

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

#### May 26, 2022 – 12:02 PM EDT

PDB ID	:	1LLO
Title	:	HEVAMINE A (A PLANT ENDOCHITINASE/LYSOZYME) COMPLEXED
		WITH ALLOSAMIDIN
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Deposited on		
Resolution	:	1.85  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 following versions of software and data (see references (1)) were used in the production of this report:

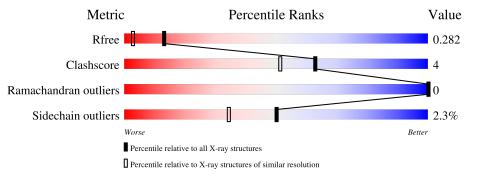
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.28.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.28.1

# 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 1.85 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R <sub>free</sub>	130704	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)

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%

Mol	Chain	Length	Quality of chain	
1	А	273	92% 7%	6.
2	В	2	100%	



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# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2319 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 Hevamine-A.

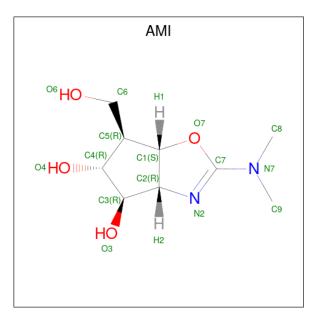
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	273	Total 2087	C 1331	N 351	O 397	S 8	0	0	0

• Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-allopyranose-(1-4)-2-ace tamido-2-deoxy-beta-D-allopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	В	2	Total 28	C N 16 2	O 10	0	0	0

• Molecule 3 is ALLOSAMIZOLINE (three-letter code: AMI) (formula:  $C_9H_{16}N_2O_4$ ).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	В	1	Total 15	C 9	N 2	0 4	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	189	Total         O           189         189	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.

• Molecule 1: Hevamine-A

Chain A:	92%			
<b>G1</b> 115 715 715 715 159 159 159 77 77 77 77 77 77 77 77 7152 7152 7152	4168 7161 1179 1195 1195 1195 1199 1199 1199 119			

• Molecule 2: 2-acetamido-2-deoxy-beta-D-allopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-allopyranose

Chain B:

100%

NAA1 NAA2



# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	52.33Å 57.99Å 82.25Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	8.00 - 1.85	Depositor
Resolution (A)	19.92 - 1.85	EDS
% Data completeness	98.9 (8.00-1.85)	Depositor
(in resolution range)	99.1 (19.92-1.85)	EDS
R <sub>merge</sub>	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$3.60 (at 1.85 \text{\AA})$	Xtriage
Refinement program	TNT	Depositor
D D.	0.146 , $0.200$	Depositor
$R, R_{free}$	0.293 , $0.282$	DCC
$R_{free}$ test set	2151 reflections $(9.94\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	13.2	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.38,90.1	EDS
L-test for twinning <sup>2</sup>	$ \langle L  \rangle = 0.49, \langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.86	EDS
Total number of atoms	2319	wwPDB-VP
Average B, all atoms $(Å^2)$	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.92% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: AMI, NAA

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	Bond	lengths	Bond angles		
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.64	0/2142	0.77	0/2914	

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	А	2087	0	2020	18	0
2	В	28	0	25	0	0
3	В	15	0	15	1	0
4	А	189	0	0	1	0
All	All	2319	0	2060	18	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 4.

The worst 5 of 18 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:158:GLN:HG2	1:A:185:ASN:HD21	1.15	1.08
1:A:238:ARG:HH11	1:A:238:ARG:HG2	1.36	0.88
1:A:158:GLN:HG2	1:A:185:ASN:ND2	1.88	0.87
1:A:70:GLN:HG3	4:A:503:HOH:O	2.00	0.60
1:A:15:THR:OG1	1:A:18:GLN:HG3	2.02	0.60

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	271/273~(99%)	265~(98%)	6~(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	A	221/221 (100%)	216~(98%)	5(2%)	50 34	

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	69	ILE
1	А	130	SER

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Mol	Chain	Res	Type
1	А	158	GLN
1	А	179	TRP
1	А	238	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	А	171	ASN
1	А	185	ASN
1	А	210	ASN
1	А	62	ASN
1	А	18	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)

2 monosaccharides 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).

Mal	Turne	Chain	Dec	Link	Bo	ond leng	ths	B	ond ang	les
	Type	Chain	nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
2	NAA	В	1	2,3	14,14,15	1.59	2 (14%)	17,19,21	1.26	3 (17%)
2	NAA	В	2	2	14,14,15	1.53	4 (28%)	17,19,21	1.91	4 (23%)

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 Ri	ings columns.
'-' means no outliers of that kind	were identified.			

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAA	В	1	2,3	-	0/6/23/26	0/1/1/1
2	NAA	В	2	2	-	2/6/23/26	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	В	1	NAA	C1-C2	4.25	1.58	1.52
2	В	2	NAA	C8-C7	-3.08	1.44	1.50
2	В	2	NAA	C1-C2	2.37	1.55	1.52
2	В	2	NAA	C3-C2	2.26	1.57	1.52
2	В	1	NAA	C4-C5	2.06	1.57	1.53

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	В	2	NAA	C1-O5-C5	-4.92	105.53	112.19
2	В	2	NAA	C2-N2-C7	3.03	127.21	122.90
2	В	1	NAA	C4-C3-C2	-3.02	106.59	111.02
2	В	2	NAA	C3-C4-C5	-2.98	104.93	110.24
2	В	2	NAA	O4-C4-C3	-2.47	104.63	110.35

There are no chirality outliers.

All (2) torsion outliers are listed below:

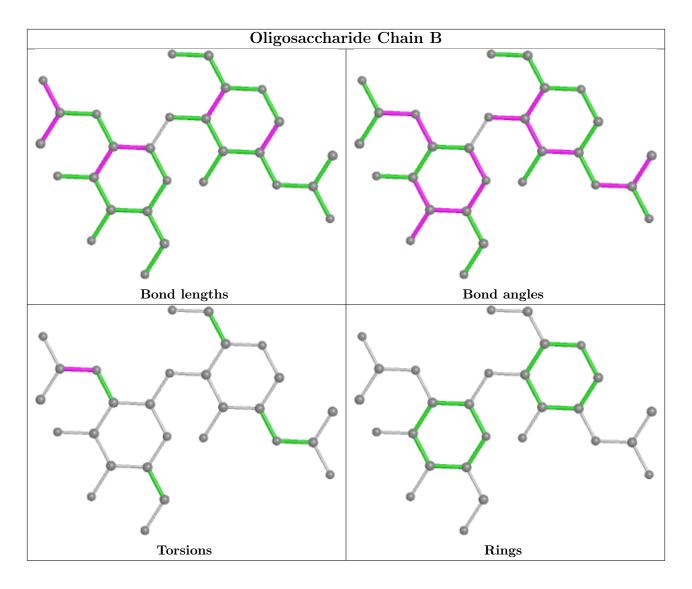
Mol	Chain	Res	Type	Atoms
2	В	2	NAA	C8-C7-N2-C2
2	В	2	NAA	O7-C7-N2-C2

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





## 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).

Γ	Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
	IVIOI					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
	3	AMI	В	3	2	13,16,16	1.74	2 (15%)	16,24,24	2.63	3 (18%)

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
3	AMI	В	3	2	-	0/6/34/34	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	В	3	AMI	C2-N2	-5.27	1.41	1.47
3	В	3	AMI	O7-C1	-2.15	1.43	1.46

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
3	В	3	AMI	O7-C7-N2	-8.87	113.10	117.80
3	В	3	AMI	C5-C4-C3	-2.92	100.05	103.81
3	В	3	AMI	C9-N7-C7	2.79	125.14	120.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	В	3	AMI	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.



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## 6 Fit of model and data (i)

## 6.1 Protein, DNA and RNA chains (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

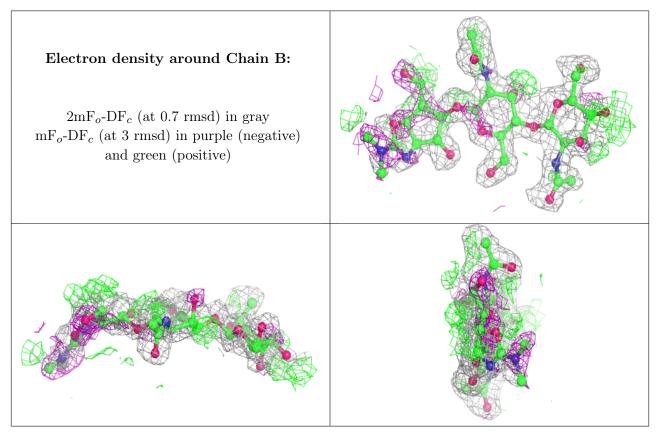
## 6.2 Non-standard residues in protein, DNA, RNA chains (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

## 6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



### 6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.



## 6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

