



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 6, 2017 – 04:01 PM EDT

PDB ID : 2YGM  
Title : THE X-RAY CRYSTAL STRUCTURE OF TANDEM CBM51 MODULES OF SP3GH98, THE FAMILY 98 GLYCOSIDE HYDROLASE FROM STREPTOCOCCUS PNEUMONIAE SP3-BS71, IN COMPLEX WITH THE BLOOD GROUP B ANTIGEN  
Authors : Higgins, M.A.; Ficko-Blean, E.; Wright, C.; Meloncelli, P.J.; Lowary, T.L.; Boraston, A.B.  
Deposited on : unknown  
Resolution : 2.35 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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20029824  
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-20029824

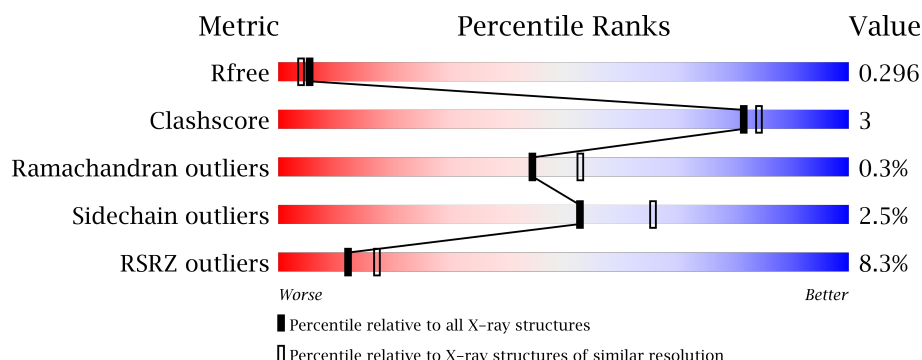
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.35 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	1522 (2.38-2.34)
Clashscore	112137	1626 (2.38-2.34)
Ramachandran outliers	110173	1605 (2.38-2.34)
Sidechain outliers	110143	1606 (2.38-2.34)
RSRZ outliers	101464	1528 (2.38-2.34)

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	354	<div> <div>10%</div> <div> <div></div> <div>91%</div> <div>7% ..</div> </div> </div>
1	B	354	<div> <div>6%</div> <div> <div></div> <div>90%</div> <div>10% .</div> </div> </div>

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 5697 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 BLOOD GROUP A-AND B-CLEAVING ENDO-BETA-GALACTOSIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	351	Total	C	N	O	S	0	1	0
			2712	1707	447	555	3			
1	B	352	Total	C	N	O	S	0	0	0
			2712	1706	447	556	3			

There are 12 discrepancies between the modelled and reference sequences:

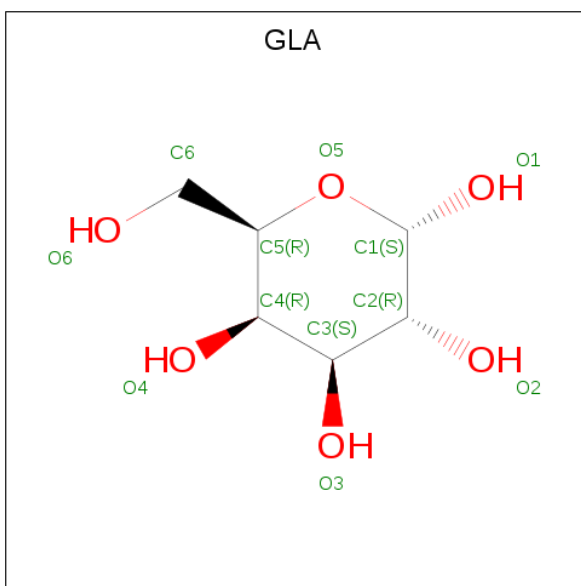
Chain	Residue	Modelled	Actual	Comment	Reference
A	60	GLY	-	expression tag	UNP C1CB04
A	61	SER	-	expression tag	UNP C1CB04
A	62	HIS	-	expression tag	UNP C1CB04
A	63	MET	-	expression tag	UNP C1CB04
A	64	ALA	-	expression tag	UNP C1CB04
A	65	SER	-	expression tag	UNP C1CB04
B	60	GLY	-	expression tag	UNP C1CB04
B	61	SER	-	expression tag	UNP C1CB04
B	62	HIS	-	expression tag	UNP C1CB04
B	63	MET	-	expression tag	UNP C1CB04
B	64	ALA	-	expression tag	UNP C1CB04
B	65	SER	-	expression tag	UNP C1CB04

- Molecule 2 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



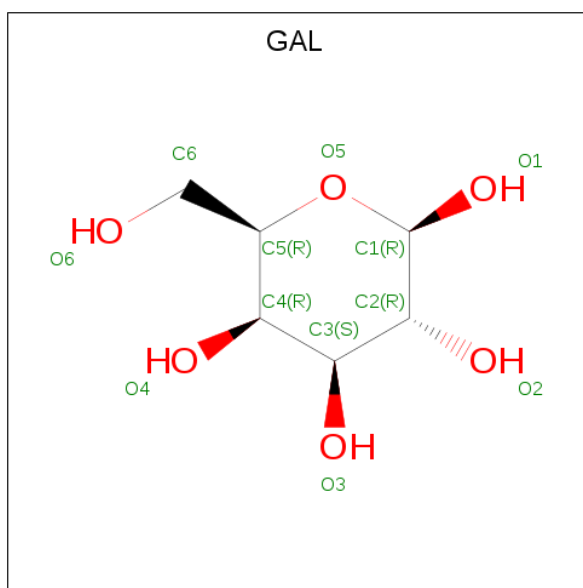
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			15	8	1	6		
2	B	1	Total	C	N	O	0	0
			15	8	1	6		

- Molecule 3 is ALPHA D-GALACTOSE (three-letter code: GLA) (formula:  $C_6H_{12}O_6$ ).



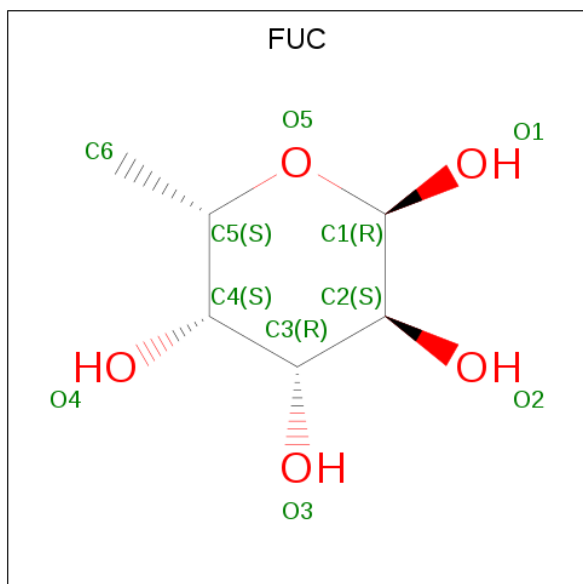
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			11	6	5		
3	B	1	Total	C	O	0	0
			11	6	5		

- Molecule 4 is BETA-D-GALACTOSE (three-letter code: GAL) (formula:  $C_6H_{12}O_6$ ).



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

- Molecule 5 is ALPHA-L-FUCOSE (three-letter code: FUC) (formula:  $C_6H_{12}O_5$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			10	6	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			10	6	4		

- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total	Na	0	0
			1	1		
7	A	1	Total	Na	0	0
			1	1		

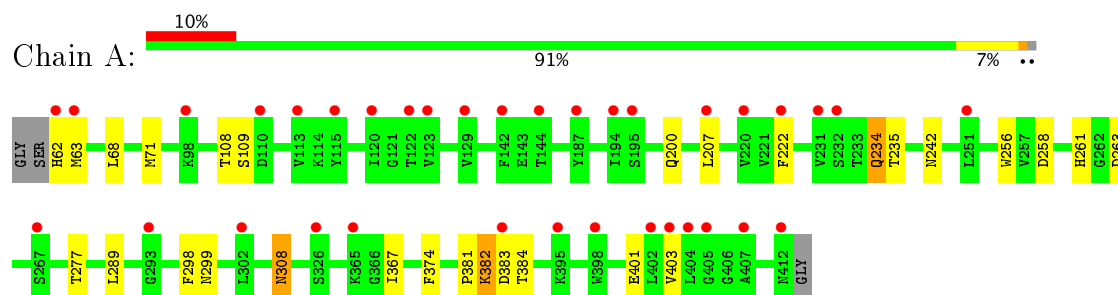
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	98	Total	O	0	0
			98	98		
8	B	77	Total	O	0	0
			77	77		

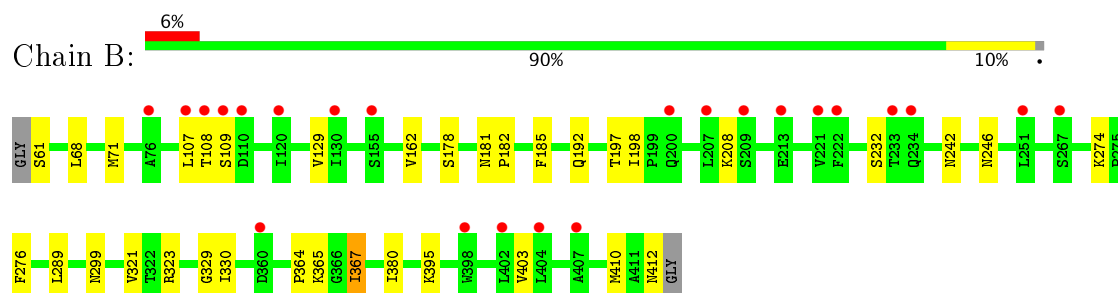
### 3 Residue-property plots [i](#)

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: BLOOD GROUP A-AND B-CLEAVING ENDO-BETA-GALACTOSIDASE



- Molecule 1: BLOOD GROUP A-AND B-CLEAVING ENDO-BETA-GALACTOSIDASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.70 Å 78.50 Å 131.58 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.35 29.25 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.9 (40.00-2.35) 100.0 (29.25-2.35)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.85 (at 2.36 Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.245 , 0.297 0.245 , 0.296	Depositor DCC
$R_{free}$ test set	1690 reflections (5.34%)	DCC
Wilson B-factor (Å <sup>2</sup> )	46.4	Xtriage
Anisotropy	0.052	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 33.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.027 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5697	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, GLA, CA, GAL, FUC, NA

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	0.35	0/2768	0.49	0/3748
1	B	0.34	0/2765	0.49	0/3744
All	All	0.35	0/5533	0.49	0/7492

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	2712	0	2644	16	0
1	B	2712	0	2641	17	0
2	A	15	0	14	0	0
2	B	15	0	14	0	0
3	A	11	0	10	0	0
3	B	11	0	10	0	0
4	A	11	0	8	0	0
4	B	11	0	8	0	0
5	A	10	0	10	0	0
5	B	10	0	10	0	0
6	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	1	0	0	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
8	A	98	0	0	1	0
8	B	77	0	0	0	0
All	All	5697	0	5369	33	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 (33) 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:382:LYS:HD3	1:A:383:ASP:H	1.28	0.94
1:B:108:THR:HG22	1:B:109:SER:H	1.52	0.73
1:B:181:ASN:HD21	1:B:192:GLN:HG3	1.55	0.71
1:A:382:LYS:HD3	1:A:383:ASP:N	2.07	0.68
1:A:382:LYS:HE2	1:A:382:LYS:HA	1.81	0.62
1:A:108:THR:HG22	1:A:109:SER:H	1.67	0.59
1:B:68:LEU:HD23	1:B:71:MET:HE3	1.85	0.58
1:A:382:LYS:CD	1:A:383:ASP:H	2.10	0.58
1:A:367:ILE:HG21	1:A:374:PHE:HE2	1.72	0.54
1:B:61:SER:N	1:B:232:SER:HG	2.05	0.54
1:B:330:ILE:HG13	1:B:367:ILE:HD11	1.90	0.52
1:B:181:ASN:ND2	1:B:192:GLN:HG3	2.25	0.49
1:A:261:HIS:HD2	1:A:263:ASP:H	1.60	0.49
1:A:68:LEU:HD23	1:A:71:MET:HE3	1.93	0.49
1:B:242:ASN:ND2	1:B:299:ASN:H	2.11	0.49
1:B:289:LEU:HD21	1:B:403:VAL:HG23	1.93	0.49
1:A:234:GLN:NE2	8:A:602:HOH:O	2.49	0.46
1:A:207:LEU:HD23	1:A:222:PHE:CG	2.52	0.45
1:A:242:ASN:ND2	1:A:299:ASN:H	2.15	0.45
1:A:242:ASN:HD21	1:A:298:PHE:HA	1.82	0.45
1:B:323:ARG:HB2	1:B:410:MET:HB2	1.99	0.45
1:A:277:THR:OG1	1:A:401:GLU:OE2	2.28	0.44
1:A:289:LEU:HD21	1:A:403:VAL:HG23	1.99	0.44
1:B:329:GLY:HA2	1:B:367:ILE:HD12	1.98	0.44
1:B:162:VAL:O	1:B:185:PHE:N	2.51	0.44
1:B:178:SER:O	1:B:182:PRO:HA	2.17	0.44
1:A:256:TRP:CD1	1:A:258:ASP:HA	2.53	0.43
1:B:129:VAL:HG22	1:B:208:LYS:HG2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:108:THR:HG22	1:B:109:SER:N	2.27	0.42
1:A:381:PRO:O	1:A:384:THR:OG1	2.25	0.40
1:B:364:PRO:HG2	1:B:365:LYS:HE2	2.02	0.40
1:B:68:LEU:HA	1:B:71:MET:HE2	2.03	0.40
1:B:321:VAL:HG12	1:B:380:ILE:HG13	2.02	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	350/354 (99%)	334 (95%)	15 (4%)	1 (0%)	44	53
1	B	350/354 (99%)	337 (96%)	12 (3%)	1 (0%)	44	53
All	All	700/708 (99%)	671 (96%)	27 (4%)	2 (0%)	44	53

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	276	PHE
1	A	308	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	303/303 (100%)	296 (98%)	7 (2%)	56	68
1	B	303/303 (100%)	295 (97%)	8 (3%)	51	64
All	All	606/606 (100%)	591 (98%)	15 (2%)	53	66

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	62	HIS
1	A	63	MET
1	A	200	GLN
1	A	234	GLN
1	A	235	THR
1	A	308	ASN
1	A	382	LYS
1	B	107	LEU
1	B	197	THR
1	B	198	ILE
1	B	246	ASN
1	B	274	LYS
1	B	367	ILE
1	B	395	LYS
1	B	412	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	88	GLN
1	A	150	GLN
1	A	181	ASN
1	A	234	GLN
1	A	242	ASN
1	A	261	HIS
1	A	285	ASN
1	A	335	ASN
1	A	412	ASN
1	B	153	ASN
1	B	181	ASN
1	B	242	ASN
1	B	261	HIS
1	B	412	ASN

### 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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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	NAG	A	501	4	15,15,15	0.48	0	21,21,21	1.18	3 (14%)
3	GLA	A	502	4	11,11,12	0.50	0	13,15,17	1.34	1 (7%)
4	GAL	A	503	3,2,5	11,11,12	0.72	0	13,15,17	1.11	2 (15%)
5	FUC	A	504	4	9,10,11	0.60	0	13,14,16	0.51	0
2	NAG	B	501	4	15,15,15	0.45	0	21,21,21	0.98	1 (4%)
3	GLA	B	502	4	11,11,12	0.56	0	13,15,17	0.70	1 (7%)
4	GAL	B	503	3,2,5	11,11,12	0.62	0	13,15,17	1.08	2 (15%)
5	FUC	B	504	4	9,10,11	0.68	0	13,14,16	0.85	1 (7%)

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	4	-	0/6/26/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GLA	A	502	4	-	0/2/19/22	0/1/1/1
4	GAL	A	503	3,2,5	-	0/2/19/22	0/1/1/1
5	FUC	A	504	4	-	0/0/17/20	0/1/1/1
2	NAG	B	501	4	-	0/6/26/26	0/1/1/1
3	GLA	B	502	4	-	0/2/19/22	0/1/1/1
4	GAL	B	503	3,2,5	-	0/2/19/22	0/1/1/1
5	FUC	B	504	4	-	0/0/17/20	0/1/1/1

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	503	GAL	O3-C3-C2	-2.40	105.66	110.02
4	A	503	GAL	O3-C3-C2	-2.13	106.15	110.02
2	A	501	NAG	O5-C5-C4	2.02	113.39	109.66
5	B	504	FUC	C1-C2-C3	2.07	112.28	109.65
4	A	503	GAL	C1-C2-C3	2.17	112.40	109.65
3	B	502	GLA	C1-O5-C5	2.23	115.24	112.17
2	B	501	NAG	C4-C3-C2	2.33	113.78	110.33
2	A	501	NAG	C3-C4-C5	2.48	114.59	110.22
4	B	503	GAL	C1-C2-C3	2.51	112.84	109.65
2	A	501	NAG	C4-C3-C2	2.82	114.51	110.33
3	A	502	GLA	C1-O5-C5	4.57	118.46	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 [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	351/354 (99%)	0.62	35 (9%) <b>8</b> <b>12</b>	31, 45, 62, 67	0
1	B	352/354 (99%)	0.57	23 (6%) <b>20</b> <b>27</b>	33, 47, 58, 61	0
All	All	703/708 (99%)	0.60	58 (8%) <b>12</b> <b>17</b>	31, 46, 59, 67	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	120	ILE	4.4
1	A	398	TRP	4.3
1	B	404	LEU	4.2
1	B	200	GLN	3.9
1	B	110	ASP	3.9
1	A	232	SER	3.8
1	A	404	LEU	3.6
1	B	120	ILE	3.3
1	A	144	THR	3.2
1	A	194	ILE	3.2
1	B	251	LEU	3.1
1	A	220	VAL	3.1
1	B	213	GLU	3.0
1	B	130	ILE	3.0
1	B	108	THR	3.0
1	A	251	LEU	3.0
1	B	267	SER	3.0
1	A	402	LEU	3.0
1	B	221	VAL	3.0
1	A	231	VAL	2.9
1	B	234	GLN	2.9
1	A	395	LYS	2.8
1	B	107	LEU	2.8
1	A	403	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	207	LEU	2.6
1	B	233	THR	2.6
1	A	407	ALA	2.6
1	A	267	SER	2.5
1	A	222	PHE	2.5
1	A	115	TYR	2.4
1	A	195	SER	2.4
1	A	302	LEU	2.4
1	B	109	SER	2.4
1	B	407	ALA	2.4
1	B	209	SER	2.4
1	A	129	VAL	2.4
1	B	360	ASP	2.3
1	B	76	ALA	2.3
1	A	122	THR	2.3
1	B	402	LEU	2.2
1	A	412	ASN	2.2
1	A	113	VAL	2.2
1	A	142	PHE	2.2
1	A	293	GLY	2.2
1	A	98	LYS	2.2
1	B	222	PHE	2.2
1	A	110	ASP	2.2
1	A	365	LYS	2.1
1	A	207	LEU	2.1
1	B	155	SER	2.1
1	A	383	ASP	2.1
1	A	187	TYR	2.1
1	A	123	VAL	2.1
1	A	326	SER	2.1
1	A	405	GLY	2.1
1	A	62	HIS	2.1
1	B	398	TRP	2.0
1	A	63	MET	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.



### 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, 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	NA	B	505	1/1	0.97	0.19	0.65	34,34,34,34	0
7	NA	A	506	1/1	0.89	0.20	0.21	43,43,43,43	0
2	NAG	B	501	15/15	0.88	0.17	-0.19	53,55,55,55	0
3	GLA	A	502	11/12	0.92	0.14	-0.29	53,53,54,55	0
6	CA	B	506	1/1	0.98	0.14	-0.66	53,53,53,53	0
3	GLA	B	502	11/12	0.95	0.10	-1.74	50,50,51,51	0
4	GAL	A	503	11/12	0.95	0.10	-1.85	55,56,56,57	0
6	CA	A	505	1/1	0.96	0.05	-2.65	44,44,44,44	0
4	GAL	B	503	11/12	0.94	0.14	-	51,52,53,53	0
2	NAG	A	501	15/15	0.81	0.18	-	58,59,60,60	0
5	FUC	B	504	10/11	0.91	0.17	-	50,51,51,51	0
5	FUC	A	504	10/11	0.88	0.18	-	57,58,58,58	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.