



# wwPDB X-ray Structure Validation Summary Report

Jun 15, 2024 – 10:31 PM EDT

PDB ID : 1TM0  
Title : Crystal Structure of the putative proline racemase from *Brucella melitensis*, Northeast Structural Genomics Target LR31  
Authors : Forouhar, F.; Chen, Y.; Xiao, R.; Ho, C.K.; Ma, L.-C.; Cooper, B.; Acton, T.B.; Montelione, G.T.; Hunt, J.F.; Tong, L.; Northeast Structural Genomics Consortium (NESG)  
Deposited on : 2004-06-10  
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 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 : 2022.3.0, CSD as543be (2022)  
Xtrriage (Phenix) : 1.20.1  
EDS : 2.37.1  
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

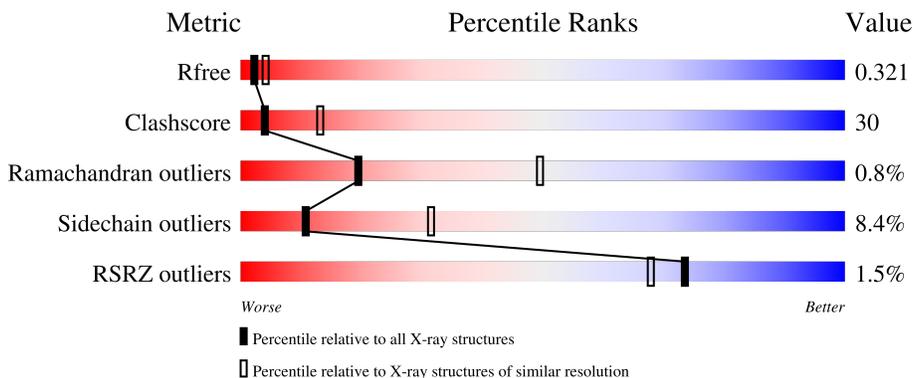
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
$R_{free}$	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (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 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	350	 50% 35% 11%
1	B	350	 46% 39% 11%

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 4718 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 PROLINE RACEMASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	311	2342	1471	416	439	6	10	0	0	0
1	B	311	2342	1471	416	439	6	10	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6
A	76	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6
A	81	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6
A	89	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6
A	109	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6
A	116	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6
A	164	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6
A	263	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6
A	272	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6
A	321	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6
A	343	LEU	-	CLONING ARTIFACT	UNP Q8YFD6
A	344	GLU	-	CLONING ARTIFACT	UNP Q8YFD6
A	345	HIS	-	EXPRESSION TAG	UNP Q8YFD6
A	346	HIS	-	EXPRESSION TAG	UNP Q8YFD6
A	347	HIS	-	EXPRESSION TAG	UNP Q8YFD6
A	348	HIS	-	EXPRESSION TAG	UNP Q8YFD6
A	349	HIS	-	EXPRESSION TAG	UNP Q8YFD6
A	350	HIS	-	EXPRESSION TAG	UNP Q8YFD6
B	1	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6
B	76	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6
B	81	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6
B	89	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6
B	109	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6
B	116	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6
B	164	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	263	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6
B	272	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6
B	321	MSE	MET	MODIFIED RESIDUE	UNP Q8YFD6
B	343	LEU	-	CLONING ARTIFACT	UNP Q8YFD6
B	344	GLU	-	CLONING ARTIFACT	UNP Q8YFD6
B	345	HIS	-	EXPRESSION TAG	UNP Q8YFD6
B	346	HIS	-	EXPRESSION TAG	UNP Q8YFD6
B	347	HIS	-	EXPRESSION TAG	UNP Q8YFD6
B	348	HIS	-	EXPRESSION TAG	UNP Q8YFD6
B	349	HIS	-	EXPRESSION TAG	UNP Q8YFD6
B	350	HIS	-	EXPRESSION TAG	UNP Q8YFD6

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	11	Total O 11 11	0	0
2	B	23	Total O 23 23	0	0



S309	G310	R311	A312	Q319	L320	D323	P324	Y332	ARG	LEU	SER	ASP	THR	TRP	PRO	ARG	ASP	GLU	LEU	GLU	HIS	HIS	HIS	HIS	HIS	HIS
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## 4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	138.03Å 77.36Å 77.42Å 90.00° 124.11° 90.00°	Depositor
Resolution (Å)	28.57 – 2.80 28.57 – 2.84	Depositor EDS
% Data completeness (in resolution range)	84.3 (28.57-2.80) 91.5 (28.57-2.84)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.81 (at 2.85Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.236 , 0.312 0.253 , 0.321	Depositor DCC
$R_{free}$ test set	2766 reflections (9.46%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	38.3	Xtriage
Anisotropy	0.398	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 0.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.015 for $1/2^*h+1/2^*k+2^*l, 1/2^*h+1/2^*k, -1/2^*h+1/2^*k-l$ 0.015 for $-1/2^*h-3/2^*k-l, -1/2^*h+1/2^*k-l, 1/2^*h+1/2^*k$ 0.016 for $-1/2^*h+3/2^*k-l, 1/2^*h+1/2^*k+l, 1/2^*h-1/2^*k$ 0.014 for $1/2^*h-1/2^*k+2^*l, -1/2^*h+1/2^*k, -1/2^*h-1/2^*k-l$ 0.014 for $-h+k-l, -l, -k$ 0.015 for $-h-k-l, l, k$ 0.015 for $-1/2^*h-1/2^*k+l, -1/2^*h-1/2^*k-l, 1/2^*h-1/2^*k$ 0.014 for $-1/2^*h+1/2^*k+l, 1/2^*h-1/2^*k+l, 1/2^*h+1/2^*k$ 0.016 for $1/2^*h+3/2^*k, 1/2^*h-1/2^*k, -1/2^*h-1/2^*k-l$ 0.016 for $1/2^*h-3/2^*k, -1/2^*h-1/2^*k, -1/2^*h+1/2^*k-l$ 0.469 for $-h-2^*l, -k, l$	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	4718	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

<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.

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.78% of the height of the origin peak. No significant pseudotranslation is detected.*

## 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	0.42	0/2379	0.61	0/3209
1	B	0.44	0/2379	0.63	0/3209
All	All	0.43	0/4758	0.62	0/6418

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 [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	2342	0	2344	134	0
1	B	2342	0	2344	151	0
2	A	11	0	0	1	0
2	B	23	0	0	4	0
All	All	4718	0	4688	283	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 30.

The worst 5 of 283 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:143:ASN:HD22	1:A:144:VAL:N	1.50	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:143:ASN:HD22	1:B:144:VAL:N	1.50	1.08
1:A:143:ASN:ND2	1:A:144:VAL:H	1.56	1.02
1:B:143:ASN:ND2	1:B:144:VAL:H	1.57	1.02
1:A:272:MSE:HE1	1:A:278:PHE:HB2	1.42	1.01

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	301/350 (86%)	264 (88%)	36 (12%)	1 (0%)	41	72
1	B	301/350 (86%)	264 (88%)	33 (11%)	4 (1%)	12	36
All	All	602/700 (86%)	528 (88%)	69 (12%)	5 (1%)	19	49

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	255	THR
1	A	215	GLU
1	B	215	GLU
1	B	217	ASP
1	B	281	LYS

### 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	255/279 (91%)	235 (92%)	20 (8%)	12	35
1	B	255/279 (91%)	232 (91%)	23 (9%)	9	28
All	All	510/558 (91%)	467 (92%)	43 (8%)	11	31

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	152	ASP
1	B	283	VAL
1	B	166	ASP
1	B	212	ARG
1	B	290	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	53	ASN
1	B	143	ASN
1	B	330	HIS
1	B	181	GLN
1	B	133	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](#)

There are no ligands in this entry.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	301/350 (86%)	-0.15	4 (1%) 77 72	4, 29, 64, 78	0
1	B	301/350 (86%)	-0.16	5 (1%) 70 63	5, 28, 66, 77	0
All	All	602/700 (86%)	-0.15	9 (1%) 73 68	4, 28, 66, 78	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	188	PRO	3.1
1	B	204	ALA	2.8
1	B	286	THR	2.7
1	A	183	GLY	2.4
1	B	256	GLY	2.4

### 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](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.