



wwPDB X-ray Structure Validation Summary Report

Mar 1, 2014 – 04:07 AM GMT

PDB ID : 4J3U
Title : Crystal structure of barley limit dextrinase in complex with maltosyl-S-betacyclodextrin
Authors : Sim, L.; Windahl, M.S.; Moeller, M.S.; Henriksen, A.
Deposited on : 2013-02-06
Resolution : 1.70 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>

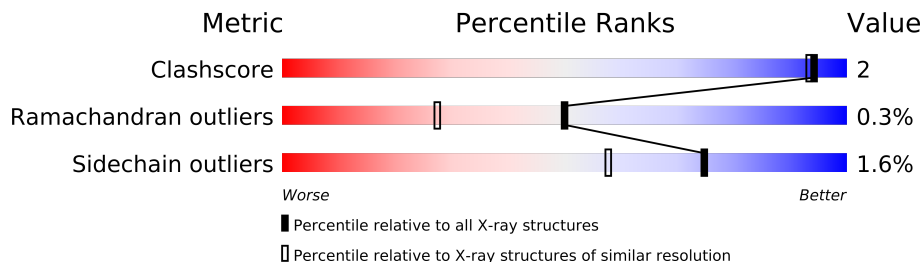
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : **FAILED**
Percentile statistics : 21963
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 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	2929 (1.70-1.70)
Ramachandran outliers	78287	2878 (1.70-1.70)
Sidechain outliers	78261	2878 (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 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.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	905	
1	B	905	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 15402 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 Limit dextrinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	870	Total	C	N	O	S	0	9	0
			6799	4296	1163	1308	32			
1	B	864	Total	C	N	O	S	0	9	0
			6752	4274	1153	1293	32			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP Q9FYY0
A	-18	GLY	-	EXPRESSION TAG	UNP Q9FYY0
A	-17	SER	-	EXPRESSION TAG	UNP Q9FYY0
A	-16	SER	-	EXPRESSION TAG	UNP Q9FYY0
A	-15	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	-14	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	-13	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	-12	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	-11	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	-10	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	-9	SER	-	EXPRESSION TAG	UNP Q9FYY0
A	-8	SER	-	EXPRESSION TAG	UNP Q9FYY0
A	-7	GLY	-	EXPRESSION TAG	UNP Q9FYY0
A	-6	LEU	-	EXPRESSION TAG	UNP Q9FYY0
A	-5	VAL	-	EXPRESSION TAG	UNP Q9FYY0
A	-4	PRO	-	EXPRESSION TAG	UNP Q9FYY0
A	-3	ARG	-	EXPRESSION TAG	UNP Q9FYY0
A	-2	GLY	-	EXPRESSION TAG	UNP Q9FYY0
A	-1	SER	-	EXPRESSION TAG	UNP Q9FYY0
A	0	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	1	MET	-	EXPRESSION TAG	UNP Q9FYY0
A	82	ARG	LYS	SEE REMARK 999	UNP Q9FYY0
A	213	ALA	THR	SEE REMARK 999	UNP Q9FYY0
A	395	ARG	CYS	SEE REMARK 999	UNP Q9FYY0
B	-19	MET	-	EXPRESSION TAG	UNP Q9FYY0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	EXPRESSION TAG	UNP Q9FYY0
B	-17	SER	-	EXPRESSION TAG	UNP Q9FYY0
B	-16	SER	-	EXPRESSION TAG	UNP Q9FYY0
B	-15	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	-14	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	-13	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	-12	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	-11	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	-10	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	-9	SER	-	EXPRESSION TAG	UNP Q9FYY0
B	-8	SER	-	EXPRESSION TAG	UNP Q9FYY0
B	-7	GLY	-	EXPRESSION TAG	UNP Q9FYY0
B	-6	LEU	-	EXPRESSION TAG	UNP Q9FYY0
B	-5	VAL	-	EXPRESSION TAG	UNP Q9FYY0
B	-4	PRO	-	EXPRESSION TAG	UNP Q9FYY0
B	-3	ARG	-	EXPRESSION TAG	UNP Q9FYY0
B	-2	GLY	-	EXPRESSION TAG	UNP Q9FYY0
B	-1	SER	-	EXPRESSION TAG	UNP Q9FYY0
B	0	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	1	MET	-	EXPRESSION TAG	UNP Q9FYY0
B	82	ARG	LYS	SEE REMARK 999	UNP Q9FYY0
B	213	ALA	THR	SEE REMARK 999	UNP Q9FYY0
B	395	ARG	CYS	SEE REMARK 999	UNP Q9FYY0

- Molecule 2 is a polymer of unknown type called SUGAR (7-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	7	Total	C	O	S	0	0
			77	42	34	1		
2	B	7	Total	C	O	S	0	0
			77	42	34	1		

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP Q9FYY0
A	-18	GLY	-	EXPRESSION TAG	UNP Q9FYY0
A	-17	SER	-	EXPRESSION TAG	UNP Q9FYY0
A	-16	SER	-	EXPRESSION TAG	UNP Q9FYY0
A	-15	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	-14	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	-13	HIS	-	EXPRESSION TAG	UNP Q9FYY0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	-11	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	-10	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	-9	SER	-	EXPRESSION TAG	UNP Q9FYY0
A	-8	SER	-	EXPRESSION TAG	UNP Q9FYY0
A	-7	GLY	-	EXPRESSION TAG	UNP Q9FYY0
A	-6	LEU	-	EXPRESSION TAG	UNP Q9FYY0
A	-5	VAL	-	EXPRESSION TAG	UNP Q9FYY0
A	-4	PRO	-	EXPRESSION TAG	UNP Q9FYY0
A	-3	ARG	-	EXPRESSION TAG	UNP Q9FYY0
A	-2	GLY	-	EXPRESSION TAG	UNP Q9FYY0
A	-1	SER	-	EXPRESSION TAG	UNP Q9FYY0
A	0	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	1	MET	-	EXPRESSION TAG	UNP Q9FYY0
A	82	ARG	LYS	SEE REMARK 999	UNP Q9FYY0
A	213	ALA	THR	SEE REMARK 999	UNP Q9FYY0
A	395	ARG	CYS	SEE REMARK 999	UNP Q9FYY0
B	-19	MET	-	EXPRESSION TAG	UNP Q9FYY0
B	-18	GLY	-	EXPRESSION TAG	UNP Q9FYY0
B	-17	SER	-	EXPRESSION TAG	UNP Q9FYY0
B	-16	SER	-	EXPRESSION TAG	UNP Q9FYY0
B	-15	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	-14	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	-13	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	-12	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	-11	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	-10	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	-9	SER	-	EXPRESSION TAG	UNP Q9FYY0
B	-8	SER	-	EXPRESSION TAG	UNP Q9FYY0
B	-7	GLY	-	EXPRESSION TAG	UNP Q9FYY0
B	-6	LEU	-	EXPRESSION TAG	UNP Q9FYY0
B	-5	VAL	-	EXPRESSION TAG	UNP Q9FYY0
B	-4	PRO	-	EXPRESSION TAG	UNP Q9FYY0
B	-3	ARG	-	EXPRESSION TAG	UNP Q9FYY0
B	-2	GLY	-	EXPRESSION TAG	UNP Q9FYY0
B	-1	SER	-	EXPRESSION TAG	UNP Q9FYY0
B	0	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	1	MET	-	EXPRESSION TAG	UNP Q9FYY0
B	82	ARG	LYS	SEE REMARK 999	UNP Q9FYY0
B	213	ALA	THR	SEE REMARK 999	UNP Q9FYY0
B	395	ARG	CYS	SEE REMARK 999	UNP Q9FYY0

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	2	Total	C	O	0	0
			22	12	10		
3	B	2	Total	C	O	0	0
			22	12	10		

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP Q9FYY0
A	-18	GLY	-	EXPRESSION TAG	UNP Q9FYY0
A	-17	SER	-	EXPRESSION TAG	UNP Q9FYY0
A	-16	SER	-	EXPRESSION TAG	UNP Q9FYY0
A	-15	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	-14	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	-13	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	-12	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	-11	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	-10	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	-9	SER	-	EXPRESSION TAG	UNP Q9FYY0
A	-8	SER	-	EXPRESSION TAG	UNP Q9FYY0
A	-7	GLY	-	EXPRESSION TAG	UNP Q9FYY0
A	-6	LEU	-	EXPRESSION TAG	UNP Q9FYY0
A	-5	VAL	-	EXPRESSION TAG	UNP Q9FYY0
A	-4	PRO	-	EXPRESSION TAG	UNP Q9FYY0
A	-3	ARG	-	EXPRESSION TAG	UNP Q9FYY0
A	-2	GLY	-	EXPRESSION TAG	UNP Q9FYY0
A	-1	SER	-	EXPRESSION TAG	UNP Q9FYY0
A	0	HIS	-	EXPRESSION TAG	UNP Q9FYY0
A	1	MET	-	EXPRESSION TAG	UNP Q9FYY0
A	82	ARG	LYS	SEE REMARK 999	UNP Q9FYY0
A	213	ALA	THR	SEE REMARK 999	UNP Q9FYY0
A	395	ARG	CYS	SEE REMARK 999	UNP Q9FYY0
B	-19	MET	-	EXPRESSION TAG	UNP Q9FYY0
B	-18	GLY	-	EXPRESSION TAG	UNP Q9FYY0
B	-17	SER	-	EXPRESSION TAG	UNP Q9FYY0
B	-16	SER	-	EXPRESSION TAG	UNP Q9FYY0
B	-15	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	-14	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	-13	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	-12	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	-11	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	-10	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	-9	SER	-	EXPRESSION TAG	UNP Q9FYY0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	SER	-	EXPRESSION TAG	UNP Q9FYY0
B	-7	GLY	-	EXPRESSION TAG	UNP Q9FYY0
B	-6	LEU	-	EXPRESSION TAG	UNP Q9FYY0
B	-5	VAL	-	EXPRESSION TAG	UNP Q9FYY0
B	-4	PRO	-	EXPRESSION TAG	UNP Q9FYY0
B	-3	ARG	-	EXPRESSION TAG	UNP Q9FYY0
B	-2	GLY	-	EXPRESSION TAG	UNP Q9FYY0
B	-1	SER	-	EXPRESSION TAG	UNP Q9FYY0
B	0	HIS	-	EXPRESSION TAG	UNP Q9FYY0
B	1	MET	-	EXPRESSION TAG	UNP Q9FYY0
B	82	ARG	LYS	SEE REMARK 999	UNP Q9FYY0
B	213	ALA	THR	SEE REMARK 999	UNP Q9FYY0
B	395	ARG	CYS	SEE REMARK 999	UNP Q9FYY0

- Molecule 4 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	12	Total I 13 13	0	1
4	A	20	Total I 22 22	0	2

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total Cl 1 1	0	0
6	A	1	Total Cl 1 1	0	0

- Molecule 7 is water.

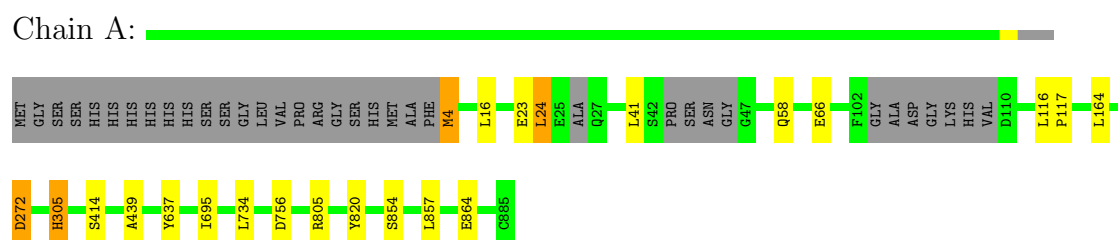
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	791	Total 791	O 791	0	0
7	B	821	Total 821	O 821	0	0

3 Residue-property plots

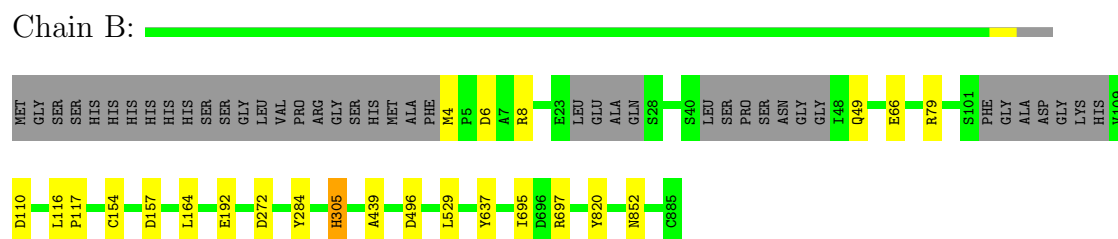
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS failed to run properly.

- Molecule 1: Limit dextrinase



- Molecule 1: Limit dextrinase



4 Data and refinement statistics

EDS failed to run properly - this section will therefore be incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	195.43Å 84.61Å 121.79Å 90.00° 119.91° 90.00°	Depositor
Resolution (Å)	29.76 – 1.70	Depositor
% Data completeness (in resolution range)	99.5 (29.76-1.70)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.19 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.172 , 0.218	Depositor
Wilson B-factor (Å ²)	15.2	Xtriage
Anisotropy	0.119	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 188324 reflections	Xtriage
Total number of atoms	15402	wwPDB-VP
Average B, all atoms (Å ²)	20.0	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 36.88 % 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 4.6671e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: IOD, CA, GLC, SGD, CL

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	0.29	0/6982	0.54	1/9492 (0.0%)
1	B	0.29	0/6944	0.54	0/9441
All	All	0.29	0/13926	0.54	1/18933 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	734	LEU	CA-CB-CG	5.15	127.15	115.30

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	6799	0	0	7	0
1	B	6752	0	0	10	0
2	A	77	0	0	0	0
2	B	77	0	0	1	0
3	A	22	0	0	0	0
3	B	22	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	22	0	0	5	0
4	B	13	0	0	0	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	A	791	0	0	4	0
7	B	821	0	0	3	0
All	All	15402	0	0	21	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 2.

The worst 5 of 21 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:A:914:IOD:I	7:A:1468:HOH:O	2.72	0.78
4:A:912:IOD:I	7:A:1606:HOH:O	2.80	0.69
1:A:23:GLU:O	1:A:24:LEU:CB	2.49	0.59
4:A:913:IOD:I	7:A:1509:HOH:O	2.87	0.58
1:B:154[A]:CYS:SG	1:B:192:GLU:CG	2.92	0.58

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	871/905 (96%)	850 (98%)	18 (2%)	3 (0%)	50 27
1	B	865/905 (96%)	845 (98%)	18 (2%)	2 (0%)	56 33
All	All	1736/1810 (96%)	1695 (98%)	36 (2%)	5 (0%)	50 27

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	24	LEU
1	A	439	ALA
1	B	439	ALA
1	A	695	ILE
1	B	695	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	739/760 (97%)	725 (98%)	14 (2%)	69	50
1	B	736/760 (97%)	725 (98%)	11 (2%)	76	60
All	All	1475/1520 (97%)	1450 (98%)	25 (2%)	75	55

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	820	TYR
1	A	864	GLU
1	B	637	TYR
1	A	857	LEU
1	B	4	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

18 carbohydrates 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	$\# Z > 2$
2	GLC	A	901	2	10,11,12	0.49	0	11,15,17	0.88	0
2	GLC	A	902	2	10,11,12	0.48	0	11,15,17	0.69	0
2	GLC	A	903	2	10,11,12	0.46	0	11,15,17	0.95	1 (9%)
2	SGD	A	904	3,2	10,11,12	0.82	0	11,15,17	1.38	2 (18%)
2	GLC	A	905	2	10,11,12	0.47	0	11,15,17	0.68	0
2	GLC	A	906	2	10,11,12	0.40	0	11,15,17	0.87	0
2	GLC	A	907	2	10,11,12	0.50	0	11,15,17	0.69	0
3	GLC	A	908	3,2	10,11,12	0.45	0	11,15,17	0.55	0
3	GLC	A	909	3	10,11,12	0.40	0	11,15,17	0.87	1 (9%)
2	GLC	B	901	2	10,11,12	0.46	0	11,15,17	1.13	1 (9%)
2	GLC	B	902	2	10,11,12	0.49	0	11,15,17	0.58	0
2	GLC	B	903	2	10,11,12	0.46	0	11,15,17	0.90	1 (9%)
2	SGD	B	904	3,2	10,11,12	0.81	0	11,15,17	1.28	2 (18%)
2	GLC	B	905	2	10,11,12	0.48	0	11,15,17	0.75	0
2	GLC	B	906	2	10,11,12	0.45	0	11,15,17	0.68	0
2	GLC	B	907	2	10,11,12	0.48	0	11,15,17	0.54	0
3	GLC	B	908	3,2	10,11,12	0.46	0	11,15,17	0.52	0
3	GLC	B	909	3	10,11,12	0.40	0	11,15,17	0.81	1 (9%)

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	GLC	A	901	2	-	0/2/19/22	0/1/1/1
2	GLC	A	902	2	-	0/2/19/22	0/1/1/1
2	GLC	A	903	2	-	0/2/19/22	0/1/1/1
2	SGD	A	904	3,2	-	0/2/19/22	0/1/1/1
2	GLC	A	905	2	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLC	A	906	2	-	0/2/19/22	0/1/1/1
2	GLC	A	907	2	-	0/2/19/22	0/1/1/1
3	GLC	A	908	3,2	-	0/2/19/22	0/1/1/1
3	GLC	A	909	3	-	0/2/19/22	0/1/1/1
2	GLC	B	901	2	-	0/2/19/22	0/1/1/1
2	GLC	B	902	2	-	0/2/19/22	0/1/1/1
2	GLC	B	903	2	-	0/2/19/22	0/1/1/1
2	SGD	B	904	3,2	-	0/2/19/22	0/1/1/1
2	GLC	B	905	2	-	0/2/19/22	0/1/1/1
2	GLC	B	906	2	-	0/2/19/22	0/1/1/1
2	GLC	B	907	2	-	0/2/19/22	0/1/1/1
3	GLC	B	908	3,2	-	0/2/19/22	0/1/1/1
3	GLC	B	909	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	904	SGD	C5-C6-S1	-3.26	109.26	114.47
2	B	904	SGD	C5-C6-S1	-2.94	109.76	114.47
2	B	901	GLC	O5-C5-C4	2.69	114.06	110.65
3	A	909	GLC	O5-C5-C6	2.57	109.68	106.98
3	B	909	GLC	O5-C5-C6	2.46	109.56	106.98

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.6 Ligand geometry ⓘ

Of 41 ligands modelled in this entry, 41 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.

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 ⓘ

EDS failed to run properly - this section will therefore be empty.

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

EDS failed to run properly - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS failed to run properly - this section will therefore be empty.

6.4 Ligands ⓘ

EDS failed to run properly - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS failed to run properly - this section will therefore be empty.