



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 14, 2017 – 01:08 AM EDT

PDB ID : 5E5L  
Title : Crystal structure of Mycobacterium tuberculosis L,D-transpeptidase 1 at 1.89 Angstrom  
Authors : Kumar, P.; Lamichhane, G.; Ginell, S.L.  
Deposited on : unknown  
Resolution : 1.89 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

<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
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20029824
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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-20029824

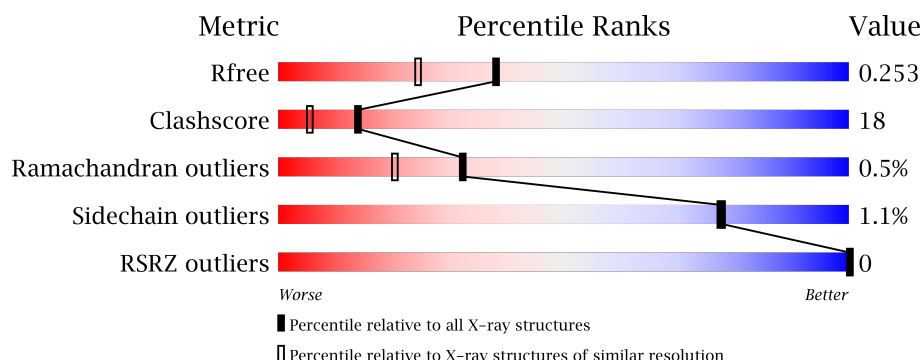
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.89 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))
$R_{free}$	100719	5047 (1.90-1.90)
Clashscore	112137	5731 (1.90-1.90)
Ramachandran outliers	110173	5669 (1.90-1.90)
Sidechain outliers	110143	5670 (1.90-1.90)
RSRZ outliers	101464	5100 (1.90-1.90)

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	223	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 56%, yellow 56%, yellow 84%, green 84%, green 100%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>56%</span> <span>28%</span> <span>• 15%</span> </div> </div>
1	B	223	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 58%, yellow 58%, yellow 89%, green 89%, green 100%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>58%</span> <span>31%</span> <span>• 10%</span> </div> </div>
1	C	223	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 55%, yellow 55%, yellow 84%, green 84%, green 100%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>55%</span> <span>29%</span> <span>• 15%</span> </div> </div>
1	D	223	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 56%, yellow 56%, yellow 86%, green 86%, green 100%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>56%</span> <span>30%</span> <span>14%</span> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6224 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 L,D-transpeptidase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	190	Total	C	N	O	S	0	0	0
			1445	913	263	265	4			
1	B	200	Total	C	N	O	S	0	0	0
			1512	959	274	275	4			
1	C	190	Total	C	N	O	S	0	0	0
			1440	910	259	267	4			
1	D	192	Total	C	N	O	S	0	0	0
			1469	928	267	270	4			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	29	GLY	-	expression tag	UNP O53638
A	30	HIS	-	expression tag	UNP O53638
A	31	MET	-	expression tag	UNP O53638
B	29	GLY	-	expression tag	UNP O53638
B	30	HIS	-	expression tag	UNP O53638
B	31	MET	-	expression tag	UNP O53638
C	29	GLY	-	expression tag	UNP O53638
C	30	HIS	-	expression tag	UNP O53638
C	31	MET	-	expression tag	UNP O53638
D	29	GLY	-	expression tag	UNP O53638
D	30	HIS	-	expression tag	UNP O53638
D	31	MET	-	expression tag	UNP O53638

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	99	Total	O	0	0
			99	99		
2	B	67	Total	O	0	0
			67	67		

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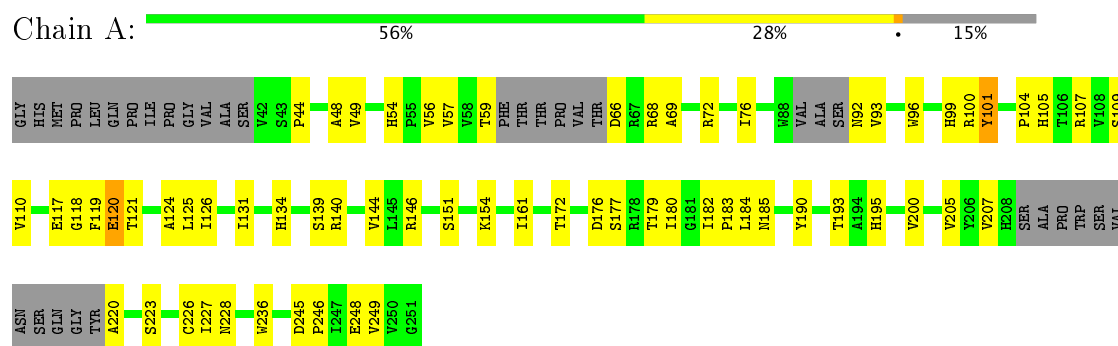
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	87	Total 87	O 87	0	0
2	D	105	Total 105	O 105	0	0

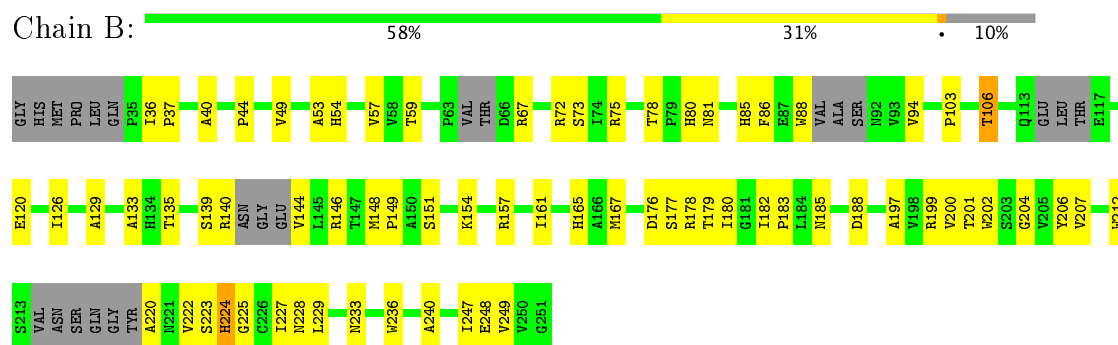
### 3 Residue-property plots

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.

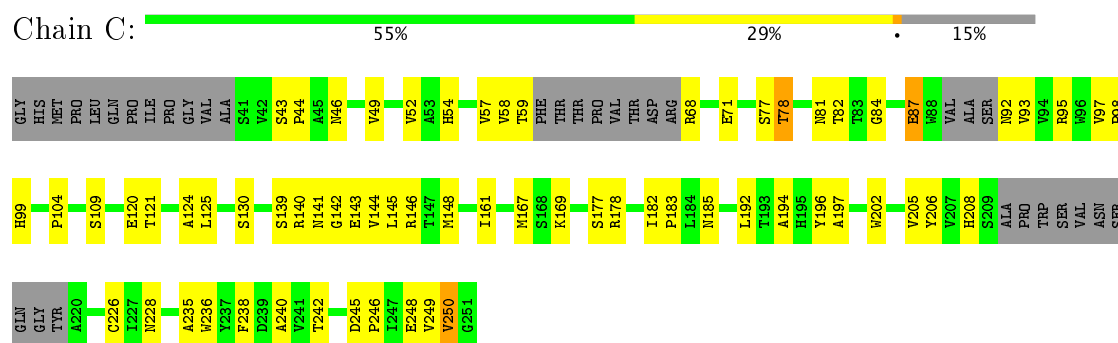
#### • Molecule 1: L,D-transpeptidase 1



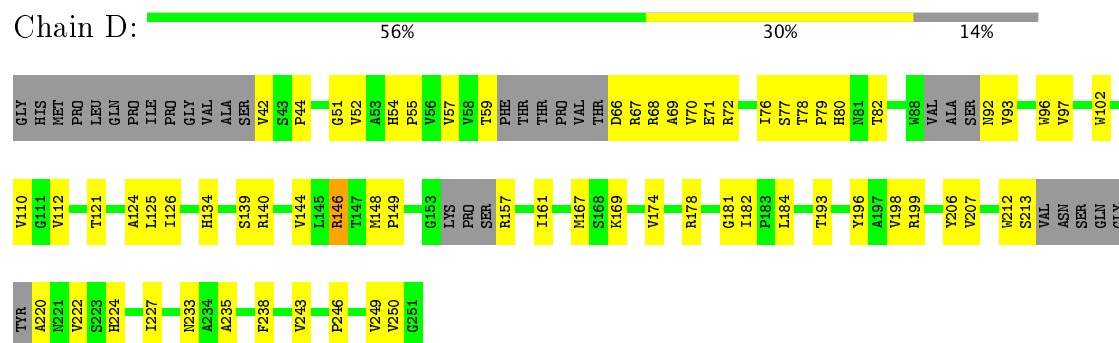
#### • Molecule 1: L,D-transpeptidase 1



#### • Molecule 1: L,D-transpeptidase 1



#### • Molecule 1: L,D-transpeptidase 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.73 Å 57.73 Å 256.60 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	24.54 – 1.89 24.54 – 1.89	Depositor EDS
% Data completeness (in resolution range)	93.2 (24.54-1.89) 92.8 (24.54-1.89)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	8.56 (at 1.89 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.208 , 0.257 0.206 , 0.253	Depositor DCC
$R_{free}$ test set	1979 reflections (2.72%)	DCC
Wilson B-factor (Å <sup>2</sup> )	16.4	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 46.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.33$ , $\langle L^2 \rangle = 0.16$	Xtriage
Estimated twinning fraction	0.478 for -h,-k,l 0.499 for h,-h-k,-l 0.478 for -k,-h,-l	Xtriage
Reported twinning fraction	0.500 for -h,-k,l	Depositor
Outliers	0 of 71314 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	6224	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% 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	0.47	0/1483	0.66	0/2030
1	B	0.48	0/1555	0.69	0/2131
1	C	0.51	0/1479	0.70	1/2026 (0.0%)
1	D	0.50	0/1509	0.71	0/2066
All	All	0.49	0/6026	0.69	1/8253 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	192	LEU	CA-CB-CG	5.29	127.47	115.30

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	1445	0	1408	52	0
1	B	1512	0	1471	55	0
1	C	1440	0	1397	50	0
1	D	1469	0	1421	52	0
2	A	99	0	0	10	3
2	B	67	0	0	6	3
2	C	87	0	0	12	1
2	D	105	0	0	16	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6224	0	5697	203	4

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 18.

The worst 5 of 203 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:193:THR:H	1:B:81:ASN:HD21	1.18	0.92
1:D:92:ASN:ND2	2:D:301:HOH:O	1.90	0.90
1:D:207:VAL:HG22	1:D:227:ILE:HD11	1.57	0.84
1:C:49:VAL:HG22	1:C:120:GLU:HB3	1.61	0.83
1:D:92:ASN:OD1	2:D:303:HOH:O	1.99	0.80

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:358:HOH:O	2:D:334:HOH:O[1_455]	2.08	0.12
2:A:368:HOH:O	2:B:327:HOH:O[3_454]	2.11	0.09
2:A:336:HOH:O	2:B:308:HOH:O[3_454]	2.13	0.07
2:A:371:HOH:O	2:C:382:HOH:O[1_545]	2.14	0.06

## 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	182/223 (82%)	174 (96%)	7 (4%)	1 (0%)	32	20
1	B	188/223 (84%)	176 (94%)	11 (6%)	1 (0%)	32	20
1	C	182/223 (82%)	174 (96%)	7 (4%)	1 (0%)	32	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	182/223 (82%)	171 (94%)	10 (6%)	1 (0%)	32	20
All	All	734/892 (82%)	695 (95%)	35 (5%)	4 (0%)	32	20

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	101	TYR
1	B	224	HIS
1	D	250	VAL
1	C	250	VAL

### 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	157/186 (84%)	156 (99%)	1 (1%)	89	90
1	B	165/186 (89%)	164 (99%)	1 (1%)	89	90
1	C	158/186 (85%)	155 (98%)	3 (2%)	62	57
1	D	160/186 (86%)	158 (99%)	2 (1%)	73	72
All	All	640/744 (86%)	633 (99%)	7 (1%)	78	77

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	87	GLU
1	D	146	ARG
1	C	242	THR
1	B	106	THR
1	D	52	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	81	ASN
1	B	81	ASN
1	C	81	ASN
1	C	221	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	190/223 (85%)	-0.59	0 100 100	9, 16, 25, 37	0
1	B	200/223 (89%)	-0.55	0 100 100	9, 17, 32, 45	0
1	C	190/223 (85%)	-0.61	0 100 100	10, 16, 24, 41	0
1	D	192/223 (86%)	-0.58	0 100 100	9, 16, 29, 34	0
All	All	772/892 (86%)	-0.58	0 100 100	9, 16, 28, 45	0

There are no RSRZ outliers to report.

### 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.