W O R L D W I D E
wwPDB
P R O T E I N   D A T A   B A N K

Full wwPDB X-ray Structure Validation Report (i)

Feb 26, 2014 – 07:19 PM GMT

PDB ID : 1IVU

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 validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at http://wwpdb.org/ValidationPDFNotes.html


The following versions of software and data (see references) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683
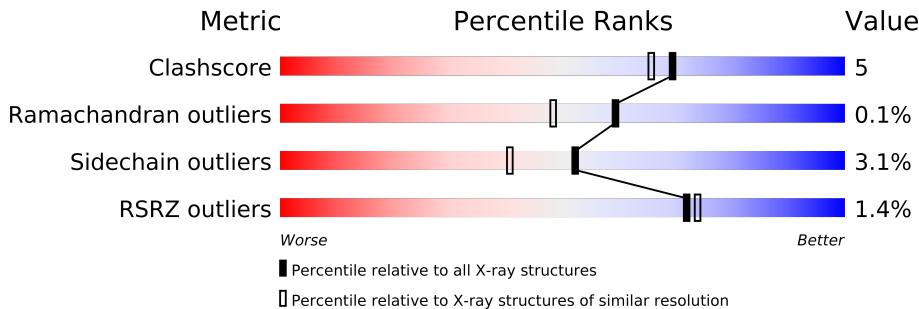
1 Overall quality at a glance (i)
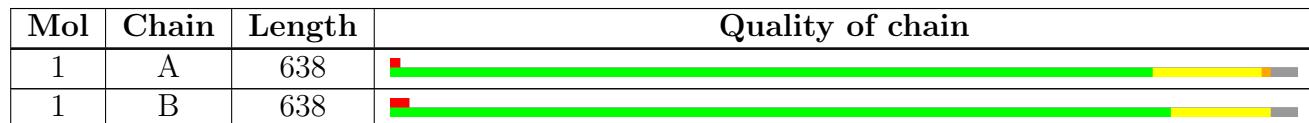
The reported resolution of this entry is 1.90 Å.

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	Percentile Ranks	Value
Clashscore		5
Ramachandran outliers		0.1%
Sidechain outliers		3.1%
RSRZ outliers		1.4%

Worse   Better

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	4465 (1.90-1.90)
Ramachandran outliers	78287	4413 (1.90-1.90)
Sidechain outliers	78261	4414 (1.90-1.90)
RSRZ outliers	66119	3686 (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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	638	
1	B	638	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 10954 atoms, of which 0 are hydrogen and 0 are deuterium.

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 4871	C 3077	N 857	O 928	S 9	0	1	0
1	B	620	Total 4871	C 3077	N 857	O 928	S 9	0	1	0

- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

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

- Molecule 3 is water.
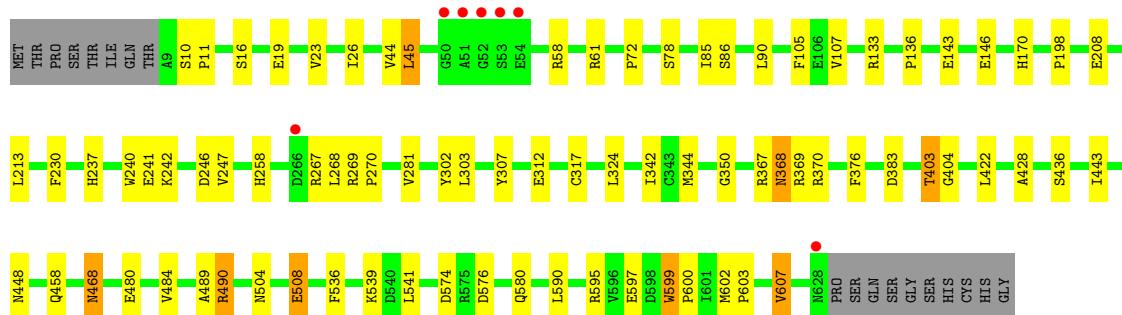
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	568	Total 568	O 568	0	0
3	B	642	Total 642	O 642	0	0

3 Residue-property plots ⓘ

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.
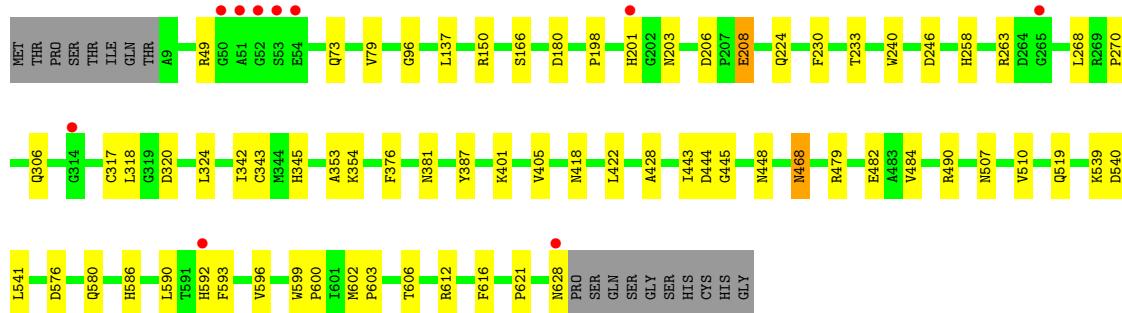
• Molecule 1: amine oxidase

Chain A:

• Molecule 1: amine oxidase

Chain B:

4 Data and refinement statistics (i)

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 69.96 – 1.79	Depositor EDS
% Data completeness (in resolution range)	(Not available) (7.00-1.90) 97.3 (69.96-1.79)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.48 (at 1.80Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.199 , 0.258 0.211 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å^2)	18.5	Xtriage
Anisotropy	0.781	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 61.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$< |L| > = 0.50, < L^2 > = 0.33$	Xtriage
Outliers	2 of 153547 reflections (0.001%)	Xtriage
F_o,F_c correlation	0.95	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.*

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[1]Intensities estimated from amplitudes.

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	0.57	1/5000 (0.0%)	0.81	0/6810
1	B	0.54	0/5000	0.79	1/6810 (0.0%)
All	All	0.55	1/10000 (0.0%)	0.80	1/13620 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	599	TRP	NE1-CE2	8.62	1.48	1.37

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	593	PHE	N-CA-C	-5.27	96.77	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2   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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4871	0	4691	50	0
1	B	4871	0	4693	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	88	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

All (88) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(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: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: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:44:VAL:HG23	3:A:1453:HOH:O	1.98	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: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:468:ASN:H	1:B:468:ASN:HD22	1.54	0.55
1:B:201:HIS:HB3	3:B:1441:HOH:O	2.07	0.55
1:A:247:VAL:HG21	1:A:344:MET:HE1	1.89	0.54
1:B:596:VAL:HG23	3:B:1201:HOH:O	2.08	0.54
1:A:576:ASP:O	1:A:580:GLN:HG3	2.07	0.54
1:A:237:HIS:HD2	1:A:246:ASP:OD1	1.92	0.53
1:B:484:VAL:HG12	1:B:539:LYS:HG3	1.90	0.53
1:A:468:ASN:HD22	1:A:468:ASN:H	1.57	0.53
1:B:263:ARG:NH1	1:B:268:LEU:HD13	2.24	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
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:HA	1:A:133:ARG:NE	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:403:THR:HG21	1:B:354:LYS:N	2.30	0.45
1:A:241:GLU:O	1:A:242:LYS:HB2	2.16	0.45
1:B:387:TYR:CE1	1:B:401:LYS:HD2	2.51	0.45
1:B:270:PRO:HG2	1:B:445:GLY:N	2.32	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
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

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
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:247:VAL:HG21	1:A:344:MET:HE2	2.00	0.41
1:A:484:VAL:HG12	1:A:539:LYS:HG3	2.02	0.41
1:B:510:VAL:HB	1:B:616:PHE:HA	2.03	0.41
1:B:324:LEU:HB2	1:B:342:ILE:HB	2.01	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:B:602:MET:HA	1:B:603:PRO:HD3	1.95	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%)	56	44
1	B	619/638 (97%)	594 (96%)	25 (4%)	0	100	100
All	All	1238/1276 (97%)	1185 (96%)	52 (4%)	1 (0%)	59	48

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	303	LEU

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	515/530 (97%)	496 (96%)	19 (4%)	45	32
1	B	515/530 (97%)	502 (98%)	13 (2%)	60	50
All	All	1030/1060 (97%)	998 (97%)	32 (3%)	52	41

All (32) 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	143	GLU
1	A	208	GLU
1	A	213	LEU
1	A	268	LEU
1	A	281	VAL
1	A	312	GLU
1	A	368	ASN
1	A	370	ARG
1	A	376	PHE
1	A	383	ASP
1	A	403	THR
1	A	468	ASN
1	A	490	ARG
1	A	508	GLU
1	A	541	LEU
1	A	607	VAL
1	B	49	ARG
1	B	73	GLN
1	B	79	VAL
1	B	198	PRO
1	B	208	GLU
1	B	233	THR
1	B	318	LEU
1	B	376	PHE
1	B	444	ASP
1	B	468	ASN

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Mol	Chain	Res	Type
1	B	519	GLN
1	B	541	LEU
1	B	628	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	170	HIS
1	A	237	HIS
1	A	273	ASN
1	A	309	ASN
1	A	368	ASN
1	A	421	GLN
1	A	448	ASN
1	A	458	GLN
1	A	468	ASN
1	A	515	HIS
1	A	573	GLN
1	A	628	ASN
1	B	203	ASN
1	B	224	GLN
1	B	237	HIS
1	B	273	ASN
1	B	334	ASN
1	B	448	ASN
1	B	468	ASN
1	B	515	HIS
1	B	519	GLN
1	B	561	HIS
1	B	586	HIS

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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.

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 ⓘ

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%)	-0.17	7 (1%)	77	79	6, 21, 41, 88	0
1	B	620/638 (97%)	-0.22	10 (1%)	68	70	4, 18, 37, 90	0
All	All	1240/1276 (97%)	-0.20	17 (1%)	72	74	4, 19, 39, 90	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	51	ALA	12.1
1	B	52	GLY	11.8
1	B	50	GLY	11.0
1	B	51	ALA	10.2
1	A	52	GLY	10.0
1	A	53	SER	6.4
1	A	54	GLU	5.3
1	B	54	GLU	5.1
1	B	53	SER	4.6
1	A	50	GLY	3.2
1	A	266	ASP	2.9
1	B	201	HIS	2.7
1	B	592[A]	HIS	2.6
1	B	628	ASN	2.6
1	B	314	GLY	2.4
1	B	265	GLY	2.2
1	A	628	ASN	2.1

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3   Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4   Ligands ⓘ

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, 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	RSR	LLDF	B-factors($Å^2$)	Q<0.9
2	CU	A	1001	1/1	0.10	-0.63	19,19,19,19	0
2	CU	B	1002	1/1	0.07	-1.01	19,19,19,19	0

6.5   Other polymers ⓘ

There are no such residues in this entry.