



## wwPDB EM Map/Model Validation Report

Apr 10, 2016 – 01:43 PM BST

PDB ID : 3J08  
EMDB ID: : EMD-5271  
Title : High resolution helical reconstruction of the bacterial p-type ATPase copper transporter CopA  
Authors : Wu, C.; Allen, G.S.; Cardozo, T.; Stokes, D.L.  
Deposited on : 2011-05-09  
Resolution : 10.00 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry. For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting. We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org). A user guide is available at <http://wwpdb.org/validation/2016/EMValidationReportHelp>

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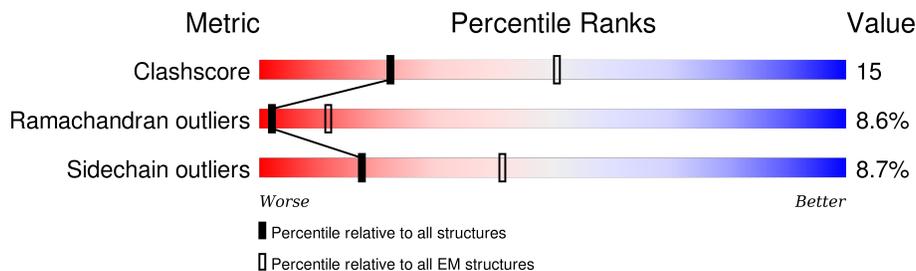
MolProbity : 4.02b-467  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk27241

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 10.00 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)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	645	70% 20% 7% .
1	B	645	69% 20% 7% .

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 9734 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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.

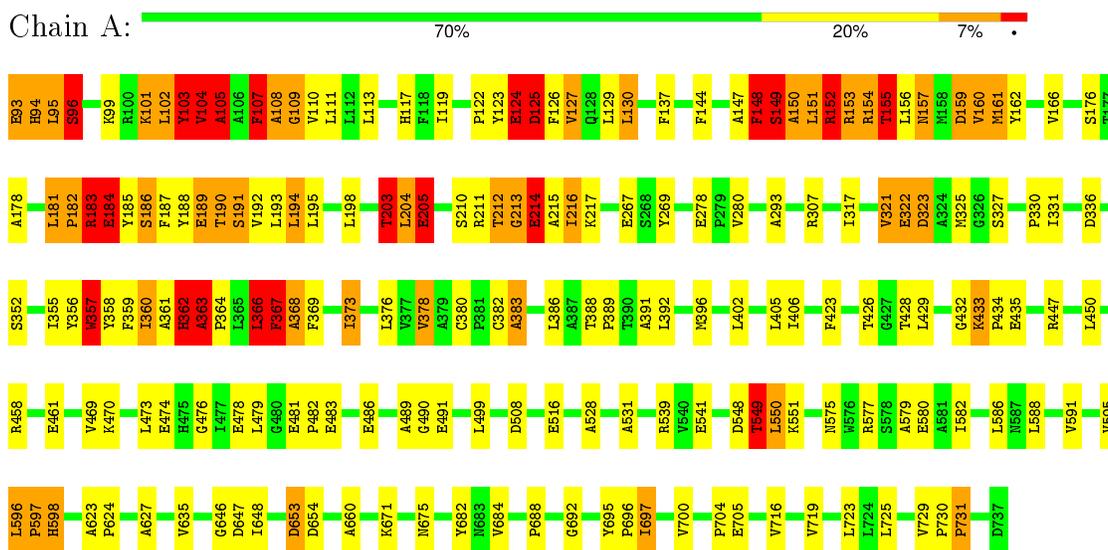
- Molecule 1 is a protein called copper-exporting P-type ATPase A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	645	Total 4867	C 3139	N 819	O 894	S 15	0	0
1	B	645	Total 4867	C 3139	N 819	O 894	S 15	0	0

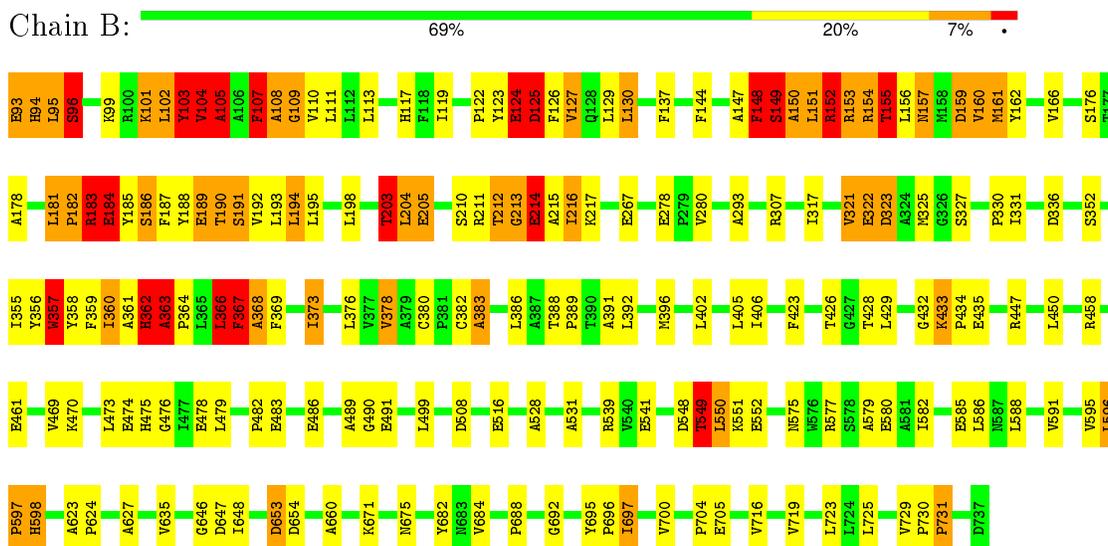
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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: copper-exporting P-type ATPase A



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



## 4 Experimental information

Property	Value	Source
Reconstruction method	HELICAL	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	two-fold phase residual	Depositor
CTF correction method	each tube-crystal	Depositor
Microscope	FEI/PHILIPS CM200FEG	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	Not provided	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	50000	Depositor
Image detector	Kodak SO-163	Depositor

## 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  >2	RMSZ	# Z  >2
1	A	0.76	0/4941	1.14	30/6700 (0.4%)
1	B	0.76	0/4941	1.14	31/6700 (0.5%)
All	All	0.76	0/9882	1.14	61/13400 (0.5%)

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	A	0	30
1	B	0	30
All	All	0	60

There are no bond length outliers.

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	B	96	SER	N-CA-CB	6.87	120.80	110.50
1	A	96	SER	N-CA-CB	6.85	120.77	110.50
1	A	155	THR	N-CA-CB	6.20	122.07	110.30
1	B	155	THR	N-CA-CB	6.18	122.05	110.30
1	B	149	SER	O-C-N	5.95	132.22	122.70

There are no chirality outliers.

5 of 60 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	102	LEU	Peptide
1	A	103	TYR	Peptide
1	A	107	PHE	Peptide
1	A	95	LEU	Peptide

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Mol	Chain	Res	Type	Group
1	A	96	SER	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	4867	0	5113	188	0
1	B	4867	0	5113	190	0
All	All	9734	0	10226	299	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 15.

The worst 5 of 299 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:280:VAL:HG11	1:B:474:GLU:CD	1.21	1.48
1:A:458:ARG:NH1	1:B:473:LEU:HG	1.18	1.43
1:A:479:LEU:N	1:B:478:GLU:HA	1.39	1.35
1:A:458:ARG:HH12	1:B:473:LEU:CG	1.39	1.34
1:A:280:VAL:CG1	1:B:474:GLU:CD	2.01	1.27

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 PDB entries followed by that with respect to all EM entries.

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	643/645 (100%)	518 (81%)	70 (11%)	55 (9%)	1	17
1	B	643/645 (100%)	518 (81%)	70 (11%)	55 (9%)	1	17
All	All	1286/1290 (100%)	1036 (81%)	140 (11%)	110 (9%)	2	17

5 of 110 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	96	SER
1	A	101	LYS
1	A	103	TYR
1	A	104	VAL
1	A	105	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 PDB entries followed by that with respect to all EM entries.

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	515/515 (100%)	470 (91%)	45 (9%)	13	45
1	B	515/515 (100%)	470 (91%)	45 (9%)	13	45
All	All	1030/1030 (100%)	940 (91%)	90 (9%)	17	45

5 of 90 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	682	TYR
1	B	137	PHE
1	B	588	LEU
1	A	697	ILE
1	B	94	HIS

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

### 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 carbohydrates 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.