

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

#### Oct 23, 2023 – 04:53 PM EDT

PDB ID	:	3D5H
Title	:	Crystal structure of haementhin from Haemanthus multiflorus at 2.0A reso-
		lution: Formation of a novel loop on a TIM barrel fold and its functional
		significance
Authors	:	Kumar, S.; Singh, N.; Sinha, M.; Singh, S.B.; Bhushan, A.; Kaur, P.; Srini-
		vasan, A.; Sharma, S.; Singh, T.P.
Deposited on		
Resolution	:	2.00  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:

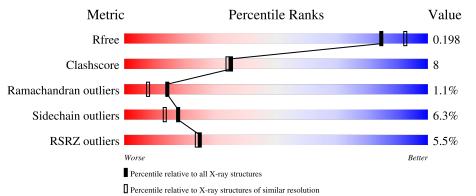
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 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 2.00 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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% 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	А	272	<u>6%</u> 80%	15%	•••



#### 3D5H

# 2 Entry composition (i)

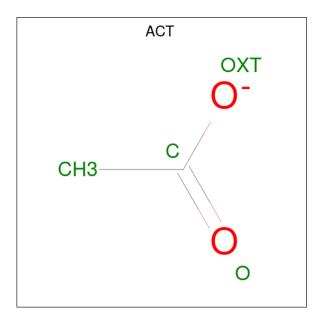
There are 4 unique types of molecules in this entry. The entry contains 2417 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Haementhin.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	272	Total 2108	C 1356	N 351	O 393	S 8	0	0	0

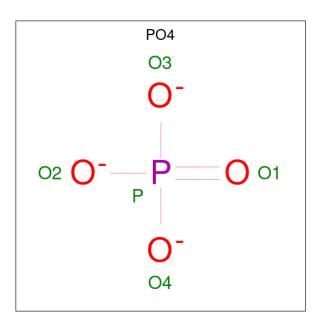
• Molecule 2 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	А	1	Total 4	C 2	0 2	0	0

• Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula:  $O_4P$ ).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	А	1	Total 5	0 4	Р 1	0	0

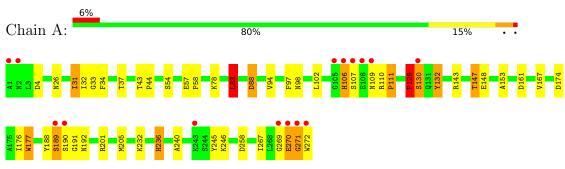
• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	300	Total O 300 300	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 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.



• Molecule 1: Haementhin



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	42.80Å 65.40Å 49.44Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $102.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	48.22 - 2.00	Depositor
Resolution (A)	17.39 - 2.00	EDS
% Data completeness	97.5(48.22-2.00)	Depositor
(in resolution range)	97.7(17.39-2.00)	EDS
R <sub>merge</sub>	(Not available)	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.67 (at 2.00 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.0	Depositor
$R, R_{free}$	0.152 , $0.186$	Depositor
It, Itfree	0.167 , $0.198$	DCC
$R_{free}$ test set	889 reflections $(5.03\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	22.8	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.34, $51.6$	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	2417	wwPDB-VP
Average B, all atoms $(Å^2)$	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.88% 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: PO4, ACT

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	Chain Bond leng			ond angles
NIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.85	0/2175	1.07	18/2962~(0.6%)

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
1	А	129	PRO	CA-C-N	-7.43	100.86	117.20
1	А	269	GLY	N-CA-C	-7.10	95.36	113.10
1	А	174	ASP	CB-CG-OD2	6.88	124.49	118.30
1	А	107	SER	CB-CA-C	6.80	123.02	110.10
1	А	109	ASN	C-N-CA	6.43	137.78	121.70
1	А	161	ASP	CB-CG-OD2	5.93	123.64	118.30
1	А	132	TYR	CB-CG-CD1	-5.88	117.47	121.00
1	А	258	ASP	CB-CG-OD2	5.81	123.53	118.30
1	А	31	ILE	O-C-N	-5.74	113.51	122.70
1	А	109	ASN	N-CA-C	5.57	126.03	111.00
1	А	83	LEU	CA-CB-CG	5.48	127.90	115.30
1	А	4	ASP	CB-CG-OD2	5.28	123.06	118.30
1	А	107	SER	CA-C-N	5.25	128.75	117.20
1	А	270	GLU	C-N-CA	5.18	133.17	122.30
1	А	132	TYR	CB-CG-CD2	5.17	124.10	121.00
1	А	190	SER	CB-CA-C	-5.08	100.46	110.10
1	А	88	ASP	CB-CG-OD2	5.03	122.82	118.30
1	А	129	PRO	CA-N-CD	-5.02	104.47	111.50

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	2108	0	2004	34	0
2	А	4	0	3	0	0
3	А	5	0	0	0	0
4	А	300	0	0	9	0
All	All	2417	0	2007	34	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 8.

All (34) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A. 1		Interatomic	Clash
Atom-1	Atom-2	distance $(\text{\AA})$	overlap (Å)
1:A:153:ALA:HB3	1:A:176:ILE:CD1	2.10	0.82
1:A:232:LYS:O	1:A:236:HIS:HB2	1.86	0.74
1:A:153:ALA:HB3	1:A:176:ILE:HD12	1.72	0.71
1:A:31:ILE:HD11	1:A:177:TRP:CZ2	2.26	0.71
1:A:189:SER:O	1:A:192:ASN:HB3	1.96	0.65
1:A:201:ARG:O	1:A:205:MET:HG3	1.98	0.64
1:A:188:TYR:OH	1:A:191:GLY:HA2	2.02	0.59
1:A:94:VAL:O	1:A:98:ASN:ND2	2.36	0.59
1:A:129:PRO:O	1:A:132:TYR:HD1	1.87	0.58
1:A:98:ASN:HD22	1:A:98:ASN:H	1.52	0.57
1:A:26:ASN:HD21	1:A:271:GLY:HA3	1.71	0.56
1:A:32:ILE:HD12	4:A:6517:HOH:O	2.06	0.55
1:A:57:GLU:HB3	1:A:58:PRO:HD3	1.91	0.53
1:A:97:PHE:CE2	1:A:102:LEU:HD11	2.45	0.52
1:A:267:ILE:CG2	1:A:267:ILE:O	2.59	0.51
1:A:26:ASN:ND2	1:A:271:GLY:HA3	2.26	0.50
1:A:245:TYR:HA	4:A:6562:HOH:O	2.11	0.50
1:A:245:TYR:CE2	1:A:246:LYS:HG3	2.47	0.49
1:A:111:PRO:HD3	4:A:6534:HOH:O	2.12	0.49
1:A:37:THR:O	1:A:44:PRO:HA	2.13	0.48
1:A:245:TYR:CA	4:A:6562:HOH:O	2.62	0.48
1:A:240:ALA:HB1	4:A:6406:HOH:O	2.13	0.47
1:A:130:SER:O	4:A:6323:HOH:O	2.20	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:PHE:HD2	4:A:6477:HOH:O	1.98	0.45
1:A:167:VAL:HG23	4:A:6521:HOH:O	2.17	0.45
1:A:98:ASN:HD22	1:A:98:ASN:N	2.13	0.44
1:A:245:TYR:CD2	1:A:246:LYS:HG3	2.53	0.44
1:A:267:ILE:O	1:A:267:ILE:HG22	2.19	0.43
1:A:143:ARG:HA	1:A:147:THR:O	2.18	0.43
1:A:245:TYR:HB3	4:A:6562:HOH:O	2.19	0.42
1:A:110:ARG:HA	1:A:111:PRO:HD2	1.93	0.42
1:A:83:LEU:HD22	1:A:88:ASP:HB3	2.01	0.42
1:A:129:PRO:O	1:A:132:TYR:CD1	2.70	0.42
1:A:33:GLY:HA2	1:A:34:PHE:HA	1.82	0.41

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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	270/272~(99%)	255~(94%)	12 (4%)	3(1%)	14 8

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	106	HIS
1	А	271	GLY
1	А	270	GLU

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	analysed Rotameric		Percentiles	
1	А	222/222~(100%)	208~(94%)	14 (6%)	18 13	

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	43	THR
1	А	54	SER
1	А	78	LYS
1	А	83	LEU
1	А	106	HIS
1	А	111	PRO
1	А	129	PRO
1	А	130	SER
1	А	147	THR
1	А	148	GLU
1	А	177	TRP
1	А	189	SER
1	А	236	HIS
1	А	272	TRP

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

Mol	Chain	Res	Type
1	А	26	ASN
1	А	98	ASN
1	А	169	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)

2 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 Link		B	ond leng	gths	B	ond ang	gles
IVIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2
3	PO4	А	6265	-	4,4,4	1.03	0	$6,\!6,\!6$	0.37	0
2	ACT	А	1209	-	3,3,3	0.80	0	$3,\!3,\!3$	1.42	0

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 (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)

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,  $95^{th}$  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	А	272/272~(100%)	-0.22	15 (5%) 25	24	13, 21, 44, 69	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	106	HIS	9.7
1	А	272	TRP	8.7
1	А	2	ASN	4.5
1	А	269	GLY	4.1
1	А	105	GLY	3.6
1	А	107	SER	3.6
1	А	108	GLU	3.5
1	А	271	GLY	3.5
1	А	1	ALA	2.9
1	А	190	SER	2.6
1	А	243	LYS	2.3
1	А	109	ASN	2.3
1	А	130	SER	2.2
1	А	270	GLU	2.1
1	А	189	SER	2.0

## 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 monosaccharides 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,  $95^{th}$  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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
2	ACT	А	1209	4/4	0.88	0.19	71,71,71,71	0
3	PO4	А	6265	5/5	0.97	0.36	41,41,42,44	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

