



## Full wwPDB X-ray Structure Validation Report ⓘ

Jan 4, 2021 – 04:05 pm GMT

PDB ID : 6ZB8  
Title : Exo-beta-1,3-glucanase from moose rumen microbiome, active site mutant E167Q/E295Q  
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Deposited on : 2020-06-08  
Resolution : 1.35 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](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.

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The following versions of software and data (see [references ⓘ](#)) 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 : 2.16  
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)  
Validation Pipeline (wwPDB-VP) : 2.16

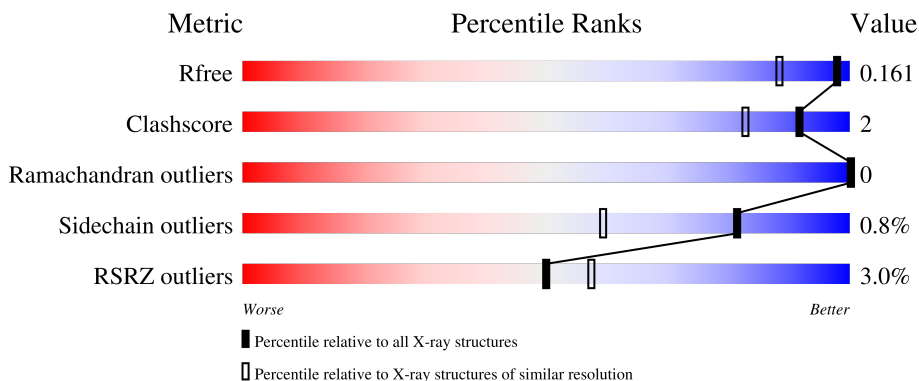
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.35 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))
$R_{free}$	130704	1509 (1.38-1.34)
Clashscore	141614	1551 (1.38-1.34)
Ramachandran outliers	138981	1530 (1.38-1.34)
Sidechain outliers	138945	1530 (1.38-1.34)
RSRZ outliers	127900	1487 (1.38-1.34)

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	391	 2% 91% 6%
1	B	391	 4% 91% 5%

## 2 Entry composition [i](#)

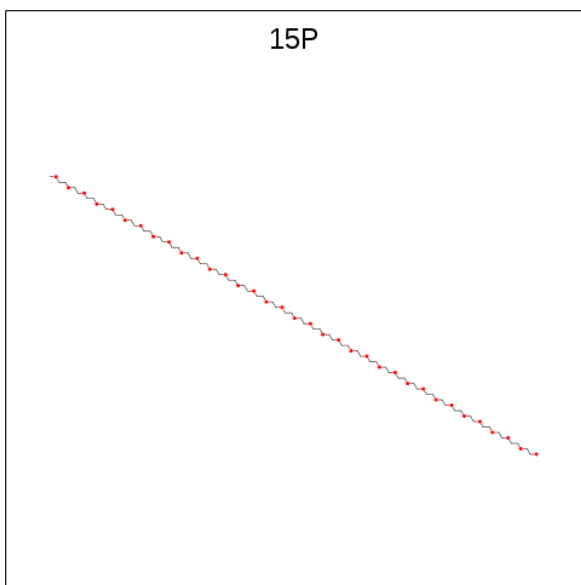
There are 3 unique types of molecules in this entry. The entry contains 12830 atoms, of which 6039 are hydrogens and 0 are deuteriums.

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 Exo-beta-1,3-glucanase variant E167Q/E295Q.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	367	6032	1980	2982	496	554	20	0	4	0
1	B	370	6079	1994	3003	501	562	19	0	4	0

- Molecule 2 is POLYETHYLENE GLYCOL (N=34) (three-letter code: 15P) (formula: C<sub>69</sub>H<sub>140</sub>O<sub>35</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
2	A	1	56	16	32	8	0	0
2	B	1	39	11	22	6	0	0

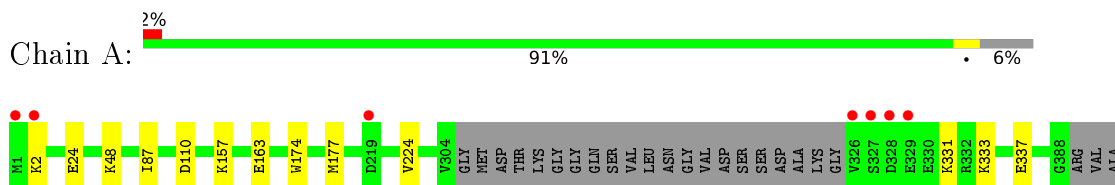
- Molecule 3 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
3	A	303	Total 303	O 303	0	0
3	B	321	Total 321	O 321	0	0

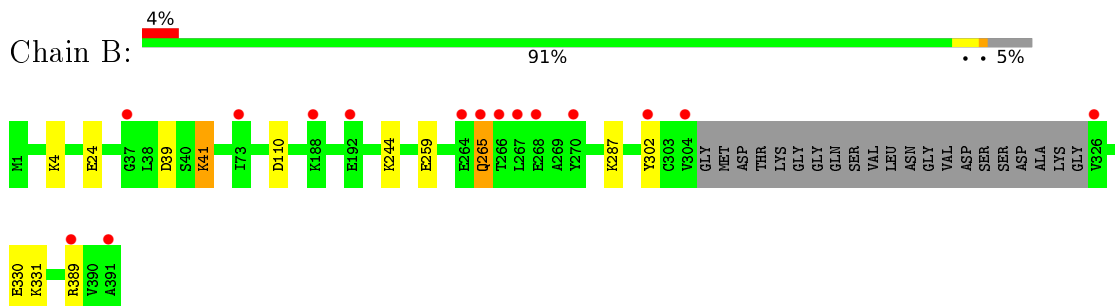
### 3 Residue-property plots [i](#)

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.

- Molecule 1: Exo-beta-1,3-glucanase variant E167Q/E295Q



- Molecule 1: Exo-beta-1,3-glucanase variant E167Q/E295Q



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.63Å 87.79Å 70.86Å 90.00° 100.96° 90.00°	Depositor
Resolution (Å)	29.35 – 1.35 29.35 – 1.35	Depositor EDS
% Data completeness (in resolution range)	95.2 (29.35-1.35) 95.2 (29.35-1.35)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.41 (at 1.35Å)	Xtrriage
Refinement program	PHENIX (1.15.2_3472: ???)	Depositor
R, $R_{free}$	0.153 , 0.163 0.153 , 0.161	Depositor DCC
$R_{free}$ test set	2000 reflections (1.44%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.6	Xtrriage
Anisotropy	0.273	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.46 , 46.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	12830	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.29% of the height of the origin peak. No significant pseudotranslation is detected.*

<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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 15P

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	0.44	0/3152	0.65	0/4260
1	B	0.45	0/3173	0.64	0/4290
All	All	0.45	0/6325	0.65	0/8550

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

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	3050	2982	2969	11	0
1	B	3076	3003	3003	8	0
2	A	24	32	30	2	0
2	B	17	22	20	0	0
3	A	303	0	0	6	1
3	B	321	0	0	4	0
All	All	6791	6039	6022	19	1

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 2.

All (19) 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:B:24:GLU:HA	1:B:24:GLU:OE1	1.99	0.61
1:B:4:LYS:NZ	3:B:505:HOH:O	2.34	0.61
1:B:287:LYS:NZ	3:B:506:HOH:O	2.34	0.60
1:B:244:LYS:HD2	3:B:504:HOH:O	2.06	0.55
1:A:177:MET:CE	2:A:401:15P:H132	2.41	0.50
1:B:39[B]:ASP:OD1	1:B:41:LYS:NZ	2.44	0.47
1:B:259:GLU:HG2	1:B:265:GLN:OE1	2.15	0.46
1:B:331[B]:LYS:NZ	3:B:514:HOH:O	2.49	0.45
1:A:157:LYS:HE2	3:A:532:HOH:O	2.15	0.45
1:A:24:GLU:OE1	3:A:501:HOH:O	2.21	0.45
1:B:302:TYR:OH	1:B:330:GLU:OE2	2.28	0.45
1:A:157:LYS:HE3	3:A:572:HOH:O	2.17	0.45
1:A:2:LYS:HG3	3:A:516:HOH:O	2.17	0.45
1:A:331:LYS:HD3	3:A:662:HOH:O	2.18	0.44
1:A:333[B]:LYS:HZ2	1:A:337:GLU:HG3	1.82	0.43
1:A:48:LYS:HE3	1:A:87:ILE:HG21	2.00	0.42
1:A:174:TRP:NE1	3:A:504:HOH:O	2.36	0.42
1:A:177:MET:HE1	2:A:401:15P:H132	2.01	0.42
1:A:163:GLU:HA	1:A:224:VAL:O	2.20	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:525:HOH:O	3:A:786:HOH:O[2_555]	2.10	0.10

## 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	367/391 (94%)	355 (97%)	12 (3%)	0	<b>100</b> <b>100</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	370/391 (95%)	357 (96%)	13 (4%)	0	100	100
All	All	737/782 (94%)	712 (97%)	25 (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	324/337 (96%)	323 (100%)	1 (0%)	92	83
1	B	326/337 (97%)	322 (99%)	4 (1%)	71	42
All	All	650/674 (96%)	645 (99%)	5 (1%)	81	59

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

Mol	Chain	Res	Type
1	A	110	ASP
1	B	41	LYS
1	B	110	ASP
1	B	265	GLN
1	B	389	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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

### 6.1 Protein, DNA and RNA chains

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	367/391 (93%)	0.01	7 (1%) 66 71	12, 16, 32, 47	0
1	B	370/391 (94%)	0.09	15 (4%) 37 43	11, 17, 31, 45	0
All	All	737/782 (94%)	0.05	22 (2%) 50 57	11, 16, 32, 47	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	326	VAL	8.3
1	B	391	ALA	6.9
1	B	326	VAL	5.4
1	B	265	GLN	3.8
1	A	327	SER	3.2
1	B	302	TYR	2.8
1	A	2	LYS	2.7
1	A	219	ASP	2.7
1	B	267	LEU	2.6
1	B	304	VAL	2.6
1	A	328	ASP	2.5
1	B	270	TYR	2.4
1	B	389	ARG	2.3
1	B	188	LYS	2.2
1	A	329	GLU	2.1
1	B	268	GLU	2.1
1	B	266	THR	2.1
1	B	192	GLU	2.1
1	A	1	MET	2.1
1	B	264	GLU	2.1
1	B	73	ILE	2.1
1	B	37	GLY	2.0

## 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 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<sup>th</sup> 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	B-factors( $\text{\AA}^2$ )	Q<0.9
2	15P	B	401	17/104	0.82	0.14	34,51,61,61	0
2	15P	A	401	24/104	0.85	0.15	29,51,66,67	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.