



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 3PFN
Title : Crystal Structure of human NAD kinase
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Deposited on : 2010-10-28
Resolution : 2.70 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	FAILED
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

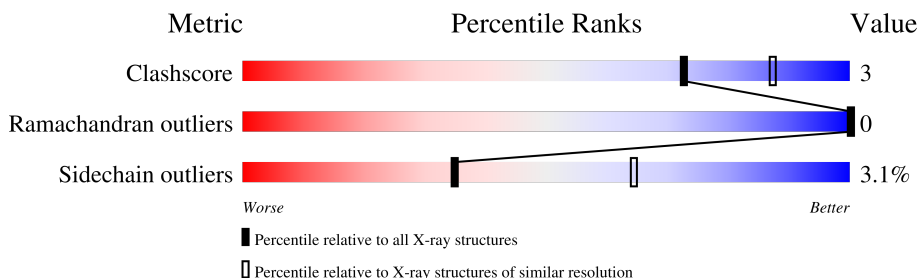
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	180529	3684 (2.70-2.70)
Ramachandran outliers	177936	3633 (2.70-2.70)
Sidechain outliers	177891	3633 (2.70-2.70)

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 $\leq 5\%$. 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.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	365	
1	B	365	
1	C	365	
1	D	365	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9218 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 NAD kinase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	327	Total	C	N	O	S	Se	0	0	0
			2388	1528	400	444	8	8			
1	B	327	Total	C	N	O	S	Se	0	0	0
			2330	1496	384	434	8	8			
1	C	321	Total	C	N	O	S	Se	0	0	0
			2222	1426	370	411	7	8			
1	D	317	Total	C	N	O	S	Se	0	0	0
			2216	1426	368	406	8	8			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	67	MSE	-	expression tag	UNP O95544
A	262	LYS	ASN	variant	UNP O95544
A	427	HIS	-	expression tag	UNP O95544
A	428	HIS	-	expression tag	UNP O95544
A	429	HIS	-	expression tag	UNP O95544
A	430	HIS	-	expression tag	UNP O95544
A	431	HIS	-	expression tag	UNP O95544
B	67	MSE	-	expression tag	UNP O95544
B	262	LYS	ASN	variant	UNP O95544
B	427	HIS	-	expression tag	UNP O95544
B	428	HIS	-	expression tag	UNP O95544
B	429	HIS	-	expression tag	UNP O95544
B	430	HIS	-	expression tag	UNP O95544
B	431	HIS	-	expression tag	UNP O95544
C	67	MSE	-	expression tag	UNP O95544
C	262	LYS	ASN	variant	UNP O95544
C	427	HIS	-	expression tag	UNP O95544
C	428	HIS	-	expression tag	UNP O95544
C	429	HIS	-	expression tag	UNP O95544
C	430	HIS	-	expression tag	UNP O95544
C	431	HIS	-	expression tag	UNP O95544

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Chain	Residue	Modelled	Actual	Comment	Reference
D	67	MSE	-	expression tag	UNP O95544
D	262	LYS	ASN	variant	UNP O95544
D	427	HIS	-	expression tag	UNP O95544
D	428	HIS	-	expression tag	UNP O95544
D	429	HIS	-	expression tag	UNP O95544
D	430	HIS	-	expression tag	UNP O95544
D	431	HIS	-	expression tag	UNP O95544

- Molecule 2 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	21	Total X 21 21	0	0
2	B	20	Total X 20 20	0	0
2	C	14	Total X 14 14	0	0
2	D	7	Total X 7 7	0	0

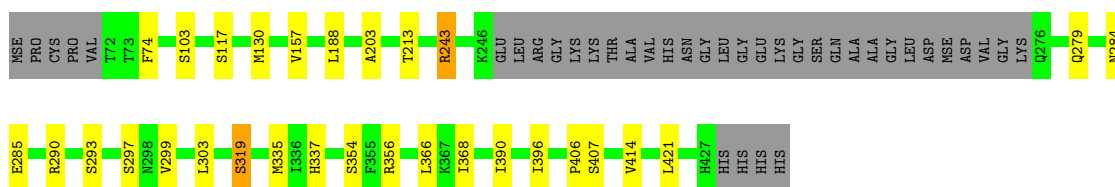
3 Residue-property plots

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.


Note EDS failed to run properly.

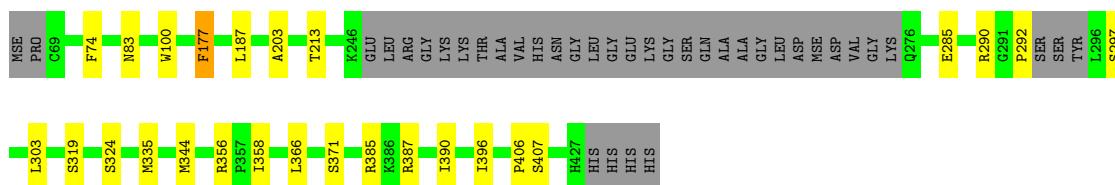
- Molecule 1: NAD kinase

Chain A: 




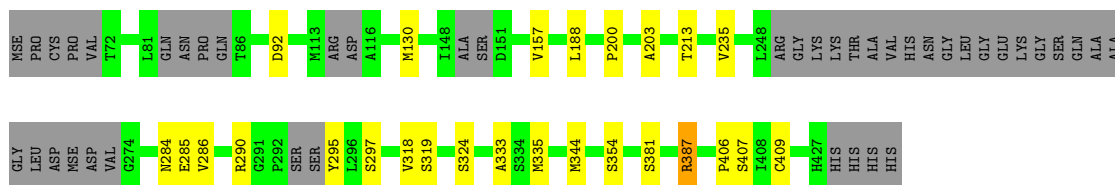
- Molecule 1: NAD kinase

Chain B: 




- Molecule 1: NAD kinase

Chain C: 



- Molecule 1: NAD kinase

Chain D: 





4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	66.09Å 133.59Å 162.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.84 – 2.70	Depositor
% Data completeness (in resolution range)	(Not available) (29.84-2.70)	Depositor
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.13 (at 2.68Å)	Xtriage
Refinement program	BUSTER-TNT BUSTER 2.8.0, BUSTER 2.8.0	Depositor
R, R_{free}	0.209 , 0.236	Depositor
Wilson B-factor (Å ²)	52.6	Xtriage
Anisotropy	0.510	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	9218	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.13% 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: UNX

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	0.49	0/2433	0.67	0/3310
1	B	0.49	0/2373	0.68	0/3237
1	C	0.48	0/2260	0.67	0/3085
1	D	0.46	0/2256	0.67	0/3082
All	All	0.48	0/9322	0.67	0/12714

There are no bond length outliers.

There are no bond angle outliers.

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	2388	0	2262	18	0
1	B	2330	0	2159	14	0
1	C	2222	0	1965	13	0
1	D	2216	0	2001	20	0
2	A	21	0	0	1	0
2	B	20	0	0	0	0
2	C	14	0	0	0	0
2	D	7	0	0	0	0
All	All	9218	0	8387	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:A:188:LEU:HD21	1:A:284:ASN:ND2	2.00	0.77
1:B:290:ARG:HB3	1:B:297:SER:HB3	1.79	0.64
1:C:188:LEU:HD21	1:C:284:ASN:ND2	2.12	0.64
1:A:319:SER:OG	2:A:8:UNX:UNK	1.79	0.63
1:B:390:ILE:HG13	1:B:396:ILE:HD11	1.79	0.63

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	323/365 (88%)	311 (96%)	12 (4%)	0	100	100
1	B	321/365 (88%)	310 (97%)	11 (3%)	0	100	100
1	C	309/365 (85%)	299 (97%)	10 (3%)	0	100	100
1	D	305/365 (84%)	295 (97%)	10 (3%)	0	100	100
All	All	1258/1460 (86%)	1215 (97%)	43 (3%)	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	245/305 (80%)	238 (97%)	7 (3%)	37	67
1	B	229/305 (75%)	220 (96%)	9 (4%)	27	56
1	C	201/305 (66%)	194 (96%)	7 (4%)	31	60
1	D	207/305 (68%)	203 (98%)	4 (2%)	52	79
All	All	882/1220 (72%)	855 (97%)	27 (3%)	35	64

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	387	ARG
1	C	295	TYR
1	D	319	SER
1	C	285	GLU
1	C	319	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	219	ASN
1	A	284	ASN
1	C	231	ASN
1	C	284	ASN
1	D	219	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 62 ligands modelled in this entry, 62 are unknown - leaving 0 for Mogul analysis.

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

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

6.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

6.4 Ligands

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers

EDS failed to run properly - this section is therefore empty.