

# Full wwPDB X-ray Structure Validation Report (i)

#### May 28, 2020 – 09:58 pm BST

PDB ID	:	2HX9
$\operatorname{Title}$	:	Crystal structure of Cu(I) Azurin with the metal-binding loop sequence "CTF-
		PGHSALM" replaced with "CSPHQGAGM", at pH4
Authors	:	Banfield, M.J.
Deposited on	:	2006-08-03
$\operatorname{Resolution}$	:	1.70  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 https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

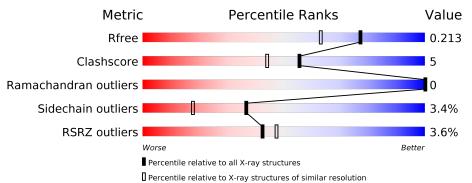
$\operatorname{MolProbity}$	:	4.02b-467
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
$\operatorname{Refmac}$	:	5.8.0158
$\operatorname{CCP4}$	:	$7.0.044 (\mathrm{Gargrove})$
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	$egin{array}{c} {f Whole archive}\ (\#{f Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
$R_{free}$	130704	4298 (1.70-1.70)
Clashscore	141614	4695(1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 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 <=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	А	127	3% 	8%	•••
1	В	127	90%	7%	•••



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2304 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Λ	124	Total	С	Ν	Ο	$\mathbf{S}$	0	4	0
		124	940	584	158	188	10	0	4	0
1	р	125	Total	С	Ν	Ο	S	0	2	0
	В	120	954	592	160	193	9		3	0

• Molecule 1 is a protein called Azurin.

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	THR	SEE REMARK 999	UNP P00282
A	113	SER	PHE	SEE REMARK 999	UNP P00282
A	115	HIS	GLY	SEE REMARK 999	UNP P00282
A	116	GLN	HIS	SEE REMARK 999	UNP P00282
A	117	GLY	SER	SEE REMARK 999	UNP P00282
A	119	GLY	LEU	SEE REMARK 999	UNP P00282
В	?	-	THR	SEE REMARK 999	UNP P00282
В	113	SER	PHE	SEE REMARK 999	UNP P00282
В	115	HIS	GLY	SEE REMARK 999	UNP P00282
В	116	GLN	HIS	SEE REMARK 999	UNP P00282
В	117	GLY	SER	SEE REMARK 999	UNP P00282
В	119	GLY	LEU	SEE REMARK 999	UNP P00282

There are 12 discrepancies between the modelled and reference sequences:

• Molecule 2 is COPPER (I) ION (three-letter code: CU1) (formula: Cu).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	В	1	Total Cu 1 1	0	0
2	А	1	Total Cu 1 1	0	0

• Molecule 3 is water.

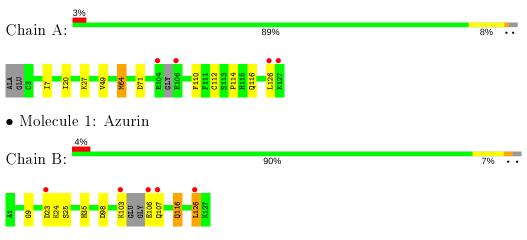


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	192	Total O 192 192	0	0
3	В	216	Total         O           216         216	0	0



## 3 Residue-property plots (i)

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: Azurin



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	38.42Å $65.33$ Å $97.24$ Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	33.00 - 1.70	Depositor
	27.12 - 1.70	EDS
% Data completeness	99.7(33.00-1.70)	Depositor
(in resolution range)	99.7(27.12-1.70)	EDS
R <sub>merge</sub>	0.05	Depositor
$R_{sym}$	0.05	Depositor
$< I/\sigma(I) > 1$	$6.02 (at 1.70 \text{\AA})$	Xtriage
Refinement program	REFMAC	Depositor
$R, R_{free}$	0.170 , $0.218$	Depositor
$\Pi, \Pi_{free}$	0.167 , $0.213$	DCC
$R_{free}$ test set	1378 reflections $(5.00\%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	17.9	Xtriage
Anisotropy	0.469	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.34 , $50.2$	EDS
L-test for twinning <sup>2</sup>	$ \langle L  \rangle = 0.48, \langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	2304	wwPDB-VP
Average B, all atoms $(Å^2)$	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.45% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: CU1

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		
	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.79	0/967	0.73	0/1303	
1	В	0.79	0/978	0.82	0/1318	
All	All	0.79	0/1945	0.78	0/2621	

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	А	940	0	903	7	0
1	В	954	0	924	12	0
2	А	1	0	0	0	0
2	В	1	0	0	0	0
3	А	192	0	0	1	0
3	В	216	0	0	4	0
All	All	2304	0	1827	19	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 5.

All (19) close contacts within the same asymmetric unit are listed below, sorted by their clash



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:24:LYS:HA	1:B:126:LEU:CD2	1.97	0.95
1:B:24:LYS:HA	1:B:126:LEU:HD22	1.60	0.84
1:B:24:LYS:HA	1:B:126:LEU:HD21	1.68	0.76
1:B:98[A]:ASP:OD1	3:B:403:HOH:O	2.02	0.75
1:A:71:ASP:HB3	3:A:253:HOH:O	1.88	0.73
1:B:24:LYS:CA	1:B:126:LEU:HD22	2.28	0.64
1:A:64[A]:MET:HE3	1:A:64[A]:MET:HA	1.83	0.61
1:B:107:GLN:HA	3:B:417:HOH:O	2.02	0.58
1:B:25:SER:HB2	3:B:332:HOH:O	2.02	0.57
1:B:23:ASP:HB2	3:B:341:HOH:O	2.08	0.52
1:A:112:CYS:SG	1:A:114:PRO:HD2	2.50	0.52
1:A:7:ILE:HD11	1:A:20:ILE:HD11	1.92	0.51
1:A:64[A]:MET:SD	1:A:114:PRO:HA	2.54	0.47
1:A:7:ILE:CD1	1:A:20:ILE:HD11	2.47	0.44
1:B:23:ASP:OD1	1:B:23:ASP:C	2.56	0.44
1:B:116:GLN:HE21	1:B:116:GLN:HB3	1.67	0.43
1:A:49:VAL:O	1:A:110:PHE:HA	2.19	0.42
1:B:106:GLU:HG3	1:B:107:GLN:N	2.36	0.41
1:B:9:GLY:O	1:B:35:HIS:HA	2.22	0.40

magnitude.

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	Perce	ntiles
1	А	124/127~(98%)	122 (98%)	2(2%)	0	100	100
1	В	124/127~(98%)	123~(99%)	1 (1%)	0	100	100
All	All	248/254~(98%)	245~(99%)	3~(1%)	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	А	106/108~(98%)	101~(95%)	5(5%)	26 10
1	В	108/108~(100%)	105~(97%)	3 (3%)	43 25
All	All	214/216~(99%)	206~(96%)	8 (4%)	37 15

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	27	LYS
1	А	64[A]	MET
1	А	64[B]	MET
1	А	116	GLN
1	А	126	LEU
1	В	103	LYS
1	В	116	GLN
1	В	126	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	12	GLN
1	А	116	GLN
1	В	116	GLN

#### 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)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

#### 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 $>2$	$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q<0.9
1	А	124/127~(97%)	0.12	4 (3%) 47 52	11, 16, 28, 34	1 (0%)
1	В	125/127~(98%)	0.07	5 (4%) 38 42	10, 14, 24, 32	0
All	All	249/254~(98%)	0.10	9 (3%) 42 47	10, 15, 27, 34	1 (0%)

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	107	GLN	3.5
1	В	103	LYS	3.2
1	А	106	GLU	3.1
1	А	126	LEU	2.7
1	В	126	LEU	2.6
1	А	104	GLU	2.5
1	В	23	ASP	2.2
1	В	106	GLU	2.1
1	A	127	LYS	2.1

### 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,



Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q<0.9
2	CU1	В	201	1/1	1.00	0.04	$15,\!15,\!15,\!15$	0
2	CU1	А	201	1/1	1.00	0.04	$17,\!17,\!17,\!17$	0

median,  $95^{th}$  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.

### 6.5 Other polymers (i)

There are no such residues in this entry.

