



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 11:29 am GMT

PDB ID : 2E7T  
Title : Crystal structure of basic winged bean lectin in complex with a blood group trisaccharide  
Authors : Kulkarni, K.A.; Katiyar, S.; Surolia, A.; Vijayan, M.; Suguna, K.  
Deposited on : 2007-01-13  
Resolution : 2.65 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](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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
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)	:	recalc28949

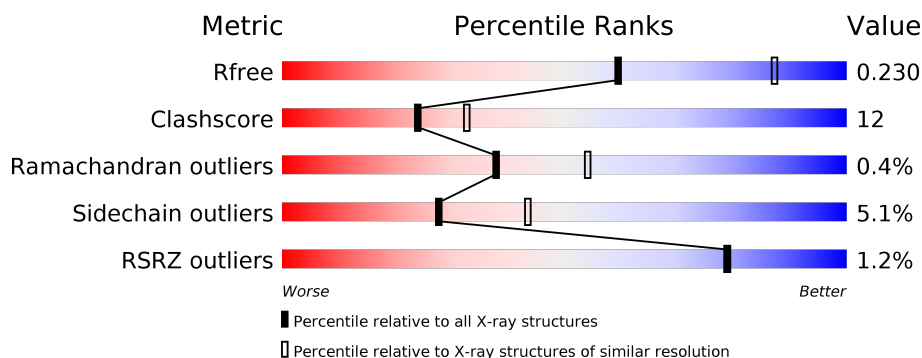
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.65 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	3491 (2.70-2.62)
Clashscore	112137	1026 (2.68-2.64)
Ramachandran outliers	110173	1010 (2.68-2.64)
Sidechain outliers	110143	1010 (2.68-2.64)
RSRZ outliers	101464	3511 (2.70-2.62)

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	237	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 73%, green 23%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> <span>%</span> <span>73%</span> <span>23%</span> <span>•</span> </div> </div>
1	B	237	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 83%, green 15%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> <span>%</span> <span>83%</span> <span>15%</span> <span>•</span> </div> </div>
1	C	237	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 72%, green 25%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> <span>%</span> <span>72%</span> <span>25%</span> <span>•</span> </div> </div>
1	D	237	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 77%, green 20%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> <span>%</span> <span>77%</span> <span>20%</span> <span>•</span> </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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	B	501	-	-	-	X
2	NAG	B	603	-	-	X	-
4	NAG	C	501	-	-	-	X
4	BMA	C	504	-	-	-	X

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 7945 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 Basic agglutinin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	236	Total	C	N	O	0	0	0
			1831	1177	307	347			
1	B	237	Total	C	N	O	0	0	0
			1823	1174	303	346			
1	C	237	Total	C	N	O	0	0	0
			1825	1175	304	346			
1	D	237	Total	C	N	O	0	0	0
			1810	1168	299	343			

- 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
			38	22	2	14		
2	A	3	Total	C	N	O	0	0
			38	22	2	14		
2	B	3	Total	C	N	O	0	0
			38	22	2	14		
2	B	3	Total	C	N	O	0	0
			38	22	2	14		
2	D	3	Total	C	N	O	0	0
			38	22	2	14		
2	D	3	Total	C	N	O	0	0
			38	22	2	14		

- 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
			37	20	1	16		
3	B	3	Total	C	N	O	0	0
			37	20	1	16		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	C	3	Total	C	N	O	0	0
			37	20	1	16		

- Molecule 4 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	C	4	Total	C	N	O	0	0
			49	28	2	19		

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	C	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 6 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Mn	0	0
			1	1		
6	A	1	Total	Mn	0	0
			1	1		
6	D	1	Total	Mn	0	0
			1	1		
6	C	1	Total	Mn	0	0
			1	1		

- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total	Ca	0	0
			1	1		
7	A	1	Total	Ca	0	0
			1	1		
7	D	1	Total	Ca	0	0
			1	1		
7	C	1	Total	Ca	0	0
			1	1		

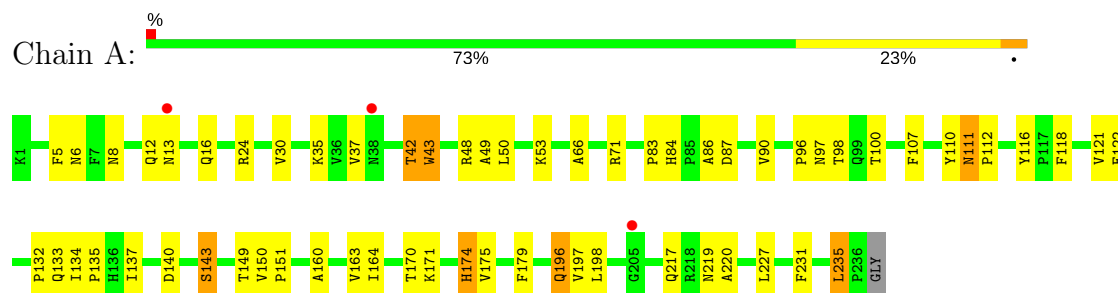
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	76	Total 76	O 76	0	0
8	B	57	Total 57	O 57	0	0
8	C	46	Total 46	O 46	0	0
8	D	53	Total 53	O 53	0	0

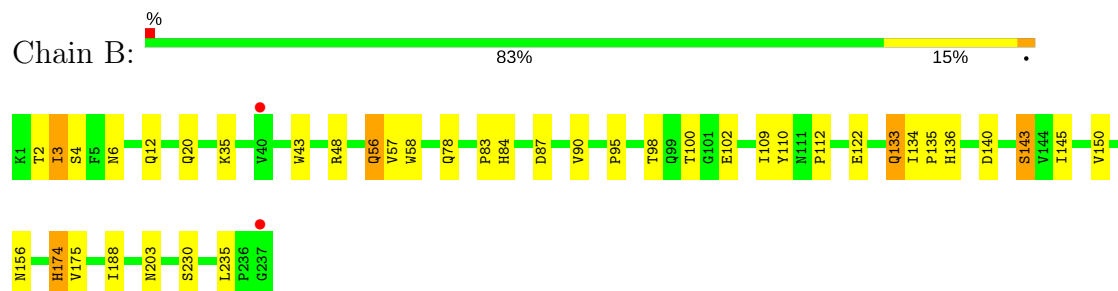
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

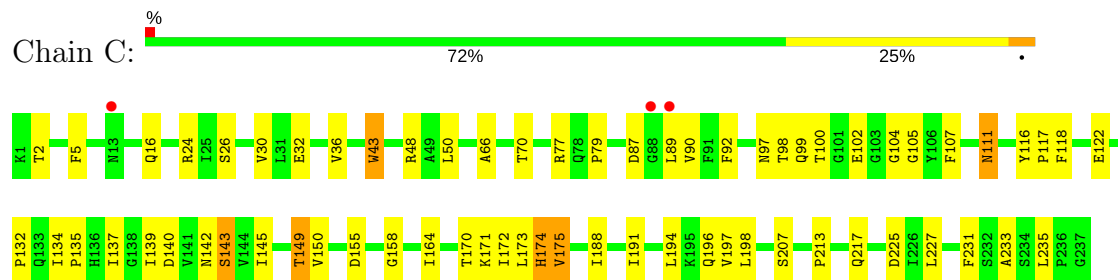
#### • Molecule 1: Basic agglutinin



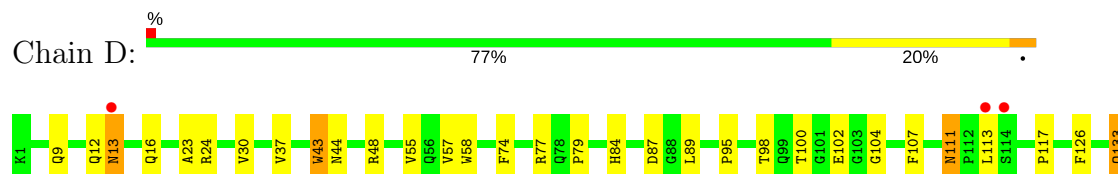
#### • Molecule 1: Basic agglutinin



#### • Molecule 1: Basic agglutinin



#### • Molecule 1: Basic agglutinin



I134	P135	D140	S143	V144	I145	F152	D155	G158	I164	T170	K171	I172	L173	H174	V175	Y186	T191	V197	L198	D212	P213	Q217	A220	L235	P236	G237
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	157.73Å 91.13Å 73.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.00 – 2.65 29.00 – 2.64	Depositor EDS
% Data completeness (in resolution range)	96.4 (29.00-2.65) 95.7 (29.00-2.64)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.92 (at 2.64Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.192 , 0.244 0.186 , 0.230	Depositor DCC
$R_{free}$ test set	1219 reflections (4.16%)	DCC
Wilson B-factor (Å <sup>2</sup> )	42.1	Xtriage
Anisotropy	0.542	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 48.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7945	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% 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, 0.333 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: A2G, BMA, NAG, CA, GLC, GAL, FUC, MN

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	0.51	0/1884	0.69	0/2580
1	B	0.52	0/1876	0.69	0/2571
1	C	0.47	0/1878	0.70	0/2571
1	D	0.48	0/1862	0.68	0/2554
All	All	0.50	0/7500	0.69	0/10276

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 [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	1831	0	1773	39	0
1	B	1823	0	1756	29	0
1	C	1825	0	1765	52	0
1	D	1810	0	1741	48	0
2	A	76	0	68	5	0
2	B	76	0	68	11	0
2	D	76	0	68	7	0
3	A	37	0	33	2	0
3	B	37	0	33	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	37	0	33	4	0
4	C	49	0	43	2	0
5	C	28	0	25	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
8	A	76	0	0	2	0
8	B	57	0	0	1	0
8	C	46	0	0	2	0
8	D	53	0	0	2	0
All	All	7945	0	7406	189	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 12.

The worst 5 of 189 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:D:111:ASN:HD21	1:D:113:LEU:HD23	1.26	0.98
1:A:196:GLN:HE22	1:D:145:ILE:HB	1.38	0.89
1:D:111:ASN:ND2	1:D:113:LEU:HD23	1.96	0.81
2:B:602:FUC:H5	2:B:603:NAG:C1	2.11	0.81
1:C:16:GLN:NE2	1:C:16:GLN:HA	1.96	0.78

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	234/237 (99%)	222 (95%)	11 (5%)	1 (0%)	38	54
1	B	235/237 (99%)	225 (96%)	10 (4%)	0	100	100
1	C	235/237 (99%)	225 (96%)	9 (4%)	1 (0%)	38	54
1	D	235/237 (99%)	223 (95%)	10 (4%)	2 (1%)	20	31
All	All	939/948 (99%)	895 (95%)	40 (4%)	4 (0%)	38	54

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	107	PHE
1	D	13	ASN
1	C	107	PHE
1	D	107	PHE

### 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	203/206 (98%)	191 (94%)	12 (6%)	23	36
1	B	200/206 (97%)	188 (94%)	12 (6%)	22	36
1	C	201/206 (98%)	194 (96%)	7 (4%)	41	60
1	D	197/206 (96%)	187 (95%)	10 (5%)	28	43
All	All	801/824 (97%)	760 (95%)	41 (5%)	28	43

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	102	GLU
1	B	175	VAL
1	D	133	GLN
1	B	133	GLN
1	B	143	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such

sidechains are listed below:

Mol	Chain	Res	Type
1	B	133	GLN
1	C	16	GLN
1	D	111	ASN
1	B	174	HIS
1	B	217	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 ⓘ

33 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	$\# Z  > 2$
3	A2G	A	400	3	14,14,15	0.85	0	15,19,21	1.00	1 (6%)
3	GAL	A	401	3	11,11,12	0.48	0	13,15,17	0.92	2 (15%)
3	GLC	A	402	3	12,12,12	0.66	0	17,17,17	0.58	0
2	NAG	A	501	1,2	14,14,15	0.62	0	15,19,21	0.88	1 (6%)
2	FUC	A	502	2	9,10,11	0.50	0	13,14,16	0.45	0
2	NAG	A	503	2	14,14,15	0.64	0	15,19,21	0.68	0
2	NAG	A	601	1,2	14,14,15	0.77	0	15,19,21	1.19	2 (13%)
2	FUC	A	602	2	9,10,11	0.72	0	13,14,16	0.43	0
2	NAG	A	603	2	14,14,15	0.67	0	15,19,21	0.89	1 (6%)
3	A2G	B	400	3	14,14,15	0.97	0	15,19,21	0.88	1 (6%)
3	GAL	B	401	3	11,11,12	0.84	0	13,15,17	0.90	1 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	GLC	B	402	3	12,12,12	0.53	0	17,17,17	0.61	0
2	NAG	B	501	1,2	14,14,15	0.61	0	15,19,21	0.78	0
2	FUC	B	502	2	9,10,11	0.56	0	13,14,16	0.45	0
2	NAG	B	503	2	14,14,15	0.58	0	15,19,21	0.79	1 (6%)
2	NAG	B	601	1,2	14,14,15	0.75	0	15,19,21	0.76	0
2	FUC	B	602	2	9,10,11	0.53	0	13,14,16	0.51	0
2	NAG	B	603	2	14,14,15	0.73	1 (7%)	15,19,21	0.77	0
3	A2G	C	400	3	14,14,15	0.74	0	15,19,21	1.96	2 (13%)
3	GAL	C	401	3	11,11,12	1.26	1 (9%)	13,15,17	1.36	3 (23%)
3	GLC	C	402	3	12,12,12	1.35	1 (8%)	17,17,17	0.87	0
4	NAG	C	501	1,4	14,14,15	0.64	0	15,19,21	0.85	1 (6%)
4	FUC	C	502	4	9,10,11	0.57	0	13,14,16	0.40	0
4	NAG	C	503	4	14,14,15	0.65	0	15,19,21	0.70	0
4	BMA	C	504	4	11,11,12	0.74	0	13,15,17	0.95	1 (7%)
5	NAG	C	601	1,5	14,14,15	0.74	0	15,19,21	0.81	0
5	NAG	C	603	5	14,14,15	0.65	0	15,19,21	0.75	0
2	NAG	D	501	1,2	14,14,15	0.57	0	15,19,21	0.69	0
2	FUC	D	502	2	9,10,11	0.83	0	13,14,16	0.41	0
2	NAG	D	503	2	14,14,15	0.57	0	15,19,21	0.83	1 (6%)
2	NAG	D	601	1,2	14,14,15	0.58	0	15,19,21	0.86	0
2	FUC	D	602	2	9,10,11	0.61	0	13,14,16	0.52	0
2	NAG	D	603	2	14,14,15	0.67	0	15,19,21	0.76	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
3	A2G	A	400	3	-	0/6/23/26	0/1/1/1
3	GAL	A	401	3	-	0/2/19/22	0/1/1/1
3	GLC	A	402	3	-	0/2/22/22	0/1/1/1
2	NAG	A	501	1,2	-	0/6/23/26	0/1/1/1
2	FUC	A	502	2	-	0/0/17/20	0/1/1/1
2	NAG	A	503	2	-	0/6/23/26	0/1/1/1
2	NAG	A	601	1,2	-	0/6/23/26	0/1/1/1
2	FUC	A	602	2	-	0/0/17/20	0/1/1/1
2	NAG	A	603	2	-	0/6/23/26	0/1/1/1
3	A2G	B	400	3	-	0/6/23/26	0/1/1/1
3	GAL	B	401	3	-	0/2/19/22	0/1/1/1
3	GLC	B	402	3	-	0/2/22/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	501	1,2	-	0/6/23/26	0/1/1/1
2	FUC	B	502	2	-	0/0/17/20	0/1/1/1
2	NAG	B	503	2	-	0/6/23/26	0/1/1/1
2	NAG	B	601	1,2	-	0/6/23/26	0/1/1/1
2	FUC	B	602	2	-	0/0/17/20	0/1/1/1
2	NAG	B	603	2	-	0/6/23/26	0/1/1/1
3	A2G	C	400	3	-	0/6/23/26	0/1/1/1
3	GAL	C	401	3	-	0/2/19/22	0/1/1/1
3	GLC	C	402	3	-	0/2/22/22	0/1/1/1
4	NAG	C	501	1,4	-	0/6/23/26	0/1/1/1
4	FUC	C	502	4	-	0/0/17/20	0/1/1/1
4	NAG	C	503	4	-	0/6/23/26	0/1/1/1
4	BMA	C	504	4	-	0/2/19/22	1/1/1/1
5	NAG	C	601	1,5	-	0/6/23/26	0/1/1/1
5	NAG	C	603	5	-	0/6/23/26	0/1/1/1
2	NAG	D	501	1,2	-	0/6/23/26	0/1/1/1
2	FUC	D	502	2	-	0/0/17/20	0/1/1/1
2	NAG	D	503	2	-	0/6/23/26	0/1/1/1
2	NAG	D	601	1,2	-	0/6/23/26	0/1/1/1
2	FUC	D	602	2	-	0/0/17/20	0/1/1/1
2	NAG	D	603	2	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	401	GAL	C2-C3	-3.23	1.48	1.52
2	B	603	NAG	C1-C2	2.16	1.55	1.52
3	C	402	GLC	O4-C4	2.59	1.48	1.43

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	401	GAL	C3-C4-C5	-2.99	104.94	110.22
2	A	603	NAG	C2-N2-C7	-2.68	119.04	122.94
2	A	501	NAG	C2-N2-C7	-2.40	119.44	122.94
3	C	400	A2G	C8-C7-N2	-2.37	111.84	116.11
4	C	501	NAG	C2-N2-C7	-2.30	119.58	122.94

There are no chirality outliers.

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	504	BMA	C1-C2-C3-C4-C5-O5

23 monomers are involved in 33 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	401	GAL	2	0
3	A	402	GLC	2	0
2	A	501	NAG	1	0
2	A	601	NAG	4	0
2	A	602	FUC	4	0
3	B	401	GAL	2	0
3	B	402	GLC	2	0
2	B	501	NAG	3	0
2	B	502	FUC	3	0
2	B	601	NAG	3	0
2	B	602	FUC	4	0
2	B	603	NAG	8	0
3	C	400	A2G	1	0
3	C	401	GAL	2	0
3	C	402	GLC	3	0
4	C	501	NAG	1	0
4	C	503	NAG	1	0
4	C	504	BMA	1	0
2	D	501	NAG	1	0
2	D	503	NAG	1	0
2	D	601	NAG	4	0
2	D	602	FUC	3	0
2	D	603	NAG	2	0

## 5.6 Ligand geometry

Of 8 ligands modelled in this entry, 8 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.

No monomer is involved in short contacts.



## 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 [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, 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	236/237 (99%)	-0.30	3 (1%) 77 77	21, 33, 52, 63	0
1	B	237/237 (100%)	-0.30	2 (0%) 86 86	20, 34, 55, 64	0
1	C	237/237 (100%)	-0.27	3 (1%) 77 77	25, 36, 55, 73	0
1	D	237/237 (100%)	-0.27	3 (1%) 77 77	24, 36, 59, 70	0
All	All	947/948 (99%)	-0.28	11 (1%) 79 79	20, 35, 56, 73	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	237	GLY	3.7
1	D	113	LEU	3.0
1	C	89	LEU	2.8
1	D	13	ASN	2.7
1	C	13	ASN	2.5

### 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( $\text{\AA}^2$ )	Q<0.9
4	NAG	C	501	14/15	0.90	0.20	4.35	49,53,56,58	0
4	BMA	C	504	11/12	0.77	0.22	3.70	67,69,70,71	0
2	NAG	B	501	14/15	0.87	0.26	2.60	49,55,62,63	0
2	NAG	D	501	14/15	0.91	0.23	1.55	60,66,71,75	0
3	A2G	C	400	14/15	0.94	0.19	1.02	41,46,48,50	0
2	NAG	B	601	14/15	0.86	0.28	0.77	53,59,66,71	0
3	A2G	A	400	14/15	0.90	0.19	0.71	41,46,48,50	0
3	A2G	B	400	14/15	0.96	0.17	0.18	40,43,44,45	0
2	NAG	A	501	14/15	0.92	0.15	-0.24	45,48,55,55	0
3	GLC	C	402	12/12	0.79	0.35	-	63,65,68,69	0
2	NAG	B	503	14/15	0.86	0.33	-	65,68,69,70	0
2	FUC	A	602	10/11	0.59	0.36	-	81,84,85,86	0
3	GLC	B	402	12/12	0.72	0.40	-	57,66,67,67	0
2	NAG	A	503	14/15	0.87	0.25	-	56,60,63,65	0
2	NAG	D	601	14/15	0.91	0.22	-	62,67,75,77	0
2	NAG	A	601	14/15	0.82	0.29	-	64,70,78,80	0
2	NAG	D	603	14/15	0.83	0.31	-	82,86,87,88	0
4	FUC	C	502	10/11	0.94	0.23	-	60,62,64,65	0
5	NAG	C	603	14/15	0.84	0.27	-	78,79,81,83	0
3	GLC	A	402	12/12	0.53	0.45	-	63,65,68,69	0
2	NAG	D	503	14/15	0.82	0.38	-	79,81,85,85	0
5	NAG	C	601	14/15	0.77	0.23	-	64,69,77,80	0
2	FUC	A	502	10/11	0.92	0.17	-	57,58,59,59	0
2	FUC	B	502	10/11	0.77	0.27	-	67,69,70,71	0
2	NAG	A	603	14/15	0.77	0.36	-	85,88,89,90	0
2	NAG	B	603	14/15	0.77	0.39	-	75,79,80,81	0
2	FUC	B	602	10/11	0.90	0.33	-	61,62,63,63	0
4	NAG	C	503	14/15	0.89	0.18	-	53,59,64,65	0
3	GAL	B	401	11/12	0.90	0.16	-	45,50,53,55	0
3	GAL	A	401	11/12	0.82	0.21	-	55,61,62,63	0
3	GAL	C	401	11/12	0.85	0.16	-	55,61,62,63	0
2	FUC	D	502	10/11	0.81	0.29	-	72,74,75,75	0
2	FUC	D	602	10/11	0.74	0.44	-	79,81,83,84	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( $\text{\AA}^2$ )	Q<0.9
7	CA	A	303	1/1	0.98	0.16	-0.25	30,30,30,30	0
7	CA	C	2303	1/1	0.95	0.14	-0.41	31,31,31,31	0
7	CA	D	3303	1/1	0.98	0.11	-0.96	31,31,31,31	0
6	MN	A	300	1/1	0.95	0.13	-1.05	46,46,46,46	0
6	MN	B	1300	1/1	0.99	0.10	-1.58	35,35,35,35	0
7	CA	B	1303	1/1	0.96	0.08	-2.40	27,27,27,27	0
6	MN	C	2300	1/1	0.99	0.05	-2.79	40,40,40,40	0
6	MN	D	3300	1/1	0.98	0.05	-3.55	41,41,41,41	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.