



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 19, 2016 – 10:02 PM GMT

PDB ID : 5C6T
Title : Crystal structure of HCMV glycoprotein B in complex with 1G2 Fab
Authors : Chandramouli, S.; Ciferri, C.; Settembre, E.C.; Carfi, A.
Deposited on : 2015-06-23
Resolution : 3.60 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
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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
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) : rb-20026982

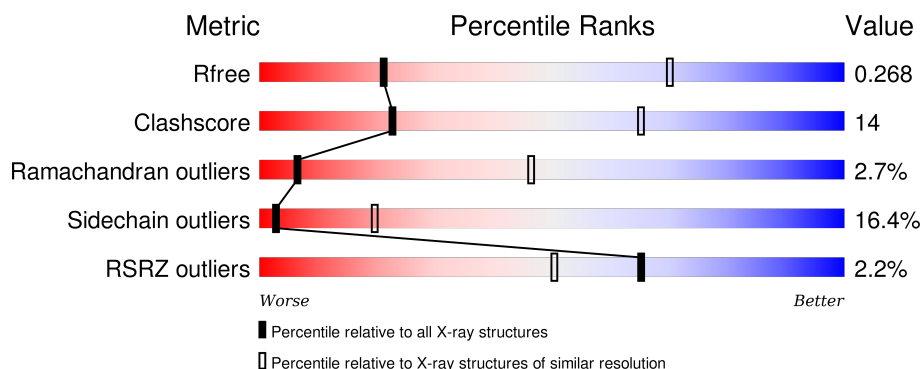
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 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	1408 (3.80-3.40)
Clashscore	102246	1010 (3.74-3.46)
Ramachandran outliers	100387	1007 (3.76-3.44)
Sidechain outliers	100360	1007 (3.76-3.44)
RSRZ outliers	91569	1003 (3.78-3.42)

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	636	
2	H	233	
3	L	214	

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
4	NAG	A	1009	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6411 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 Envelope glycoprotein B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	566	Total	C	N	O	S	0	1	0
			4578	2900	781	873	24			

There are 31 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	63	MET	-	expression tag	UNP P13201
A	64	GLU	-	expression tag	UNP P13201
A	65	SER	-	expression tag	UNP P13201
A	66	ARG	-	expression tag	UNP P13201
A	67	ILE	-	expression tag	UNP P13201
A	68	TRP	-	expression tag	UNP P13201
A	69	CYS	-	expression tag	UNP P13201
A	70	LEU	-	expression tag	UNP P13201
A	71	VAL	-	expression tag	UNP P13201
A	72	VAL	-	expression tag	UNP P13201
A	73	CYS	-	expression tag	UNP P13201
A	74	VAL	-	expression tag	UNP P13201
A	75	ASN	-	expression tag	UNP P13201
A	76	LEU	-	expression tag	UNP P13201
A	77	CYS	-	expression tag	UNP P13201
A	78	ILE	-	expression tag	UNP P13201
A	79	VAL	-	expression tag	UNP P13201
A	80	CYS	-	expression tag	UNP P13201
A	81	LEU	-	expression tag	UNP P13201
A	82	GLY	-	expression tag	UNP P13201
A	83	ALA	-	expression tag	UNP P13201
A	84	ALA	-	expression tag	UNP P13201
A	85	VAL	-	expression tag	UNP P13201
A	86	SER	-	expression tag	UNP P13201
A	156	HIS	ILE	engineered mutation	UNP P13201
A	157	ARG	HIS	engineered mutation	UNP P13201
A	240	ASN	TRP	engineered mutation	UNP P13201

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Chain	Residue	Modelled	Actual	Comment	Reference
A	242	THR	TYR	engineered mutation	UNP P13201
A	246	SER	CYS	engineered mutation	UNP P13201
A	457	SER	ARG	engineered mutation	UNP P13201
A	460	SER	ARG	engineered mutation	UNP P13201

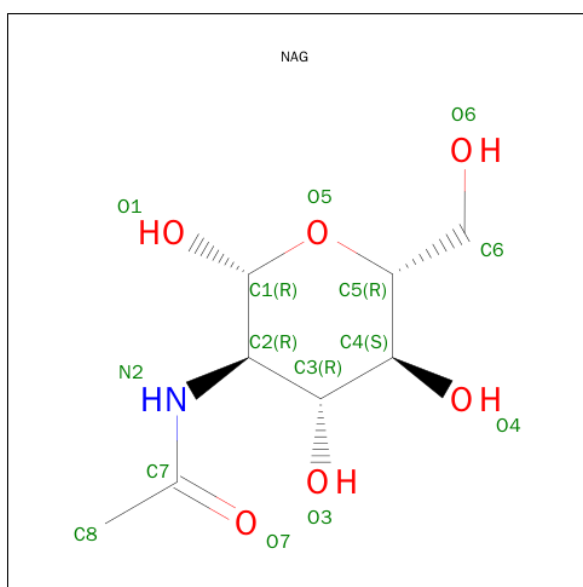
- Molecule 2 is a protein called 1G2 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	113	Total	C	N	O	S	0	0	0
			908	586	152	168	2			

- Molecule 3 is a protein called 1G2 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	104	Total	C	N	O	S	0	0	0
			784	486	135	161	2			

- Molecule 4 is 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	A	1	Total	C	N	O		0	0
			14	8	1	5			
4	A	1	Total	C	N	O		0	0
			14	8	1	5			

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

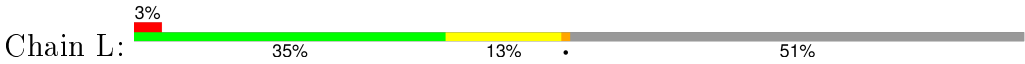
- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		

GLY THR ALA ALA LEU GLY CYS LEU VAL LYS ASP TYR PHE PRO GLU ASP LYS ARG VAL THR VAL SER TRP SER ASN CYS SER GLY ALA LEU THR SER GLU ASN GLY VAL HIS THR PHE PRO ALA VAL LEU GLN SER SER GLY TYR SER LEU SER SER VAL THR VAL PRO SER SER SER SER LEU GLY THR THR

TYR ILE CYS ASN VAL ASN HIS LYS PRO LYS SER ASN TYR THR LYS VAL ASP LYS ARG VAL GLU PRO LYS LYS SER CYS ASP LYS GLY SER GLU ASN LEU LEU THR PHE GLN

● Molecule 3: 1G2 Fab light chain



GLN SER VAL I4 T5 Q6 P7 P8 P14 G15 Q16 R17 S23 N28 Y33 V34 S35 F40 P41 G42 Y50 R51 N52 N53 Q54 G58 S64 L74 A75 I76 S77 R80 S81 E82 A85 C89 G90 T91 W92 S96 W97 G100 T106 V107 LEU

GLY GLN SER VAL LYS ALA PRO ALA SER VAL THR THR PHE PRO PRO SER SER GLU GLU LEU LEU GLN TRP LYS SER ALA ASN LYS ALA THR LEU VAL CYS GLN VAL ILE THR HIS ASP PHE GLY THR PRO GLY ALA VAL THR VAL VAL ALA TRP LYS ALA ASP SER SER PRO VAL LYS ALA GLY VAL GLU VAL THR THR THR THR PRO SER LYS

GLN SER ASN ASN LYS TYR ALA ALA SER SER TYR TYR LEU SER LEU LEU THR PRO GLU GLN TRP LYS SER HIS ARG SER TYR SER CYS GLN VAL THR THR HIS GLU GLY SER THR VAL GLU LYS THR VAL VAL ALA PRO THR GLU CYS SER

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	176.49 Å 176.49 Å 176.49 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.98 – 3.60 19.98 – 3.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.98-3.60) 100.0 (19.98-3.40)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.56 (at 3.44 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.212 , 0.260 0.224 , 0.268	Depositor DCC
R_{free} test set	1072 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	117.2	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 77.0	EDS
Estimated twinning fraction	0.028 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 25331 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6411	wwPDB-VP
Average B, all atoms (Å ²)	138.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.17% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, NAG

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	0.32	0/4680	0.56	0/6342
2	H	0.25	0/934	0.50	0/1274
3	L	0.24	0/804	0.48	0/1095
All	All	0.30	0/6418	0.54	0/8711

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	608	THR	Peptide

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	4578	0	4384	113	0
2	H	908	0	872	42	0
3	L	784	0	736	20	0
4	A	140	0	129	5	0
5	A	1	0	0	0	0
All	All	6411	0	6121	170	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 14.

The worst 5 of 170 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:148:THR:HG23	1:A:166:THR:HB	1.57	0.86
1:A:150:ARG:HB2	1:A:150:ARG:HH11	1.47	0.78
1:A:167:GLU:OE1	1:A:191:ARG:NH2	2.17	0.77
1:A:352:SER:HA	1:A:370:LYS:HD3	1.68	0.75
1:A:169:VAL:HG11	1:A:189:TYR:CZ	2.23	0.74

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	557/636 (88%)	479 (86%)	61 (11%)	17 (3%)	5	43
2	H	109/233 (47%)	93 (85%)	14 (13%)	2 (2%)	11	54
3	L	102/214 (48%)	87 (85%)	13 (13%)	2 (2%)	9	53
All	All	768/1083 (71%)	659 (86%)	88 (12%)	21 (3%)	6	46

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	132	ASN
1	A	302	ASN
1	A	405	ASN
1	A	603	LEU
3	L	53	ASN

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	504/576 (88%)	409 (81%)	95 (19%)	2	13
2	H	97/202 (48%)	84 (87%)	13 (13%)	5	29
3	L	87/182 (48%)	82 (94%)	5 (6%)	25	67
All	All	688/960 (72%)	575 (84%)	113 (16%)	3	20

5 of 113 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	386	ASP
1	A	522	LYS
2	H	106	ASP
1	A	389	LEU
1	A	427	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	249	ASN
2	H	79	GLN
3	L	16	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 11 ligands modelled in this entry, 1 is monoatomic - leaving 10 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	$\# Z > 2$
4	NAG	A	1001	1	14,14,15	0.29	0	15,19,21	0.21	0
4	NAG	A	1002	1	14,14,15	0.33	0	15,19,21	0.69	1 (6%)
4	NAG	A	1003	1	14,14,15	0.18	0	15,19,21	0.33	0
4	NAG	A	1004	1	14,14,15	0.31	0	15,19,21	0.22	0
4	NAG	A	1005	1	14,14,15	0.23	0	15,19,21	0.39	0
4	NAG	A	1006	4	14,14,15	1.08	1 (7%)	15,19,21	1.12	1 (6%)
4	NAG	A	1007	1,4	14,14,15	0.76	1 (7%)	15,19,21	0.96	1 (6%)
4	NAG	A	1008	1	14,14,15	0.55	0	15,19,21	0.30	0
4	NAG	A	1009	1	14,14,15	0.40	0	15,19,21	0.45	0
4	NAG	A	1010	1	14,14,15	0.56	0	15,19,21	0.44	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	1001	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1002	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1003	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1004	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	A	1005	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1006	4	-	0/6/23/26	0/1/1/1
4	NAG	A	1007	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	1008	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1009	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1010	1	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1007	NAG	C1-C2	2.04	1.55	1.52
4	A	1006	NAG	O5-C1	3.74	1.49	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1002	NAG	C1-O5-C5	2.31	115.53	112.14
4	A	1007	NAG	C1-O5-C5	3.06	116.64	112.14
4	A	1006	NAG	C1-O5-C5	3.92	117.90	112.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1002	NAG	1	0
4	A	1006	NAG	1	0
4	A	1007	NAG	1	0
4	A	1009	NAG	1	0
4	A	1010	NAG	2	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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, 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	566/636 (88%)	-0.50	2 (0%) 93 88	60, 100, 167, 230	0
2	H	113/233 (48%)	0.39	9 (7%) 15 10	114, 223, 284, 349	0
3	L	104/214 (48%)	0.39	6 (5%) 26 18	151, 228, 266, 310	0
All	All	783/1083 (72%)	-0.26	17 (2%) 65 50	60, 114, 257, 349	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	8	GLY	6.5
2	H	9	PRO	4.9
3	L	89	CYS	4.4
2	H	7	SER	3.6
2	H	38	TRP	3.4

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, 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(\AA^2)	Q<0.9
4	NAG	A	1009	14/15	0.87	0.44	2.66	145,157,161,161	0
4	NAG	A	1002	14/15	0.92	0.25	0.49	97,109,118,123	0
4	NAG	A	1007	14/15	0.87	0.20	-0.19	137,152,161,162	0
4	NAG	A	1004	14/15	0.71	0.49	-	228,238,246,246	0
5	MG	A	1011	1/1	0.91	0.23	-	99,99,99,99	1
4	NAG	A	1005	14/15	0.68	0.52	-	228,240,254,258	0
4	NAG	A	1001	14/15	0.77	0.38	-	172,195,199,201	0
4	NAG	A	1006	14/15	0.79	0.46	-	158,174,182,189	0
4	NAG	A	1010	14/15	0.91	0.20	-	134,146,164,165	0
4	NAG	A	1008	14/15	0.83	0.45	-	157,176,183,184	0
4	NAG	A	1003	14/15	0.61	0.52	-	175,192,205,209	0

6.5 Other polymers [i](#)

There are no such residues in this entry.