



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2018 – 04:49 PM EDT

PDB ID : 5NBS  
Title : Structural studies of a Glycoside Hydrolase Family 3 beta-glucosidase from the Model Fungus *Neurospora crassa*  
Authors : Gudmundsson, M.; Karkehabadi, S.; Kaper, T.; Sandgren, M.  
Deposited on : 2017-03-02  
Resolution : 2.25 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.

---

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

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

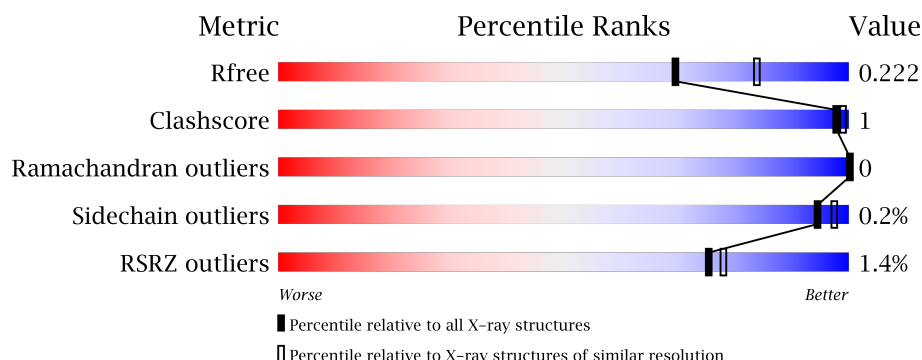
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.25 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	1062 (2.26-2.26)
Clashscore	112137	1178 (2.26-2.26)
Ramachandran outliers	110173	1145 (2.26-2.26)
Sidechain outliers	110143	1146 (2.26-2.26)
RSRZ outliers	101464	1066 (2.26-2.26)

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	857	<div> <div style="width: 100%; height: 10px; background-color: red; position: relative;"> <span style="position: absolute; right: 0; top: -10px;">%</span> </div> <div style="width: 95%; height: 10px; background-color: green; position: relative;"> <span style="position: absolute; right: 0; top: -10px;">95%</span> </div> </div>
1	B	857	<div> <div style="width: 100%; height: 10px; background-color: red; position: relative;"> <span style="position: absolute; right: 0; top: -10px;">2%</span> </div> <div style="width: 96%; height: 10px; background-color: green; position: relative;"> <span style="position: absolute; right: 0; top: -10px;">96%</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	A	1129	-	-	-	X
2	NAG	A	1141	-	-	-	X
2	NAG	A	1145	-	-	-	X
2	NAG	B	1124	-	-	-	X
2	NAG	B	1134	-	-	-	X
2	NAG	B	1137	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 15111 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 Beta-glucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	842	Total	C	N	O	S	0	13	0
			6613	4184	1123	1279	27			
1	B	841	Total	C	N	O	S	0	4	0
			6523	4131	1102	1264	26			

- 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
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

*Continued on next page...*

*Continued from previous page...*

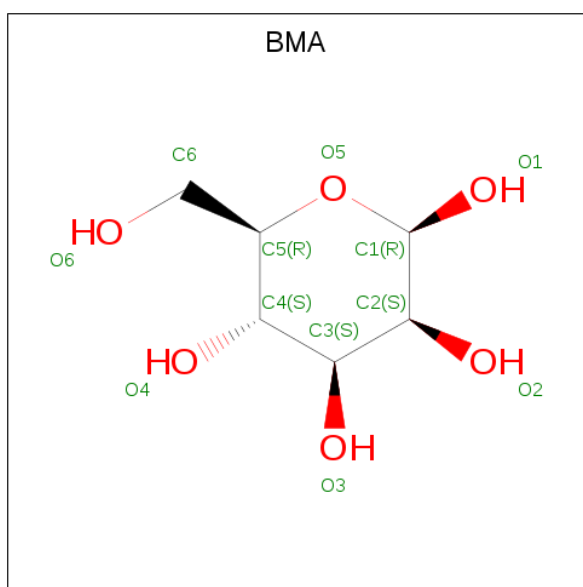
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1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

*Continued on next page...*

Continued from previous page...

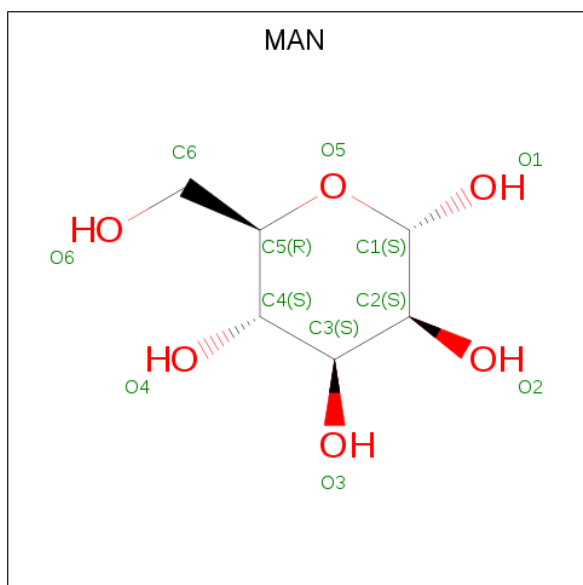
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1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

- Molecule 3 is BETA-D-MANNOSE (three-letter code: BMA) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).



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

- Molecule 4 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).



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

*Continued on next page...*

*Continued from previous page...*

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

*Continued on next page...*



*Continued from previous page...*

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

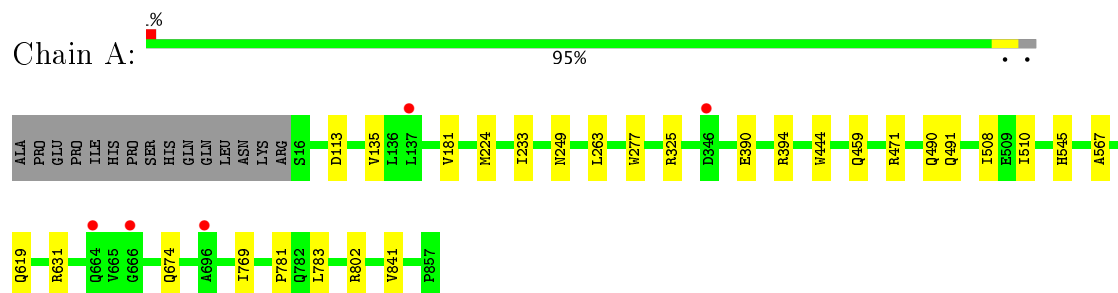
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	625	Total	O	0	0
			625	625		
5	B	329	Total	O	0	0
			329	329		

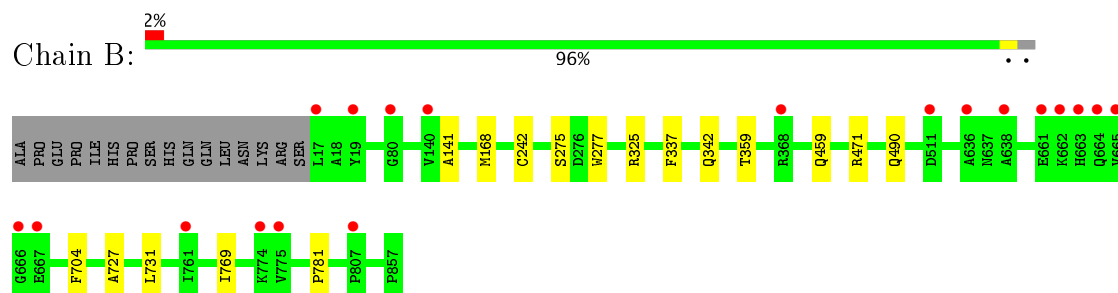
### 3 Residue-property plots [i](#)

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: Beta-glucosidase



#### • Molecule 1: Beta-glucosidase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	142.93Å 286.84Å 58.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.00 – 2.25 47.00 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.2 (47.00-2.25) 99.2 (47.00-2.25)	Depositor EDS
$R_{merge}$	0.03	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.30 (at 2.24Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.180 , 0.220 0.185 , 0.222	Depositor DCC
$R_{free}$ test set	5627 reflections (5.21%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.7	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 34.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.42$ , $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	15111	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 2.46% 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: BMA, NAG, 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	0.45	0/6793	0.65	2/9246 (0.0%)
1	B	0.41	0/6703	0.61	1/9131 (0.0%)
All	All	0.43	0/13496	0.63	3/18377 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	325	ARG	NE-CZ-NH1	6.66	123.63	120.30
1	A	325	ARG	NE-CZ-NH2	-6.02	117.29	120.30
1	B	325	ARG	NE-CZ-NH1	5.52	123.06	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6613	0	6320	18	0
1	B	6523	0	6230	10	0
2	A	266	0	234	0	0
2	B	238	0	209	1	0
3	A	66	0	51	0	0
3	B	55	0	42	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	220	0	189	0	0
4	B	176	0	152	0	0
5	A	625	0	0	0	0
5	B	329	0	0	1	0
All	All	15111	0	13427	26	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 1.

All (26) 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:B:337:PHE:CE1	1:B:342:GLN:HG2	2.29	0.68
1:A:802[A]:ARG:HH11	1:A:802[A]:ARG:HG2	1.60	0.64
1:A:802[A]:ARG:NH1	1:A:802[A]:ARG:HG2	2.13	0.64
1:A:471:ARG:HH22	1:A:490:GLN:HE22	1.50	0.59
1:A:249:ASN:HD21	1:A:619:GLN:HE22	1.52	0.58
1:A:224[A]:MET:SD	1:A:631:ARG:NH1	2.82	0.52
1:B:141:ALA:HB2	1:B:168:MET:SD	2.51	0.51
1:A:769:ILE:HD11	1:A:781:PRO:HB3	1.91	0.51
1:A:459[B]:GLN:HG2	1:B:459:GLN:HG2	1.96	0.48
1:A:233:ILE:HD11	1:A:263:LEU:HD12	1.97	0.46
1:A:444:TRP:CZ3	1:A:510:ILE:HD12	2.51	0.45
1:A:135:VAL:HG22	1:A:181:VAL:HB	1.99	0.44
1:A:783:LEU:HD11	1:A:841:VAL:HG13	1.98	0.44
1:B:704:PHE:CZ	2:B:1102:NAG:H82	2.53	0.44
1:A:113:ASP:OD2	1:A:802[A]:ARG:NH1	2.51	0.43
1:B:769:ILE:HD11	1:B:781:PRO:HB3	1.99	0.43
1:B:342:GLN:NE2	5:B:1202:HOH:O	2.51	0.42
1:A:783:LEU:CD1	1:A:841:VAL:HG13	2.49	0.42
1:A:802[A]:ARG:CG	1:A:802[A]:ARG:HH11	2.27	0.42
1:B:242:CYS:SG	1:B:275:SER:HA	2.60	0.41
1:B:727:ALA:HB1	1:B:731:LEU:HD12	2.02	0.41
1:B:471:ARG:HH22	1:B:490:GLN:HE22	1.69	0.41
1:A:390:GLU:OE2	1:A:394[B]:ARG:NH1	2.54	0.41
1:A:545:HIS:CD2	1:A:567:ALA:HB3	2.56	0.41
1:A:491:GLN:CG	1:B:359:THR:OG1	2.69	0.41
1:A:444:TRP:CD1	1:A:508:ILE:HB	2.57	0.40

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	853/857 (100%)	827 (97%)	26 (3%)	0	100	100
1	B	843/857 (98%)	818 (97%)	25 (3%)	0	100	100
All	All	1696/1714 (99%)	1645 (97%)	51 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	699/700 (100%)	696 (100%)	3 (0%)	93	95
1	B	689/700 (98%)	688 (100%)	1 (0%)	94	99
All	All	1388/1400 (99%)	1384 (100%)	4 (0%)	94	97

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

Mol	Chain	Res	Type
1	A	277	TRP
1	A	674[A]	GLN
1	A	674[B]	GLN
1	B	277	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	197	GLN
1	A	261	ASN
1	A	302	ASN
1	A	433	ASN
1	A	462	GLN
1	A	467	GLN
1	A	490	GLN
1	A	491	GLN
1	A	619	GLN
1	A	703	GLN
1	B	126	GLN
1	B	186	HIS
1	B	207	ASN
1	B	261	ASN
1	B	433	ASN
1	B	450	ASN
1	B	462	GLN
1	B	479	HIS
1	B	490	GLN
1	B	725	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

83 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	$\# Z  > 2$
2	NAG	A	1101	1,2	14,14,15	0.35	0	15,19,21	0.58	0
2	NAG	A	1102	3,2	14,14,15	0.35	0	15,19,21	0.70	0
3	BMA	A	1103	2,4	11,11,12	0.39	0	13,15,17	0.54	0
4	MAN	A	1104	3,4	11,11,12	0.36	0	13,15,17	0.70	0
4	MAN	A	1105	4	11,11,12	0.53	0	13,15,17	0.64	0
4	MAN	A	1106	3	11,11,12	0.56	0	13,15,17	0.51	0
2	NAG	A	1107	1	14,14,15	0.29	0	15,19,21	0.72	0
2	NAG	A	1108	1	14,14,15	0.53	0	15,19,21	1.65	3 (20%)
2	NAG	A	1109	1,2	14,14,15	0.31	0	15,19,21	0.80	0
2	NAG	A	1110	3,2	14,14,15	0.38	0	15,19,21	1.09	0
3	BMA	A	1111	2,4	11,11,12	0.25	0	13,15,17	1.16	3 (23%)
4	MAN	A	1112	3,4	11,11,12	0.30	0	13,15,17	1.04	1 (7%)
4	MAN	A	1113	4	11,11,12	0.32	0	13,15,17	0.67	0
4	MAN	A	1114	3,4	11,11,12	0.65	0	13,15,17	0.67	0
4	MAN	A	1115	4	11,11,12	0.55	0	13,15,17	0.93	0
4	MAN	A	1116	4	11,11,12	0.54	0	13,15,17	0.64	0
2	NAG	A	1117	1,2	14,14,15	0.41	0	15,19,21	1.09	0
2	NAG	A	1118	3,2	14,14,15	0.27	0	15,19,21	0.72	1 (6%)
3	BMA	A	1119	2,4	11,11,12	0.50	0	13,15,17	1.49	3 (23%)
4	MAN	A	1120	3	11,11,12	0.47	0	13,15,17	0.85	0
2	NAG	A	1121	1,2	14,14,15	0.35	0	15,19,21	1.01	1 (6%)
2	NAG	A	1122	3,2	14,14,15	0.48	0	15,19,21	0.81	0
3	BMA	A	1123	2,4	11,11,12	0.32	0	13,15,17	1.11	1 (7%)
4	MAN	A	1124	3	11,11,12	0.61	0	13,15,17	1.01	0
4	MAN	A	1125	3,4	11,11,12	0.50	0	13,15,17	1.17	1 (7%)
4	MAN	A	1126	4	11,11,12	0.41	0	13,15,17	0.92	0
4	MAN	A	1127	4	11,11,12	0.47	0	13,15,17	0.75	0
4	MAN	A	1128	4	11,11,12	0.37	0	13,15,17	0.84	0
2	NAG	A	1129	1	14,14,15	0.66	0	15,19,21	1.26	2 (13%)
2	NAG	A	1130	1,2	14,14,15	0.46	0	15,19,21	0.99	0
2	NAG	A	1131	2	14,14,15	0.50	0	15,19,21	1.15	1 (6%)
2	NAG	A	1132	1,2	14,14,15	0.31	0	15,19,21	0.99	1 (6%)
2	NAG	A	1133	3,2	14,14,15	0.36	0	15,19,21	1.20	1 (6%)
3	BMA	A	1134	2,4	11,11,12	0.44	0	13,15,17	0.81	0
4	MAN	A	1135	3,4	11,11,12	0.42	0	13,15,17	1.02	1 (7%)
4	MAN	A	1136	4	11,11,12	0.83	1 (9%)	13,15,17	1.33	2 (15%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	MAN	A	1137	3,4	11,11,12	0.45	0	13,15,17	0.82	0
4	MAN	A	1138	4	11,11,12	0.46	0	13,15,17	0.97	1 (7%)
4	MAN	A	1139	4	11,11,12	0.43	0	13,15,17	0.76	0
4	MAN	A	1140	4	11,11,12	0.58	0	13,15,17	0.76	0
2	NAG	A	1141	1	14,14,15	0.55	0	15,19,21	1.03	0
2	NAG	A	1142	1,2	14,14,15	0.34	0	15,19,21	0.95	0
2	NAG	A	1143	3,2	14,14,15	0.38	0	15,19,21	1.24	1 (6%)
3	BMA	A	1144	2	11,11,12	0.40	0	13,15,17	0.88	0
2	NAG	A	1145	1	14,14,15	0.33	0	15,19,21	1.22	2 (13%)
2	NAG	B	1101	1,2	14,14,15	0.39	0	15,19,21	0.81	0
2	NAG	B	1102	3,2	14,14,15	0.28	0	15,19,21	1.02	1 (6%)
3	BMA	B	1103	2,4	11,11,12	0.27	0	13,15,17	0.54	0
4	MAN	B	1104	3,4	11,11,12	0.34	0	13,15,17	1.18	1 (7%)
4	MAN	B	1105	4	11,11,12	0.43	0	13,15,17	0.56	0
4	MAN	B	1106	3	11,11,12	0.65	0	13,15,17	0.63	0
2	NAG	B	1107	1,2	14,14,15	0.33	0	15,19,21	0.96	1 (6%)
2	NAG	B	1108	3,2	14,14,15	0.30	0	15,19,21	0.82	0
3	BMA	B	1109	2,4	11,11,12	0.34	0	13,15,17	0.57	0
4	MAN	B	1110	3,4	11,11,12	0.49	0	13,15,17	1.09	2 (15%)
4	MAN	B	1111	4	11,11,12	0.51	0	13,15,17	0.72	0
2	NAG	B	1112	1,2	14,14,15	0.33	0	15,19,21	1.14	2 (13%)
2	NAG	B	1113	3,2	14,14,15	0.33	0	15,19,21	1.27	1 (6%)
3	BMA	B	1114	2,4	11,11,12	0.36	0	13,15,17	0.42	0
4	MAN	B	1115	3	11,11,12	0.37	0	13,15,17	0.85	0
2	NAG	B	1116	1,2	14,14,15	0.33	0	15,19,21	1.03	1 (6%)
2	NAG	B	1117	3,2	14,14,15	0.49	0	15,19,21	0.83	0
3	BMA	B	1118	2,4	11,11,12	0.35	0	13,15,17	0.68	0
4	MAN	B	1119	3	11,11,12	0.40	0	13,15,17	1.06	0
4	MAN	B	1120	3,4	11,11,12	0.40	0	13,15,17	1.09	1 (7%)
4	MAN	B	1121	4	11,11,12	0.36	0	13,15,17	0.93	0
4	MAN	B	1122	4	11,11,12	0.48	0	13,15,17	0.78	0
4	MAN	B	1123	4	11,11,12	0.41	0	13,15,17	0.67	0
2	NAG	B	1124	1	14,14,15	0.49	0	15,19,21	0.99	0
2	NAG	B	1125	1	14,14,15	0.34	0	15,19,21	0.64	0
2	NAG	B	1126	1,2	14,14,15	0.36	0	15,19,21	0.63	0
2	NAG	B	1127	3,2	14,14,15	0.40	0	15,19,21	1.10	2 (13%)
3	BMA	B	1128	2,4	11,11,12	0.60	0	13,15,17	0.81	0
4	MAN	B	1129	3,4	11,11,12	0.41	0	13,15,17	0.69	0
4	MAN	B	1130	4	11,11,12	0.36	0	13,15,17	0.82	1 (7%)
4	MAN	B	1131	4	11,11,12	0.35	0	13,15,17	0.81	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	MAN	B	1132	3	11,11,12	0.50	0	13,15,17	0.77	0
4	MAN	B	1133	4	11,11,12	0.32	0	13,15,17	0.85	1 (7%)
2	NAG	B	1134	1	14,14,15	0.50	0	15,19,21	1.56	2 (13%)
2	NAG	B	1135	1,2	14,14,15	0.41	0	15,19,21	0.91	0
2	NAG	B	1136	2	14,14,15	0.49	0	15,19,21	0.78	0
2	NAG	B	1137	1,2	14,14,15	0.34	0	15,19,21	1.19	2 (13%)
2	NAG	B	1138	2	14,14,15	0.52	0	15,19,21	0.84	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	1101	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1102	3,2	-	0/6/23/26	0/1/1/1
3	BMA	A	1103	2,4	-	0/2/19/22	0/1/1/1
4	MAN	A	1104	3,4	-	0/2/19/22	0/1/1/1
4	MAN	A	1105	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1106	3	-	0/2/19/22	0/1/1/1
2	NAG	A	1107	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1108	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1109	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1110	3,2	-	0/6/23/26	0/1/1/1
3	BMA	A	1111	2,4	-	0/2/19/22	0/1/1/1
4	MAN	A	1112	3,4	-	0/2/19/22	0/1/1/1
4	MAN	A	1113	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1114	3,4	-	0/2/19/22	0/1/1/1
4	MAN	A	1115	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1116	4	-	0/2/19/22	0/1/1/1
2	NAG	A	1117	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1118	3,2	-	0/6/23/26	0/1/1/1
3	BMA	A	1119	2,4	-	0/2/19/22	0/1/1/1
4	MAN	A	1120	3	-	0/2/19/22	0/1/1/1
2	NAG	A	1121	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1122	3,2	-	0/6/23/26	0/1/1/1
3	BMA	A	1123	2,4	-	0/2/19/22	0/1/1/1
4	MAN	A	1124	3	-	0/2/19/22	0/1/1/1
4	MAN	A	1125	3,4	-	0/2/19/22	0/1/1/1
4	MAN	A	1126	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1127	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1128	4	-	0/2/19/22	0/1/1/1

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	1129	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1130	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1131	2	-	0/6/23/26	0/1/1/1
2	NAG	A	1132	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1133	3,2	-	0/6/23/26	0/1/1/1
3	BMA	A	1134	2,4	-	0/2/19/22	0/1/1/1
4	MAN	A	1135	3,4	-	0/2/19/22	0/1/1/1
4	MAN	A	1136	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1137	3,4	-	0/2/19/22	0/1/1/1
4	MAN	A	1138	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1139	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1140	4	-	0/2/19/22	0/1/1/1
2	NAG	A	1141	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1142	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1143	3,2	-	0/6/23/26	0/1/1/1
3	BMA	A	1144	2	-	0/2/19/22	0/1/1/1
2	NAG	A	1145	1	-	0/6/23/26	0/1/1/1
2	NAG	B	1101	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	1102	3,2	-	0/6/23/26	0/1/1/1
3	BMA	B	1103	2,4	-	0/2/19/22	0/1/1/1
4	MAN	B	1104	3,4	-	0/2/19/22	0/1/1/1
4	MAN	B	1105	4	-	0/2/19/22	0/1/1/1
4	MAN	B	1106	3	-	0/2/19/22	0/1/1/1
2	NAG	B	1107	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	1108	3,2	-	0/6/23/26	0/1/1/1
3	BMA	B	1109	2,4	-	0/2/19/22	0/1/1/1
4	MAN	B	1110	3,4	-	0/2/19/22	0/1/1/1
4	MAN	B	1111	4	-	0/2/19/22	0/1/1/1
2	NAG	B	1112	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	1113	3,2	-	0/6/23/26	0/1/1/1
3	BMA	B	1114	2,4	-	0/2/19/22	0/1/1/1
4	MAN	B	1115	3	-	0/2/19/22	0/1/1/1
2	NAG	B	1116	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	1117	3,2	-	0/6/23/26	0/1/1/1
3	BMA	B	1118	2,4	-	0/2/19/22	0/1/1/1
4	MAN	B	1119	3	-	0/2/19/22	0/1/1/1
4	MAN	B	1120	3,4	-	0/2/19/22	0/1/1/1
4	MAN	B	1121	4	-	0/2/19/22	0/1/1/1
4	MAN	B	1122	4	-	0/2/19/22	0/1/1/1
4	MAN	B	1123	4	-	0/2/19/22	0/1/1/1
2	NAG	B	1124	1	-	0/6/23/26	0/1/1/1
2	NAG	B	1125	1	-	0/6/23/26	0/1/1/1

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	1126	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	1127	3,2	-	0/6/23/26	0/1/1/1
3	BMA	B	1128	2,4	-	0/2/19/22	0/1/1/1
4	MAN	B	1129	3,4	-	0/2/19/22	0/1/1/1
4	MAN	B	1130	4	-	0/2/19/22	0/1/1/1
4	MAN	B	1131	4	-	0/2/19/22	0/1/1/1
4	MAN	B	1132	3	-	0/2/19/22	0/1/1/1
4	MAN	B	1133	4	-	0/2/19/22	0/1/1/1
2	NAG	B	1134	1	-	0/6/23/26	0/1/1/1
2	NAG	B	1135	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	1136	2	-	0/6/23/26	0/1/1/1
2	NAG	B	1137	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	1138	2	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1136	MAN	C2-C3	2.14	1.55	1.52

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1134	NAG	O5-C1-C2	-3.64	106.41	111.47
4	B	1104	MAN	O5-C1-C2	-3.24	105.71	110.79
2	B	1137	NAG	O5-C1-C2	-3.10	107.16	111.47
4	A	1136	MAN	O5-C1-C2	-3.05	106.00	110.79
2	B	1116	NAG	O4-C4-C5	-3.00	101.72	109.28
2	A	1143	NAG	O4-C4-C3	-2.85	104.16	110.36
2	A	1133	NAG	O4-C4-C3	-2.79	104.29	110.36
2	A	1121	NAG	O4-C4-C5	-2.61	102.72	109.28
3	A	1119	BMA	C6-C5-C4	-2.56	107.01	113.00
2	B	1127	NAG	O4-C4-C3	-2.45	105.02	110.36
4	B	1110	MAN	O2-C2-C1	-2.39	104.31	109.18
2	B	1112	NAG	O5-C1-C2	-2.38	108.16	111.47
4	B	1133	MAN	O5-C1-C2	-2.27	107.23	110.79
3	A	1123	BMA	O3-C3-C4	-2.27	105.43	110.36
4	A	1138	MAN	O5-C1-C2	-2.25	107.27	110.79
4	A	1135	MAN	O5-C1-C2	-2.24	107.28	110.79
4	A	1125	MAN	O6-C6-C5	-2.18	104.01	111.34
2	A	1145	NAG	O5-C1-C2	-2.15	108.49	111.47
3	A	1111	BMA	O3-C3-C4	-2.14	105.71	110.36
2	A	1108	NAG	O7-C7-C8	-2.13	118.17	122.06

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1119	BMA	O4-C4-C3	-2.13	105.71	110.36
2	B	1107	NAG	C4-C3-C2	-2.13	107.89	111.02
4	B	1110	MAN	O5-C1-C2	-2.12	107.48	110.79
4	B	1130	MAN	O5-C1-C2	-2.09	107.51	110.79
4	B	1120	MAN	O6-C6-C5	-2.07	104.39	111.34
3	A	1111	BMA	O4-C4-C3	-2.03	105.94	110.36
3	A	1111	BMA	O5-C1-C2	-2.02	107.63	110.79
4	A	1112	MAN	O2-C2-C1	-2.01	105.09	109.18
2	A	1118	NAG	O4-C4-C3	-2.00	106.00	110.36
4	A	1136	MAN	C1-O5-C5	2.20	115.20	112.17
2	A	1129	NAG	C2-N2-C7	2.32	126.33	122.94
2	B	1127	NAG	C2-N2-C7	2.33	126.33	122.94
3	A	1119	BMA	C3-C4-C5	2.33	114.32	110.22
2	B	1112	NAG	C1-O5-C5	2.37	115.44	112.17
2	B	1102	NAG	C1-O5-C5	2.42	115.50	112.17
2	B	1113	NAG	C1-O5-C5	2.43	115.52	112.17
2	A	1108	NAG	C8-C7-N2	2.47	120.57	116.11
2	A	1131	NAG	C1-O5-C5	2.59	115.73	112.17
2	B	1137	NAG	C1-O5-C5	2.66	115.84	112.17
2	A	1132	NAG	C1-C2-N2	2.68	115.06	110.49
2	A	1145	NAG	C1-O5-C5	2.95	116.23	112.17
2	A	1129	NAG	C1-O5-C5	3.31	116.73	112.17
2	B	1134	NAG	C1-O5-C5	3.75	117.34	112.17
2	A	1108	NAG	C2-N2-C7	3.85	128.56	122.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1102	NAG	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, 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	842/857 (98%)	-0.32	5 (0%) 89 89	17, 26, 39, 55	0
1	B	841/857 (98%)	-0.12	19 (2%) 61 64	25, 42, 62, 81	0
All	All	1683/1714 (98%)	-0.22	24 (1%) 75 78	17, 33, 57, 81	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	17	LEU	4.2
1	B	774	LYS	4.0
1	B	775	VAL	3.2
1	B	666	GLY	3.2
1	B	761	ILE	3.2
1	B	665	VAL	3.0
1	B	638	ALA	2.9
1	B	667	GLU	2.9
1	B	807	PRO	2.9
1	B	664	GLN	2.8
1	A	346	ASP	2.6
1	B	663	HIS	2.5
1	B	368	ARG	2.3
1	B	662	LYS	2.3
1	A	696	ALA	2.3
1	B	636	ALA	2.3
1	B	80	GLY	2.3
1	B	661	GLU	2.2
1	B	140	VAL	2.1
1	A	664	GLN	2.1
1	A	666	GLY	2.1
1	B	19	TYR	2.1
1	B	511	ASP	2.0
1	A	137	LEU	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](#)

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(Å <sup>2</sup> )	Q<0.9
2	NAG	A	1129	14/15	0.81	0.23	12.36	41,44,47,47	0
2	NAG	A	1141	14/15	0.91	0.20	4.17	30,31,33,33	0
2	NAG	B	1137	14/15	0.90	0.22	3.59	64,66,67,70	0
2	NAG	B	1134	14/15	0.82	0.20	3.07	47,49,52,53	0
2	NAG	A	1145	14/15	0.91	0.20	2.59	41,42,45,45	0
2	NAG	B	1124	14/15	0.87	0.18	2.04	51,53,55,55	0
2	NAG	B	1135	14/15	0.90	0.11	1.62	46,47,50,54	0
2	NAG	B	1126	14/15	0.90	0.24	1.35	44,46,49,50	0
2	NAG	B	1113	14/15	0.95	0.16	0.79	55,58,60,63	0
2	NAG	B	1127	14/15	0.93	0.20	0.77	46,47,50,51	0
2	NAG	A	1108	14/15	0.94	0.13	0.75	22,22,23,23	0
4	MAN	B	1122	11/12	0.92	0.14	0.62	46,48,49,49	0
4	MAN	B	1123	11/12	0.91	0.16	0.09	49,49,51,51	0
2	NAG	A	1101	14/15	0.96	0.10	0.02	33,34,35,37	0
2	NAG	B	1107	14/15	0.90	0.13	-0.04	49,51,55,56	0
2	NAG	B	1112	14/15	0.96	0.11	-0.05	47,48,50,53	0
2	NAG	B	1101	14/15	0.96	0.12	-0.22	41,42,42,43	0
2	NAG	B	1117	14/15	0.92	0.14	-0.22	48,49,51,51	0
2	NAG	B	1116	14/15	0.90	0.13	-0.39	46,48,50,51	0
2	NAG	A	1102	14/15	0.94	0.12	-0.40	40,42,44,49	0
4	MAN	A	1127	11/12	0.95	0.08	-0.43	25,25,26,26	0
2	NAG	B	1108	14/15	0.92	0.14	-0.47	55,56,58,58	0
2	NAG	A	1132	14/15	0.96	0.09	-0.53	24,25,26,26	0
2	NAG	A	1142	14/15	0.96	0.09	-0.63	27,27,29,32	0
2	NAG	A	1133	14/15	0.96	0.10	-0.77	28,29,31,34	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	A	1118	14/15	0.94	0.12	-0.85	36,38,40,44	0
2	NAG	A	1117	14/15	0.97	0.09	-0.86	30,31,32,35	0
2	NAG	A	1121	14/15	0.96	0.09	-0.86	27,28,29,30	0
2	NAG	B	1102	14/15	0.94	0.12	-0.88	43,46,49,51	0
2	NAG	A	1110	14/15	0.98	0.09	-1.03	29,30,31,33	0
2	NAG	A	1109	14/15	0.97	0.09	-1.09	24,25,26,27	0
4	MAN	A	1126	11/12	0.97	0.07	-1.31	25,26,26,26	0
2	NAG	A	1122	14/15	0.96	0.09	-1.52	27,28,29,29	0
4	MAN	A	1105	11/12	0.86	0.31	-	63,64,66,66	0
4	MAN	B	1131	11/12	0.86	0.20	-	47,50,50,50	0
4	MAN	A	1135	11/12	0.89	0.32	-	52,55,57,59	0
3	BMA	B	1128	11/12	0.87	0.27	-	53,55,57,61	0
3	BMA	B	1103	11/12	0.92	0.15	-	54,56,58,63	0
3	BMA	A	1134	11/12	0.92	0.15	-	37,39,42,46	0
2	NAG	B	1125	14/15	0.91	0.12	-	49,51,51,53	0
4	MAN	A	1112	11/12	0.96	0.10	-	41,42,43,45	0
4	MAN	B	1133	11/12	0.91	0.40	-	66,68,69,69	0
4	MAN	A	1116	11/12	0.80	0.24	-	60,63,65,65	0
4	MAN	B	1105	11/12	0.89	0.30	-	57,58,59,59	0
4	MAN	A	1128	11/12	0.97	0.07	-	27,28,28,28	0
3	BMA	A	1111	11/12	0.93	0.15	-	36,39,43,46	0
4	MAN	A	1136	11/12	0.79	0.41	-	64,66,67,67	0
4	MAN	B	1110	11/12	0.88	0.24	-	61,63,64,64	0
4	MAN	B	1115	11/12	0.89	0.22	-	78,79,80,80	0
3	BMA	A	1123	11/12	0.97	0.07	-	27,29,30,32	0
4	MAN	A	1139	11/12	0.92	0.16	-	44,45,46,46	0
4	MAN	A	1113	11/12	0.92	0.15	-	48,49,51,56	0
2	NAG	A	1143	14/15	0.94	0.15	-	35,37,40,45	0
4	MAN	B	1111	11/12	0.83	0.16	-	64,66,68,69	0
4	MAN	A	1138	11/12	0.88	0.18	-	46,47,50,50	0
3	BMA	B	1109	11/12	0.88	0.19	-	60,62,63,63	0
3	BMA	A	1103	11/12	0.93	0.14	-	54,58,61,63	0
2	NAG	B	1138	14/15	0.89	0.34	-	73,75,76,77	0
4	MAN	A	1104	11/12	0.88	0.20	-	62,65,67,68	0
3	BMA	A	1144	11/12	0.82	0.22	-	50,53,55,56	0
2	NAG	A	1131	14/15	0.86	0.28	-	44,48,49,50	0
4	MAN	B	1130	11/12	0.88	0.30	-	51,54,56,57	0
4	MAN	B	1132	11/12	0.86	0.39	-	65,68,69,70	0
4	MAN	A	1125	11/12	0.97	0.09	-	26,27,27,27	0
4	MAN	A	1106	11/12	0.79	0.22	-	65,68,69,70	0
4	MAN	B	1106	11/12	0.83	0.34	-	67,70,72,73	0
4	MAN	A	1124	11/12	0.93	0.13	-	33,35,36,36	0

*Continued on next page...*



*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	BMA	A	1119	11/12	0.82	0.19	-	48,53,55,57	0
4	MAN	B	1120	11/12	0.93	0.13	-	49,50,51,52	0
4	MAN	A	1120	11/12	0.74	0.23	-	61,63,65,65	0
2	NAG	A	1130	14/15	0.92	0.10	-	32,33,36,40	0
4	MAN	A	1137	11/12	0.94	0.16	-	44,46,47,51	0
4	MAN	A	1114	11/12	0.81	0.26	-	50,51,53,54	0
4	MAN	B	1121	11/12	0.94	0.12	-	50,51,51,51	0
2	NAG	A	1107	14/15	0.89	0.21	-	50,54,56,56	0
3	BMA	B	1118	11/12	0.94	0.14	-	50,52,53,55	0
4	MAN	B	1104	11/12	0.92	0.24	-	56,57,59,60	0
4	MAN	A	1140	11/12	0.84	0.33	-	54,55,57,58	0
4	MAN	A	1115	11/12	0.87	0.32	-	56,58,58,59	0
4	MAN	B	1129	11/12	0.92	0.21	-	54,56,58,62	0
3	BMA	B	1114	11/12	0.85	0.17	-	68,73,76,76	0
4	MAN	B	1119	11/12	0.92	0.17	-	57,59,60,60	0
2	NAG	B	1136	14/15	0.84	0.23	-	57,59,62,62	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.