



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 09:38 PM UTC

PDB ID : 4IM4 / pdb\_00004im4  
Title : Multifunctional cellulase, xylanase, mannanase  
Authors : Bianchetti, C.M.; Takasuka, T.E.; Fox, B.G.  
Deposited on : 2013-01-02  
Resolution : 2.42 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

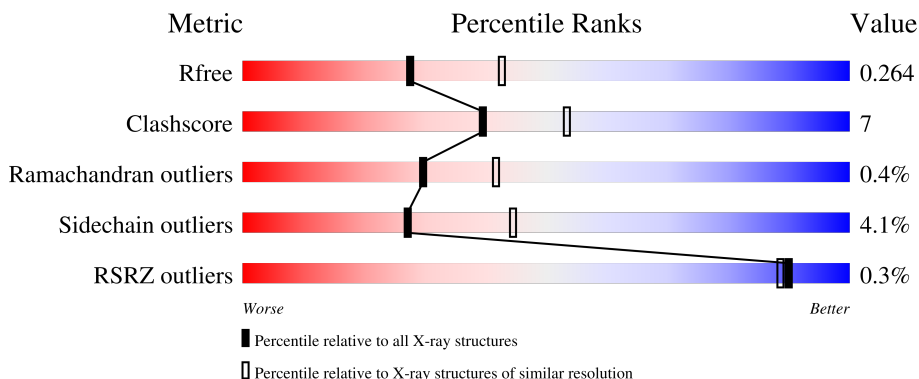
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.42 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	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
Sidechain outliers	187428	6482 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

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	336	 82% 15%
1	B	336	 86% 13%
1	C	336	 78% 21%
1	D	336	 88% 12%
1	E	336	 80% 18%

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Mol	Chain	Length	Quality of chain
1	F	336	 85% 15%

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 17521 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 E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	336	2702	1715	469	508	10	0	1	0
1	B	336	2702	1715	469	508	10	0	1	0
1	C	336	2720	1731	469	510	10	0	2	0
1	D	336	2694	1710	466	508	10	0	0	0
1	E	336	2694	1710	466	508	10	0	0	0
1	F	336	2697	1712	466	509	10	0	1	0

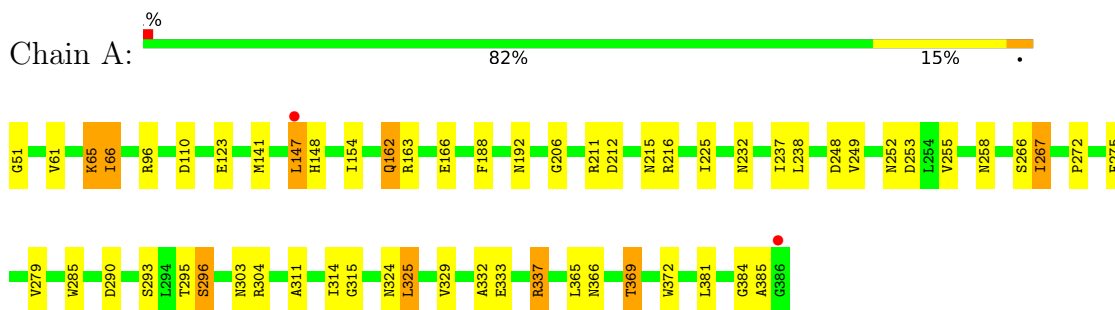
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	248	Total 248	O 248	0	0
2	B	205	Total 205	O 205	0	0
2	C	228	Total 228	O 228	0	0
2	D	205	Total 205	O 205	0	0
2	E	208	Total 208	O 208	0	0
2	F	218	Total 218	O 218	0	0

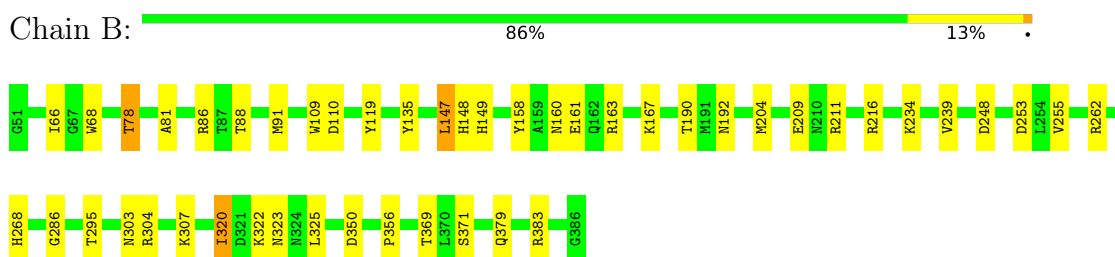
### 3 Residue-property plots [i](#)

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.

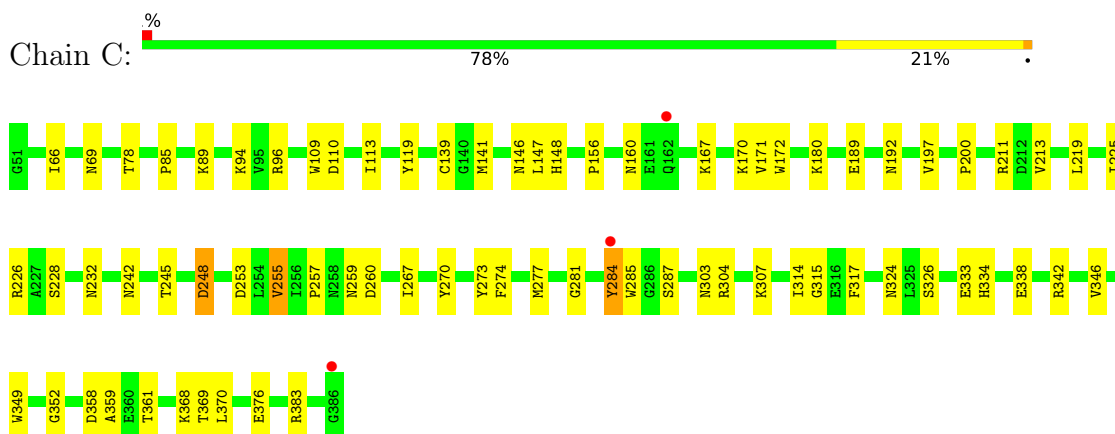
- Molecule 1: Endoglucanase E



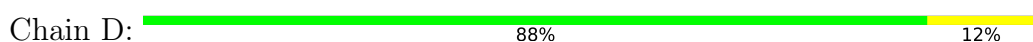
- Molecule 1: Endoglucanase E

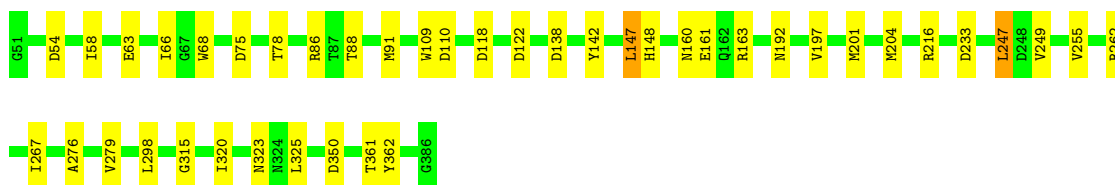


- Molecule 1: Endoglucanase E



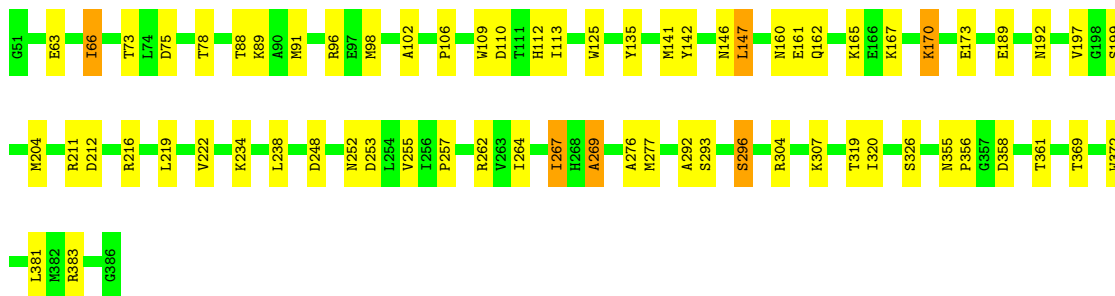
- Molecule 1: Endoglucanase E





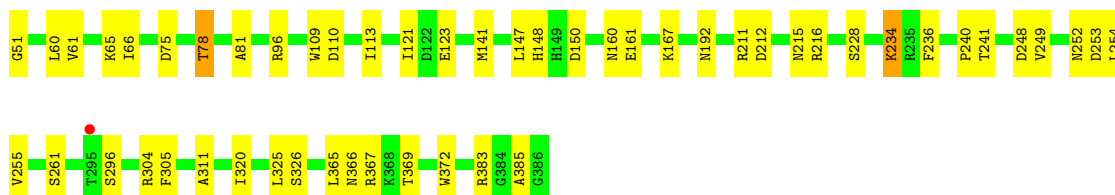
- Molecule 1: Endoglucanase E

Chain E: 80% 18%



- Molecule 1: Endoglucanase E

Chain F: 85% 15%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	92.41Å 111.70Å 120.37Å 90.00° 97.29° 90.00°	Depositor
Resolution (Å)	47.35 – 2.42 47.35 – 2.42	Depositor EDS
% Data completeness (in resolution range)	99.5 (47.35-2.42) 91.2 (47.35-2.42)	Depositor EDS
$R_{merge}$	0.19	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.84 (at 2.42Å)	Xtrriage
Refinement program	PHENIX 1.8_1069	Depositor
R, $R_{free}$	0.209 , 0.264 0.211 , 0.264	Depositor DCC
$R_{free}$ test set	1994 reflections (2.15%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.6	Xtrriage
Anisotropy	0.505	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 36.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	17521	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	14.0	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 22.96 % 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 5.1293e-03. 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	0.59	0/2773	0.86	0/3775
1	B	0.53	0/2773	0.82	1/3775 (0.0%)
1	C	0.54	0/2799	0.87	1/3811 (0.0%)
1	D	0.52	0/2762	0.84	0/3761
1	E	0.56	0/2762	0.87	1/3761 (0.0%)
1	F	0.53	0/2768	0.87	0/3769
All	All	0.55	0/16637	0.86	3/22652 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	269	ALA	N-CA-C	5.62	116.60	107.32
1	C	273	TYR	N-CA-C	5.11	117.25	111.11
1	B	135	TYR	N-CA-C	-5.09	105.73	111.28

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	2702	0	2610	37	0
1	B	2702	0	2610	25	0
1	C	2720	0	2628	49	0
1	D	2694	0	2597	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2694	0	2597	46	0
1	F	2697	0	2602	31	0
2	A	248	0	0	13	0
2	B	205	0	0	7	0
2	C	228	0	0	20	0
2	D	205	0	0	9	0
2	E	208	0	0	16	0
2	F	218	0	0	9	0
All	All	17521	0	15644	213	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 7.

The worst 5 of 213 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)
2:A:593:HOH:O	1:E:204:MET:SD	1.91	1.25
1:E:304:ARG:NH2	2:E:567:HOH:O	1.95	0.99
1:D:118:ASP:OD1	2:D:567:HOH:O	1.82	0.95
1:C:285:TRP:O	2:C:610:HOH:O	1.89	0.91
1:E:369:THR:OG1	2:E:444:HOH:O	1.87	0.88

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	335/336 (100%)	320 (96%)	13 (4%)	2 (1%)	21 30
1	B	335/336 (100%)	320 (96%)	14 (4%)	1 (0%)	36 49
1	C	337/336 (100%)	322 (96%)	14 (4%)	1 (0%)	36 49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	334/336 (99%)	319 (96%)	14 (4%)	1 (0%)	36	49
1	E	334/336 (99%)	320 (96%)	13 (4%)	1 (0%)	36	49
1	F	335/336 (100%)	320 (96%)	13 (4%)	2 (1%)	21	30
All	All	2010/2016 (100%)	1921 (96%)	81 (4%)	8 (0%)	30	42

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	110	ASP
1	B	110	ASP
1	C	110	ASP
1	D	110	ASP
1	E	110	ASP

### 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	285/284 (100%)	270 (95%)	15 (5%)	20	34
1	B	285/284 (100%)	276 (97%)	9 (3%)	34	54
1	C	287/284 (101%)	274 (96%)	13 (4%)	24	40
1	D	284/284 (100%)	272 (96%)	12 (4%)	26	43
1	E	284/284 (100%)	271 (95%)	13 (5%)	24	39
1	F	285/284 (100%)	274 (96%)	11 (4%)	28	46
All	All	1710/1704 (100%)	1637 (96%)	73 (4%)	27	42

5 of 73 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	267	ILE
1	F	325	LEU
1	E	296	SER
1	F	123	GLU

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Mol	Chain	Res	Type
1	C	66	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	323	ASN
1	F	151	ASN
1	C	334	HIS
1	F	242	ASN
1	E	151	ASN

### 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	336/336 (100%)	-0.08	2 (0%) 85   84	6, 12, 22, 40	1 (0%)
1	B	336/336 (100%)	-0.17	0 100   100	6, 13, 25, 34	1 (0%)
1	C	336/336 (100%)	0.06	3 (0%) 81   79	5, 14, 24, 40	2 (0%)
1	D	336/336 (100%)	-0.08	0 100   100	7, 14, 28, 39	0
1	E	336/336 (100%)	-0.05	0 100   100	6, 12, 22, 35	0
1	F	336/336 (100%)	0.05	1 (0%) 90   88	8, 14, 26, 34	1 (0%)
All	All	2016/2016 (100%)	-0.04	6 (0%) 90   88	5, 13, 25, 40	5 (0%)

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	284[A]	TYR	6.5
1	C	162	GLN	2.7
1	A	147	LEU	2.4
1	A	386	GLY	2.2
1	C	386	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 oligosaccharides in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers

There are no such residues in this entry.