



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 3AMD / pdb\_00003amd  
Title : Crystal structures of *Thermotoga maritima* Cel5A, apo form and tetramer/au  
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Deposited on : 2010-08-19  
Resolution : 2.00 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

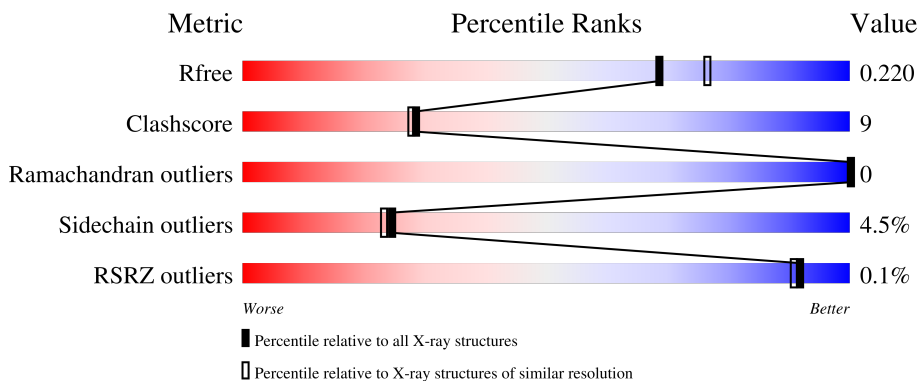
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	317	
1	B	317	
1	C	317	
1	D	317	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11201 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 Endoglucanase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	311	Total 2610	C 1698	N 445	O 463	S 4	0	0	0
1	B	312	Total 2618	C 1703	N 446	O 464	S 5	0	0	0
1	C	309	Total 2602	C 1694	N 443	O 461	S 4	0	0	0
1	D	311	Total 2610	C 1698	N 445	O 463	S 4	0	0	0

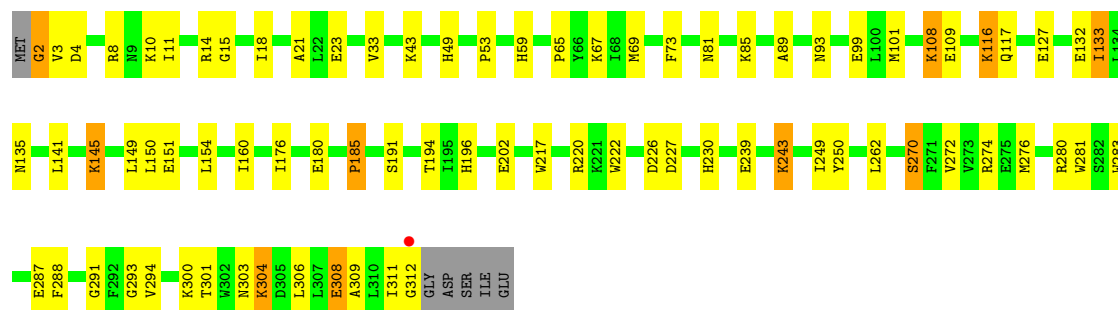
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	207	Total 207	O 207	0	0
2	B	201	Total 201	O 201	0	0
2	C	175	Total 175	O 175	0	0
2	D	178	Total 178	O 178	0	0



- Molecule 1: Endoglucanase

Chain D:  73% 22% ..



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	82.27Å 75.33Å 93.57Å 90.00° 90.41° 90.00°	Depositor
Resolution (Å)	25.00 – 2.00 25.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	95.8 (25.00-2.00) 95.8 (25.00-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.05 (at 1.99Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.168 , 0.219 0.167 , 0.220	Depositor DCC
$R_{free}$ test set	3797 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	17.3	Xtrriage
Anisotropy	0.622	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 46.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.026 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	11201	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 69.86 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.4447e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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	1.04	2/2691 (0.1%)	1.22	21/3640 (0.6%)
1	B	1.03	1/2699 (0.0%)	1.20	15/3650 (0.4%)
1	C	1.03	4/2683 (0.1%)	1.23	26/3630 (0.7%)
1	D	1.02	5/2691 (0.2%)	1.16	17/3640 (0.5%)
All	All	1.03	12/10764 (0.1%)	1.20	79/14560 (0.5%)

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	1
All	All	0	2

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1	MET	SD-CE	7.33	1.97	1.79
1	C	21	ALA	CA-C	7.26	1.55	1.52
1	C	52	ILE	CA-CB	6.95	1.60	1.54
1	D	2	GLY	N-CA	6.33	1.55	1.45
1	A	2	GLY	N-CA	6.15	1.55	1.45

The worst 5 of 79 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	293	GLY	N-CA-C	10.98	124.55	111.93
1	C	133	ILE	N-CA-C	10.65	121.31	110.23
1	A	293	GLY	N-CA-C	10.03	123.47	111.93
1	B	288	PHE	N-CA-C	9.53	121.26	111.07
1	A	133	ILE	N-CA-C	9.33	119.94	110.23

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	250	TYR	Sidechain
1	B	250	TYR	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	2610	0	2543	47	0
1	B	2618	0	2555	47	0
1	C	2602	0	2537	46	0
1	D	2610	0	2543	48	0
2	A	207	0	0	9	0
2	B	201	0	0	3	0
2	C	175	0	0	8	0
2	D	178	0	0	11	0
All	All	11201	0	10178	182	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 9.

The worst 5 of 182 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:C:304:LYS:HG2	2:C:698:HOH:O	1.60	0.99
1:B:308:GLU:OE1	1:B:312:GLY:HA3	1.63	0.99
1:B:98:GLU:HG3	2:B:354:HOH:O	1.69	0.91
1:D:133:ILE:HD11	1:D:154:LEU:HD11	1.57	0.87
1:C:33:VAL:O	1:C:35:LYS:HD2	1.77	0.85

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	A	309/317 (98%)	301 (97%)	8 (3%)	0	100	100
1	B	310/317 (98%)	299 (96%)	11 (4%)	0	100	100
1	C	307/317 (97%)	295 (96%)	12 (4%)	0	100	100
1	D	309/317 (98%)	302 (98%)	7 (2%)	0	100	100
All	All	1235/1268 (97%)	1197 (97%)	38 (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	272/277 (98%)	262 (96%)	10 (4%)	30	30
1	B	273/277 (99%)	261 (96%)	12 (4%)	25	24
1	C	272/277 (98%)	259 (95%)	13 (5%)	23	21
1	D	272/277 (98%)	258 (95%)	14 (5%)	21	19
All	All	1089/1108 (98%)	1040 (96%)	49 (4%)	24	23

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	144	GLU
1	D	10	LYS
1	C	186	LYS

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Mol	Chain	Res	Type
1	C	226	ASP
1	D	108	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	20	ASN
1	D	59	HIS
1	D	230	HIS
1	B	81	ASN
1	B	138	HIS

### 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	311/317 (98%)	-0.62	0 <a href="#">100</a> <a href="#">100</a>	9, 17, 29, 39	0
1	B	312/317 (98%)	-0.62	0 <a href="#">100</a> <a href="#">100</a>	10, 17, 29, 40	0
1	C	309/317 (97%)	-0.54	0 <a href="#">100</a> <a href="#">100</a>	12, 19, 29, 42	0
1	D	311/317 (98%)	-0.55	1 (0%) <a href="#">90</a> <a href="#">89</a>	10, 19, 32, 38	0
All	All	1243/1268 (98%)	-0.58	1 (0%) <a href="#">92</a> <a href="#">91</a>	9, 18, 29, 42	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	312	GLY	2.3

### 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.