

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

Oct 23, 2021 – 12:30 PM EDT

PDB ID : 1EGN

Title: CELLOBIOHYDROLASE CEL7A (E223S, A224H, L225V, T226A, D262G)

MUTANT

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Deposited on : 2000-02-16

Resolution : 1.60 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) : 1.13 EDS : 2.23.2

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

Refmac : 5.8.0158

CCP4 : 7.0.044 (Gargrove)

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

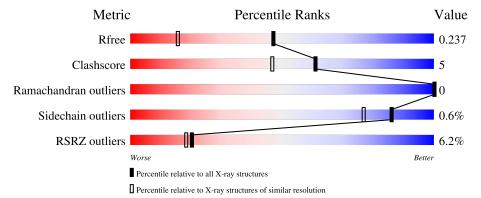
 $\begin{tabular}{lll} Validation Pipeline (wwPDB-VP) & : & 2.23.2 \end{tabular}$ 

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY\ DIFFRACTION$ 

The reported resolution of this entry is 1.60 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{\rm A})}) \end{array}$
$R_{free}$	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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 >=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% 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	
			6%	
1	A	434	90%	10%



## 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3589 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.

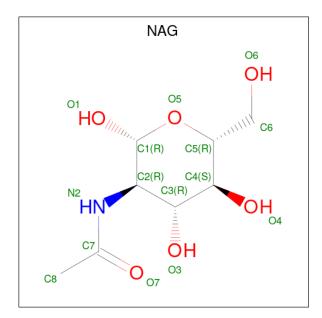
• Molecule 1 is a protein called 1,4-BETA-D-GLUCAN CELLOBIOHYDROLASE CEL7A.

Mol	Chain	Residues		Atoms			ZeroOcc	AltConf	Trace	
1	٨	434	Total	С	N	О	S	0	0	0
1	A	404	3219	1974	535	684	26	0	U	

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	94	ASP	GLY	SEE REMARK 999	UNP P62694
A	223	SER	GLU	engineered mutation	UNP P62694
A	224	HIS	ALA	engineered mutation	UNP P62694
A	225	VAL	LEU	engineered mutation	UNP P62694
A	226	ALA	THR	engineered mutation	UNP P62694
A	262	GLY	ASP	engineered mutation	UNP P62694

• Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	С	N	O	0	0
			14	8	1	$^{\mathrm{G}}$		

 $\bullet$  Molecule 3 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Co 2 2	0	0

• Molecule 4 is water.

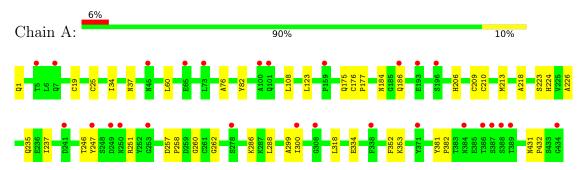
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	354	Total O 354 354	0	0



## 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: 1,4-BETA-D-GLUCAN CELLOBIOHYDROLASE CEL7A





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants	83.11Å 83.34Å 110.61Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	20.00 - 1.60	Depositor
Resolution (A)	23.74 - 1.60	EDS
% Data completeness	100.0 (20.00-1.60)	Depositor
(in resolution range)	99.9 (23.74-1.60)	EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	4.99  (at  1.60Å)	Xtriage
Refinement program	CNS	Depositor
D.D.	0.240 , $0.270$	Depositor
$R, R_{free}$	0.203 , $0.237$	DCC
$R_{free}$ test set	1038 reflections $(2.04\%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	10.2	Xtriage
Anisotropy	0.497	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.49, 60.3	EDS
L-test for twinning <sup>2</sup>	$< L > = 0.50, < L^2> = 0.34$	Xtriage
Estimated twinning fraction	0.009 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3589	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.86% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

## 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: CO, NAG, PCA

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).

Mal	Chain	Bond	lengths	Bond angles		
MIOI	Mol Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.30	0/3288	0.67	0/4482	

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	3219	0	2919	28	0
2	A	14	0	13	0	0
3	A	2	0	0	0	0
4	A	354	0	0	4	0
All	All	3589	0	2932	28	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 5.

All (28) 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	${\rm distance} \ ({\rm \AA})$	overlap (Å)
1:A:299:ALA:C	1:A:300:ILE:HD12	2.13	0.67
1:A:300:ILE:HD12	1:A:300:ILE:N	2.10	0.67
1:A:175:GLN:OE1	1:A:246:THR:HG23	1.98	0.64
1:A:258:PRO:HG3	4:A:535:HOH:O	1.98	0.61
1:A:218:ALA:HB2	1:A:223:SER:HA	1.86	0.58
1:A:246:THR:HG22	1:A:251:ARG:HH12	1.70	0.56
1:A:226:ALA:HB2	1:A:262:GLY:HA2	1.87	0.56
1:A:318:LEU:HD21	1:A:334:GLU:HA	1.88	0.55
1:A:251:ARG:O	1:A:258:PRO:HG2	2.07	0.54
1:A:186:GLN:HG2	4:A:777:HOH:O	2.07	0.54
1:A:213:MET:HB2	1:A:352:PHE:HZ	1.74	0.52
1:A:177:PRO:HA	1:A:247:TYR:CD2	2.47	0.49
1:A:34:ILE:HA	1:A:108:LEU:HD23	1.94	0.49
1:A:381:TYR:HA	1:A:382:PRO:C	2.34	0.48
1:A:431:ASN:HB3	1:A:432:PRO:HD2	1.96	0.47
1:A:257:ASP:OD2	1:A:260:GLY:HA2	2.15	0.47
1:A:209:CYS:O	1:A:210:CYS:HB3	2.15	0.46
1:A:60:LEU:HD22	4:A:783:HOH:O	2.15	0.46
1:A:176:CYS:N	1:A:177:PRO:CD	2.78	0.45
1:A:209:CYS:O	1:A:235:GLN:HA	2.16	0.45
1:A:76:ALA:HB1	1:A:82:TYR:CE2	2.51	0.45
1:A:300:ILE:N	1:A:300:ILE:CD1	2.77	0.43
1:A:184:ASN:HD21	1:A:235:GLN:HE22	1.66	0.43
1:A:123:LEU:HD21	1:A:353:LYS:HE3	2.01	0.43
1:A:286:LYS:HD3	4:A:817:HOH:O	2.19	0.42
1:A:206:HIS:CG	1:A:237:ILE:HD11	2.56	0.40
1:A:19:CYS:HA	1:A:25:CYS:HA	2.03	0.40
1:A:288:LEU:HD23	1:A:288:LEU:N	2.37	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	entiles
1	A	432/434 (100%)	423 (98%)	9 (2%)	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	Analysed Rotameric		Percentiles		
1	A	355/355 (100%)	353 (99%)	2 (1%)	86 77		

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

Mol	Chain	Res	Type
1	A	37	ASN
1	A	224	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	GLN
1	A	98	GLN
1	A	184	ASN
1	A	186	GLN
1	A	224	HIS
1	A	250	ASN
1	A	307	ASN
1	A	373	ASN
1	A	413	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)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Pos	Link	Bond lengths			Bond angles		
MIOI	туре	Chain	nes	Link	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	PCA	A	1	1	7,8,9	2.21	1 (14%)	9,10,12	1.32	2 (22%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PCA	A	1	1	-	0/0/11/13	0/1/1/1

#### All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$Ideal(\AA)$
1	A	1	PCA	CD-N	5.34	1.48	1.34

#### All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}(^{o})$
1	A	1	PCA	CB-CA-C	-2.32	109.51	112.70
1	A	1	PCA	CA-N-CD	-2.26	105.84	113.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.



### 5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type Chain Res Lini		Link	Bond lengths			Bond angles			
MIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAG	A	435	1	14,14,15	0.54	0	17,19,21	0.73	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	435	1	-	0/6/23/26	0/1/1/1

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)

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,  $95^{th}$  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>	# RSRZ > 2	$OWAB(A^2)$	Q<0.9
1	A	433/434 (99%)	0.42	27 (6%) 20 18	6, 10, 19, 30	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	249	ASP	5.7
1	A	101	GLN	4.6
1	A	253	GLY	4.3
1	A	45	ASN	4.2
1	A	247	TYR	4.1
1	A	389	THR	3.8
1	A	241	ASP	3.7
1	A	7	GLN	3.7
1	A	384	ASN	3.6
1	A	434	GLY	3.4
1	A	371	TYR	3.1
1	A	5	THR	3.1
1	A	388	SER	3.1
1	A	278	SER	3.1
1	A	159	PRO	3.0
1	A	100	ALA	2.9
1	A	386	THR	2.6
1	A	250	ASN	2.3
1	A	193	GLU	2.3
1	A	73	LEU	2.2
1	A	387	SER	2.2
1	A	196	SER	2.2
1	A	300	ILE	2.2
1	A	338	PHE	2.1
1	A	186	GLN	2.1
1	A	65	GLU	2.1
1	A	308	GLY	2.1



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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median,  $95^{th}$  percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
1	PCA	A	1	8/9	0.92	0.11	11,11,12,12	0

### 6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

### 6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median,  $95^{th}$  percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	NAG	A	435	14/15	0.82	0.16	14,15,19,19	0
3	CO	A	471	1/1	0.92	0.08	28,28,28,28	0
3	CO	A	470	1/1	0.99	0.05	7,7,7,7	1

### 6.5 Other polymers (i)

There are no such residues in this entry.

