



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 06:08 AM UTC

PDB ID : 1TP8 / pdb\_00001tp8  
Title : CRYSTAL STRUCTURE OF A GALACTOSE SPECIFIC LECTIN FROM ARTOCARPUS HIRSUTA IN COMPLEX WITH METHYL- $\alpha$ -D-GALACTOSE  
Authors : Rao, K.N.; Suresh, C.G.; Katre, U.V.; Gaikwad, S.M.; Khan, M.I.  
Deposited on : 2004-06-16  
Resolution : 3.00 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

---

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

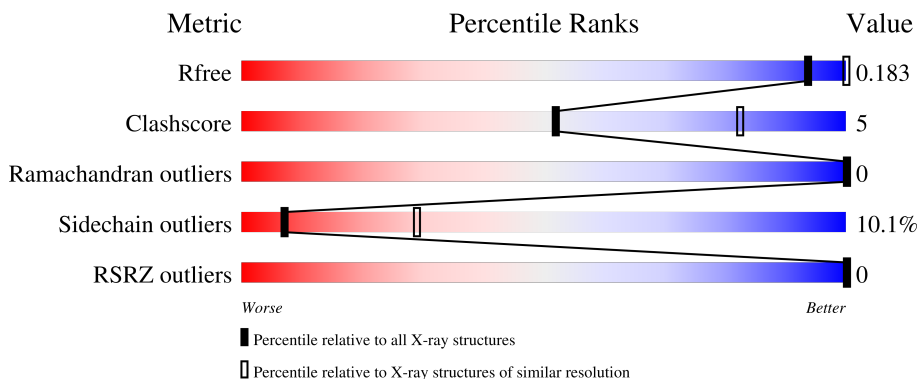
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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))
$R_{free}$	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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	133	77% 18% 5%
1	C	133	78% 20% .
1	E	133	74% 22% .
1	G	133	78% 19% .
2	B	20	60% 10% 10% 20%

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
2	D	20	
2	F	20	
2	H	20	

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
3	AMG	E	502	X	-	-	-

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4705 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.

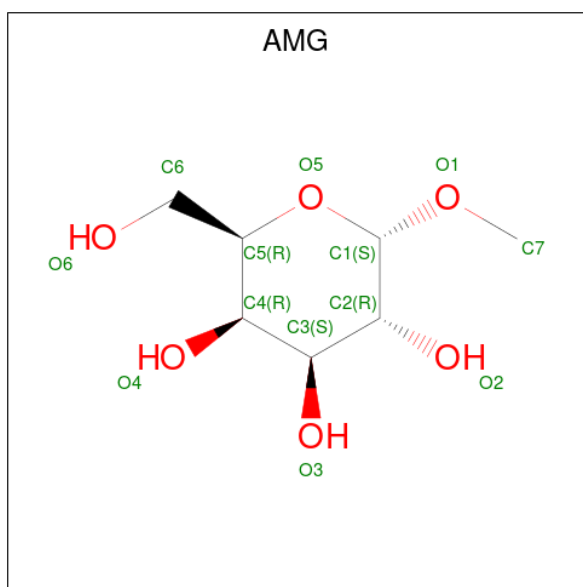
- Molecule 1 is a protein called AGGLUTININ ALPHA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	133	1035	673	159	201	2	4	0	0
1	C	133	1035	673	159	201	2	4	0	0
1	E	133	1035	673	159	201	2	4	0	0
1	G	133	1035	673	159	201	2	4	0	0

- Molecule 2 is a protein called AGGLUTININ BETA CHAIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	16	111	71	20	20	8	0	0
2	D	16	111	71	20	20	4	0	0
2	F	16	111	71	20	20	8	0	0
2	H	16	111	71	20	20	4	0	0

- Molecule 3 is methyl alpha-D-galactopyranoside (CCD ID: AMG) (formula: C<sub>7</sub>H<sub>14</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 13 7 6	0	0
3	C	1	Total C O 13 7 6	0	0
3	E	1	Total C O 13 7 6	0	0
3	G	1	Total C O 13 7 6	0	0


- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	19	Total O 19 19	0	0
4	B	3	Total O 3 3	0	0
4	C	17	Total O 17 17	0	0
4	E	14	Total O 14 14	0	0
4	F	1	Total O 1 1	0	0
4	G	15	Total O 15 15	0	0

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


These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

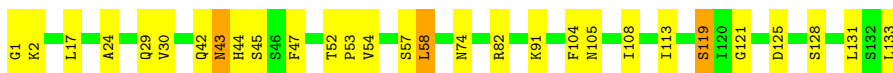
- Molecule 1: AGGLUTININ ALPHA CHAIN

Chain A: 



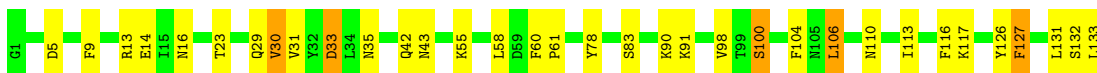
- Molecule 1: AGGLUTININ ALPHA CHAIN

Chain C: 




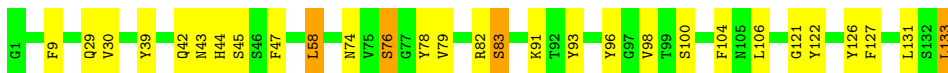
- Molecule 1: AGGLUTININ ALPHA CHAIN

Chain E: 



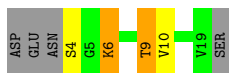
- Molecule 1: AGGLUTININ ALPHA CHAIN

Chain G: 



- Molecule 2: AGGLUTININ BETA CHAIN

Chain B: 



- Molecule 2: AGGLUTININ BETA CHAIN

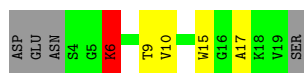
Chain D: 



- Molecule 2: AGGLUTININ BETA CHAIN



- Molecule 2: AGGLUTININ BETA CHAIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.90Å 121.90Å 131.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00 20.00 – 3.01	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-3.00) 72.4 (20.00-3.01)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	8.41 (at 3.00Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.193 , 0.237 0.181 , 0.183	Depositor DCC
$R_{free}$ test set	1465 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.2	Xtrriage
Anisotropy	0.652	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 20.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.33$ , $\langle L^2 \rangle = 0.15$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4705	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.88% 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: AMG

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	0.61	0/1064	1.59	14/1443 (1.0%)
1	C	0.62	0/1064	1.64	12/1443 (0.8%)
1	E	0.58	0/1064	1.54	11/1443 (0.8%)
1	G	0.64	0/1064	1.71	13/1443 (0.9%)
2	B	0.87	1/113 (0.9%)	1.81	1/152 (0.7%)
2	D	0.72	0/113	1.65	1/152 (0.7%)
2	F	0.87	0/113	1.83	3/152 (2.0%)
2	H	0.68	0/113	1.73	2/152 (1.3%)
All	All	0.63	1/4708 (0.0%)	1.64	57/6380 (0.9%)

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
2	D	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	6	LYS	CB-CG	-5.66	1.35	1.52

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	74	ASN	OD1-CG-ND2	8.88	131.48	122.60
1	G	44	HIS	CA-CB-CG	-7.79	106.01	113.80
1	C	105	ASN	OD1-CG-ND2	7.70	130.30	122.60
1	A	132	SER	N-CA-C	7.33	119.28	108.14

*Continued on next page...*

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	E	110	ASN	OD1-CG-ND2	-6.96	115.64	122.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	18	LYS	Mainchain

## 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	1035	0	995	12	0
1	C	1035	0	995	9	0
1	E	1035	0	995	11	0
1	G	1035	0	995	12	0
2	B	111	0	112	0	0
2	D	111	0	112	2	0
2	F	111	0	112	1	0
2	H	111	0	112	2	0
3	A	13	0	14	0	0
3	C	13	0	14	0	0
3	E	13	0	14	2	0
3	G	13	0	14	1	0
4	A	19	0	0	0	0
4	B	3	0	0	0	0
4	C	17	0	0	0	0
4	E	14	0	0	0	0
4	F	1	0	0	0	0
4	G	15	0	0	0	0
All	All	4705	0	4484	46	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 5.

The worst 5 of 46 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:C:108:ILE:HD11	1:C:113:ILE:HD11	1.73	0.70
1:E:14:GLU:OE2	1:E:55:LYS:HE2	1.99	0.63
1:G:58:LEU:H	1:G:58:LEU:HD22	1.64	0.61
1:G:29:GLN:HG3	1:G:43:ASN:HB2	1.82	0.61
2:F:10:VAL:HG12	1:G:133:LEU:HD13	1.83	0.61

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	131/133 (98%)	125 (95%)	6 (5%)	0	100	100
1	C	131/133 (98%)	125 (95%)	6 (5%)	0	100	100
1	E	131/133 (98%)	126 (96%)	5 (4%)	0	100	100
1	G	131/133 (98%)	127 (97%)	4 (3%)	0	100	100
2	B	14/20 (70%)	13 (93%)	1 (7%)	0	100	100
2	D	14/20 (70%)	13 (93%)	1 (7%)	0	100	100
2	F	14/20 (70%)	14 (100%)	0	0	100	100
2	H	14/20 (70%)	14 (100%)	0	0	100	100
All	All	580/612 (95%)	557 (96%)	23 (4%)	0	100	100

There are no Ramachandran outliers to report.

#### 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	113/113 (100%)	102 (90%)	11 (10%)	8 30
1	C	113/113 (100%)	106 (94%)	7 (6%)	16 49
1	E	113/113 (100%)	102 (90%)	11 (10%)	8 30
1	G	113/113 (100%)	104 (92%)	9 (8%)	11 38
2	B	11/16 (69%)	7 (64%)	4 (36%)	0 1
2	D	11/16 (69%)	9 (82%)	2 (18%)	2 9
2	F	11/16 (69%)	8 (73%)	3 (27%)	0 2
2	H	11/16 (69%)	8 (73%)	3 (27%)	0 2
All	All	496/516 (96%)	446 (90%)	50 (10%)	7 29

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	91	LYS
2	F	9	THR
2	H	10	VAL
1	E	100	SER
1	E	127	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	110	ASN
2	F	8	GLN
2	H	8	GLN
1	G	43	ASN
2	B	8	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

4 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
3	AMG	E	502	-	13,13,13	0.39	0	18,18,18	2.25	6 (33%)
3	AMG	G	503	-	13,13,13	0.43	0	18,18,18	1.44	3 (16%)
3	AMG	C	501	-	13,13,13	0.53	0	18,18,18	1.75	5 (27%)
3	AMG	A	500	-	13,13,13	0.55	0	18,18,18	1.41	1 (5%)

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	AMG	G	503	-	-	0/4/24/24	0/1/1/1
3	AMG	C	501	-	-	0/4/24/24	0/1/1/1
3	AMG	A	500	-	-	0/4/24/24	0/1/1/1
3	AMG	E	502	-	1/1/5/5	3/4/24/24	0/1/1/1

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	502	AMG	C1-C2-C3	4.90	120.31	110.01
3	A	500	AMG	O1-C1-C2	-4.08	103.43	108.14
3	C	501	AMG	O3-C3-C2	-4.00	100.95	110.38
3	E	502	AMG	O1-C1-C2	-3.71	103.86	108.14
3	E	502	AMG	O5-C1-O1	3.17	118.32	110.94

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	E	502	AMG	C2

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	502	AMG	O5-C1-O1-C7
3	E	502	AMG	C2-C1-O1-C7
3	E	502	AMG	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	502	AMG	2	0
3	G	503	AMG	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 [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	133/133 (100%)	-1.82	0 100 100	20, 33, 43, 54	1 (0%)
1	C	133/133 (100%)	-1.82	0 100 100	22, 31, 43, 50	1 (0%)
1	E	133/133 (100%)	-1.82	0 100 100	23, 35, 46, 56	1 (0%)
1	G	133/133 (100%)	-1.84	0 100 100	19, 31, 42, 47	1 (0%)
2	B	16/20 (80%)	-1.60	0 100 100	21, 27, 52, 67	2 (12%)
2	D	16/20 (80%)	-1.63	0 100 100	22, 31, 47, 69	1 (6%)
2	F	16/20 (80%)	-1.58	0 100 100	21, 27, 50, 66	2 (12%)
2	H	16/20 (80%)	-1.68	0 100 100	24, 32, 46, 68	1 (6%)
All	All	596/612 (97%)	-1.80	0 100 100	19, 32, 45, 69	10 (1%)

There are no RSRZ outliers to report.

### 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 oligosaccharides 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. 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	B-factors( $\text{\AA}^2$ )	Q<0.9
3	AMG	A	500	13/13	0.99	0.03	28,30,31,31	0
3	AMG	C	501	13/13	1.00	0.02	28,30,33,33	0
3	AMG	E	502	13/13	1.00	0.03	27,30,31,32	0
3	AMG	G	503	13/13	1.00	0.02	31,31,32,32	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.