



# Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 03:34 am BST

PDB ID : 3QQX  
Title : Reduced Native Intermediate of the Multicopper Oxidase CueO  
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Deposited on : 2011-02-16  
Resolution : 1.50 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](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
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

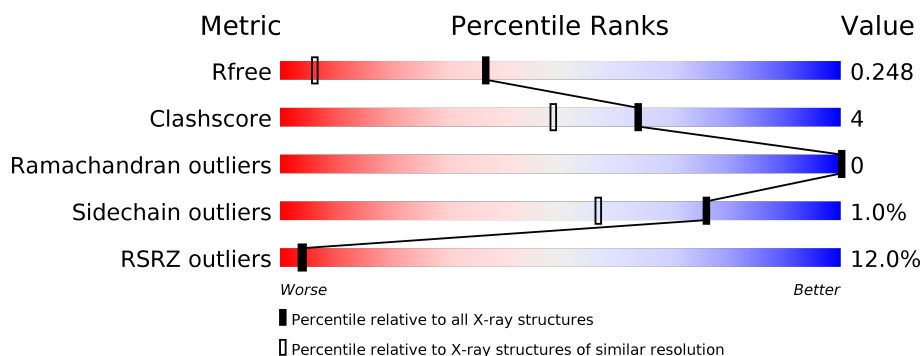
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.50 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))
$R_{free}$	130704	2936 (1.50-1.50)
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

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 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	505	

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
4	O	A	702	-	-	-	X

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 4341 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 Blue copper oxidase CueO.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	474	Total	C	N	O	S	0	15	0
			3752	2373	655	697	27			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	506	ASP	GLU	ENGINEERED MUTATION	UNP P36649
A	517	LEU	-	EXPRESSION TAG	UNP P36649
A	518	GLN	-	EXPRESSION TAG	UNP P36649
A	519	GLY	-	EXPRESSION TAG	UNP P36649
A	520	ASP	-	EXPRESSION TAG	UNP P36649
A	521	HIS	-	EXPRESSION TAG	UNP P36649
A	522	GLY	-	EXPRESSION TAG	UNP P36649
A	523	LEU	-	EXPRESSION TAG	UNP P36649
A	524	SER	-	EXPRESSION TAG	UNP P36649
A	525	ALA	-	EXPRESSION TAG	UNP P36649
A	526	TRP	-	EXPRESSION TAG	UNP P36649
A	527	SER	-	EXPRESSION TAG	UNP P36649
A	528	HIS	-	EXPRESSION TAG	UNP P36649
A	529	PRO	-	EXPRESSION TAG	UNP P36649
A	530	ASN	-	EXPRESSION TAG	UNP P36649
A	531	PHE	-	EXPRESSION TAG	UNP P36649
A	532	GLU	-	EXPRESSION TAG	UNP P36649
A	533	LYS	-	EXPRESSION TAG	UNP P36649

- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Cu	0	0
			3	3		

- Molecule 3 is COPPER (I) ION (three-letter code: CU1) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	5	Total	Cu	0	0
			5	5		

- Molecule 4 is OXYGEN ATOM (three-letter code: O) (formula: O).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	O	0	0
			2	2		

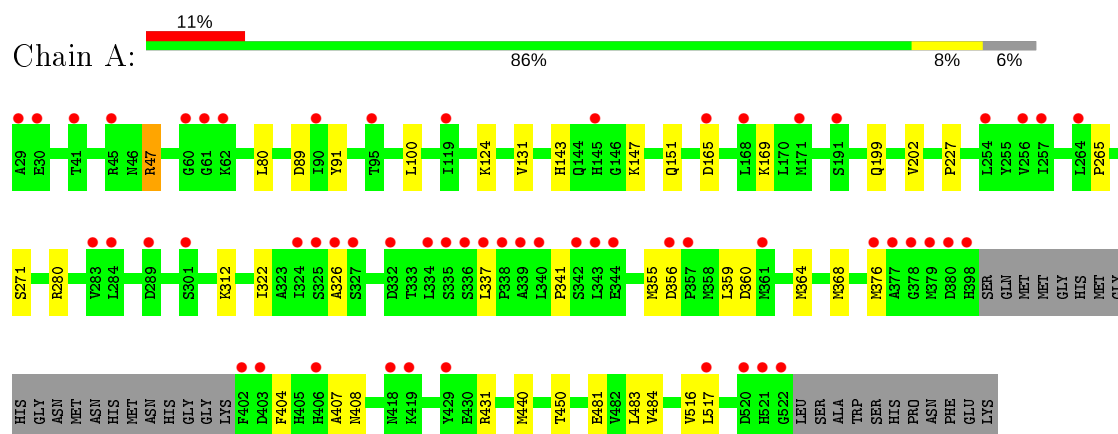
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	579	Total	O	0	1
			579	579		

### 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: Blue copper oxidase CueO



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	50.17Å 91.38Å 54.33Å 90.00° 102.22° 90.00°	Depositor
Resolution (Å)	24.35 – 1.50 24.35 – 1.50	Depositor EDS
% Data completeness (in resolution range)	96.4 (24.35-1.50) 96.4 (24.35-1.50)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.91 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.206 , 0.242 0.213 , 0.248	Depositor DCC
$R_{free}$ test set	3721 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	20.3	Xtriage
Anisotropy	0.172	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 46.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4341	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.68% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: O, CU, 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	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.66	0/3842	0.78	2/5217 (0.0%)

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	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	47	ARG	NE-CZ-NH2	-6.49	117.05	120.30
1	A	47	ARG	NE-CZ-NH1	6.23	123.41	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	322	ILE	Mainchain

### 5.2 Too-close contacts

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	3752	0	3692	31	0
2	A	3	0	0	0	0
3	A	5	0	0	0	0
4	A	2	0	0	0	0
5	A	579	0	0	10	0
All	All	4341	0	3692	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.

All (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:A:431:ARG:HD2	1:A:481:GLU:OE1	1.84	0.76
1:A:337:LEU:HD13	5:A:844:HOH:O	1.95	0.66
1:A:355:MET:HG2	1:A:408:ASN:ND2	2.10	0.65
1:A:431:ARG:NH1	1:A:481:GLU:OE1	2.21	0.65
1:A:517:LEU:HD12	5:A:900:HOH:O	1.99	0.63
1:A:202:VAL:HG23	5:A:551:HOH:O	1.98	0.61
1:A:364:MET:O	1:A:368:MET:HG2	2.03	0.58
1:A:516:VAL:O	1:A:517:LEU:HD23	2.06	0.56
1:A:227:PRO:HB2	1:A:326[A]:ALA:HB2	1.88	0.54
1:A:450:THR:HG21	1:A:484:VAL:CG2	2.40	0.51
1:A:80:LEU:HB3	1:A:131:VAL:HG21	1.93	0.51
1:A:376:MET:CE	5:A:1068:HOH:O	2.59	0.50
1:A:356:ASP:HB2	5:A:937:HOH:O	2.13	0.49
1:A:165:ASP:O	1:A:169:LYS:HE2	2.13	0.48
1:A:271[B]:SER:OG	5:A:786:HOH:O	2.20	0.48
1:A:376:MET:HE3	5:A:1068:HOH:O	2.14	0.47
1:A:359:LEU:HD22	1:A:407:ALA:HB3	1.96	0.47
1:A:202:VAL:HG22	1:A:404:PHE:CD1	2.50	0.46
1:A:341:PRO:HD2	1:A:483:LEU:CD2	2.45	0.46
1:A:450:THR:HG21	1:A:484:VAL:HG23	1.97	0.46
1:A:91:TYR:OH	1:A:124:LYS:HE3	2.16	0.45
1:A:376:MET:HE2	5:A:1004:HOH:O	2.16	0.44
1:A:431:ARG:CD	1:A:481:GLU:OE1	2.63	0.44
1:A:227:PRO:HB2	1:A:326[B]:ALA:HB2	2.01	0.43
1:A:100:LEU:HD23	1:A:100:LEU:C	2.40	0.43
1:A:440:MET:CE	5:A:1068:HOH:O	2.66	0.42
1:A:47:ARG:HD3	1:A:89:ASP:OD2	2.20	0.41
1:A:265:PRO:HD3	1:A:337:LEU:HD22	2.02	0.41
1:A:91:TYR:CZ	1:A:124:LYS:HE3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:147:LYS:O	1:A:151:GLN:HG3	2.22	0.40
1:A:312:LYS:NZ	5:A:975:HOH:O	2.54	0.40

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	484/505 (96%)	467 (96%)	17 (4%)	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	402/414 (97%)	398 (99%)	4 (1%)	76	57

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	143	HIS
1	A	199	GLN
1	A	280	ARG
1	A	360	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	314	HIS
1	A	408	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 10 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	380:ASP	C	398:HIS	N	32.71

## 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, 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	474/505 (93%)	0.98	57 (12%) 4 4	20, 27, 41, 59	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	29	ALA	13.4
1	A	380	ASP	9.8
1	A	378	GLY	7.7
1	A	379	MET	7.2
1	A	522	GLY	6.1
1	A	324[A]	ILE	5.9
1	A	520	ASP	5.5
1	A	339	ALA	5.1
1	A	517	LEU	5.1
1	A	327[A]	SER	4.9
1	A	61	GLY	4.7
1	A	344	GLU	4.7
1	A	418	ASN	4.5
1	A	171	MET	4.4
1	A	377	ALA	4.1
1	A	340	LEU	4.0
1	A	337	LEU	3.9
1	A	402	PHE	3.9
1	A	165	ASP	3.7
1	A	338	PRO	3.7
1	A	376	MET	3.7
1	A	521	HIS	3.7
1	A	30	GLU	3.6
1	A	403	ASP	3.4
1	A	301[A]	SER	3.4
1	A	398	HIS	3.3
1	A	336	SER	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	325[A]	SER	3.1
1	A	343	LEU	2.9
1	A	361[A]	MET	2.9
1	A	334	LEU	2.8
1	A	326[A]	ALA	2.7
1	A	256	VAL	2.7
1	A	168	LEU	2.7
1	A	406	HIS	2.7
1	A	342	SER	2.7
1	A	45	ARG	2.6
1	A	62	LYS	2.6
1	A	289	ASP	2.5
1	A	254	LEU	2.5
1	A	356	ASP	2.5
1	A	191	SER	2.4
1	A	429	TYR	2.3
1	A	357	PRO	2.2
1	A	264	LEU	2.2
1	A	60	GLY	2.2
1	A	90	ILE	2.2
1	A	257	ILE	2.2
1	A	419	LYS	2.2
1	A	284	LEU	2.1
1	A	95	THR	2.1
1	A	335[A]	SER	2.1
1	A	332	ASP	2.1
1	A	41	THR	2.0
1	A	145	HIS	2.0
1	A	119	ILE	2.0
1	A	283	VAL	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

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(Å <sup>2</sup> )	Q<0.9
4	O	A	702	1/1	0.65	0.46	34,34,34,34	0
4	O	A	701	1/1	0.86	0.35	31,31,31,31	0
3	CU1	A	607	1/1	0.90	0.16	74,74,74,74	0
3	CU1	A	606	1/1	0.99	0.12	47,47,47,47	0
2	CU	A	608	1/1	0.99	0.38	62,62,62,62	0
3	CU1	A	605	1/1	1.00	0.05	25,25,25,25	1
3	CU1	A	603	1/1	1.00	0.04	29,29,29,29	0
3	CU1	A	604	1/1	1.00	0.04	26,26,26,26	0
2	CU	A	602	1/1	1.00	0.04	28,28,28,28	0
2	CU	A	601	1/1	1.00	0.13	31,31,31,31	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.