



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:19 PM GMT

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 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  
<http://wwpdb.org/validation/2016/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  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

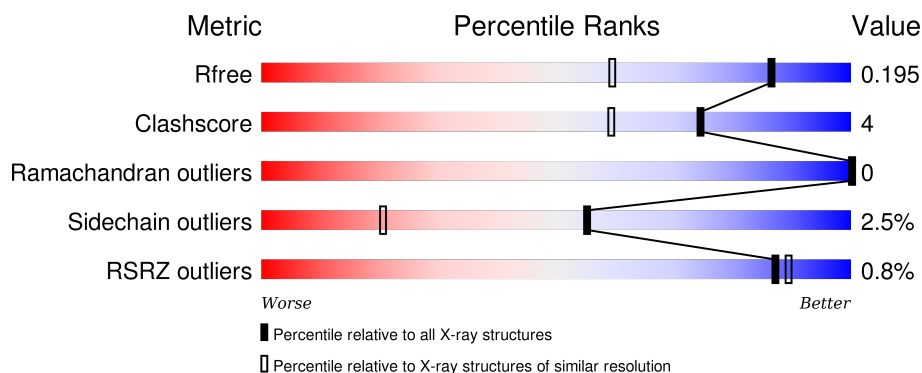
# 1 Overall quality at a glance ⓘ

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))
$R_{free}$	91344	2072 (1.50-1.50)
Clashscore	102246	2274 (1.50-1.50)
Ramachandran outliers	100387	2218 (1.50-1.50)
Sidechain outliers	100360	2216 (1.50-1.50)
RSRZ outliers	91569	2075 (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. 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	<div> <div> <div></div> <div>83%</div> <div>10%</div> <div>6%</div> </div> </div>
1	B	339	<div> <div> <div></div> <div>84%</div> <div>9%</div> <div>7%</div> </div> </div>
1	C	339	<div> <div> <div></div> <div>80%</div> <div>12%</div> <div>7%</div> </div> </div>

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
3	OXY	A	1405	-	-	-	X
3	OXY	B	2403	-	-	-	X
3	OXY	C	3403	-	-	-	X

## 2 Entry composition

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	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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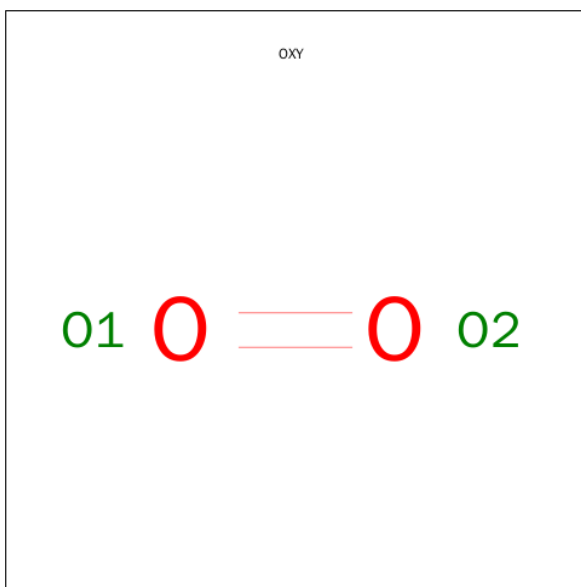
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Chain	Residue	Modelled	Actual	Comment	Reference
B	2335	HIS	-	EXPRESSION TAG	UNP C0STU6
B	2336	HIS	-	EXPRESSION TAG	UNP C0STU6
B	2337	HIS	-	EXPRESSION TAG	UNP C0STU6
B	2338	HIS	-	EXPRESSION TAG	UNP C0STU6
B	2339	HIS	-	EXPRESSION TAG	UNP C0STU6
C	3001	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 (three-letter code: CU) (formula: Cu).

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

- Molecule 3 is OXYGEN MOLECULE (three-letter code: 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	C	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

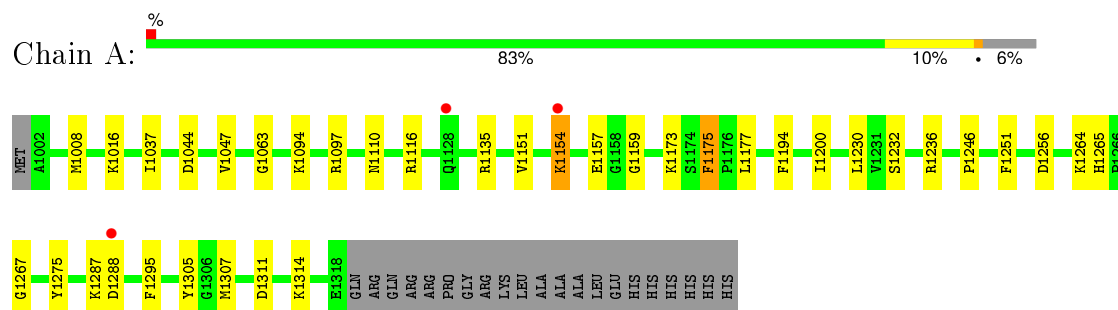
- Molecule 5 is water.

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

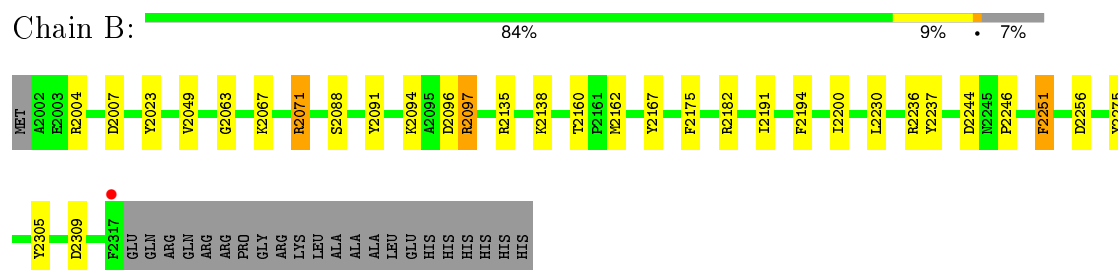
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

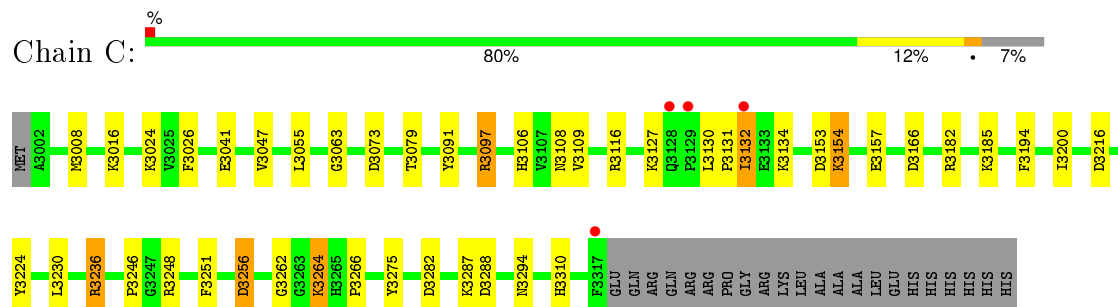
#### • Molecule 1: Multicopper oxidase



#### • Molecule 1: Multicopper oxidase



#### • Molecule 1: Multicopper oxidase



## 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 101.17Å 124.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.50 16.32 – 1.50	Depositor EDS
% Data completeness (in resolution range)	94.5 (10.00-1.50) 99.3 (16.32-1.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.07 (at 1.50Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, $R_{free}$	0.172 , (Not available) 0.161 , 0.195	Depositor DCC
$R_{free}$ test set	7439 reflections (5.25%)	DCC
Wilson B-factor (Å <sup>2</sup> )	10.9	Xtriage
Anisotropy	0.444	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 62.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 149676 reflections	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>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, 0.375 respectively for untwinned datasets, and 0.333, 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, CU, CL

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	B	0.51	0/2615	1.20	15/3561 (0.4%)
1	C	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.

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	1135	ARG	NE-CZ-NH2	-9.03	115.78	120.30
1	B	2167	TYR	CB-CG-CD1	-8.05	116.17	121.00
1	B	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
1	B	2182	ARG	NE-CZ-NH1	-6.78	116.91	120.30
1	C	3091	TYR	CB-CG-CD2	6.66	125.00	121.00
1	C	3216	ASP	CB-CG-OD1	6.40	124.06	118.30
1	B	2175	PHE	CB-CG-CD1	-6.36	116.35	120.80
1	B	2135	ARG	CD-NE-CZ	6.34	132.48	123.60
1	B	2004	ARG	NE-CZ-NH1	-6.28	117.16	120.30
1	A	1116	ARG	NE-CZ-NH2	-6.24	117.18	120.30
1	C	3182	ARG	NE-CZ-NH2	6.17	123.39	120.30
1	C	3248	ARG	NE-CZ-NH1	-6.01	117.29	120.30
1	C	3224	TYR	CB-CG-CD1	5.99	124.60	121.00
1	C	3251	PHE	CB-CG-CD2	5.98	124.99	120.80
1	C	3236	ARG	NE-CZ-NH2	-5.77	117.41	120.30
1	A	1175	PHE	CB-CG-CD1	-5.77	116.76	120.80
1	B	2007	ASP	CB-CG-OD1	5.77	123.49	118.30
1	B	2309	ASP	CB-CG-OD1	5.76	123.49	118.30
1	A	1305	TYR	CB-CG-CD2	5.74	124.44	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2071	ARG	NE-CZ-NH2	5.73	123.16	120.30
1	B	2097	ARG	NE-CZ-NH1	5.64	123.12	120.30
1	B	2305	TYR	CB-CG-CD1	-5.57	117.66	121.00
1	C	3166	ASP	CB-CG-OD1	5.54	123.28	118.30
1	C	3097	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	C	3224	TYR	CB-CG-CD2	-5.45	117.73	121.00
1	C	3236	ARG	NE-CZ-NH1	5.41	123.01	120.30
1	B	2244	ASP	CB-CG-OD1	5.29	123.06	118.30
1	B	2091	TYR	CD1-CE1-CZ	5.28	124.55	119.80
1	C	3116	ARG	NE-CZ-NH2	5.24	122.92	120.30
1	C	3091	TYR	CD1-CE1-CZ	5.23	124.50	119.80
1	B	2237	TYR	CZ-CE2-CD2	-5.22	115.10	119.80
1	B	2167	TYR	CG-CD1-CE1	-5.13	117.19	121.30
1	C	3256	ASP	CB-CG-OD1	5.05	122.85	118.30
1	C	3282	ASP	CB-CG-OD1	-5.03	113.77	118.30
1	C	3091	TYR	CG-CD2-CE2	5.03	125.32	121.30
1	C	3091	TYR	CB-CG-CD1	-5.00	118.00	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	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2539	0	2439	24	0
1	B	2519	0	2404	14	0
1	C	2533	0	2429	25	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	2	0	0	0	0
3	C	2	0	0	0	0
4	A	1	0	0	0	0
5	A	251	0	0	2	0
5	B	280	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	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.

All (60) 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: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
1:A:1173[B]:LYS:HD3	1:A:1177:LEU:O	1.99	0.62
1:C:3024:LYS:HE2	1:C:3153:ASP:O	2.00	0.60
1:A:1154:LYS:HE2	1:A:1157:GLU:OE1	2.02	0.59
1:A:1037:ILE:HG12	1:A:1307:MET:HE3	1.84	0.59
1:B:2160:THR:HB	1:B:2162:MET:HE1	1.84	0.58
1:A:1008[A]:MET:HE2	1:A:1307:MET:HE1	1.86	0.57
1:C:3131:PRO:O	1:C:3134:LYS:HB2	2.04	0.57
1:B:2138:LYS:HD3	5:B:2741:HOH:O	2.02	0.57
1:A:1016:LYS:HE3	5:A:5173:HOH:O	2.03	0.56
1:C:3185[B]:LYS:HD2	1:C:3246:PRO:CG	2.36	0.55
1:C:3200[A]:ILE:HG22	1:C:3230:LEU:HD11	1.88	0.55
1:C:3262:GLY:O	1:C:3264:LYS:HE2	2.08	0.54
1:A:1008[A]:MET:HE3	1:A:1047:VAL:HG11	1.91	0.53
1:A:1063:GLY:O	1:A:1097:ARG:HG2	2.10	0.52
1:B:2246:PRO:HA	1:B:2275:TYR:CG	2.45	0.52
1:C:3008[B]:MET:HG3	1:C:3047:VAL:HG13	1.93	0.50
1:B:2200[A]:ILE:HG22	1:B:2230:LEU:HD11	1.93	0.50
1:C:3130:LEU:HB3	1:C:3132:ILE:CD1	2.42	0.50
1:A:1246:PRO:HA	1:A:1275:TYR:CG	2.47	0.50
1:A:1173[B]:LYS:HD2	1:A:1295:PHE:HE1	1.77	0.49
1:B:2094:LYS:HD3	1:B:2096[B]:ASP:OD1	2.12	0.49
1:A:1110:ASN:HB2	1:A:1159:GLY:O	2.13	0.49
1:A:1232[A]:SER:OG	1:B:2230:LEU:HD13	2.11	0.49
1:C:3063:GLY:O	1:C:3097:ARG:HG2	2.12	0.48
1:C:3106:HIS:HA	1:C:3109:VAL:HG12	1.95	0.47
1:C:3130:LEU:HD13	1:C:3132:ILE:HD11	1.98	0.46
1:B:2063:GLY:O	1:B:2097:ARG:HG2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1200[A]:ILE:CG2	1:A:1230:LEU:HD11	2.45	0.46
1:B:2191:ILE:HD13	1:B:2251:PHE:CE1	2.51	0.46
1:C:3200[A]:ILE:CG2	1:C:3230:LEU:HD11	2.47	0.45
1:A:1044:ASP:OD1	1:A:1094:LYS:HE2	2.17	0.45
1:A:1173[A]:LYS:HD3	5:A:5136:HOH:O	2.16	0.45
1:C:3008[B]:MET:HG3	1:C:3047:VAL:CG1	2.47	0.44
1:B:2138:LYS:HB2	1:B:2138:LYS:HE2	1.74	0.44
1:C:3073:ASP:HB3	1:C:3079:THR:HG21	2.00	0.44
1:A:1008[A]:MET:HB2	1:A:1008[A]:MET:HE2	1.65	0.43
1:A:1265:HIS:CE1	1:C:3109:VAL:HG22	2.53	0.43
1:A:1311:ASP:HA	1:A:1314:LYS:CD	2.45	0.43
1:C:3185[B]:LYS:HD2	1:C:3246:PRO:HG3	2.00	0.43
1:C:3246:PRO:HA	1:C:3275:TYR:CG	2.54	0.43
1:B:2049:VAL:O	1:B:2088:SER:HA	2.19	0.42
1:B:2191:ILE:HD13	1:B:2251:PHE:HE1	1.83	0.42
1:A:1200[A]:ILE:HG22	1:A:1230:LEU:HD11	2.01	0.42
1:A:1265:HIS:CD2	1:C:3108:ASN:HA	2.54	0.41
1:C:3041:GLU:O	1:C:3127:LYS:HE3	2.20	0.41
1:A:1287:LYS:O	1:A:1288:ASP:HB2	2.21	0.41
1:B:2162:MET:HB2	1:B:2162:MET:HE2	1.68	0.41
1:B:2071:ARG:HH11	1:B:2071:ARG:HD2	1.63	0.41
1:C:3026:PHE:CZ	1:C:3055:LEU:HD12	2.55	0.41
1:C:3287:LYS:O	1:C:3288:ASP:HB2	2.21	0.41
1:C:3130:LEU:HB3	1:C:3132:ILE:HD11	2.03	0.41
1:A:1175:PHE:O	1:A:1267:GLY:HA2	2.21	0.41
1:C:3154:LYS:HE2	1:C:3157:GLU:CD	2.40	0.41
1:B:2246:PRO:HA	1:B:2275:TYR:CD2	2.56	0.40
1:C:3294:ASN:HB3	1:C:3310:HIS:CE1	2.57	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	322/339 (95%)	316 (98%)	6 (2%)	0	100	100
1	B	319/339 (94%)	312 (98%)	7 (2%)	0	100	100
1	C	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 ⓘ

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%)	60	25
1	B	273/287 (95%)	267 (98%)	6 (2%)	60	25
1	C	275/287 (96%)	267 (97%)	8 (3%)	50	16
All	All	824/861 (96%)	804 (98%)	20 (2%)	55	22

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1154	LYS
1	A	1194	PHE
1	A	1236	ARG
1	A	1251	PHE
1	A	1256	ASP
1	A	1264	LYS
1	B	2023	TYR
1	B	2067	LYS
1	B	2194	PHE
1	B	2236	ARG
1	B	2251	PHE
1	B	2256	ASP
1	C	3016	LYS
1	C	3132	ILE
1	C	3154	LYS

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Mol	Chain	Res	Type
1	C	3194	PHE
1	C	3236	ARG
1	C	3256	ASP
1	C	3264	LYS
1	C	3266	PRO

Some 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 carbohydrates 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	A	1405	2	1,1,1	0.32	0	0,0,0	0.00	-
3	OXY	B	2403	2	1,1,1	0.31	0	0,0,0	0.00	-
3	OXY	C	3403	2	1,1,1	0.32	0	0,0,0	0.00	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	OXY	A	1405	2	-	0/0/0/0	0/0/0/0
3	OXY	B	2403	2	-	0/0/0/0	0/0/0/0
3	OXY	C	3403	2	-	0/0/0/0	0/0/0/0

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%)	-0.29	3 (0%) 85 87	6, 12, 27, 47	0
1	B	316/339 (93%)	-0.36	1 (0%) 94 95	6, 12, 25, 45	0
1	C	316/339 (93%)	-0.26	4 (1%) 79 82	6, 11, 29, 67	0
All	All	949/1017 (93%)	-0.30	8 (0%) 87 89	6, 12, 27, 67	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	3132	ILE	3.1
1	C	3128	GLN	3.0
1	C	3317	PHE	2.9
1	C	3129	PRO	2.7
1	A	1128	GLN	2.6
1	A	1288	ASP	2.3
1	B	2317	PHE	2.3
1	A	1154	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. LLDF column lists the quality of electron



density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	OXY	A	1405	2/2	0.94	0.17	10.20	10,10,10,11	2
3	OXY	B	2403	2/2	0.97	0.15	8.09	10,10,10,17	2
3	OXY	C	3403	2/2	0.97	0.10	3.08	9,9,9,12	2
2	CU	B	2402	1/1	0.99	0.08	0.93	17,17,17,17	1
2	CU	C	3402	1/1	1.00	0.04	-1.98	14,14,14,14	1
2	CU	B	2404	1/1	0.99	0.05	-2.12	10,10,10,10	0
4	CL	A	1406	1/1	0.99	0.04	-2.84	13,13,13,13	0
2	CU	A	1404	1/1	0.99	0.04	-3.03	17,17,17,17	1
2	CU	B	2401	1/1	0.99	0.04	-3.07	13,13,13,13	1
2	CU	A	1403	1/1	0.99	0.03	-3.20	13,13,13,13	1
2	CU	B	2405	1/1	0.99	0.03	-3.71	10,10,10,10	1
2	CU	A	1402	1/1	0.99	0.03	-4.09	11,11,11,11	1
2	CU	C	3405	1/1	1.00	0.03	-4.65	11,11,11,11	1
2	CU	A	1401	1/1	0.99	0.04	-5.01	12,12,12,12	0
2	CU	C	3404	1/1	0.99	0.04	-5.09	11,11,11,11	0
2	CU	C	3401	1/1	1.00	0.04	-5.12	12,12,12,12	1

## 6.5 Other polymers

There are no such residues in this entry.