



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:51 PM GMT

PDB ID : 4DO6
Title : Pharmacological chaperones for human alpha-N-acetylgalactosaminidase
Authors : Clark, N.E.; Garman, S.C.
Deposited on : 2012-02-09
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
<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 (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

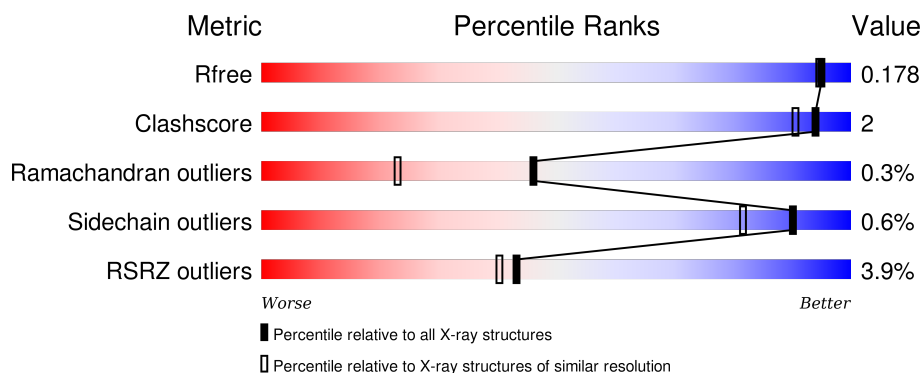
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

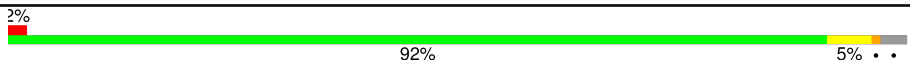
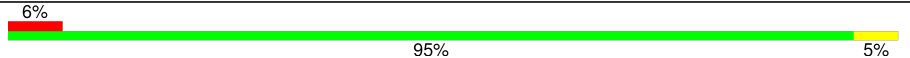
The reported resolution of this entry is 1.60 Å.

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))
R_{free}	91344	2475 (1.60-1.60)
Clashscore	102246	2732 (1.60-1.60)
Ramachandran outliers	100387	2654 (1.60-1.60)
Sidechain outliers	100360	2653 (1.60-1.60)
RSRZ outliers	91569	2479 (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 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	400	 2% 92% 5% . .
1	B	400	 6% 95% 5%

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	CIT	A	510	-	-	-	X

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 7426 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-N-acetylgalactosaminidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	388	Total	C	N	O	S	0	6	0
			3137	2001	531	577	28			
1	B	400	Total	C	N	O	S	0	2	0
			3209	2044	548	589	28			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	201	GLN	ASN	ENGINEERED MUTATION	UNP P17050
A	412	HIS	-	EXPRESSION TAG	UNP P17050
A	413	HIS	-	EXPRESSION TAG	UNP P17050
A	414	HIS	-	EXPRESSION TAG	UNP P17050
A	415	HIS	-	EXPRESSION TAG	UNP P17050
A	416	HIS	-	EXPRESSION TAG	UNP P17050
A	417	HIS	-	EXPRESSION TAG	UNP P17050
B	201	GLN	ASN	ENGINEERED MUTATION	UNP P17050
B	412	HIS	-	EXPRESSION TAG	UNP P17050
B	413	HIS	-	EXPRESSION TAG	UNP P17050
B	414	HIS	-	EXPRESSION TAG	UNP P17050
B	415	HIS	-	EXPRESSION TAG	UNP P17050
B	416	HIS	-	EXPRESSION TAG	UNP P17050
B	417	HIS	-	EXPRESSION TAG	UNP P17050

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

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

- Molecule 3 is a polymer of unknown type called SUGAR (5-MER).

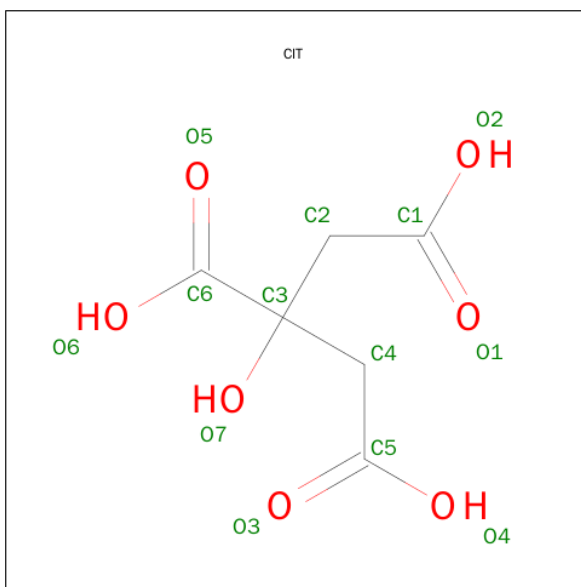
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	5	Total	C	N	O	0	0
			61	34	2	25		
3	B	5	Total	C	N	O	0	0
			61	34	2	25		

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



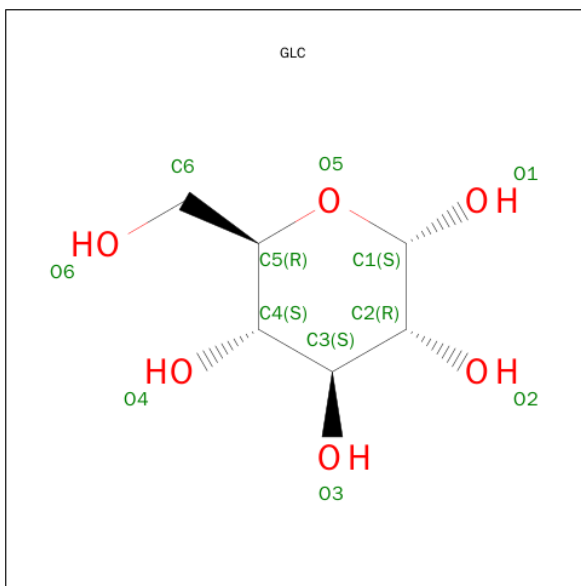
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			13	6	7		

- Molecule 6 is SUGAR (ALPHA-D-GLUCOSE) (three-letter code: GLC) (formula: $C_6H_{12}O_6$).

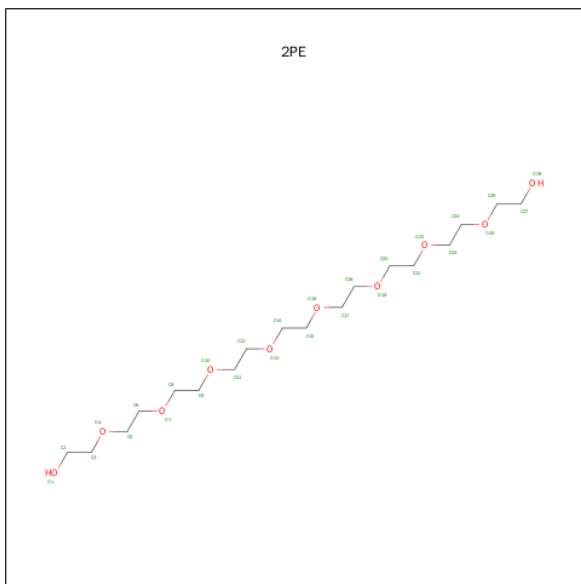


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			12	6	6		
6	A	1	Total	C	O	0	0
			12	6	6		
6	B	1	Total	C	O	0	0
			12	6	6		

- Molecule 7 is a polymer of unknown type called SUGAR (3-MER).

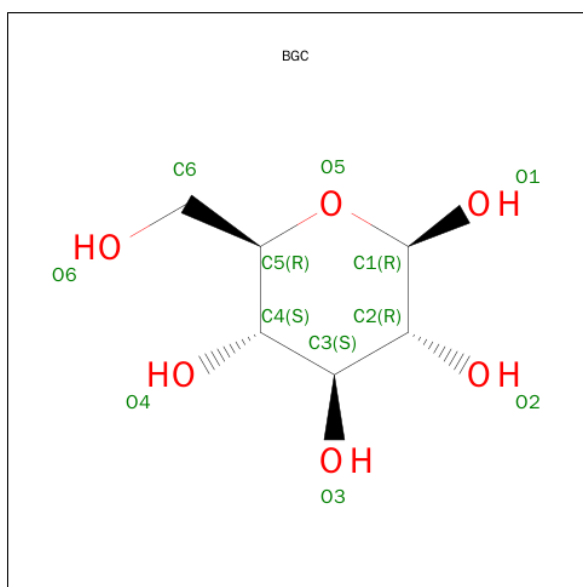
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 8 is NONAETHYLENE GLYCOL (three-letter code: 2PE) (formula: $C_{18}H_{38}O_{10}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			3	2	1		
8	B	1	Total	C	O	0	0
			3	2	1		

- Molecule 9 is SUGAR (BETA-D-GLUCOSE) (three-letter code: BGC) (formula: $C_6H_{12}O_6$).



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

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	445	Total	O	0	0
			445	445		
10	B	341	Total	O	0	0
			341	341		

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 ($RSRZ > 2$). 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.

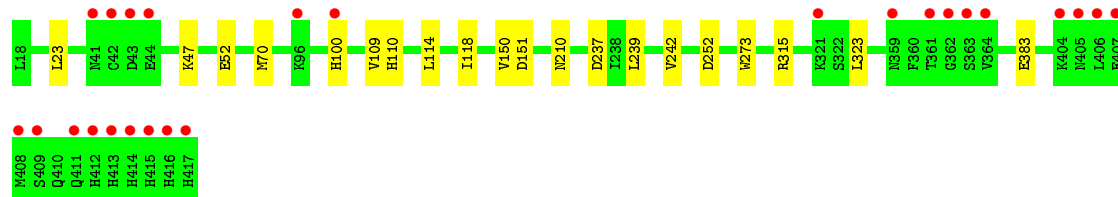
- Molecule 1: Alpha-N-acetylgalactosaminidase

Chain A: 



- Molecule 1: Alpha-N-acetylgalactosaminidase

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	153.31Å 114.30Å 68.57Å 90.00° 96.43° 90.00°	Depositor
Resolution (Å)	43.79 – 1.60 39.20 – 1.60	Depositor EDS
% Data completeness (in resolution range)	94.7 (43.79-1.60) 94.7 (39.20-1.60)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.28 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.154 , 0.170 0.162 , 0.178	Depositor DCC
R_{free} test set	7782 reflections (5.63%)	DCC
Wilson B-factor (Å ²)	21.7	Xtriage
Anisotropy	0.080	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 49.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 145693 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7426	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.65% 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, 0.375 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: BGC, NAG, GLC, BMA, 2PE, FUC, CIT, MAN

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	0.43	0/3225	0.66	2/4385 (0.0%)
1	B	0.40	0/3303	0.59	0/4492
All	All	0.42	0/6528	0.62	2/8877 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	315[A]	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	A	315[B]	ARG	NE-CZ-NH2	-5.46	117.57	120.30

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	3137	0	3031	12	0
1	B	3209	0	3082	11	0
2	A	39	0	34	0	0
3	A	61	0	52	0	0
3	B	61	0	52	0	0
4	A	14	0	13	1	0
4	B	14	0	13	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	13	0	5	0	0
6	A	24	0	24	0	0
6	B	12	0	12	0	0
7	B	38	0	34	0	0
8	B	6	0	4	0	0
9	B	12	0	12	1	0
10	A	445	0	0	2	0
10	B	341	0	0	2	0
All	All	7426	0	6368	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 2.

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:128:MET:SD	10:A:890:HOH:O	2.35	0.83
1:B:70:MET:HE3	10:B:922:HOH:O	1.93	0.69
1:A:275[A]:VAL:HG11	1:A:339:VAL:HG23	1.77	0.66
1:A:90:ARG:HD3	10:A:755:HOH:O	2.01	0.60
1:B:110:HIS:HE1	1:B:151:ASP:OD2	1.86	0.58
1:A:109:VAL:HG13	1:A:114:LEU:HB2	1.84	0.58
1:B:110:HIS:HD2	10:B:905:HOH:O	1.87	0.58
1:B:237:ASP:OD1	1:B:315:ARG:NH2	2.37	0.54
1:A:240:GLN:HG3	1:A:315[A]:ARG:HG2	1.91	0.52
1:A:237:ASP:OD1	1:A:315[A]:ARG:NH2	2.44	0.51
1:B:239:LEU:O	1:B:242:VAL:HG22	2.14	0.47
1:A:275[A]:VAL:HG11	1:A:339:VAL:CG2	2.43	0.46
1:A:383:GLU:O	4:A:509:NAG:H82	2.16	0.45
1:A:118:ILE:HG22	1:A:150:VAL:HG11	1.99	0.45
1:B:383:GLU:O	4:B:509:NAG:H82	2.17	0.44
1:B:118:ILE:HG22	1:B:150:VAL:HG11	2.00	0.44
1:B:109:VAL:HG13	1:B:114:LEU:HB2	2.00	0.43
1:A:404:LYS:O	1:A:405:ASN:HB2	2.18	0.43
1:B:323:LEU:HD12	9:B:511:BGC:H6C2	2.01	0.43
1:B:52:GLU:OE2	1:B:100:HIS:HD2	2.03	0.42
1:A:312:ILE:HG21	1:A:330:PRO:HG2	2.01	0.42
1:A:360:PHE:CE1	1:A:400:LEU:HD23	2.55	0.41
1:B:23:LEU:HD12	1:B:210:ASN:HB3	2.02	0.41

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	392/400 (98%)	379 (97%)	12 (3%)	1 (0%)	46	23
1	B	400/400 (100%)	388 (97%)	11 (3%)	1 (0%)	46	23
All	All	792/800 (99%)	767 (97%)	23 (3%)	2 (0%)	46	23

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	252	ASP
1	B	252	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	340/346 (98%)	338 (99%)	2 (1%)	90	82
1	B	348/346 (101%)	346 (99%)	2 (1%)	90	82
All	All	688/692 (99%)	684 (99%)	4 (1%)	90	82

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	273	TRP
1	A	404	LYS
1	B	47	LYS
1	B	273	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	143	GLN
1	A	235	HIS
1	B	100	HIS
1	B	110	HIS
1	B	143	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 ⓘ

16 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	501	1,2	14,14,15	0.54	0	15,19,21	1.14	1 (6%)
2	NAG	A	502	2	14,14,15	0.52	0	15,19,21	0.81	0
2	BMA	A	503	2	11,11,12	0.29	0	14,15,17	0.72	0
3	NAG	A	504	1,3	14,14,15	0.57	0	15,19,21	0.57	0
3	NAG	A	505	3	14,14,15	0.53	0	15,19,21	0.64	0
3	BMA	A	506	3	11,11,12	0.38	0	14,15,17	0.92	0
3	MAN	A	507	3	11,11,12	0.56	0	14,15,17	0.87	1 (7%)
3	MAN	A	508	3	11,11,12	0.56	0	14,15,17	1.00	2 (14%)
7	NAG	B	501	1,7	14,14,15	0.47	0	15,19,21	0.85	1 (6%)
7	NAG	B	502	7	14,14,15	0.52	0	15,19,21	0.67	0
7	FUC	B	503	7	10,10,11	0.55	0	14,14,16	0.87	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	B	504	1,3	14,14,15	0.59	0	15,19,21	0.74	0
3	NAG	B	505	3	14,14,15	0.55	0	15,19,21	0.85	1 (6%)
3	BMA	B	506	3	11,11,12	0.37	0	14,15,17	0.77	0
3	MAN	B	507	3	11,11,12	0.58	0	14,15,17	0.83	0
3	MAN	B	508	3	11,11,12	0.53	0	14,15,17	1.21	2 (14%)

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	501	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	502	2	-	0/6/23/26	0/1/1/1
2	BMA	A	503	2	-	0/2/19/22	0/1/1/1
3	NAG	A	504	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	505	3	-	0/6/23/26	0/1/1/1
3	BMA	A	506	3	-	0/2/19/22	0/1/1/1
3	MAN	A	507	3	-	0/2/19/22	0/1/1/1
3	MAN	A	508	3	-	0/2/19/22	0/1/1/1
7	NAG	B	501	1,7	-	0/6/23/26	0/1/1/1
7	NAG	B	502	7	-	0/6/23/26	0/1/1/1
7	FUC	B	503	7	-	0/0/17/20	0/1/1/1
3	NAG	B	504	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	505	3	-	0/6/23/26	0/1/1/1
3	BMA	B	506	3	-	0/2/19/22	0/1/1/1
3	MAN	B	507	3	-	0/2/19/22	0/1/1/1
3	MAN	B	508	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	505	NAG	O4-C4-C3	-2.03	105.76	110.34
3	A	508	MAN	C1-C2-C3	2.06	111.98	109.54
2	A	501	NAG	O7-C7-N2	2.06	126.07	121.86
7	B	501	NAG	C1-O5-C5	2.18	115.02	112.25
3	B	508	MAN	C1-C2-C3	2.28	112.24	109.54
3	A	507	MAN	C1-C2-C3	2.29	112.25	109.54
3	A	508	MAN	C1-O5-C5	2.41	115.31	112.25
3	B	508	MAN	C1-O5-C5	3.52	116.72	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

9 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	509	1	14,14,15	0.48	0	15,19,21	0.84	1 (6%)
5	CIT	A	510	-	3,12,12	0.65	0	3,17,17	1.10	0
6	GLC	A	511	-	12,12,12	0.48	0	17,17,17	0.93	0
6	GLC	A	512	-	12,12,12	0.48	0	17,17,17	0.60	0
4	NAG	B	509	1	14,14,15	0.44	0	15,19,21	0.84	1 (6%)
8	2PE	B	510	-	2,2,27	0.45	0	1,1,26	0.34	0
9	BGC	B	511	-	12,12,12	0.52	0	17,17,17	0.64	0
6	GLC	B	512	-	12,12,12	0.43	0	17,17,17	0.76	0
8	2PE	B	513	-	2,2,27	0.46	0	1,1,26	0.33	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
4	NAG	A	509	1	-	0/6/23/26	0/1/1/1
5	CIT	A	510	-	-	0/6/16/16	0/0/0/0
6	GLC	A	511	-	-	0/2/22/22	0/1/1/1
6	GLC	A	512	-	-	0/2/22/22	0/1/1/1
4	NAG	B	509	1	-	0/6/23/26	0/1/1/1
8	2PE	B	510	-	-	0/0/0/25	0/0/0/0
9	BGC	B	511	-	-	0/2/22/22	0/1/1/1
6	GLC	B	512	-	-	0/2/22/22	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	2PE	B	513	-	-	0/0/0/25	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	509	NAG	C1-O5-C5	2.43	115.33	112.25
4	A	509	NAG	C1-O5-C5	2.46	115.38	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	509	NAG	1	0
4	B	509	NAG	1	0
9	B	511	BGC	1	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, 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	388/400 (97%)	-0.34	6 (1%) 76 75	13, 21, 42, 72	0
1	B	400/400 (100%)	-0.01	25 (6%) 23 21	14, 28, 55, 123	0
All	All	788/800 (98%)	-0.17	31 (3%) 43 40	13, 24, 51, 123	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	417	HIS	11.8
1	B	415	HIS	9.2
1	A	361	THR	7.8
1	B	408	MET	6.3
1	B	413	HIS	5.9
1	B	363	SER	5.5
1	B	412	HIS	5.1
1	B	42	CYS	4.5
1	B	409	SER	4.1
1	B	416	HIS	4.1
1	A	363	SER	4.1
1	B	414	HIS	3.9
1	B	361	THR	3.7
1	B	407	GLU	3.3
1	B	406	LEU	3.3
1	B	405	ASN	3.3
1	A	362	GLY	3.2
1	B	411	GLN	3.1
1	A	405	ASN	2.9
1	B	43	ASP	2.9
1	B	359	ASN	2.7
1	B	404	LYS	2.6
1	B	41	ASN	2.5
1	A	383	GLU	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	96	LYS	2.5
1	B	364	VAL	2.4
1	B	100	HIS	2.4
1	A	360	PHE	2.3
1	B	321	LYS	2.3
1	B	44	GLU	2.2
1	B	362	GLY	2.1

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, 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
3	NAG	A	504	14/15	0.95	0.10	0.66	21,29,39,42	0
3	NAG	B	504	14/15	0.97	0.06	-0.65	19,26,32,37	0
3	NAG	B	505	14/15	0.95	0.13	-	25,36,47,54	0
3	NAG	A	505	14/15	0.91	0.19	-	27,36,50,53	0
7	NAG	B	501	14/15	0.78	0.21	-	58,66,96,105	0
2	NAG	A	502	14/15	0.88	0.36	-	59,67,85,91	0
2	BMA	A	503	11/12	0.42	0.46	-	86,97,101,102	0
3	BMA	B	506	11/12	0.83	0.29	-	53,72,88,99	0
3	BMA	A	506	11/12	0.89	0.17	-	31,47,65,80	0
3	MAN	A	507	11/12	0.64	0.25	-	74,87,93,96	0
3	MAN	A	508	11/12	0.74	0.50	-	96,101,106,108	0
7	NAG	B	502	14/15	0.60	0.47	-	84,107,112,112	0
2	NAG	A	501	14/15	0.81	0.22	-	39,47,57,63	0
3	MAN	B	507	11/12	0.72	0.30	-	83,92,96,99	0
7	FUC	B	503	10/11	0.65	0.56	-	114,120,122,123	0
3	MAN	B	508	11/12	0.45	0.59	-	111,115,120,122	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, 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
5	CIT	A	510	13/13	0.94	0.24	4.67	33,45,57,62	0
6	GLC	B	512	12/12	0.91	0.10	1.98	23,33,43,48	0
6	GLC	A	511	12/12	0.91	0.16	1.57	26,57,65,69	0
9	BGC	B	511	12/12	0.86	0.17	1.20	26,50,60,62	0
6	GLC	A	512	12/12	0.95	0.09	0.03	21,31,43,43	0
8	2PE	B	510	3/28	0.84	0.09	-	58,58,60,65	0
8	2PE	B	513	3/28	0.82	0.07	-	57,57,58,60	0
4	NAG	B	509	14/15	0.80	0.36	-	75,91,100,101	0
4	NAG	A	509	14/15	0.81	0.36	-	69,83,97,97	0

6.5 Other polymers [i](#)

There are no such residues in this entry.