



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:10 AM GMT

PDB ID : 3HG2  
Title : Human alpha-galactosidase catalytic mechanism 1. Empty active site  
Authors : Guce, A.I.; Clark, N.E.; Garman, S.C.  
Deposited on : 2009-05-13  
Resolution : 2.30 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

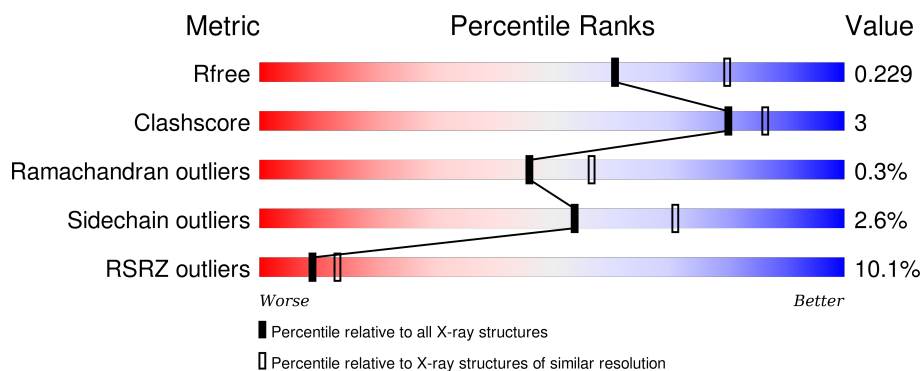
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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))
$R_{free}$	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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  $\geq 3$ , 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	398	<div> <div>9%</div> <div>91%</div> <div>6% ..</div> </div>
1	B	398	<div> <div>11%</div> <div>88%</div> <div>10% ..</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
5	SO4	A	822	-	-	-	X

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6765 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-galactosidase A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	390	Total	C	N	O	S	0	0	0
			3122	1988	534	574	26			
1	B	391	Total	C	N	O	S	0	0	0
			3131	1993	536	576	26			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	2	Total	C	N	O	0	0
			24	14	1	9		

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	3	Total	C	N	O	0	0
			39	22	2	15		
3	B	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



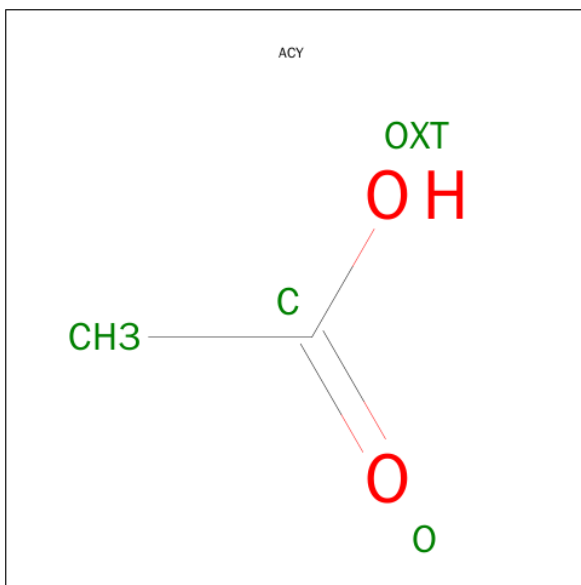
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		

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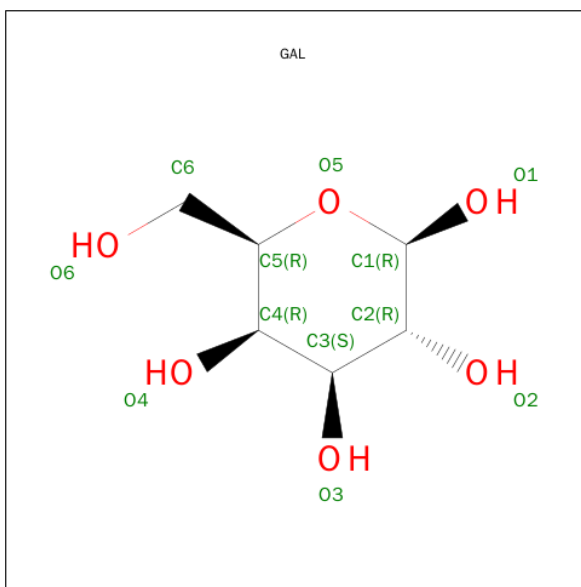
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is ACETIC ACID (three-letter code: ACY) (formula: C<sub>2</sub>H<sub>4</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		
6	B	1	Total	C	O	0	0
			4	2	2		
6	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is SUGAR (BETA-D-GALACTOSE) (three-letter code: GAL) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			12	6	6		

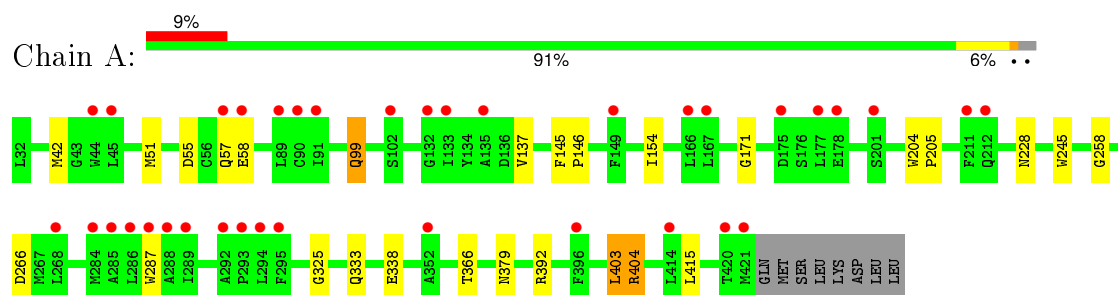
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	194	Total	O	0	0
			194	194		
8	B	135	Total	O	0	0
			135	135		

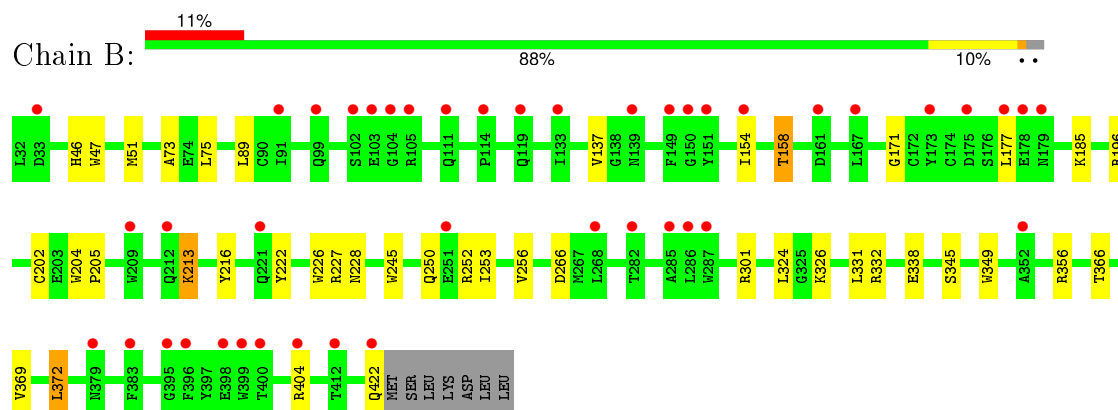
### 3 Residue-property plots [i](#)

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 ( $\text{RSRZ} > 2$ ). 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-galactosidase A



#### • Molecule 1: Alpha-galactosidase A





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.81Å 90.81Å 217.17Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	28.31 – 2.30 28.30 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.3 (28.31-2.30) 97.3 (28.30-2.30)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.38 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.176 , 0.202 0.214 , 0.229	Depositor DCC
$R_{free}$ test set	2338 reflections (5.13%)	DCC
Wilson B-factor (Å <sup>2</sup> )	33.9	Xtriage
Anisotropy	0.002	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 39.0	EDS
Estimated twinning fraction	0.029 for -h,-k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 45598 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6765	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.37% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, NAG, GAL, SO4, ACY, FUC

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	0.41	0/3209	0.55	0/4358
1	B	0.41	0/3218	0.53	0/4370
All	All	0.41	0/6427	0.54	0/8728

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-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 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	3122	0	2981	18	0
1	B	3131	0	2989	24	0
2	A	24	0	22	0	0
3	A	39	0	34	0	0
3	B	39	0	34	0	0
4	A	14	0	13	0	0
4	B	28	0	26	0	0
5	A	10	0	0	0	0
5	B	5	0	0	0	0
6	A	4	0	3	0	0
6	B	8	0	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	12	0	12	2	0
8	A	194	0	0	5	0
8	B	135	0	0	1	0
All	All	6765	0	6120	42	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 (42) 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:366:THR:HG22	1:A:404:ARG:HD3	1.75	0.68
1:A:403:LEU:HD11	1:A:415:LEU:HD13	1.78	0.64
1:B:250:GLN:NE2	7:B:803:GAL:H1	2.16	0.61
1:B:137:VAL:HG12	1:B:171:GLY:HA2	1.88	0.56
1:B:250:GLN:HE21	7:B:803:GAL:H1	1.71	0.55
1:B:75:LEU:CD1	1:B:301:ARG:HG2	2.37	0.55
1:B:154:ILE:O	1:B:158:THR:HG22	2.07	0.54
1:A:403:LEU:HD11	1:A:415:LEU:CD1	2.37	0.54
1:B:369:VAL:HA	1:B:372:LEU:HD22	1.89	0.54
1:B:213:LYS:HD2	8:B:1294:HOH:O	2.08	0.54
1:A:154:ILE:HG12	8:A:1306:HOH:O	2.07	0.54
1:A:99:GLN:HB3	8:A:1328:HOH:O	2.08	0.53
1:A:55:ASP:OD2	1:A:58:GLU:HB2	2.08	0.52
1:B:75:LEU:HD11	1:B:301:ARG:HG2	1.91	0.52
1:B:366:THR:HG22	1:B:404:ARG:HG2	1.92	0.51
1:A:42:MET:HE1	8:A:1258:HOH:O	2.10	0.51
1:A:228:ASN:HB3	1:A:245:TRP:CH2	2.46	0.50
1:B:228:ASN:HB3	1:B:245:TRP:CH2	2.47	0.49
1:A:204:TRP:HB3	1:A:205:PRO:HD3	1.95	0.49
1:B:366:THR:CG2	1:B:404:ARG:HG2	2.45	0.46
1:A:42:MET:CE	8:A:1169:HOH:O	2.63	0.46
1:A:137:VAL:HG12	1:A:171:GLY:HA2	1.99	0.45
1:A:333:GLN:HG3	1:A:338:GLU:HG2	2.00	0.44
1:B:216:TYR:HE1	1:B:228:ASN:HD21	1.65	0.44
1:B:253:ILE:O	1:B:256:VAL:HG22	2.17	0.44
1:A:204:TRP:HB3	1:A:205:PRO:CD	2.48	0.44
1:A:392:ARG:NH2	8:A:1040:HOH:O	2.47	0.43
1:B:202:CYS:O	1:B:226:TRP:HA	2.19	0.42
1:A:145:PHE:HB3	1:A:146:PRO:CD	2.49	0.42
1:B:204:TRP:HB3	1:B:205:PRO:HD3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:422:GLN:HE21	1:B:422:GLN:HB2	1.68	0.41
1:A:145:PHE:HB3	1:A:146:PRO:HD2	2.02	0.41
1:B:213:LYS:NZ	1:B:252:ARG:HH22	2.19	0.41
1:B:73:ALA:HB2	1:B:89:LEU:HD22	2.03	0.41
1:B:331:LEU:HG	1:B:332:ARG:HG3	2.01	0.41
1:A:366:THR:CG2	1:A:404:ARG:HD3	2.48	0.40
1:B:213:LYS:HG3	1:B:252:ARG:HH12	1.86	0.40
1:B:185:LYS:HG2	1:B:222:TYR:CZ	2.56	0.40
1:B:47:TRP:O	1:B:51:MET:HG2	2.21	0.40
1:A:258:GLY:HA2	1:A:325:GLY:O	2.22	0.40
1:B:338:GLU:OE2	1:B:356:ARG:NH1	2.55	0.40
1:B:205:PRO:HG2	1:B:227:ARG:O	2.22	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	388/398 (98%)	375 (97%)	12 (3%)	1 (0%)	46	57
1	B	389/398 (98%)	378 (97%)	10 (3%)	1 (0%)	46	57
All	All	777/796 (98%)	753 (97%)	22 (3%)	2 (0%)	46	57

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	266	ASP
1	B	266	ASP

### 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	331/339 (98%)	324 (98%)	7 (2%)	61	78
1	B	332/339 (98%)	322 (97%)	10 (3%)	48	65
All	All	663/678 (98%)	646 (97%)	17 (3%)	54	71

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	MET
1	A	57	GLN
1	A	99	GLN
1	A	287	TRP
1	A	379	ASN
1	A	403	LEU
1	A	404	ARG
1	B	46	HIS
1	B	158	THR
1	B	177	LEU
1	B	196	ARG
1	B	213	LYS
1	B	324	LEU
1	B	326	LYS
1	B	345	SER
1	B	349	TRP
1	B	372	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	A	111	GLN
1	A	228	ASN
1	A	249	ASN
1	A	379	ASN

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Mol	Chain	Res	Type
1	B	179	ASN
1	B	228	ASN
1	B	386	GLN
1	B	416	GLN
1	B	422	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules 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 ⓘ

8 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	NAG	A	639	1,2	14,14,15	0.46	0	15,19,21	1.04	1 (6%)
2	FUC	A	644	2	10,10,11	0.65	0	14,14,16	1.06	1 (7%)
3	NAG	A	692	1,3	14,14,15	0.47	0	15,19,21	0.81	0
3	NAG	A	693	3	14,14,15	0.49	0	15,19,21	0.79	0
3	BMA	A	694	3	11,11,12	0.43	0	14,15,17	0.85	1 (7%)
3	NAG	B	692	1,3	14,14,15	0.54	0	15,19,21	1.16	2 (13%)
3	NAG	B	693	3	14,14,15	0.51	0	15,19,21	1.06	1 (6%)
3	BMA	B	694	3	11,11,12	0.51	0	14,15,17	0.85	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
2	NAG	A	639	1,2	-	0/6/23/26	0/1/1/1
2	FUC	A	644	2	-	0/0/17/20	0/1/1/1
3	NAG	A	692	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	693	3	-	0/6/23/26	0/1/1/1
3	BMA	A	694	3	-	0/2/19/22	0/1/1/1
3	NAG	B	692	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	693	3	-	0/6/23/26	0/1/1/1
3	BMA	B	694	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	644	FUC	O5-C5-C6	2.13	109.66	106.13
3	A	694	BMA	C1-O5-C5	2.34	115.22	112.25
3	B	692	NAG	C1-O5-C5	2.40	115.29	112.25
3	B	692	NAG	C2-N2-C7	2.50	126.25	123.04
3	B	693	NAG	C4-C3-C2	2.69	115.41	111.23
2	A	639	NAG	C1-O5-C5	2.94	115.98	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.6 Ligand geometry ⓘ

10 ligands 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	$\# Z  > 2$
4	NAG	A	715	1	14,14,15	0.53	0	15,19,21	1.01	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	SO4	A	822	-	4,4,4	0.22	0	6,6,6	0.08	0
5	SO4	A	823	-	4,4,4	0.32	0	6,6,6	0.31	0
6	ACY	A	841	-	1,3,3	0.98	0	0,3,3	0.00	-
4	NAG	B	639	1	14,14,15	0.60	0	15,19,21	1.24	2 (13%)
4	NAG	B	715	1	14,14,15	0.49	0	15,19,21	0.70	0
7	GAL	B	803	-	12,12,12	0.59	0	17,17,17	0.97	1 (5%)
5	SO4	B	821	-	4,4,4	0.22	0	6,6,6	0.15	0
6	ACY	B	842	-	1,3,3	1.41	0	0,3,3	0.00	-
6	ACY	B	843	-	1,3,3	1.35	0	0,3,3	0.00	-

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
4	NAG	A	715	1	-	0/6/23/26	0/1/1/1
5	SO4	A	822	-	-	0/0/0/0	0/0/0/0
5	SO4	A	823	-	-	0/0/0/0	0/0/0/0
6	ACY	A	841	-	-	0/0/0/0	0/0/0/0
4	NAG	B	639	1	-	0/6/23/26	0/1/1/1
4	NAG	B	715	1	-	0/6/23/26	0/1/1/1
7	GAL	B	803	-	-	0/2/22/22	0/1/1/1
5	SO4	B	821	-	-	0/0/0/0	0/0/0/0
6	ACY	B	842	-	-	0/0/0/0	0/0/0/0
6	ACY	B	843	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	803	GAL	C4-C3-C2	2.01	114.55	110.79
4	B	639	NAG	C4-C3-C2	2.36	114.90	111.23
4	A	715	NAG	C1-O5-C5	2.51	115.44	112.25
4	B	639	NAG	C2-N2-C7	2.55	126.31	123.04

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	803	GAL	2	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	390/398 (97%)	0.34	36 (9%) 11 16	30, 35, 42, 51	0
1	B	391/398 (98%)	0.48	43 (10%) 7 11	30, 35, 42, 55	0
All	All	781/796 (98%)	0.41	79 (10%) 9 13	30, 35, 42, 55	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	421	MET	5.6
1	B	102	SER	5.6
1	B	149	PHE	5.4
1	A	211	PHE	5.1
1	A	102	SER	4.9
1	A	91	ILE	4.1
1	A	133	ILE	4.1
1	B	103	GLU	3.7
1	B	286	LEU	3.6
1	A	45	LEU	3.6
1	A	90	CYS	3.6
1	B	178	GLU	3.6
1	B	422	GLN	3.5
1	A	287	TRP	3.4
1	A	57	GLN	3.2
1	A	288	ALA	3.2
1	A	285	ALA	3.1
1	B	150	GLY	3.1
1	A	268	LEU	3.0
1	A	286	LEU	3.0
1	B	104	GLY	3.0
1	B	133	ILE	3.0
1	B	396	PHE	3.0
1	B	99	GLN	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	294	LEU	2.9
1	B	379	ASN	2.9
1	B	154	ILE	2.8
1	B	175	ASP	2.8
1	A	166	LEU	2.8
1	A	420	THR	2.7
1	B	119	GLN	2.7
1	A	289	ILE	2.7
1	A	295	PHE	2.7
1	B	173	TYR	2.7
1	B	352	ALA	2.6
1	A	177	LEU	2.6
1	B	395	GLY	2.6
1	A	44	TRP	2.5
1	B	398	GLU	2.5
1	A	58	GLU	2.5
1	A	175	ASP	2.5
1	A	178	GLU	2.4
1	B	151	TYR	2.4
1	B	167	LEU	2.4
1	B	177	LEU	2.4
1	B	383	PHE	2.4
1	B	33	ASP	2.4
1	B	179	ASN	2.3
1	A	89	LEU	2.3
1	A	396	PHE	2.3
1	A	167	LEU	2.3
1	A	284	MET	2.3
1	B	251	GLU	2.3
1	B	285	ALA	2.3
1	B	209	TRP	2.3
1	B	139	ASN	2.2
1	A	132	GLY	2.2
1	B	399	TRP	2.2
1	A	352	ALA	2.2
1	B	221	GLN	2.2
1	A	414	LEU	2.2
1	B	268	LEU	2.2
1	A	149	PHE	2.2
1	B	111	GLN	2.2
1	B	114	PRO	2.2
1	B	282	THR	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	404	ARG	2.1
1	A	201	SER	2.1
1	B	161	ASP	2.1
1	B	105	ARG	2.1
1	B	212	GLN	2.1
1	B	400	THR	2.1
1	B	412	THR	2.1
1	B	91	ILE	2.1
1	A	292	ALA	2.0
1	B	287	TRP	2.0
1	A	212	GLN	2.0
1	A	293	PRO	2.0
1	A	135	ALA	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](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	NAG	A	639	14/15	0.75	0.31	1.83	58,62,67,71	0
3	NAG	B	692	14/15	0.85	0.20	-0.18	52,57,60,62	0
3	NAG	A	692	14/15	0.94	0.14	-0.69	45,46,49,52	0
3	NAG	A	693	14/15	0.93	0.18	-0.74	55,58,59,62	0
3	BMA	B	694	11/12	0.43	0.34	-	72,74,74,75	0
2	FUC	A	644	10/11	0.80	0.49	-	73,75,75,76	0
3	NAG	B	693	14/15	0.87	0.27	-	63,65,67,70	0
3	BMA	A	694	11/12	0.79	0.30	-	64,66,67,67	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
5	SO4	A	822	5/5	0.88	0.41	5.58	92,92,92,93	0
4	NAG	B	639	14/15	0.70	0.37	1.23	56,61,61,61	0
5	SO4	B	821	5/5	0.98	0.18	0.64	60,60,61,61	0
7	GAL	B	803	12/12	0.71	0.20	0.35	68,68,69,69	0
5	SO4	A	823	5/5	0.98	0.10	-0.27	49,49,50,50	0
6	ACY	A	841	4/4	0.73	0.20	-	67,67,67,67	0
6	ACY	B	842	4/4	0.87	0.18	-	66,66,66,66	0
4	NAG	B	715	14/15	0.70	0.40	-	58,62,64,65	0
4	NAG	A	715	14/15	0.91	0.24	-	53,57,58,58	0
6	ACY	B	843	4/4	0.93	0.15	-	70,70,70,70	0

## 6.5 Other polymers

There are no such residues in this entry.