



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 31, 2023 – 07:20 AM EDT

PDB ID : 3OTV  
Title : Crystal structure of the intracellular domain of Rv3910 from Mycobacterium tuberculosis  
Authors : Gee, C.L.; Alber, T.  
Deposited on : 2010-09-14  
Resolution : 3.09 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  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
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) : 2.36

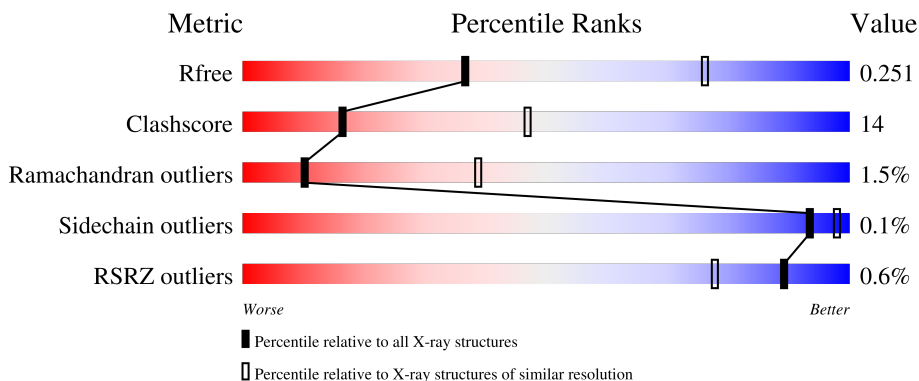
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.09 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	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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	285	 % 63% 25% 11%
1	B	285	 60% 25% 14%
1	C	285	 68% 21% 10%
1	D	285	 % 64% 22% 13%

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7513 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 PROBABLE CONSERVED TRANSMEMBRANE PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	254	Total 1890	C 1182	N 350	O 355	S 3	63	0	0
1	B	244	Total 1815	C 1135	N 336	O 341	S 3	34	0	0
1	C	257	Total 1911	C 1193	N 353	O 362	S 3	60	0	0
1	D	248	Total 1837	C 1150	N 338	O 346	S 3	64	0	0

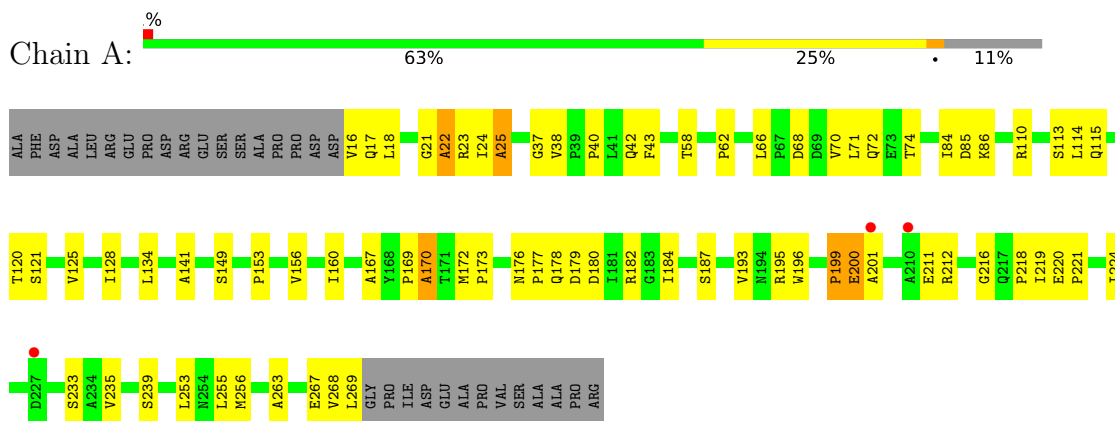
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	7	Total 7	O 7	0	0
2	B	28	Total 28	O 28	0	0
2	C	11	Total 11	O 11	0	0
2	D	14	Total 14	O 14	0	0

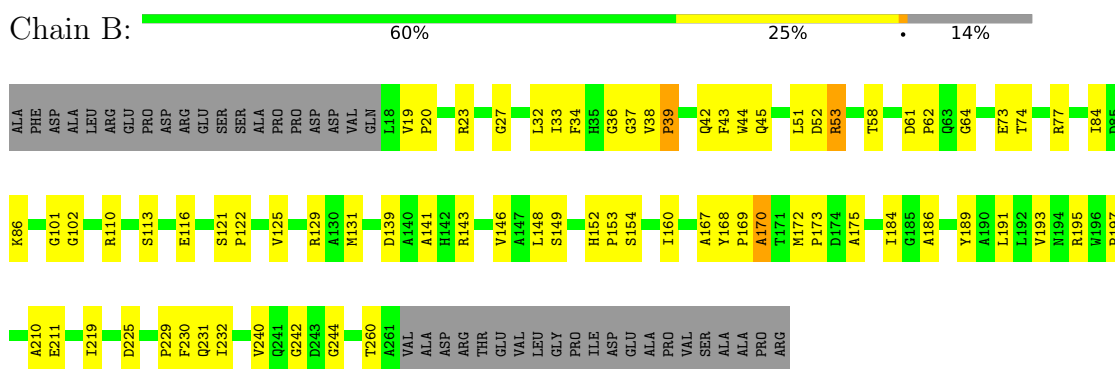
### 3 Residue-property plots [i](#)

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

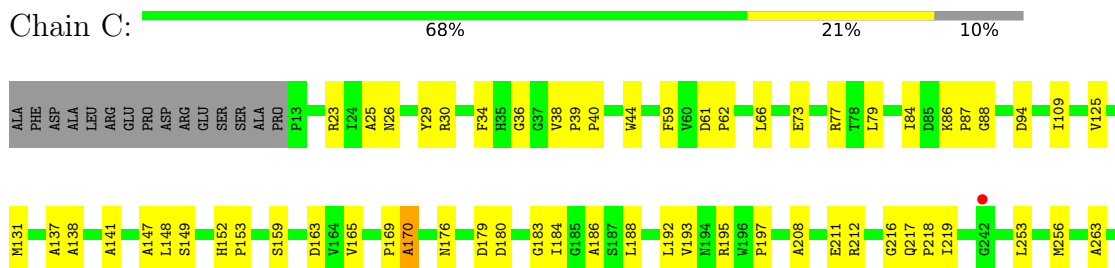
- Molecule 1: PROBABLE CONSERVED TRANSMEMBRANE PROTEIN



- Molecule 1: PROBABLE CONSERVED TRANSMEMBRANE PROTEIN



- Molecule 1: PROBABLE CONSERVED TRANSMEMBRANE PROTEIN



T266	E267
V268	L269
GLY	PRO
ILE	ASP
GLU	ALA
PRO	VAL
SER	ALA
ALA	PRO
PRO	ARG

● Molecule 1: PROBABLE CONSERVED TRANSMEMBRANE PROTEIN



ALA	V16	A22	R23	I24	R30	L31	F34	H35	G36	G37	V38	P39	F43	T58	F59	V60	D61	P62	R77	I84	D85	K86	V89	A90	R91	E107	I128	R129	A130	M131	A137
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A138	D139	V146	A147	I150	H152	P153	L166	A167	Y168	P169	A170	P173	M176	P177	I184	L188	A201	G202	V203	E211	R212	D213	Q217	P218	I219	D223	I224	D225	R226	Q231	A234	V235	A236	A237	R238	Q241	G242	D243	G244	A249	L252
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M256	Q257	Q258	V262	A263	ASP	ARG	THR	GLU	VAL	LEU	GLY	PRO	ILE	ASP	GLU	ALA	PRO	VAL	SER	ALA	ALA	PRO	ARG
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## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	58.04Å 59.69Å 145.06Å 90.00° 97.21° 90.00°	Depositor
Resolution (Å)	40.81 – 3.09 40.81 – 3.09	Depositor EDS
% Data completeness (in resolution range)	87.3 (40.81-3.09) 87.4 (40.81-3.09)	Depositor EDS
$R_{merge}$	0.63	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.81 (at 3.12Å)	Xtrriage
Refinement program	ELVES, PHENIX (phenix.refine: 1.6.1_357)	Depositor
R, $R_{free}$	0.189 , 0.248 0.188 , 0.251	Depositor DCC
$R_{free}$ test set	829 reflections (5.19%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	65.0	Xtrriage
Anisotropy	0.122	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 48.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7513	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.87% 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	0/1924	0.65	0/2630
1	B	0.49	0/1849	0.72	0/2527
1	C	0.47	0/1945	0.67	0/2659
1	D	0.44	0/1871	0.64	0/2559
All	All	0.47	0/7589	0.67	0/10375

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	1890	0	1912	55	0
1	B	1815	0	1833	62	0
1	C	1911	0	1922	47	0
1	D	1837	0	1853	44	0
2	A	7	0	0	0	0
2	B	28	0	0	1	0
2	C	11	0	0	0	0
2	D	14	0	0	0	0
All	All	7513	0	7520	207	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 14.

The worst 5 of 207 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:16:VAL:HG12	1:A:17:GLN:H	1.12	1.09
1:B:131:MET:CE	1:B:184:ILE:HG23	2.08	0.84
1:A:16:VAL:HG12	1:A:17:GLN:N	1.93	0.84
1:B:113:SER:OG	1:B:116:GLU:HG3	1.77	0.83
1:C:40:PRO:HG3	1:C:66:LEU:HD11	1.63	0.81

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	252/285 (88%)	224 (89%)	22 (9%)	6 (2%)	<b>6</b> 27
1	B	242/285 (85%)	222 (92%)	18 (7%)	2 (1%)	19 <b>54</b>
1	C	255/285 (90%)	240 (94%)	14 (6%)	1 (0%)	34 <b>69</b>
1	D	246/285 (86%)	224 (91%)	16 (6%)	6 (2%)	<b>6</b> 27
All	All	995/1140 (87%)	910 (92%)	70 (7%)	15 (2%)	<b>10</b> 39

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	170	ALA
1	C	170	ALA
1	B	170	ALA
1	D	170	ALA
1	A	200	GLU



### 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	196/221 (89%)	196 (100%)	0	100	100
1	B	188/221 (85%)	187 (100%)	1 (0%)	88	94
1	C	198/221 (90%)	198 (100%)	0	100	100
1	D	190/221 (86%)	190 (100%)	0	100	100
All	All	772/884 (87%)	771 (100%)	1 (0%)	93	98

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

Mol	Chain	Res	Type
1	B	53	ARG

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

Mol	Chain	Res	Type
1	A	254	ASN
1	C	257	GLN
1	D	132	GLN
1	D	257	GLN

### 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 [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	254/285 (89%)	-0.20	3 (1%) 79 61	34, 62, 96, 115	13 (5%)
1	B	244/285 (85%)	-0.40	0 100 100	35, 51, 74, 105	8 (3%)
1	C	257/285 (90%)	-0.25	1 (0%) 92 84	35, 61, 92, 101	13 (5%)
1	D	248/285 (87%)	-0.35	2 (0%) 86 72	36, 61, 85, 96	13 (5%)
All	All	1003/1140 (87%)	-0.30	6 (0%) 89 78	34, 58, 90, 115	47 (4%)

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	227	ASP	3.1
1	C	242	GLY	2.7
1	D	262	VAL	2.4
1	A	201	ALA	2.1
1	D	202	GLY	2.1

### 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.