



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 14, 2023 – 12:09 AM JST

PDB ID : 5YIL  
Title : Hoisting-loop in bacterial multidrug exporter AcrB is a highly flexible hinge that enables the large motion of the subdomains  
Authors : Zwama, M.; Sakurai, K.; Hayashi, K.; Nakashima, R.; Kitagawa, K.; Nishino, K.; Yamaguchi, A.  
Deposited on : 2017-10-05  
Resolution : 3.00 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

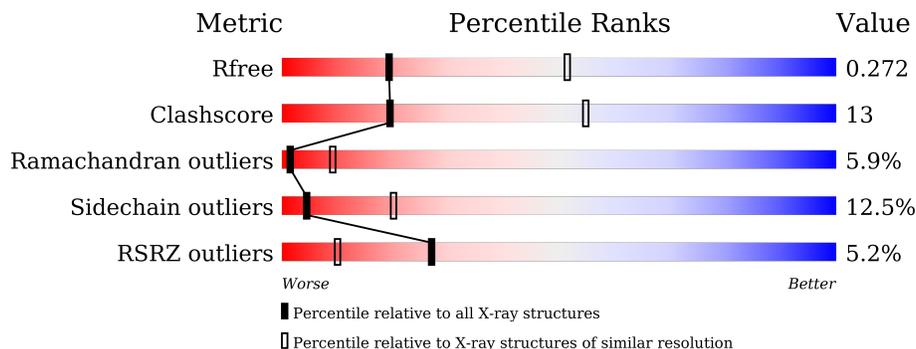
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	1050	 4% 72% 24% ..
1	B	1050	 6% 65% 28% ..
1	C	1050	 6% 58% 33% 6% ..

## 2 Entry composition i

There is only 1 type of molecule in this entry. The entry contains 23566 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 Multidrug efflux pump subunit AcrB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	1041	7918	5091	1310	1473	44	0	0	0
1	B	1030	7824	5037	1290	1453	44	0	0	0
1	C	1030	7824	5037	1290	1453	44	0	0	0

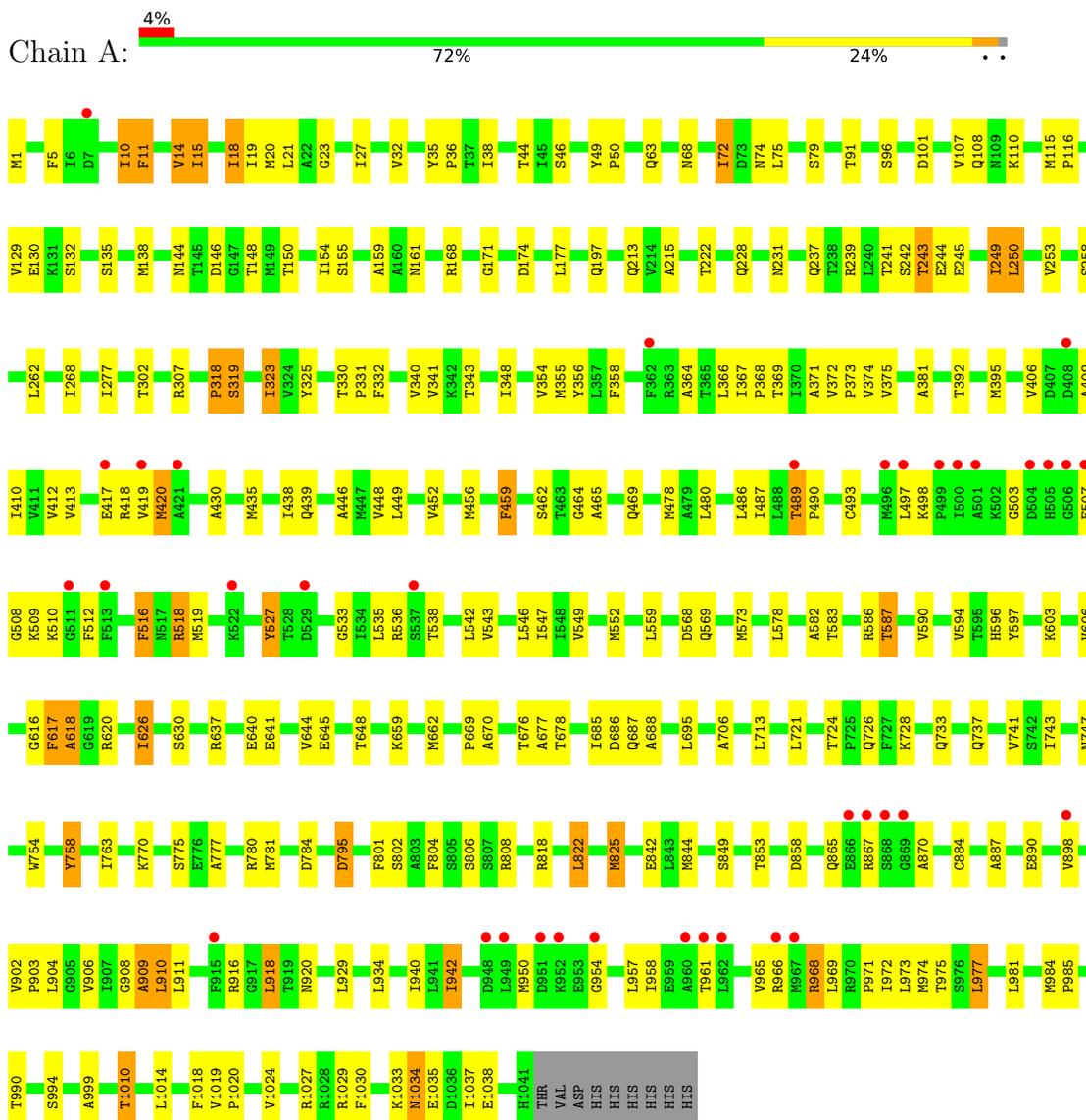
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1047	HIS	-	expression tag	UNP P31224
A	1048	HIS	-	expression tag	UNP P31224
A	1049	HIS	-	expression tag	UNP P31224
A	1050	HIS	-	expression tag	UNP P31224
B	1047	HIS	-	expression tag	UNP P31224
B	1048	HIS	-	expression tag	UNP P31224
B	1049	HIS	-	expression tag	UNP P31224
B	1050	HIS	-	expression tag	UNP P31224
C	1047	HIS	-	expression tag	UNP P31224
C	1048	HIS	-	expression tag	UNP P31224
C	1049	HIS	-	expression tag	UNP P31224
C	1050	HIS	-	expression tag	UNP P31224

### 3 Residue-property plots

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.

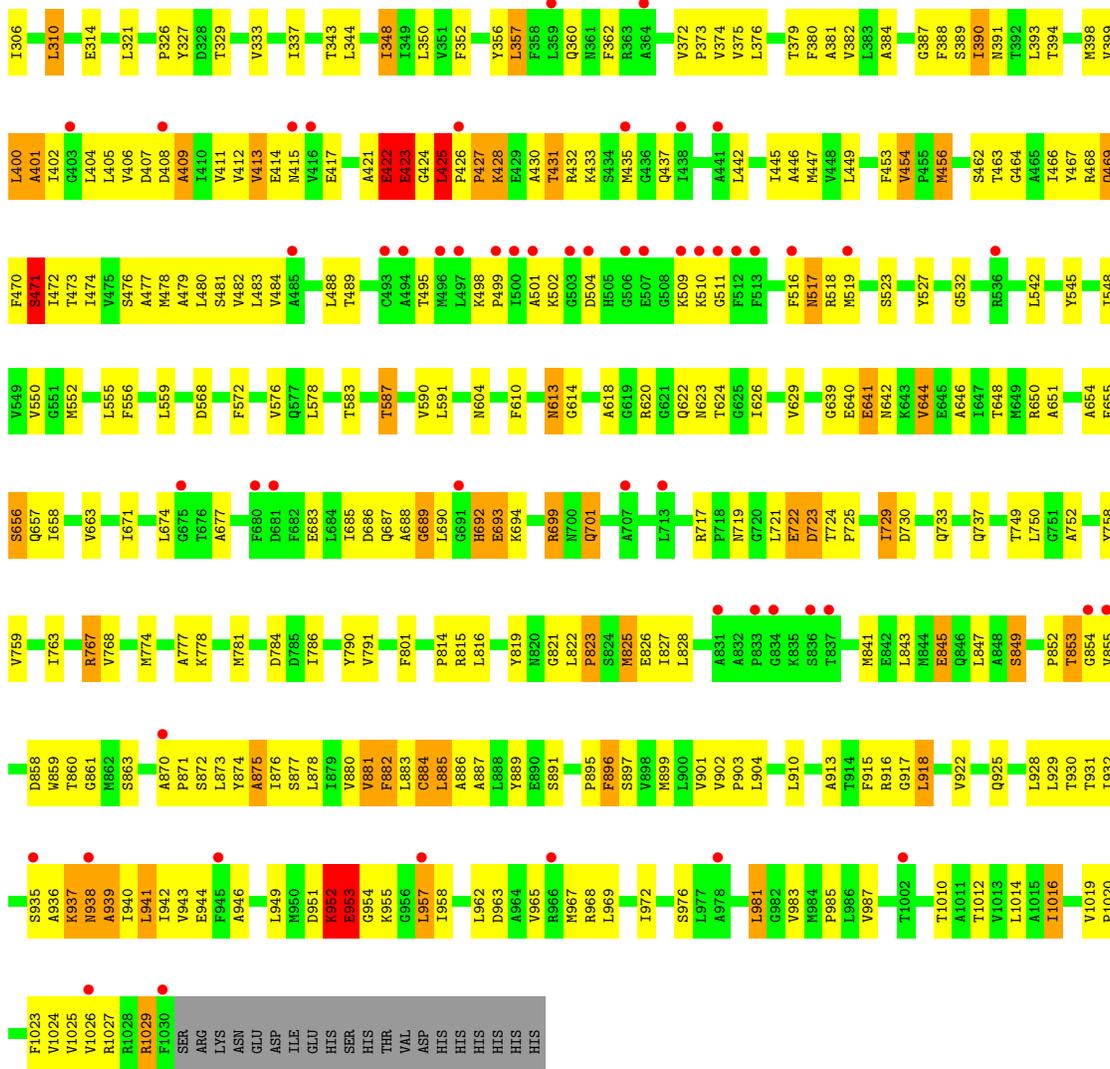
- Molecule 1: Multidrug efflux pump subunit AcrB



- Molecule 1: Multidrug efflux pump subunit AcrB







## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	135.98Å 139.81Å 285.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 3.00 98.45 – 3.00	Depositor EDS
% Data completeness (in resolution range)	94.5 (100.00-3.00) 94.5 (98.45-3.00)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.61 (at 3.01Å)	Xtrriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.224 , 0.273 0.226 , 0.272	Depositor DCC
$R_{free}$ test set	5112 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	67.9	Xtrriage
Anisotropy	0.025	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 74.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.026 for k,h,-l	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	23566	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	87.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.21% 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	0.69	0/8070	0.86	0/10957
1	B	0.64	0/7974	0.83	0/10829
1	C	0.69	0/7974	0.89	2/10829 (0.0%)
All	All	0.67	0/24018	0.86	2/32615 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	128	SER	CB-CA-C	-6.51	97.73	110.10
1	C	131	LYS	N-CA-C	-5.49	96.18	111.00

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	7918	0	8059	127	0
1	B	7824	0	7976	221	0
1	C	7824	0	7976	283	0
All	All	23566	0	24011	608	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 13.

The worst 5 of 608 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:344:LEU:HD23	1:B:402:ILE:CD1	1.46	1.45
1:B:449:LEU:HB3	1:B:478:MET:CE	1.52	1.37
1:B:344:LEU:CD2	1:B:402:ILE:CD1	2.18	1.20
1:B:344:LEU:CD2	1:B:402:ILE:HD11	1.79	1.12
1:B:449:LEU:HB3	1:B:478:MET:HE2	1.23	1.10

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	1039/1050 (99%)	877 (84%)	116 (11%)	46 (4%)	2	15
1	B	1028/1050 (98%)	825 (80%)	148 (14%)	55 (5%)	2	11
1	C	1028/1050 (98%)	791 (77%)	155 (15%)	82 (8%)	1	4
All	All	3095/3150 (98%)	2493 (80%)	419 (14%)	183 (6%)	1	9

5 of 183 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	319	SER
1	A	366	LEU
1	A	464	GLY
1	A	543	VAL
1	A	582	ALA

### 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	847/856 (99%)	748 (88%)	99 (12%)	5	22
1	B	836/856 (98%)	737 (88%)	99 (12%)	5	22
1	C	836/856 (98%)	719 (86%)	117 (14%)	3	16
All	All	2519/2568 (98%)	2204 (88%)	315 (12%)	4	20

5 of 315 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	301	ASP
1	C	825	MET
1	C	389	SER
1	C	583	THR
1	C	918	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	109	ASN
1	C	613	ASN
1	C	181	GLN
1	C	298	ASN
1	C	719	ASN

### 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	1041/1050 (99%)	0.07	37 (3%) 42 17	21, 70, 147, 190	0
1	B	1030/1050 (98%)	0.26	66 (6%) 19 6	27, 98, 147, 173	0
1	C	1030/1050 (98%)	0.24	58 (5%) 24 8	24, 87, 142, 207	0
All	All	3101/3150 (98%)	0.19	161 (5%) 27 10	21, 86, 147, 207	0

The worst 5 of 161 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	500	ILE	9.7
1	C	6	ILE	5.8
1	C	497	LEU	5.5
1	C	707	ALA	5.4
1	B	497	LEU	5.2

### 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.