

# Full wwPDB X-ray Structure Validation Report (i)

#### Jan 28, 2024 - 01:57 PM EST

PDB ID	:	1ENO
Title	:	BRASSICA NAPUS ENOYL ACP REDUCTASE/NAD BINARY COMPLEX
		AT PH 8.0 AND ROOM TEMPERATURE
Authors	:	Rafferty, J.B.; Rice, D.W.
Deposited on		
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:

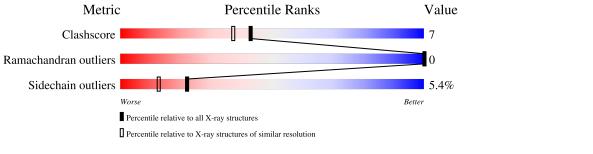
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
$\mathrm{EDS}$	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 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
Metric	$(\# {\rm Entries})$	$(\# { m Entries},  { m resolution}  { m range}({ m \AA}))$
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	312	78%	15%	• 5%



#### 1ENO

# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2335 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.

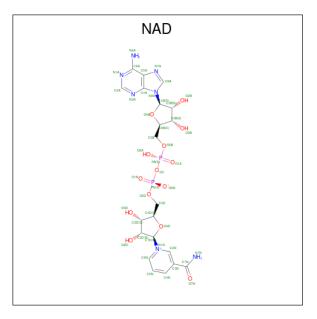
• Molecule 1 is a protein called ENOYL ACYL CARRIER PROTEIN REDUCTASE.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	297	Total 2181	C 1386	N 369	O 420	S 6	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	311	ASP	ASN	conflict	UNP P80030

• Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula:  $C_{21}H_{27}N_7O_{14}P_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	А	1	Total 44	C 21	N 7	0 14	Р 2	0	0

• Molecule 3 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	110	Total         O           110         110	0	0

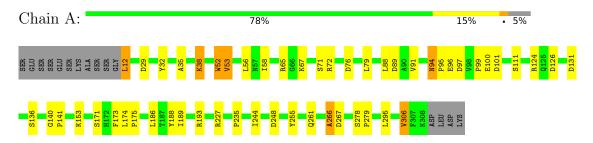


# 3 Residue-property plots (i)

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: ENOYL ACYL CARRIER PROTEIN REDUCTASE





## 4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants	70.50Å $70.50$ Å $117.80$ Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	10.00 - 1.90	Depositor
% Data completeness	(Not available) (10.00-1.90)	Depositor
(in resolution range)	(100 available) (10.00 1.50)	Depositor
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	TNT	Depositor
$R, R_{free}$	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2335	wwPDB-VP
Average B, all atoms $(Å^2)$	23.0	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: NAD

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).

Mal	Chain	Bo	nd lengths	Bond angles		
Mol	Unain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	1.01	6/2224~(0.3%)	1.15	16/3028~(0.5%)	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	А	0	2

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
1	А	306	VAL	C-N	13.10	1.64	1.34
1	А	100	GLU	C-N	-7.86	1.16	1.34
1	А	266	ALA	C-N	-7.58	1.16	1.34
1	А	52	TRP	C-N	7.31	1.50	1.34
1	А	171	SER	CB-OG	-5.65	1.34	1.42
1	А	235	PRO	C-N	-5.61	1.21	1.34

All (6) bond length outliers are listed below:

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	72	ARG	NE-CZ-NH2	-9.42	115.59	120.30
1	А	306	VAL	C-N-CA	-9.03	99.13	121.70
1	А	72	ARG	NE-CZ-NH1	8.42	124.51	120.30
1	А	76	ASP	CB-CG-OD1	-6.78	112.20	118.30
1	А	52	TRP	C-N-CA	-6.63	105.12	121.70
1	А	97	ASP	CB-CG-OD1	-6.29	112.64	118.30
1	А	76	ASP	CB-CG-OD2	6.12	123.81	118.30

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Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	А	53	VAL	O-C-N	-6.08	109.56	121.10
1	А	29	ASP	CB-CG-OD1	5.59	123.33	118.30
1	А	131	ASP	CB-CG-OD2	-5.40	113.44	118.30
1	А	29	ASP	CB-CG-OD2	-5.40	113.44	118.30
1	А	126	ASP	CB-CG-OD1	-5.39	113.45	118.30
1	А	248	ASP	CB-CG-OD2	5.22	123.00	118.30
1	А	100	GLU	C-N-CA	5.19	134.66	121.70
1	А	227	ARG	NE-CZ-NH2	-5.14	117.73	120.30
1	А	193	ARG	NE-CZ-NH2	-5.12	117.74	120.30

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There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	306	VAL	Mainchain
1	А	53	VAL	Mainchain

## 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	2181	0	2155	27	0
2	А	44	0	25	10	0
3	А	110	0	0	2	0
All	All	2335	0	2180	30	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.

All (30) 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:35:ALA:HB2	1:A:266:ALA:HB1	1.66	0.76
1:A:94:ASN:HB2	1:A:95:PRO:CD	2.22	0.69
2:A:501:NAD:O2A	2:A:501:NAD:H3B	1.93	0.68

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		Interatomic	Clash
Atom-1	Atom-2	distance $(\text{\AA})$	overlap (Å)
1:A:94:ASN:HB2	1:A:95:PRO:HD2	1.79	0.64
1:A:94:ASN:ND2	1:A:96:GLU:HG2	2.13	0.64
1:A:99:PRO:HB2	1:A:101:ASP:HB3	1.79	0.62
1:A:35:ALA:CB	1:A:266:ALA:HB1	2.32	0.59
1:A:188:TYR:CG	2:A:501:NAD:N7N	2.71	0.58
2:A:501:NAD:O5B	2:A:501:NAD:C5D	2.53	0.56
1:A:65:ARG:NH1	1:A:67:LYS:HE2	2.23	0.53
1:A:188:TYR:CD1	2:A:501:NAD:N7N	2.77	0.53
1:A:89:ASP:OD1	1:A:91:VAL:HG22	2.09	0.52
1:A:12:LEU:N	3:A:530:HOH:O	2.43	0.51
1:A:186:LEU:HB2	2:A:501:NAD:O3D	2.11	0.50
1:A:65:ARG:CZ	1:A:67:LYS:HE2	2.43	0.49
1:A:94:ASN:CB	1:A:95:PRO:CD	2.89	0.49
1:A:136:SER:HA	2:A:501:NAD:O3D	2.13	0.48
1:A:174:LEU:N	1:A:175:PRO:HD2	2.29	0.47
1:A:267:ASP:HB2	3:A:588:HOH:O	2.15	0.46
1:A:140:GLY:HA2	1:A:141:PRO:HD2	1.83	0.45
1:A:174:LEU:N	1:A:175:PRO:CD	2.80	0.45
1:A:32:TYR:HD2	2:A:501:NAD:O4D	2.01	0.44
1:A:38:LYS:HD2	1:A:71:SER:O	2.19	0.43
1:A:52:TRP:HA	1:A:88:LEU:O	2.19	0.43
1:A:173:PHE:C	1:A:175:PRO:HD2	2.39	0.42
1:A:32:TYR:CD2	2:A:501:NAD:O4D	2.73	0.42
1:A:136:SER:C	2:A:501:NAD:H3D	2.40	0.42
1:A:278:SER:HB2	1:A:279:PRO:HD2	2.02	0.42
2:A:501:NAD:H6N	2:A:501:NAD:H2D	1.68	0.41
1:A:255:TYR:O	1:A:261:GLN:HG3	2.21	0.40

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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	А	295/312~(95%)	285~(97%)	10 (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	А	224/245~(91%)	212~(95%)	12 (5%)	22 13		

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	12	LEU
1	А	38	LYS
1	А	56	LEU
1	А	58	ILE
1	А	79	LEU
1	А	94	ASN
1	А	111	SER
1	А	124	ARG
1	А	153	LYS
1	А	189	ILE
1	А	244	ILE
1	А	295	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	94	ASN
1	А	256	ASN
1	А	271	ASN



#### 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)

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	Bos	Link	Bo	ond leng	ths	B	ond ang	gles
WIOI	Type	Ullalli	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
2	NAD	А	501	-	42,48,48	2.00	5 (11%)	50,73,73	2.01	10 (20%)

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.

$\mathbf{M}$	ol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2		NAD	А	501	-	-	14/26/62/62	0/5/5/5

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	А	501	NAD	C2N-N1N	8.31	1.45	1.35
2	А	501	NAD	O2D-C2D	-5.46	1.30	1.43
2	А	501	NAD	C3N-C7N	5.46	1.58	1.50

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Contra	Continued from previous page									
Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)			
2	А	501	NAD	C3D-C4D	-2.84	1.45	1.53			
2	А	501	NAD	C6N-N1N	2.20	1.40	1.35			

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All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
2	А	501	NAD	C6N-C5N-C4N	6.39	128.72	119.44
2	А	501	NAD	C5N-C4N-C3N	-6.08	113.14	120.34
2	А	501	NAD	O4D-C1D-C2D	-5.01	99.60	106.93
2	А	501	NAD	C2N-C3N-C4N	4.52	123.39	118.26
2	А	501	NAD	O2D-C2D-C3D	-3.86	99.32	111.82
2	А	501	NAD	C5N-C6N-N1N	-3.41	115.50	120.40
2	А	501	NAD	C5A-C6A-N6A	2.69	124.44	120.35
2	А	501	NAD	C1B-N9A-C4A	-2.36	122.50	126.64
2	А	501	NAD	C3N-C2N-N1N	-2.36	118.12	120.43
2	А	501	NAD	C3D-C2D-C1D	2.21	104.30	100.98

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	А	501	NAD	C5D-O5D-PN-O1N
2	А	501	NAD	C3D-C4D-C5D-O5D
2	А	501	NAD	O4D-C1D-N1N-C2N
2	А	501	NAD	O4D-C1D-N1N-C6N
2	А	501	NAD	C2D-C1D-N1N-C2N
2	А	501	NAD	C2D-C1D-N1N-C6N
2	А	501	NAD	O4D-C4D-C5D-O5D
2	А	501	NAD	C4D-C5D-O5D-PN
2	А	501	NAD	PN-O3-PA-O5B
2	А	501	NAD	PA-O3-PN-O5D
2	А	501	NAD	C4B-C5B-O5B-PA
2	А	501	NAD	C5D-O5D-PN-O3
2	А	501	NAD	C5D-O5D-PN-O2N
2	А	501	NAD	O4B-C4B-C5B-O5B

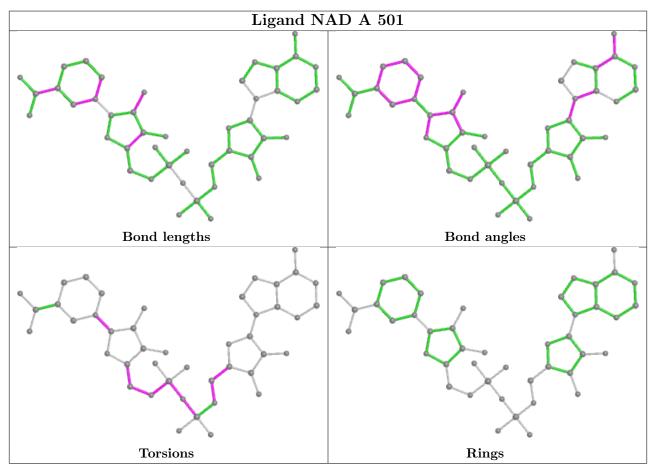
There are no ring outliers.

1 monomer is involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	А	501	NAD	10	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 sufficient 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)

The following chains have linkage breaks:



Mol	Chain	Number of breaks
1	А	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	306:VAL	С	307:PHE	Ν	1.64
1	А	100:GLU	С	101:ASP	Ν	1.16
1	А	266:ALA	С	267:ASP	Ν	1.16



## 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.

