

Full wwPDB X-ray Structure Validation Report (i)

Oct 11, 2021 – 03:06 PM EDT

PDB ID : 2FY7

Title : Crystal structure of the catalytic domain of the human beta1,4-galactosyltra

nsferase mutant M339H in apo form

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Deposited on : 2006-02-07

Resolution : 1.70 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 following versions of software and data (see references (1)) 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 : 2.23.2

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)

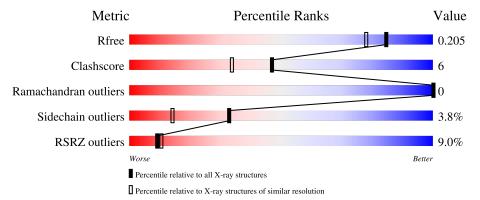
Validation Pipeline (wwPDB-VP) : 2.23.2

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 1.70 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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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	
			8%	
1	A	287	85%	6% • 7%



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2516 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 Beta-1,4-galactosyltransferase 1.

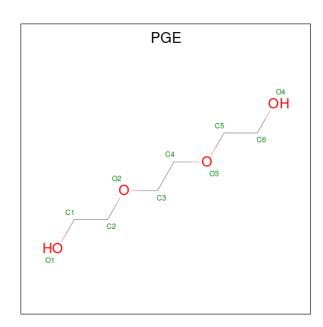
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	268	Total	С	N	О	S	0	0	0
1	A	200	2167	1389	376	391	11	0	U	

There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	112	ALA	-	cloning artifact	UNP P15291
A	113	SER	-	cloning artifact	UNP P15291
A	114	MET	-	cloning artifact	UNP P15291
A	115	THR	-	cloning artifact	UNP P15291
A	116	GLY	-	cloning artifact	UNP P15291
A	117	GLY	_	cloning artifact	UNP P15291
A	118	GLN	-	cloning artifact	UNP P15291
A	119	GLN	-	cloning artifact	UNP P15291
A	120	MET	-	cloning artifact	UNP P15291
A	121	GLY	-	cloning artifact	UNP P15291
A	122	ARG	-	cloning artifact	UNP P15291
A	123	GLY	-	cloning artifact	UNP P15291
A	124	SER	-	cloning artifact	UNP P15291
A	125	ALA	-	cloning artifact	UNP P15291
A	337	THR	ARG	engineered mutation	UNP P15291
A	338	THR	CYS	engineered mutation	UNP P15291
A	340	HIS	MET	engineered mutation	UNP P15291

• Molecule 2 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 10 6 4	0	0
2	A	1	Total C O 10 6 4	0	0

• Molecule 3 is water.

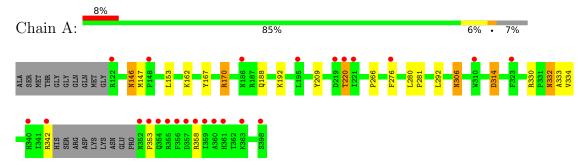
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	329	Total O 329 329	0	0



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: Beta-1,4-galactosyltransferase 1





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants	70.35Å 137.77Å 66.21Å	Donositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.75 - 1.70	Depositor
Resolution (A)	19.75 - 1.60	EDS
% Data completeness	94.2 (19.75-1.70)	Depositor
(in resolution range)	90.2 (19.75-1.60)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$< I/\sigma(I) > 1$	1.14 (at 1.60Å)	Xtriage
Refinement program	CNS 1.0	Depositor
D D.	0.187 , 0.222	Depositor
R, R_{free}	0.168 , 0.205	DCC
R_{free} test set	3875 reflections (10.02%)	wwPDB-VP
Wilson B-factor (Å ²)	21.8	Xtriage
Anisotropy	0.160	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.35, 48.1	EDS
L-test for twinning ²	$ < L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2516	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.39% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities 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: PGE

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	Mol Chain	Bond	$\mathbf{lengths}$	Bond angles	
MIOI		RMSZ	# Z > 5	RMSZ	# Z > 5
1	A	0.69	0/2226	0.82	0/3023

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	2167	0	2113	27	0
2	A	20	0	28	0	1
3	A	329	0	0	3	0
All	All	2516	0	2141	27	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 6.

All (27) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{aligned} ext{Clash} \ ext{overlap } (ext{Å}) \end{aligned}$
1:A:306:ASN:H	1:A:306:ASN:HD22	1.36	0.74

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A 1 1		Interatomic	Clash
Atom-1	Atom-2	${\rm distance}(\mathring{\rm A})$	overlap (Å)
1:A:146:ASN:HD22	1:A:146:ASN:H	1.44	0.66
1:A:170:ARG:HA	1:A:170:ARG:HE	1.61	0.65
1:A:170:ARG:HA	1:A:170:ARG:NE	2.12	0.65
1:A:276:PHE:CE2	1:A:353:PRO:HD3	2.36	0.61
1:A:170:ARG:HE	1:A:170:ARG:CA	2.14	0.60
1:A:342:ARG:HG3	1:A:342:ARG:HH11	1.68	0.58
1:A:332:ASN:HD22	1:A:334:VAL:H	1.53	0.56
1:A:220:THR:HG23	3:A:742:HOH:O	2.04	0.56
1:A:276:PHE:CZ	1:A:353:PRO:HD3	2.44	0.53
1:A:281:PRO:HB3	1:A:353:PRO:HG2	1.92	0.51
1:A:266:PRO:HB3	1:A:292:LEU:CD2	2.41	0.50
1:A:306:ASN:HD22	1:A:306:ASN:N	1.99	0.49
1:A:342:ARG:H	1:A:342:ARG:NH1	2.11	0.47
1:A:266:PRO:HB3	1:A:292:LEU:HD21	1.96	0.47
1:A:280:LEU:HD21	1:A:330:ARG:CZ	2.45	0.47
1:A:314:ASP:HB2	3:A:558:HOH:O	2.15	0.47
1:A:332:ASN:HD22	1:A:332:ASN:C	2.19	0.46
1:A:170:ARG:HD3	3:A:635:HOH:O	2.17	0.45
1:A:146:ASN:HD22	1:A:146:ASN:N	2.06	0.45
1:A:332:ASN:HD22	1:A:333:ALA:N	2.16	0.44
1:A:146:ASN:H	1:A:146:ASN:ND2	2.14	0.44
1:A:306:ASN:H	1:A:306:ASN:ND2	2.07	0.43
1:A:167:TYR:HB3	1:A:209:TYR:CE2	2.52	0.43
1:A:332:ASN:ND2	1:A:334:VAL:H	2.14	0.43
1:A:188:GLN:O	1:A:192:LYS:HG3	2.18	0.43
1:A:162:LYS:NZ	1:A:162:LYS:HB3	2.37	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	$egin{array}{c} ext{Interatomic} \ ext{distance} \ (ext{Å}) \end{array}$	$egin{aligned} \operatorname{Clash} \ \operatorname{overlap}\ (ext{\AA}) \end{aligned}$
2:A:403:PGE:O4	2:A:403:PGE:O4[3_555]	1.61	0.59

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	264/287 (92%)	258 (98%)	6 (2%)	0	100 10	0

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	237/252 (94%)	228 (96%)	9 (4%)	33 14	

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	146	ASN
1	A	147	MET
1	A	153	LEU
1	A	170	ARG
1	A	220	THR
1	A	306	ASN
1	A	314	ASP
1	A	332	ASN
1	A	358	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	146	ASN
1	A	306	ASN
1	A	332	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)

2 ligands 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	Type	ype Chain	Dec	Res Link	В	ond leng	gths	Bond angles		
IVIOI	туре	Chain	n Res Link	Lilik	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
2	PGE	A	404	-	9,9,9	0.56	0	8,8,8	0.40	0
2	PGE	A	403	-	9,9,9	0.42	0	8,8,8	0.38	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	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PGE	A	404	-	-	3/7/7/7	-
2	PGE	A	403	-	-	5/7/7/7	_

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.



All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	403	PGE	O1-C1-C2-O2
2	A	404	PGE	O1-C1-C2-O2
2	A	403	PGE	O3-C5-C6-O4
2	A	403	PGE	C3-C4-O3-C5
2	A	403	PGE	C6-C5-O3-C4
2	A	403	PGE	C4-C3-O2-C2
2	A	404	PGE	C4-C3-O2-C2
2	A	404	PGE	O3-C5-C6-O4

There are no ring outliers.

1 monomer is involved in 1 short contact:

\mathbf{Mol}	Chain	Res	Type	Clashes	Symm-Clashes
2	A	403	PGE	0	1

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	$OWAB(A^2)$	Q < 0.9
1	A	268/287 (93%)	0.46	24 (8%) 9 10	11, 17, 35, 59	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	342	ARG	7.4
1	A	356	PHE	6.0
1	A	352	ASN	5.7
1	A	357	ASP	5.7
1	A	354	GLN	4.9
1	A	358	ARG	4.8
1	A	360	ALA	4.5
1	A	353	PRO	4.5
1	A	148	PRO	3.9
1	A	359	ILE	3.4
1	A	398	SER	3.3
1	A	220	THR	3.3
1	A	361	HIS	3.0
1	A	310	TRP	2.9
1	A	355	ARG	2.7
1	A	363	LYS	2.6
1	A	323	PHE	2.5
1	A	219	ASP	2.4
1	A	221	ILE	2.3
1	A	340	HIS	2.1
1	A	122	ARG	2.1
1	A	186	ASN	2.1
1	A	195	LEU	2.0
1	A	276	PHE	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^{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	PGE	A	403	10/10	0.78	0.20	51,53,54,54	0
2	PGE	A	404	10/10	0.78	0.21	34,37,47,50	0

6.5 Other polymers (i)

There are no such residues in this entry.

