



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 5, 2018 – 06:43 PM EST

PDB ID : 1NM9
Title : Crystal structure of recombinant human salivary amylase mutant W58A
Authors : Ramasubbu, N.; Ragunath, C.; Mishra, P.J.; Thomas, L.M.
Deposited on : 2003-01-09
Resolution : 2.10 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030736
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030736

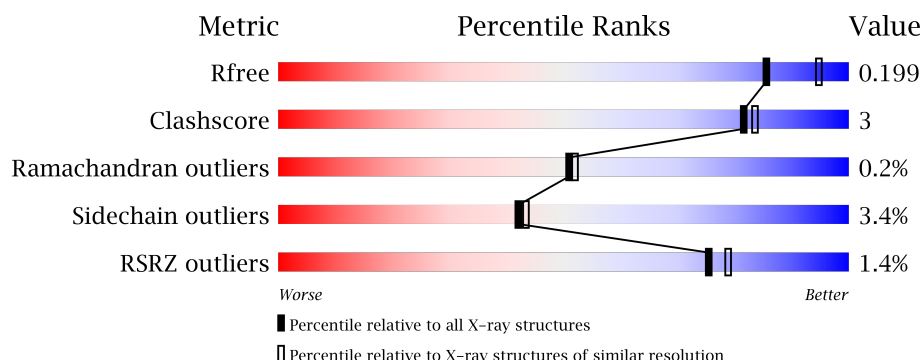
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	100719	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

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. 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	496	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -5px; left: 0; width: 100%;"></div> <div style="position: absolute; top: 5px; left: 0; width: 100%;"></div> </div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> % 92% 7% </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	HMC	A	504	-	-	-	X
4	GLC	A	551	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GLC	A	552	-	-	-	X

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 4260 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.

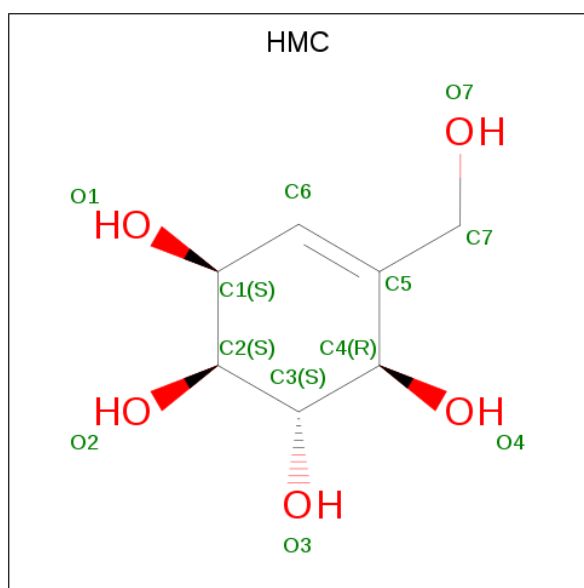
- Molecule 1 is a protein called Alpha-amylase, salivary.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	496	3937	2485	695	736	21	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	PCA	GLN	MODIFIED RESIDUE	UNP P04745
A	58	ALA	TRP	ENGINEERED	UNP P04745

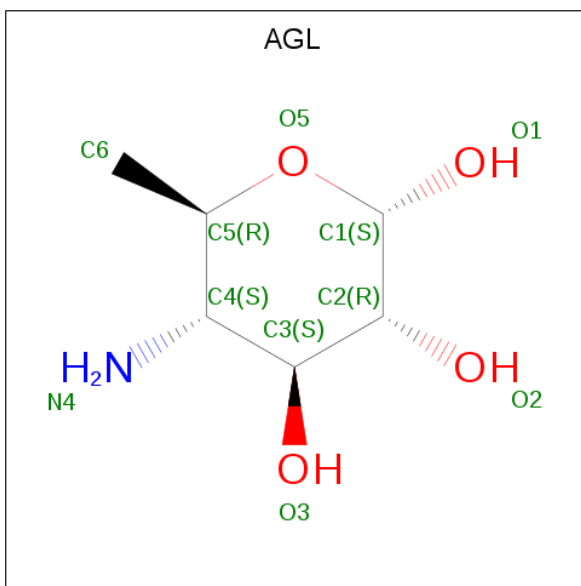
- Molecule 2 is 5-HYDROXYMETHYL-CHONDURITOL (three-letter code: HMC) (formula: $C_7H_{12}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	11	7	4	0	0

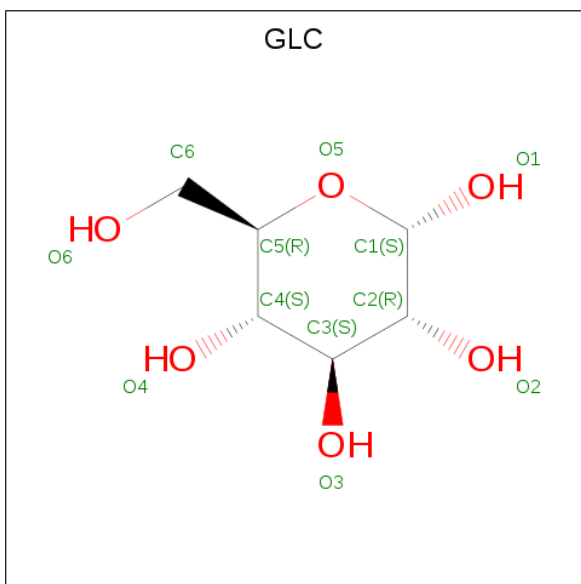
- Molecule 3 is 4,6-DIDEOXY-4-AMINO-ALPHA-D-GLUCOSE (three-letter code: AGL)

(formula: $C_6H_{13}NO_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			10	6	1	3		
3	A	1	Total	C	N	O	0	0
			10	6	1	3		

- Molecule 4 is ALPHA-D-GLUCOSE (three-letter code: GLC) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			12	6	6		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			11	6	5		
4	A	1	Total	C	O	0	0
			12	6	6		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Ca	0	0
			1	1		

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

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

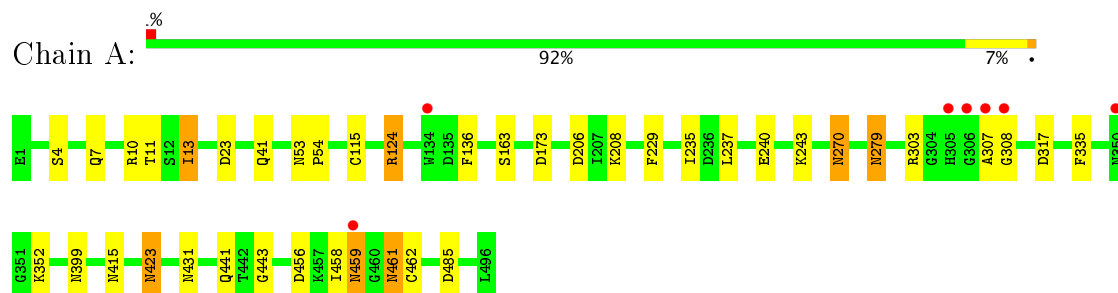
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	255	Total	O	0	0
			255	255		

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 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: Alpha-amylase, salivary



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.95Å 74.06Å 134.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.64 – 2.10 42.53 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.5 (42.64-2.10) 99.5 (42.53-2.10)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.43 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.160 , 0.196 0.165 , 0.199	Depositor DCC
R_{free} test set	1561 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	24.0	Xtriage
Anisotropy	0.018	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 45.2	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	0.96	EDS
Total number of atoms	4260	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.43% 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: AGL, CL, CA, GLC, PCA, HMC

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	0.45	0/4042	0.70	6/5486 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	206	ASP	CB-CG-OD2	5.80	123.52	118.30
1	A	23	ASP	CB-CG-OD2	5.53	123.28	118.30
1	A	485	ASP	CB-CG-OD2	5.21	122.99	118.30
1	A	456	ASP	CB-CG-OD2	5.14	122.93	118.30
1	A	317	ASP	CB-CG-OD2	5.14	122.92	118.30
1	A	173	ASP	CB-CG-OD2	5.13	122.92	118.30

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	3937	0	3702	23	0
2	A	11	0	10	0	0
3	A	20	0	20	0	0
4	A	35	0	32	0	0
5	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	1	0	0	0	0
7	A	255	0	0	4	0
All	All	4260	0	3764	23	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 3.

All (23) 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:441:GLN:HE21	1:A:443:GLY:H	1.36	0.74
1:A:279:ASN:H	1:A:279:ASN:HD22	1.44	0.66
1:A:461:ASN:HD22	1:A:462:CYS:H	1.44	0.65
1:A:308:GLY:O	7:A:859:HOH:O	2.16	0.60
1:A:13:ILE:HD11	1:A:41:GLN:HB2	1.84	0.59
1:A:308:GLY:N	7:A:838:HOH:O	2.35	0.59
1:A:235:ILE:HG21	1:A:307:ALA:HB2	1.87	0.57
1:A:423:ASN:H	1:A:423:ASN:HD22	1.53	0.55
1:A:13:ILE:HG23	1:A:335:PHE:HE1	1.72	0.54
1:A:461:ASN:ND2	1:A:462:CYS:H	2.07	0.52
1:A:124:ARG:HG2	1:A:136:PHE:CD1	2.45	0.52
1:A:415:ASN:HB3	1:A:431:ASN:HB3	1.92	0.50
1:A:240:GLU:O	1:A:243:LYS:HE2	2.14	0.48
1:A:7:GLN:HB2	1:A:10:ARG:HD2	1.95	0.47
1:A:13:ILE:CD1	1:A:41:GLN:HB2	2.44	0.47
1:A:124:ARG:NH2	7:A:811:HOH:O	2.48	0.47
1:A:441:GLN:NE2	1:A:443:GLY:H	2.11	0.44
1:A:4:SER:HA	1:A:229:PHE:CG	2.55	0.42
1:A:308:GLY:CA	7:A:838:HOH:O	2.68	0.42
1:A:270:ASN:HD22	1:A:270:ASN:HA	1.72	0.41
1:A:423:ASN:N	1:A:423:ASN:HD22	2.17	0.41
1:A:11:THR:OG1	1:A:399:ASN:ND2	2.54	0.41
1:A:53:ASN:HA	1:A:54:PRO:HA	1.96	0.41

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	494/496 (100%)	482 (98%)	11 (2%)	1 (0%)	51	52

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	459	ASN

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	417/417 (100%)	403 (97%)	14 (3%)	42	43

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ILE
1	A	115	CYS
1	A	124	ARG
1	A	163	SER
1	A	208	LYS
1	A	237	LEU
1	A	270	ASN
1	A	279	ASN
1	A	303	ARG
1	A	352	LYS

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Mol	Chain	Res	Type
1	A	423	ASN
1	A	458	ILE
1	A	459	ASN
1	A	461	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	270	ASN
1	A	279	ASN
1	A	396	ASN
1	A	399	ASN
1	A	408	ASN
1	A	423	ASN
1	A	441	GLN
1	A	461	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	PCA	A	1	1	8,8,9	2.06	3 (37%)	9,10,12	2.08	5 (55%)

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	PCA	A	1	1	-	0/0/11/13	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1	PCA	CA-C	2.21	1.53	1.50
1	A	1	PCA	CA-N	3.26	1.50	1.46
1	A	1	PCA	CD-N	4.20	1.46	1.34

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1	PCA	CA-N-CD	-3.26	102.41	113.58
1	A	1	PCA	OE-CD-CG	-2.80	121.70	126.86
1	A	1	PCA	O-C-CA	-2.27	119.86	125.15
1	A	1	PCA	CB-CA-N	2.05	109.19	103.30
1	A	1	PCA	CG-CD-N	2.36	115.04	108.33

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 for Mogul analysis.

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	HMC	A	504	3	10,11,12	0.87	0	7,15,17	1.92	2 (28%)
3	AGL	A	505	2,4	9,10,11	0.62	0	12,14,16	0.93	0
4	GLC	A	506	3	12,12,12	0.59	0	17,17,17	0.62	0
3	AGL	A	550	4	9,10,11	0.57	0	12,14,16	0.60	0
4	GLC	A	551	3	11,11,12	0.50	0	13,15,17	2.88	3 (23%)
4	GLC	A	552	-	12,12,12	0.67	0	17,17,17	1.92	5 (29%)

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	HMC	A	504	3	-	0/2/19/22	0/1/1/1
3	AGL	A	505	2,4	-	0/0/17/20	0/1/1/1
4	GLC	A	506	3	-	0/2/22/22	0/1/1/1
3	AGL	A	550	4	-	0/0/17/20	0/1/1/1
4	GLC	A	551	3	-	0/2/19/22	0/1/1/1
4	GLC	A	552	-	-	0/2/22/22	0/1/1/1

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	504	HMC	O7-C7-C5	-3.80	103.28	112.63
4	A	552	GLC	C6-C5-C4	-2.33	107.55	113.00
4	A	552	GLC	O5-C5-C6	2.09	111.42	106.41
2	A	504	HMC	O3-C3-C2	2.12	113.88	110.02
4	A	552	GLC	C1-C2-C3	2.49	115.15	110.65
4	A	552	GLC	C1-O5-C5	3.52	119.73	113.39
4	A	551	GLC	C1-C2-C3	4.44	115.28	109.65
4	A	552	GLC	O5-C1-C2	5.35	118.92	110.04
4	A	551	GLC	O5-C1-C2	5.92	120.06	110.79
4	A	551	GLC	C1-O5-C5	6.92	121.70	112.17

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

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 [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	495/496 (99%)	-0.34	7 (1%) 75 79	15, 22, 33, 48	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	134	TRP	5.9
1	A	308	GLY	4.3
1	A	350	ASN	4.0
1	A	307	ALA	3.7
1	A	459	ASN	3.3
1	A	306	GLY	2.7
1	A	305	HIS	2.6

6.2 Non-standard residues in protein, DNA, RNA chains [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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
1	PCA	A	1	8/9	0.97	0.10	-	22,22,23,24	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	HMC	A	504	11/12	0.90	0.14	5.52	20,23,25,26	0
4	GLC	A	551	11/12	0.91	0.13	3.12	38,40,41,42	0
4	GLC	A	552	12/12	0.87	0.18	2.41	43,44,46,47	0
3	AGL	A	505	10/11	0.92	0.14	0.35	24,28,29,29	0
4	GLC	A	506	12/12	0.91	0.15	-0.07	28,34,36,37	0
5	CA	A	497	1/1	1.00	0.04	-2.60	22,22,22,22	0
6	CL	A	498	1/1	1.00	0.08	-2.89	20,20,20,20	0
3	AGL	A	550	10/11	0.89	0.18	-	43,43,44,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.