

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

Dec 3, 2023 - 07:38 pm GMT

PDB ID : 1EB9

Title : Structure Determinants of Substrate Specificity of Hydroxynitrile Lyase from

Manihot esculenta

Authors: Lauble, H.; Miehlich, B.; Foerster, S.; Kobler, C.; Wajant, H.; Effenberger, F.

Deposited on : 2001-07-24

Resolution : 2.10 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 (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 : 1.8.4, 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)

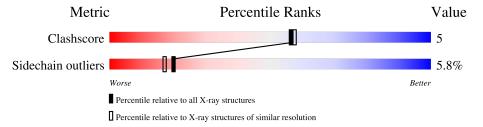
Validation Pipeline (wwPDB-VP) : 2.36

# 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 2.10 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}({\rm \AA})) \end{array}$
Clashscore	141614	5710 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)

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	262	81%	15%	<del>-</del>
1	В	262	84%	13%	



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4467 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.

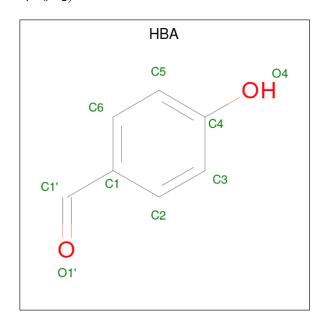
• Molecule 1 is a protein called HYDROXYNITRILE LYASE.

	$\mathbf{Mol}$	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
	1	Λ	262	Total	С	N	О	S	0	0	0
	1	A	202	2095	1351	348	388	8	0	U	0
ĺ	1	D	258	Total	С	N	О	S	0	0	0
	1	Б	250	2065	1331	343	383	8	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	128	ALA	TRP	engineered mutation	UNP P52705
В	128	ALA	TRP	engineered mutation	UNP P52705

• Molecule 2 is P-HYDROXYBENZALDEHYDE (three-letter code: HBA) (formula:  $C_7H_6O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 9	C 7	O 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 9 7 2	0	0
2	В	1	Total C O 9 7 2	0	0
2	В	1	Total C O 9 7 2	0	0

#### • Molecule 3 is water.

]	Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
	3	A	132	Total O 132 132	0	0
	3	В	139	Total O 139 139	0	0

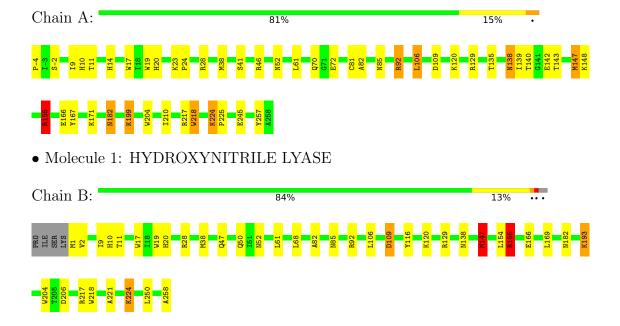


# 3 Residue-property plots (i)

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: HYDROXYNITRILE LYASE





# 4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 41 21 2	Depositor	
Cell constants	106.34Å 106.34Å 188.84Å	Depositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	8.00 - 2.10	Depositor	
% Data completeness	97.1 (8.00-2.10)	Depositor	
(in resolution range)	31.1 (0.00-2.10)	Depositor	
$R_{merge}$	0.05	Depositor	
$R_{sym}$	(Not available)	Depositor	
Refinement program	X-PLOR 3.851	Depositor	
$R, R_{free}$	0.197 , 0.244	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	4467	wwPDB-VP	
Average B, all atoms (Å <sup>2</sup> )	28.0	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: HBA

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		
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.85	0/2145	1.55	$24/2905 \ (0.8\%)$	
1	В	0.88	0/2114	1.44	28/2864 (1.0%)	
All	All	0.86	0/4259	1.50	52/5769~(0.9%)	

There are no bond length outliers.

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	155	ARG	NE-CZ-NH2	-20.00	110.30	120.30
1	A	155	ARG	NE-CZ-NH1	18.77	129.68	120.30
1	В	155	ARG	NE-CZ-NH2	-12.99	113.81	120.30
1	A	129	ARG	NE-CZ-NH1	10.17	125.39	120.30
1	A	92	ARG	NE-CZ-NH2	-10.06	115.27	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	A	2095	0	2096	26	0
1	В	2065	0	2060	15	0
2	A	18	0	12	1	0
2	В	18	0	12	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	132	0	0	1	0
3	В	139	0	0	1	0
All	All	4467	0	4180	42	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 5.

The worst 5 of 42 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{array}{ll}  ext{Interatomic} \  ext{distance} \ ( ext{Å}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:B:10:HIS:HE1	1:B:38:MET:H	1.20	0.88
1:B:147:MET:CE	2:B:1259:HBA:H3	2.05	0.85
1:A:52:ASN:HD22	1:A:138:ASN:HB2	1.41	0.84
1:A:10:HIS:HE1	1:A:38:MET:H	1.23	0.82
1:B:147:MET:HE2	2:B:1259:HBA:H3	1.61	0.82

There are no symmetry-related clashes.

#### 5.3 Torsion angles (i)

#### 5.3.1 Protein backbone (i)

There are no protein backbone outliers to report in this entry.

#### 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	226/226 (100%)	211 (93%)	15 (7%)	16	14	
1	В	222/226 (98%)	211 (95%)	11 (5%)	24	23	
All	All	448/452 (99%)	422 (94%)	26 (6%)	20	17	

5 of 26 residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	A	224	LYS
1	В	120	LYS
1	В	224	LYS
1	В	106	LEU
1	В	147	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	В	10	HIS
1	В	20	HIS
1	В	182	ASN
1	В	52	ASN
1	В	85	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)

4 ligands are 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 Li		Link	В	Bond lengths			Bond angles		
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
2	HBA	A	1259	-	9,9,9	1.25	1 (11%)	11,11,11	1.16	1 (9%)
2	HBA	В	1260	-	9,9,9	1.32	1 (11%)	11,11,11	0.67	0
2	HBA	В	1259	-	9,9,9	1.20	1 (11%)	11,11,11	1.92	4 (36%)
2	HBA	A	1260	-	9,9,9	1.54	1 (11%)	11,11,11	0.87	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.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HBA	A	1259	-	-	0/2/2/2	0/1/1/1
2	HBA	В	1260	-	-	2/2/2/2	0/1/1/1
2	HBA	В	1259	-	-	0/2/2/2	0/1/1/1
2	HBA	A	1260	-	-	2/2/2/2	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
2	A	1260	HBA	C3-C4	2.76	1.44	1.38
2	В	1260	HBA	C3-C4	2.41	1.43	1.38
2	A	1259	HBA	C3-C4	2.23	1.43	1.38
2	В	1259	HBA	C5-C4	2.08	1.42	1.38

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$Ideal(^{o})$
2	В	1259	HBA	C6-C1-C2	3.44	122.74	117.64
2	A	1259	HBA	C6-C1-C2	2.73	121.67	117.64
2	В	1259	HBA	C3-C2-C1	-2.41	118.11	121.25
2	В	1259	HBA	C6-C5-C4	-2.23	117.43	119.88
2	В	1259	HBA	O4-C4-C3	-2.19	113.77	120.02

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	1260	HBA	C2-C1-C1'-O1'
2	В	1260	HBA	C6-C1-C1'-O1'
2	A	1260	HBA	C2-C1-C1'-O1'

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Mol	Chain	Res	Type	Atoms
2	A	1260	HBA	C6-C1-C1'-O1'

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1259	HBA	1	0
2	В	1259	HBA	3	0
2	A	1260	HBA	1	0

## 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.

