

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

Jan 7, 2024 – 05:56 am GMT

PDB ID 6HFI

> Title Human dihydroorotase mutant F1563A apo structure

Authors Ramon-Maiques, S.; Grande Garcia, A.

2018-08-21 Deposited on

1.46 Å(reported) Resolution

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

> 1.8.4, CSD as541be (2020) Mogul

Xtriage (Phenix) 1.13 EDS 2.36

20191225.v01 (using entries in the PDB archive December 25th 2019) Percentile statistics

> Refmac 5.8.0158

CCP4 7.0.044 (Gargrove) Engh & Huber (2001)

Ideal geometry (proteins) Ideal geometry (DNA, RNA) Parkinson et al. (1996)

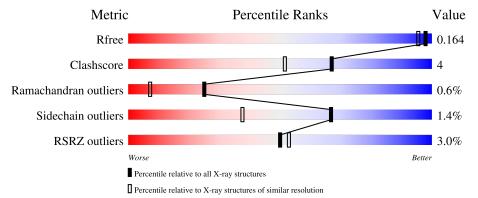
Validation Pipeline (wwPDB-VP) 2.36

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$ 

The reported resolution of this entry is 1.46 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \ resolution} \\ (\#{\rm Entries, \ resolution \ range(\AA)}) \end{array}$
$R_{free}$	130704	1156 (1.46-1.46)
Clashscore	141614	1202 (1.46-1.46)
Ramachandran outliers	138981	1178 (1.46-1.46)
Sidechain outliers	138945	1178 (1.46-1.46)
RSRZ outliers	127900	1139 (1.46-1.46)

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	
			3%	
1	A	393	82%	9% • 8%



## 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6209 atoms, of which 2907 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 CAD protein.

$\mathbf{Mol}$	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	A	362	Total 5800	C 1844	H 2902	N 509	O 529	S 16	3	24	0

There are 3 discrepancies between the modelled and reference sequences:

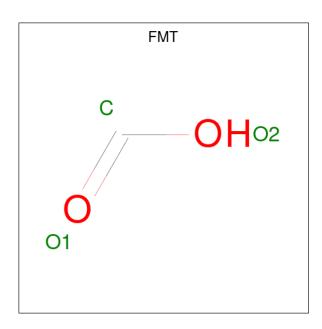
Chain	Residue	Modelled	Actual	Comment	Reference
A	1454	GLY	-	expression tag	UNP P27708
A	1455	PRO	-	expression tag	UNP P27708
A	1563	ALA	PHE	engineered mutation	UNP P27708

• Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	4	Total Zn 4 4	0	0

• Molecule 3 is FORMIC ACID (three-letter code: FMT) (formula: CH<sub>2</sub>O<sub>2</sub>).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C H O 4 1 1 2	0	0
3	A	1	Total C H O 4 1 1 2	0	1
3	A	1	Total C H O 4 1 1 2	0	0
3	A	1	Total C H O 4 1 1 2	0	0
3	A	1	Total C H O 4 1 1 2	0	0

#### • Molecule 4 is water.

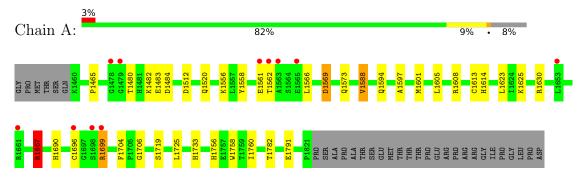
$\mathbf{Mol}$	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
4	A	385	Total O 385 385	0	0



## 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: CAD protein





## 4 Data and refinement statistics (i)

Property	Value	Source	
Space group	C 2 2 21	Depositor	
Cell constants	81.80Å 159.09Å 61.30Å	Donogitor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	28.25 - 1.46	Depositor	
Resolution (A)	72.75 - 1.46	EDS	
% Data completeness	99.0 (28.25-1.46)	Depositor	
(in resolution range)	99.7 (72.75-1.46)	EDS	
$R_{merge}$	(Not available)	Depositor	
$R_{sym}$	(Not available)	Depositor	
$< I/\sigma(I) > 1$	2.76 (at 1.46Å)	Xtriage	
Refinement program	PHENIX 1.12_2829	Depositor	
P. P.	0.128 , 0.164	Depositor	
$R, R_{free}$	0.129 , $0.164$	DCC	
$R_{free}$ test set	3474 reflections $(5.00%)$	wwPDB-VP	
Wilson B-factor (Å <sup>2</sup> )	15.9	Xtriage	
Anisotropy	0.477	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.41, 51.6	EDS	
L-test for twinning <sup>2</sup>	$ < L >=0.48, < L^2>=0.31$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
$F_o, F_c$ correlation	0.98	EDS	
Total number of atoms	6209	wwPDB-VP	
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.73% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  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: ZN, FMT, KCX

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	Bo	nd lengths	Bo	nd angles	
10	101	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
	1	A	0.62	3/3037 (0.1%)	0.77	8/4139 (0.2%)

#### All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
1	A	1588[A]	VAL	CB-CG1	-5.84	1.40	1.52
1	A	1588[B]	VAL	CB-CG1	-5.84	1.40	1.52
1	A	1594	GLN	CB-CG	-5.30	1.38	1.52

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$Ideal(^{o})$
1	A	1566	LEU	CB-CG-CD2	6.87	122.68	111.00
1	A	1512	ASP	CB-CG-OD1	5.72	123.45	118.30
1	A	1566	LEU	CB-CG-CD1	5.41	120.20	111.00
1	A	1667	ARG	NE-CZ-NH2	5.36	122.98	120.30
1	A	1725	LEU	CB-CG-CD1	5.28	119.97	111.00
1	A	1608	ARG	NE-CZ-NH1	-5.20	117.70	120.30
1	A	1704	PHE	CB-CG-CD1	5.09	124.36	120.80
1	A	1484	ASP	CB-CG-OD2	5.04	122.83	118.30

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



.1	,	1 0	$\alpha_1$ 1	1. /	, 1, 1	1 1
the asymmetr	ne unit	whereas S	vmm-Clashes	lists svr	${ m mmetry}$ -related	clashes
one only minimous	ic aiii.	WILCI COD D	y IIIIII CIGOTICO	TID UD D Y I	difficulty followed	CIGOTICS.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2898	2902	2845	23	2
2	A	4	0	0	0	0
3	A	15	5	5	1	0
4	A	385	0	0	4	2
All	All	3302	2907	2850	23	4

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.

All (23) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A	A	Interatomic	Clash
Atom-1	Atom-2	${\rm distance}(\mathring{\rm A})$	overlap (Å)
1:A:1601[B]:MET:CE	1:A:1605:LEU:HD11	2.13	0.78
1:A:1588[A]:VAL:CG1	1:A:1613[A]:CYS:SG	2.73	0.76
1:A:1630[A]:ARG:NH2	3:A:1908:FMT:O1	2.30	0.63
1:A:1482:LYS:NZ	1:A:1690:HIS:ND1	2.47	0.61
1:A:1667:ARG:HH21	1:A:1667:ARG:HG3	1.71	0.55
1:A:1601[B]:MET:HE1	1:A:1605:LEU:HD11	1.85	0.54
1:A:1588[A]:VAL:HG12	1:A:1613[A]:CYS:SG	2.48	0.53
1:A:1758:TRP:NE1	1:A:1782[A]:THR:HG22	2.27	0.50
1:A:1625[A]:LYS:NZ	4:A:2009:HOH:O	2.42	0.50
1:A:1791:GLU:OE1	4:A:2002:HOH:O	2.20	0.50
1:A:1719[B]:SER:OG	4:A:2001:HOH:O	2.19	0.47
1:A:1480:THR:HA	1:A:1483:GLU:O	2.16	0.45
1:A:1558[B]:TYR:CE2	1:A:1562:THR:HG23	2.52	0.45
1:A:1630[A]:ARG:HH21	1:A:1630[A]:ARG:HG3	1.83	0.44
1:A:1756:HIS:ND1	1:A:1782[A]:THR:HG21	2.32	0.44
1:A:1588[A]:VAL:HG13	1:A:1613[A]:CYS:SG	2.55	0.43
1:A:1758:TRP:CZ3	1:A:1760[B]:ILE:HD13	2.53	0.43
1:A:1597:ALA:HB2	1:A:1623:LEU:HD21	2.00	0.43
1:A:1520:GLN:HG2	4:A:2013:HOH:O	2.19	0.42
1:A:1465:PRO:HB2	1:A:1733:HIS:CE1	2.54	0.42
1:A:1569:ASP:N	1:A:1573:GLN:OE1	2.51	0.42
1:A:1601[B]:MET:HE2	1:A:1605:LEU:HD11	2.01	0.41
1:A:1699:ARG:HG3	1:A:1699:ARG:O	2.20	0.41

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.



Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:A:1696:CYS:HG	1:A:1696:CYS:HG[3_454]	0.89	0.71
1:A:1696:CYS:SG	1:A:1696:CYS:HG[3_454]	1.41	0.19
4:A:2008:HOH:O	4:A:2269:HOH:O[3_554]	2.05	0.15
4:A:2234:HOH:O	4:A:2370:HOH:O[3_554]	2.18	0.02

### 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	A	383/393 (98%)	366 (96%)	15 (4%)	2 (0%)	29 9

#### All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1614	HIS
1	A	1706	GLY

#### 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	317/321 (99%)	313 (99%)	4 (1%)	69 40	

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

Mol	Chain	Res	Type
1	A	1561	GLU

Continued on next page...



Continued from previous page...

Mol	Chain	Res	Type
1	A	1569	ASP
1	A	1667	ARG
1	A	1699	ARG

Sometimes 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)

1 non-standard protein/DNA/RNA residue 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	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain Pos	Pos	es Link	Bond lengths			Bond angles		
		туре		nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2								
	1	KCX	A	1556	2,1	9,11,12	2.01	3 (33%)	5,12,14	2.11	1 (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.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	KCX	A	1556	2,1	-	0/9/10/12	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\mathring{\mathrm{A}})$	$\operatorname{Ideal}(\text{\AA})$
1	A	1556	KCX	CX-NZ	3.86	1.42	1.35
1	A	1556	KCX	CA-N	-3.34	1.38	1.48
1	A	1556	KCX	OQ1-CX	2.42	1.26	1.21



All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$Ideal(^{o})$
1	A	1556	KCX	OQ1-CX-NZ	-4.16	118.51	124.96

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 for Mogul analysis.

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
3	FMT	A	1905[A]	-	2,2,2	0.71	0	1,1,1	0.13	0
3	FMT	A	1904	-	2,2,2	1.04	0	1,1,1	0.37	0
3	FMT	A	1907	-	2,2,2	0.78	0	1,1,1	0.67	0
3	FMT	A	1906	-	2,2,2	0.42	0	1,1,1	0.25	0
3	FMT	A	1908	-	2,2,2	0.93	0	1,1,1	0.60	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.

1 monomer is involved in 1 short contact:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1908	FMT	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)

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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	361/393 (91%)	-0.11	11 (3%) 50 53	11, 19, 37, 57	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1563	ALA	4.7
1	A	1561	GLU	4.2
1	A	1699	ARG	4.2
1	A	1696	CYS	3.2
1	A	1562	THR	2.8
1	A	1479	GLY	2.7
1	A	1653	LEU	2.3
1	A	1698	SER	2.1
1	A	1661	ARG	2.1
1	A	1478	GLY	2.1
1	A	1565	GLU	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains (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	$ m B ext{-}factors(\AA^2)$	Q<0.9
1	KCX	A	1556	12/13	0.97	0.09	11,16,20,22	0

### 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
3	FMT	A	1906	3/3	0.82	0.13	54,54,54,65	0
3	FMT	A	1907	3/3	0.95	0.10	46,46,47,55	0
3	FMT	A	1908	3/3	0.97	0.10	40,41,41,49	0
2	ZN	A	1903	1/1	0.98	0.13	26,26,26,26	1
2	ZN	A	1909	1/1	0.99	0.30	34,34,34,34	0
3	FMT	A	1904	3/3	0.99	0.08	15,16,18,19	0
3	FMT	A	1905[A]	3/3	0.99	0.09	13,13,13,16	4
2	ZN	A	1902	1/1	1.00	0.09	13,13,13,13	1
2	ZN	A	1901	1/1	1.00	0.08	14,14,14,14	1

### 6.5 Other polymers (i)

There are no such residues in this entry.

