Full wwPDB X-ray Structure Validation Report ⓘ

Jan 13, 2024 – 07:42 pm GMT

PDB ID	:	6HZJ
Title	:	Apo structure of TP domain from clinical penicillin-resistant mutant Neisseria gonorrhoea strain 6140 Penicillin-Binding Protein 2 (PBP2)
Authors	:	Bellini, D.; Koekemoer, L.; Newman, H.; Dowson, C.G.
Deposited on	:	2018-10-23
Resolution	:	1.43 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:

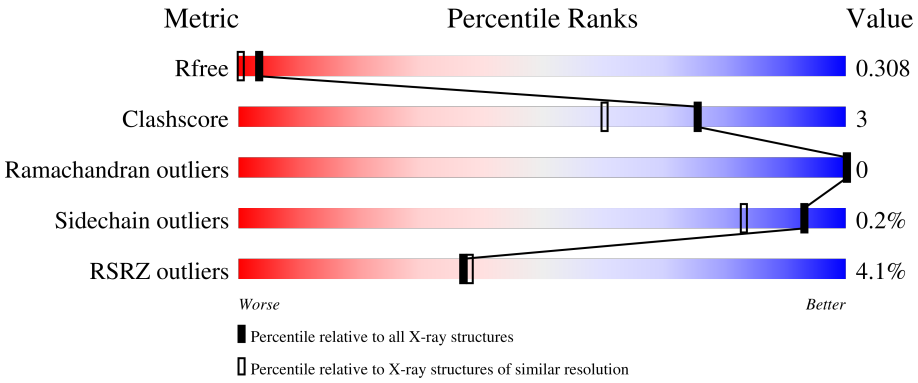
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.43 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	2021 (1.46-1.42)
Clashscore	141614	2086 (1.46-1.42)
Ramachandran outliers	138981	2047 (1.46-1.42)
Sidechain outliers	138945	2047 (1.46-1.42)
RSRZ outliers	127900	1993 (1.46-1.42)

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 <=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	339	4% 89% 7% .
1	B	339	4% 90% 6% .

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 5379 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 peptidoglycan D,D-transpeptidase PenA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	326	Total	C	N	O	S	0	1	0
			2486	1572	445	462	7			
1	B	327	Total	C	N	O	S	0	0	0
			2488	1572	446	463	7			

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	230	GLY	-	expression tag	UNP E5KLA8
A	231	PRO	-	expression tag	UNP E5KLA8
A	232	GLY	-	expression tag	UNP E5KLA8
A	233	TYR	-	expression tag	UNP E5KLA8
A	234	GLN	-	expression tag	UNP E5KLA8
A	235	ASP	-	expression tag	UNP E5KLA8
A	236	PRO	-	expression tag	UNP E5KLA8
A	237	ARG	-	expression tag	UNP E5KLA8
A	297	GLY	ALA	conflict	UNP E5KLA8
A	?	-	TYR	deletion	UNP E5KLA8
A	?	-	ASP	deletion	UNP E5KLA8
A	?	-	PRO	deletion	UNP E5KLA8
A	?	-	ASN	deletion	UNP E5KLA8
A	?	-	ARG	deletion	UNP E5KLA8
A	?	-	PRO	deletion	UNP E5KLA8
A	?	-	GLY	deletion	UNP E5KLA8
A	?	-	ARG	deletion	UNP E5KLA8
A	?	-	ALA	deletion	UNP E5KLA8
A	?	-	ASP	deletion	UNP E5KLA8
A	?	-	SER	deletion	UNP E5KLA8
A	?	-	GLU	deletion	UNP E5KLA8
A	?	-	GLN	deletion	UNP E5KLA8
A	?	-	ARG	deletion	UNP E5KLA8
B	230	GLY	-	expression tag	UNP E5KLA8
B	231	PRO	-	expression tag	UNP E5KLA8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	232	GLY	-	expression tag	UNP E5KLA8
B	233	TYR	-	expression tag	UNP E5KLA8
B	234	GLN	-	expression tag	UNP E5KLA8
B	235	ASP	-	expression tag	UNP E5KLA8
B	236	PRO	-	expression tag	UNP E5KLA8
B	237	ARG	-	expression tag	UNP E5KLA8
B	297	GLY	ALA	conflict	UNP E5KLA8
B	?	-	TYR	deletion	UNP E5KLA8
B	?	-	ASP	deletion	UNP E5KLA8
B	?	-	PRO	deletion	UNP E5KLA8
B	?	-	ASN	deletion	UNP E5KLA8
B	?	-	ARG	deletion	UNP E5KLA8
B	?	-	PRO	deletion	UNP E5KLA8
B	?	-	GLY	deletion	UNP E5KLA8
B	?	-	ARG	deletion	UNP E5KLA8
B	?	-	ALA	deletion	UNP E5KLA8
B	?	-	ASP	deletion	UNP E5KLA8
B	?	-	SER	deletion	UNP E5KLA8
B	?	-	GLU	deletion	UNP E5KLA8
B	?	-	GLN	deletion	UNP E5KLA8
B	?	-	ARG	deletion	UNP E5KLA8

- Molecule 2 is water.

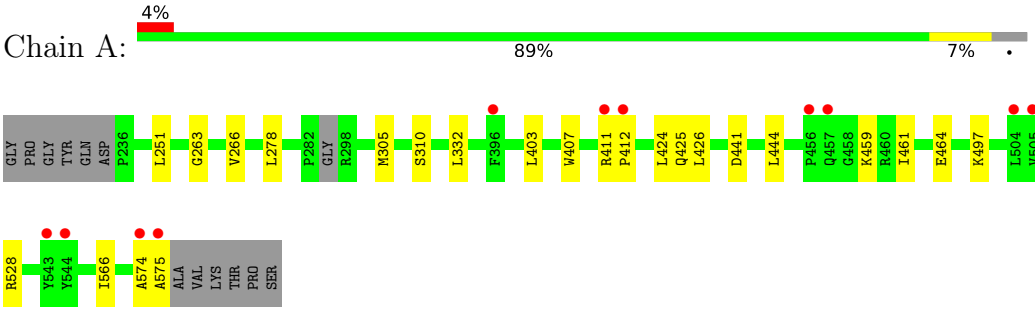
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	192	Total O 192 192	0	0
2	B	213	Total O 213 213	0	0

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.

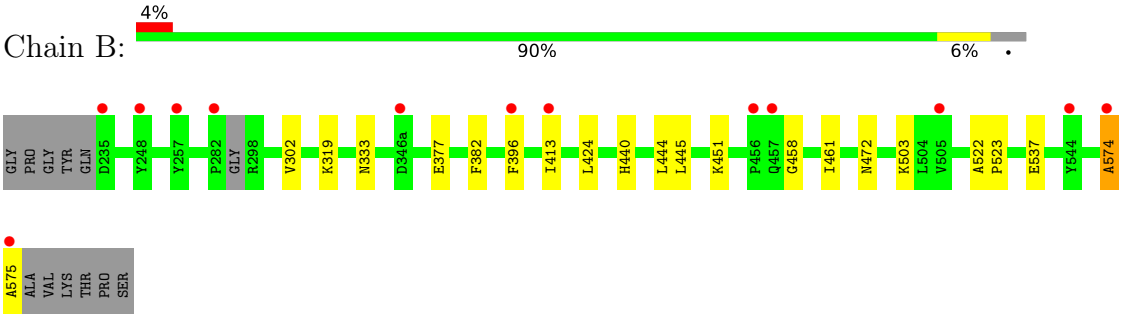
• Molecule 1: Probable peptidoglycan D,D-transpeptidase PenA

Chain A:



• Molecule 1: Probable peptidoglycan D,D-transpeptidase PenA

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	52.65Å 77.59Å 81.87Å 90.00° 98.61° 90.00°	Depositor
Resolution (Å)	56.01 – 1.43 47.11 – 1.43	Depositor EDS
% Data completeness (in resolution range)	91.2 (56.01-1.43) 91.2 (47.11-1.43)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.62 (at 1.43Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.278 , 0.301 0.287 , 0.308	Depositor DCC
R_{free} test set	5428 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å^2)	8.7	Xtriage
Anisotropy	0.584	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 34.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	5379	wwPDB-VP
Average B, all atoms (Å^2)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.10% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.52	1/2539 (0.0%)	0.64	0/3439
1	B	0.52	0/2538	0.65	1/3439 (0.0%)
All	All	0.52	1/5077 (0.0%)	0.65	1/6878 (0.0%)

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	A	407	TRP	CD2-CE2	5.57	1.48	1.41

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	574	ALA	C-N-CA	6.36	137.59	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	574	ALA	Peptide

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	2486	0	2517	20	3
1	B	2488	0	2514	12	3
2	A	192	0	0	1	1
2	B	213	0	0	4	1
All	All	5379	0	5031	31	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 3.

All (31) 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:472:ASN:HB3	2:B:792:HOH:O	1.63	0.98
1:A:412:PRO:O	2:A:601:HOH:O	1.80	0.97
1:A:305:MET:HE3	1:A:425:GLN:HB2	1.65	0.79
1:A:305:MET:CE	1:A:425:GLN:HB2	2.25	0.66
1:B:458:GLY:N	2:B:601:HOH:O	2.16	0.65
1:A:424:LEU:C	1:A:424:LEU:HD12	2.24	0.56
1:A:424:LEU:HD12	1:A:424:LEU:O	2.09	0.52
1:A:441:ASP:HB3	1:A:464:GLU:HG2	1.91	0.52
1:A:305:MET:HE1	1:A:403:LEU:HB2	1.90	0.52
1:A:305:MET:HE3	1:A:403:LEU:HB3	1.93	0.50
1:B:440:HIS:CD2	1:B:445:LEU:HD21	2.47	0.49
1:B:444:LEU:HD22	1:B:461:ILE:HD11	1.96	0.47
1:A:528:ARG:HG2	1:A:566:ILE:HD13	1.97	0.47
1:B:413:ILE:HG13	2:B:761:HOH:O	2.15	0.46
1:A:459:LYS:HD3	1:B:377:GLU:HG2	1.98	0.46
1:B:522:ALA:HA	1:B:523:PRO:C	2.36	0.46
1:B:424:LEU:C	1:B:424:LEU:HD12	2.37	0.45
1:A:305:MET:CE	1:A:403:LEU:HB3	2.47	0.45
1:A:528:ARG:HG2	1:A:566:ILE:CD1	2.46	0.45
1:A:305:MET:HE2	1:A:425:GLN:CD	2.37	0.45
1:B:503:LYS:NZ	1:B:537:GLU:OE2	2.38	0.44
1:A:444:LEU:HD22	1:A:461:ILE:HD11	2.00	0.44
1:A:574:ALA:O	1:A:575:ALA:C	2.55	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:MET:CE	1:A:403:LEU:CB	2.95	0.44
1:A:251:LEU:HD11	1:A:263:GLY:HA3	2.00	0.44
1:A:266:VAL:HG22	1:A:278:LEU:HD12	2.00	0.43
1:B:302:VAL:HG11	1:B:396:PHE:HB2	2.01	0.42
1:B:451:LYS:HD3	2:B:606:HOH:O	2.19	0.42
1:A:310:SER:O	1:A:497:LYS:HE2	2.20	0.41
1:B:319:LYS:HD2	1:B:382:PHE:CG	2.56	0.41
1:A:411:ARG:NH1	1:A:412:PRO:HD2	2.36	0.41

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)
1:A:575:ALA:C	1:B:333:ASN:CB[2_645]	1.97	0.23
1:A:575:ALA:CA	1:B:333:ASN:N[2_645]	1.98	0.22
1:A:332:LEU:CA	1:B:575:ALA:CB[2_646]	2.02	0.18
2:A:607:HOH:O	2:B:715:HOH:O[2_645]	2.18	0.02

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	323/339 (95%)	318 (98%)	5 (2%)	0	100	100
1	B	323/339 (95%)	319 (99%)	4 (1%)	0	100	100
All	All	646/678 (95%)	637 (99%)	9 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	260/268 (97%)	259 (100%)	1 (0%)	91 80
1	B	260/268 (97%)	260 (100%)	0	100 100
All	All	520/536 (97%)	519 (100%)	1 (0%)	93 83

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

Mol	Chain	Res	Type
1	A	426	LEU

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

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

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

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, 95^{th} 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	326/339 (96%)	0.27	14 (4%)	35	36	8, 14, 29, 66	0
1	B	327/339 (96%)	0.18	13 (3%)	38	39	9, 14, 27, 40	0
All	All	653/678 (96%)	0.22	27 (4%)	37	38	8, 14, 28, 66	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	575	ALA	17.8
1	B	575	ALA	7.6
1	A	506	ASN	5.7
1	A	505	VAL	5.5
1	A	507	GLY	4.5
1	A	412	PRO	4.1
1	B	413	ILE	3.9
1	A	574	ALA	3.8
1	B	456	PRO	3.7
1	A	456	PRO	3.5
1	A	411	ARG	3.4
1	B	574	ALA	3.3
1	B	544	TYR	3.2
1	A	544	TYR	3.1
1	A	457	GLN	3.1
1	A	396	PHE	3.0
1	B	505	VAL	3.0
1	A	508	ARG	2.9
1	A	504	LEU	2.8
1	B	457	GLN	2.8
1	A	543	TYR	2.8
1	B	235	ASP	2.6
1	B	282	PRO	2.2
1	B	396	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	257	TYR	2.1
1	B	346(a)	ASP	2.1
1	B	248	TYR	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.