

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

May 28, 2020 – 07:46 pm BST

PDB ID : 1J83

Title : STRUCTURE OF FAM17 CARBOHYDRATE BINDING MODULE FROM

CLOSTRIDIUM CELLULOVORANS

Authors: Notenboom, V.; Boraston, A.B.; Chiu, P.; Freelove, A.C.J.; Kilburn, D.G.;

Rose, D.R.

Deposited on : 2001-05-20

Resolution : 1.70 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 following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : NOT EXECUTED EDS : NOT EXECUTED

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

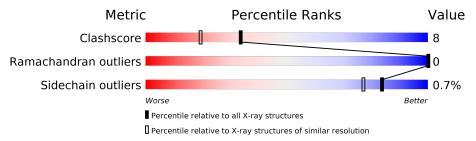
Validation Pipeline (wwPDB-VP) : 2.11

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar  resolution} \\ (\#{\rm Entries,  resolution  range(\AA)}) \end{array}$
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)

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 on 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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain					
1	A	180	87%	13%				
1	В	180	85%	14%	•			



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2995 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 ENDO-1,4-BETA GLUCANASE ENGF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	180	Total 1363	C 850	N 231	O 280	Se 2	0	0	0
1	В	180	Total 1363	C 850		O 280	Se 2	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1112	MSE	MET	MODIFIED RESIDUE	UNP P94622
A	1186	MSE	MET	MODIFIED RESIDUE	UNP P94622
В	2112	MSE	MET	MODIFIED RESIDUE	UNP P94622
В	2186	MSE	MET	MODIFIED RESIDUE	UNP P94622

• Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	В	1	Total Ca 1 1	0	0
2	A	1	Total Ca 1 1	0	0

• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	127	Total O 127 127	0	0
3	В	140	Total O 140 140	0	0

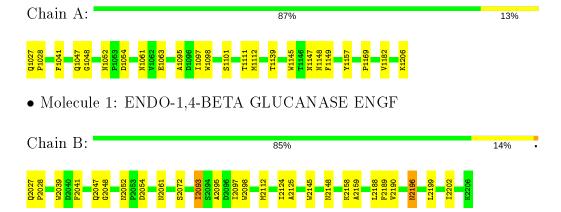


# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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. 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. 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.

Note EDS was not executed.

• Molecule 1: ENDO-1,4-BETA GLUCANASE ENGF





# 4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source	
Space group	C 1 2 1	Depositor	
Cell constants	131.26Å 37.68Å 71.23Å	Depositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 91.93° 90.00°	Depositor	
Resolution (Å)	24.54 - 1.70	Depositor	
% Data completeness	94.3 (24.54-1.70)	Depositor	
(in resolution range)	34.9 (24.04 1.10)	Depositor	
$R_{merge}$	0.05	Depositor	
$R_{sym}$	(Not available)	Depositor	
Refinement program	CNS 1.0	Depositor	
$R, R_{free}$	0.198 , 0.219	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	2995	wwPDB-VP	
Average B, all atoms (Å <sup>2</sup> )	11.0	wwPDB-VP	



# 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: CA

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	0.33	0/1391	0.64	0/1901	
1	В	0.34	0/1391	0.63	0/1901	
All	All	0.34	0/2782	0.64	0/3802	

There are no bond length outliers.

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	1363	0	1298	16	0
1	В	1363	0	1298	29	0
2	A	1	0	0	0	0
2	В	1	0	0	0	0
3	A	127	0	0	0	0
3	В	140	0	0	0	0
All	All	2995	0	2596	45	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 8.

All (45) close contacts within the same asymmetric unit are listed below, sorted by their clash



magnitude.

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${f distance}\;({f \AA})$	$-$ overlap $(\AA)$
1:A:1145:TRP:H	1:A:1148:ASN:HD22	1.15	0.94
1:B:2093:ILE:HD11	1:B:2188:LEU:HB2	1.50	0.92
1:B:2145:TRP:H	1:B:2148:ASN:HD22	1.20	0.85
1:B:2027:GLN:HB2	1:B:2028:PRO:CD	2.09	0.82
1:B:2112:MSE:HE1	1:B:2199:LEU:HD13	1.63	0.81
1:B:2112:MSE:HE3	1:B:2202:ILE:HG12	1.67	0.77
1:A:1145:TRP:H	1:A:1148:ASN:ND2	1.87	0.71
1:B:2093:ILE:CD1	1:B:2188:LEU:HB2	2.21	0.70
1:B:2027:GLN:HB2	1:B:2028:PRO:HD3	1.73	0.69
1:B:2093:ILE:HD13	1:B:2188:LEU:O	1.98	0.64
1:B:2145:TRP:H	1:B:2148:ASN:ND2	1.96	0.62
1:B:2095:ALA:HB1	1:B:2098:TRP:HB2	1.81	0.61
1:B:2093:ILE:HD13	1:B:2093:ILE:H	1.66	0.60
1:B:2145:TRP:N	1:B:2148:ASN:HD22	1.97	0.60
1:A:1139:THR:HG23	1:A:1169:PRO:HD3	1.85	0.59
1:A:1095:ALA:HB1	1:A:1098:TRP:HB2	1.85	0.58
1:A:1041:PHE:H	1:A:1047:GLN:NE2	2.03	0.57
1:B:2112:MSE:HE2	1:B:2199:LEU:HD22	1.87	0.56
1:A:1145:TRP:N	1:A:1148:ASN:HD22	1.96	0.55
1:A:1052:ASN:ND2	1:A:1054:ASP:H	2.04	0.55
1:B:2027:GLN:CB	1:B:2028:PRO:CD	2.85	0.55
1:B:2052:ASN:ND2	1:B:2054:ASP:H	2.04	0.54
1:A:1027:GLN:N	1:A:1028:PRO:CD	2.73	0.52
1:B:2112:MSE:CE	1:B:2199:LEU:HD13	2.39	0.51
1:B:2048:GLY:HA2	1:B:2097:ILE:HG13	1.93	0.51
1:B:2041:PHE:H	1:B:2047:GLN:NE2	2.10	0.49
1:B:2061:ASN:HB2	1:B:2072:SER:HB2	1.94	0.49
1:A:1048:GLY:HA2	1:A:1097:ILE:HG13	1.95	0.48
1:B:2112:MSE:HE2	1:B:2199:LEU:HB3	1.94	0.48
1:B:2196:ASN:HD22	1:B:2196:ASN:C	2.17	0.48
1:B:2124:ILE:HD11	1:B:2190:VAL:HG13	1.96	0.48
1:B:2125:ALA:HB3	1:B:2189:PHE:HB2	1.96	0.48
1:A:1061:ASN:ND2	1:A:1063:GLU:OE1	2.48	0.47
1:A:1101:SER:HB2	1:A:1182:VAL:CG1	2.45	0.45
1:B:2196:ASN:ND2	1:B:2196:ASN:C	2.72	0.43
1:B:2124:ILE:CD1	1:B:2190:VAL:HG13	2.47	0.43
1:A:1147:ASN:HD22	1:A:1147:ASN:H	1.68	0.42
1:B:2093:ILE:N	1:B:2093:ILE:HD13	2.33	0.42
1:B:2112:MSE:CE	1:B:2199:LEU:HB3	2.50	0.42
1:B:2039:TRP:HB2	1:B:2202:ILE:HB	2.03	0.41
1:B:2158:LYS:HG2	1:B:2159:ALA:N	2.34	0.41

Continued on next page...



Continued from previous page...

Atom-1	Atom-2	$egin{aligned}  ext{Interatomic} \  ext{distance} \ ( ext{Å}) \end{aligned}$	$egin{array}{c} \operatorname{Clash} \ \operatorname{overlap}\ ( ext{Å}) \end{array}$
1:A:1111:THR:HG22	1:A:1112:MSE:N	2.35	0.41
1:A:1149:PHE:HB3	1:A:1157:TYR:HB3	2.02	0.41
1:A:1145:TRP:HB2	1:A:1147:ASN:ND2	2.36	0.41
1:A:1206:LYS:HE2	1:A:1206:LYS:HB3	1.82	0.40

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	Perce	${f ntiles}$
1	A	178/180 (99%)	173 (97%)	5 (3%)	0	100	100
1	В	178/180 (99%)	171 (96%)	7 (4%)	0	100	100
All	All	356/360~(99%)	344 (97%)	12 (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	153/151 (101%)	153 (100%)	0	100 100
1	В	153/151 (101%)	151 (99%)	2 (1%)	69 56
All	All	306/302 (101%)	304 (99%)	2 (1%)	84 77



All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	2093	ILE
1	В	2196	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1047	GLN
1	A	1052	ASN
1	A	1061	ASN
1	A	1075	ASN
1	A	1100	GLN
1	A	1147	ASN
1	A	1148	ASN
1	A	1152	GLN
1	В	2047	GLN
1	В	2052	ASN
1	В	2061	ASN
1	В	2066	ASN
1	В	2075	ASN
1	В	2100	GLN
1	В	2147	ASN
1	В	2148	ASN
1	В	2152	GLN
1	В	2196	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 carbohydrates in this entry.



### 5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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)

EDS was not executed - this section is therefore empty.

#### 6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

### 6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

#### 6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

