

# wwPDB X-ray Structure Validation Summary Report (i)

#### Dec 12, 2023 – 11:44 am GMT

PDB ID : 2XX0

Title : STRUCTURE OF THE N90S-H254F MUTANT OF NITRITE REDUCTASE

FROM ALCALIGENES XYLOSOXIDANS

Authors: Antonyuk, S.V.; Leferink, N.G.H.; Han, C.; Heyes, D.J.; Rigby, S.E.J.; Hough,

M.A.; Eady, R.R.; Scrutton, N.S.; Hasnain, S.S.

Deposited on : 2010-11-07

Resolution : 1.46 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) 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 (1)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.36

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)

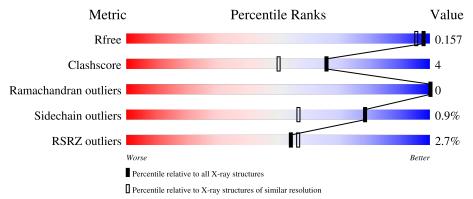
Validation Pipeline (wwPDB-VP) : 2.36

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$ 

The reported resolution of this entry is 1.46 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	1156 (1.46-1.46)
Clashscore	141614	1202 (1.46-1.46)
Ramachandran outliers	138981	1178 (1.46-1.46)
Sidechain outliers	138945	1178 (1.46-1.46)
RSRZ outliers	127900	1139 (1.46-1.46)

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 <=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	336	92%	7% •
1	В	336	94%	5% •



# 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 6071 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 RE-DUCTASE.

Mol	Chain	Residues	${f Atoms}$				ZeroOcc	AltConf	Trace	
1	A	335	Total 2657	C 1702	N 456	O 486	S 13	0	16	0
1	В	336	Total 2660	C 1707	N 455	O 486	S 12	0	16	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLU	-	expression tag	UNP O68601
A	90	SER	GLN	engineered mutation	UNP O68601
A	254	PHE	HIS	engineered mutation	UNP O68601
В	1	GLU	-	expression tag	UNP O68601
В	90	SER	GLN	engineered mutation	UNP O68601
В	254	PHE	HIS	engineered mutation	UNP O68601

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

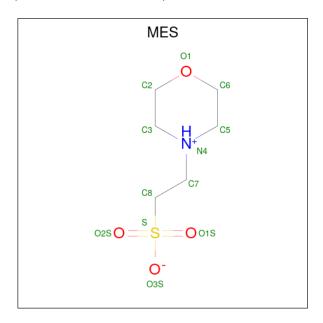
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Cu 2 2	0	0
2	В	2	Total Cu 2 2	0	0

• Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	3	Total Zn 3 3	0	0
3	В	3	Total Zn 3 3	0	0

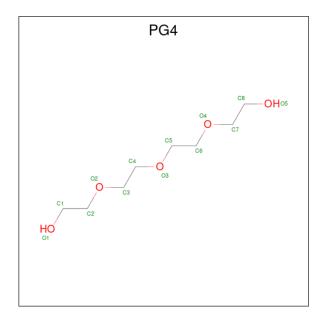


• Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula:  $C_6H_{13}NO_4S$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
1	Λ	1	Total	С	N	О	S	0	0
4	Α	1	12	6	1	4	1	0	0
1	D	1	Total	С	N	О	S	0	0
4	Ъ	1	12	6	1	4	1	0	U

• Molecule 5 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula:  $C_8H_{18}O_5$ ).





$\mathbf{Mol}$	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 13 8 5	0	0
5	В	1	Total C O 13 8 5	0	0

## $\bullet\,$ Molecule 6 is water.

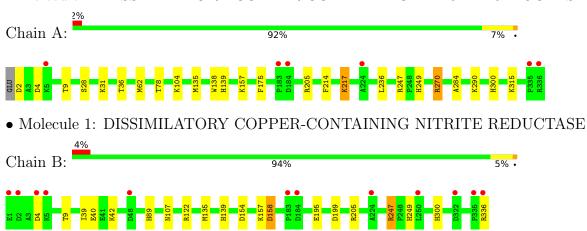
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	367	Total O 367 367	0	0
6	В	327	Total O 327 327	0	0



# 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: DISSIMILATORY COPPER-CONTAINING NITRITE REDUCTASE





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3	Depositor
Cell constants	89.25Å 89.25Å 288.27Å	Donogitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	23.00 - 1.46	Depositor
Resolution (A)	22.70 - 1.46	EDS
% Data completeness	98.9 (23.00-1.46)	Depositor
(in resolution range)	93.6 (22.70-1.46)	EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.33 (at 1.46Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
Ρ. Р.	0.125 , 0.151	Depositor
$R, R_{free}$	0.135 , $0.157$	DCC
$R_{free}$ test set	6961 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	17.1	Xtriage
Anisotropy	0.418	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.35, 46.9	EDS
L-test for twinning <sup>2</sup>	$< L >=0.48, < L^2>=0.31$	Xtriage
Estimated twinning fraction	0.033 for -h-k,k,-l	Xtriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	6071	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	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 45.21 % 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 1.3656e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: ZN, PG4, MES, 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	
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.79	0/2773	0.87	8/3767 (0.2%)	
1	В	0.79	1/2777 (0.0%)	0.86	6/3774~(0.2%)	
All	All	0.79	1/5550 (0.0%)	0.87	$14/7541 \ (0.2\%)$	

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	В	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\textup{\AA})$	Ideal(Å)
1	В	195	GLU	CB-CG	-6.41	1.40	1.52

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
1	В	122	ARG	NE-CZ-NH1	7.20	123.90	120.30
1	В	122	ARG	NE-CZ-NH2	-7.17	116.72	120.30
1	В	205	ARG	NE-CZ-NH2	-6.26	117.17	120.30
1	В	158	ASP	CB-CG-OD2	-6.24	112.69	118.30
1	A	270[A]	ARG	NE-CZ-NH2	-5.95	117.32	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	A	300	HIS	Peptide
1	В	300	HIS	Peptide

### 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)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
1	A	2657	0	2678	29	0
1	В	2660	0	2676	14	0
2	A	2	0	0	0	0
2	В	2	0	0	0	0
3	A	3	0	0	0	0
3	В	3	0	0	0	0
4	A	12	0	12	0	0
4	В	12	0	12	0	0
5	A	13	0	18	0	0
5	В	13	0	18	0	0
6	A	367	0	0	13	2
6	В	327	0	0	8	0
All	All	6071	0	5414	43	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.

The worst 5 of 43 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{aligned} \operatorname{Clash} \ \operatorname{overlap}\ (\mathring{\mathbf{A}}) \end{aligned}$
1:A:270[A]:ARG:NH2	6:A:2306:HOH:O	1.81	1.10
1:A:135[B]:MET:HE1	1:A:139:HIS:HE2	1.22	0.99
1:A:249:HIS:NE2	6:A:2291:HOH:O	1.96	0.95
1:A:135[B]:MET:CE	1:A:139:HIS:HE2	1.82	0.90
1:B:249:HIS:NE2	6:B:2259:HOH:O	2.04	0.88

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	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance}  ({\rm \AA}) \end{array}$	Clash overlap (Å)
6:A:2290:HOH:O	6:A:2323:HOH:O[3_445]	1.93	0.27
6:A:2289:HOH:O	6:A:2289:HOH:O[3_445]	2.13	0.07

### 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	Perce	$\mathbf{ntiles}$
1	A	349/336 (104%)	343 (98%)	6 (2%)	0	100	100
1	В	350/336~(104%)	345 (99%)	5 (1%)	0	100	100
All	All	699/672 (104%)	688 (98%)	11 (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	Rotameric Outliers		Percentiles		
1	A	286/271 (106%)	283 (99%)	3 (1%)	76	52		
1	В	$285/271 \ (105\%)$	281 (99%)	4 (1%)	67	37		
All	All	571/542 (105%)	564 (99%)	7 (1%)	78	43		

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	$\operatorname{Res}$	Type
1	В	4[A]	ASP
1	В	4[B]	ASP

Continued on next page...



Continued from previous page...

Mol	Chain	Res	Type
1	В	247	ARG
1	В	158	ASP
1	A	217[B]	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	269	GLN
1	В	266	ASN

#### 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 monosaccharides in this entry.

### 5.6 Ligand geometry (i)

Of 14 ligands modelled in this entry, 10 are monoatomic - leaving 4 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	Trmo	Type Chain	, Dec	Res Link	Bond lengths			Bond angles		
MIOI	Type		nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	MES	В	1341	-	12,12,12	1.75	2 (16%)	14,16,16	5.67	9 (64%)
5	PG4	В	1342	-	12,12,12	0.49	0	11,11,11	0.55	0
5	PG4	A	1342	-	12,12,12	0.44	0	11,11,11	0.58	0
4	MES	A	1341	-	12,12,12	1.42	1 (8%)	14,16,16	5.01	8 (57%)



In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	$\operatorname{Res}$	Link	Chirals	Torsions	Rings
4	MES	В	1341	-	-	2/6/14/14	0/1/1/1
5	PG4	В	1342	-	-	1/10/10/10	-
5	PG4	A	1342	-	-	0/10/10/10	-
4	MES	A	1341	-	-	1/6/14/14	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(\text{\AA})$
4	В	1341	MES	C8-S	-4.59	1.71	1.77
4	A	1341	MES	C8-S	-3.86	1.72	1.77
4	В	1341	MES	O1S-S	3.04	1.54	1.45

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$Ideal(^{o})$
4	В	1341	MES	O1S-S-C8	-12.68	91.65	106.92
4	A	1341	MES	O2S-S-C8	-11.43	93.15	106.92
4	В	1341	MES	O2S-S-C8	-9.73	95.20	106.92
4	A	1341	MES	O3S-S-C8	-9.67	90.13	105.77
4	В	1341	MES	O3S-S-C8	-7.88	93.02	105.77

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1341	MES	C8-C7-N4-C5
4	В	1341	MES	C8-C7-N4-C5
5	В	1342	PG4	C8-C7-O4-C6
4	В	1341	MES	C8-C7-N4-C3

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 (i)

### 6.1 Protein, DNA and RNA chains (i)

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,  $95^{th}$  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	$\langle { m RSRZ} \rangle$	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	335/336~(99%)	-0.45	6 (1%) 68 69	11, 19, 30, 48	18 (5%)
1	В	336/336 (100%)	-0.34	12 (3%) 42 46	12, 21, 33, 48	23 (6%)
All	All	671/672 (99%)	-0.40	18 (2%) 54 56	11, 20, 32, 48	41 (6%)

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	336	ARG	4.7
1	В	335	PRO	4.4
1	A	336	ARG	4.2
1	В	5	LYS	3.9
1	A	5	LYS	3.6

## 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 monosaccharides 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,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
4	MES	В	1341	12/12	0.88	0.13	26,28,39,39	12
4	MES	A	1341	12/12	0.91	0.14	27,30,37,40	12
5	PG4	A	1342	13/13	0.91	0.12	34,37,47,47	0
5	PG4	В	1342	13/13	0.92	0.14	34,39,49,52	0
3	ZN	A	1343	1/1	0.99	0.02	30,30,30,30	1
3	ZN	В	1343	1/1	0.99	0.03	36,36,36,36	1
2	CU	A	1337	1/1	1.00	0.02	20,20,20,20	0
3	ZN	В	1339	1/1	1.00	0.04	14,14,14,14	1
3	ZN	В	1340	1/1	1.00	0.01	24,24,24,24	0
2	CU	A	1339	1/1	1.00	0.04	14,14,14,14	1
2	CU	В	1337	1/1	1.00	0.02	23,23,23,23	0
2	CU	В	1338	1/1	1.00	0.04	17,17,17,17	1
3	ZN	A	1338	1/1	1.00	0.04	13,13,13,13	1
3	ZN	A	1340	1/1	1.00	0.06	19,19,19,19	1

# 6.5 Other polymers (i)

There are no such residues in this entry.

