:129:VAL:HG11	1:A:204:LEU:HD21	1.93	0.51
1:B:43:LEU:CD1	1:B:53:LEU:HD11	2.41	0.50
1:B:129:VAL:HG11	1:B:204:LEU:HD21	1.95	0.47
1:A:303:CYS:HG	1:B:303:CYS:CB	2.28	0.47
1:B:250:PRO:C	1:B:251:ILE:HD12	2.35	0.46
1:A:4:LEU:HD13	1:A:64:ILE:CD1	2.46	0.46
1:A:277:LEU:C	1:A:277:LEU:HD23	2.36	0.45
1:B:11:VAL:HG23	2:B:482:HOH:O	2.17	0.45
1:B:213:VAL:HG23	1:B:217:ASP:HB2	1.99	0.43
1:B:161:ILE:CG2	1:B:165:MET:HE2	2.48	0.43
1:A:233:ILE:HD13	1:A:250:PRO:HA	2.01	0.42
1:B:165:MET:HE2	1:B:171:PHE:HD1	1.85	0.42
1:B:282:GLY:N	2:B:403:HOH:O	2.50	0.41
1:A:4:LEU:HD13	1:A:64:ILE:HD12	2.01	0.41
1:A:100:THR:HG22	1:A:127:GLY:HA3	2.02	0.41

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	295/304 (97%)	286 (97%)	9 (3%)	0	100	100
1	B	294/304 (97%)	285 (97%)	9 (3%)	0	100	100
All	All	589/608 (97%)	571 (97%)	18 (3%)	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	237/256 (93%)	232 (98%)	5 (2%)	61	47
1	B	236/256 (92%)	233 (99%)	3 (1%)	76	68
All	All	473/512 (92%)	465 (98%)	8 (2%)	68	57

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	VAL
1	A	110	ASN
1	A	175	LEU
1	A	215	ILE
1	A	241	GLU
1	B	1	MET
1	B	151	ARG
1	B	272	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	78	ASN
1	A	265	ASN
1	A	287	ASN
1	B	265	ASN
1	B	287	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(Å <sup>2</sup> )	Q<0.9
1	A	299/304 (98%)	-0.02	8 (2%) 58 53	21, 30, 51, 61	0
1	B	300/304 (98%)	-0.24	3 (1%) 84 82	20, 29, 44, 59	0
All	All	599/608 (98%)	-0.13	11 (1%) 71 67	20, 30, 48, 61	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	189	THR	4.5
1	A	115	LEU	3.5
1	A	183	TYR	3.2
1	B	228	PRO	3.0
1	A	175	LEU	2.8
1	B	190	LEU	2.3
1	A	182	GLY	2.2
1	A	190	LEU	2.2
1	A	211	ASN	2.1
1	A	178	ALA	2.0
1	B	226	ASP	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 carbohydrates in this entry.

## 6.4 Ligands

There are no ligands in this entry.

## 6.5 Other polymers

There are no such residues in this entry.