

Full wwPDB X-ray Structure Validation Report (i)

Jun 12, 2024 – 06:53 AM EDT

PDB ID	:	1EJ2
Title	:	Crystal structure of methanobacterium thermoautotrophicum nicotinamide
		mononucleotide adenylyl transferase with bound $NAD+$
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		Consortium (NESG)
Deposited on	:	2000-02-29
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 (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:

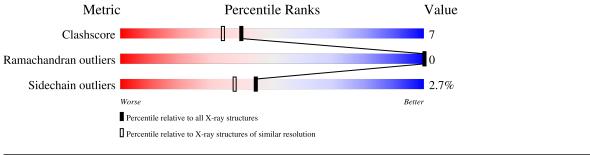
Xtriage (Phenix)	: : :	2022.3.0, CSD as543be (2022) NOT EXECUTED NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)		<u> </u>
Ideal geometry (DNA, RNA)		
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

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

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	Similar resolution
Methe	$(\# { m Entries})$	$(\# { m Entries}, { m resolution} { m range}({ m \AA}))$
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain		
1	А	181	80%	12%	• 8%



2 Entry composition (i)

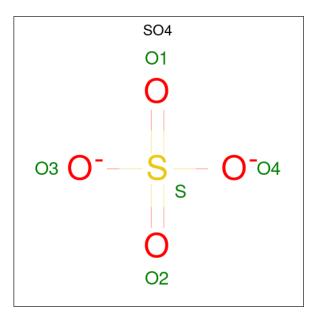
There are 5 unique types of molecules in this entry. The entry contains 1510 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 NICOTINAMIDE MONONUCLEOTIDE ADENYLYLTRANS-FERASE.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	А	167	Total 1340	C 851	N 237	0 244	S 8	0	0	0

• Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	А	1	Total 5	0 4	S 1	0	0

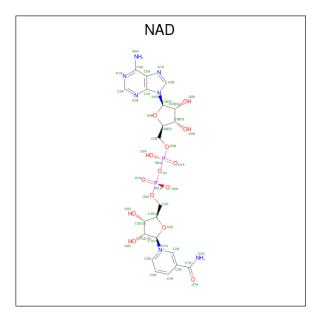
• Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	Total Na 1 1	0	0

• Molecule 4 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD)



(formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
4	Δ	1	Total	С	Ν	Ο	Р	0	0
4	Π	1	44	21	7	14	2	0	U

• Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	А	120	Total 120	O 120	0	0

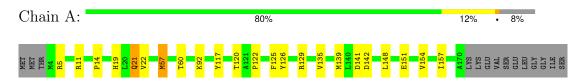


3 Residue-property plots (i)

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. 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: NICOTINAMIDE MONONUCLEOTIDE ADENYLYLTRANSFERASE





4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 63 2 2	Depositor	
Cell constants	89.08Å 89.08Å 109.93Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor	
Resolution (Å)	28.30 - 1.90	Depositor	
% Data completeness	91.0 (28.30-1.90)	Depositor	
(in resolution range)	51.0 (20.00-1.00)	Depositor	
R_{merge}	0.04	Depositor	
R_{sym}	(Not available)	Depositor	
Refinement program	$CNS \ 0.5$	Depositor	
R, R_{free}	0.211 , 0.241	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	1510	wwPDB-VP	
Average B, all atoms $(Å^2)$	36.0	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: NA, NAD, SO4

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		
	Unain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.72	0/1369	0.82	1/1854~(0.1%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	A	5	ARG	NE-CZ-NH2	-6.14	117.23	120.30

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	А	1340	0	1344	20	0
2	А	5	0	0	0	0
3	А	1	0	0	0	0
4	А	44	0	26	1	0
5	А	120	0	0	0	0
All	All	1510	0	1370	20	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 7.



$1 \mathrm{EJ2}$

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:MET:HE2	1:A:57:MET:HA	1.20	1.15
1:A:57:MET:HA	1:A:57:MET:CE	1.97	0.94
1:A:21:GLN:HG3	1:A:22:VAL:N	1.89	0.87
1:A:21:GLN:HE21	1:A:125:PHE:HB2	1.38	0.85
1:A:92:LYS:HE2	1:A:117:TYR:OH	1.93	0.68
1:A:21:GLN:HG2	1:A:125:PHE:HB2	1.75	0.68
1:A:151:GLU:O	1:A:154:VAL:HG22	1.98	0.63
1:A:21:GLN:NE2	1:A:125:PHE:HB2	2.13	0.63
1:A:21:GLN:HG2	1:A:125:PHE:CB	2.31	0.60
1:A:151:GLU:HA	1:A:154:VAL:HG22	1.86	0.57
1:A:135:VAL:O	1:A:139:MET:HG3	2.05	0.57
1:A:151:GLU:O	1:A:154:VAL:CG2	2.58	0.51
1:A:19:HIS:O	1:A:22:VAL:HG12	2.10	0.50
1:A:139:MET:HE1	1:A:157:ILE:HD13	1.97	0.47
1:A:11:ARG:HH11	1:A:11:ARG:HG3	1.80	0.47
1:A:141:ASP:O	1:A:142:ASP:HB2	2.17	0.45
1:A:120:THR:O	1:A:122:PRO:HD3	2.19	0.43
1:A:57:MET:HE2	1:A:60:THR:HB	2.01	0.43
1:A:126:TYR:HB3	1:A:129:ARG:HG2	2.01	0.41
1:A:11:ARG:HG2	4:A:1339:NAD:H3D	2.04	0.40

All (20) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

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	Perce	entiles
1	А	$165/181 \ (91\%)$	164 (99%)	1 (1%)	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	А	148/160~(92%)	144 (97%)	4 (3%)	44 38	

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	14	PRO
1	А	21	GLN
1	А	57	MET
1	А	148	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	21	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 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.



 $1 \mathrm{EJ2}$

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	Turne	Chain	Res	Link	В	ond leng	gths	B	ond ang	les
	Type	Unain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAD	А	1339	-	42,48,48	2.67	11 (26%)	50,73,73	2.07	9 (18%)
2	SO4	А	1759	3	4,4,4	0.31	0	6,6,6	0.28	0

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.

Mo	l Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAD	А	1339	-	-	8/26/62/62	0/5/5/5

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	Ideal(Å)
4	А	1339	NAD	PN-O3	7.78	1.67	1.59
4	А	1339	NAD	C4N-C3N	7.68	1.51	1.39
4	А	1339	NAD	C5N-C4N	7.42	1.51	1.38
4	А	1339	NAD	C2N-C3N	5.01	1.46	1.39
4	А	1339	NAD	O7N-C7N	4.51	1.32	1.24
4	А	1339	NAD	C2N-N1N	4.10	1.39	1.35
4	А	1339	NAD	C6N-N1N	3.00	1.42	1.35
4	А	1339	NAD	O4D-C4D	2.69	1.51	1.45
4	А	1339	NAD	C2A-N1A	2.65	1.38	1.33
4	А	1339	NAD	C7N-N7N	-2.57	1.28	1.33
4	А	1339	NAD	C6N-C5N	-2.25	1.33	1.38

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
4	А	1339	NAD	C5N-C4N-C3N	-8.06	112.44	120.36
4	А	1339	NAD	C4D-O4D-C1D	-5.48	104.91	109.92
4	А	1339	NAD	C5A-C6A-N6A	3.86	126.20	120.31
4	А	1339	NAD	C6N-C5N-C4N	3.80	124.92	119.45
4	А	1339	NAD	C5D-C4D-C3D	-3.76	101.66	115.21

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1 EJ 2

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
4	А	1339	NAD	C6N-N1N-C2N	-3.49	118.91	121.88
4	А	1339	NAD	O7N-C7N-C3N	2.37	122.50	119.60
4	А	1339	NAD	PN-O5D-C5D	-2.24	108.50	121.35
4	А	1339	NAD	O7N-C7N-N7N	-2.17	119.48	122.62

Continued from previous page...

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	А	1339	NAD	C5D-O5D-PN-O3
4	А	1339	NAD	C5D-O5D-PN-O1N
4	А	1339	NAD	C5D-O5D-PN-O2N
4	А	1339	NAD	C3D-C4D-C5D-O5D
4	А	1339	NAD	O4D-C4D-C5D-O5D
4	А	1339	NAD	C3B-C4B-C5B-O5B
4	А	1339	NAD	O4B-C4B-C5B-O5B
4	А	1339	NAD	PN-O3-PA-O5B

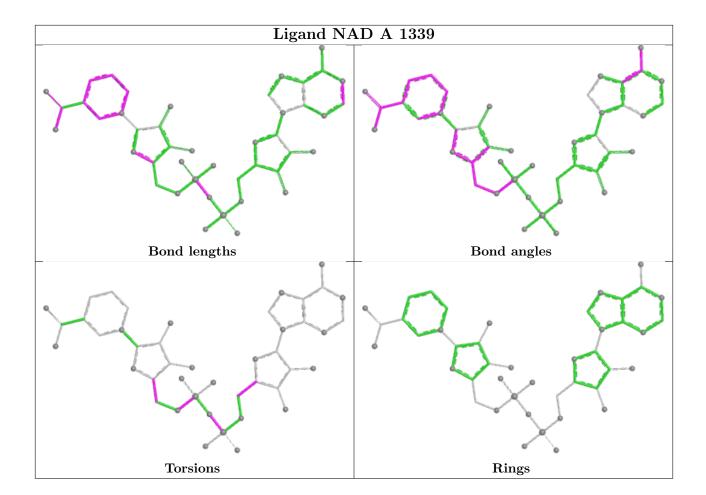
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	А	1339	NAD	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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.

