



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 12:05 AM UTC

PDB ID : 8XGX / pdb_00008xgx
Title : beta-1,4-galactosyltransferase
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Deposited on : 2023-12-15
Resolution : 2.41 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

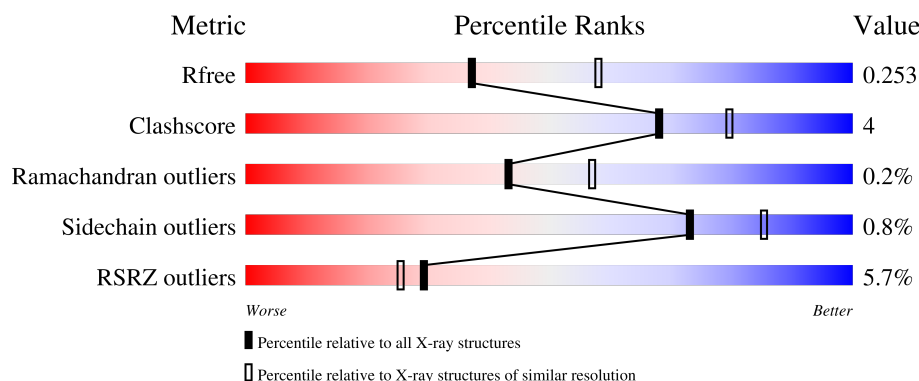
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

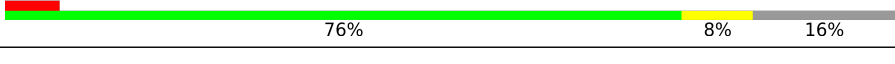
The reported resolution of this entry is 2.41 Å.

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}	180053	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
Sidechain outliers	187428	6482 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

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 $\leq 5\%$. 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	251	
1	B	251	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3562 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 Glycosyltransferase family 25 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	210	Total	C	N	O	S	0	2	0
			1741	1125	286	322	8			
1	B	211	Total	C	N	O	S	0	0	0
			1737	1121	285	323	8			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	234	ILE	-	expression tag	UNP A0A5D0ENI3
A	235	ASN	-	expression tag	UNP A0A5D0ENI3
A	236	LEU	-	expression tag	UNP A0A5D0ENI3
A	237	LYS	-	expression tag	UNP A0A5D0ENI3
A	238	TYR	-	expression tag	UNP A0A5D0ENI3
A	239	GLU	-	expression tag	UNP A0A5D0ENI3
A	240	LYS	-	expression tag	UNP A0A5D0ENI3
A	241	ARG	-	expression tag	UNP A0A5D0ENI3
A	242	LYS	-	expression tag	UNP A0A5D0ENI3
A	243	HIS	-	expression tag	UNP A0A5D0ENI3
A	244	LEU	-	expression tag	UNP A0A5D0ENI3
A	245	GLU	-	expression tag	UNP A0A5D0ENI3
A	246	HIS	-	expression tag	UNP A0A5D0ENI3
A	247	HIS	-	expression tag	UNP A0A5D0ENI3
A	248	HIS	-	expression tag	UNP A0A5D0ENI3
A	249	HIS	-	expression tag	UNP A0A5D0ENI3
A	250	HIS	-	expression tag	UNP A0A5D0ENI3
A	251	HIS	-	expression tag	UNP A0A5D0ENI3
B	234	ILE	-	expression tag	UNP A0A5D0ENI3
B	235	ASN	-	expression tag	UNP A0A5D0ENI3
B	236	LEU	-	expression tag	UNP A0A5D0ENI3
B	237	LYS	-	expression tag	UNP A0A5D0ENI3
B	238	TYR	-	expression tag	UNP A0A5D0ENI3
B	239	GLU	-	expression tag	UNP A0A5D0ENI3
B	240	LYS	-	expression tag	UNP A0A5D0ENI3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	241	ARG	-	expression tag	UNP A0A5D0ENI3
B	242	LYS	-	expression tag	UNP A0A5D0ENI3
B	243	HIS	-	expression tag	UNP A0A5D0ENI3
B	244	LEU	-	expression tag	UNP A0A5D0ENI3
B	245	GLU	-	expression tag	UNP A0A5D0ENI3
B	246	HIS	-	expression tag	UNP A0A5D0ENI3
B	247	HIS	-	expression tag	UNP A0A5D0ENI3
B	248	HIS	-	expression tag	UNP A0A5D0ENI3
B	249	HIS	-	expression tag	UNP A0A5D0ENI3
B	250	HIS	-	expression tag	UNP A0A5D0ENI3
B	251	HIS	-	expression tag	UNP A0A5D0ENI3

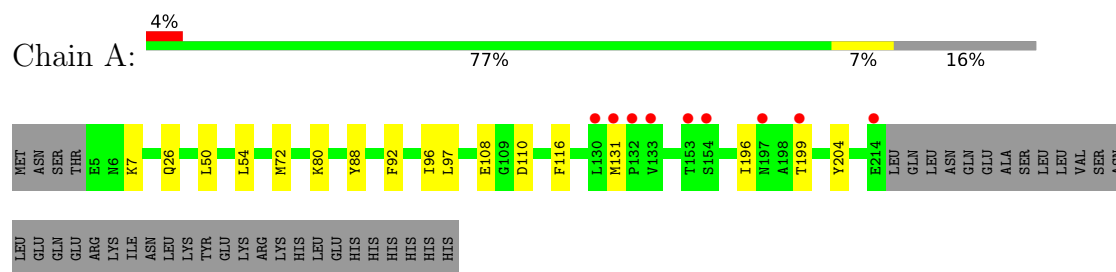
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	47	Total O 47 47	0	2
2	B	37	Total O 37 37	0	0

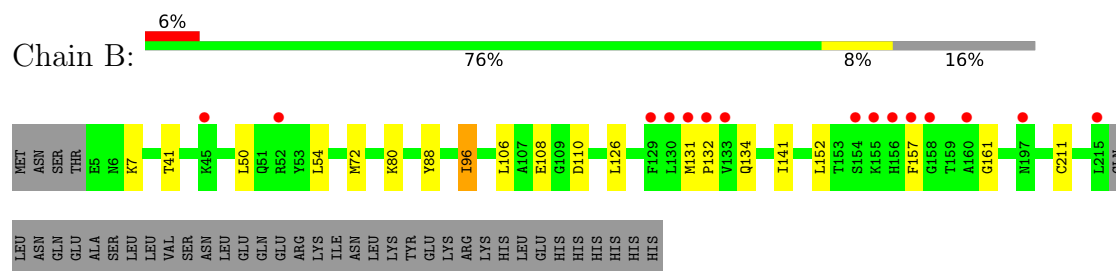
3 Residue-property plots [i](#)

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: Glycosyltransferase family 25 protein



- Molecule 1: Glycosyltransferase family 25 protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	87.84Å 87.84Å 140.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.54 – 2.41 46.54 – 2.41	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.54-2.41) 100.0 (46.54-2.41)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.43 (at 2.42Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.208 , 0.253 0.211 , 0.253	Depositor DCC
R_{free} test set	1070 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	39.4	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 23.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3562	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 71.10 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.7885e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical 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	0.98	0/1787	1.37	1/2419 (0.0%)
1	B	0.98	1/1776 (0.1%)	1.38	0/2404
All	All	0.98	1/3563 (0.0%)	1.37	1/4823 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	41	THR	N-CA	5.33	1.49	1.46

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	199	THR	CB-CA-C	5.64	119.24	110.67

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	1741	0	1717	15	0
1	B	1737	0	1710	15	0
2	A	47	0	0	0	1
2	B	37	0	0	2	2
All	All	3562	0	3427	25	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 4.

All (25) 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:96:ILE:HD11	1:B:211:CYS:SG	2.34	0.68
1:B:108:GLU:OE2	2:B:301:HOH:O	2.14	0.64
1:B:134:GLN:HG3	2:B:324:HOH:O	2.01	0.59
1:B:50:LEU:HD23	1:B:72:MET:CE	2.33	0.58
1:A:50:LEU:HD23	1:A:72:MET:CE	2.37	0.54
1:B:50:LEU:HD23	1:B:72:MET:HE2	1.91	0.51
1:B:108:GLU:HG3	1:B:110:ASP:H	1.77	0.49
1:A:108:GLU:HG3	1:A:110:ASP:H	1.77	0.49
1:A:96:ILE:C	1:A:97[A]:LEU:HD12	2.38	0.48
1:A:131:MET:SD	1:B:131:MET:SD	3.11	0.48
1:A:26:GLN:HE22	1:A:97[A]:LEU:HA	1.79	0.48
1:A:26:GLN:HE22	1:A:97[B]:LEU:HA	1.79	0.47
1:B:132:PRO:HA	1:B:157:PHE:CE2	2.50	0.47
1:A:116:PHE:CE1	1:B:141:ILE:HD13	2.51	0.45
1:A:50:LEU:HD23	1:A:72:MET:HE2	1.98	0.44
1:A:204:TYR:CE1	1:B:141:ILE:HD12	2.54	0.43
1:B:7:LYS:HD2	1:B:88:TYR:CZ	2.53	0.43
1:B:50:LEU:O	1:B:54:LEU:C	2.62	0.43
1:A:196:ILE:HD11	1:B:152:LEU:HD23	2.00	0.43
1:A:50:LEU:O	1:A:54:LEU:C	2.63	0.42
1:A:7:LYS:HD2	1:A:88:TYR:CZ	2.54	0.42
1:B:106:LEU:HD21	1:B:126:LEU:HD13	2.01	0.42
1:A:92:PHE:CD1	1:A:96:ILE:HD13	2.56	0.41
1:A:204:TYR:CZ	1:B:141:ILE:CD1	3.04	0.41

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)
2:B:333:HOH:O	2:B:333:HOH:O[2_545]	1.95	0.25
2:A:338:HOH:O	2:B:303:HOH:O[3_444]	2.12	0.08

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	210/251 (84%)	201 (96%)	9 (4%)	0	100	100
1	B	209/251 (83%)	203 (97%)	5 (2%)	1 (0%)	24	35
All	All	419/502 (84%)	404 (96%)	14 (3%)	1 (0%)	43	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	161	GLY

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	192/230 (84%)	191 (100%)	1 (0%)	81	90
1	B	191/230 (83%)	189 (99%)	2 (1%)	68	82
All	All	383/460 (83%)	380 (99%)	3 (1%)	73	85

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	80	LYS
1	B	80	LYS
1	B	96	ILE

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	26	GLN
1	A	197	ASN
1	B	145	GLN

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 oligosaccharides 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

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	210/251 (83%)	0.27	9 (4%)	40 35	21, 41, 65, 81	2 (0%)
1	B	211/251 (84%)	0.34	15 (7%)	22 18	26, 41, 74, 114	0
All	All	421/502 (83%)	0.30	24 (5%)	29 25	21, 41, 70, 114	2 (0%)

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	155	LYS	4.8
1	B	156	HIS	4.8
1	B	157	PHE	4.3
1	B	129	PHE	3.9
1	A	131	MET	3.6
1	B	215	LEU	3.6
1	A	154	SER	3.6
1	A	133	VAL	3.5
1	A	132	PRO	3.4
1	B	154	SER	3.0
1	A	214	GLU	3.0
1	B	131	MET	2.9
1	B	132	PRO	2.8
1	A	153	THR	2.7
1	B	160	ALA	2.7
1	B	130	LEU	2.6
1	B	197	ASN	2.4
1	B	133	VAL	2.4
1	A	199	THR	2.3
1	B	45	LYS	2.3
1	A	197	ASN	2.3
1	B	158	GLY	2.1
1	A	130	LEU	2.1
1	B	52	ARG	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.