



wwPDB X-ray Structure Validation Summary Report ⓘ

May 29, 2020 – 05:12 am BST

PDB ID : 4K73
Title : X-ray crystal structure of an L,D-transpeptidase from Mycobacterium tuberculosis H37Rv
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2013-04-16
Resolution : 1.65 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

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	:	2.11
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)	:	2.11

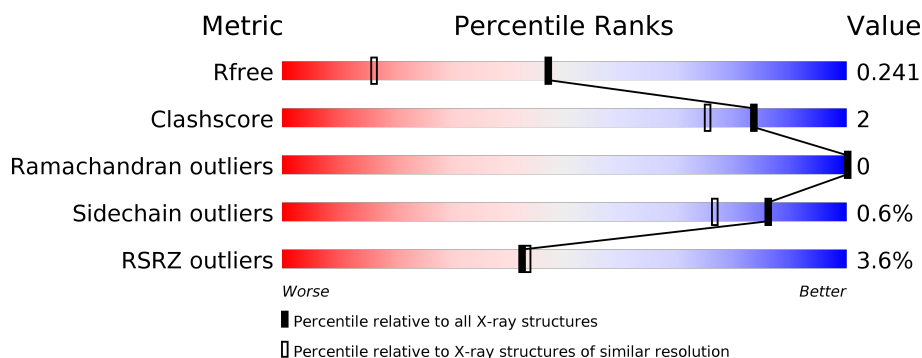
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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	1827 (1.66-1.66)
Clashscore	141614	1931 (1.66-1.66)
Ramachandran outliers	138981	1891 (1.66-1.66)
Sidechain outliers	138945	1891 (1.66-1.66)
RSRZ outliers	127900	1791 (1.66-1.66)

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 ≥ 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	274	<div> <div>3%</div> <div>77%</div> <div>19%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1940 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	221	Total	C	N	O	S	0	5	0
			1687	1074	285	323	5			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	MET	-	EXPRESSION TAG	UNP O06825
A	-1	ALA	-	EXPRESSION TAG	UNP O06825
A	0	HIS	-	EXPRESSION TAG	UNP O06825
A	1	HIS	-	EXPRESSION TAG	UNP O06825
A	2	HIS	-	EXPRESSION TAG	UNP O06825
A	3	HIS	-	EXPRESSION TAG	UNP O06825
A	4	HIS	-	EXPRESSION TAG	UNP O06825
A	5	HIS	-	EXPRESSION TAG	UNP O06825
A	6	MET	-	EXPRESSION TAG	UNP O06825
A	7	GLY	-	EXPRESSION TAG	UNP O06825
A	8	THR	-	EXPRESSION TAG	UNP O06825
A	9	LEU	-	EXPRESSION TAG	UNP O06825
A	10	GLU	-	EXPRESSION TAG	UNP O06825
A	11	ALA	-	EXPRESSION TAG	UNP O06825
A	12	GLN	-	EXPRESSION TAG	UNP O06825
A	13	THR	-	EXPRESSION TAG	UNP O06825
A	14	GLN	-	EXPRESSION TAG	UNP O06825
A	15	GLY	-	EXPRESSION TAG	UNP O06825
A	16	PRO	-	EXPRESSION TAG	UNP O06825
A	17	GLY	-	EXPRESSION TAG	UNP O06825
A	18	SER	-	EXPRESSION TAG	UNP O06825
A	19	MET	-	EXPRESSION TAG	UNP O06825

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Ca 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	252	Total 252	O 252	0	0

- Molecule 1: L,D-transpeptidase

Residue	Conservation	Frequency	Position	Frequency	Conservation	Residue
HIS	0.00	0.00	159	0.00	0.00	MET
R159	0.00	0.00		0.00	0.00	ALA
G163	0.00	0.00		0.00	0.00	HIS
E164	0.00	0.00		0.00	0.00	HIS
D165	0.00	0.00		0.00	0.00	HIS
Y177	0.00	0.00		0.00	0.00	HIS
S192	0.00	0.00		0.00	0.00	MET
S198	0.00	0.00		0.00	0.00	GLY
SER	0.00	0.00		0.00	0.00	LEU
VAL	0.00	0.00		0.00	0.00	GLY
ILE	0.00	0.00		0.00	0.00	ALA
PRO	0.00	0.00		0.00	0.00	GLN
VAL	0.00	0.00		0.00	0.00	GLN
ASP	0.00	0.00		0.00	0.00	GLY
ASP	0.00	0.00		0.00	0.00	PRO
PRO	0.00	0.00		0.00	0.00	GLY
ASP	0.00	0.00		0.00	0.00	SER
G209	0.00	0.00		0.00	0.00	MET
D215	0.00	0.00		0.00	0.00	ALA
L239	0.00	0.00		0.00	0.00	ALA
E244	0.00	0.00		0.00	0.00	ASP
E271	0.00	0.00		0.00	0.00	ILE
	0.00	0.00		0.00	0.00	HIS
	0.00	0.00		0.00	0.00	LEU
	0.00	0.00		0.00	0.00	VAL
	0.00	0.00		0.00	0.00	ALA
	0.00	0.00		0.00	0.00	ALA
	0.00	0.00		0.00	0.00	LYS
	0.00	0.00		0.00	0.00	GLN
	0.00	0.00		0.00	0.00	S33
	0.00	0.00		0.00	0.00	F34
	0.00	0.00		0.00	0.00	L42
	0.00	0.00		0.00	0.00	I63
	0.00	0.00		0.00	0.00	R69
	0.00	0.00		0.00	0.00	T81
	0.00	0.00		0.00	0.00	N93
	0.00	0.00		0.00	0.00	R102
	0.00	0.00		0.00	0.00	E111
	0.00	0.00		0.00	0.00	F150
	0.00	0.00		0.00	0.00	PRO
	0.00	0.00		0.00	0.00	PRO
	0.00	0.00		0.00	0.00	LEU
	0.00	0.00		0.00	0.00	PRO
	0.00	0.00		0.00	0.00	ALA
	0.00	0.00		0.00	0.00	ALA
	0.00	0.00		0.00	0.00	PRO
	0.00	0.00		0.00	0.00	HIS

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	44.24Å 46.44Å 111.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.48 – 1.65 46.44 – 1.65	Depositor EDS
% Data completeness (in resolution range)	99.1 (46.48-1.65) 99.1 (46.44-1.65)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.04 (at 1.65Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.196 , 0.231 0.206 , 0.241	Depositor DCC
R_{free} test set	1416 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	16.7	Xtriage
Anisotropy	0.144	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 37.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.037 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	1940	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.78% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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	0.73	0/1733	0.87	2/2374 (0.1%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	102	ARG	NE-CZ-NH1	6.37	123.48	120.30
1	A	102	ARG	NE-CZ-NH2	-5.77	117.41	120.30

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	1687	0	1597	8	0
2	A	1	0	0	0	0
3	A	252	0	0	2	0
All	All	1940	0	1597	8	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 2.

The worst 5 of 8 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:42:LEU:HD22	3:A:535:HOH:O	1.71	0.91
1:A:69[B]:ARG:HH11	1:A:69[B]:ARG:HG2	1.61	0.65
1:A:165[B]:ASP:OD1	1:A:165[B]:ASP:N	2.26	0.63
1:A:69[B]:ARG:CG	1:A:69[B]:ARG:HH11	2.21	0.54
1:A:93:ASN:HB2	3:A:561:HOH:O	2.12	0.49

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	219/274 (80%)	213 (97%)	6 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	180/225 (80%)	179 (99%)	1 (1%)	86	76

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	215	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	221/274 (80%)	0.09	8 (3%) 42 43	9, 19, 38, 43	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	239	LEU	4.6
1	A	150	PRO	3.2
1	A	244	HIS	3.1
1	A	163	GLY	2.6
1	A	209	GLY	2.6

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](#)

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
2	CA	A	301	1/1	0.99	0.06	8,8,8,8	0

6.5 Other polymers [i](#)

There are no such residues in this entry.