



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2018 – 02:25 pm GMT

PDB ID : 1C93  
Title : Endo-Beta-N-Acetylglucosaminidase H, D130N/E132Q Double Mutant  
Authors : Rao, V.; Cui, T.; Guan, C.; Van Roey, P.  
Deposited on : 1999-07-30  
Resolution : 2.10 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  
Xtriage (Phenix) : 1.13  
EDS : trunk30967  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30967

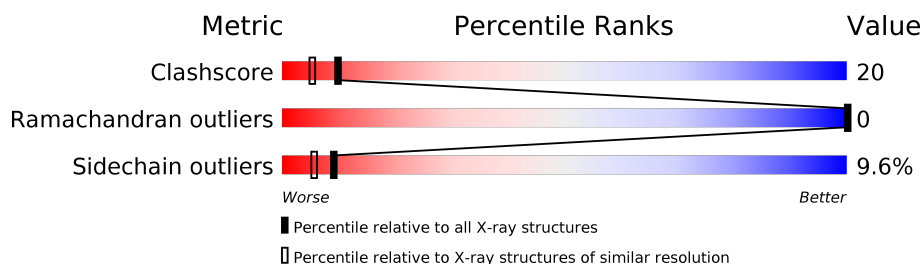
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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))
Clashscore	122126	5109 (2.10-2.10)
Ramachandran outliers	120053	5059 (2.10-2.10)
Sidechain outliers	120020	5060 (2.10-2.10)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	265	 70% 26% .

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2140 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-BETA-N-ACETYLGLUCOSAMINIDASE H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	265	Total	C	N	O	S	0	0	0
			2016	1266	349	399	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	132	GLN	GLU	ENGINEERED	UNP P04067
A	130	ASN	ASP	ENGINEERED	UNP P04067

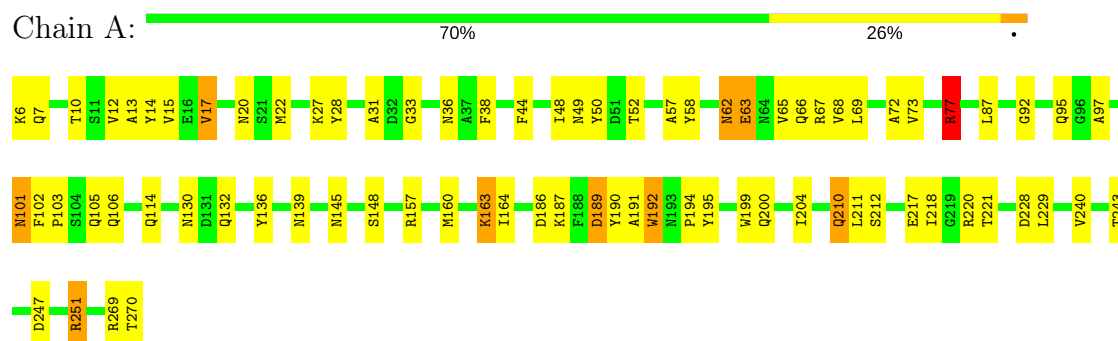
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	124	Total	O	0	0
			124	124		

### 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.

• Molecule 1: ENDO-BETA-N-ACETYLGLUCOSAMINIDASE H



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	44.30Å 55.50Å 46.70Å 90.00° 104.50° 90.00°	Depositor
Resolution (Å)	10.00 – 2.10 45.21 – 2.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-2.10) 95.6 (45.21-2.10)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.05 (at 2.10Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, $R_{free}$	0.200 , (Not available) 0.368 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	10.5	Xtriage
Anisotropy	0.242	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 67.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.68	EDS
Total number of atoms	2140	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 9.95% 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 [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	0.64	0/2058	0.85	0/2803

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	77	ARG	Sidechain

### 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	2016	0	1935	81	1
2	A	124	0	0	4	2
All	All	2140	0	1935	81	2

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 20.

All (81) 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:A:72:ALA:HB1	1:A:77:ARG:CZ	1.90	1.01
1:A:17:VAL:HG21	1:A:65:VAL:HG22	1.47	0.97
1:A:72:ALA:HB1	1:A:77:ARG:NH2	1.83	0.93
1:A:73:VAL:HA	1:A:77:ARG:HD3	1.49	0.93
1:A:62:ASN:HD22	1:A:65:VAL:HG23	1.35	0.89
1:A:62:ASN:ND2	1:A:65:VAL:HG23	1.96	0.80
1:A:72:ALA:CB	1:A:77:ARG:NH1	2.49	0.76
1:A:17:VAL:HG13	1:A:22:MET:HE3	1.72	0.71
1:A:17:VAL:HG12	1:A:68:VAL:HG21	1.71	0.71
1:A:72:ALA:HB1	1:A:77:ARG:NH1	2.05	0.71
1:A:73:VAL:CA	1:A:77:ARG:HD3	2.21	0.70
1:A:72:ALA:CB	1:A:77:ARG:CZ	2.69	0.70
1:A:17:VAL:HG22	1:A:44:PHE:O	1.92	0.70
1:A:101:ASN:ND2	1:A:136:TYR:HD2	1.91	0.69
1:A:77:ARG:N	1:A:77:ARG:HD2	2.09	0.67
1:A:221:THR:HG22	2:A:388:HOH:O	1.94	0.66
1:A:77:ARG:H	1:A:77:ARG:HD2	1.61	0.65
1:A:72:ALA:O	1:A:77:ARG:HD2	1.97	0.64
1:A:101:ASN:ND2	1:A:136:TYR:CD2	2.67	0.62
1:A:12:VAL:O	1:A:243:THR:HB	2.01	0.61
1:A:52:THR:HG22	1:A:139:ASN:HB3	1.82	0.60
1:A:212:SER:HB2	1:A:240:VAL:HB	1.84	0.60
1:A:72:ALA:HB3	1:A:77:ARG:NH1	2.16	0.59
1:A:72:ALA:O	1:A:77:ARG:CD	2.52	0.58
1:A:58:TYR:HA	1:A:114:GLN:HE22	1.68	0.58
1:A:62:ASN:ND2	1:A:65:VAL:H	2.02	0.57
1:A:17:VAL:CG1	1:A:22:MET:HE3	2.34	0.57
1:A:191:ALA:HB3	1:A:211:LEU:CD2	2.35	0.57
1:A:15:VAL:HB	1:A:22:MET:SD	2.45	0.56
1:A:66:GLN:HG3	1:A:67:ARG:HH11	1.71	0.55
1:A:73:VAL:HA	1:A:77:ARG:CD	2.32	0.55
1:A:101:ASN:CG	1:A:136:TYR:HD2	2.10	0.55
1:A:145:ASN:OD1	1:A:148:SER:HB2	2.06	0.54
1:A:17:VAL:HG13	1:A:22:MET:CE	2.36	0.54
1:A:72:ALA:C	1:A:77:ARG:HD3	2.29	0.53
1:A:218:ILE:CG2	1:A:251:ARG:HG2	2.39	0.52
1:A:218:ILE:HG12	1:A:243:THR:HG23	1.91	0.52
1:A:73:VAL:O	1:A:77:ARG:HB2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:ASP:O	1:A:210:GLN:HB2	2.09	0.51
1:A:28:TYR:CE2	1:A:269:ARG:HB2	2.45	0.51
1:A:217:GLU:H	1:A:221:THR:CG2	2.24	0.51
1:A:194:PRO:HG2	1:A:195:TYR:CE1	2.46	0.50
1:A:50:TYR:H	1:A:95:GLN:NE2	2.09	0.50
1:A:87:LEU:HD21	1:A:164:ILE:CG2	2.41	0.50
1:A:48:ILE:O	1:A:48:ILE:HG23	2.11	0.50
1:A:157:ARG:NH1	1:A:163:LYS:O	2.39	0.49
1:A:63:GLU:O	1:A:67:ARG:HG2	2.13	0.48
1:A:190:TYR:HA	1:A:210:GLN:O	2.14	0.48
1:A:12:VAL:HG21	1:A:192:TRP:CZ3	2.49	0.48
1:A:73:VAL:HG23	2:A:293:HOH:O	2.13	0.48
1:A:73:VAL:N	1:A:77:ARG:HD3	2.27	0.48
1:A:17:VAL:CG2	1:A:65:VAL:HG22	2.34	0.48
1:A:48:ILE:HG22	1:A:92:GLY:HA2	1.96	0.47
1:A:199:TRP:HB2	1:A:229:LEU:CD2	2.45	0.47
1:A:62:ASN:HD22	1:A:65:VAL:CG2	2.19	0.46
1:A:14:TYR:HD1	1:A:44:PHE:HD1	1.63	0.45
1:A:15:VAL:HB	1:A:22:MET:CE	2.47	0.45
1:A:13:ALA:HB2	1:A:38:PHE:CD1	2.53	0.45
1:A:49:ASN:O	1:A:57:ALA:HA	2.17	0.44
1:A:160:MET:HB2	1:A:163:LYS:HB2	2.00	0.44
1:A:31:ALA:C	1:A:33:GLY:H	2.20	0.44
1:A:27:LYS:O	1:A:269:ARG:HA	2.18	0.43
1:A:102:PHE:N	1:A:148:SER:OG	2.51	0.43
1:A:17:VAL:CG1	1:A:68:VAL:HG21	2.43	0.43
1:A:50:TYR:CD1	1:A:97:ALA:HB2	2.54	0.43
1:A:102:PHE:HA	1:A:103:PRO:HD3	1.86	0.43
1:A:157:ARG:NH2	1:A:187:LYS:O	2.48	0.42
1:A:57:ALA:HB2	1:A:97:ALA:HB1	2.01	0.42
1:A:36:ASN:HB3	2:A:275:HOH:O	2.18	0.42
1:A:221:THR:CG2	2:A:388:HOH:O	2.62	0.42
1:A:130:ASN:OD1	1:A:132:GLN:HG3	2.20	0.42
1:A:87:LEU:HD21	1:A:164:ILE:HG22	2.01	0.42
1:A:269:ARG:HG2	1:A:270:THR:N	2.34	0.42
1:A:191:ALA:HB3	1:A:211:LEU:HD23	2.02	0.41
1:A:217:GLU:H	1:A:221:THR:HG23	1.85	0.41
1:A:101:ASN:CG	1:A:136:TYR:CD2	2.91	0.41
1:A:20:ASN:ND2	1:A:247:ASP:CB	2.84	0.41
1:A:87:LEU:HD21	1:A:164:ILE:HG21	2.03	0.41
1:A:218:ILE:CG1	1:A:243:THR:HG23	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:LYS:HA	1:A:163:LYS:HD2	1.87	0.40
1:A:192:TRP:HB3	1:A:212:SER:HB3	2.03	0.40

All (2) 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)
1:A:228:ASP:OD1	2:A:353:HOH:O[2_748]	2.13	0.07
2:A:334:HOH:O	2:A:370:HOH:O[2_858]	2.16	0.04

## 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	263/265 (99%)	251 (95%)	12 (5%)	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	208/208 (100%)	188 (90%)	20 (10%)	9	6

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LYS
1	A	7	GLN
1	A	10	THR
1	A	17	VAL
1	A	62	ASN
1	A	63	GLU
1	A	69	LEU
1	A	77	ARG
1	A	101	ASN
1	A	105	GLN
1	A	106	GLN
1	A	163	LYS
1	A	186	ASP
1	A	189	ASP
1	A	192	TRP
1	A	200	GLN
1	A	204	ILE
1	A	210	GLN
1	A	220	ARG
1	A	251	ARG

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

Mol	Chain	Res	Type
1	A	7	GLN
1	A	20	ASN
1	A	36	ASN
1	A	62	ASN
1	A	82	GLN
1	A	93	ASN
1	A	95	GLN
1	A	101	ASN
1	A	105	GLN
1	A	114	GLN
1	A	139	ASN
1	A	159	ASN
1	A	200	GLN

### 5.3.3 RNA ⓘ

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](#)

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](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.