



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 10:13 AM UTC

PDB ID : 4E9X / pdb\_00004e9x  
Title : Multicopper Oxidase mgLAC (data3)  
Authors : Komori, H.; Miyazaki, K.; Higuchi, Y.  
Deposited on : 2012-03-21  
Resolution : 1.14 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

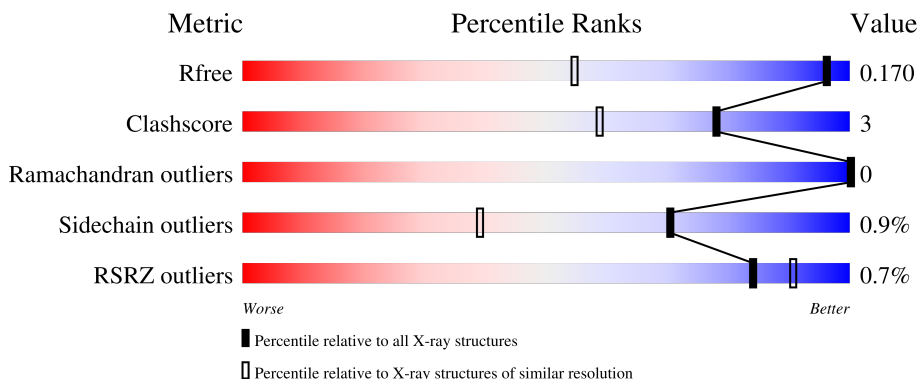
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.14 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))
$R_{free}$	180053	1380 (1.16-1.12)
Clashscore	190562	1393 (1.16-1.12)
Ramachandran outliers	187476	1369 (1.16-1.12)
Sidechain outliers	187428	1369 (1.16-1.12)
RSRZ outliers	180081	1379 (1.16-1.12)

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  $\geq 3$ , 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	339	84% 9% • 6%
1	B	339	87% 6% 7%
1	C	339	83% 8% •• 7%

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 8478 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
			Total	C	N	O	S			
1	A	317	Total 2539	C 1633	N 425	O 469	S 12	0	7	0
1	B	316	Total 2519	C 1617	N 423	O 468	S 11	0	5	0
1	C	316	Total 2533	C 1631	N 424	O 467	S 11	0	7	0

There are 42 discrepancies between the modelled and reference sequences:

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

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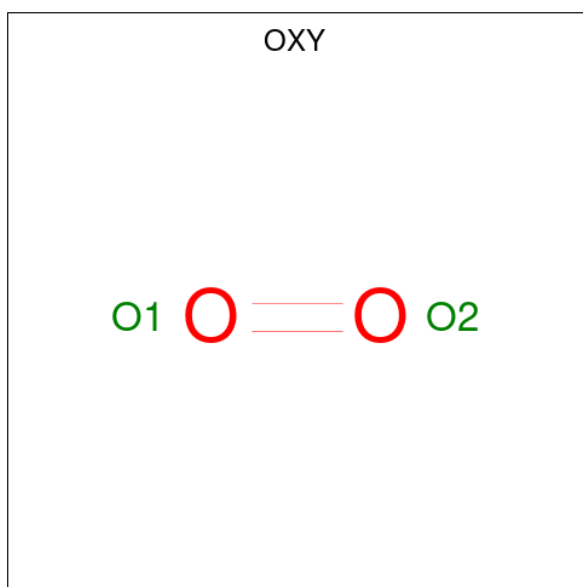
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Chain	Residue	Modelled	Actual	Comment	Reference
B	2335	HIS	-	expression tag	UNP C0STU6
B	2336	HIS	-	expression tag	UNP C0STU6
B	2337	HIS	-	expression tag	UNP C0STU6
B	2338	HIS	-	expression tag	UNP C0STU6
B	2339	HIS	-	expression tag	UNP C0STU6
C	3001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

- Molecule 2 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	4	Total Cu 4 4	0	0
2	B	4	Total Cu 4 4	0	0
2	C	4	Total Cu 4 4	0	0

- Molecule 3 is OXYGEN MOLECULE (CCD ID: OXY) (formula: O<sub>2</sub>).



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

- Molecule 4 is CHLORIDE ION (CCD ID: 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	271	Total O 272 272	0	1
5	B	308	Total O 308 308	0	0
5	C	288	Total O 288 288	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	74.74Å 101.16Å 123.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.14 10.00 – 1.14	Depositor EDS
% Data completeness (in resolution range)	94.2 (10.00-1.14) 99.0 (10.00-1.14)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.62 (at 1.14Å)	Xtrriage
Refinement program	SHELXL-97	Depositor
R, $R_{free}$	0.141 , (Not available) 0.139 , 0.170	Depositor DCC
$R_{free}$ test set	16984 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	9.4	Xtrriage
Anisotropy	0.464	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.44 , 59.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	8478	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	14.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.44% 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: 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	0.91	1/2641 (0.0%)	1.34	16/3594 (0.4%)
1	B	0.91	1/2615 (0.0%)	1.28	12/3561 (0.3%)
1	C	0.93	1/2637 (0.0%)	1.33	18/3590 (0.5%)
All	All	0.92	3/7893 (0.0%)	1.32	46/10745 (0.4%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	2062	HIS	CD2-NE2	-5.53	1.31	1.37
1	C	3062	HIS	ND1-CE1	5.50	1.38	1.32
1	A	1062	HIS	CD2-NE2	-5.27	1.32	1.37

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1238	ASP	CA-CB-CG	7.36	119.96	112.60
1	B	2071	ARG	NE-CZ-NH1	-7.01	114.49	121.50
1	A	1115	VAL	CA-C-O	-7.00	114.00	119.46
1	A	1128	GLN	CA-C-O	6.77	129.27	120.74
1	C	3287	LYS	CA-C-N	-6.72	112.50	123.05

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	2539	0	2439	14	0
1	B	2519	0	2404	12	0
1	C	2533	0	2429	18	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
2	C	4	0	0	0	0
3	A	2	0	0	0	0
3	B	4	0	0	0	0
4	A	1	0	0	0	0
5	A	272	0	0	1	0
5	B	308	0	0	1	0
5	C	288	0	0	0	0
All	All	8478	0	7272	41	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 3.

The worst 5 of 41 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:1008[A]:MET:HE2	1:A:1307:MET:HE1	1.64	0.79
1:C:3261:ALA:O	1:C:3264:LYS:HE2	1.88	0.72
1:C:3132:ILE:H	1:C:3132:ILE:HD13	1.64	0.63
1:C:3024:LYS:HE2	1:C:3153:ASP:O	2.00	0.62
1:C:3154:LYS:HE2	1:C:3157:GLU:OE1	2.06	0.56

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	322/339 (95%)	316 (98%)	6 (2%)	0	100	100
1	B	319/339 (94%)	313 (98%)	6 (2%)	0	100	100
1	C	321/339 (95%)	314 (98%)	7 (2%)	0	100	100
All	All	962/1017 (95%)	943 (98%)	19 (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%)	272 (99%)	4 (1%)	59	21
1	B	273/287 (95%)	273 (100%)	0	100	100
1	C	275/287 (96%)	272 (99%)	3 (1%)	65	31
All	All	824/861 (96%)	817 (99%)	7 (1%)	70	42

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1264	LYS
1	C	3132	ILE
1	C	3264	LYS
1	C	3154	LYS
1	A	1194	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1048	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 oligosaccharides 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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	OXY	B	2406	2	1,1,1	0.22	0	-		
3	OXY	B	2403	2	1,1,1	0.10	0	-		
3	OXY	A	1405	2	1,1,1	0.23	0	-		

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	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	317/339 (93%)	-0.50	1 (0%) 90 94	5, 12, 23, 42	7 (2%)
1	B	316/339 (93%)	-0.55	1 (0%) 90 94	5, 11, 21, 33	5 (1%)
1	C	316/339 (93%)	-0.50	5 (1%) 70 78	5, 11, 25, 51	7 (2%)
All	All	949/1017 (93%)	-0.52	7 (0%) 84 91	5, 11, 23, 51	19 (2%)

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	3129	PRO	3.7
1	C	3132	ILE	3.6
1	C	3128	GLN	2.7
1	C	3153	ASP	2.4
1	C	3130	LEU	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 oligosaccharides 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	OXY	B	2403	2/2	0.89	0.11	11,11,11,15	2
3	OXY	A	1405	2/2	0.93	0.08	10,10,10,13	2
3	OXY	B	2406	2/2	0.95	0.07	9,9,9,13	2
4	CL	A	1406	1/1	0.99	0.04	11,11,11,11	0
2	CU	B	2401	1/1	1.00	0.02	13,13,13,13	1
2	CU	B	2402	1/1	1.00	0.08	14,14,14,14	1
2	CU	B	2404	1/1	1.00	0.01	9,9,9,9	0
2	CU	B	2405	1/1	1.00	0.03	9,9,9,9	1
2	CU	C	3401	1/1	1.00	0.01	12,12,12,12	1
2	CU	C	3402	1/1	1.00	0.05	11,11,11,11	1
2	CU	C	3403	1/1	1.00	0.01	11,11,11,11	0
2	CU	C	3404	1/1	1.00	0.02	9,9,9,9	1
2	CU	A	1401	1/1	1.00	0.01	12,12,12,12	0
2	CU	A	1402	1/1	1.00	0.02	10,10,10,10	1
2	CU	A	1403	1/1	1.00	0.04	12,12,12,12	1
2	CU	A	1404	1/1	1.00	0.06	13,13,13,13	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.