

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

#### Oct 31, 2023 – 02:27 PM EDT

PDB ID : 3N18

Title : Crystal stricture of E145G/Y227F chitinase in complex with NAG from Bacil-

lus cereus NCTU2

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Deposited on : 2010-05-15

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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

 $Mol Probity \quad : \quad 4.02b\text{--}467$ 

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

Xtriage (Phenix) : 1.13

EDS : 2.36

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

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

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

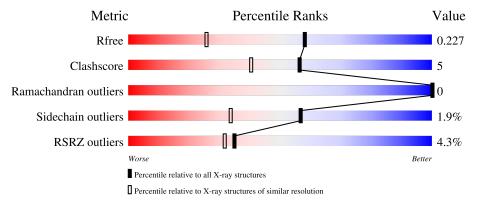
Validation Pipeline (wwPDB-VP) : 2.36

## 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 1.60 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	Whole archive	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	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	
1	A	333	4%	89%	8% ••
2	В	4	25%	50%	25%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:



Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	В	1	-	-	-	X
2	NAG	В	2	-	-	-	X



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2889 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.

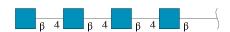
• Molecule 1 is a protein called Chitinase A.

$\mathbf{Mol}$	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	327	Total 2511	C 1612	N 414	O 478	S 7	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	145	GLY	GLU	engineered mutation	UNP D0VV09
A	227	PHE	TYR	engineered mutation	UNP D0VV09
A	277	VAL	ALA	SEE REMARK 999	UNP D0VV09

• Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a cetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
2	В	4	Total 57	C 32	N 4	O 21	0	0	0

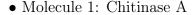
• Molecule 3 is water.

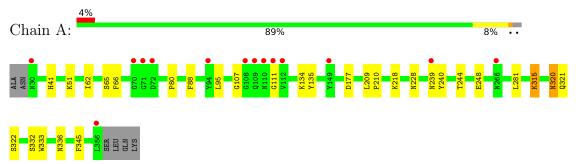
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	321	Total O 321 321	0	0



## 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.





 $\bullet \ \, \text{Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2$ 

Chain B: 25% 50% 25%





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	48.68Å 75.07Å 79.41Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 - 1.60	Depositor
Resolution (A)	28.47 - 1.60	EDS
% Data completeness	98.2 (20.00-1.60)	Depositor
(in resolution range)	98.2 (28.47-1.60)	EDS
$R_{merge}$	0.03	Depositor
$R_{sym}$	0.04	Depositor
$< I/\sigma(I) > 1$	5.51 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.4.0067	Depositor
P. P.	0.197 , 0.227	Depositor
$R, R_{free}$	0.197 , $0.227$	DCC
$R_{free}$ test set	1927 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.6	Xtriage
Anisotropy	0.378	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.36, 43.0	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	2889	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.19% 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: NAG

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	Iol Chain Bond lengths		lengths	Bond angles	
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	A	0.23	0/2577	0.41	0/3498

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	2511	0	2432	23	0
2	В	57	0	51	4	0
3	A	321	0	0	0	0
All	All	2889	0	2483	25	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 (25) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{aligned} \operatorname{Clash} \ \operatorname{overlap}\ (\begin{subarray}{c} \begin{subarray}{c} \begi$
1:A:177:ASP:OD1	1:A:218:LYS:NZ	2.03	0.91

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A 4 1	A 4 0	Interatomic	Clash
Atom-1	Atom-2	${\rm distance}(\mathring{\rm A})$	overlap (Å)
1:A:228:ASN:HD22	2:B:2:NAG:H61	1.52	0.71
1:A:62:ILE:HD12	1:A:95:LEU:HD13	1.79	0.64
1:A:134:LYS:HE2	1:A:135:TYR:CZ	2.35	0.61
2:B:2:NAG:H62	2:B:3:NAG:C1	2.31	0.60
1:A:240:TYR:CE2	1:A:315:LYS:HD2	2.37	0.58
1:A:134:LYS:HE2	1:A:135:TYR:CE2	2.38	0.58
1:A:240:TYR:OH	1:A:315:LYS:CD	2.53	0.57
1:A:320:ASN:C	1:A:320:ASN:HD22	2.12	0.52
1:A:240:TYR:HE2	1:A:315:LYS:HD2	1.76	0.51
1:A:240:TYR:OH	1:A:315:LYS:HD3	2.11	0.49
1:A:41:HIS:H	1:A:336:ASN:ND2	2.13	0.47
1:A:320:ASN:HD22	1:A:322:SER:H	1.62	0.47
1:A:336:ASN:H	1:A:336:ASN:HD22	1.61	0.47
1:A:244:THR:O	1:A:248:GLU:HG2	2.17	0.45
1:A:333:TRP:HB2	2:B:3:NAG:H83	1.99	0.44
1:A:332:SER:HB2	1:A:345:PHE:CZ	2.54	0.43
1:A:65:SER:HA	1:A:66:PHE:HA	1.72	0.43
1:A:80:PRO:HB3	1:A:88:PHE:CG	2.54	0.42
1:A:41:HIS:H	1:A:336:ASN:HD21	1.68	0.42
1:A:62:ILE:CD1	1:A:95:LEU:HD13	2.48	0.42
1:A:107:GLY:O	1:A:111:GLY:HA3	2.21	0.41
2:B:2:NAG:C6	2:B:3:NAG:C1	2.97	0.41
1:A:209:LEU:N	1:A:210:PRO:HD2	2.36	0.41
1:A:281:LEU:O	1:A:332:SER:HA	2.21	0.41

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 Allowe		Outliers	Percentiles	
1	A	325/333~(98%)	313 (96%)	12 (4%)	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	265/270 (98%)	260 (98%)	5 (2%)	57 34	

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	LYS
1	A	239	ASN
1	A	315	LYS
1	A	320	ASN
1	A	321	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	ASN
1	A	118	ASN
1	A	126	ASN
1	A	159	ASN
1	A	238	ASN
1	A	239	ASN
1	A	257	HIS
1	A	266	ASN
1	A	304	ASN
1	A	320	ASN
1	A	321	GLN
1	A	336	ASN
1	A	342	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)

4 monosaccharides are 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	Tuno	Chain	Res	es Link	Bond lengths			Bond angles		
Mol   Type	Type				Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAG	В	1	2	15,15,15	0.56	0	21,21,21	1.11	2 (9%)
2	NAG	В	2	2	14,14,15	0.54	0	17,19,21	0.86	0
2	NAG	В	3	2	14,14,15	0.56	0	17,19,21	1.97	3 (17%)
2	NAG	В	4	2	14,14,15	0.51	0	17,19,21	0.83	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	$\mathbf{Type}$	Chain	$\operatorname{Res}$	Link	Chirals	Torsions	Rings
2	NAG	В	1	2	-	4/6/26/26	0/1/1/1
2	NAG	В	2	2	-	2/6/23/26	0/1/1/1
2	NAG	В	3	2	-	0/6/23/26	0/1/1/1
2	NAG	В	4	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$Ideal(^{o})$
2	В	3	NAG	C2-N2-C7	-6.36	113.85	122.90
2	В	1	NAG	O5-C1-C2	3.05	112.58	109.52
2	В	3	NAG	C1-O5-C5	2.60	115.72	112.19
2	В	3	NAG	O7-C7-N2	-2.20	117.92	121.95
2	В	1	NAG	C1-C2-N2	-2.04	108.36	110.73



There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	1	NAG	C1-C2-N2-C7
2	В	1	NAG	C8-C7-N2-C2
2	В	1	NAG	O7-C7-N2-C2
2	В	2	NAG	C8-C7-N2-C2
2	В	2	NAG	O7-C7-N2-C2
2	В	1	NAG	C3-C2-N2-C7

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	2	NAG	3	0
2	В	3	NAG	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



## 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,  $95^{th}$  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		$OWAB(Å^2)$	Q<0.9	
1	A	327/333 (98%)	0.30	14 (4%)	35	32	10, 15, 24, 26	1 (0%)

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	30	ASN	7.4
1	A	111	GLY	6.8
1	A	109	GLN	6.5
1	A	108	GLY	4.8
1	A	70	GLY	4.7
1	A	266	ASN	3.6
1	A	110	ASN	3.5
1	A	356	LEU	3.1
1	A	94	TYR	3.0
1	A	239	ASN	2.6
1	A	71	GLY	2.3
1	A	112	VAL	2.1
1	A	149	TYR	2.1
1	A	72	ASP	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.

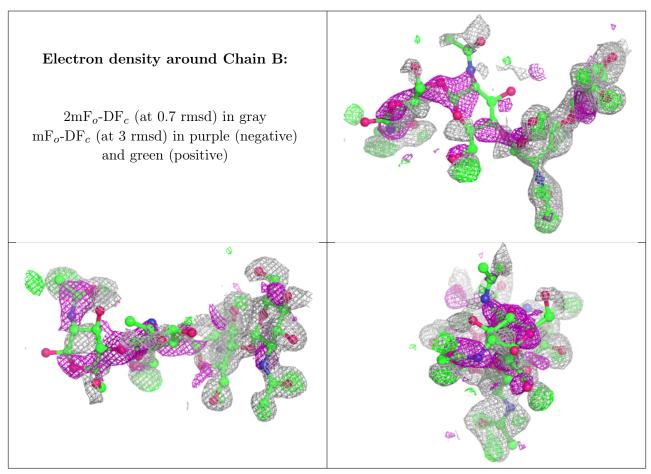
### 6.3 Carbohydrates (i)

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	В	1	15/15	-0.13	0.71	51,52,52,52	0
2	NAG	В	2	14/15	0.18	0.61	49,51,51,51	0
2	NAG	В	4	14/15	0.28	0.33	45,46,46,46	0
2	NAG	В	3	14/15	0.52	0.29	47,47,48,48	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



## 6.4 Ligands (i)

There are no ligands in this entry.

### 6.5 Other polymers (i)

There are no such residues in this entry.

