



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 19, 2023 – 09:00 AM EST

PDB ID : 1IV8
Title : Crystal Structure of Maltooligosyl trehalose synthase
Authors : Kobayashi, M.; Kubota, M.; Matsuura, Y.
Deposited on : 2002-03-15
Resolution : 1.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

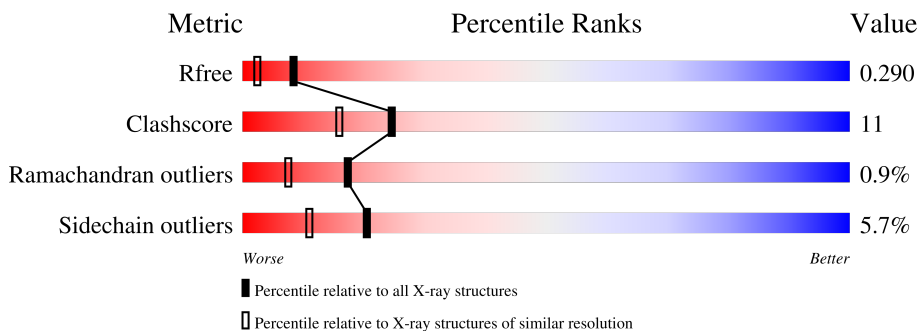
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


The reported resolution of this entry is 1.90 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}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)

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 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	720	 78% 19% .

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 6379 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 MALTOOLIGOSYL TREHALOSE SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	720	6013	3879	991	1122	21	0	0	0

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	MLZ	LYS	modified residue	UNP Q53688
A	105	MLZ	LYS	modified residue	UNP Q53688
A	108	MLZ	LYS	modified residue	UNP Q53688
A	109	MLY	LYS	modified residue	UNP Q53688
A	111	MLY	LYS	modified residue	UNP Q53688
A	206	MLY	LYS	modified residue	UNP Q53688
A	216	MLY	LYS	modified residue	UNP Q53688
A	250	MLY	LYS	modified residue	UNP Q53688
A	310	MLZ	LYS	modified residue	UNP Q53688
A	326	MLZ	LYS	modified residue	UNP Q53688
A	390	MLY	LYS	modified residue	UNP Q53688
A	467	MLZ	LYS	modified residue	UNP Q53688
A	504	MLY	LYS	modified residue	UNP Q53688
A	508	MLZ	LYS	modified residue	UNP Q53688
A	513	MLZ	LYS	modified residue	UNP Q53688
A	519	MLZ	LYS	modified residue	UNP Q53688
A	558	MLY	LYS	modified residue	UNP Q53688
A	616	MLY	LYS	modified residue	UNP Q53688
A	638	MLZ	LYS	modified residue	UNP Q53688

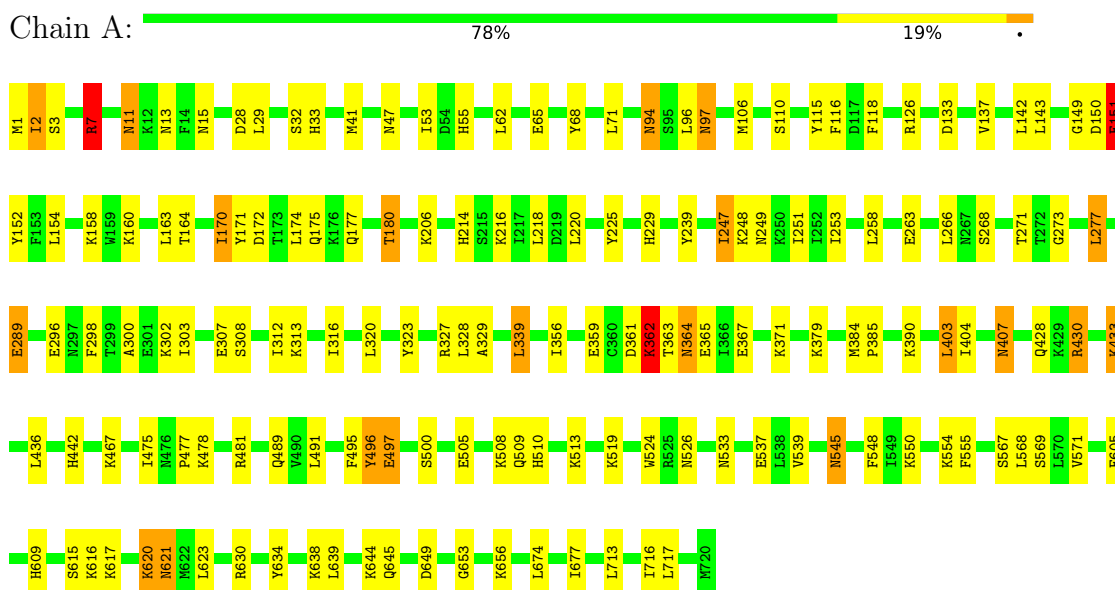
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	366	Total	O	0	0
			366	366		

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.

- Molecule 1: MALTOOLIGOSYL TREHALOSE SYNTHASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	56.50Å 68.50Å 93.77Å 90.00° 101.46° 90.00°	Depositor
Resolution (Å)	8.00 – 1.90 29.39 – 1.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-1.90) 93.3 (29.39-1.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.66 (at 1.91Å)	Xtrriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.197 , 0.256 0.257 , 0.290	Depositor DCC
R_{free} test set	3667 reflections (7.09%)	wwPDB-VP
Wilson B-factor (Å ²)	19.2	Xtrriage
Anisotropy	0.016	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 51.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6379	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.26% 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: MLY, MLZ

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	0.38	0/5930	0.65	4/7992 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	258	LEU	CA-CB-CG	6.19	129.54	115.30
1	A	273	GLY	N-CA-C	5.27	126.27	113.10
1	A	277	LEU	CA-CB-CG	5.12	127.07	115.30
1	A	7	ARG	NE-CZ-NH1	5.05	122.83	120.30

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	6013	0	6024	131	0
2	A	366	0	0	20	0
All	All	6379	0	6024	131	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.

The worst 5 of 131 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:621:ASN:HD21	1:A:630:ARG:HH22	1.08	1.01
1:A:94:ASN:HD22	1:A:96:LEU:H	1.10	0.94
1:A:359:GLU:OE2	2:A:902:HOH:O	1.92	0.86
1:A:362:LYS:HE2	1:A:364:ASN:HD21	1.38	0.86
1:A:94:ASN:ND2	1:A:96:LEU:H	1.75	0.85

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	699/720 (97%)	663 (95%)	30 (4%)	6 (1%)	17 7

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	151	GLU
1	A	362	LYS
1	A	496	TYR
1	A	2	ILE
1	A	497	GLU

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	647/647 (100%)	610 (94%)	37 (6%)	20 11

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	491	LEU
1	A	674	LEU
1	A	526	ASN
1	A	620	LYS
1	A	247	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	331	GLN
1	A	442	HIS
1	A	621	ASN
1	A	407	ASN
1	A	472	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

19 non-standard protein/DNA/RNA residues 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	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	MLZ	A	310	1	8,9,10	0.37	0	4,9,11	0.79	0
1	MLY	A	504	1	9,10,11	0.48	0	6,11,13	0.71	0
1	MLY	A	111	1	9,10,11	0.58	0	6,11,13	0.55	0
1	MLZ	A	108	1	8,9,10	0.54	0	4,9,11	0.58	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLY	A	390	1	9,10,11	0.49	0	6,11,13	0.62	0
1	MLY	A	616	1	9,10,11	0.47	0	6,11,13	0.82	0
1	MLY	A	109	1	9,10,11	0.39	0	6,11,13	0.64	0
1	MLZ	A	27	1	8,9,10	0.39	0	4,9,11	0.81	0
1	MLZ	A	105	1	8,9,10	0.43	0	4,9,11	0.63	0
1	MLZ	A	508	1	8,9,10	0.38	0	4,9,11	0.65	0
1	MLY	A	558	1	9,10,11	0.52	0	6,11,13	0.67	0
1	MLZ	A	326	1	8,9,10	0.39	0	4,9,11	0.68	0
1	MLY	A	216	1	9,10,11	0.52	0	6,11,13	0.91	0
1	MLY	A	250	1	9,10,11	0.52	0	6,11,13	0.49	0
1	MLZ	A	513	1	8,9,10	0.48	0	4,9,11	0.66	0
1	MLZ	A	519	1	8,9,10	0.44	0	4,9,11	0.72	0
1	MLY	A	206	1	9,10,11	0.44	0	6,11,13	0.63	0
1	MLZ	A	467	1	8,9,10	0.34	0	4,9,11	0.76	0
1	MLZ	A	638	1	8,9,10	0.35	0	4,9,11	0.61	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
1	MLZ	A	310	1	-	0/7/8/10	-
1	MLY	A	504	1	-	0/8/9/11	-
1	MLY	A	111	1	-	0/8/9/11	-
1	MLZ	A	108	1	-	1/7/8/10	-
1	MLY	A	390	1	-	2/8/9/11	-
1	MLY	A	616	1	-	0/8/9/11	-
1	MLY	A	109	1	-	1/8/9/11	-
1	MLZ	A	27	1	-	0/7/8/10	-
1	MLZ	A	105	1	-	0/7/8/10	-
1	MLZ	A	508	1	-	1/7/8/10	-
1	MLY	A	558	1	-	0/8/9/11	-
1	MLZ	A	326	1	-	0/7/8/10	-
1	MLY	A	216	1	-	1/8/9/11	-
1	MLY	A	250	1	-	0/8/9/11	-
1	MLZ	A	513	1	-	0/7/8/10	-
1	MLZ	A	519	1	-	0/7/8/10	-
1	MLY	A	206	1	-	0/8/9/11	-
1	MLZ	A	467	1	-	0/7/8/10	-
1	MLZ	A	638	1	-	1/7/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	390	MLY	O-C-CA-CB
1	A	638	MLZ	CA-CB-CG-CD
1	A	109	MLY	CE-CD-CG-CB
1	A	216	MLY	CE-CD-CG-CB
1	A	108	MLZ	CE-CD-CG-CB

There are no ring outliers.

9 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	390	MLY	1	0
1	A	616	MLY	1	0
1	A	508	MLZ	1	0
1	A	216	MLY	1	0
1	A	513	MLZ	1	0
1	A	519	MLZ	1	0
1	A	206	MLY	1	0
1	A	467	MLZ	1	0
1	A	638	MLZ	2	0

5.5 Carbohydrates [i](#)

There are no monosaccharides 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

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.