



Full wwPDB X-ray Structure Validation Report ⓘ

May 27, 2018 – 10:35 PM EDT

PDB ID : 6C4M
Title : Yersinopine dehydrogenase (YpODH) - NADP⁺ bound
Authors : McFarlane, J.S.; Davis, C.L.; Lamb, A.L.
Deposited on : 2018-01-12
Resolution : 1.94 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : rb-20031172
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20031172

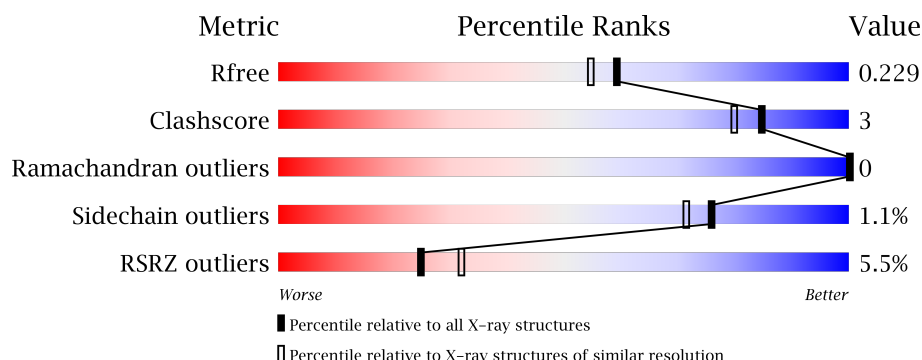
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.94 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}	111664	3622 (1.96-1.92)
Clashscore	122126	3795 (1.96-1.92)
Ramachandran outliers	120053	3757 (1.96-1.92)
Sidechain outliers	120020	3757 (1.96-1.92)
RSRZ outliers	108989	3554 (1.96-1.92)

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. 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.

Mol	Chain	Length	Quality of chain
1	C	474	<div> <div>5%</div> <div>83%</div> <div>5%</div> <div>12%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6758 atoms, of which 3273 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.

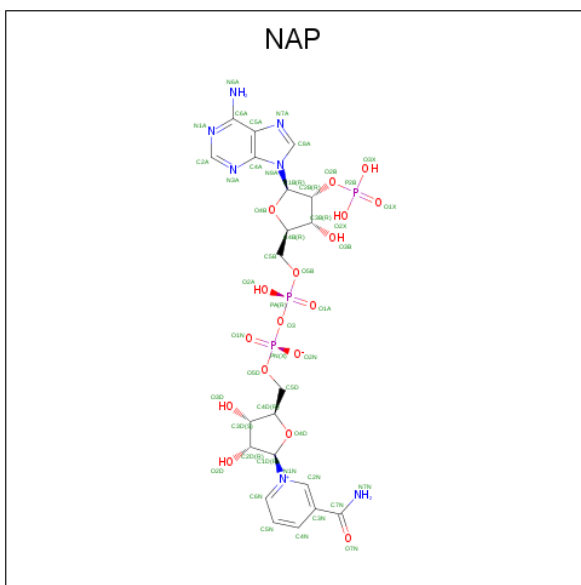
- Molecule 1 is a protein called Yersinopine dehydrogenase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	C	418	6569	2111	3273	570	604	11	0	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-17	HIS	-	expression tag	UNP Q8CKU7
C	-16	HIS	-	expression tag	UNP Q8CKU7
C	-15	HIS	-	expression tag	UNP Q8CKU7
C	-14	HIS	-	expression tag	UNP Q8CKU7
C	-13	HIS	-	expression tag	UNP Q8CKU7
C	-12	HIS	-	expression tag	UNP Q8CKU7
C	-11	SER	-	expression tag	UNP Q8CKU7
C	-10	SER	-	expression tag	UNP Q8CKU7
C	-9	GLY	-	expression tag	UNP Q8CKU7
C	-8	ARG	-	expression tag	UNP Q8CKU7
C	-7	GLU	-	expression tag	UNP Q8CKU7
C	-6	ASN	-	expression tag	UNP Q8CKU7
C	-5	LEU	-	expression tag	UNP Q8CKU7
C	-4	TYR	-	expression tag	UNP Q8CKU7
C	-3	PHE	-	expression tag	UNP Q8CKU7
C	-2	GLN	-	expression tag	UNP Q8CKU7
C	-1	GLY	-	expression tag	UNP Q8CKU7
C	0	HIS	-	expression tag	UNP Q8CKU7

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃).

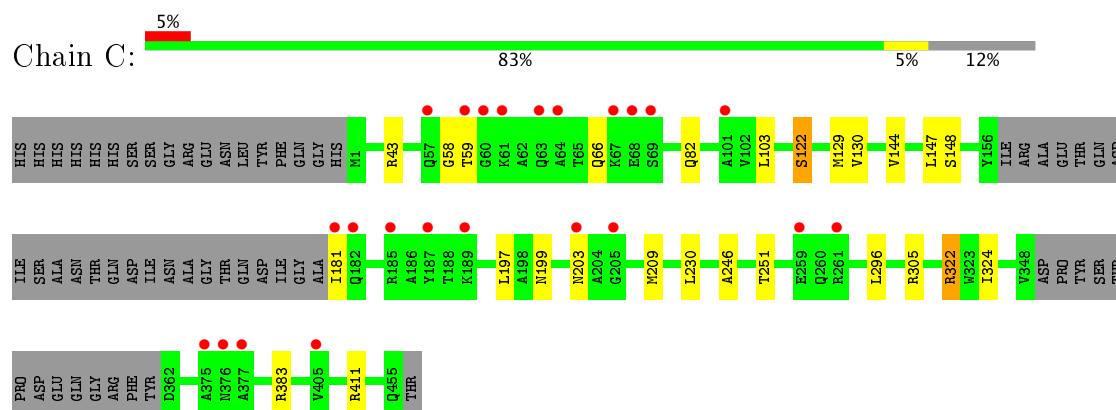


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	141	Total O 141 141	0	0

- Molecule 1: Yersinopine dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	98.39Å 125.67Å 88.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.73 – 1.94 38.74 – 1.94	Depositor EDS
% Data completeness (in resolution range)	98.8 (38.73-1.94) 98.8 (38.74-1.94)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.73 (at 1.94Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.190 , 0.229 0.190 , 0.229	Depositor DCC
R_{free} test set	1996 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	31.5	Xtriage
Anisotropy	0.894	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 44.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6758	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.60% 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: NAP

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	C	0.48	0/3370	0.63	1/4596 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	C	129	MET	CG-SD-CE	-5.51	91.39	100.20

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	C	3296	3273	3316	17	0
2	C	48	0	24	0	0
3	C	141	0	0	6	0
All	All	3485	3273	3340	17	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.

All (17) 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:C:322:ARG:NH2	3:C:602:HOH:O	2.13	0.81
1:C:122:SER:O	3:C:601:HOH:O	2.07	0.73
1:C:43:ARG:NH2	1:C:181:ILE:O	2.23	0.71
1:C:148:SER:O	3:C:601:HOH:O	2.12	0.66
1:C:411:ARG:NH1	3:C:605:HOH:O	2.34	0.60
1:C:144:VAL:O	1:C:199:ASN:HA	2.06	0.56
1:C:322:ARG:NH1	3:C:608:HOH:O	2.39	0.56
1:C:203:ASN:O	1:C:209:MET:HE2	2.10	0.52
1:C:103:LEU:CD1	1:C:130:VAL:HG22	2.43	0.49
1:C:147:LEU:HD23	1:C:197:LEU:HB3	1.96	0.48
1:C:197:LEU:HD12	1:C:197:LEU:C	2.36	0.46
1:C:230:LEU:HD21	1:C:296:LEU:HD13	1.97	0.46
1:C:246:ALA:HA	1:C:251:THR:HG21	2.00	0.43
1:C:58:GLY:HA3	1:C:66:GLN:O	2.19	0.42
1:C:305:ARG:HA	1:C:324:ILE:HG23	2.01	0.41
1:C:82:GLN:OE1	3:C:603:HOH:O	2.22	0.41
1:C:197:LEU:HD13	1:C:209:MET:SD	2.62	0.40

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	C	412/474 (87%)	403 (98%)	9 (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	Outliers	Percentiles	
1	C	350/397 (88%)	346 (99%)	4 (1%)	76	71

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

Mol	Chain	Res	Type
1	C	59	THR
1	C	122	SER
1	C	322	ARG
1	C	383	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

1 ligand is modelled in this entry.

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	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAP	C	501	-	44,52,52	3.57	19 (43%)	53,80,80	2.49	7 (13%)

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	Res	Link	Chirals	Torsions	Rings
2	NAP	C	501	-	-	0/27/67/67	0/5/5/5

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	501	NAP	C3B-C4B	-9.35	1.28	1.53
2	C	501	NAP	C3D-C4D	-8.09	1.32	1.53
2	C	501	NAP	O4D-C1D	-7.36	1.31	1.41
2	C	501	NAP	O7N-C7N	-3.49	1.17	1.24
2	C	501	NAP	O2D-C2D	-3.09	1.35	1.43
2	C	501	NAP	C5A-C4A	-2.64	1.34	1.40
2	C	501	NAP	C5N-C4N	-2.16	1.34	1.38
2	C	501	NAP	C4A-N3A	2.07	1.38	1.35
2	C	501	NAP	C2A-N1A	2.19	1.38	1.33
2	C	501	NAP	C3N-C7N	2.74	1.54	1.50
2	C	501	NAP	C2A-N3A	2.90	1.36	1.32
2	C	501	NAP	C6A-N6A	3.13	1.46	1.34
2	C	501	NAP	O3D-C3D	3.46	1.51	1.43
2	C	501	NAP	O4B-C4B	4.97	1.56	1.45
2	C	501	NAP	C3B-C2B	5.46	1.65	1.53
2	C	501	NAP	C7N-N7N	5.80	1.44	1.33
2	C	501	NAP	P2B-O2B	5.85	1.70	1.59
2	C	501	NAP	O4D-C4D	6.76	1.60	1.45
2	C	501	NAP	O4B-C1B	8.94	1.53	1.41

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	501	NAP	N3A-C2A-N1A	-10.15	120.17	128.86
2	C	501	NAP	C1B-N9A-C4A	-8.43	112.06	126.64
2	C	501	NAP	N6A-C6A-N1A	-6.31	105.48	118.57
2	C	501	NAP	C4B-O4B-C1B	-4.49	105.15	109.83
2	C	501	NAP	C2N-C3N-C4N	2.07	120.64	118.26
2	C	501	NAP	C2D-C3D-C4D	2.29	107.01	102.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	501	NAP	C5A-C6A-N6A	7.25	135.25	120.47

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

6.1 Protein, DNA and RNA chains

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, 95th 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	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	C	418/474 (88%)	0.47	23 (5%)	25 32	25, 36, 54, 72	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	61	LYS	4.2
1	C	375	ALA	4.2
1	C	64	ALA	4.1
1	C	67	LYS	3.7
1	C	261	ARG	3.6
1	C	57	GLN	3.3
1	C	376	ASN	3.1
1	C	187	TYR	3.0
1	C	181	ILE	2.9
1	C	405	VAL	2.9
1	C	68	GLU	2.6
1	C	189	LYS	2.5
1	C	59	THR	2.5
1	C	259	GLU	2.5
1	C	377	ALA	2.4
1	C	60	GLY	2.4
1	C	185	ARG	2.4
1	C	203	ASN	2.4
1	C	182	GLN	2.4
1	C	205	GLY	2.3
1	C	63	GLN	2.1
1	C	69	SER	2.1
1	C	101	ALA	2.1

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 carbohydrates 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, 95th 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	B-factors(\AA^2)	Q<0.9
2	NAP	C	501	48/48	0.96	0.14	34,40,48,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.