



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 10:43 PM UTC

PDB ID : 1IVU / pdb_00001ivu
Title : Crystal structure of copper amine oxidase from *Arthrobacter globiformis*: Initial intermediate in topaquinone biogenesis
Authors : Kim, M.; Okajima, T.; Kishishita, S.; Yoshimura, M.; Kawamori, A.; Tanizawa, K.; Yamaguchi, H.
Deposited on : 2002-03-29
Resolution : 1.90 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

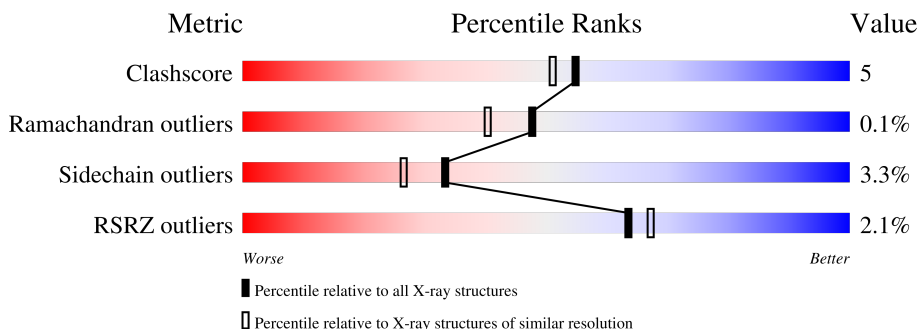
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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))
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	638	2% 81% 15% • •
1	B	638	2% 83% 13% • •

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10954 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 amine oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	620	Total	C	N	O	S	0	1	0
			4871	3077	857	928	9			
1	B	620	Total	C	N	O	S	0	1	0
			4871	3077	857	928	9			

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

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

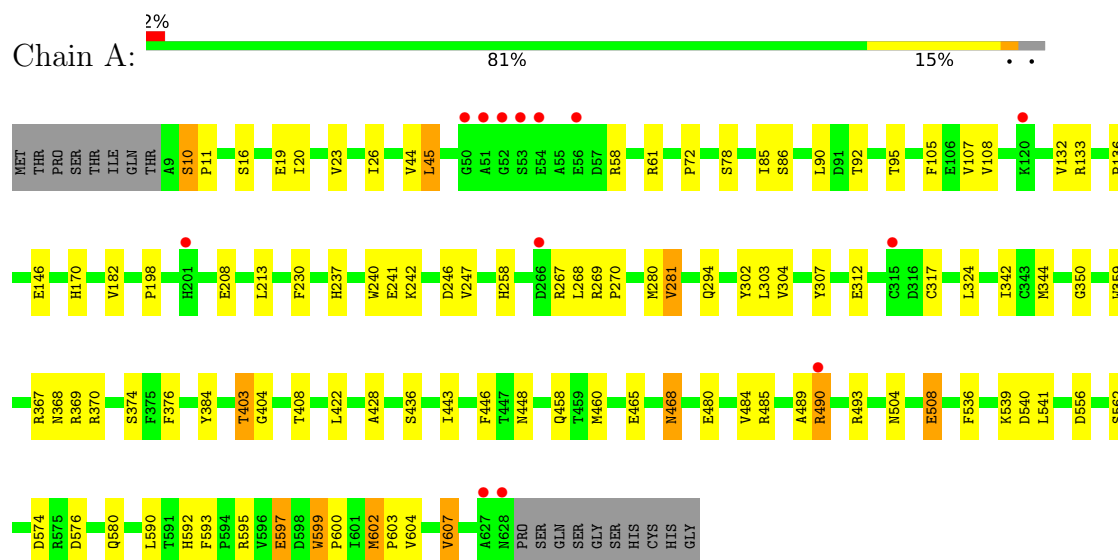
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	568	Total	O	0	0
			568	568		
3	B	642	Total	O	0	0
			642	642		

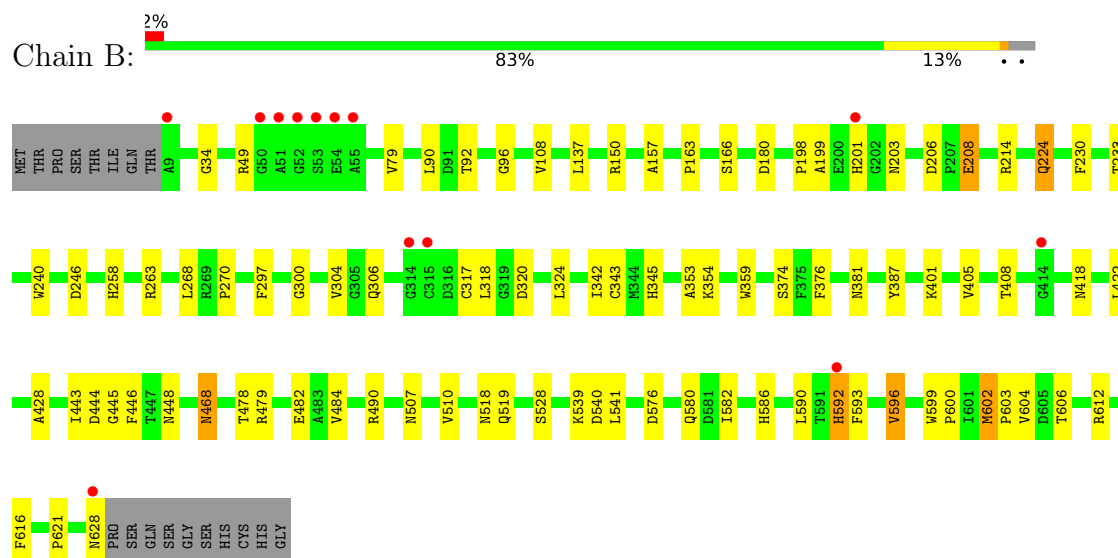
3 Residue-property plots

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: amine oxidase



• Molecule 1: amine oxidase



4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	157.88Å 63.18Å 184.28Å 90.00° 111.81° 90.00°	Depositor
Resolution (Å)	7.00 – 1.90 7.00 – 1.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (7.00-1.90) 96.7 (7.00-1.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.48 (at 1.80Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.199 , 0.258 0.202 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	18.5	Xtriage
Anisotropy	0.781	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.57 , 116.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10954	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 36.08 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.2840e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.71	3/5000 (0.1%)	1.06	21/6810 (0.3%)
1	B	0.67	0/5000	1.09	25/6810 (0.4%)
All	All	0.69	3/10000 (0.0%)	1.08	46/13620 (0.3%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	599	TRP	NE1-CE2	10.27	1.48	1.37
1	A	593	PHE	N-CA	-5.90	1.40	1.46
1	A	593	PHE	CA-C	-5.79	1.47	1.52

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	446	PHE	N-CA-C	7.54	122.23	112.89
1	B	224	GLN	CA-C-N	7.29	127.63	119.32
1	B	224	GLN	C-N-CA	7.29	127.63	119.32
1	B	592[A]	HIS	N-CA-C	7.13	120.14	108.52
1	B	592[B]	HIS	N-CA-C	7.13	120.14	108.52
1	B	199	ALA	N-CA-C	7.05	122.13	112.90
1	B	108	VAL	N-CA-C	6.96	117.66	110.36
1	A	408	THR	N-CA-C	6.71	120.00	110.14
1	A	446	PHE	N-CA-C	6.51	121.06	113.18
1	B	359	TRP	N-CA-C	6.37	118.23	111.28
1	A	108	VAL	N-CA-C	6.35	116.52	110.42
1	B	34	GLY	CA-C-N	6.27	126.18	119.28
1	B	34	GLY	C-N-CA	6.27	126.18	119.28
1	A	359	TRP	N-CA-C	6.25	118.09	111.28
1	B	92	THR	N-CA-C	6.13	119.59	111.75
1	B	602	MET	N-CA-C	5.88	118.14	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	518	ASN	N-CA-C	5.86	119.74	112.24
1	A	374	SER	N-CA-C	5.73	117.68	109.14
1	A	562	SER	N-CA-C	5.72	117.19	111.07
1	A	294	GLN	N-CA-C	5.72	117.38	109.15
1	B	163	PRO	N-CA-C	5.70	121.45	113.53
1	B	582	ILE	N-CA-C	5.69	117.04	108.96
1	A	592[A]	HIS	N-CA-C	5.66	117.63	108.41
1	A	592[B]	HIS	N-CA-C	5.66	117.63	108.41
1	A	485	ARG	N-CA-C	5.65	118.93	109.95
1	B	604	VAL	N-CA-C	5.62	116.66	109.30
1	A	281	VAL	CB-CA-C	-5.58	102.89	111.31
1	A	92	THR	N-CA-C	5.56	118.11	111.71
1	A	20	ILE	N-CA-C	-5.50	105.36	110.53
1	A	604	VAL	N-CA-C	5.47	116.46	109.30
1	B	374	SER	N-CA-C	5.47	117.11	108.96
1	B	300	GLY	N-CA-C	5.45	119.08	112.49
1	B	408	THR	N-CA-C	5.40	118.45	110.46
1	B	90	LEU	N-CA-C	5.34	117.94	109.24
1	A	10	SER	CA-C-N	5.34	125.42	119.87
1	A	10	SER	C-N-CA	5.34	125.42	119.87
1	B	478	THR	N-CA-C	5.32	119.85	112.45
1	A	304	VAL	N-CA-C	5.27	117.64	111.05
1	B	157	ALA	N-CA-C	5.27	118.81	109.96
1	A	493	ARG	N-CA-C	5.22	117.91	110.24
1	A	95	THR	N-CA-C	5.19	119.30	112.92
1	B	593	PHE	N-CA-C	-5.11	96.77	108.27
1	A	132	VAL	N-CA-C	5.08	115.08	107.51
1	B	297	PHE	N-CA-C	-5.06	99.08	108.24
1	B	304	VAL	N-CA-C	5.04	117.35	111.05
1	A	540	ASP	N-CA-C	5.00	118.53	112.23

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	4871	0	4691	53	0
1	B	4871	0	4693	43	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	568	0	0	10	0
3	B	642	0	0	8	0
All	All	10954	0	9384	91	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 5.

All (91) 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:B:317:CYS:HG	1:B:343:CYS:HG	0.94	0.92
1:A:170:HIS:CE1	3:A:1232:HOH:O	2.35	0.79
1:A:458:GLN:HE22	1:B:418:ASN:HD21	1.29	0.78
1:A:599:TRP:CD2	1:A:600:PRO:HA	2.18	0.77
1:A:26:ILE:HD13	3:A:1506:HOH:O	1.85	0.77
1:A:599:TRP:CG	1:A:600:PRO:HA	2.20	0.77
1:B:507:ASN:HB2	3:B:1551:HOH:O	1.88	0.73
1:A:247:VAL:HG21	1:A:344:MET:HE1	1.70	0.72
1:A:443:ILE:H	1:A:448:ASN:HD21	1.37	0.72
1:A:170:HIS:HE1	3:A:1232:HOH:O	1.71	0.71
1:B:166:SER:H	1:B:203:ASN:HD21	1.36	0.69
1:B:443:ILE:H	1:B:448:ASN:HD21	1.43	0.67
1:A:247:VAL:HG21	1:A:344:MET:CE	2.25	0.67
1:A:170:HIS:HD2	1:A:198:PRO:O	1.80	0.65
1:A:280:MET:HE1	1:A:384:TYR:CZ	2.34	0.63
1:A:44:VAL:HG23	3:A:1453:HOH:O	1.98	0.62
1:B:96:GLY:HA2	3:B:1175:HOH:O	1.98	0.62
1:B:263:ARG:HH11	1:B:268:LEU:HD13	1.64	0.62
1:A:350:GLY:HA2	1:A:367:ARG:NH2	2.16	0.61
1:A:403:THR:HG21	1:B:354:LYS:H	1.67	0.59
1:B:401:LYS:HG2	1:B:606:THR:HG22	1.85	0.59
1:A:280:MET:HE1	1:A:384:TYR:CE2	2.39	0.58
1:A:422:LEU:HD11	1:A:428:ALA:HB2	1.85	0.58
1:B:590:LEU:HD13	1:B:592[B]:HIS:CE1	2.39	0.57
1:A:595:ARG:HG3	1:A:597:GLU:HG2	1.87	0.56
1:B:201:HIS:HB3	3:B:1441:HOH:O	2.07	0.55
1:B:468:ASN:HD22	1:B:468:ASN:H	1.54	0.55
1:A:576:ASP:O	1:A:580:GLN:HG3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:596:VAL:HG23	3:B:1201:HOH:O	2.08	0.54
1:A:237:HIS:HD2	1:A:246:ASP:OD1	1.92	0.53
1:A:468:ASN:HD22	1:A:468:ASN:H	1.57	0.53
1:B:484:VAL:HG12	1:B:539:LYS:HG3	1.90	0.53
1:B:263:ARG:NH1	1:B:268:LEU:HD13	2.24	0.52
1:B:599:TRP:CD2	1:B:600:PRO:HA	2.44	0.52
1:A:599:TRP:CG	1:A:600:PRO:CA	2.92	0.52
1:A:58:ARG:HG3	3:A:1453:HOH:O	2.09	0.52
1:B:490:ARG:NE	3:B:1117:HOH:O	2.38	0.52
1:B:137:LEU:HD23	3:B:1319:HOH:O	2.10	0.51
3:A:1288:HOH:O	1:B:621:PRO:HD2	2.10	0.51
1:A:489:ALA:H	1:A:490:ARG:HH21	1.59	0.49
1:B:166:SER:H	1:B:203:ASN:ND2	2.09	0.49
1:A:133:ARG:NE	1:A:133:ARG:HA	2.28	0.49
1:A:590:LEU:HG	1:A:607:VAL:HG22	1.94	0.48
1:A:146:GLU:HG2	3:A:1511:HOH:O	2.13	0.48
1:A:78:SER:HB2	1:A:85:ILE:HD11	1.95	0.48
1:A:436:SER:HB2	1:A:536:PHE:CE2	2.49	0.48
1:A:246:ASP:HB2	1:A:258:HIS:HB2	1.96	0.47
1:A:403:THR:HG22	1:A:404:GLY:H	1.79	0.47
1:A:324:LEU:HB2	1:A:342:ILE:HB	1.96	0.46
1:A:368:ASN:ND2	1:A:369:ARG:H	2.14	0.46
1:B:206:ASP:OD2	1:B:208:GLU:HB3	2.16	0.46
1:A:10:SER:HA	1:A:11:PRO:HD3	1.81	0.45
1:A:241:GLU:O	1:A:242:LYS:HB2	2.16	0.45
1:A:403:THR:HG21	1:B:354:LYS:N	2.30	0.45
1:B:270:PRO:HG2	1:B:445:GLY:N	2.32	0.45
1:B:387:TYR:CE1	1:B:401:LYS:HD2	2.51	0.45
1:B:345:HIS:HE1	3:B:1289:HOH:O	2.00	0.45
1:B:246:ASP:HB2	1:B:258:HIS:HB2	1.98	0.45
1:A:26:ILE:HG21	3:A:1506:HOH:O	2.16	0.44
1:A:602:MET:HA	1:A:603:PRO:HD3	1.87	0.44
1:B:422:LEU:HD11	1:B:428:ALA:HB2	1.98	0.44
1:A:504:ASN:OD1	1:A:508:GLU:HG3	2.18	0.44
1:B:612:ARG:NH1	3:B:1262:HOH:O	2.50	0.44
1:B:576:ASP:O	1:B:580:GLN:HG3	2.17	0.44
1:B:317:CYS:HG	1:B:343:CYS:CB	2.25	0.44
1:A:403:THR:HG21	1:B:353:ALA:HA	1.99	0.43
1:A:230:PHE:HB3	1:A:240:TRP:HB2	1.99	0.43
1:A:72:PRO:HG2	1:A:90:LEU:HB2	2.01	0.43
1:B:230:PHE:HB3	1:B:240:TRP:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:302:TYR:O	1:A:307:TYR:HE2	2.02	0.43
1:B:224:GLN:HE21	1:B:320:ASP:HB3	1.83	0.42
1:A:269:ARG:HA	1:A:270:PRO:HD3	1.88	0.42
1:A:45:LEU:HD13	1:A:61:ARG:HB2	2.02	0.42
1:A:16:SER:HB3	3:A:1478:HOH:O	2.19	0.42
1:B:540:ASP:O	1:B:586:HIS:HD2	2.03	0.42
1:B:590:LEU:HB3	1:B:592[B]:HIS:NE2	2.34	0.42
1:A:267:ARG:HG2	1:A:267:ARG:HH11	1.85	0.41
1:A:484:VAL:HG12	1:A:539:LYS:HG3	2.02	0.41
1:B:324:LEU:HB2	1:B:342:ILE:HB	2.01	0.41
1:B:510:VAL:HB	1:B:616:PHE:HA	2.03	0.41
1:A:317:CYS:HB2	3:A:1514:HOH:O	2.21	0.41
1:A:480:GLU:HB2	1:A:574:ASP:HA	2.02	0.41
1:A:19:GLU:O	1:A:23:VAL:HG23	2.20	0.41
1:B:306:GLN:HE21	1:B:306:GLN:HB2	1.72	0.41
1:A:460:MET:HE1	1:B:528:SER:HA	2.03	0.41
1:B:602:MET:HA	1:B:603:PRO:HD3	1.95	0.41
1:A:61:ARG:HH22	1:A:556:ASP:CG	2.29	0.41
1:B:381:ASN:HB2	1:B:405:VAL:O	2.22	0.40
1:B:479:ARG:O	1:B:482:GLU:HG2	2.20	0.40
1:B:150:ARG:HD2	1:B:180:ASP:OD2	2.21	0.40
1:A:105:PHE:HD1	1:A:136:PRO:HB2	1.87	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	619/638 (97%)	591 (96%)	27 (4%)	1 (0%)	43	36
1	B	619/638 (97%)	594 (96%)	25 (4%)	0	100	100
All	All	1238/1276 (97%)	1185 (96%)	52 (4%)	1 (0%)	48	40

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	303	LEU

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	515/530 (97%)	495 (96%)	20 (4%)	28	21
1	B	515/530 (97%)	501 (97%)	14 (3%)	39	34
All	All	1030/1060 (97%)	996 (97%)	34 (3%)	33	26

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	LEU
1	A	86	SER
1	A	107	VAL
1	A	182	VAL
1	A	208	GLU
1	A	213	LEU
1	A	268	LEU
1	A	281	VAL
1	A	312	GLU
1	A	370	ARG
1	A	376	PHE
1	A	403	THR
1	A	465	GLU
1	A	468	ASN
1	A	490	ARG
1	A	508	GLU
1	A	541	LEU
1	A	597	GLU
1	A	602	MET
1	A	607	VAL
1	B	49	ARG
1	B	79	VAL

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Mol	Chain	Res	Type
1	B	198	PRO
1	B	208	GLU
1	B	214	ARG
1	B	233	THR
1	B	318	LEU
1	B	376	PHE
1	B	444	ASP
1	B	468	ASN
1	B	519	GLN
1	B	541	LEU
1	B	596	VAL
1	B	628	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	126	ASN
1	A	170	HIS
1	A	237	HIS
1	A	309	ASN
1	A	368	ASN
1	A	418	ASN
1	A	448	ASN
1	A	468	ASN
1	A	515	HIS
1	B	203	ASN
1	B	224	GLN
1	B	237	HIS
1	B	273	ASN
1	B	306	GLN
1	B	334	ASN
1	B	418	ASN
1	B	448	ASN
1	B	458	GLN
1	B	468	ASN
1	B	515	HIS
1	B	586	HIS

5.3.3 RNA ⓘ

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 2 ligands modelled in this entry, 2 are monoatomic - 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 [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	620/638 (97%)	-0.19	13 (2%) 63 67	6, 21, 41, 88	1 (0%)
1	B	620/638 (97%)	-0.32	13 (2%) 63 67	4, 18, 37, 90	1 (0%)
All	All	1240/1276 (97%)	-0.26	26 (2%) 63 67	4, 19, 39, 90	2 (0%)

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	50	GLY	12.7
1	B	52	GLY	9.8
1	A	51	ALA	8.4
1	B	51	ALA	7.5
1	A	53	SER	6.9
1	A	52	GLY	5.1
1	A	50	GLY	4.4
1	A	54	GLU	4.3
1	B	53	SER	4.3
1	B	54	GLU	4.0
1	B	201	HIS	3.5
1	B	9	ALA	2.8
1	B	55	ALA	2.6
1	B	314	GLY	2.6
1	A	266	ASP	2.6
1	A	627	ALA	2.6
1	B	628	ASN	2.5
1	A	490	ARG	2.4
1	B	414	GLY	2.3
1	B	592[A]	HIS	2.3
1	A	56	GLU	2.2
1	A	315	CYS	2.2
1	A	628	ASN	2.1
1	A	120	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	315	CYS	2.0
1	A	201	HIS	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
2	CU	B	1002	1/1	0.93	0.05	19,19,19,19	0
2	CU	A	1001	1/1	0.98	0.08	19,19,19,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.