



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 07:23 PM GMT

PDB ID : 4S0F
Title : Crystal structure of the peptidase-containing ABC transporter PCAT1 E648Q mutant complexed with ATPgS in an occluded conformation
Authors : Lin, D.L.; Huang, S.; Chen, J.
Deposited on : 2014-12-30
Resolution : 5.51 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20026982

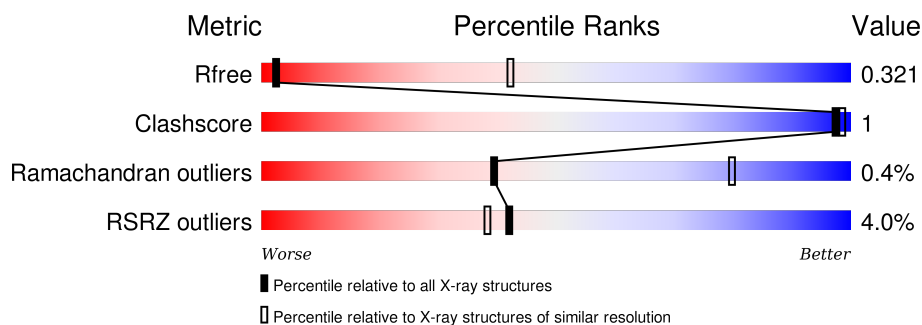
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 5.51 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}	91344	1017 (7.40-3.62)
Clashscore	102246	1020 (7.10-3.70)
Ramachandran outliers	100387	1017 (7.40-3.64)
RSRZ outliers	91569	1016 (7.40-3.62)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	<div> <div>3%</div> <div>76%</div> <div>23%</div> </div>
1	B	730	<div> <div>3%</div> <div>76%</div> <div>23%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	AGS	B	801	-	-	-	X

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5636 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.

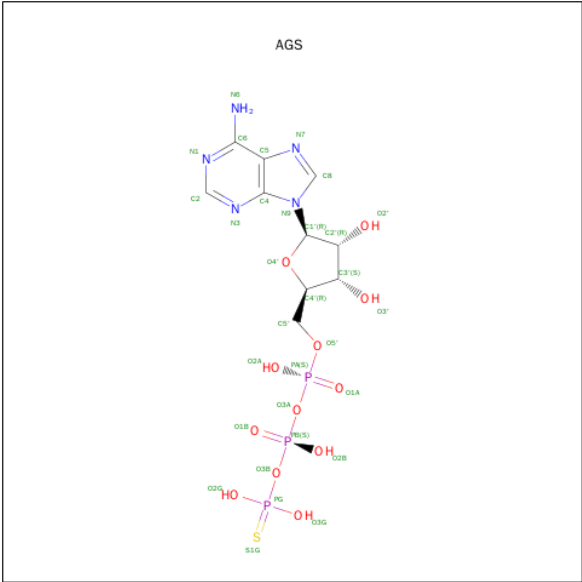
- Molecule 1 is a protein called ABC-type bacteriocin transporter.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	565	Total	C	N	O	0	0	0
			2787	1657	565	565			
1	B	565	Total	C	N	O	0	0	0
			2787	1657	565	565			

There are 8 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
A	648	GLN	GLU	ENGINEERED MUTATION	UNP A3DCU1
B	-2	SER	-	EXPRESSION TAG	UNP A3DCU1
B	-1	ASN	-	EXPRESSION TAG	UNP A3DCU1
B	0	ALA	-	EXPRESSION TAG	UNP A3DCU1
B	648	GLN	GLU	ENGINEERED MUTATION	UNP A3DCU1

- Molecule 2 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (three-letter code: AGS) (formula: C₁₀H₁₆N₅O₁₂P₃S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	0
			31	10	5	12	3	1		
2	B	1	Total	C	N	O	P	S	0	0
			31	10	5	12	3	1		

4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	230.00 Å 230.00 Å 89.40 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.98 – 5.51 41.66 – 5.51	Depositor EDS
% Data completeness (in resolution range)	80.9 (19.98-5.51) 81.4 (41.66-5.51)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.28 (at 5.38 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1839)	Depositor
R, R_{free}	0.300 , 0.314 0.311 , 0.321	Depositor DCC
R_{free} test set	307 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	277.2	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	1 of 6630 reflections (0.015%)	Xtriage
F_o, F_c correlation	0.78	EDS
Total number of atoms	5636	wwPDB-VP
Average B, all atoms (Å ²)	223.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.98% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: AGS

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	0.23	0/2786	0.42	0/3876
1	B	0.23	0/2786	0.43	0/3876
All	All	0.23	0/5572	0.42	0/7752

There are no bond length outliers.

There are no bond angle outliers.

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	2787	0	1271	5	0
1	B	2787	0	1271	4	0
2	A	31	0	12	2	0
2	B	31	0	12	3	0
All	All	5636	0	2566	10	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 1.

All (10) 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:522:GLY:HA2	2:B:801:AGS:H4'	1.47	0.95
2:B:801:AGS:H8	2:B:801:AGS:H5'2	1.57	0.85
2:A:801:AGS:O2G	2:A:801:AGS:O2B	2.13	0.67
1:A:522:GLY:HA2	2:A:801:AGS:H5'1	1.90	0.53
1:A:561:LYS:O	1:A:642:ASP:N	2.43	0.51
1:A:363:ALA:HB2	1:B:583:GLY:HA2	1.96	0.47
1:A:490:ASN:O	1:A:541:GLY:HA3	2.16	0.45
1:B:490:ASN:O	1:B:541:GLY:HA3	2.17	0.45
1:B:644:LEU:O	1:B:674:VAL:HA	2.17	0.43
1:A:624:SER:HA	2:B:801:AGS:H5'1	2.01	0.42

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	563/730 (77%)	535 (95%)	26 (5%)	2 (0%)	39	80
1	B	563/730 (77%)	535 (95%)	26 (5%)	2 (0%)	39	80
All	All	1126/1460 (77%)	1070 (95%)	52 (5%)	4 (0%)	39	80

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	474	ASP
1	A	478	PHE
1	A	524	GLY
1	B	524	GLY

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	AGS	A	801	-	26,33,33	0.71	1 (3%)	24,52,52	1.00	1 (4%)
2	AGS	B	801	-	26,33,33	0.72	1 (3%)	24,52,52	0.73	1 (4%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	AGS	A	801	-	-	0/17/38/38	0/3/3/3
2	AGS	B	801	-	-	0/17/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	AGS	PG-S1G	2.23	1.94	1.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	AGS	PG-S1G	2.49	1.95	1.90

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	AGS	PB-O3B-PG	-3.69	119.31	132.71
2	B	801	AGS	PB-O3B-PG	-3.28	120.80	132.71

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	AGS	2	0
2	B	801	AGS	3	0

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	565/730 (77%)	-0.25	21 (3%)	45 41	79, 201, 310, 383	0
1	B	565/730 (77%)	-0.12	24 (4%)	40 37	89, 235, 394, 486	0
All	All	1130/1460 (77%)	-0.18	45 (3%)	42 38	79, 214, 375, 486	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	568	ASP	13.0
1	B	566	SER	8.1
1	B	567	GLN	7.8
1	B	654	ASP	6.2
1	A	679	HIS	5.3
1	B	569	VAL	5.1
1	A	702	GLY	4.6
1	A	520	GLU	4.5
1	B	655	SER	4.3
1	B	695	ASP	4.3
1	A	519	GLY	4.3
1	A	701	SER	4.2
1	B	570	PHE	4.0
1	A	568	ASP	3.9
1	B	696	GLY	3.6
1	B	657	THR	3.6
1	A	651	SER	3.5
1	B	603	ASP	3.4
1	A	523	SER	3.2
1	B	481	SER	3.0
1	A	657	THR	2.9
1	B	602	HIS	2.9
1	B	653	LEU	2.8
1	B	601	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	656	ILE	2.8
1	A	700	GLU	2.7
1	A	618	GLU	2.7
1	A	634	ALA	2.6
1	A	567	GLN	2.6
1	B	605	ILE	2.6
1	B	600	ASN	2.5
1	B	660	HIS	2.5
1	A	650	THR	2.4
1	B	503	LYS	2.3
1	A	619	SER	2.3
1	A	600	ASN	2.3
1	B	604	PHE	2.2
1	A	599	ALA	2.2
1	A	680	ARG	2.2
1	A	638	LEU	2.2
1	A	595	ALA	2.2
1	B	565	VAL	2.1
1	B	595	ALA	2.1
1	B	590	ASP	2.0
1	A	678	ALA	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 carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	AGS	B	801	31/31	0.82	0.43	0.09	257,257,257,257	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	AGS	A	801	31/31	0.76	0.33	-0.51	248,248,248,248	0

6.5 Other polymers [i](#)

There are no such residues in this entry.