



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:13 AM UTC

PDB ID : 1HAW / pdb_00001haw
Title : X-RAY STRUCTURE OF A BLUE COPPER NITRITE REDUCTASE AT HIGH PH AND IN COPPER FREE FORM AT 1.9 Å RESOLUTION
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Deposited on : 2001-04-09
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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

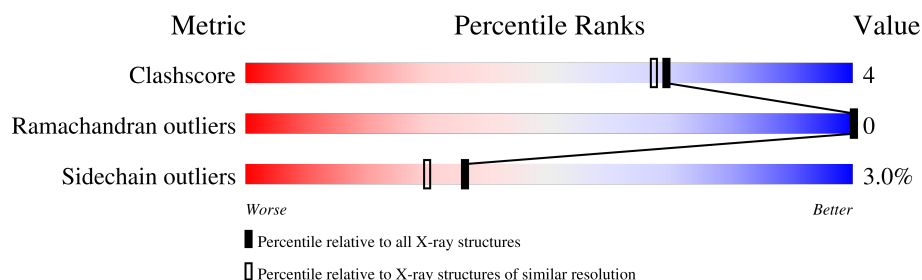
1 Overall quality at a glance

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)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	336	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2725 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 DISSIMILATORY COPPER-CONTAINING NITRITE REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	118	0	0
			2575	1639	448	477	11			

- Molecule 2 is COPPER (I) ION (CCD ID: CU1) (formula: Cu).

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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	149	Total	O	0	0
			149	149		

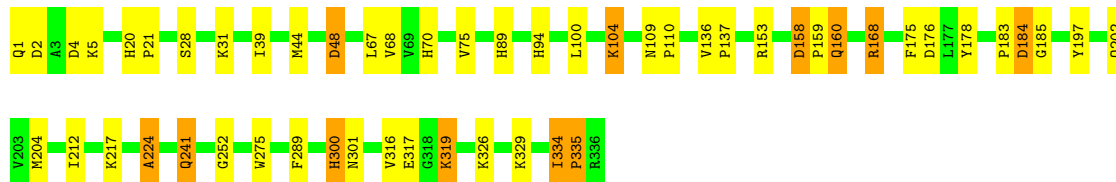
3 Residue-property plots [i](#)

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. 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. 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.

Note EDS was not executed.

- Molecule 1: DISSIMILATORY COPPER-CONTAINING NITRITE REDUCTASE

Chain A:  84% 12% .



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	106.11Å 106.11Å 63.65Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 1.90	Depositor
% Data completeness (in resolution range)	91.2 (20.00-1.90)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.171 , 0.199	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2725	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CU1

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	1.56	13/2645 (0.5%)	1.96	45/3600 (1.2%)

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	3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	334	ILE	C-N	-37.57	0.89	1.33
1	A	160	GLN	CD-NE2	-33.35	0.63	1.33
1	A	224	ALA	CA-CB	31.16	2.04	1.53
1	A	2	ASP	CB-CG	-23.91	0.92	1.52
1	A	335	PRO	C-N	-17.09	1.09	1.33
1	A	168	ARG	CG-CD	14.19	1.95	1.52
1	A	326	LYS	CD-CE	11.64	1.87	1.52
1	A	217	LYS	CG-CD	9.39	1.80	1.52
1	A	4	ASP	CB-CG	-9.06	1.29	1.52
1	A	319	LYS	CB-CG	-7.56	1.29	1.52
1	A	202	GLN	CB-CG	-5.21	1.36	1.52
1	A	329	LYS	CG-CD	-5.14	1.37	1.52
1	A	48	ASP	CA-CB	-5.09	1.44	1.53

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	334	ILE	O-C-N	-38.86	76.80	121.10
1	A	160	GLN	CG-CD-NE2	-26.90	76.05	116.40
1	A	334	ILE	CA-C-N	25.44	146.61	119.90
1	A	334	ILE	C-N-CA	25.44	146.61	119.90
1	A	224	ALA	N-CA-CB	21.96	144.04	110.22
1	A	224	ALA	CB-CA-C	-15.39	82.15	110.63
1	A	335	PRO	O-C-N	-13.33	108.17	123.10
1	A	2	ASP	CA-CB-CG	12.22	124.82	112.60
1	A	48	ASP	CB-CA-C	-10.68	90.79	110.01
1	A	1	GLN	OE1-CD-NE2	-9.77	112.83	122.60
1	A	326	LYS	CG-CD-CE	-9.59	89.24	111.30
1	A	5	LYS	CA-C-N	9.00	135.43	121.03
1	A	5	LYS	C-N-CA	9.00	135.43	121.03
1	A	217	LYS	CB-CG-CD	-8.74	91.19	111.30
1	A	44	MET	CA-CB-CG	8.62	131.35	114.10
1	A	5	LYS	O-C-N	-8.52	111.26	122.42
1	A	300	HIS	CE1-NE2-CD2	8.43	117.43	109.00
1	A	185	GLY	N-CA-C	-8.00	101.96	115.08
1	A	301	ASN	N-CA-C	-6.98	95.70	107.99
1	A	48	ASP	N-CA-CB	6.91	121.01	110.44
1	A	1	GLN	CG-CD-NE2	6.63	126.35	116.40
1	A	300	HIS	ND1-CE1-NE2	-6.37	102.03	108.40
1	A	160	GLN	OE1-CD-NE2	-6.30	116.30	122.60
1	A	2	ASP	CB-CG-OD1	6.15	132.54	118.40
1	A	334	ILE	C-N-CD	-6.14	99.84	125.00
1	A	252	GLY	N-CA-C	-6.12	107.25	115.21
1	A	70	HIS	CA-CB-CG	-5.85	107.95	113.80
1	A	153	ARG	CD-NE-CZ	5.84	132.57	124.40
1	A	317	GLU	CB-CG-CD	5.83	122.51	112.60
1	A	300	HIS	CG-CD2-NE2	-5.66	101.54	107.20
1	A	2	ASP	CB-CG-OD2	-5.62	105.48	118.40
1	A	175	PHE	CA-CB-CG	-5.61	108.19	113.80
1	A	158	ASP	CA-CB-CG	5.57	118.17	112.60
1	A	178	TYR	CA-C-N	-5.34	118.75	122.59
1	A	178	TYR	C-N-CA	-5.34	118.75	122.59
1	A	176	ASP	CA-CB-CG	5.33	117.94	112.60
1	A	75	VAL	CA-C-N	-5.32	115.30	123.07
1	A	75	VAL	C-N-CA	-5.32	115.30	123.07
1	A	241	GLN	OE1-CD-NE2	-5.31	117.29	122.60
1	A	289	PHE	CA-CB-CG	-5.27	108.53	113.80
1	A	212	ILE	CA-C-O	-5.23	115.07	120.25
1	A	197	TYR	N-CA-C	5.22	117.38	111.02
1	A	301	ASN	N-CA-CB	5.09	117.93	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	217	LYS	N-CA-C	5.07	116.23	108.42
1	A	316	VAL	N-CA-C	5.01	115.18	108.17

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	160	GLN	Sidechain
1	A	334	ILE	Mainchain
1	A	335	PRO	Mainchain

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	2575	0	2537	17	1
2	A	1	0	0	0	0
3	A	149	0	0	1	2
All	All	2725	0	2537	17	2

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 (17) 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:224:ALA:CA	1:A:224:ALA:CB	2.04	1.33
1:A:224:ALA:CB	1:A:224:ALA:C	2.37	0.98
1:A:137:PRO:HB2	1:A:204:MET:HE1	1.73	0.70
1:A:20:HIS:HE1	1:A:68:VAL:H	1.46	0.64
1:A:100:LEU:HD12	1:A:104:LYS:HD3	1.84	0.59
1:A:20:HIS:CE1	1:A:68:VAL:H	2.23	0.57
1:A:224:ALA:CB	1:A:224:ALA:O	2.53	0.56
1:A:39:ILE:HD13	1:A:89:HIS:HB2	1.95	0.47
1:A:300:HIS:ND1	1:A:300:HIS:O	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:VAL:HB	1:A:137:PRO:HD3	1.99	0.44
1:A:20:HIS:HD2	1:A:21:PRO:O	2.01	0.43
1:A:224:ALA:O	1:A:224:ALA:HB1	2.19	0.43
1:A:168:ARG:HG2	3:A:2111:HOH:O	2.20	0.41
1:A:183:PRO:O	1:A:184:ASP:C	2.62	0.41
1:A:31:LYS:HE2	1:A:31:LYS:HB3	1.85	0.41
1:A:109:ASN:HB3	1:A:110:PRO:HD2	2.03	0.40
1:A:158:ASP:HB2	1:A:159:PRO:CD	2.52	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:2042:HOH:O	3:A:2136:HOH:O[3_665]	1.92	0.28
1:A:94:HIS:NE2	3:A:2136:HOH:O[3_665]	2.11	0.09

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	333/336 (99%)	327 (98%)	6 (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	271/271 (100%)	263 (97%)	8 (3%)	36	30

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	SER
1	A	48	ASP
1	A	67	LEU
1	A	104	LYS
1	A	184	ASP
1	A	241	GLN
1	A	275	TRP
1	A	319	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	HIS
1	A	211	HIS
1	A	269	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 1 ligands modelled in this entry, 1 is 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1:GLN	C	2:ASP	N	2.38
1	A	335:PRO	C	336:ARG	N	1.09
1	A	334:ILE	C	335:PRO	N	0.89

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.