



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 22, 2024 – 12:54 AM EDT

PDB ID : 3LO7
Title : Crystal structure of PBPA from Mycobacterium tuberculosis
Authors : Fedarovich, A.; Davies, C.
Deposited on : 2010-02-03
Resolution : 2.05 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	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

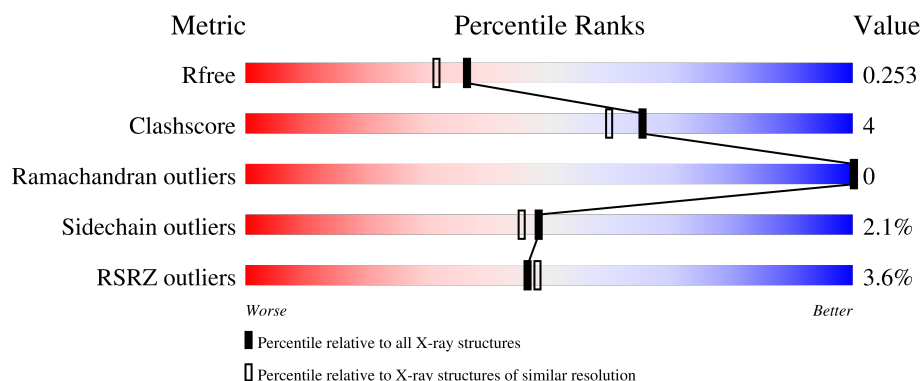
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.05 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}	164625	2096 (2.04-2.04)
Clashscore	180529	2229 (2.04-2.04)
Ramachandran outliers	177936	2217 (2.04-2.04)
Sidechain outliers	177891	2217 (2.04-2.04)
RSRZ outliers	164620	2096 (2.04-2.04)

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	483	
1	B	483	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 5984 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 Penicillin-binding protein A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	420	Total	C	N	O	S	0	0	0
			3093	1936	550	598	9			
1	B	383	Total	C	N	O	S	0	0	0
			2815	1761	501	544	9			

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9	MET	-	expression tag	UNP P71586
A	10	SER	-	expression tag	UNP P71586
A	11	TYR	-	expression tag	UNP P71586
A	12	TYR	-	expression tag	UNP P71586
A	13	HIS	-	expression tag	UNP P71586
A	14	HIS	-	expression tag	UNP P71586
A	15	HIS	-	expression tag	UNP P71586
A	16	HIS	-	expression tag	UNP P71586
A	17	HIS	-	expression tag	UNP P71586
A	18	HIS	-	expression tag	UNP P71586
A	19	ASP	-	expression tag	UNP P71586
A	20	TYR	-	expression tag	UNP P71586
A	21	ASP	-	expression tag	UNP P71586
A	22	ILE	-	expression tag	UNP P71586
A	23	PRO	-	expression tag	UNP P71586
A	24	THR	-	expression tag	UNP P71586
A	25	GLU	-	expression tag	UNP P71586
A	26	ASN	-	expression tag	UNP P71586
A	27	LEU	-	expression tag	UNP P71586
A	28	TYR	-	expression tag	UNP P71586
A	29	PHE	-	expression tag	UNP P71586
A	30	GLN	-	expression tag	UNP P71586
A	31	GLY	-	expression tag	UNP P71586
A	32	ALA	-	expression tag	UNP P71586
A	33	MET	-	expression tag	UNP P71586

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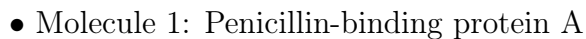
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Chain	Residue	Modelled	Actual	Comment	Reference
A	34	GLY	-	expression tag	UNP P71586
B	9	MET	-	expression tag	UNP P71586
B	10	SER	-	expression tag	UNP P71586
B	11	TYR	-	expression tag	UNP P71586
B	12	TYR	-	expression tag	UNP P71586
B	13	HIS	-	expression tag	UNP P71586
B	14	HIS	-	expression tag	UNP P71586
B	15	HIS	-	expression tag	UNP P71586
B	16	HIS	-	expression tag	UNP P71586
B	17	HIS	-	expression tag	UNP P71586
B	18	HIS	-	expression tag	UNP P71586
B	19	ASP	-	expression tag	UNP P71586
B	20	TYR	-	expression tag	UNP P71586
B	21	ASP	-	expression tag	UNP P71586
B	22	ILE	-	expression tag	UNP P71586
B	23	PRO	-	expression tag	UNP P71586
B	24	THR	-	expression tag	UNP P71586
B	25	GLU	-	expression tag	UNP P71586
B	26	ASN	-	expression tag	UNP P71586
B	27	LEU	-	expression tag	UNP P71586
B	28	TYR	-	expression tag	UNP P71586
B	29	PHE	-	expression tag	UNP P71586
B	30	GLN	-	expression tag	UNP P71586
B	31	GLY	-	expression tag	UNP P71586
B	32	ALA	-	expression tag	UNP P71586
B	33	MET	-	expression tag	UNP P71586
B	34	GLY	-	expression tag	UNP P71586

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	57	Total O 57 57	0	0
2	B	19	Total O 19 19	0	0

- Molecule 1: Penicillin-binding protein A



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	120.60Å 120.60Å 92.20Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.30 – 2.05 36.30 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.8 (36.30-2.05) 99.8 (36.30-2.05)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.16 (at 2.05Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.215 , 0.252 0.213 , 0.253	Depositor DCC
R_{free} test set	2388 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	42.8	Xtriage
Anisotropy	0.260	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 34.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.039 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5984	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 67.65 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.9725e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

5.1 Standard geometry

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	0.54	0/3155	0.61	0/4308
1	B	0.55	1/2869 (0.0%)	0.60	0/3918
All	All	0.54	1/6024 (0.0%)	0.61	0/8226

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	132	GLY	N-CA	12.77	1.65	1.46

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	72	PHE	Peptide

5.2 Too-close contacts

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	3093	0	3087	21	0
1	B	2815	0	2804	26	0
2	A	57	0	0	0	0
2	B	19	0	0	0	0
All	All	5984	0	5891	44	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 4.

All (44) 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:B:190:ASN:HD22	1:B:193:VAL:HG23	1.31	0.95
1:B:141:ARG:HD3	1:B:488:GLN:HE21	1.35	0.89
1:B:170:GLY:O	1:B:365:PRO:HA	1.88	0.73
1:B:141:ARG:HD3	1:B:488:GLN:NE2	2.09	0.68
1:A:474:LEU:HD13	1:B:155:TYR:OH	2.01	0.61
1:A:112:ASP:HB3	1:A:115:LEU:HD12	1.85	0.59
1:A:94:ARG:HD2	1:A:95:TYR:CZ	2.39	0.57
1:A:307:LEU:HD21	1:A:344:LEU:HD11	1.86	0.57
1:A:467:LEU:HD11	1:B:463:GLY:HA2	1.86	0.57
1:B:60:GLN:HG3	1:B:140:PRO:HG2	1.87	0.56
1:A:364:ARG:HB2	1:A:387:GLN:HG3	1.90	0.54
1:A:141:ARG:NH2	1:A:488:GLN:HB2	2.24	0.52
1:B:473:ALA:O	1:B:477:PRO:HD3	2.10	0.51
1:A:155:TYR:HB2	1:B:468:SER:HB3	1.93	0.50
1:A:162:VAL:HG11	1:A:482:VAL:HG21	1.93	0.50
1:A:201:LEU:HD13	1:A:209:LEU:HD21	1.93	0.49
1:B:159:LYS:HE3	1:B:212:ARG:HH11	1.78	0.49
1:A:94:ARG:HD2	1:A:95:TYR:CE1	2.49	0.48
1:B:307:LEU:HD21	1:B:344:LEU:HD11	1.96	0.47
1:A:53:GLY:HA3	1:A:132:GLY:O	2.14	0.47
1:B:141:ARG:CD	1:B:488:GLN:HE21	2.18	0.47
1:A:216:GLU:HG2	1:A:218:TYR:CZ	2.50	0.46
1:A:84:TYR:CE2	1:A:143:GLN:HG2	2.52	0.45
1:B:239:GLU:HA	1:B:274:LEU:HB3	1.99	0.45
1:A:222:SER:HB2	1:A:426:GLY:HA3	1.98	0.44
1:A:438:PRO:HB2	1:A:462:ASN:HB3	1.99	0.44
1:B:70:GLY:C	1:B:72:PHE:H	2.20	0.44
1:A:159:LYS:HD2	1:A:212:ARG:NH1	2.33	0.44
1:B:159:LYS:HE3	1:B:212:ARG:NH1	2.34	0.43
1:B:175:LEU:HD21	1:B:211:ASN:HD21	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:VAL:HG22	1:A:147:TRP:CD1	2.53	0.43
1:A:249:ILE:HG13	1:A:250:PRO:HD2	2.00	0.42
1:B:83:VAL:HG22	1:B:147:TRP:CD1	2.54	0.42
1:B:70:GLY:C	1:B:72:PHE:N	2.72	0.42
1:B:310:PRO:HA	1:B:311:PRO:HD3	1.92	0.42
1:B:190:ASN:HD21	1:B:192:GLU:HB3	1.83	0.42
1:A:484:GLU:O	1:A:488:GLN:HG3	2.19	0.42
1:B:162:VAL:HB	1:B:176:VAL:HB	2.02	0.42
1:B:105:ASP:O	1:B:109:ASN:N	2.53	0.41
1:B:137:THR:HB	1:B:171:LYS:HB2	2.03	0.41
1:B:190:ASN:ND2	1:B:192:GLU:HB3	2.36	0.41
1:A:110:GLY:HA2	1:A:115:LEU:HD13	2.03	0.41
1:B:244:THR:HG21	1:B:249:ILE:HD12	2.04	0.40
1:B:181:TYR:O	1:B:183:PRO:HD3	2.22	0.40

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	412/483 (85%)	400 (97%)	12 (3%)	0	100	100
1	B	371/483 (77%)	353 (95%)	18 (5%)	0	100	100
All	All	783/966 (81%)	753 (96%)	30 (4%)	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	320/370 (86%)	314 (98%)	6 (2%)	52	50
1	B	291/370 (79%)	284 (98%)	7 (2%)	44	40
All	All	611/740 (83%)	598 (98%)	13 (2%)	48	45

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	LEU
1	A	222	SER
1	A	240	THR
1	A	248	THR
1	A	380	SER
1	A	385	TYR
1	B	68	THR
1	B	82	GLU
1	B	222	SER
1	B	328	ASP
1	B	450	GLN
1	B	466	ARG
1	B	488	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	190	ASN
1	B	412	GLN
1	B	488	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.1 Protein, DNA and RNA chains

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	420/483 (86%)	0.09	13 (3%) 51 53	28, 42, 68, 78	0
1	B	383/483 (79%)	0.48	16 (4%) 41 43	31, 56, 88, 113	0
All	All	803/966 (83%)	0.28	29 (3%) 46 48	28, 47, 81, 113	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	68	THR	4.1
1	B	72	PHE	3.8
1	A	45	LEU	3.6
1	B	419	VAL	3.5
1	A	258	LEU	3.2
1	B	132	GLY	3.2
1	A	261	TYR	3.1
1	B	59	GLY	3.1
1	A	48	TYR	2.9
1	B	250	PRO	2.8
1	B	70	GLY	2.8
1	A	47	GLU	2.8
1	A	50	ARG	2.7
1	A	383	VAL	2.7
1	B	449	ALA	2.7
1	B	271	THR	2.6
1	A	46	ASP	2.5
1	B	470	THR	2.4
1	B	69	ASP	2.3
1	B	249	ILE	2.3
1	B	106	PRO	2.3
1	B	71	ARG	2.3
1	A	115	LEU	2.3
1	B	108	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	436	HIS	2.2
1	A	381	THR	2.1
1	A	415	ALA	2.1
1	A	250	PRO	2.0
1	B	191	PRO	2.0

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.