



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 21, 2026 – 12:30 PM JST

PDB ID : 9UM5 / pdb\_00009um5  
Title : CaPETaseM9 SEC loop of 10CL variant  
Authors : Kim, K.; Ki, D.; Park, J.  
Deposited on : 2025-04-21  
Resolution : 1.73 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](mailto: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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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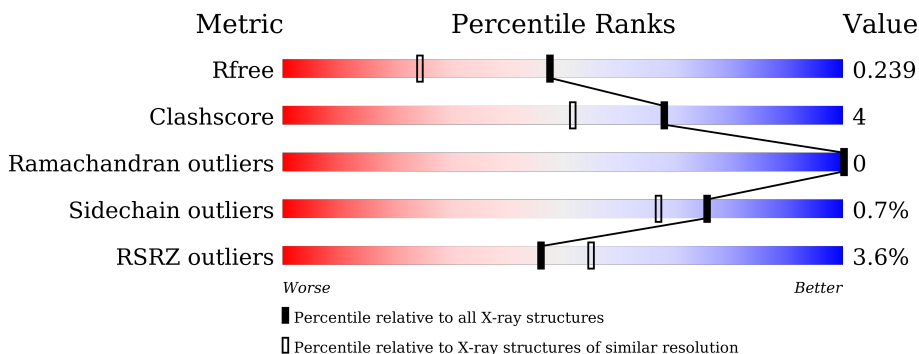
The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

**i**

## X-RAY DIFFRACTION

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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
R <sub>free</sub>	180053	1187 (1.74-1.74)
Clashscore	190562	1207 (1.74-1.74)
Ramachandran outliers	187476	1200 (1.74-1.74)
Sidechain outliers	187428	1200 (1.74-1.74)
RSRZ outliers	180081	1188 (1.74-1.74)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	A	264	88%	8% ..
1	B	264	87%	10% ..
1	C	264	85%	13% .
1	D	264	88%	9% ..

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8248 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 Cutinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	259	Total	C	N	O	S	0	0	0
			1973	1252	341	370	10			
1	B	259	Total	C	N	O	S	0	0	0
			1966	1247	341	368	10			
1	C	260	Total	C	N	O	S	0	0	0
			1978	1255	342	371	10			
1	D	258	Total	C	N	O	S	0	0	0
			1964	1247	340	367	10			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	109	ALA	ASN	engineered mutation	UNP A0A1M7II12
A	129	THR	VAL	engineered mutation	UNP A0A1M7II12
A	155	ARG	ALA	engineered mutation	UNP A0A1M7II12
A	180	CYS	LEU	engineered mutation	UNP A0A1M7II12
A	196	THR	GLY	engineered mutation	UNP A0A1M7II12
A	198	LYS	ARG	engineered mutation	UNP A0A1M7II12
A	202	CYS	ALA	engineered mutation	UNP A0A1M7II12
A	242	CYS	ARG	engineered mutation	UNP A0A1M7II12
A	283	ARG	SER	engineered mutation	UNP A0A1M7II12
A	284	ASP	THR	engineered mutation	UNP A0A1M7II12
A	288	GLY	ALA	engineered mutation	UNP A0A1M7II12
A	289	GLU	PRO	engineered mutation	UNP A0A1M7II12
A	291	CYS	SER	engineered mutation	UNP A0A1M7II12
A	300	LEU	-	expression tag	UNP A0A1M7II12
A	301	GLU	-	expression tag	UNP A0A1M7II12
A	302	HIS	-	expression tag	UNP A0A1M7II12
A	303	HIS	-	expression tag	UNP A0A1M7II12
A	304	HIS	-	expression tag	UNP A0A1M7II12
B	109	ALA	ASN	engineered mutation	UNP A0A1M7II12
B	129	THR	VAL	engineered mutation	UNP A0A1M7II12
B	155	ARG	ALA	engineered mutation	UNP A0A1M7II12

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Chain	Residue	Modelled	Actual	Comment	Reference
B	180	CYS	LEU	engineered mutation	UNP A0A1M7II12
B	196	THR	GLY	engineered mutation	UNP A0A1M7II12
B	198	LYS	ARG	engineered mutation	UNP A0A1M7II12
B	202	CYS	ALA	engineered mutation	UNP A0A1M7II12
B	242	CYS	ARG	engineered mutation	UNP A0A1M7II12
B	283	ARG	SER	engineered mutation	UNP A0A1M7II12
B	284	ASP	THR	engineered mutation	UNP A0A1M7II12
B	288	GLY	ALA	engineered mutation	UNP A0A1M7II12
B	289	GLU	PRO	engineered mutation	UNP A0A1M7II12
B	291	CYS	SER	engineered mutation	UNP A0A1M7II12
B	300	LEU	-	expression tag	UNP A0A1M7II12
B	301	GLU	-	expression tag	UNP A0A1M7II12
B	302	HIS	-	expression tag	UNP A0A1M7II12
B	303	HIS	-	expression tag	UNP A0A1M7II12
B	304	HIS	-	expression tag	UNP A0A1M7II12
C	109	ALA	ASN	engineered mutation	UNP A0A1M7II12
C	129	THR	VAL	engineered mutation	UNP A0A1M7II12
C	155	ARG	ALA	engineered mutation	UNP A0A1M7II12
C	180	CYS	LEU	engineered mutation	UNP A0A1M7II12
C	196	THR	GLY	engineered mutation	UNP A0A1M7II12
C	198	LYS	ARG	engineered mutation	UNP A0A1M7II12
C	202	CYS	ALA	engineered mutation	UNP A0A1M7II12
C	242	CYS	ARG	engineered mutation	UNP A0A1M7II12
C	283	ARG	SER	engineered mutation	UNP A0A1M7II12
C	284	ASP	THR	engineered mutation	UNP A0A1M7II12
C	288	GLY	ALA	engineered mutation	UNP A0A1M7II12
C	289	GLU	PRO	engineered mutation	UNP A0A1M7II12
C	291	CYS	SER	engineered mutation	UNP A0A1M7II12
C	300	LEU	-	expression tag	UNP A0A1M7II12
C	301	GLU	-	expression tag	UNP A0A1M7II12
C	302	HIS	-	expression tag	UNP A0A1M7II12
C	303	HIS	-	expression tag	UNP A0A1M7II12
C	304	HIS	-	expression tag	UNP A0A1M7II12
D	109	ALA	ASN	engineered mutation	UNP A0A1M7II12
D	129	THR	VAL	engineered mutation	UNP A0A1M7II12
D	155	ARG	ALA	engineered mutation	UNP A0A1M7II12
D	180	CYS	LEU	engineered mutation	UNP A0A1M7II12
D	196	THR	GLY	engineered mutation	UNP A0A1M7II12
D	198	LYS	ARG	engineered mutation	UNP A0A1M7II12
D	202	CYS	ALA	engineered mutation	UNP A0A1M7II12
D	242	CYS	ARG	engineered mutation	UNP A0A1M7II12
D	283	ARG	SER	engineered mutation	UNP A0A1M7II12

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Chain	Residue	Modelled	Actual	Comment	Reference
D	284	ASP	THR	engineered mutation	UNP A0A1M7II12
D	288	GLY	ALA	engineered mutation	UNP A0A1M7II12
D	289	GLU	PRO	engineered mutation	UNP A0A1M7II12
D	291	CYS	SER	engineered mutation	UNP A0A1M7II12
D	300	LEU	-	expression tag	UNP A0A1M7II12
D	301	GLU	-	expression tag	UNP A0A1M7II12
D	302	HIS	-	expression tag	UNP A0A1M7II12
D	303	HIS	-	expression tag	UNP A0A1M7II12
D	304	HIS	-	expression tag	UNP A0A1M7II12

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	106	Total 106	O 106	0	0
2	B	101	Total 101	O 101	0	0
2	C	96	Total 96	O 96	0	0
2	D	64	Total 64	O 64	0	0

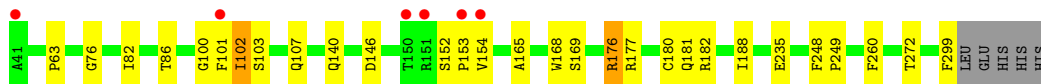
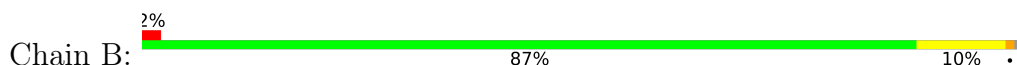
### 3 Residue-property plots [i](#)

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.

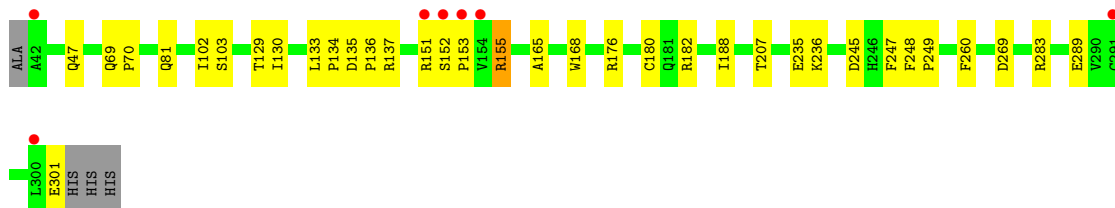
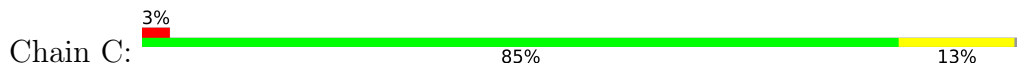
- Molecule 1: Cutinase



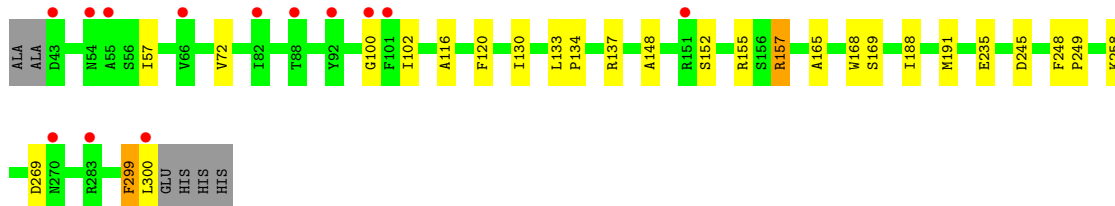
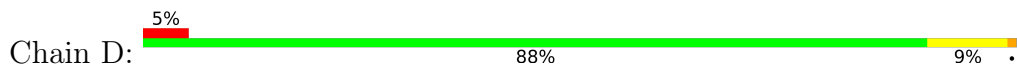
- Molecule 1: Cutinase



- Molecule 1: Cutinase



- Molecule 1: Cutinase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	46.57Å 75.78Å 77.24Å 118.73° 95.89° 102.03°	Depositor
Resolution (Å)	25.83 – 1.73 25.83 – 1.73	Depositor EDS
% Data completeness (in resolution range)	95.2 (25.83-1.73) 95.5 (25.83-1.73)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.78 (at 1.73Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, $R_{free}$	0.183 , 0.225 0.197 , 0.239	Depositor DCC
$R_{free}$ test set	4392 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.4	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 32.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8248	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.44% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<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.

## 5 Model quality

### 5.1 Standard geometry

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	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.72	0/2031	1.19	9/2777 (0.3%)
1	B	0.72	0/2024	1.17	5/2768 (0.2%)
1	C	0.74	0/2036	1.14	6/2784 (0.2%)
1	D	0.71	0/2022	1.12	3/2765 (0.1%)
All	All	0.72	0/8113	1.16	23/11094 (0.2%)

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
1	B	0	2
1	C	0	5
1	D	0	3
All	All	0	11

There are no bond length outliers.

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	283	ARG	CB-CA-C	-6.78	99.33	109.90
1	C	47	GLN	CB-CA-C	-6.69	99.47	109.90
1	D	269	ASP	CA-CB-CG	6.49	119.09	112.60
1	B	180	CYS	CB-CA-C	6.38	120.99	110.90
1	B	248	PHE	CA-CB-CG	6.30	120.10	113.80

There are no chirality outliers.

5 of 11 planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	A	283	ARG	Sidechain
1	B	176	ARG	Sidechain
1	B	182	ARG	Sidechain
1	C	137	ARG	Sidechain
1	C	151	ARG	Sidechain

## 5.2 Too-close contacts

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	1973	0	1891	15	1
1	B	1966	0	1884	16	1
1	C	1978	0	1896	18	0
1	D	1964	0	1885	13	0
2	A	106	0	0	0	0
2	B	101	0	0	0	0
2	C	96	0	0	0	0
2	D	64	0	0	0	0
All	All	8248	0	7556	55	1

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 55 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:B:82:ILE:HD13	1:B:154:VAL:HG11	1.51	0.92
1:D:102:ILE:HA	1:D:130:ILE:HG12	1.68	0.76
1:B:152:SER:OG	1:B:153:PRO:HD2	1.94	0.68
1:B:82:ILE:CD1	1:B:154:VAL:HG11	2.24	0.68
1:D:248:PHE:CG	1:D:249:PRO:HD3	2.34	0.63

All (1) 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	Interatomic distance (Å)	Clash overlap (Å)
1:A:283:ARG:NH2	1:B:86:THR:O[1_554]	2.17	0.03

## 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	257/264 (97%)	251 (98%)	6 (2%)	0	100	100
1	B	257/264 (97%)	250 (97%)	7 (3%)	0	100	100
1	C	258/264 (98%)	248 (96%)	10 (4%)	0	100	100
1	D	256/264 (97%)	249 (97%)	7 (3%)	0	100	100
All	All	1028/1056 (97%)	998 (97%)	30 (3%)	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	206/209 (99%)	205 (100%)	1 (0%)	81	75
1	B	204/209 (98%)	203 (100%)	1 (0%)	81	75
1	C	206/209 (99%)	203 (98%)	3 (2%)	57	38
1	D	205/209 (98%)	204 (100%)	1 (0%)	81	75
All	All	821/836 (98%)	815 (99%)	6 (1%)	76	67

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	283	ARG
1	C	289	GLU
1	D	72	VAL
1	B	102	ILE
1	A	102	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	107	GLN
1	C	81	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	259/264 (98%)	0.11	11 (4%) 40 49	9, 18, 32, 63	0
1	B	259/264 (98%)	0.10	6 (2%) 61 69	11, 19, 33, 63	0
1	C	260/264 (98%)	0.18	7 (2%) 56 64	12, 20, 34, 64	0
1	D	258/264 (97%)	0.47	13 (5%) 34 42	13, 24, 39, 48	0
All	All	1036/1056 (98%)	0.22	37 (3%) 46 55	9, 20, 35, 64	0

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	43	ASP	4.7
1	C	42	ALA	4.7
1	B	153	PRO	4.0
1	D	101	PHE	3.9
1	A	287	PHE	3.8

### 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 oligosaccharides in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.