



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 11:10 PM UTC

PDB ID : 1GCY / pdb_00001gcy
Title : HIGH RESOLUTION CRYSTAL STRUCTURE OF MALTOTETRAOSE-FORMING EXO-AMYLASE
Authors : Mezaki, Y.; Katsuya, Y.; Kubota, M.; Matsuura, Y.
Deposited on : 2000-08-14
Resolution : 1.60 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

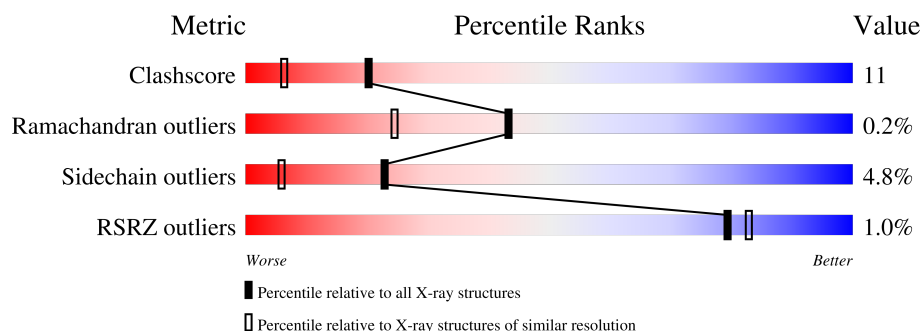
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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	527	59% 17% • 21%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3503 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 GLUCAN 1,4-ALPHA-MALTOTETRAHYDROLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	415	Total	C	N	O	S	0	0	0
			3279	2061	593	615	10			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	334	ASP	SER	conflict	UNP P13507

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Ca	0	0
			2	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	222	Total	O	0	0
			222	222		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	69.42Å 171.66Å 46.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 1.60 8.00 – 1.60	Depositor EDS
% Data completeness (in resolution range)	89.6 (8.00-1.60) 88.9 (8.00-1.60)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.36 (at 1.60Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.259 , 0.304 0.241 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	17.4	Xtriage
Anisotropy	0.460	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.51 , 73.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3503	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.21% of the height of the origin peak. No significant pseudotranslation is detected.*

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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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	0.42	0/3383	0.93	15/4604 (0.3%)

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	139	ASP	N-CA-C	-10.40	100.33	113.23
1	A	25	TRP	N-CA-C	7.27	120.13	111.33
1	A	116	ASN	N-CA-C	6.87	118.77	111.28
1	A	19	ILE	N-CA-C	6.11	118.45	108.97
1	A	11	ARG	N-CA-C	6.03	118.98	109.39
1	A	183	SER	N-CA-C	6.02	117.92	111.36
1	A	122	TYR	CA-C-N	5.80	125.01	118.97
1	A	122	TYR	C-N-CA	5.80	125.01	118.97
1	A	334	ASP	N-CA-C	5.68	117.47	111.28
1	A	336	MET	N-CA-C	5.60	117.47	111.36
1	A	339	TRP	N-CA-C	5.58	119.78	112.92
1	A	301	GLN	N-CA-C	5.56	118.87	110.64
1	A	210	SER	N-CA-C	5.34	120.80	113.97
1	A	405	ALA	N-CA-C	-5.11	107.59	113.88
1	A	257	ALA	N-CA-C	-5.04	105.87	111.36

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	3279	0	3000	71	0
2	A	2	0	0	0	0
3	A	222	0	0	2	0
All	All	3503	0	3000	71	0

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 11.

All (71) 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:317:GLN:H	1:A:317:GLN:HE21	1.08	0.94
1:A:277:ASN:HD22	1:A:279:ASP:H	1.20	0.86
1:A:216:CYS:O	1:A:252:PRO:HD2	1.79	0.82
1:A:292:ASN:ND2	1:A:295:THR:H	1.81	0.77
1:A:292:ASN:ND2	1:A:294:ASP:H	1.83	0.75
1:A:292:ASN:HD21	1:A:295:THR:H	1.35	0.73
1:A:317:GLN:H	1:A:317:GLN:NE2	1.86	0.73
1:A:292:ASN:C	1:A:292:ASN:HD22	1.97	0.72
1:A:145:ASN:ND2	1:A:155:ARG:H	1.90	0.69
1:A:145:ASN:HD21	1:A:155:ARG:H	1.46	0.64
1:A:292:ASN:HD22	1:A:294:ASP:H	1.47	0.62
1:A:277:ASN:ND2	1:A:279:ASP:H	1.94	0.61
1:A:200:PRO:HB3	1:A:245:TRP:CD1	2.39	0.58
1:A:317:GLN:HE21	1:A:317:GLN:N	1.89	0.57
1:A:56:MET:HG3	1:A:109:VAL:HG13	1.86	0.57
1:A:125:LYS:HE2	1:A:127:ILE:O	2.04	0.57
1:A:311:GLN:O	1:A:311:GLN:HG3	2.03	0.57
1:A:71:LYS:HD3	1:A:302:ASN:HD22	1.70	0.56
1:A:11:ARG:HH22	1:A:204:ASN:ND2	2.04	0.56
1:A:26:ASN:HD22	1:A:29:ARG:HH11	1.54	0.54
1:A:80:TRP:HE1	1:A:114:VAL:HB	1.73	0.54
1:A:61:ARG:NE	1:A:84:ASN:HB3	2.24	0.53
1:A:62:ASP:O	1:A:75:GLY:HA2	2.10	0.52
1:A:325:SER:HB2	1:A:326:PRO:CD	2.40	0.52
1:A:355:ALA:HB2	1:A:383:LEU:HD21	1.92	0.52
1:A:61:ARG:CD	1:A:84:ASN:HB3	2.40	0.51
1:A:211:ALA:HB1	1:A:214:SER:OG	2.11	0.51
1:A:71:LYS:HD2	1:A:72:SER:H	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:299:PRO:HD3	1:A:334:ASP:CG	2.37	0.49
1:A:271:LYS:HE3	1:A:272:HIS:CE1	2.48	0.49
1:A:143:PRO:HG2	1:A:146:TYR:CE2	2.48	0.48
1:A:92:ASP:O	1:A:96:ARG:HG3	2.14	0.48
1:A:71:LYS:HD3	1:A:301:GLN:OE1	2.13	0.48
1:A:137:ARG:HB2	1:A:151:ASP:HB2	1.96	0.47
1:A:301:GLN:HB2	3:A:685:HOH:O	2.13	0.47
1:A:86:ASN:ND2	1:A:92:ASP:H	2.11	0.47
1:A:292:ASN:HD21	1:A:294:ASP:HB3	1.79	0.47
1:A:325:SER:HB2	1:A:326:PRO:HD2	1.96	0.46
1:A:261:ARG:NE	1:A:261:ARG:HA	2.31	0.46
1:A:26:ASN:ND2	1:A:29:ARG:HH11	2.14	0.45
1:A:122:TYR:HA	1:A:123:PRO:HD3	1.84	0.45
1:A:11:ARG:HH12	1:A:204:ASN:HD22	1.64	0.45
1:A:50:GLY:CA	1:A:353:ARG:HH12	2.29	0.45
1:A:406:VAL:HB	1:A:415:VAL:HB	1.99	0.45
1:A:12:TYR:CD2	1:A:12:TYR:C	2.95	0.45
1:A:82:ASP:HA	1:A:127:ILE:HD12	1.98	0.45
1:A:196:ARG:CZ	1:A:222:LYS:HD2	2.47	0.45
1:A:143:PRO:HG2	1:A:146:TYR:HE2	1.82	0.45
1:A:50:GLY:HA3	1:A:353:ARG:HH12	1.83	0.44
1:A:80:TRP:CD1	1:A:80:TRP:H	2.34	0.44
1:A:334:ASP:OD1	1:A:338:ASP:OD1	2.36	0.44
1:A:299:PRO:HD3	1:A:334:ASP:OD2	2.18	0.43
1:A:2:GLN:O	1:A:14:GLY:HA3	2.18	0.43
1:A:113:VAL:O	1:A:115:PRO:HD3	2.18	0.43
1:A:111:TYR:CD1	1:A:187:ALA:HB2	2.54	0.43
1:A:195:VAL:HG22	1:A:219:GLU:O	2.16	0.43
1:A:31:ALA:N	1:A:32:PRO:HD3	2.34	0.43
1:A:119:ASN:C	1:A:119:ASN:HD22	2.26	0.43
1:A:145:ASN:HD21	1:A:154:ASP:HB3	1.84	0.43
1:A:332:TYR:HB3	1:A:335:HIS:HD2	1.84	0.42
1:A:326:PRO:HG3	1:A:361:SER:O	2.19	0.42
1:A:71:LYS:HD2	1:A:72:SER:N	2.34	0.42
1:A:80:TRP:NE1	1:A:114:VAL:HB	2.34	0.42
1:A:30:GLU:C	1:A:32:PRO:HD3	2.45	0.42
1:A:394:PRO:HD3	1:A:416:TRP:CE2	2.54	0.42
1:A:21:GLN:O	1:A:333:TRP:HB2	2.19	0.41
1:A:171:TYR:CD1	1:A:171:TYR:C	2.98	0.41
1:A:224:PRO:O	1:A:234:ASN:HA	2.20	0.41
1:A:292:ASN:ND2	1:A:294:ASP:N	2.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:316:ARG:HB2	3:A:622:HOH:O	2.21	0.41
1:A:56:MET:CG	1:A:109:VAL:HG13	2.52	0.40

There are no symmetry-related clashes.

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	411/527 (78%)	395 (96%)	15 (4%)	1 (0%)	43 24

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	157	ILE

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	331/413 (80%)	315 (95%)	16 (5%)	23 6

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	GLN

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Mol	Chain	Res	Type
1	A	12	TYR
1	A	41	GLN
1	A	65	SER
1	A	67	SER
1	A	71	LYS
1	A	125	LYS
1	A	162	ASP
1	A	182	ARG
1	A	205	SER
1	A	229	ASN
1	A	239	GLN
1	A	292	ASN
1	A	301	GLN
1	A	311	GLN
1	A	317	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2	GLN
1	A	8	ASN
1	A	26	ASN
1	A	33	ASN
1	A	86	ASN
1	A	119	ASN
1	A	145	ASN
1	A	180	ASN
1	A	204	ASN
1	A	234	ASN
1	A	277	ASN
1	A	292	ASN
1	A	302	ASN
1	A	311	GLN
1	A	317	GLN
1	A	335	HIS
1	A	347	GLN
1	A	388	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are 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](#)

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	415/527 (78%)	-0.19	4 (0%) 79 83	11, 17, 32, 50	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	301	GLN	2.6
1	A	311	GLN	2.3
1	A	358	ARG	2.3
1	A	67	SER	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](#)

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, 95th 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	B-factors(Å ²)	Q<0.9
2	CA	A	528	1/1	0.99	0.03	17,17,17,17	0
2	CA	A	529	1/1	0.99	0.02	21,21,21,21	0

6.5 Other polymers [i](#)

There are no such residues in this entry.