



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 06:18 AM UTC

PDB ID : 4RY2 / pdb_00004ry2
Title : Crystal structure of the peptidase-containing ABC transporter PCAT1
Authors : Lin, D.L.; Huang, S.; Chen, J.
Deposited on : 2014-12-13
Resolution : 3.61 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

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

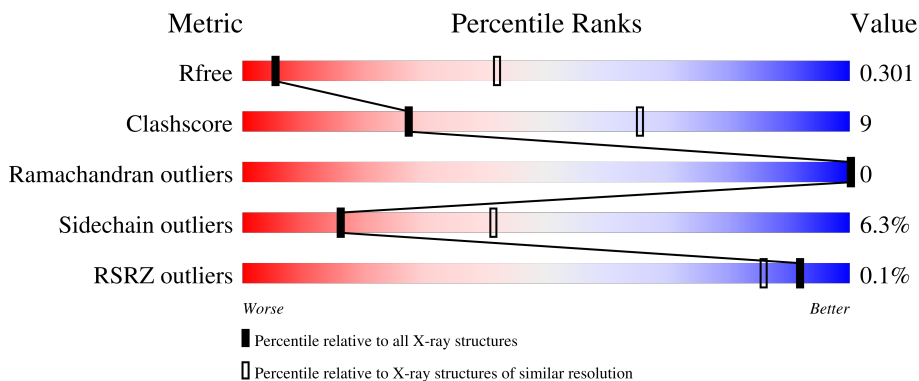
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.61 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	1062 (3.72-3.52)
Clashscore	190562	1092 (3.72-3.52)
Ramachandran outliers	187476	1057 (3.72-3.52)
Sidechain outliers	187428	1055 (3.72-3.52)
RSRZ outliers	180081	1060 (3.72-3.52)

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	730	
1	B	730	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 9927 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 ABC-type bacteriocin transporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	701	4970	3192	813	939	26	0	0	0
1	B	699	4957	3186	809	936	26	0	0	0

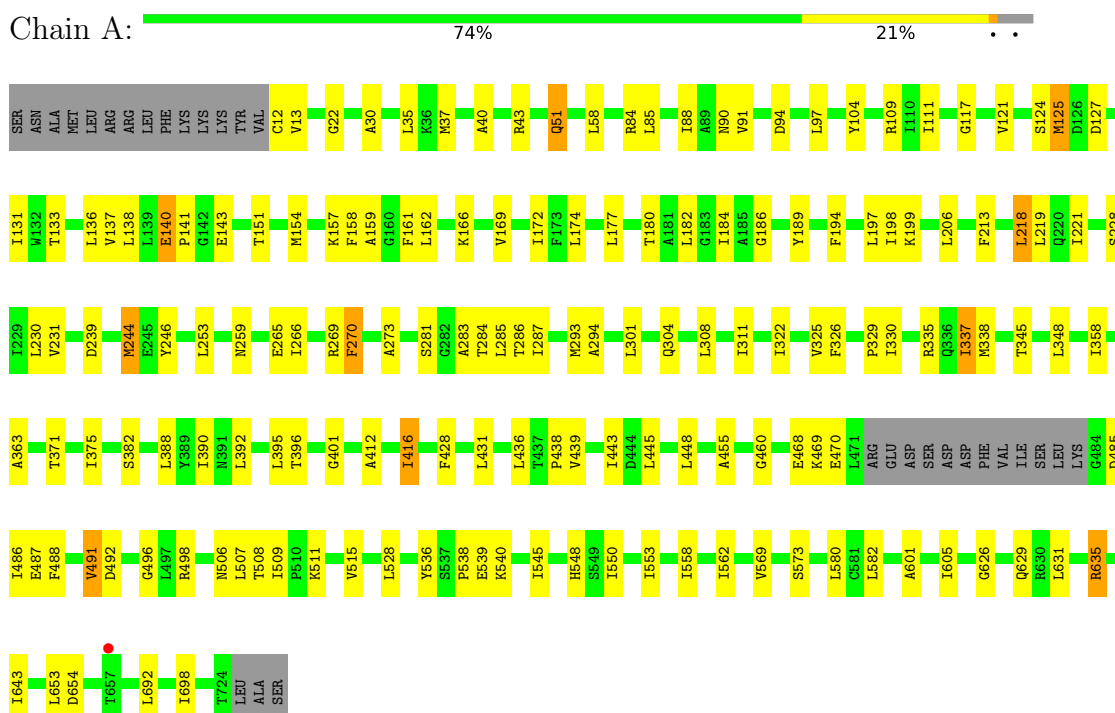
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP A3DCU1
A	-1	ASN	-	expression tag	UNP A3DCU1
A	0	ALA	-	expression tag	UNP A3DCU1
B	-2	SER	-	expression tag	UNP A3DCU1
B	-1	ASN	-	expression tag	UNP A3DCU1
B	0	ALA	-	expression tag	UNP A3DCU1

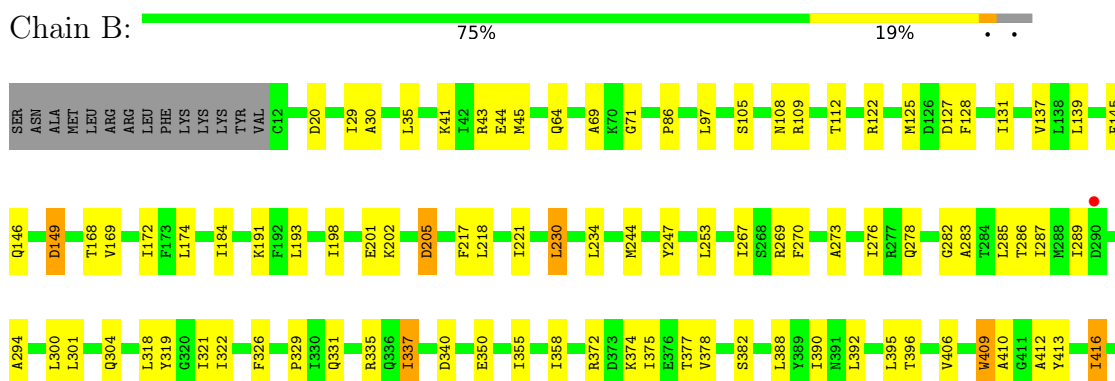
3 Residue-property plots [i](#)

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: ABC-type bacteriocin transporter



- Molecule 1: ABC-type bacteriocin transporter



A427	L582	ALA
LA31	G583	SER
P438	D590	
D444	A596	
T451	M600	
E468	A601	
K469	H602	
E470	D603	
L471	F604	
ARG	I605	
GLU	L608	
ASP	Y612	
SER	D613	
ASP	T614	
ASP	F615	
PHE	L616	
VAL	N617	
ILE	E618	
SER	A621	
LEU	Q627	
LYS	K628	
G484	Q629	
E487	R630	
V491	R635	
D492	L638	
T508	P641	
I509	L644	
P510	I645	
E520	L653	
A529	D654	
P538	S655	
I543	I656	
S549	T657	
I553	I677	
S554	A678	
L555	H679	
I588	I684	
F564	V685	
Y691	I690	
K577	Y691	
E578	E722	
N579	ASN	
L580	THR	
C581	LEU	

4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.59Å 89.73Å 296.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.97 – 3.61 19.97 – 3.61	Depositor EDS
% Data completeness (in resolution range)	75.2 (19.97-3.61) 74.7 (19.97-3.61)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.07 (at 3.57Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: dev_1839)	Depositor
R, R_{free}	0.266 , 0.289 0.280 , 0.301	Depositor DCC
R_{free} test set	1069 reflections (3.52%)	wwPDB-VP
Wilson B-factor (Å ²)	130.0	Xtrriage
Anisotropy	0.130	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 100.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.035 for k,h,-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9927	wwPDB-VP
Average B, all atoms (Å ²)	169.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.48% 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	0.33	0/5045	0.82	6/6865 (0.1%)
1	B	0.32	0/5031	0.80	1/6841 (0.0%)
All	All	0.32	0/10076	0.81	7/13706 (0.1%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	654	ASP	N-CA-C	5.85	118.16	111.02
1	A	143	GLU	CB-CA-C	-5.60	109.61	117.23
1	A	509	ILE	CA-C-N	5.58	126.02	119.99
1	A	509	ILE	C-N-CA	5.58	126.02	119.99
1	B	654	ASP	N-CA-C	5.51	117.74	111.02

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	4970	0	4654	93	0
1	B	4957	0	4656	92	0
All	All	9927	0	9310	174	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 9.

The worst 5 of 174 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:109:ARG:HD2	1:A:125:MET:HE1	1.63	0.79
1:A:273:ALA:HA	1:A:455:ALA:HB1	1.68	0.76
1:A:169:VAL:HG23	1:A:285:LEU:HD12	1.68	0.75
1:A:337:ILE:HD11	1:A:382:SER:HA	1.71	0.73
1:B:301:LEU:HD21	1:B:431:LEU:HB3	1.73	0.71

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	697/730 (96%)	660 (95%)	37 (5%)	0	100	100
1	B	695/730 (95%)	662 (95%)	33 (5%)	0	100	100
All	All	1392/1460 (95%)	1322 (95%)	70 (5%)	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	463/625 (74%)	434 (94%)	29 (6%)	16	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	462/625 (74%)	433 (94%)	29 (6%)	16	41
All	All	925/1250 (74%)	867 (94%)	58 (6%)	16	41

5 of 58 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	635	ARG
1	B	653	LEU
1	B	221	ILE
1	B	603	ASP
1	B	492	ASP

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	64	GLN
1	A	327	ASN
1	A	334	ASN
1	B	441	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 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	701/730 (96%)	-0.29	1 (0%) 92 86	83, 169, 240, 268	0
1	B	699/730 (95%)	-0.30	1 (0%) 92 86	84, 187, 251, 289	0
All	All	1400/1460 (95%)	-0.30	2 (0%) 92 86	83, 176, 246, 289	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	657	THR	2.7
1	B	290	ASP	2.3

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.