



wwPDB X-ray Structure Validation Summary Report ⓘ

May 17, 2020 – 03:53 am BST

PDB ID : 5I5I
Title : Shewanella denitrificans nitrous oxide reductase, app form
Authors : Schneider, L.K.; Einsle, O.
Deposited on : 2016-02-15
Resolution : 2.14 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 ⓘ symbol.

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

MolProbity : 4.02b-467
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

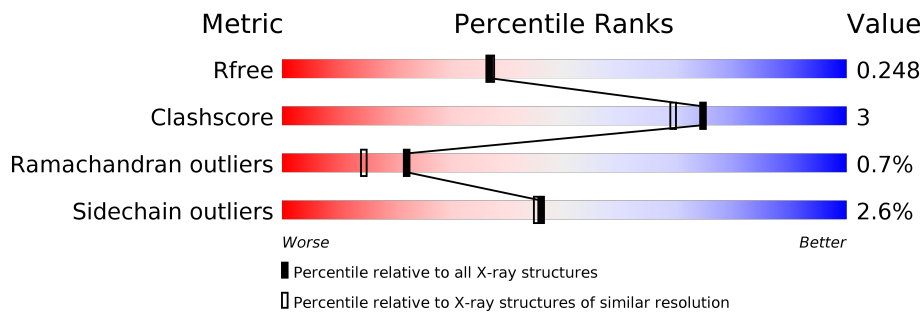
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.14 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))
R_{free}	130704	2523 (2.16-2.12)
Clashscore	141614	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)

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	636	 74% 9% 15%
1	B	636	 77% 7% 16%

2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 8589 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 Nitrous-oxide reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	539	4254	2687	742	795	30	0	0	0
1	B	537	4243	2682	741	790	30	0	2	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	629	LEU	-	expression tag	UNP Q12M27
A	630	GLU	-	expression tag	UNP Q12M27
A	631	HIS	-	expression tag	UNP Q12M27
A	632	HIS	-	expression tag	UNP Q12M27
A	633	HIS	-	expression tag	UNP Q12M27
A	634	HIS	-	expression tag	UNP Q12M27
A	635	HIS	-	expression tag	UNP Q12M27
A	636	HIS	-	expression tag	UNP Q12M27
B	629	LEU	-	expression tag	UNP Q12M27
B	630	GLU	-	expression tag	UNP Q12M27
B	631	HIS	-	expression tag	UNP Q12M27
B	632	HIS	-	expression tag	UNP Q12M27
B	633	HIS	-	expression tag	UNP Q12M27
B	634	HIS	-	expression tag	UNP Q12M27
B	635	HIS	-	expression tag	UNP Q12M27
B	636	HIS	-	expression tag	UNP Q12M27

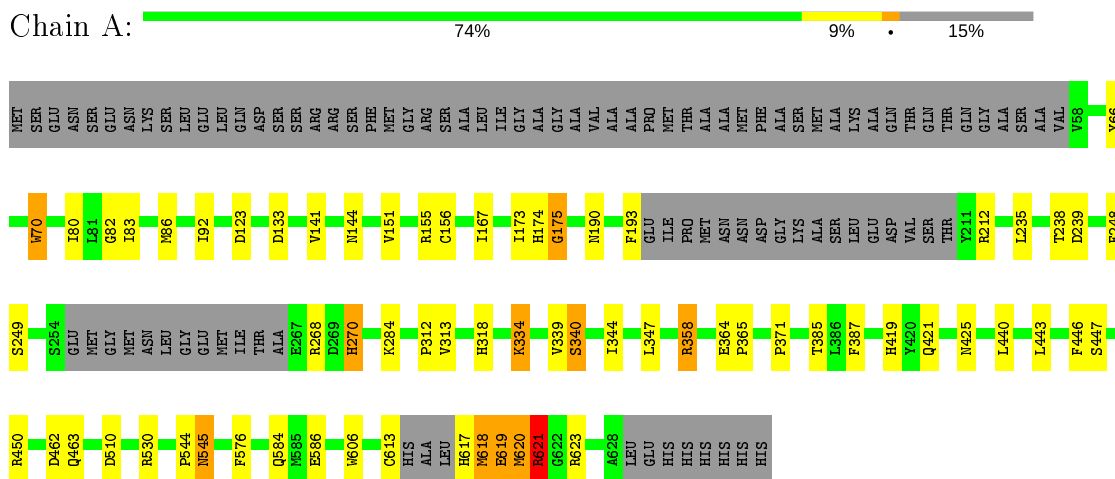
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	50	Total	O	0	0
			50	50		
2	B	42	Total	O	0	0
			42	42		

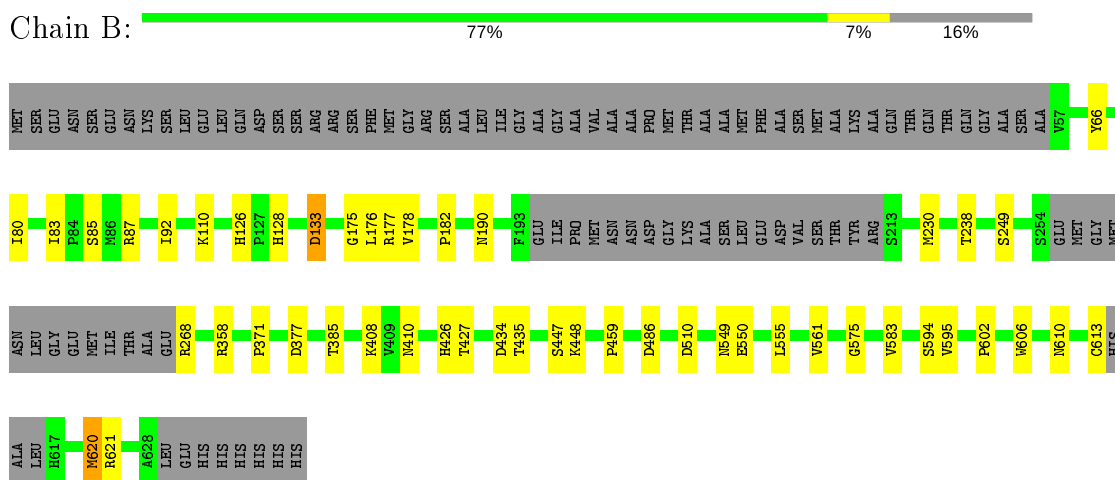
3 Residue-property plots i

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: Nitrous-oxide reductase



- Molecule 1: Nitrous-oxide reductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.08Å 121.62Å 178.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.54 – 2.14 48.10 – 1.57	Depositor EDS
% Data completeness (in resolution range)	99.3 (100.54-2.14) 97.2 (48.10-1.57)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.43 (at 1.57Å)	Xtrriage
Refinement program	REFMAC 5.8.0131	Depositor
R, R_{free}	0.237 , 0.286 0.251 , 0.248	Depositor DCC
R_{free} test set	8559 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	2.4	Xtrriage
Anisotropy	0.404	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 58.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.80	EDS
Total number of atoms	8589	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 43.18 % 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 1.8313e-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 [i](#)

5.1 Standard geometry [i](#)

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	0.76	1/4352 (0.0%)	0.89	7/5889 (0.1%)
1	B	0.75	0/4348	0.88	4/5885 (0.1%)
All	All	0.76	1/8700 (0.0%)	0.88	11/11774 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	70	TRP	CB-CG	-6.86	1.38	1.50

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	268	ARG	NE-CZ-NH1	6.58	123.59	120.30
1	A	239	ASP	CB-CG-OD1	6.09	123.78	118.30
1	B	268	ARG	NE-CZ-NH2	-6.05	117.28	120.30
1	A	123	ASP	CB-CG-OD1	5.80	123.52	118.30
1	B	377	ASP	CB-CG-OD1	5.67	123.40	118.30

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	4254	0	4154	31	0
1	B	4243	0	4149	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	50	0	0	1	0
2	B	42	0	0	1	0
All	All	8589	0	8303	54	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 3.

The worst 5 of 54 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:80:ILE:HD11	1:B:92:ILE:HD11	1.69	0.74
1:A:80:ILE:HD11	1:A:92:ILE:HD11	1.78	0.65
1:A:238:THR:HG22	1:A:249:SER:OG	1.96	0.64
1:B:190:ASN:OD1	1:B:238:THR:HG23	1.97	0.64
1:A:270:HIS:ND1	2:A:701:HOH:O	2.31	0.61

There are no symmetry-related clashes.

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	531/636 (84%)	505 (95%)	21 (4%)	5 (1%)	17 10
1	B	531/636 (84%)	502 (94%)	27 (5%)	2 (0%)	34 29
All	All	1062/1272 (84%)	1007 (95%)	48 (4%)	7 (1%)	22 14

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	620	MET
1	A	175	GLY

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Mol	Chain	Res	Type
1	A	618	MET
1	A	620	MET
1	A	133	ASP

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	466/541 (86%)	451 (97%)	15 (3%)	39	37
1	B	466/541 (86%)	457 (98%)	9 (2%)	57	59
All	All	932/1082 (86%)	908 (97%)	24 (3%)	46	45

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	545	ASN
1	A	619	GLU
1	B	613	CYS
1	A	586	GLU
1	A	613	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	421	GLN
1	A	463	GLN
1	B	410	ASN
1	A	321	ASN
1	B	270	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](#)

There are no ligands in this entry.

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

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

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

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

6.3 Carbohydrates

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

6.4 Ligands

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

6.5 Other polymers

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