

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

#### Mar 10, 2024 – 05:04 AM EDT

PDB ID : 4E9Y

Title : Multicopper Oxidase mgLAC (data4) Authors : Komori, H.; Miyazaki, K.; Higuchi, Y.

Deposited on : 2012-03-21

Resolution : 1.50 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
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

MolProbity : 4.02b-467

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.36

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove) roteins) : Engh & Huber (2001)

Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

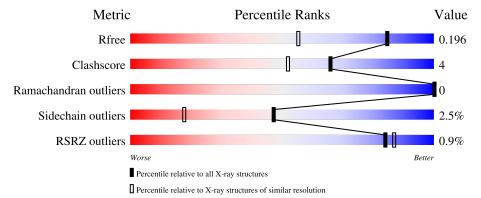
Validation Pipeline (wwPDB-VP) : 2.36

## 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 1.50 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{A})}) \end{array}$
$R_{free}$	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 of 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	A	339	83%	10%	• 6%
1	В	339	84%	9%	• 7%
1	С	339	80%	12%	• 7%



## 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 8400 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 Multicopper oxidase.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	۸	917	Total	С	N	О	S	0	7	0
1	A	317	2539	1633	425	469	12	0	(	
1	В	316	Total	С	N	О	S	0	E	0
1	Б	310	2519	1617	423	468	11	0	9	
1	С	316	Total	С	N	О	S	0	7	0
	310	2533	1631	424	467	11				

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1001	MET	-	expression tag	UNP COSTU6
A	1327	LYS	-	expression tag	UNP COSTU6
A	1328	LEU	-	expression tag	UNP COSTU6
A	1329	ALA	-	expression tag	UNP COSTU6
A	1330	ALA	-	expression tag	UNP COSTU6
A	1331	ALA	-	expression tag	UNP C0STU6
A	1332	LEU	_	expression tag	UNP COSTU6
A	1333	GLU	-	expression tag	UNP C0STU6
A	1334	HIS	-	expression tag	UNP COSTU6
A	1335	HIS	-	expression tag	UNP C0STU6
A	1336	HIS	-	expression tag	UNP COSTU6
A	1337	HIS	-	expression tag	UNP COSTU6
A	1338	HIS	-	expression tag	UNP COSTU6
A	1339	HIS	-	expression tag	UNP COSTU6
В	2001	MET	-	expression tag	UNP COSTU6
В	2327	LYS	-	expression tag	UNP COSTU6
В	2328	LEU	-	expression tag	UNP COSTU6
В	2329	ALA	-	expression tag	UNP COSTU6
В	2330	ALA	-	expression tag	UNP COSTU6
В	2331	ALA	-	expression tag	UNP COSTU6
В	2332	LEU	-	expression tag	UNP COSTU6
В	2333	GLU	-	expression tag	UNP C0STU6
В	2334	HIS	-	expression tag	UNP COSTU6

Continued on next page...



Continued from previous page...

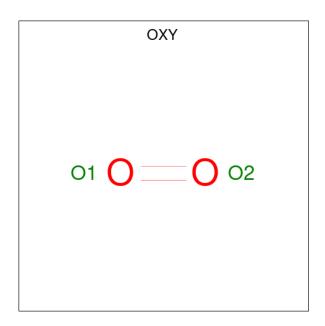
Chain	Residue	Modelled	Actual	Comment	Reference
В	2335	HIS	-	expression tag	UNP COSTU6
В	2336	HIS	-	expression tag	UNP COSTU6
В	2337	HIS	-	expression tag	UNP COSTU6
В	2338	HIS	-	expression tag	UNP C0STU6
В	2339	HIS	-	expression tag	UNP C0STU6
С	3001	MET	-	expression tag	UNP COSTU6
С	3327	LYS	-	expression tag	UNP C0STU6
С	3328	LEU	-	expression tag	UNP COSTU6
С	3329	ALA	-	expression tag	UNP COSTU6
С	3330	ALA	-	expression tag	UNP COSTU6
С	3331	ALA	-	expression tag	UNP COSTU6
С	3332	LEU	-	expression tag	UNP C0STU6
С	3333	GLU	-	expression tag	UNP COSTU6
С	3334	HIS	-	expression tag	UNP C0STU6
С	3335	HIS	-	expression tag	UNP COSTU6
С	3336	HIS	-	expression tag	UNP COSTU6
С	3337	HIS	-	expression tag	UNP COSTU6
С	3338	HIS	-	expression tag	UNP COSTU6
С	3339	HIS	-	expression tag	UNP COSTU6

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	4	Total Cu 4 4	0	0
2	В	4	Total Cu 4 4	0	0
2	С	4	Total Cu 4 4	0	0

 $\bullet$  Molecule 3 is OXYGEN MOLECULE (three-letter code: OXY) (formula: O2).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O 2 2	0	0
3	В	1	Total O 2 2	0	0
3	С	1	Total O 2 2	0	0

• Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Cl 1 1	0	0

• Molecule 5 is water.

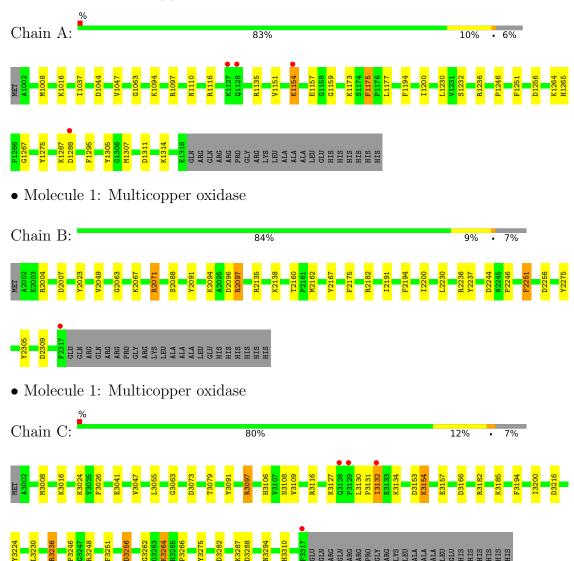
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	250	Total O 251 251	0	1
5	В	280	Total O 280 280	0	0
5	С	259	Total O 259 259	0	0



## 3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Multicopper oxidase





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	74.74Å 101.17Å 124.00Å	Donositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 - 1.50	Depositor
Resolution (A)	16.32 - 1.50	EDS
% Data completeness	94.5 (10.00-1.50)	Depositor
(in resolution range)	99.3 (16.32-1.50)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.07 (at 1.50Å)	Xtriage
Refinement program	SHELXL-97	Depositor
D D.	0.172 , (Not available)	Depositor
$R, R_{free}$	0.161 , 0.196	DCC
$R_{free}$ test set	7475 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	10.9	Xtriage
Anisotropy	0.444	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.38, 62.9	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.50, < L^2>=0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	8400	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.47% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  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: OXY, CL, CU

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	0.49	0/2641	1.16	6/3594~(0.2%)
1	В	0.51	0/2615	1.20	$15/3561 \ (0.4\%)$
1	С	0.51	0/2637	1.20	$17/3590 \ (0.5\%)$
All	All	0.50	0/7893	1.18	38/10745 (0.4%)

There are no bond length outliers.

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	1135	ARG	NE-CZ-NH2	-9.03	115.78	120.30
1	В	2167	TYR	CB-CG-CD1	-8.05	116.17	121.00
1	В	2071	ARG	NE-CZ-NH1	-8.01	116.30	120.30
1	A	1116	ARG	NE-CZ-NH1	7.84	124.22	120.30
1	A	1305	TYR	CB-CG-CD1	-6.83	116.90	121.00

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	$\mathbf{H}(\mathbf{model})$	H(added)	Clashes	Symm-Clashes
1	A	2539	0	2439	24	0
1	В	2519	0	2404	14	0
1	С	2533	0	2429	25	0

Continued on next page...



Continued	trom	mmoninonic	maaa
COHABABACA		DIEUIUU	DUIUE
0 0 1000100000			

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	4	0	0	0	0
2	В	4	0	0	0	0
2	С	4	0	0	0	0
3	A	2	0	0	0	0
3	В	2	0	0	0	0
3	С	2	0	0	0	0
4	A	1	0	0	0	0
5	A	251	0	0	2	0
5	В	280	0	0	1	0
5	С	259	0	0	0	0
All	All	8400	0	7272	60	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 60 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{array}{c} { m Clash} \\ { m overlap} \ ({ m \AA}) \end{array}$
1:A:1287:LYS:HE3	1:A:1288:ASP:OD2	1.86	0.75
1:C:3132:ILE:H	1:C:3132:ILE:HD13	1.52	0.73
1:A:1311:ASP:HA	1:A:1314:LYS:HD2	1.75	0.68
1:C:3154:LYS:HE2	1:C:3157:GLU:OE1	1.93	0.68
1:A:1151:VAL:HA	1:A:1154:LYS:HD3	1.79	0.64

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	entiles
1	A	322/339~(95%)	316 (98%)	6 (2%)	0	100	100
1	В	319/339 (94%)	312 (98%)	7 (2%)	0	100	100

Continued on next page...



Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
1	С	321/339 (95%)	314 (98%)	7 (2%)	0	100	100
All	All	962/1017 (95%)	942 (98%)	20 (2%)	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	$276/287 \ (96\%)$	270 (98%)	6 (2%)	52 22		
1	В	273/287 (95%)	267 (98%)	6 (2%)	52 22		
1	С	275/287 (96%)	267 (97%)	8 (3%)	42 13		
All	All	824/861 (96%)	804 (98%)	20 (2%)	47 19		

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	С	3154	LYS
1	С	3256	ASP
1	С	3266	PRO
1	С	3264	LYS
1	В	2023	TYR

Sometimes 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 monosaccharides in this entry.

### 5.6 Ligand geometry (i)

Of 16 ligands modelled in this entry, 13 are monoatomic - leaving 3 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).

Mal	Mol Type	Chain	Res	Res Link	Bond lengths		Bond angles		
MIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	$\mid \text{RMSZ} \mid \# Z  > 2$
3	OXY	С	3403	2	1,1,1	0.16	0	-	
3	OXY	В	2403	2	1,1,1	0.15	0	-	
3	OXY	A	1405	2	1,1,1	0.16	0	1	

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,  $95^{th}$  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>	#RSRZ>2		$\mathrm{OWAB}(\mathrm{\AA}^2)$	Q < 0.9
1	A	317/339 (93%)	-0.29	4 (1%) 77	81	6, 12, 27, 47	0
1	В	316/339 (93%)	-0.36	1 (0%) 94	95	6, 12, 25, 45	0
1	С	316/339 (93%)	-0.26	4 (1%) 77	81	6, 11, 29, 67	0
All	All	949/1017 (93%)	-0.30	9 (0%) 84	87	6, 12, 27, 67	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ	
1	С	3132	ILE	3.2	
1	С	3128	GLN	3.0	
1	С	3317	PHE	2.8	
1	С	3129	PRO	2.7	
1	A	1128	GLN	2.6	

### 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 monosaccharides 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,  $95^{th}$  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.



Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathring{\mathbf{A}}^2)$	Q<0.9
3	OXY	A	1405	2/2	0.94	0.17	10,10,10,11	2
3	OXY	В	2403	2/2	0.97	0.15	10,10,10,17	2
3	OXY	С	3403	2/2	0.97	0.10	9,9,9,12	2
2	CU	A	1404	1/1	0.99	0.04	17,17,17,17	1
2	CU	В	2401	1/1	0.99	0.04	13,13,13,13	1
2	CU	В	2402	1/1	0.99	0.08	17,17,17,17	1
2	CU	В	2404	1/1	0.99	0.05	10,10,10,10	0
2	CU	В	2405	1/1	0.99	0.03	10,10,10,10	1
2	CU	С	3404	1/1	0.99	0.04	11,11,11,11	0
2	CU	A	1401	1/1	0.99	0.04	12,12,12,12	0
2	CU	A	1402	1/1	0.99	0.03	11,11,11,11	1
2	CU	A	1403	1/1	0.99	0.03	13,13,13,13	1
4	CL	A	1406	1/1	0.99	0.04	13,13,13,13	0
2	CU	С	3401	1/1	1.00	0.04	12,12,12,12	1
2	CU	С	3405	1/1	1.00	0.03	11,11,11,11	1
2	CU	С	3402	1/1	1.00	0.05	14,14,14,14	1

# 6.5 Other polymers (i)

There are no such residues in this entry.

