

Full wwPDB X-ray Structure Validation Report (i)

May 29, 2024 – 12:50 PM EDT

PDB ID : 1NZR

Title : CRYSTAL STRUCTURE OF THE AZURIN MUTANT NICKEL-

TRP48MET FROM PSEUDOMONAS AERUGINOSA AT 2.2 ANGSTROMS

RESOLUTION

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Deposited on : 1994-12-09

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 (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 (i)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : NOT EXECUTED EDS : NOT EXECUTED

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

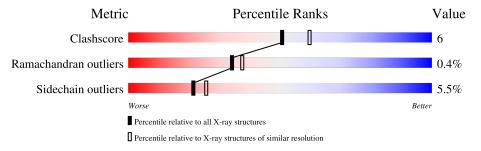
Validation Pipeline (wwPDB-VP) : 2.36.2

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 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
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 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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain		
1	A	128	79%	20%	•
1	В	128	79%	20%	.
1	С	128	84%	14%	.
1	D	128	75%	22%	•



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5751 atoms, of which 1538 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 AZURIN.

Mol	Chain	Residues		Atoms					ZeroOcc	AltConf	Trace
1	Λ	128	Total	С	Н	N	О	S	0	0	0
1	A		1183	601	216	163	193	10	0		
1	В	128	Total	С	Н	N	О	S	0	0	0
1	Ъ	120	1183	601	216	163	193	10		0	0
1	С	128	Total	С	Н	N	О	S	0	0	0
1		120	1183	601	216	163	193	10	0		
1	D	128	Total	С	Н	N	О	S	0	0	0
1	ע	120	1183	601	216	163	193	10	U	U	

There are 4 discrepancies between the modelled and reference sequences:

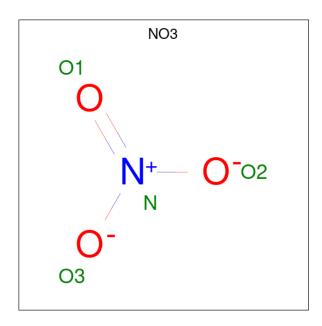
Chain	Residue	Modelled	Actual	Comment	Reference
A	48	MET	TRP	engineered mutation	UNP P00282
В	48	MET	TRP	engineered mutation	UNP P00282
С	48	MET	TRP	engineered mutation	UNP P00282
D	48	MET	TRP	engineered mutation	UNP P00282

• Molecule 2 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ni 1 1	0	0
2	В	1	Total Ni 1 1	0	0
2	С	1	Total Ni 1 1	0	0
2	D	1	Total Ni 1 1	0	0

• Molecule 3 is NITRATE ION (three-letter code: NO3) (formula: NO₃).





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
3	A	1	Total 4	N 1	O 3	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	89	Total H	О	0	0
	11	00	267 178	89	Ü	0
4	В	92	Total H	O	0	0
4	Б	92	276 184	92	U	U
4	С	78	Total H	О	0	0
4		10	234 156	78	U	U
4	D	78	Total H	О	0	0
4	ש	10	234 156	78	U	U

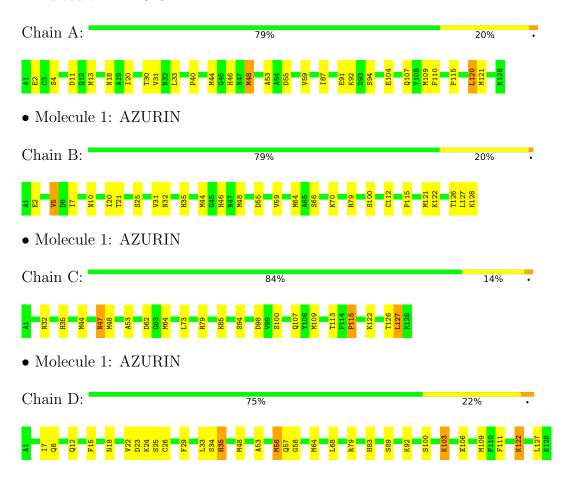


3 Residue-property plots (i)

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: AZURIN





4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	57.40Å 80.40Å 110.30Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.20	Depositor
% Data completeness	(Not available) ((Not available)-2.20)	Depositor
(in resolution range)	, , ,	Беровног
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.170 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5751	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP



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: NI, NO3

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	Clasia	Bond	lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.79	0/982	1.34	2/1322~(0.2%)	
1	В	0.79	0/982	1.41	4/1322~(0.3%)	
1	С	0.84	0/982	1.43	5/1322~(0.4%)	
1	D	0.83	0/982	1.44	10/1322~(0.8%)	
All	All	0.81	0/3928	1.41	21/5288 (0.4%)	

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\mathbf{Ideal}(^{o})$
1	В	79	ARG	NE-CZ-NH1	12.60	126.60	120.30
1	В	79	ARG	NE-CZ-NH2	-8.59	116.00	120.30
1	D	103	LYS	CA-CB-CG	8.36	131.78	113.40
1	С	127	LEU	CA-CB-CG	7.09	131.61	115.30
1	D	79	ARG	NE-CZ-NH1	6.97	123.78	120.30
1	D	79	ARG	NE-CZ-NH2	-6.79	116.91	120.30
1	D	127	LEU	CA-CB-CG	6.15	129.45	115.30
1	D	103	LYS	CB-CA-C	-6.13	98.13	110.40
1	D	64	MET	CA-CB-CG	-6.07	102.97	113.30
1	A	120	LEU	CA-CB-CG	6.02	129.15	115.30
1	D	103	LYS	CB-CG-CD	-5.52	97.24	111.60
1	D	122	LYS	CA-CB-CG	5.50	125.50	113.40
1	С	79	ARG	NE-CZ-NH2	-5.47	117.57	120.30
1	A	2	GLU	CA-CB-CG	-5.36	101.61	113.40
1	D	12	GLN	CA-CB-CG	5.32	125.09	113.40
1	В	44	MET	CA-CB-CG	5.27	122.27	113.30
1	D	56	MET	CG-SD-CE	-5.18	91.92	100.20
1	В	122	LYS	CG-CD-CE	-5.16	96.42	111.90
1	С	44	MET	CA-CB-CG	5.11	121.99	113.30
1	С	73	LEU	CA-CB-CG	5.10	127.04	115.30

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Mol	Chain	Res	Type	Atoms	${f Z}$	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
1	С	62	ASP	CB-CG-OD1	5.01	122.81	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	967	216	951	14	0
1	В	967	216	951	11	1
1	С	967	216	951	8	0
1	D	967	216	951	14	1
2	A	1	0	0	0	0
2	В	1	0	0	0	0
2	С	1	0	0	0	0
2	D	1	0	0	0	0
3	A	4	0	0	0	0
4	A	89	178	0	1	0
4	В	92	184	0	2	0
4	С	78	156	0	0	0
4	D	78	156	0	0	0
All	All	4213	1538	3804	44	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 6.

All (44) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:C:47:ASN:HD21	1:C:113:THR:H	1.43	0.66
1:A:13:MET:HE3	1:A:120:LEU:HG	1.79	0.64
1:A:53:ALA:HA	1:A:109:MET:HG2	1.85	0.59
1:C:107:GLN:HE22	1:D:58:GLY:HA2	1.69	0.58
1:C:32:ASN:HA	1:C:94:SER:HB3	1.85	0.58
1:A:33:LEU:O	1:A:92:LYS:HD2	2.04	0.57

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		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:A:11:ASP:HA	1:A:44:MET:HG2	1.87	0.56	
1:D:48:MET:O	1:D:83:HIS:HA	2.06	0.54	
1:A:104:GLU:HG2	4:A:674:HOH:O	2.08	0.54	
1:C:122:LYS:NZ	1:D:57:GLN:HE22	2.06	0.54	
1:D:23:ASP:HB3	1:D:26:CYS:SG	2.50	0.52	
1:D:7:ILE:HG23	1:D:33:LEU:HD12	1.91	0.52	
1:B:46:HIS:CE1	1:B:121:MET:SD	3.04	0.51	
1:D:34:SER:HB3	1:D:92:LYS:HD3	1.95	0.49	
1:B:31:VAL:HG11	1:B:48:MET:HG3	1.93	0.49	
1:A:46:HIS:CE1	1:A:121:MET:SD	3.06	0.49	
1:B:7:ILE:HG22	1:B:32:ASN:O	2.13	0.49	
1:C:53:ALA:HA	1:C:109:MET:HG2	1.95	0.48	
1:A:13:MET:HG2	1:A:44:MET:SD	2.55	0.46	
1:B:46:HIS:HA	1:B:112:CYS:SG	2.55	0.46	
1:A:55:ASP:O	1:A:59:VAL:HG23	2.15	0.46	
1:A:4:SER:HA	1:A:30:THR:O	2.15	0.46	
1:D:22:VAL:HG13	1:D:29:PHE:CD1	2.52	0.45	
1:D:103:LYS:HD3	1:D:106:GLU:HB2	1.99	0.44	
1:B:10:ASN:HB2	4:B:716:HOH:O	2.16	0.44	
1:D:35:HIS:O	1:D:89:SER:HA	2.18	0.44	
1:C:85:LYS:HB3	1:C:85:LYS:HE2	1.81	0.44	
1:C:107:GLN:NE2	1:D:58:GLY:HA2	2.31	0.43	
1:A:20:ILE:HG13	1:A:110:PHE:CE1	2.53	0.43	
1:B:21:THR:HG23	1:B:128:LYS:HB2	2.00	0.43	
1:D:103:LYS:HE2	1:D:103:LYS:HB3	1.71	0.43	
1:C:64:MET:HG3	1:C:115:PRO:HG3	2.01	0.43	
1:D:53:ALA:HA	1:D:109:MET:HG2	2.00	0.43	
1:D:8:GLN:O	1:D:15:PHE:HA	2.19	0.42	
1:B:64:MET:HG3	1:B:115:PRO:HG3	2.01	0.42	
1:A:31:VAL:HG21	1:A:48:MET:HE3	2.01	0.42	
1:B:64:MET:HB2	4:B:796:HOH:O	2.19	0.42	
1:A:31:VAL:HG21	1:A:48:MET:CE	2.50	0.41	
1:B:5:VAL:HG11	1:B:20:ILE:HD13	2.02	0.41	
1:D:56:MET:HG3	1:D:111:PHE:CE1	2.55	0.41	
1:B:66:SER:O	1:B:70:LYS:HG2	2.20	0.41	
1:A:87:ILE:HB	1:A:91:GLU:HB2	2.02	0.41	
1:A:4:SER:HB3	1:A:30:THR:HB	2.03	0.41	
1:B:55:ASP:O	1:B:59:VAL:HG23	2.21	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	$egin{aligned} & ext{Interatomic} \ & ext{distance} \ & ext{(Å)} \end{aligned}$	Clash overlap (Å)
1:B:100:SER:HG	1:D:24:LYS:HZ2[2_564]	1.27	0.33

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	entiles
1	A	126/128 (98%)	123 (98%)	2 (2%)	1 (1%)	19	19
1	В	$126/128 \; (98\%)$	119 (94%)	6 (5%)	1 (1%)	19	19
1	C	$126/128 \; (98\%)$	119 (94%)	7 (6%)	0	100	100
1	D	126/128 (98%)	122 (97%)	4 (3%)	0	100	100
All	All	$504/512 \ (98\%)$	483 (96%)	19 (4%)	2 (0%)	34	37

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	2	GLU
1	A	115	PRO

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	110/110 (100%)	105 (96%)	5 (4%)	27	34	
1	В	110/110 (100%)	105 (96%)	5 (4%)	27	34	
1	С	110/110 (100%)	102 (93%)	8 (7%)	14	15	

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Mol	Chain	Analysed	Rotameric	Outliers	Perce	\mathbf{ntiles}
1	D	110/110 (100%)	104 (94%) 6 (6%)		21	26
All	All	440/440 (100%)	416 (94%)	24 (6%)	21	26

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	ASN
1	A	40	PRO
1	A A A	48	MET
1	A	94	SER
1	A	107	GLN
1	В	5	VAL
1	В	25	SER
1	В	35	HIS
1	В	126	THR
1	В	127	LEU
1	С	35	HIS
1	B C C C C C C C C C	47	ASN
1	С	48	MET
1	С	98	ASP
1	С	100	SER
1	С	115	PRO
1	С	126	THR
1		127	LEU
1	D	18	ASN
1	D	25	SER
1	D	35	HIS
1	D	68	LEU
1	D	100	SER
1	D	122	LYS

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

Mol	Chain	Res	Type	
1	В	38	ASN	
1	С	38	ASN	
1	С	2 47 AS		
1	С	107	GLN	
1	D	8	GLN	
1	D	18	ASN	
1	D	57	GLN	



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 5 ligands modelled in this entry, 4 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	n Pos	$_{ m s}\mid_{ m Link}$	\mathbf{B}	Bond lengths		Bond angles			
	Type	Chain	filalli Ites	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NO3	A	130	-	1,3,3	0.61	0	0,3,3	-	-

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)

There are no chain breaks in this entry.



6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

