



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:28 PM UTC

PDB ID : 5FPW / pdb\_00005fpw  
Title : proCathepsin B S9 from Trypanosoma congolense  
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Deposited on : 2015-12-03  
Resolution : 2.10 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  
Xtrriage (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

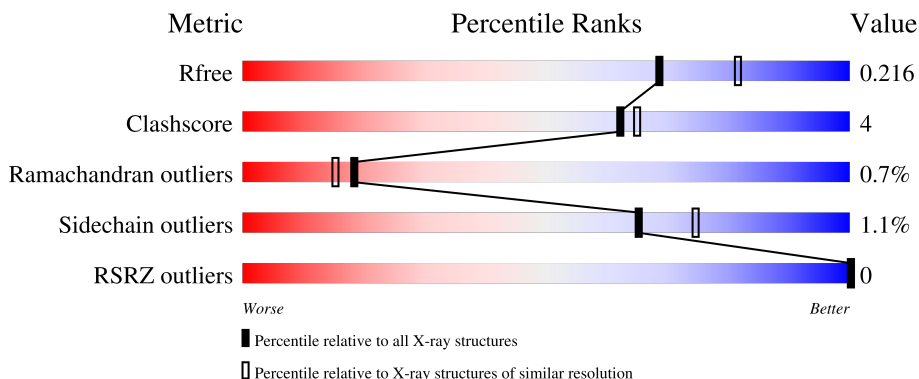
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	321	 82% 9% 9%
1	B	321	 80% 10% 8%
1	C	321	 84% 7% 9%

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 7566 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 PRO CATHEPSIN B S9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	293	2302	1474	389	424	15	0	0	1
1	B	294	2308	1477	390	426	15	5	0	1
1	C	293	2300	1473	388	424	15	5	0	1

There are 33 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	ALA	-	expression tag	UNP B2C331
A	-2	GLU	-	expression tag	UNP B2C331
A	-1	PHE	-	expression tag	UNP B2C331
A	0	HIS	-	expression tag	UNP B2C331
A	1	HIS	-	expression tag	UNP B2C331
A	2	HIS	-	expression tag	UNP B2C331
A	3	HIS	-	expression tag	UNP B2C331
A	4	HIS	-	expression tag	UNP B2C331
A	5	HIS	-	expression tag	UNP B2C331
A	192	GLN	ASN	engineered mutation	UNP B2C331
A	208	SER	ASN	engineered mutation	UNP B2C331
B	997	ALA	-	expression tag	UNP B2C331
B	998	GLU	-	expression tag	UNP B2C331
B	999	PHE	-	expression tag	UNP B2C331
B	1000	HIS	-	expression tag	UNP B2C331
B	1001	HIS	-	expression tag	UNP B2C331
B	1002	HIS	-	expression tag	UNP B2C331
B	1003	HIS	-	expression tag	UNP B2C331
B	1004	HIS	-	expression tag	UNP B2C331
B	1005	HIS	-	expression tag	UNP B2C331
B	1192	GLN	ASN	engineered mutation	UNP B2C331
B	1208	SER	ASN	engineered mutation	UNP B2C331
C	1997	ALA	-	expression tag	UNP B2C331

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1998	GLU	-	expression tag	UNP B2C331
C	1999	PHE	-	expression tag	UNP B2C331
C	2000	HIS	-	expression tag	UNP B2C331
C	2001	HIS	-	expression tag	UNP B2C331
C	2002	HIS	-	expression tag	UNP B2C331
C	2003	HIS	-	expression tag	UNP B2C331
C	2004	HIS	-	expression tag	UNP B2C331
C	2005	HIS	-	expression tag	UNP B2C331
C	2192	GLN	ASN	engineered mutation	UNP B2C331
C	2208	SER	ASN	engineered mutation	UNP B2C331

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	239	Total O 239 239	0	0
2	B	220	Total O 220 220	0	0
2	C	197	Total O 197 197	0	0



## 4 Data and refinement statistics i

Property	Value	Source
Space group	C 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	128.79Å 223.22Å 102.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.03 – 2.10 39.03 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.5 (39.03-2.10) 98.3 (39.03-2.10)	Depositor EDS
$R_{merge}$	0.01	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.16 (at 2.10Å)	Xtrriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.179 , 0.216 0.180 , 0.216	Depositor DCC
$R_{free}$ test set	4263 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.5	Xtrriage
Anisotropy	0.374	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 39.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.467 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.477 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	7566	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.05% 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 [i](#)

### 5.1 Standard geometry [i](#)

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	0.47	2/2369 (0.1%)	0.54	0/3221
1	B	0.51	2/2375 (0.1%)	0.56	0/3229
1	C	0.49	3/2367 (0.1%)	0.56	0/3218
All	All	0.49	7/7111 (0.1%)	0.55	0/9668

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1009	PRO	N-CD	-14.66	1.27	1.47
1	A	9	PRO	N-CD	-12.72	1.29	1.47
1	C	2009	PRO	N-CD	-11.62	1.31	1.47
1	B	1314	SER	C-N	-6.80	1.23	1.33
1	A	313	THR	C-N	-6.77	1.23	1.33

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	A	2302	0	2199	20	0
1	B	2308	0	2204	22	0
1	C	2300	0	2198	15	1
2	A	239	0	0	6	2
2	B	220	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	197	0	0	2	2
All	All	7566	0	6601	55	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.

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:A:95:ALA:HB3	1:A:185:ASN:HB2	1.49	0.93
1:B:1153:GLU:OE1	2:B:4138:HOH:O	1.99	0.81
1:C:2020:ASN:HD21	1:C:2029:ALA:H	1.28	0.79
1:C:2153:GLU:HG3	1:C:2154:TYR:CD2	2.25	0.72
1:A:63:THR:H	1:A:66:GLN:HE21	1.37	0.70

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	Interatomic distance (Å)	Clash overlap (Å)
2:A:4056:HOH:O	2:A:4056:HOH:O[2_655]	1.94	0.26
1:C:2053:LYS:NZ	2:C:4178:HOH:O[6_555]	2.05	0.15
2:C:4109:HOH:O	2:C:4109:HOH:O[6_555]	2.13	0.07
2:A:4050:HOH:O	2:A:4058:HOH:O[2_655]	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	289/321 (90%)	274 (95%)	13 (4%)	2 (1%)	18 15
1	B	290/321 (90%)	278 (96%)	9 (3%)	3 (1%)	12 9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	289/321 (90%)	278 (96%)	10 (4%)	1 (0%)	36	36
All	All	868/963 (90%)	830 (96%)	32 (4%)	6 (1%)	18	15

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	56	SER
1	C	2169	CYS
1	B	1055	SER
1	B	1056	SER
1	A	55	SER

### 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	242/267 (91%)	242 (100%)	0	100	100
1	B	243/267 (91%)	239 (98%)	4 (2%)	55	64
1	C	242/267 (91%)	238 (98%)	4 (2%)	53	62
All	All	727/801 (91%)	719 (99%)	8 (1%)	65	74

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	2212	LEU
1	C	2169	CYS
1	C	2051	ILE
1	B	1294	LEU
1	C	2118	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	66	GLN
1	B	1119	GLN
1	B	1162	GLN
1	C	2020	ASN
1	C	2119	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	293/321 (91%)	-1.31	0 100 100	23, 34, 60, 99	0
1	B	294/321 (91%)	-1.32	0 100 100	19, 34, 60, 118	1 (0%)
1	C	293/321 (91%)	-1.31	0 100 100	19, 34, 59, 110	1 (0%)
All	All	880/963 (91%)	-1.31	0 100 100	19, 34, 60, 118	2 (0%)

There are no RSRZ outliers to report.

### 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.