



wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 05:53 AM GMT

PDB ID : 3M6D
Title : The crystal structure of the d307a mutant of glycoside Hydrolase (family 31) from ruminococcus obeum atcc 29174
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Deposited on : 2010-03-15
Resolution : 2.90 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

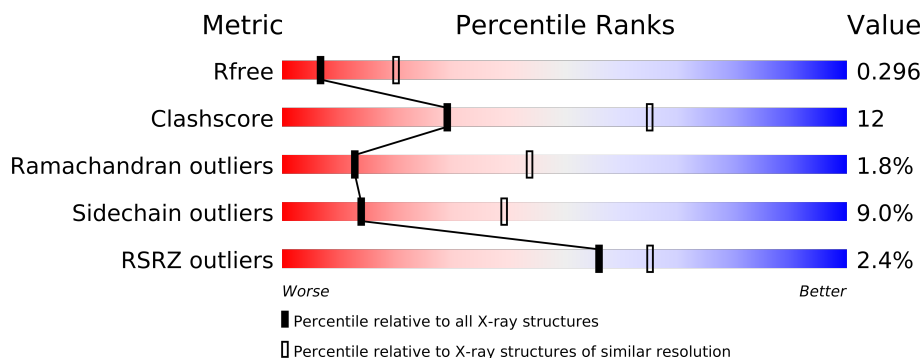
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.90 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}	66092	1053 (2.90-2.90)
Clashscore	79885	1326 (2.90-2.90)
Ramachandran outliers	78287	1290 (2.90-2.90)
Sidechain outliers	78261	1292 (2.90-2.90)
RSRZ outliers	66119	1054 (2.90-2.90)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	666	
1	B	666	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 10735 atoms, of which 0 are hydrogen and 0 are deuterium.

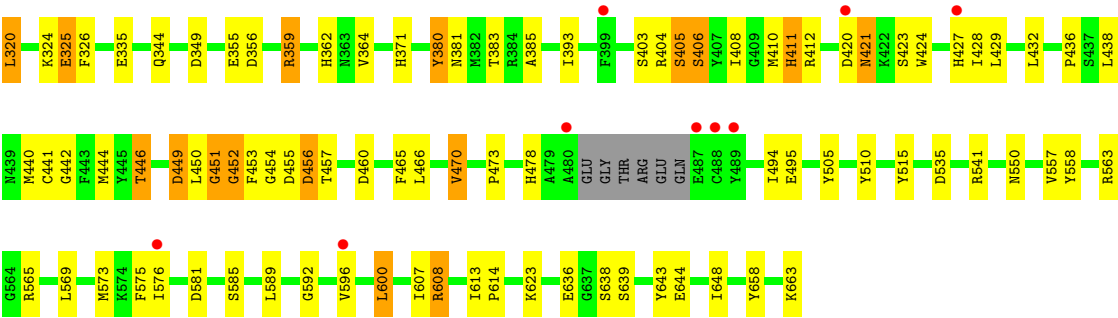
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	655	Total	C	N	O	S	0	0	0
			5357	3442	878	1003	34			
1	B	658	Total	C	N	O	S	0	0	0
			5378	3453	881	1009	35			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	EXPRESSION TAG	UNP A5ZY13
A	-1	ASN	-	EXPRESSION TAG	UNP A5ZY13
A	0	ALA	-	EXPRESSION TAG	UNP A5ZY13
A	307	ALA	ASP	ENGINEERED	UNP A5ZY13
B	-2	SER	-	EXPRESSION TAG	UNP A5ZY13
B	-1	ASN	-	EXPRESSION TAG	UNP A5ZY13
B	0	ALA	-	EXPRESSION TAG	UNP A5ZY13
B	307	ALA	ASP	ENGINEERED	UNP A5ZY13



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	64.86Å 124.03Å 87.83Å 90.00° 108.15° 90.00°	Depositor
Resolution (Å)	49.78 – 2.90 49.78 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.8 (49.78-2.90) 98.8 (49.78-2.90)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.86 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.218 , 0.297 0.219 , 0.296	Depositor DCC
R_{free} test set	1481 reflections (5.37%)	DCC
Wilson B-factor (Å ²)	54.9	Xtriage
Anisotropy	0.488	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.22 , -5.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 29072 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	10735	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.51% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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	0.67	0/5498	0.72	0/7412
1	B	0.66	0/5519	0.73	0/7441
All	All	0.66	0/11017	0.73	0/14853

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5357	0	5136	151	0
1	B	5378	0	5149	114	0
All	All	10735	0	10285	259	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 12.

The worst 5 of 259 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:450:LEU:O	1:B:451:GLY:O	1.64	1.16
1:A:514:GLU:OE2	1:A:517:LYS:HE3	1.59	1.01
1:A:270:VAL:HG12	1:A:271:TRP:H	1.29	0.94

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:429:LEU:HD22	1:B:558:TYR:CE1	2.11	0.86
1:B:230:ARG:HG3	1:B:230:ARG:HH11	1.40	0.85

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	651/666 (98%)	591 (91%)	49 (8%)	11 (2%)	14	45
1	B	654/666 (98%)	588 (90%)	53 (8%)	13 (2%)	11	40
All	All	1305/1332 (98%)	1179 (90%)	102 (8%)	24 (2%)	13	44

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	451	GLY
1	B	453	PHE
1	B	638	SER
1	A	54	GLY
1	A	540	ILE

5.3.2 Protein sidechains ⓘ

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	563/574 (98%)	511 (91%)	52 (9%)	13	38
1	B	565/574 (98%)	515 (91%)	50 (9%)	14	40
All	All	1128/1148 (98%)	1026 (91%)	102 (9%)	14	39

5 of 102 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	602	GLU
1	B	66	CYS
1	B	563	ARG
1	A	609	SER
1	A	655	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	502	ASN
1	B	70	ASN
1	B	371	HIS
1	A	493	ASN
1	B	431	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 95th 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 ²)	Q<0.9
1	A	655/666 (98%)	-0.22	18 (2%)	52	61	42, 54, 69, 104	4 (0%)
1	B	658/666 (98%)	-0.21	13 (1%)	62	71	39, 53, 70, 92	1 (0%)
All	All	1313/1332 (98%)	-0.21	31 (2%)	56	65	39, 54, 69, 104	5 (0%)

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	488	CYS	9.1
1	B	489	TYR	6.5
1	A	629	ASN	4.4
1	A	362	HIS	3.9
1	A	369	ILE	3.7

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.