



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 4OL4 / pdb_00004ol4
Title : Crystal structure of secreted proline rich antigen MTC28 (Rv0040c) from Mycobacterium tuberculosis
Authors : Kundu, P.; Biswas, R.; Mukherjee, S.; Reinhard, L.; Mueller-dieckmann, J.; Weiss, M.S.; Das, A.K.
Deposited on : 2014-01-23
Resolution : 2.80 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

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>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

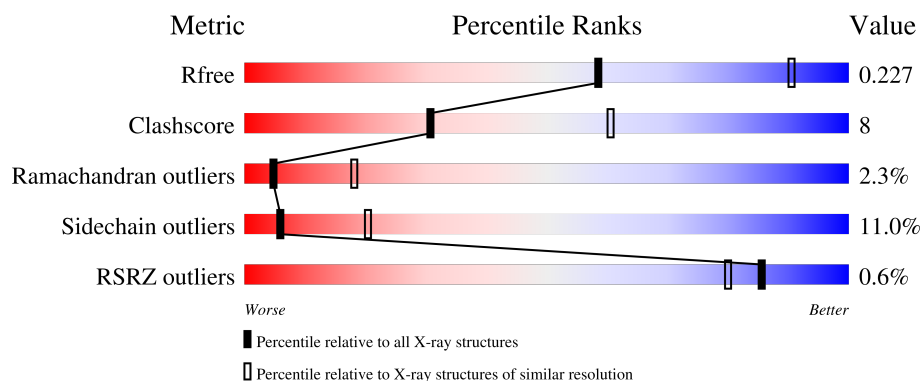
1 Overall quality at a glance

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}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (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 ≥ 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	289	45%12%•39%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1369 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-rich 28 kDa antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	177	Total	C	N	O	S	0	0	0
			1346	848	234	261	3			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	22	HIS	-	expression tag	UNP P0A5Q6
A	23	HIS	-	expression tag	UNP P0A5Q6
A	24	HIS	-	expression tag	UNP P0A5Q6
A	25	HIS	-	expression tag	UNP P0A5Q6
A	26	HIS	-	expression tag	UNP P0A5Q6
A	27	HIS	-	expression tag	UNP P0A5Q6
A	28	GLY	-	expression tag	UNP P0A5Q6
A	29	SER	-	expression tag	UNP P0A5Q6
A	30	ALA	-	expression tag	UNP P0A5Q6
A	31	CYS	-	expression tag	UNP P0A5Q6

- Molecule 2 is water.

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

- Molecule 1: Proline-rich 28 kDa antigen



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	102.22Å 102.22Å 68.72Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.48 – 2.80 19.48 – 2.81	Depositor EDS
% Data completeness (in resolution range)	99.6 (19.48-2.80) 99.6 (19.48-2.81)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.36 (at 2.79Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.180 , 0.223 0.185 , 0.227	Depositor DCC
R_{free} test set	499 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	48.4	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 30.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.035 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	1369	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.06% 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](#)

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	1.23	3/1376 (0.2%)	1.35	12/1882 (0.6%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	262	ASP	CA-C	-7.03	1.43	1.52
1	A	159	ASN	CA-C	6.33	1.56	1.53
1	A	254	ALA	C-O	5.11	1.30	1.23

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	177	PHE	N-CA-C	7.30	126.36	110.80
1	A	141	VAL	CA-C-N	-7.08	113.37	120.31
1	A	141	VAL	C-N-CA	-7.08	113.37	120.31
1	A	135	PRO	CA-C-N	7.05	127.09	119.90
1	A	135	PRO	C-N-CA	7.05	127.09	119.90
1	A	143	ASP	CA-C-N	6.66	127.63	120.83
1	A	143	ASP	C-N-CA	6.66	127.63	120.83
1	A	256	THR	CB-CA-C	5.33	119.33	110.90
1	A	159	ASN	N-CA-C	5.30	113.83	108.75
1	A	165	ASN	N-CA-C	5.20	116.98	109.07
1	A	262	ASP	CB-CA-C	-5.12	102.30	110.79
1	A	233	ILE	CB-CA-C	-5.02	105.01	111.53

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	1346	0	1322	22	0
2	A	23	0	0	3	0
All	All	1369	0	1322	22	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 8.

All (22) 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:135:PRO:O	1:A:138:TRP:HB2	1.84	0.77
1:A:159:ASN:OD1	1:A:160:SER:N	2.28	0.66
1:A:185:HIS:HE1	2:A:407:HOH:O	1.79	0.64
1:A:104:GLY:O	1:A:185:HIS:HD2	1.82	0.63
1:A:105:THR:HG21	2:A:408:HOH:O	2.00	0.61
1:A:105:THR:HG22	1:A:108:ASP:H	1.70	0.56
1:A:254:ALA:O	1:A:255:VAL:HB	2.07	0.54
1:A:107:ARG:HG2	2:A:402:HOH:O	2.07	0.53
1:A:254:ALA:O	1:A:255:VAL:CB	2.55	0.52
1:A:249:THR:HG23	1:A:253:GLN:HB2	1.92	0.49
1:A:172:ARG:CZ	1:A:174:ILE:HD11	2.42	0.49
1:A:253:GLN:HA	1:A:256:THR:HG23	1.94	0.48
1:A:249:THR:HG22	1:A:250:ALA:O	2.14	0.46
1:A:197:GLN:HE21	1:A:197:GLN:HB2	1.47	0.45
1:A:104:GLY:O	1:A:185:HIS:CD2	2.67	0.45
1:A:195:ALA:O	1:A:196:TRP:C	2.57	0.44
1:A:151:VAL:HG22	1:A:152:VAL:N	2.33	0.43
1:A:177:PHE:O	1:A:178:ASP:HB3	2.19	0.43
1:A:117:LEU:CD2	1:A:173:LEU:CD2	2.96	0.42
1:A:249:THR:CG2	1:A:250:ALA:O	2.67	0.42
1:A:137:ARG:HH11	1:A:137:ARG:HG2	1.85	0.41
1:A:217:THR:HA	1:A:225:LEU:O	2.20	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	175/289 (61%)	162 (93%)	9 (5%)	4 (2%)	5	18

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	145	ASN
1	A	160	SER
1	A	147	PRO
1	A	178	ASP

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	146/229 (64%)	130 (89%)	16 (11%)	6	20

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	105	THR
1	A	107	ARG
1	A	111	ARG
1	A	113	LYS
1	A	116	LYS
1	A	134	MET
1	A	137	ARG

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Mol	Chain	Res	Type
1	A	161	VAL
1	A	176	ASP
1	A	183	ILE
1	A	197	GLN
1	A	229	ARG
1	A	232	VAL
1	A	240	LYS
1	A	249	THR
1	A	256	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	109	HIS
1	A	120	GLN
1	A	140	GLN
1	A	165	ASN
1	A	185	HIS
1	A	197	GLN
1	A	253	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 oligosaccharides 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, 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	177/289 (61%)	-0.54	1 (0%) 85 80	24, 39, 71, 81	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	273	HIS	3.6

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 oligosaccharides 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.