



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 09:38 PM UTC

PDB ID : 9RC6 / pdb_00009rc6
Title : Laccase (multicopper oxidase) from *Pediococcus pentosaceus* 4618 mutant Y471L co-crystallized with Copper Chloride
Authors : Paredes, F.; Casino, P.
Deposited on : 2025-05-27
Resolution : 2.60 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

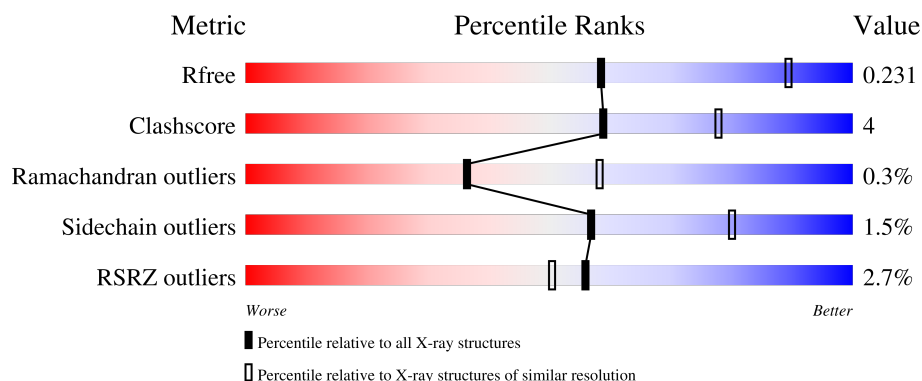
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

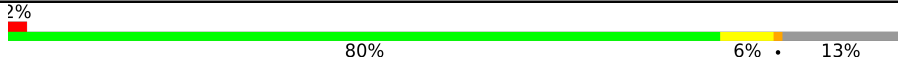
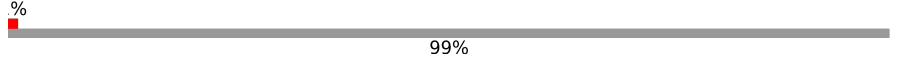
The reported resolution of this entry is 2.60 Å.

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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	532	
1	C	532	
1	G	532	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7491 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 domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	461	Total	C	N	O	S	0	1	0
			3656	2333	625	684	14			
1	C	463	Total	C	N	O	S	0	1	0
			3678	2347	628	689	14			
1	G	5	Total	C	N	O		0	0	0
			45	27	13	5				

There are 81 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	MET	-	initiating methionine	UNP A0AB73HHR8
A	-21	GLY	-	expression tag	UNP A0AB73HHR8
A	-20	SER	-	expression tag	UNP A0AB73HHR8
A	-19	SER	-	expression tag	UNP A0AB73HHR8
A	-18	HIS	-	expression tag	UNP A0AB73HHR8
A	-17	HIS	-	expression tag	UNP A0AB73HHR8
A	-16	HIS	-	expression tag	UNP A0AB73HHR8
A	-15	HIS	-	expression tag	UNP A0AB73HHR8
A	-14	HIS	-	expression tag	UNP A0AB73HHR8
A	-13	HIS	-	expression tag	UNP A0AB73HHR8
A	-12	SER	-	expression tag	UNP A0AB73HHR8
A	-11	SER	-	expression tag	UNP A0AB73HHR8
A	-10	GLY	-	expression tag	UNP A0AB73HHR8
A	-9	LEU	-	expression tag	UNP A0AB73HHR8
A	-8	VAL	-	expression tag	UNP A0AB73HHR8
A	-7	PRO	-	expression tag	UNP A0AB73HHR8
A	-6	ARG	-	expression tag	UNP A0AB73HHR8
A	-5	GLY	-	expression tag	UNP A0AB73HHR8
A	-4	SER	-	expression tag	UNP A0AB73HHR8
A	-3	HIS	-	expression tag	UNP A0AB73HHR8
A	-2	MET	-	expression tag	UNP A0AB73HHR8
A	-1	ALA	-	expression tag	UNP A0AB73HHR8
A	0	SER	-	expression tag	UNP A0AB73HHR8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	12	PRO	GLN	variant	UNP A0AB73HHR8
A	241	ASN	ASP	variant	UNP A0AB73HHR8
A	253	ALA	SER	variant	UNP A0AB73HHR8
A	471	ALA	TYR	engineered mutation	UNP A0AB73HHR8
C	-22	MET	-	initiating methionine	UNP A0AB73HHR8
C	-21	GLY	-	expression tag	UNP A0AB73HHR8
C	-20	SER	-	expression tag	UNP A0AB73HHR8
C	-19	SER	-	expression tag	UNP A0AB73HHR8
C	-18	HIS	-	expression tag	UNP A0AB73HHR8
C	-17	HIS	-	expression tag	UNP A0AB73HHR8
C	-16	HIS	-	expression tag	UNP A0AB73HHR8
C	-15	HIS	-	expression tag	UNP A0AB73HHR8
C	-14	HIS	-	expression tag	UNP A0AB73HHR8
C	-13	HIS	-	expression tag	UNP A0AB73HHR8
C	-12	SER	-	expression tag	UNP A0AB73HHR8
C	-11	SER	-	expression tag	UNP A0AB73HHR8
C	-10	GLY	-	expression tag	UNP A0AB73HHR8
C	-9	LEU	-	expression tag	UNP A0AB73HHR8
C	-8	VAL	-	expression tag	UNP A0AB73HHR8
C	-7	PRO	-	expression tag	UNP A0AB73HHR8
C	-6	ARG	-	expression tag	UNP A0AB73HHR8
C	-5	GLY	-	expression tag	UNP A0AB73HHR8
C	-4	SER	-	expression tag	UNP A0AB73HHR8
C	-3	HIS	-	expression tag	UNP A0AB73HHR8
C	-2	MET	-	expression tag	UNP A0AB73HHR8
C	-1	ALA	-	expression tag	UNP A0AB73HHR8
C	0	SER	-	expression tag	UNP A0AB73HHR8
C	12	PRO	GLN	variant	UNP A0AB73HHR8
C	241	ASN	ASP	variant	UNP A0AB73HHR8
C	253	ALA	SER	variant	UNP A0AB73HHR8
C	471	ALA	TYR	engineered mutation	UNP A0AB73HHR8
G	-1	MET	-	initiating methionine	UNP A0AB73HHR8
G	0	GLY	-	expression tag	UNP A0AB73HHR8
G	1	SER	-	expression tag	UNP A0AB73HHR8
G	2	SER	-	expression tag	UNP A0AB73HHR8
G	3	HIS	-	expression tag	UNP A0AB73HHR8
G	4	HIS	-	expression tag	UNP A0AB73HHR8
G	5	HIS	-	expression tag	UNP A0AB73HHR8
G	6	HIS	-	expression tag	UNP A0AB73HHR8
G	7	HIS	-	expression tag	UNP A0AB73HHR8
G	8	HIS	-	expression tag	UNP A0AB73HHR8
G	9	SER	-	expression tag	UNP A0AB73HHR8

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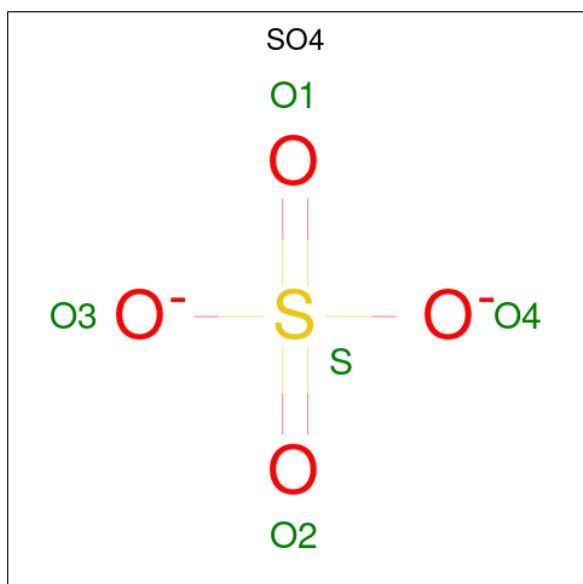
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Chain	Residue	Modelled	Actual	Comment	Reference
G	10	SER	-	expression tag	UNP A0AB73HHR8
G	11	GLY	-	expression tag	UNP A0AB73HHR8
G	12	LEU	-	expression tag	UNP A0AB73HHR8
G	13	VAL	-	expression tag	UNP A0AB73HHR8
G	14	PRO	-	expression tag	UNP A0AB73HHR8
G	15	ARG	-	expression tag	UNP A0AB73HHR8
G	16	GLY	-	expression tag	UNP A0AB73HHR8
G	17	SER	-	expression tag	UNP A0AB73HHR8
G	18	HIS	-	expression tag	UNP A0AB73HHR8
G	19	MET	-	expression tag	UNP A0AB73HHR8
G	20	ALA	-	expression tag	UNP A0AB73HHR8
G	21	SER	-	expression tag	UNP A0AB73HHR8
G	33	PRO	GLN	variant	UNP A0AB73HHR8
G	262	ASN	ASP	variant	UNP A0AB73HHR8
G	274	ALA	SER	variant	UNP A0AB73HHR8
G	492	ALA	TYR	engineered mutation	UNP A0AB73HHR8

- 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	C	4	Total Cu 4 4	0	0

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0

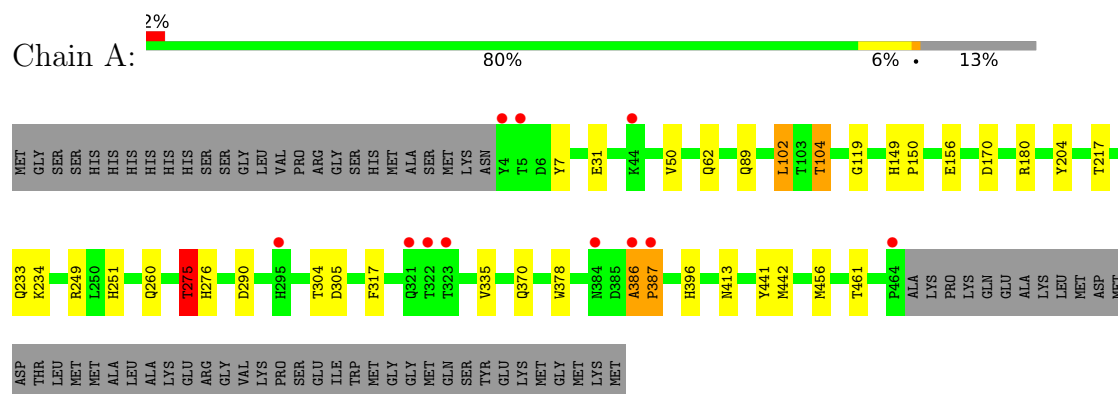
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	29	Total O 29 29	0	0
4	C	34	Total O 34 34	0	0
4	G	1	Total O 1 1	0	0

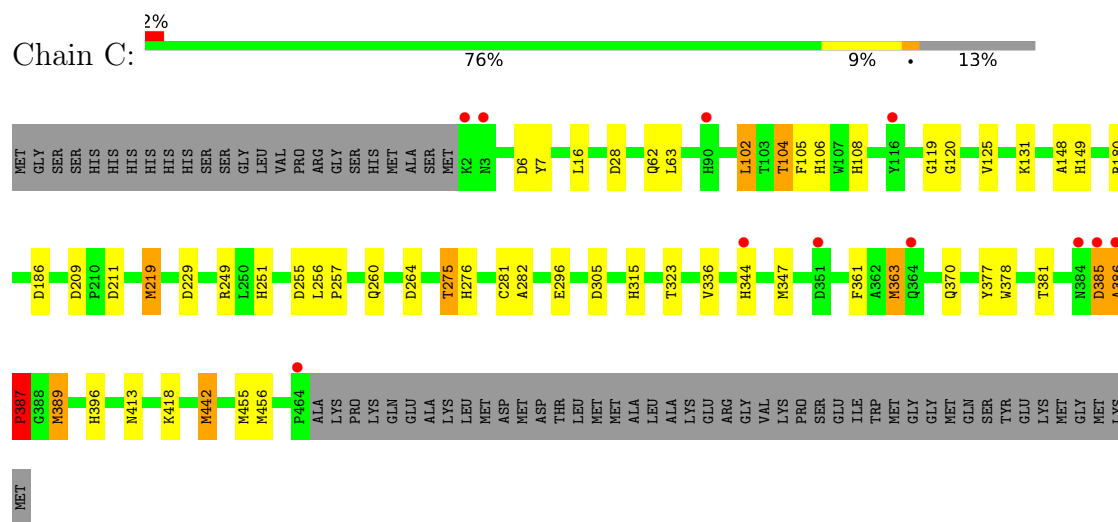
3 Residue-property plots [i](#)

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.

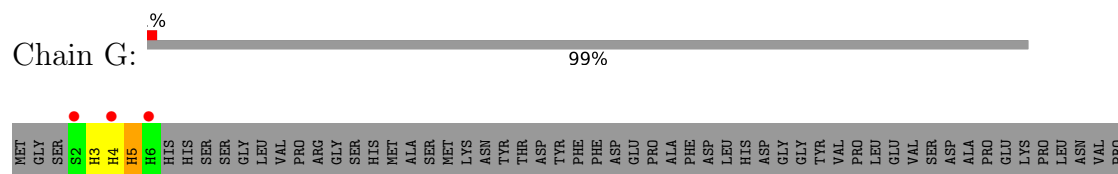
- Molecule 1: Multicopper oxidase domain-containing protein



- Molecule 1: Multicopper oxidase domain-containing protein



- Molecule 1: Multicopper oxidase domain-containing protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	123.68Å 123.68Å 181.77Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	107.11 – 2.60 107.11 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (107.11-2.60) 100.0 (107.11-2.60)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.27 (at 2.62Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.189 , 0.229 0.195 , 0.231	Depositor DCC
R_{free} test set	2472 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	55.4	Xtriage
Anisotropy	0.321	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 35.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.008 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7491	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.49% 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: CU, SO4

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	0.50	0/3771	0.96	5/5157 (0.1%)
1	C	0.51	0/3794	0.96	10/5189 (0.2%)
1	G	0.81	0/48	1.90	1/64 (1.6%)
All	All	0.51	0/7613	0.97	16/10410 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	2
All	All	0	3

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	387	PRO	N-CA-C	-6.57	98.94	112.47
1	C	275	THR	CA-CB-OG1	-6.49	99.86	109.60
1	A	31	GLU	CB-CA-C	6.29	121.02	109.46
1	A	275	THR	CA-CB-OG1	-5.84	100.84	109.60
1	C	62	GLN	N-CA-CB	5.79	120.28	110.49
1	A	335	VAL	N-CA-CB	5.70	116.74	110.53
1	C	385	ASP	CA-CB-CG	5.64	118.25	112.60
1	A	217	THR	CA-CB-OG1	-5.55	101.27	109.60
1	C	219	MET	CG-SD-CE	-5.52	88.75	100.90
1	C	28	ASP	CA-CB-CG	5.44	118.04	112.60
1	C	6	ASP	CA-CB-CG	5.22	117.82	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	28	ASP	CB-CA-C	-5.17	99.19	109.99
1	G	5	HIS	CB-CA-C	5.16	119.91	111.23
1	C	186	ASP	CA-CB-CG	5.09	117.69	112.60
1	A	62	GLN	N-CA-CB	5.08	117.91	109.88
1	C	209	ASP	CA-CB-CG	5.02	117.62	112.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	180	ARG	Sidechain
1	C	180	ARG	Sidechain
1	C	386	ALA	Peptide

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	3656	0	3477	25	0
1	C	3678	0	3497	37	0
1	G	45	0	29	2	0
2	A	4	0	0	0	0
2	C	4	0	0	0	0
3	A	15	0	0	0	0
3	C	25	0	0	0	0
4	A	29	0	0	0	0
4	C	34	0	0	0	0
4	G	1	0	0	5	0
All	All	7491	0	7003	64	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 (64) 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:C:275:THR:HG22	1:C:276:HIS:CD2	1.93	1.03
1:C:276:HIS:CE1	4:G:601:HOH:O	2.13	0.97
1:C:276:HIS:HE1	4:G:601:HOH:O	1.44	0.97
1:A:386:ALA:CB	1:A:387:PRO:HD3	2.03	0.89
1:G:3:HIS:NE2	4:G:601:HOH:O	1.96	0.81
1:A:275:THR:HG22	1:A:276:HIS:ND1	1.97	0.80
1:C:336:VAL:HG21	1:C:377:TYR:CZ	2.19	0.77
1:A:386:ALA:HB1	1:A:387:PRO:HD3	1.68	0.73
1:A:386:ALA:HB3	1:A:387:PRO:HD3	1.74	0.69
1:C:63:LEU:HD13	1:C:219:MET:HE1	1.80	0.64
1:A:275:THR:CG2	1:A:276:HIS:ND1	2.60	0.64
1:A:104:THR:HG23	1:A:119:GLY:O	1.98	0.63
1:C:7:TYR:CE1	1:C:276:HIS:HB3	2.33	0.63
1:A:260:GLN:HE22	1:A:413:ASN:HD22	1.44	0.63
1:A:386:ALA:CB	1:A:387:PRO:CD	2.74	0.63
1:C:260:GLN:HE22	1:C:413:ASN:HD22	1.45	0.63
1:C:211:ASP:OD2	1:C:389:MET:HE1	2.01	0.60
1:G:5:HIS:NE2	4:G:601:HOH:O	2.10	0.59
1:C:275:THR:HG22	1:C:276:HIS:NE2	2.19	0.57
1:A:7:TYR:CE1	1:A:276:HIS:HB3	2.41	0.55
1:A:104:THR:CG2	1:A:119:GLY:O	2.54	0.55
1:A:156:GLU:HG3	1:A:204:TYR:CD2	2.42	0.54
1:A:386:ALA:HB3	1:A:387:PRO:CD	2.38	0.54
1:C:149:HIS:HE1	1:C:456:MET:HE1	1.73	0.54
1:C:386:ALA:HB3	1:C:387:PRO:HD2	1.90	0.52
1:A:370:GLN:HE22	1:A:378:TRP:HE1	1.58	0.50
1:A:149:HIS:HE1	1:A:456:MET:HE1	1.76	0.49
1:C:102:LEU:HD12	1:C:102:LEU:C	2.37	0.49
1:C:264:ASP:HB2	1:C:418:LYS:HA	1.94	0.49
1:C:336:VAL:HG21	1:C:377:TYR:CE1	2.46	0.49
1:C:255:ASP:OD1	4:G:601:HOH:O	2.20	0.49
1:C:361:PHE:HE2	1:C:363:MET:CE	2.27	0.48
1:C:7:TYR:CZ	1:C:249:ARG:HB3	2.48	0.48
1:C:105:PHE:O	1:C:119:GLY:HA3	2.14	0.47
1:C:281:CYS:O	1:C:282:ALA:HB3	2.15	0.47
1:C:347:MET:HB3	1:C:455:MET:HE2	1.95	0.47
1:C:125:VAL:HG22	1:C:131:LYS:HG3	1.96	0.47
1:C:370:GLN:HE22	1:C:378:TRP:HE1	1.62	0.47
1:C:104:THR:CG2	1:C:119:GLY:O	2.63	0.47
1:C:386:ALA:HB3	1:C:387:PRO:CD	2.45	0.46
1:C:386:ALA:CB	1:C:387:PRO:CD	2.93	0.46
1:A:104:THR:HG21	1:A:149:HIS:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:255:ASP:HB3	1:C:275:THR:HG23	1.98	0.46
1:C:361:PHE:CE2	1:C:363:MET:CE	2.98	0.46
1:C:120:GLY:HA3	1:C:442:MET:HE3	1.97	0.46
1:C:256:LEU:HD12	1:C:257:PRO:HD2	1.98	0.45
1:C:229:ASP:OD1	1:C:315:HIS:HE1	2.00	0.45
1:A:251:HIS:HE1	1:A:305:ASP:O	2.01	0.44
1:A:396:HIS:HB2	1:A:441:TYR:HB3	1.99	0.44
1:C:251:HIS:HE1	1:C:305:ASP:O	2.00	0.43
1:A:149:HIS:N	1:A:150:PRO:CD	2.82	0.43
1:A:370:GLN:O	1:A:461:THR:HA	2.19	0.43
1:A:170:ASP:OD1	1:A:170:ASP:C	2.62	0.42
1:C:104:THR:O	1:C:148:ALA:HA	2.19	0.42
1:C:344:HIS:HE1	1:C:381:THR:OG1	2.01	0.42
1:A:102:LEU:C	1:A:102:LEU:HD12	2.45	0.42
1:A:233:GLN:HG3	1:A:317:PHE:CE1	2.55	0.42
1:A:234:LYS:CE	1:A:290:ASP:OD2	2.67	0.41
1:C:16:LEU:C	1:C:16:LEU:HD12	2.45	0.41
1:C:108:HIS:CD2	1:C:108:HIS:C	2.98	0.41
1:C:385:ASP:O	1:C:386:ALA:C	2.64	0.41
1:A:249:ARG:O	1:A:304:THR:HA	2.21	0.41
1:C:106:HIS:CE1	1:C:396:HIS:CE1	3.09	0.41
1:A:50:VAL:HB	1:A:89:GLN:NE2	2.35	0.41

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	460/532 (86%)	435 (95%)	23 (5%)	2 (0%)	30	51
1	C	462/532 (87%)	444 (96%)	17 (4%)	1 (0%)	43	66
1	G	3/532 (1%)	3 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	925/1596 (58%)	882 (95%)	40 (4%)	3 (0%)	36 58

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	386	ALA
1	C	387	PRO
1	A	387	PRO

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	393/453 (87%)	389 (99%)	4 (1%)	68 86
1	C	396/453 (87%)	389 (98%)	7 (2%)	51 76
1	G	4/453 (1%)	3 (75%)	1 (25%)	0 1
All	All	793/1359 (58%)	781 (98%)	12 (2%)	57 80

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	102	LEU
1	A	104	THR
1	A	275	THR
1	A	442	MET
1	C	102	LEU
1	C	104	THR
1	C	296	GLU
1	C	323	THR
1	C	363	MET
1	C	389	MET
1	C	442	MET
1	G	4	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	251	HIS
1	A	260	GLN
1	A	344	HIS
1	A	370	GLN
1	A	450	HIS
1	C	89	GLN
1	C	251	HIS
1	C	260	GLN
1	C	276	HIS
1	C	315	HIS
1	C	344	HIS
1	C	370	GLN
1	C	450	HIS

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, 8 are monoatomic - leaving 8 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	SO4	A	606	-	4,4,4	0.29	0	6,6,6	0.14	0
3	SO4	C	608	-	4,4,4	0.32	0	6,6,6	0.06	0
3	SO4	C	609	-	4,4,4	0.31	0	6,6,6	0.10	0
3	SO4	C	606	-	4,4,4	0.34	0	6,6,6	0.09	0
3	SO4	A	605	-	4,4,4	0.33	0	6,6,6	0.10	0
3	SO4	C	605	-	4,4,4	0.32	0	6,6,6	0.13	0
3	SO4	A	607	-	4,4,4	0.31	0	6,6,6	0.10	0
3	SO4	C	607	-	4,4,4	0.27	0	6,6,6	0.16	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

6.1 Protein, DNA and RNA chains

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	461/532 (86%)	-0.10	11 (2%) 59 54	25, 55, 81, 121	1 (0%)
1	C	463/532 (87%)	-0.17	11 (2%) 59 54	22, 52, 78, 117	1 (0%)
1	G	5/532 (0%)	2.80	3 (60%) 0 0	74, 84, 97, 102	0
All	All	929/1596 (58%)	-0.12	25 (2%) 56 50	22, 54, 81, 121	2 (0%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	2	SER	6.8
1	C	2	LYS	5.1
1	A	4	TYR	5.0
1	C	386	ALA	4.8
1	A	386	ALA	4.6
1	A	322	THR	4.1
1	A	5	THR	4.0
1	C	3	ASN	3.8
1	C	364	GLN	3.6
1	A	323	THR	3.5
1	G	6	HIS	3.3
1	C	464	PRO	3.1
1	A	387	PRO	3.1
1	C	116	TYR	3.0
1	C	385	ASP	2.9
1	C	384	ASN	2.7
1	C	351	ASP	2.3
1	A	384	ASN	2.3
1	C	344	HIS	2.2
1	A	464	PRO	2.2
1	A	295	HIS	2.2
1	A	44	LYS	2.1
1	G	4	HIS	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	90	HIS	2.1
1	A	321	GLN	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(Å ²)	Q<0.9
3	SO4	C	606	5/5	0.73	0.13	98,98,112,117	0
3	SO4	A	605	5/5	0.78	0.11	86,89,102,103	0
3	SO4	A	607	5/5	0.85	0.09	82,94,101,102	0
3	SO4	C	608	5/5	0.87	0.10	94,99,104,105	0
3	SO4	C	605	5/5	0.88	0.08	92,92,97,97	0
3	SO4	C	609	5/5	0.88	0.14	75,75,83,96	0
3	SO4	A	606	5/5	0.92	0.15	80,80,88,91	0
3	SO4	C	607	5/5	0.93	0.13	67,75,81,82	0
2	CU	A	604	1/1	0.98	0.13	79,79,79,79	0
2	CU	C	603	1/1	0.99	0.03	61,61,61,61	0
2	CU	C	604	1/1	0.99	0.09	82,82,82,82	0
2	CU	A	603	1/1	0.99	0.04	60,60,60,60	0
2	CU	A	601	1/1	0.99	0.02	52,52,52,52	0
2	CU	C	602	1/1	0.99	0.02	59,59,59,59	0
2	CU	C	601	1/1	1.00	0.02	53,53,53,53	0
2	CU	A	602	1/1	1.00	0.01	55,55,55,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.