



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 10:15 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 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 ⓘ 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 ⓘ](#)) 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

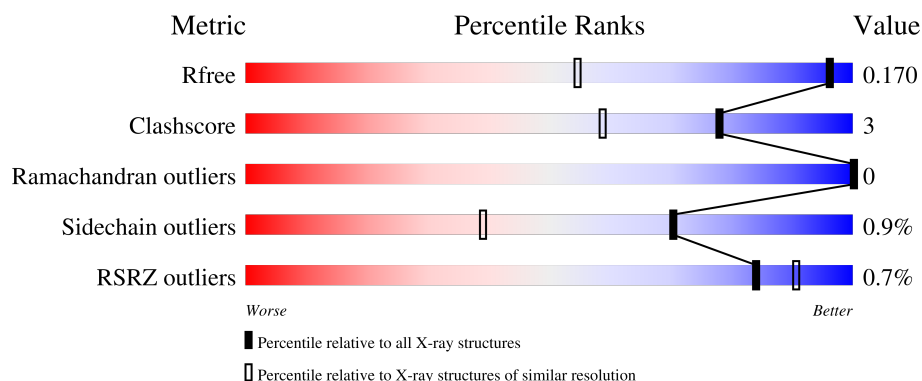
1 Overall quality at a glance

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 ≥ 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	
1	B	339	
1	C	339	

2 Entry composition

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
1	A	317	Total	C	N	O	S	0	7	0
			2539	1633	425	469	12			
1	B	316	Total	C	N	O	S	0	5	0
			2519	1617	423	468	11			
1	C	316	Total	C	N	O	S	0	7	0
			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 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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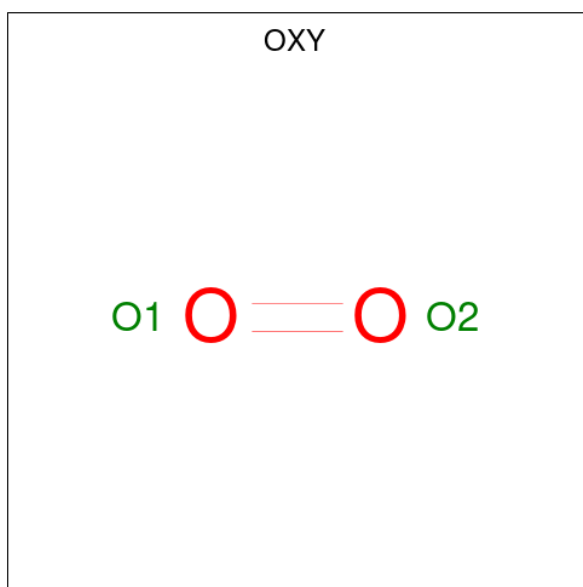
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Chain	Residue	Modelled	Actual	Comment	Reference
B	2335	HIS	-	expression tag	UNP C0STU6
B	2336	HIS	-	expression tag	UNP C0STU6
B	2337	HIS	-	expression tag	UNP C0STU6
B	2338	HIS	-	expression tag	UNP C0STU6
B	2339	HIS	-	expression tag	UNP C0STU6
C	3001	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: O₂).



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.

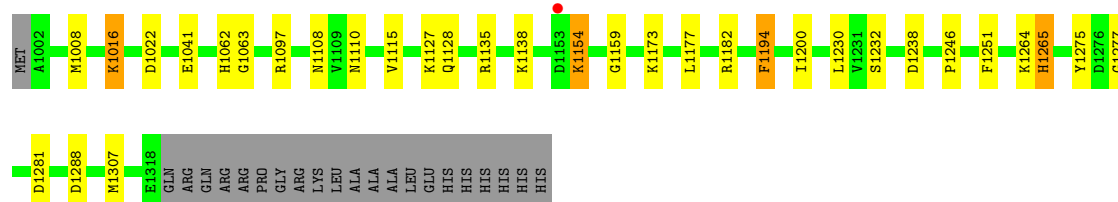
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	271	Total O 272 272	0	1
5	B	308	Total O 308 308	0	0
5	C	288	Total O 288 288	0	0

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.

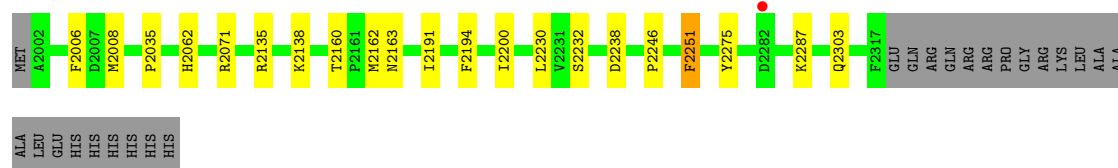
- Molecule 1: Multicopper oxidase

Chain A: 



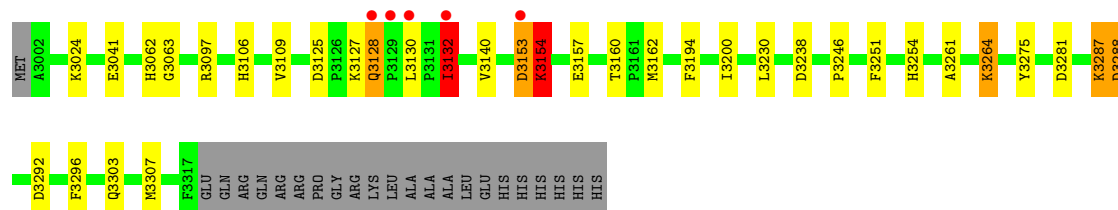
- Molecule 1: Multicopper oxidase

Chain B: 



- Molecule 1: Multicopper oxidase

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	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
$\langle I/\sigma(I) \rangle$ ¹	2.62 (at 1.14Å)	Xtriage
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 ²)	9.4	Xtriage
Anisotropy	0.464	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 59.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	8478	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtriage'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.*

¹Intensities estimated from amplitudes.

²Theoretical 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: 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

All (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
1	C	3287	LYS	C-N-CA	-6.72	112.50	123.05
1	B	2071	ARG	NE-CZ-NH2	6.64	125.18	119.20
1	C	3238	ASP	CA-CB-CG	6.46	119.06	112.60
1	C	3153	ASP	CA-CB-CG	-6.44	106.16	112.60
1	A	1277	GLY	CA-C-N	-6.43	117.96	122.59
1	A	1277	GLY	C-N-CA	-6.43	117.96	122.59
1	C	3125	ASP	CA-CB-CG	6.37	118.97	112.60
1	A	1022	ASP	CA-CB-CG	-6.29	106.31	112.60
1	C	3288	ASP	N-CA-C	6.28	120.52	112.86
1	B	2194	PHE	CA-CB-CG	6.15	119.95	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	3251	PHE	CA-CB-CG	6.11	119.91	113.80
1	C	3307	MET	CG-SD-CE	-6.11	87.47	100.90
1	A	1135	ARG	NE-CZ-NH2	-6.10	113.71	119.20
1	C	3303	GLN	OE1-CD-NE2	-5.99	116.61	122.60
1	A	1265	HIS	CA-CB-CG	5.82	119.62	113.80
1	C	3128	GLN	CA-C-O	5.82	128.07	120.74
1	B	2287	LYS	CA-C-N	-5.79	113.92	122.83
1	B	2287	LYS	C-N-CA	-5.79	113.92	122.83
1	B	2135	ARG	CD-NE-CZ	5.60	132.24	124.40
1	A	1281	ASP	CA-CB-CG	-5.58	107.02	112.60
1	B	2251	PHE	CA-CB-CG	5.57	119.37	113.80
1	B	2303	GLN	CA-C-N	-5.41	113.89	122.65
1	B	2303	GLN	C-N-CA	-5.41	113.89	122.65
1	B	2163	ASN	OD1-CG-ND2	5.34	127.94	122.60
1	C	3254	HIS	ND1-CE1-NE2	5.33	113.73	108.40
1	A	1108	ASN	OD1-CG-ND2	-5.31	117.29	122.60
1	C	3132	ILE	CA-C-N	-5.30	112.25	120.31
1	C	3132	ILE	C-N-CA	-5.30	112.25	120.31
1	A	1154	LYS	CA-C-O	5.23	126.75	120.27
1	A	1194	PHE	CA-CB-CG	5.22	119.02	113.80
1	B	2006	PHE	CA-CB-CG	-5.19	108.61	113.80
1	A	1108	ASN	CB-CG-ND2	5.18	124.17	116.40
1	A	1251	PHE	CA-CB-CG	5.17	118.97	113.80
1	A	1135	ARG	NH1-CZ-NH2	5.17	126.02	119.30
1	B	2238	ASP	CA-CB-CG	5.16	117.76	112.60
1	C	3292	ASP	CA-C-O	-5.11	115.08	120.09
1	C	3303	GLN	CB-CG-CD	5.11	121.28	112.60
1	C	3154	LYS	CB-CA-C	-5.10	103.31	111.17
1	C	3194	PHE	CA-CB-CG	5.07	118.87	113.80
1	C	3281	ASP	CA-CB-CG	-5.03	107.57	112.60
1	A	1288	ASP	CA-C-O	5.03	126.25	120.32

There are no chirality outliers.

There are no planarity outliers.

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	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.

All (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
1:C:3128:GLN:O	1:C:3128:GLN:HG2	2.07	0.53
1:B:2138:LYS:HD3	5:B:2755:HOH:O	2.07	0.52
1:A:1232[A]:SER:OG	1:B:2230:LEU:HD13	2.09	0.52
1:B:2246:PRO:HA	1:B:2275:TYR:CG	2.44	0.52
1:C:3200[A]:ILE:HG22	1:C:3230:LEU:HD11	1.91	0.52
1:B:2162:MET:HE2	1:B:2162:MET:H	1.75	0.52
1:A:1200[A]:ILE:HG22	1:A:1230:LEU:HD11	1.91	0.51
1:A:1200[A]:ILE:CG2	1:A:1230:LEU:HD11	2.41	0.51
1:B:2160:THR:OG1	1:B:2162:MET:HE2	2.11	0.51
1:A:1246:PRO:HA	1:A:1275:TYR:CG	2.46	0.51
1:C:3130:LEU:CD1	1:C:3132:ILE:HD11	2.42	0.50
1:C:3200[A]:ILE:CG2	1:C:3230:LEU:HD11	2.42	0.49
1:C:3041:GLU:O	1:C:3127:LYS:HE3	2.13	0.49
1:C:3063:GLY:O	1:C:3097:ARG:HG2	2.12	0.49
1:C:3160:THR:OG1	1:C:3162:MET:HE2	2.13	0.48
1:B:2200[A]:ILE:HG22	1:B:2230:LEU:HD11	1.96	0.48
1:A:1173[B]:LYS:HD3	1:A:1177:LEU:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3106:HIS:HA	1:C:3109:VAL:HG12	1.94	0.48
1:C:3154:LYS:HE2	1:C:3157:GLU:CD	2.39	0.47
1:A:1008[A]:MET:HE2	1:A:1307:MET:CE	2.42	0.46
1:A:1016:LYS:HE3	5:A:5179:HOH:O	2.15	0.46
1:B:2200[A]:ILE:CG2	1:B:2230:LEU:HD11	2.46	0.46
1:C:3246:PRO:HA	1:C:3275:TYR:CG	2.53	0.43
1:B:2008[A]:MET:HE2	1:B:2035:PRO:HG2	2.01	0.43
1:A:1041:GLU:O	1:A:1127:LYS:HE3	2.19	0.43
1:B:2232[A]:SER:OG	1:C:3230:LEU:HD13	2.19	0.42
1:B:2191:ILE:HD13	1:B:2251:PHE:CE1	2.55	0.42
1:A:1138:LYS:HE3	1:A:1182:ARG:O	2.20	0.42
1:A:1063:GLY:O	1:A:1097:ARG:HG2	2.20	0.42
1:A:1265:HIS:CE1	1:C:3109:VAL:HG22	2.55	0.41
1:A:1110:ASN:HB2	1:A:1159:GLY:O	2.21	0.41
1:B:2246:PRO:HA	1:B:2275:TYR:CD2	2.56	0.41
1:A:1008[A]:MET:HE2	1:A:1008[A]:MET:HB2	1.86	0.41
1:C:3287:LYS:O	1:C:3288:ASP:HB2	2.21	0.40
1:B:2138:LYS:HB2	1:B:2138:LYS:HE2	1.68	0.40
1:C:3140:VAL:HG13	1:C:3296:PHE:HB3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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 ⓘ

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

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1016	LYS
1	A	1154	LYS
1	A	1194	PHE
1	A	1264	LYS
1	C	3132	ILE
1	C	3154	LYS
1	C	3264	LYS

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 ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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, 95th 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 ²)	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%)

All (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
1	A	1153	ASP	2.0
1	B	2282	ASP	2.0

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, 95th 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.