

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

Apr 20, 2024 – 10:49 pm BST

PDB ID	:	4AFZ
Title	:	Human Chymase - Fynomer Complex
Authors	:	Schlatter, D.; Brack, S.; Banner, D.W.; Batey, S.; Benz, J.; Bertschinger,
		J.; Huber, W.; Joseph, C.; Rufer, A.; Van Der Kloosters, A.; Weber, M.;
		Grabulovski, D.; Hennig, M.
Deposited on		
Resolution	:	2.25  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:

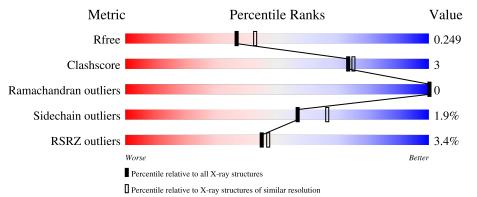
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as $541$ be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

# 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 2.25 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	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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	226	90%	9% •				
1	В	226	8%	8% •				
2	С	84	63% 8% · 27	%				
2	D	84	60% 7% • 32%					



# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4629 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.

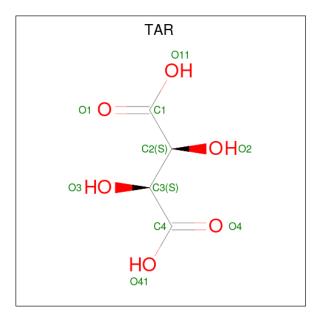
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Λ	224	Total	С	Ν	0	$\mathbf{S}$	0	2	0
	A	224	1767	1125	321	310	11	0	2	0
1	В	218	Total	С	Ν	0	S	0	1	0
	D	210	1709	1088	311	299	11	0		0

• Molecule 1 is a protein called CHYMASE.

• Molecule 2 is a protein called FYNOMER.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace	
9	С	61	Total	С	Ν	0	0	0	Ο
		01	496	325	77	94	0	0	0
9	Л	57	Total	С	Ν	0	0	0	Ο
2	2 D	57	467	307	73	87	0	0	0

• Molecule 3 is D(-)-TARTARIC ACID (three-letter code: TAR) (formula:  $C_4H_6O_6$ ).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	А	1	Total 10	$\begin{array}{c} \mathrm{C} \\ 4 \end{array}$	O 6	0	0

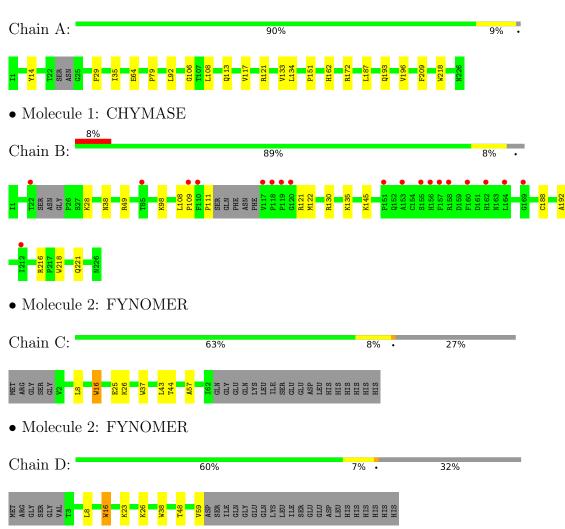
• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	97	Total O 97 97	0	0
4	В	46	Total         O           46         46	0	0
4	С	22	Total O 22 22	0	0
4	D	15	Total O 15 15	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: CHYMASE



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	60.27Å 58.34Å 93.03Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $103.76^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	45.18 - 2.25	Depositor
Resolution (A)	45.18 - 2.25	EDS
% Data completeness	95.1 (45.18-2.25)	Depositor
(in resolution range)	95.1 (45.18-2.25)	EDS
R <sub>merge</sub>	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.91 (at 2.24 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.6.0119	Depositor
D D.	0.178 , $0.241$	Depositor
$R, R_{free}$	0.185 , $0.249$	DCC
$R_{free}$ test set	1448 reflections $(5.06\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	40.2	Xtriage
Anisotropy	0.115	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.36 , $45.6$	EDS
L-test for twinning <sup>2</sup>	$ \langle L  \rangle = 0.49, \langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4629	wwPDB-VP
Average B, all atoms $(Å^2)$	50.0	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: TAR

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	Bond angles		
IVIOI			# Z  > 5	RMSZ	# Z  > 5	
1	А	0.66	1/1812~(0.1%)	0.72	0/2450	
1	В	0.58	1/1751~(0.1%)	0.64	0/2366	
2	С	0.86	2/513~(0.4%)	0.77	0/702	
2	D	0.78	2/484~(0.4%)	0.68	0/662	
All	All	0.67	6/4560~(0.1%)	0.69	0/6180	

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	218	TRP	CD2-CE2	6.53	1.49	1.41
2	С	37	TRP	CD2-CE2	5.76	1.48	1.41
2	D	38	TRP	CD2-CE2	5.74	1.48	1.41
1	В	218	TRP	CD2-CE2	5.24	1.47	1.41
2	D	16	TRP	CD2-CE2	5.05	1.47	1.41
2	С	16	TRP	CD2-CE2	5.01	1.47	1.41

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	1767	0	1772	18	0

Continued on next page...



Mol	Chain	1	H(model)	H(added)	Clashes	Symm-Clashes
1	В	1709	0	1725	14	0
2	С	496	0	462	2	0
2	D	467	0	433	2	0
3	А	10	0	4	0	0
4	А	97	0	0	1	0
4	В	46	0	0	0	0
4	С	22	0	0	0	0
4	D	15	0	0	0	0
All	All	4629	0	4396	29	0

Continued from previous page...

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 (29) 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:172:ARG:NH1	1:B:49:ARG:CZ	2.26	0.98
1:A:172:ARG:HH12	1:B:49:ARG:CZ	1.76	0.97
1:A:172:ARG:NH1	1:B:49:ARG:NH2	2.17	0.91
1:A:172:ARG:HH12	1:B:49:ARG:NH2	1.81	0.74
1:A:172:ARG:HH12	1:B:49:ARG:NH1	1.91	0.67
1:B:28:LYS:HE3	2:D:48:THR:HB	1.83	0.59
1:A:35:ILE:HD11	1:A:92:LEU:HD21	1.86	0.57
1:A:29[B]:PHE:C	1:A:29[B]:PHE:CD1	2.77	0.57
1:B:121:ARG:HD3	1:B:188:CYS:HB3	1.87	0.56
1:B:130:ARG:HD3	1:B:135:LYS:O	2.08	0.53
1:A:172:ARG:HH11	1:B:49:ARG:NH2	2.05	0.51
1:B:111:PRO:HD3	1:B:192:ALA:O	2.11	0.51
1:A:196:VAL:HG22	1:A:209:PHE:CE2	2.47	0.49
1:B:111:PRO:C	1:B:216:ARG:HD3	2.34	0.49
1:A:151:PRO:HG3	1:A:162:HIS:CD2	2.50	0.47
1:A:14:TYR:HA	1:A:106:GLY:O	2.16	0.46
1:B:108:LEU:HA	1:B:109:PRO:HD2	1.79	0.45
1:A:133:VAL:HG12	1:A:134:LEU:HG	1.99	0.44
1:B:122:MET:HE2	1:B:145:LYS:HE3	1.99	0.44
2:D:8:LEU:O	2:D:23:LYS:HG3	2.18	0.43
1:A:108:LEU:HD11	1:A:187:LEU:HD21	2.00	0.43
1:A:162:HIS:HD2	4:A:2081:HOH:O	2.02	0.42
1:A:113[A]:GLN:O	1:A:113[A]:GLN:HG2	2.19	0.42
1:A:193:GLN:HA	1:A:193:GLN:OE1	2.21	0.41
1:B:38:ASN:HB3	1:B:98:LYS:HG2	2.02	0.41

Continued on next page...



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:25:GLU:HG3	2:C:44:THR:OG1	2.20	0.41
1:A:117:VAL:HG23	1:A:121:ARG:HD2	2.03	0.40
1:A:121:ARG:HE	1:A:121:ARG:HB3	1.66	0.40
2:C:8:LEU:HD11	2:C:57:ALA:HB2	2.03	0.40

Continued from previous page...

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	222/226~(98%)	217 (98%)	5(2%)	0	100 100
1	В	213/226~(94%)	208~(98%)	5(2%)	0	100 100
2	С	59/84~(70%)	57~(97%)	2 (3%)	0	100 100
2	D	55/84~(66%)	55 (100%)	0	0	100 100
All	All	549/620~(88%)	537 (98%)	12 (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	А	191/191~(100%)	189~(99%)	2(1%)	76 84
1	В	185/191~(97%)	184 (100%)	1 (0%)	88 92

Continued on next page...



Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	С	52/72~(72%)	49~(94%)	3~(6%)	20 20
2	D	48/72~(67%)	45~(94%)	3~(6%)	18 17
All	All	476/526~(90%)	467~(98%)	9~(2%)	57 66

Continued from previous page...

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	64	GLU
1	А	79	PRO
1	В	221	GLN
2	С	16	TRP
2	С	26	LYS
2	С	43	LEU
2	D	16	TRP
2	D	26	LYS
2	D	59	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	152	GLN
1	А	162	HIS
1	А	221	GLN
1	В	152	GLN
1	В	221	GLN
2	D	28	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)

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).

Mol	Type	Chain	Res	Link	B	ond leng	gths	В	ond ang	les
WIOI	туре	Ullalli	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
3	TAR	А	1227	-	9,9,9	1.05	0	12,12,12	1.06	1 (8%)

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	TAR	А	1227	-	-	6/12/12/12	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	А	1227	TAR	O41-C4-C3	2.01	118.71	113.27

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	А	1227	TAR	O1-C1-C2-O2
3	А	1227	TAR	O3-C3-C4-O4
3	А	1227	TAR	O3-C3-C4-O41
3	А	1227	TAR	O11-C1-C2-O2
3	А	1227	TAR	O11-C1-C2-C3
3	А	1227	TAR	O1-C1-C2-C3

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	$\langle RSRZ \rangle$	# RSRZ > 2	$\mathbf{OWAB}(\mathrm{\AA}^2)$	$Q{<}0.9$
1	А	224/226~(99%)	0.06	0 100 100	28, 39, 61, 88	23 (10%)
1	В	218/226~(96%)	0.46	19 (8%) 10 11	41, 58, 94, 125	24 (11%)
2	С	61/84~(72%)	0.04	0 100 100	31, 41, 56, 84	3(4%)
2	D	57/84~(67%)	0.09	0 100 100	37,  48,  63,  65	0
All	All	560/620~(90%)	0.22	19 (3%) 45 47	28, 47, 85, 125	50~(8%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	109	PRO	6.0
1	В	162	HIS	4.4
1	В	157	PHE	3.8
1	В	120	GLY	3.5
1	В	158	ARG	3.2
1	В	164	LEU	3.2
1	В	110	PHE	3.2
1	В	118	PRO	3.2
1	В	119	PRO	3.0
1	В	22	THR	2.7
1	В	151	PRO	2.6
1	В	156	HIS	2.5
1	В	160	PHE	2.5
1	В	153	ALA	2.5
1	В	212	ILE	2.5
1	В	155	SER	2.4
1	В	85	THR	2.1
1	В	117	VAL	2.1
1	В	169	GLY	2.1



#### 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	$B-factors(Å^2)$	Q < 0.9
3	TAR	А	1227	10/10	0.87	0.23	46,70,78,80	0

#### 6.5 Other polymers (i)

There are no such residues in this entry.

