

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

Jan 30, 2024 – 03:13 PM EST

PDB ID : 1HFC

Title : 1.56 ANGSTROM STRUCTURE OF MATURE TRUNCATED HUMAN FI-

BROBLAST COLLAGENASE

Authors: Spurlino, J.C.; Smith, D.L.

Deposited on : 1994-09-13

Resolution : 1.50 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

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)

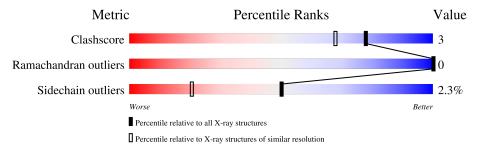
Validation Pipeline (wwPDB-VP) : 2.36

## 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.50 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	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)

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	l	
1	A	169	64%	26%	•• 7%



# 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 1360 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 FIBROBLAST COLLAGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	157	Total 1244	C 779	N 221	O 242	S 2	0	0	0

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

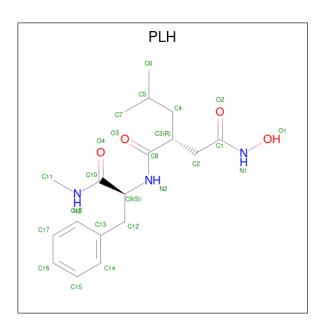
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Zn 2 2	0	0

• Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Ca 1 1	0	0

• Molecule 4 is METHYLAMINO-PHENYLALANYL-LEUCYL-HYDROXAMIC ACID (three-letter code: PLH) (formula: C<sub>18</sub>H<sub>27</sub>N<sub>3</sub>O<sub>4</sub>).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	Λ	1	Total	С	N	О	0	0
4	A	1	25	18	3	4	0	U

### • Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	88	Total O 88 88	0	0

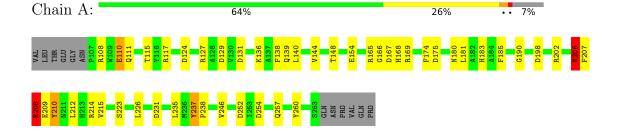


## 3 Residue-property plots (i)

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: FIBROBLAST COLLAGENASE





# 4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 21 21 21	Depositor	
Cell constants	109.21Å 44.57Å 36.28Å	Depositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	10.00 - 1.50	Depositor	
% Data completeness	(Not available) (10.00-1.50)	Depositor	
(in resolution range)	(10.00 1.90)		
$R_{merge}$	(Not available)	Depositor	
$R_{sym}$	(Not available)	Depositor	
Refinement program	PROLSQ, X-PLOR	Depositor	
$R, R_{free}$	0.174 , (Not available)	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	1360	wwPDB-VP	
Average B, all atoms (Å <sup>2</sup> )	12.0	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: CA, ZN, PLH

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	Во	ond angles
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	A	1.14	1/1281 (0.1%)	2.41	59/1743 (3.4%)

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	A	0	1

#### All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	Ideal(A)
1	A	206	ASN	CG-OD1	5.19	1.35	1.24

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	117	ARG	NE-CZ-NH1	32.67	136.64	120.30
1	A	117	ARG	NE-CZ-NH2	-23.65	108.47	120.30
1	A	202	ARG	NE-CZ-NH2	13.79	127.19	120.30
1	A	117	ARG	CD-NE-CZ	12.44	141.02	123.60
1	A	165	ARG	NE-CZ-NH1	12.32	126.46	120.30
1	A	131	ASP	CB-CG-OD1	11.82	128.94	118.30
1	A	208	ARG	NE-CZ-NH1	11.46	126.03	120.30
1	A	207	PHE	CB-CG-CD1	-11.46	112.78	120.80
1	A	202	ARG	NE-CZ-NH1	-10.96	114.82	120.30
1	A	231	ASP	CB-CG-OD2	-10.54	108.81	118.30
1	A	167	ASP	CB-CG-OD2	-9.72	109.55	118.30
1	A	108	ARG	NE-CZ-NH1	-8.54	116.03	120.30

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Mol	$\frac{\text{Chain}}{\text{Chain}}$	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{\scriptscriptstyle o})$
1	A	168	HIS	CG-ND1-CE1	8.47	120.06	108.20
1	A	154	GLU	CA-CB-CG	8.41	131.90	113.40
1	A	110	GLU	CB-CG-CD	8.18	136.28	114.20
1	A	110	GLU	OE1-CD-OE2	-8.10	113.58	123.30
1	A	237	TYR	CB-CG-CD2	-8.08	116.15	121.00
1	A	252	ASP	CB-CG-OD2	-8.01	111.09	118.30
1	A	252	ASP	CB-CG-OD1	-7.76	111.31	118.30
1	A	260	TYR	CG-CD1-CE1	7.64	127.41	121.30
1	A	165	ARG	CD-NE-CZ	7.64	134.30	123.60
1	A	252	ASP	OD1-CG-OD2	7.51	137.57	123.30
1	A	207	PHE	CB-CG-CD2	7.25	125.87	120.80
1	A	202	ARG	CD-NE-CZ	6.93	133.30	123.60
1	A	215	VAL	O-C-N	6.85	133.66	122.70
1	A	110	GLU	CG-CD-OE1	6.77	131.84	118.30
1	A	214	ARG	NE-CZ-NH2	6.71	123.65	120.30
1	A	183	HIS	CG-CD2-NE2	6.54	121.63	109.20
1	A	131	ASP	OD1-CG-OD2	-6.50	110.94	123.30
1	A	208	ARG	CG-CD-NE	-6.48	98.19	111.80
1	A	246	VAL	O-C-N	6.38	132.91	122.70
1	A	212	LEU	CB-CG-CD1	6.37	121.83	111.00
1	A	223	SER	O-C-N	6.27	132.73	122.70
1	A	117	ARG	O-C-N	6.24	132.68	122.70
1	A	167	ASP	CB-CG-OD1	6.07	123.76	118.30
1	A	198	ASP	CB-CG-OD1	5.95	123.65	118.30
1	A	226	LEU	O-C-N	5.93	132.18	122.70
1	A	127	ARG	NE-CZ-NH1	-5.92	117.34	120.30
1	A	235	LEU	CB-CG-CD1	-5.79	101.15	111.00
1	A	198	ASP	CB-CG-OD2	-5.78	113.10	118.30
1	A	166	GLY	CA-C-N	5.75	129.85	117.20
1	A	237	TYR	CB-CG-CD1	5.74	124.44	121.00
1	A	185	PHE	CB-CG-CD1	-5.62	116.87	120.80
1	A	175	ASP	N-CA-CB	-5.60	100.52	110.60
1	A	115	THR	O-C-N	5.59	131.65	122.70
1	A	148	THR	N-CA-CB	5.59	120.93	110.30
1	A	190	GLY	O-C-N	5.56	131.59	122.70
1	A	138	PHE	O-C-N	5.46	131.44	122.70
1	A	144	VAL	O-C-N	5.46	131.43	122.70
1	A	129	ASP	CB-CG-OD2	5.41	123.17	118.30
1	A	254	ASP	CB-CG-OD2	-5.39	113.45	118.30
1	A	174	PHE	CB-CG-CD2	-5.20	117.16	120.80
1	A	183	HIS	CE1-NE2-CD2	-5.20	93.61	106.60
1	A	168	HIS	ND1-CG-CD2	-5.09	98.88	106.00

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Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	257	GLN	CA-C-N	5.09	128.39	117.20
1	A	181	LEU	CB-CG-CD1	5.08	119.63	111.00
1	A	210	TYR	CB-CG-CD1	-5.07	117.96	121.00
1	A	140	LEU	CB-CG-CD1	-5.02	102.47	111.00
1	A	124	ASP	CB-CG-OD2	-5.02	113.79	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	208	ARG	Sidechain

### 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	1244	0	1141	7	0
2	A	2	0	0	0	0
3	A	1	0	0	0	0
4	A	25	0	26	1	0
5	A	88	0	0	0	0
All	All	1360	0	1167	7	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 3.

All (7) 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:206:ASN:OD1	1:A:208:ARG:NH1	2.46	0.48
1:A:110:GLU:HG3	1:A:111:GLN:N	2.29	0.48
1:A:237:TYR:CD1	1:A:238:PRO:HD2	2.53	0.43
1:A:169:ARG:N	1:A:169:ARG:HD2	2.34	0.42
1:A:237:TYR:CG	1:A:238:PRO:HD2	2.55	0.41
1:A:180:ASN:HD21	4:A:280:PLH:H22	1.85	0.41
1:A:209:GLU:HA	1:A:210:TYR:HA	1.90	0.40



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	Analysed Favoured Allowed		Outliers	Percentiles
1	A	155/169 (92%)	154 (99%)	1 (1%)	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	Analysed Rotameric (		Percentiles
1	A	130/141 (92%)	127 (98%)	3 (2%)	50 20

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	136	LYS
1	A	139	GLN
1	A	206	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	113	HIS
1	A	132	HIS

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Mol	Chain	Res	Type
1	A	156	GLN
1	A	257	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)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 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			В	ond ang	les
	туре	Chain		Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	PLH	A	280	2	25,25,25	1.14	2 (8%)	31,32,32	2.59	9 (29%)

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	$\operatorname{Res}$	Link	Chirals	Torsions	Rings
4	PLH	A	280	2	ı	0/28/28/28	0/1/1/1

All (2) bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}( ext{\AA})$
4	A	280	PLH	C10-N3	2.41	1.36	1.33
4	A	280	PLH	C1-N1	-2.29	1.29	1.32

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$Ideal(^{o})$
4	A	280	PLH	O2-C1-C2	-7.60	110.37	121.50
4	A	280	PLH	O2-C1-N1	6.42	131.15	123.27
4	A	280	PLH	O1-N1-C1	-6.02	110.90	119.79
4	A	280	PLH	O3-C8-C3	-3.84	117.12	122.12
4	A	280	PLH	C2-C3-C8	3.58	114.95	109.77
4	A	280	PLH	O3-C8-N2	2.37	127.33	122.93
4	A	280	PLH	C17-C16-C15	2.24	124.09	119.93
4	A	280	PLH	C9-C10-N3	-2.21	113.63	116.99
4	A	280	PLH	C2-C1-N1	2.19	118.45	115.14

There are no chirality outliers.

There are no torsion outliers.

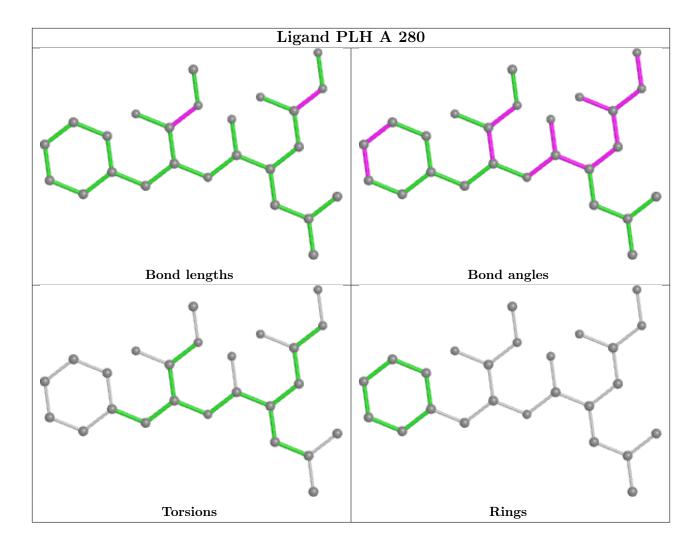
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	280	PLH	1	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 any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. 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)

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.

