



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2018 – 07:06 am GMT

PDB ID : 2ACF  
Title : NMR STRUCTURE OF SARS-COV NON-STRUCTURAL PROTEIN  
NSP3A (SARS1) FROM SARS CORONAVIRUS  
Authors : Saikatendu, K.S.; Joseph, J.S.; Subramanian, V.; Neuman, B.W.; Buchmeier,  
M.J.; Stevens, R.C.; Kuhn, P.; Joint Center for Structural Genomics (JCSG)  
Deposited on : 2005-07-18  
Resolution : 1.40 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.

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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 : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : trunk30967  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30967

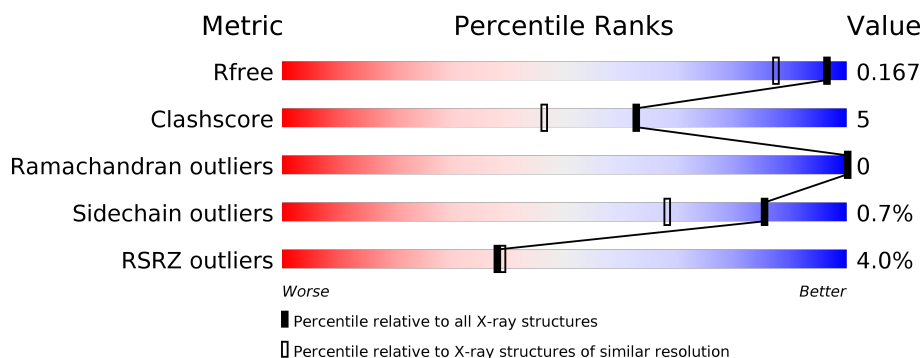
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.40 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))
$R_{free}$	111664	1450 (1.40-1.40)
Clashscore	122126	1541 (1.40-1.40)
Ramachandran outliers	120053	1500 (1.40-1.40)
Sidechain outliers	120020	1499 (1.40-1.40)
RSRZ outliers	108989	1412 (1.40-1.40)

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	182	<div> <div>4%</div> <div> <div></div> <div>88%</div> <div>5% • 5%</div> </div> </div>
1	B	182	<div> <div>3%</div> <div> <div></div> <div>88%</div> <div>7% 5%</div> </div> </div>
1	C	182	<div> <div>3%</div> <div> <div></div> <div>86%</div> <div>10% • •</div> </div> </div>
1	D	182	<div> <div>5%</div> <div> <div></div> <div>91%</div> <div>7% • •</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GOL	B	1004	-	-	X	-

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6502 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 Replicase polypeptide 1ab.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	172	Total	C	N	O	S	0	11	0
			1382	874	240	260	8			
1	B	173	Total	C	N	O	S	0	3	0
			1318	835	225	250	8			
1	C	176	Total	C	N	O	S	0	10	0
			1401	887	241	264	9			
1	D	179	Total	C	N	O	S	0	4	0
			1379	870	241	259	9			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	177	HIS	-	EXPRESSION TAG	GB 34555776
A	178	HIS	-	EXPRESSION TAG	GB 34555776
A	179	HIS	-	EXPRESSION TAG	GB 34555776
A	180	HIS	-	EXPRESSION TAG	GB 34555776
A	181	HIS	-	EXPRESSION TAG	GB 34555776
A	182	HIS	-	EXPRESSION TAG	GB 34555776
A	183	MET	-	CLONING ARTIFACT	GB 34555776
B	177	HIS	-	EXPRESSION TAG	GB 34555776
B	178	HIS	-	EXPRESSION TAG	GB 34555776
B	179	HIS	-	EXPRESSION TAG	GB 34555776
B	180	HIS	-	EXPRESSION TAG	GB 34555776
B	181	HIS	-	EXPRESSION TAG	GB 34555776
B	182	HIS	-	EXPRESSION TAG	GB 34555776
B	183	MET	-	CLONING ARTIFACT	GB 34555776
C	177	HIS	-	EXPRESSION TAG	GB 34555776
C	178	HIS	-	EXPRESSION TAG	GB 34555776
C	179	HIS	-	EXPRESSION TAG	GB 34555776
C	180	HIS	-	EXPRESSION TAG	GB 34555776
C	181	HIS	-	EXPRESSION TAG	GB 34555776
C	182	HIS	-	EXPRESSION TAG	GB 34555776
C	183	MET	-	CLONING ARTIFACT	GB 34555776

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Chain	Residue	Modelled	Actual	Comment	Reference
D	177	HIS	-	EXPRESSION TAG	GB 34555776
D	178	HIS	-	EXPRESSION TAG	GB 34555776
D	179	HIS	-	EXPRESSION TAG	GB 34555776
D	180	HIS	-	EXPRESSION TAG	GB 34555776
D	181	HIS	-	EXPRESSION TAG	GB 34555776
D	182	HIS	-	EXPRESSION TAG	GB 34555776
D	183	MET	-	CLONING ARTIFACT	GB 34555776

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	228	Total	O	0	0
			228	228		
3	B	260	Total	O	0	0
			260	260		
3	C	232	Total	O	0	0
			232	232		
3	D	230	Total	O	0	0
			230	230		



- Molecule 1: Replicase polyprotein 1ab



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.50Å 81.58Å 125.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.40 31.22 – 1.40	Depositor EDS
% Data completeness (in resolution range)	99.2 (50.00-1.40) 99.2 (31.22-1.40)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.04	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.83 (at 1.40Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.164 , 0.189 0.168 , 0.167	Depositor DCC
$R_{free}$ test set	7583 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.0	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.44 , 57.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	6502	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 25.84 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.9439e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: GOL

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	0.72	0/1403	0.82	2/1902 (0.1%)
1	B	0.85	0/1336	0.84	3/1813 (0.2%)
1	C	0.83	0/1420	0.93	7/1925 (0.4%)
1	D	0.77	0/1401	0.80	0/1900
All	All	0.79	0/5560	0.85	12/7540 (0.2%)

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	249	ASP	CB-CG-OD2	-7.30	111.73	118.30
1	B	249	ASP	CB-CG-OD2	-7.12	111.89	118.30
1	B	295	TYR	CB-CG-CD2	6.15	124.69	121.00
1	C	330	ARG	NE-CZ-NH1	6.14	123.37	120.30
1	A	248	ASP	CB-CG-OD2	-5.87	113.02	118.30

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	1382	0	1401	12	0
1	B	1318	0	1348	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1401	0	1435	15	0
1	D	1379	0	1401	11	0
2	A	12	0	16	3	0
2	B	18	0	24	4	0
2	C	36	0	48	9	0
2	D	6	0	8	0	0
3	A	228	0	0	5	0
3	B	260	0	0	6	0
3	C	232	0	0	3	0
3	D	230	0	0	4	0
All	All	6502	0	5681	53	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 53 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:227:HIS:H	1:D:244:GLN:HE22	1.25	0.84
1:B:227:HIS:H	1:B:244:GLN:HE22	1.28	0.82
1:B:210:GLN:HG3	3:B:1205:HOH:O	1.80	0.80
1:C:227:HIS:H	1:C:244:GLN:HE22	1.28	0.79
1:C:282:LEU:HB3	2:C:1011:GOL:H2	1.68	0.75

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	181/182 (100%)	178 (98%)	3 (2%)	0	100	100
1	B	174/182 (96%)	174 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	184/182 (101%)	183 (100%)	1 (0%)	0	100	100
1	D	181/182 (100%)	178 (98%)	3 (2%)	0	100	100
All	All	720/728 (99%)	713 (99%)	7 (1%)	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	151/150 (101%)	150 (99%)	1 (1%)	85	68
1	B	144/150 (96%)	144 (100%)	0	100	100
1	C	154/150 (103%)	151 (98%)	3 (2%)	60	26
1	D	151/150 (101%)	150 (99%)	1 (1%)	85	68
All	All	600/600 (100%)	595 (99%)	5 (1%)	85	64

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	181	HIS
1	C	290[A]	LEU
1	C	290[B]	LEU
1	C	345	GLN
1	D	357	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	345	GLN
1	C	213	ASN
1	D	323	GLN
1	C	187	GLN

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Mol	Chain	Res	Type
1	C	227	HIS

### 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](#)

12 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	GOL	A	1002	-	5,5,5	0.30	0	5,5,5	0.48	0
2	GOL	A	1010	-	5,5,5	0.38	0	5,5,5	0.61	0
2	GOL	B	1001	-	5,5,5	0.52	0	5,5,5	0.49	0
2	GOL	B	1004	-	5,5,5	0.59	0	5,5,5	0.75	0
2	GOL	B	1007	-	5,5,5	0.49	0	5,5,5	1.17	0
2	GOL	C	1005	-	5,5,5	1.05	0	5,5,5	0.98	0
2	GOL	C	1006	-	5,5,5	1.52	2 (40%)	5,5,5	1.05	0
2	GOL	C	1008	-	5,5,5	0.72	0	5,5,5	1.29	0
2	GOL	C	1009	-	5,5,5	0.75	0	5,5,5	1.96	2 (40%)
2	GOL	C	1011	-	5,5,5	0.46	0	5,5,5	0.27	0
2	GOL	C	1012	-	5,5,5	0.40	0	5,5,5	0.30	0
2	GOL	D	1003	-	5,5,5	0.21	0	5,5,5	0.68	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	GOL	A	1002	-	-	0/4/4/4	0/0/0/0
2	GOL	A	1010	-	-	0/4/4/4	0/0/0/0
2	GOL	B	1001	-	-	0/4/4/4	0/0/0/0
2	GOL	B	1004	-	-	0/4/4/4	0/0/0/0
2	GOL	B	1007	-	-	0/4/4/4	0/0/0/0
2	GOL	C	1005	-	-	0/4/4/4	0/0/0/0
2	GOL	C	1006	-	-	0/4/4/4	0/0/0/0
2	GOL	C	1008	-	-	0/4/4/4	0/0/0/0
2	GOL	C	1009	-	-	0/4/4/4	0/0/0/0
2	GOL	C	1011	-	-	0/4/4/4	0/0/0/0
2	GOL	C	1012	-	-	0/4/4/4	0/0/0/0
2	GOL	D	1003	-	-	0/4/4/4	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1006	GOL	C1-C2	2.17	1.60	1.52
2	C	1006	GOL	O1-C1	2.38	1.52	1.42

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1009	GOL	O3-C3-C2	-3.04	95.37	110.11
2	C	1009	GOL	O2-C2-C1	2.64	121.04	109.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1002	GOL	2	0
2	A	1010	GOL	1	0
2	B	1004	GOL	4	0
2	C	1005	GOL	1	0
2	C	1006	GOL	3	0
2	C	1008	GOL	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1009	GOL	1	0
2	C	1011	GOL	1	0
2	C	1012	GOL	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	172/182 (94%)	0.09	8 (4%)	31 31	12, 19, 33, 44	1 (0%)
1	B	173/182 (95%)	-0.03	5 (2%)	51 51	10, 15, 25, 41	0
1	C	176/182 (96%)	0.03	6 (3%)	45 45	10, 15, 26, 43	0
1	D	179/182 (98%)	0.04	9 (5%)	29 28	12, 18, 29, 47	0
All	All	700/728 (96%)	0.03	28 (4%)	38 39	10, 17, 29, 47	1 (0%)

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	180	HIS	9.1
1	D	181	HIS	8.7
1	C	183	MET	7.5
1	C	358	VAL	7.4
1	C	356	PRO	7.1

### 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. 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
2	GOL	C	1012	6/6	0.67	0.17	41,45,46,49	0
2	GOL	C	1011	6/6	0.74	0.30	46,46,47,48	0
2	GOL	A	1010	6/6	0.75	0.18	36,39,40,41	0
2	GOL	C	1009	6/6	0.80	0.20	20,33,36,36	0
2	GOL	C	1005	6/6	0.82	0.20	26,38,43,44	0
2	GOL	C	1008	6/6	0.82	0.17	21,36,37,39	0
2	GOL	A	1002	6/6	0.83	0.24	32,41,42,44	0
2	GOL	D	1003	6/6	0.84	0.20	32,40,42,42	0
2	GOL	C	1006	6/6	0.85	0.14	20,25,27,28	0
2	GOL	B	1007	6/6	0.87	0.11	22,25,32,34	0
2	GOL	B	1001	6/6	0.88	0.14	20,23,25,32	0
2	GOL	B	1004	6/6	0.91	0.16	19,28,31,33	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.