



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2018 – 05:30 am GMT

PDB ID : 3A1C  
Title : crystal structure of the P- and N-domains of CopA, a copper-transporting P-type ATPase, bound with AMPPCP-Mg  
Authors : Tsuda, T.; Toyoshima, C.  
Deposited on : 2009-03-31  
Resolution : 1.85 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.

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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  
Mogul : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : trunk30967  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30967

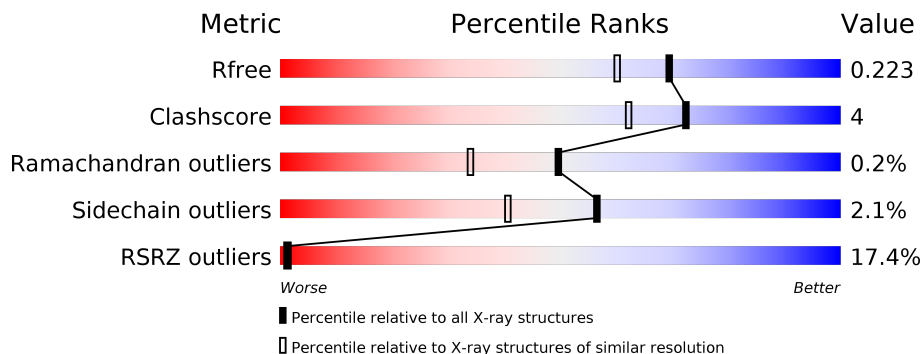
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.85 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))
$R_{free}$	111664	2111 (1.86-1.86)
Clashscore	122126	2258 (1.86-1.86)
Ramachandran outliers	120053	2234 (1.86-1.86)
Sidechain outliers	120020	2234 (1.86-1.86)
RSRZ outliers	108989	2075 (1.86-1.86)

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  $\geq 3$ , 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	287	<div> <div>9%</div> <div>83%</div> <div>9%</div> <div>7%</div> </div>
1	B	287	<div> <div>23%</div> <div>86%</div> <div>8%</div> <div>5%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4573 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.

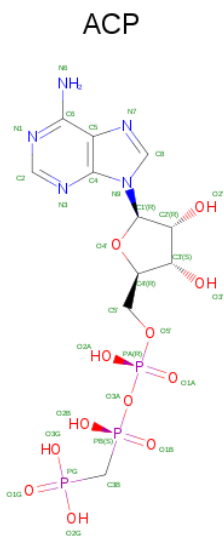
- Molecule 1 is a protein called Probable copper-exporting P-type ATPase A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	267	Total	C	N	O	S	0	0	0
			1995	1249	348	395	3			
1	B	273	Total	C	N	O	S	0	0	0
			2042	1279	356	403	4			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	387	MET	-	EXPRESSION TAG	UNP O29777
A	388	GLY	-	EXPRESSION TAG	UNP O29777
A	389	HIS	-	EXPRESSION TAG	UNP O29777
A	390	HIS	-	EXPRESSION TAG	UNP O29777
A	391	HIS	-	EXPRESSION TAG	UNP O29777
A	392	HIS	-	EXPRESSION TAG	UNP O29777
A	393	HIS	-	EXPRESSION TAG	UNP O29777
A	394	HIS	-	EXPRESSION TAG	UNP O29777
A	395	GLY	-	EXPRESSION TAG	UNP O29777
A	396	SER	-	EXPRESSION TAG	UNP O29777
A	397	ARG	-	EXPRESSION TAG	UNP O29777
B	387	MET	-	EXPRESSION TAG	UNP O29777
B	388	GLY	-	EXPRESSION TAG	UNP O29777
B	389	HIS	-	EXPRESSION TAG	UNP O29777
B	390	HIS	-	EXPRESSION TAG	UNP O29777
B	391	HIS	-	EXPRESSION TAG	UNP O29777
B	392	HIS	-	EXPRESSION TAG	UNP O29777
B	393	HIS	-	EXPRESSION TAG	UNP O29777
B	394	HIS	-	EXPRESSION TAG	UNP O29777
B	395	GLY	-	EXPRESSION TAG	UNP O29777
B	396	SER	-	EXPRESSION TAG	UNP O29777
B	397	ARG	-	EXPRESSION TAG	UNP O29777

- Molecule 2 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-letter code: ACP) (formula: C<sub>11</sub>H<sub>18</sub>N<sub>5</sub>O<sub>12</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 31	C 11	N 5	O 12	P 3	0	0
2	B	1	Total 31	C 11	N 5	O 12	P 3	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0

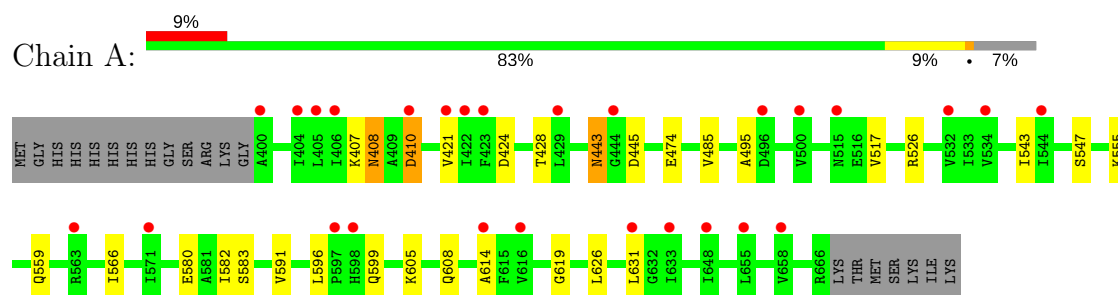
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	262	Total O 262 262	0	0
4	B	211	Total O 211 211	0	0

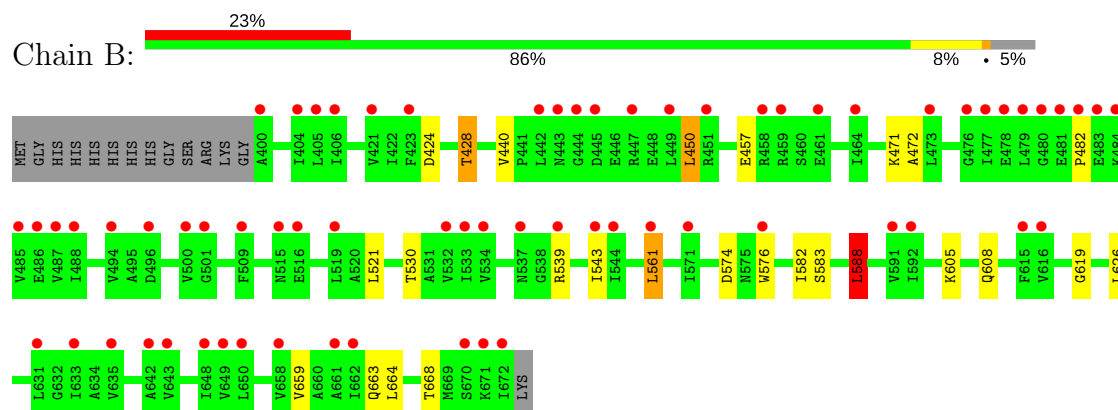
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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 copper-exporting P-type ATPase A



- Molecule 1: Probable copper-exporting P-type ATPase A



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.79Å 90.79Å 191.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.85 27.35 – 1.85	Depositor EDS
% Data completeness (in resolution range)	99.8 (20.00-1.85) 99.7 (27.35-1.85)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.00 (at 1.85Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.195 , 0.225 0.194 , 0.223	Depositor DCC
$R_{free}$ test set	3501 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.3	Xtriage
Anisotropy	0.110	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 55.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4573	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.84% 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](#)

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

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	0.55	0/2009	0.68	2/2714 (0.1%)
1	B	0.47	0/2056	0.60	1/2775 (0.0%)
All	All	0.51	0/4065	0.64	3/5489 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	526	ARG	NE-CZ-NH1	8.53	124.56	120.30
1	A	526	ARG	NE-CZ-NH2	-7.64	116.48	120.30
1	B	588	LEU	CB-CG-CD1	5.05	119.59	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	1995	0	2078	17	0
1	B	2042	0	2136	15	0
2	A	31	0	14	0	0
2	B	31	0	14	1	0
3	A	1	0	0	0	0
4	A	262	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	211	0	0	2	0
All	All	4573	0	4242	31	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.

The worst 5 of 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:664:LEU:O	1:B:668:THR:HG23	1.73	0.89
1:B:450:LEU:HD11	1:B:471:LYS:HG3	1.76	0.67
1:A:605:LYS:HA	1:A:608:GLN:HE21	1.62	0.64
1:B:605:LYS:HA	1:B:608:GLN:HE21	1.62	0.62
1:A:424:ASP:O	1:A:428:THR:HB	1.99	0.62

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	265/287 (92%)	262 (99%)	3 (1%)	0	100	100
1	B	271/287 (94%)	264 (97%)	6 (2%)	1 (0%)	36	21
All	All	536/574 (93%)	526 (98%)	9 (2%)	1 (0%)	49	34

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	482	PRO



### 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	211/228 (92%)	208 (99%)	3 (1%)	69	58
1	B	217/228 (95%)	211 (97%)	6 (3%)	47	29
All	All	428/456 (94%)	419 (98%)	9 (2%)	56	40

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	450	LEU
1	B	588	LEU
1	B	539	ARG
1	A	443	ASN
1	B	521	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	628	GLN
1	B	628	GLN
1	B	608	GLN
1	A	587	ASN
1	B	515	ASN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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	ACP	A	997	3	27,33,33	1.38	3 (11%)	30,52,52	1.88	7 (23%)
2	ACP	B	997	-	27,33,33	1.32	4 (14%)	30,52,52	1.74	4 (13%)

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	ACP	A	997	3	-	0/15/38/38	0/3/3/3
2	ACP	B	997	-	-	0/15/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	997	ACP	C2-N3	2.18	1.35	1.32
2	B	997	ACP	O4'-C1'	2.22	1.44	1.41
2	A	997	ACP	C2-N3	2.23	1.35	1.32
2	B	997	ACP	PB-O3A	2.98	1.61	1.58
2	A	997	ACP	PB-O3A	3.24	1.62	1.58

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	997	ACP	N3-C2-N1	-7.23	122.67	128.86
2	B	997	ACP	N3-C2-N1	-6.80	123.04	128.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	997	ACP	O1G-PG-C3B	-2.89	104.81	111.25
2	A	997	ACP	PA-O3A-PB	-2.61	123.93	132.42
2	B	997	ACP	C4-C5-N7	-2.48	107.02	109.41

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	997	ACP	1	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 [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	267/287 (93%)	0.63	27 (10%)	7 7	28, 39, 50, 56	0
1	B	273/287 (95%)	1.11	67 (24%)	0 0	31, 44, 67, 75	0
All	All	540/574 (94%)	0.87	94 (17%)	1 1	28, 40, 63, 75	0

The worst 5 of 94 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	672	ILE	10.0
1	B	480	GLY	7.4
1	B	481	GLU	7.0
1	B	643	VAL	6.6
1	B	670	SER	6.3

### 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 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. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	B-factors( $\text{\AA}^2$ )	Q<0.9
3	MG	A	998	1/1	0.76	0.13	74,74,74,74	0
2	ACP	B	997	31/31	0.94	0.12	44,49,52,54	0
2	ACP	A	997	31/31	0.94	0.10	34,38,54,56	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.