



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 04:17 PM EDT

PDB ID : 4E9V / pdb_00004e9v
Title : Multicopper Oxidase mgLAC (data1)
Authors : Komori, H.; Miyazaki, K.; Higuchi, Y.
Deposited on : 2012-03-21
Resolution : 1.80 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
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

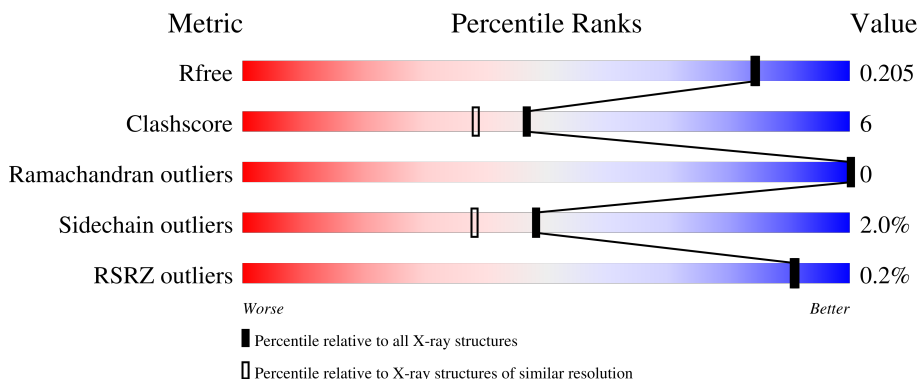
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	81% 11% • 6%
1	B	339	82% 11% • 7%
1	C	339	78% 13% • 7%

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	OH	A	1406	-	-	X	-

2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 8364 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	2539	1633	425	469	12	0	7	0
1	B	316	2519	1617	423	468	11	0	5	0
1	C	316	2533	1631	424	467	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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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

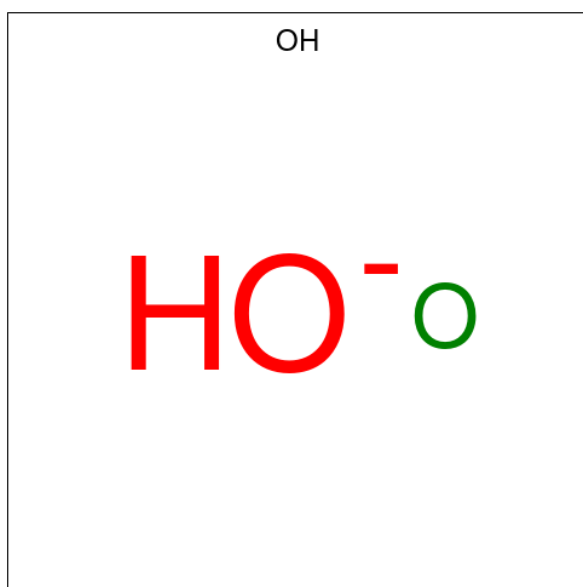
- Molecule 2 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

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 ATOM (CCD ID: O) (formula: O).

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

- Molecule 4 is HYDROXIDE ION (CCD ID: OH) (formula: HO).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O 1 1	0	0
4	B	1	Total O 1 1	0	0
4	C	1	Total O 1 1	0	0

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

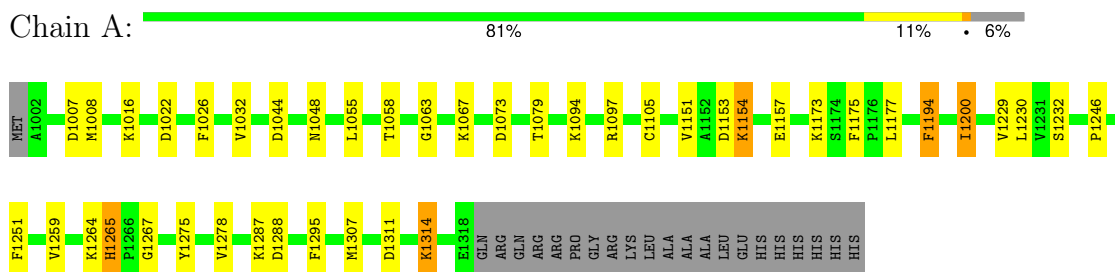
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	234	Total O 235 235	0	1
6	B	265	Total O 265 265	0	0
6	C	254	Total O 254 254	0	0

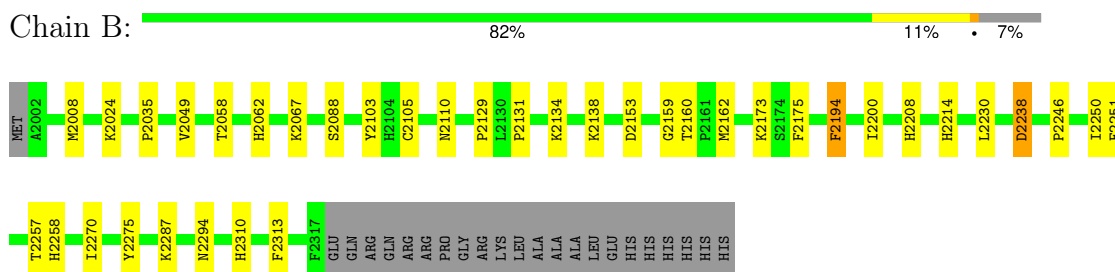
3 Residue-property plots [i](#)

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.

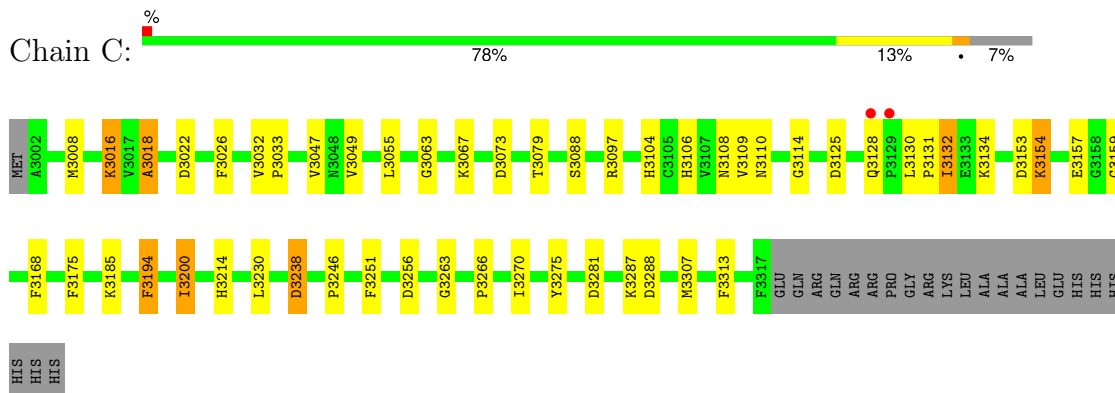
- Molecule 1: Multicopper oxidase



- 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, α , β , γ	74.73Å 101.13Å 123.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.80 10.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	95.0 (10.00-1.80) 99.3 (10.00-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.17 (at 1.80Å)	Xtrriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.163 , (Not available) 0.155 , 0.205	Depositor DCC
R_{free} test set	4387 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	10.4	Xtrriage
Anisotropy	0.415	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 71.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8364	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.40% 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 i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: O, OH, 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	0.44	0/2641	1.31	10/3594 (0.3%)
1	B	0.45	0/2615	1.31	8/3561 (0.2%)
1	C	0.44	0/2637	1.31	11/3590 (0.3%)
All	All	0.44	0/7893	1.31	29/10745 (0.3%)

There are no bond length outliers.

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1251	PHE	CA-CB-CG	9.64	123.44	113.80
1	C	3251	PHE	CA-CB-CG	8.80	122.60	113.80
1	C	3032	VAL	CA-C-O	-8.38	115.58	119.94
1	B	2194	PHE	CA-CB-CG	7.71	121.51	113.80
1	A	1032	VAL	CA-C-O	-7.62	115.98	119.94
1	C	3018	ALA	O-C-N	6.84	126.09	121.71
1	A	1194	PHE	CA-CB-CG	6.62	120.42	113.80
1	C	3153	ASP	CA-CB-CG	-6.56	106.04	112.60
1	C	3238	ASP	CA-CB-CG	6.56	119.16	112.60
1	A	1314	LYS	CA-C-N	-6.39	116.74	122.43
1	A	1314	LYS	C-N-CA	-6.39	116.74	122.43
1	C	3194	PHE	CA-CB-CG	6.36	120.16	113.80
1	C	3125	ASP	CA-CB-CG	6.34	118.94	112.60
1	A	1022	ASP	CA-CB-CG	-6.34	106.26	112.60
1	A	1278	VAL	CA-C-O	6.23	122.83	119.15
1	B	2287	LYS	CA-C-N	-6.17	113.98	123.17
1	B	2287	LYS	C-N-CA	-6.17	113.98	123.17
1	C	3168	PHE	CA-CB-CG	-5.90	107.90	113.80
1	B	2238	ASP	CA-CB-CG	5.65	118.25	112.60
1	B	2208	HIS	CA-CB-CG	5.37	119.17	113.80
1	C	3114	GLY	CA-C-N	-5.28	116.23	122.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	3114	GLY	C-N-CA	-5.28	116.23	122.36
1	B	2251	PHE	CA-CB-CG	5.28	119.08	113.80
1	A	1265	HIS	CA-CB-CG	5.27	119.07	113.80
1	B	2313	PHE	CA-CB-CG	5.21	119.01	113.80
1	B	2062	HIS	CA-CB-CG	5.10	118.90	113.80
1	A	1153	ASP	CA-C-N	-5.07	114.50	122.76
1	A	1153	ASP	C-N-CA	-5.07	114.50	122.76
1	C	3281	ASP	CA-CB-CG	-5.03	107.57	112.60

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	29	0
1	B	2519	0	2404	22	0
1	C	2533	0	2429	35	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
2	C	4	0	0	0	0
3	A	1	0	0	1	0
3	B	1	0	0	1	0
3	C	1	0	0	1	0
4	A	1	0	0	3	0
4	B	1	0	0	1	0
4	C	1	0	0	1	0
5	A	1	0	0	0	0
6	A	235	0	0	3	0
6	B	265	0	0	4	0
6	C	254	0	0	0	0
All	All	8364	0	7272	85	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 6.

All (85) 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:1311:ASP:HA	1:A:1314:LYS:HD2	1.66	0.78
1:A:1008[A]:MET:HE2	1:A:1307:MET:HE1	1.66	0.78
1:C:3016:LYS:HE2	1:C:3018:ALA:O	1.84	0.77
1:B:2173:LYS:HE2	6:B:2654:HOH:O	1.85	0.75
1:A:1287:LYS:HE3	1:A:1288:ASP:OD2	1.87	0.74
1:A:1173[B]:LYS:HD3	1:A:1177:LEU:O	1.88	0.73
1:A:1151:VAL:HA	1:A:1154:LYS:HD3	1.69	0.73
1:C:3016:LYS:HE3	1:C:3022:ASP:OD1	1.89	0.71
1:C:3132:ILE:H	1:C:3132:ILE:HD13	1.57	0.69
1:A:1016:LYS:HE3	6:A:5165:HOH:O	1.93	0.69
1:C:3131:PRO:O	1:C:3134:LYS:HB2	1.94	0.68
1:A:1173[B]:LYS:HD2	1:A:1295:PHE:HE1	1.60	0.66
1:C:3200[A]:ILE:HG22	1:C:3230:LEU:HD11	1.78	0.66
3:B:2406:O:O	4:C:3403:OH:O	2.16	0.64
1:A:1154:LYS:HE2	1:A:1157:GLU:OE1	2.00	0.60
4:A:1406:OH:O	3:C:3406:O:O	2.18	0.60
3:A:1403:O:O	4:B:2403:OH:O	2.19	0.60
1:B:2246:PRO:HA	1:B:2275:TYR:CG	2.40	0.57
1:A:1173[B]:LYS:HD2	1:A:1295:PHE:CE1	2.38	0.57
1:C:3130:LEU:HB3	1:C:3132:ILE:HG12	1.88	0.56
1:C:3026:PHE:HZ	1:C:3055:LEU:HD12	1.71	0.56
1:C:3185[B]:LYS:HD2	1:C:3246:PRO:CG	2.35	0.56
1:B:2129:PRO:HG2	1:B:2134:LYS:HE2	1.88	0.55
1:C:3008[B]:MET:HG2	1:C:3307:MET:HE1	1.88	0.55
1:A:1063:GLY:O	1:A:1097:ARG:HG2	2.08	0.54
1:A:1044:ASP:OD1	1:A:1094:LYS:HE2	2.08	0.54
1:A:1246:PRO:HA	1:A:1275:TYR:CG	2.43	0.54
1:C:3026:PHE:CZ	1:C:3055:LEU:HD12	2.43	0.53
1:A:1232[A]:SER:OG	1:B:2230:LEU:HD13	2.08	0.53
1:B:2160:THR:OG1	1:B:2162:MET:HE2	2.09	0.53
1:C:3246:PRO:HA	1:C:3275:TYR:CG	2.45	0.52
1:B:2049:VAL:O	1:B:2088:SER:HA	2.10	0.52
1:B:2214:HIS:HB2	1:B:2238:ASP:HB2	1.92	0.51
1:C:3008[B]:MET:HG3	1:C:3047:VAL:HG13	1.91	0.51
1:B:2024:LYS:HE2	1:B:2153:ASP:OD1	2.11	0.51
1:A:1311:ASP:HA	1:A:1314:LYS:CD	2.40	0.50
1:C:3008[B]:MET:HG3	1:C:3047:VAL:CG1	2.42	0.50
1:C:3214:HIS:HB2	1:C:3238:ASP:HB2	1.92	0.50
1:B:2008[A]:MET:HE2	1:B:2035:PRO:HG2	1.94	0.49
1:C:3106:HIS:HA	1:C:3109:VAL:HG12	1.94	0.49
1:A:1007:ASP:OD1	1:A:1048:ASN:HB2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1406:OH:O	1:C:3104:HIS:CE1	2.66	0.49
1:B:2200[A]:ILE:HG22	1:B:2230:LEU:HD11	1.95	0.48
1:A:1265:HIS:CD2	1:C:3108:ASN:HA	2.48	0.48
1:A:1200[A]:ILE:HG22	1:A:1230:LEU:HD11	1.96	0.48
1:B:2008[B]:MET:HE1	1:B:2103:TYR:CE1	2.48	0.48
1:C:3049:VAL:O	1:C:3088:SER:HA	2.14	0.48
1:B:2138:LYS:HB2	1:B:2138:LYS:HE2	1.57	0.47
1:C:3130:LEU:CB	1:C:3132:ILE:HG12	2.44	0.47
1:B:2110:ASN:HB2	1:B:2159:GLY:O	2.16	0.46
1:A:1200[A]:ILE:CG2	1:A:1230:LEU:HD11	2.46	0.46
1:C:3154:LYS:HE2	1:C:3157:GLU:OE1	2.16	0.46
1:C:3063:GLY:O	1:C:3097:ARG:HG2	2.16	0.45
1:C:3154:LYS:HE2	1:C:3157:GLU:CD	2.40	0.45
1:C:3131:PRO:HA	1:C:3134:LYS:HD2	1.98	0.45
1:B:2294:ASN:HB3	1:B:2310:HIS:CE1	2.52	0.44
1:B:2246:PRO:HA	1:B:2275:TYR:CD2	2.52	0.44
1:C:3185[B]:LYS:HD2	1:C:3246:PRO:HG3	1.99	0.44
1:A:1259:VAL:HG21	1:C:3109:VAL:CG2	2.47	0.44
4:A:1406:OH:O	1:C:3104:HIS:HE1	2.01	0.43
1:A:1175:PHE:O	1:A:1267:GLY:HA2	2.18	0.43
1:A:1008[A]:MET:HE2	1:A:1307:MET:CE	2.42	0.42
1:A:1026:PHE:CZ	1:A:1055:LEU:HD12	2.54	0.42
1:A:1200[A]:ILE:HD13	1:A:1232[A]:SER:HB2	2.00	0.42
1:A:1173[A]:LYS:NZ	6:A:5002[A]:HOH:O	2.50	0.42
1:C:3008[B]:MET:CG	1:C:3307:MET:HE1	2.47	0.42
1:B:2162:MET:HE1	1:C:3263:GLY:HA2	2.01	0.42
1:A:1287:LYS:O	1:A:1288:ASP:HB2	2.20	0.42
1:A:1058:THR:O	1:A:1105:CYS:HA	2.20	0.42
1:A:1200[A]:ILE:HD13	1:A:1232[A]:SER:CB	2.50	0.42
6:B:2726:HOH:O	1:C:3256:ASP:HB3	2.20	0.41
1:C:3110:ASN:HB2	1:C:3159:GLY:O	2.20	0.41
1:B:2257:THR:HG23	6:B:2585:HOH:O	2.20	0.41
1:C:3073:ASP:HB3	1:C:3079:THR:HG21	2.03	0.41
1:A:1073:ASP:HB3	1:A:1079:THR:HG21	2.03	0.41
1:A:1229:VAL:HG13	6:A:5221:HOH:O	2.20	0.41
1:C:3033:PRO:HD2	1:C:3313:PHE:CG	2.56	0.41
1:C:3175:PHE:HB2	1:C:3270:ILE:HB	2.03	0.41
1:C:3200[A]:ILE:CG2	1:C:3230:LEU:HD11	2.50	0.40
1:B:2058:THR:O	1:B:2105:CYS:HA	2.21	0.40
1:B:2131:PRO:O	1:B:2134:LYS:HB2	2.21	0.40
1:B:2175:PHE:HB2	1:B:2270:ILE:HB	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3287:LYS:O	1:C:3288:ASP:HB2	2.22	0.40
1:B:2138:LYS:HD3	6:B:2730:HOH:O	2.22	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%)	318 (99%)	4 (1%)	0	100	100
1	B	319/339 (94%)	312 (98%)	7 (2%)	0	100	100
1	C	321/339 (95%)	313 (98%)	8 (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%)	270 (98%)	6 (2%)	45	34
1	B	273/287 (95%)	270 (99%)	3 (1%)	65	60
1	C	275/287 (96%)	266 (97%)	9 (3%)	33	21
All	All	824/861 (96%)	806 (98%)	18 (2%)	48	34

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1067	LYS
1	A	1154	LYS
1	A	1194	PHE
1	A	1200[A]	ILE
1	A	1200[B]	ILE
1	A	1264	LYS
1	B	2067	LYS
1	B	2194	PHE
1	B	2250	ILE
1	C	3016	LYS
1	C	3067	LYS
1	C	3128	GLN
1	C	3132	ILE
1	C	3154	LYS
1	C	3194	PHE
1	C	3200[A]	ILE
1	C	3200[B]	ILE
1	C	3266	PRO

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 16 are monoatomic and 3 are modelled with single atom - 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

There are no such residues in this entry.

5.8 Polymer linkage issues

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%)	-0.74	0 100 100	4, 11, 26, 48	7 (2%)
1	B	316/339 (93%)	-0.80	0 100 100	4, 11, 24, 45	5 (1%)
1	C	316/339 (93%)	-0.74	2 (0%) 85 86	4, 11, 28, 69	7 (2%)
All	All	949/1017 (93%)	-0.76	2 (0%) 91 91	4, 11, 26, 69	19 (2%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	3128	GLN	2.9
1	C	3129	PRO	2.4

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(Å ²)	Q<0.9
4	OH	C	3403	1/1	0.64	0.18	14,14,14,14	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	OH	B	2403	1/1	0.66	0.20	18,18,18,18	1
4	OH	A	1406	1/1	0.70	0.20	19,19,19,19	1
3	O	B	2406	1/1	0.81	0.12	6,6,6,6	1
3	O	A	1403	1/1	0.88	0.09	8,8,8,8	1
3	O	C	3406	1/1	0.90	0.07	7,7,7,7	1
2	CU	C	3401	1/1	0.98	0.03	16,16,16,16	1
2	CU	C	3405	1/1	0.98	0.03	14,14,14,14	1
2	CU	A	1404	1/1	0.98	0.03	18,18,18,18	1
2	CU	B	2402	1/1	0.98	0.04	18,18,18,18	1
2	CU	B	2401	1/1	0.99	0.03	19,19,19,19	1
2	CU	A	1402	1/1	0.99	0.03	16,16,16,16	1
2	CU	B	2405	1/1	0.99	0.02	14,14,14,14	1
2	CU	A	1401	1/1	0.99	0.02	11,11,11,11	0
2	CU	C	3402	1/1	0.99	0.02	14,14,14,14	1
2	CU	A	1405	1/1	0.99	0.02	17,17,17,17	1
2	CU	C	3404	1/1	1.00	0.01	10,10,10,10	0
2	CU	B	2404	1/1	1.00	0.01	9,9,9,9	0
5	CL	A	1407	1/1	1.00	0.01	12,12,12,12	0

6.5 Other polymers [i](#)

There are no such residues in this entry.