Full wwPDB X-ray Structure Validation Report (i)

Feb 6, 2024 – 12:52 PM EST

PDB ID	:	2EBN
Title	:	CRYSTAL STRUCTURE OF ENDO-BETA-N-ACETYLGLUCOSAMINIDASE F1, AN ALPHA(SLASH)BETA-BARREL ENZYME ADAPTED FOR A COMPLEX SUBSTRATE
Authors	:	Van Roey, P.
Deposited on	:	1994-08-30
Resolution	:	2.00 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 (i)) were used in the production of this report:

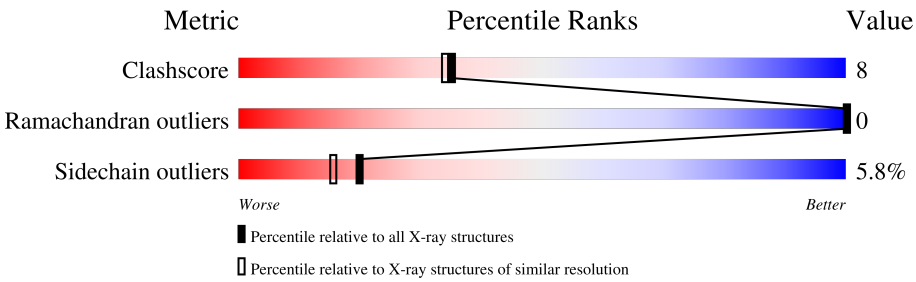
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.00 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	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	289	80% 17% ...

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2457 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 F1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	285	2213	1403	373	430	7	0	0	0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
2	A	1	1	1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	243	243	243	0	0

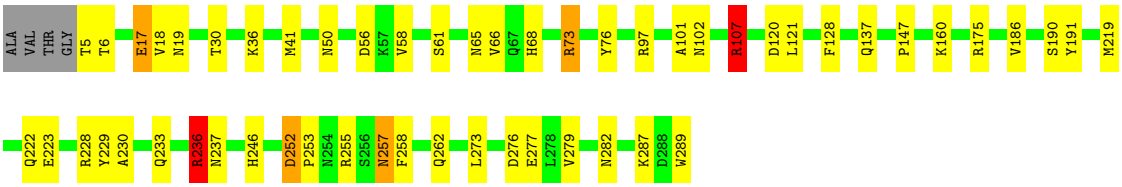
3 Residue-property plots (i)

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. 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-BETA-N-ACETYLGLUCOSAMINIDASE F1

Chain A:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α, β, γ	70.64Å 70.64Å 103.31Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	10.00 – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROFFT, X-PLOR	Depositor
R, R_{free}	0.158 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2457	wwPDB-VP
Average B, all atoms ($Å^2$)	19.0	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: ZN

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	0.95	1/2263 (0.0%)	1.47	20/3076 (0.7%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	17	GLU	CD-OE2	5.18	1.31	1.25

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	107	ARG	NE-CZ-NH1	12.51	126.55	120.30
1	A	175	ARG	NE-CZ-NH2	-12.17	114.22	120.30
1	A	175	ARG	NE-CZ-NH1	9.04	124.82	120.30
1	A	97	ARG	NE-CZ-NH2	-8.12	116.24	120.30
1	A	120	ASP	CB-CG-OD2	-8.11	111.00	118.30
1	A	97	ARG	NE-CZ-NH1	7.45	124.03	120.30
1	A	17	GLU	CG-CD-OE1	6.95	132.20	118.30
1	A	17	GLU	OE1-CD-OE2	-6.55	115.44	123.30
1	A	236	ARG	NE-CZ-NH1	6.50	123.55	120.30
1	A	252	ASP	CB-CG-OD2	6.34	124.00	118.30
1	A	17	GLU	CB-CG-CD	6.05	130.53	114.20
1	A	277	GLU	CG-CD-OE2	6.01	130.32	118.30
1	A	120	ASP	CB-CG-OD1	5.69	123.42	118.30
1	A	236	ARG	NE-CZ-NH2	-5.57	117.51	120.30
1	A	228	ARG	CD-NE-CZ	5.55	131.38	123.60
1	A	128	PHE	CB-CG-CD2	-5.55	116.91	120.80
1	A	277	GLU	OE1-CD-OE2	-5.47	116.73	123.30
1	A	277	GLU	CB-CG-CD	5.35	128.65	114.20
1	A	58	VAL	CB-CA-C	5.11	121.10	111.40
1	A	276	ASP	CB-CG-OD1	5.08	122.87	118.30

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	2213	0	2160	36	0
2	A	1	0	0	0	0
3	A	243	0	0	9	1
All	All	2457	0	2160	36	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 8.

All (36) 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:73:ARG:HG3	1:A:73:ARG:HH11	1.30	0.93
1:A:68:HIS:NE2	3:A:437:HOH:O	2.04	0.91
1:A:252:ASP:H	1:A:262:GLN:HE22	1.23	0.86
1:A:236:ARG:HH11	1:A:236:ARG:HG3	1.43	0.83
1:A:30:THR:HG21	3:A:569:HOH:O	1.80	0.81
1:A:233:GLN:O	1:A:237:ASN:ND2	2.11	0.81
1:A:236:ARG:HH11	1:A:236:ARG:CG	2.05	0.69
1:A:73:ARG:NH1	3:A:336:HOH:O	2.26	0.69
1:A:56:ASP:CG	1:A:107:ARG:HH22	1.97	0.67
1:A:287:LYS:NZ	1:A:289:TRP:O	2.22	0.61
1:A:30:THR:CG2	3:A:569:HOH:O	2.46	0.59
1:A:76:TYR:OH	3:A:437:HOH:O	1.79	0.59
1:A:137:GLN:O	3:A:465:HOH:O	2.17	0.59
1:A:236:ARG:CG	1:A:236:ARG:NH1	2.65	0.58
1:A:73:ARG:HH11	1:A:73:ARG:CG	2.09	0.58
1:A:73:ARG:HG3	1:A:73:ARG:NH1	2.07	0.57
1:A:19:ASN:ND2	1:A:65:ASN:HD22	2.04	0.55
1:A:253:PRO:HA	1:A:258:PHE:CD1	2.42	0.55
1:A:56:ASP:O	1:A:107:ARG:NH2	2.42	0.53
1:A:19:ASN:HD22	1:A:65:ASN:HD22	1.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:LYS:HG2	1:A:191:TYR:HA	1.94	0.50
1:A:50:ASN:HD22	1:A:61:SER:CB	2.26	0.48
1:A:68:HIS:ND1	3:A:333:HOH:O	2.01	0.48
1:A:17:GLU:CD	3:A:510:HOH:O	2.52	0.47
1:A:186:VAL:CG1	1:A:190:SER:HB2	2.44	0.47
1:A:50:ASN:HD22	1:A:61:SER:HB3	1.80	0.47
1:A:222:GLN:HE21	1:A:229:TYR:HA	1.80	0.47
1:A:255:ARG:HD2	1:A:257:ASN:ND2	2.30	0.47
1:A:186:VAL:HG13	1:A:190:SER:HB2	1.97	0.45
1:A:233:GLN:NE2	3:A:418:HOH:O	2.50	0.44
1:A:101:ALA:O	1:A:147:PRO:HA	2.19	0.43
1:A:222:GLN:NE2	1:A:230:ALA:H	2.17	0.42
1:A:18:VAL:HG21	1:A:66:VAL:HG22	2.00	0.42
1:A:56:ASP:OD1	1:A:107:ARG:NH2	2.33	0.41
1:A:255:ARG:HD2	1:A:257:ASN:HD21	1.86	0.41
1:A:219:MET:O	1:A:246:HIS:HD2	2.04	0.40

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:323:HOH:O	3:A:537:HOH:O[5_564]	1.95	0.25

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	283/289 (98%)	273 (96%)	10 (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	240/242 (99%)	226 (94%)	14 (6%)	20 15

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	THR
1	A	6	THR
1	A	36	LYS
1	A	41	MET
1	A	73	ARG
1	A	102	ASN
1	A	107	ARG
1	A	121	LEU
1	A	223	GLU
1	A	236	ARG
1	A	257	ASN
1	A	273	LEU
1	A	279	VAL
1	A	282	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	ASN
1	A	28	ASN
1	A	48	ASN
1	A	50	ASN
1	A	62	ASN
1	A	67	GLN
1	A	81	GLN
1	A	94	ASN
1	A	102	ASN
1	A	137	GLN
1	A	222	GLN

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Mol	Chain	Res	Type
1	A	246	HIS
1	A	257	ASN
1	A	262	GLN
1	A	282	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 1 ligands modelled in this entry, 1 is 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.