



Full wwPDB X-ray Structure Validation Report ⓘ

May 28, 2020 – 08:08 pm BST

PDB ID : 1NID
Title : THE STRUCTURE OF CU-NITRITE REDUCTASE FROM ACHROMOBACTER CYCLOCLASTES AT FIVE PH VALUES, WITH NITRITE BOUND AND WITH TYPE II CU DEPLETED
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Deposited on : 1995-07-03
Resolution : 2.20 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

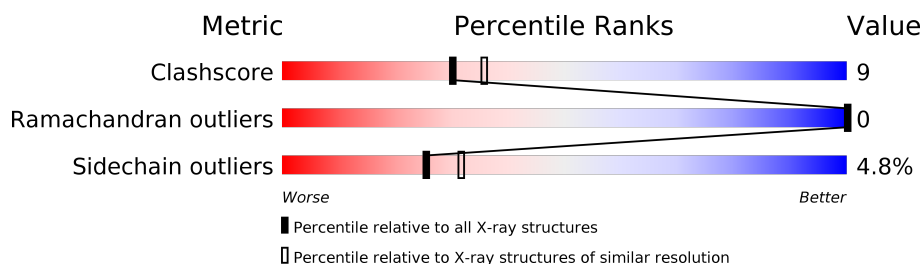
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)

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 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	340	

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
3	NO2	A	503	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2780 atoms, of which 28 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.

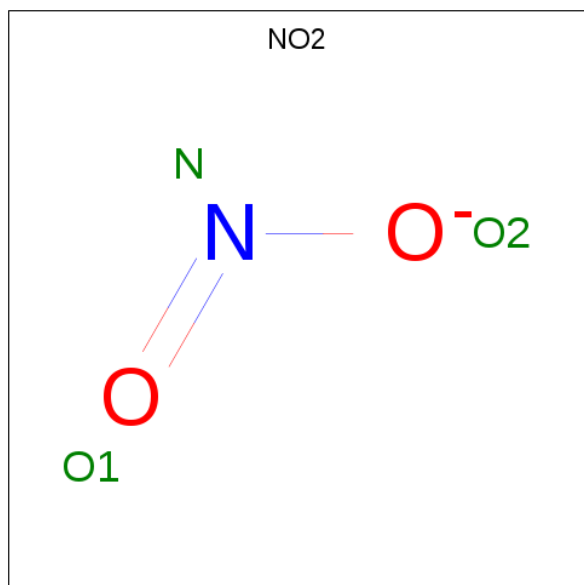
- Molecule 1 is a protein called NITRITE REDUCTASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	333	Total	C	H	N	O	S	20	0	0
			2603	1640	28	441	484	10			

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

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

- Molecule 3 is NITRITE ION (three-letter code: NO2) (formula: NO₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	N	O	0	0
			3	1	2		

- Molecule 4 is water.

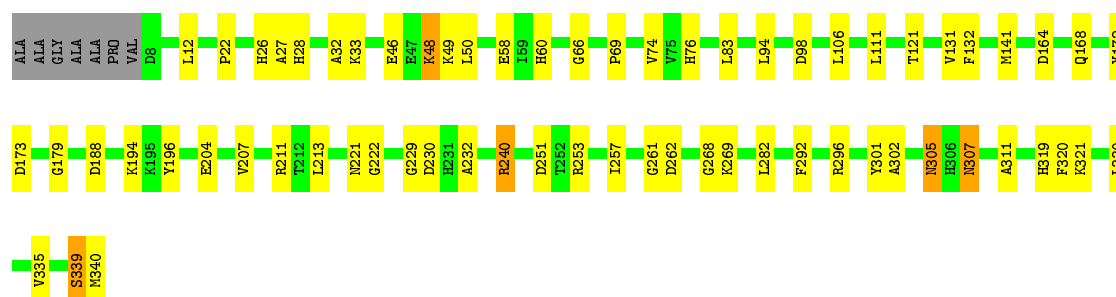
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	172	Total 172	O 172	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

• Molecule 1: NITRITE REDUCTASE

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	97.60 Å 97.60 Å 97.60 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.20 28.17 – 2.22	Depositor EDS
% Data completeness (in resolution range)	92.0 (10.00-2.20) 92.2 (28.17-2.22)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.65 (at 2.22 Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.149 , (Not available) 0.200 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	16.2	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 52.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.060 for l,-k,h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2780	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% 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: NO2, 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	0.95	0/2645	1.00	10/3605 (0.3%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	98	ASP	CB-CG-OD1	8.85	126.26	118.30
1	A	240	ARG	NE-CZ-NH1	7.47	124.03	120.30
1	A	307	ASN	N-CA-C	-7.11	91.82	111.00
1	A	251	ASP	CB-CG-OD1	5.82	123.54	118.30
1	A	305	ASN	N-CA-C	-5.70	95.61	111.00
1	A	261	GLY	N-CA-C	-5.52	99.31	113.10
1	A	282	LEU	CA-CB-CG	5.50	127.95	115.30
1	A	188	ASP	CB-CG-OD1	5.09	122.88	118.30
1	A	222	GLY	N-CA-C	5.06	125.76	113.10
1	A	268	GLY	N-CA-C	5.02	125.64	113.10

There are no chirality outliers.

There are no planarity outliers.

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	28	2503	45	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	2	0	0	0	0
3	A	3	0	0	2	0
4	A	172	0	0	16	1
All	All	2752	28	2503	47	1

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 9.

All (47) 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)
3:A:503:NO2:N	3:A:503:NO2:O1	1.68	1.27
3:A:503:NO2:N	3:A:503:NO2:O2	1.66	1.27
1:A:204:GLU:HG2	4:A:1201:HOH:O	1.74	0.86
1:A:339:SER:O	1:A:340:MET:HG3	1.76	0.85
1:A:141:MET:HG3	4:A:1145:HOH:O	1.83	0.78
1:A:76:HIS:NE2	4:A:1076:HOH:O	2.17	0.78
1:A:335:VAL:HG12	4:A:1336:HOH:O	1.89	0.71
1:A:141:MET:CE	4:A:1145:HOH:O	2.38	0.70
1:A:60:HIS:HD2	4:A:3060:HOH:O	1.73	0.69
1:A:335:VAL:CG1	4:A:1336:HOH:O	2.39	0.69
1:A:26:HIS:HE1	1:A:74:VAL:H	1.39	0.69
1:A:22:PRO:HB2	1:A:221:ASN:HD21	1.58	0.69
1:A:229:GLY:O	1:A:321:LYS:NZ	2.27	0.66
1:A:76:HIS:HD2	4:A:2079:HOH:O	1.82	0.62
1:A:60:HIS:HE1	1:A:196:TYR:O	1.85	0.60
1:A:26:HIS:CE1	1:A:74:VAL:H	2.17	0.59
1:A:28:HIS:HE1	1:A:172:TYR:OH	1.87	0.57
1:A:319:HIS:HD2	4:A:1229:HOH:O	1.89	0.55
1:A:32:ALA:HA	4:A:1076:HOH:O	2.07	0.55
1:A:232:ALA:CB	1:A:321:LYS:HZ3	2.22	0.52
1:A:141:MET:HE3	4:A:1145:HOH:O	2.06	0.51
1:A:240:ARG:HB3	1:A:292:PHE:CZ	2.45	0.51
1:A:232:ALA:CB	1:A:321:LYS:NZ	2.74	0.51
1:A:76:HIS:CD2	4:A:1076:HOH:O	2.58	0.51
1:A:132:PHE:CE2	1:A:269:LYS:HE3	2.46	0.49
1:A:221:ASN:ND2	4:A:1221:HOH:O	2.22	0.49
1:A:232:ALA:HB2	1:A:321:LYS:HZ3	1.77	0.49
1:A:173:ASP:OD2	1:A:240:ARG:HD3	2.13	0.48
1:A:26:HIS:HD2	1:A:27:ALA:O	1.96	0.48
1:A:83:LEU:O	1:A:121:THR:HA	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:MET:CG	4:A:1145:HOH:O	2.54	0.47
1:A:48:LYS:HE2	1:A:66:GLY:O	2.15	0.47
1:A:207:VAL:O	1:A:211:ARG:HG3	2.14	0.46
1:A:69:PRO:HG3	1:A:179:GLY:HA3	1.97	0.46
1:A:26:HIS:O	1:A:28:HIS:HD2	1.99	0.46
1:A:305:ASN:O	1:A:311:ALA:HB2	2.16	0.46
1:A:301:TYR:HB2	1:A:320:PHE:HB2	1.98	0.45
1:A:49:LYS:HD2	1:A:58:GLU:CD	2.36	0.45
1:A:257:ILE:HD12	1:A:302:ALA:HB3	1.99	0.44
1:A:232:ALA:HB3	1:A:321:LYS:NZ	2.32	0.44
1:A:141:MET:HE2	4:A:1145:HOH:O	2.10	0.43
1:A:46:GLU:HG2	1:A:48:LYS:HD3	2.00	0.43
1:A:232:ALA:HB2	1:A:321:LYS:NZ	2.32	0.43
1:A:262:ASP:OD2	1:A:296:ARG:NH2	2.53	0.42
1:A:164:ASP:OD2	1:A:168:GLN:HB2	2.21	0.41
1:A:335:VAL:HG11	4:A:1336:HOH:O	2.11	0.41
1:A:194:LYS:HZ2	1:A:194:LYS:HG2	1.82	0.40

All (1) 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)
1:A:12:LEU:O	4:A:2159:HOH:O[11_545]	1.97	0.23

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	331/340 (97%)	324 (98%)	7 (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	271/273 (99%)	258 (95%)	13 (5%)	25	32

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	LYS
1	A	48	LYS
1	A	50	LEU
1	A	94	LEU
1	A	106	LEU
1	A	111	LEU
1	A	131	VAL
1	A	213	LEU
1	A	230	ASP
1	A	253	ARG
1	A	307	ASN
1	A	330	LEU
1	A	339	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	HIS
1	A	28	HIS
1	A	60	HIS
1	A	76	HIS
1	A	78	ASN
1	A	307	ASN
1	A	319	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	NO2	A	503	2	1,2,2	9.06	1 (100%)	0,1,1	0.00	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	503	NO2	O1-N	9.06	1.68	1.22

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	503	NO2	2	0

5.7 Other polymers [i](#)

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](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.