

# wwPDB X-ray Structure Validation Summary Report (i)

#### Oct 23, 2023 – 11:21 AM EDT

PDB ID	:	3ALX
Title	:	Crystal structure of the measles virus hemagglutinin bound to its cellular re-
		ceptor SLAM (MV-H(L482R)-SLAM(N102H/R108Y) fusion)
Authors	:	Hashiguchi, T.; Ose, T.; Kubota, M.; Maita, N.; Kamishikiryo, J.; Maenaka,
		K.; Yanagi, Y.
Deposited on	:	2010-08-09
Resolution	:	3.15  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 https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 3.15 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R <sub>free</sub>	130704	1665 (3.20-3.12)
Clashscore	141614	1804 (3.20-3.12)
Ramachandran outliers	138981	1770 (3.20-3.12)
Sidechain outliers	138945	1769 (3.20-3.12)
RSRZ outliers	127900	1616 (3.20-3.12)

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 >=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 <=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	А	559	% <b>4</b> 1%	40%	11% • 8%
1	В	559	3%	44%	<b>6%</b> • 6%
1	С	559	35%	46%	10% • 8%
1	D	559	31%	51%	8% 10%

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	
	2110	- D	0.01					1

IVIOI	Type	Chain	Res	Chirality	Geometry	Clasnes	Electron density
2	NAG	В	801	-	-	-	Х
2	NAG	С	801	-	-	-	Х
2	NAG	D	901	-	-	-	Х



# 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 16313 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Λ	515	Total	С	Ν	Ο	$\mathbf{S}$	0	0	0
1	A	515	4053	2598	677	750	28	0	0	U
1	1 B	526	Total	С	Ν	0	S	0	0	0
1		520	4141	2651	695	767	28			
1	1 C	C 514	Total	С	Ν	0	S	0	0	0
1			4051	2599	676	748	28	0	0	U
1	1 D	504	Total	С	Ν	0	S	0	0	0
	304	3984	2562	663	732	27	0	0	U	

• Molecule 1 is a protein called Hemagglutinin,LINKER,CDw150.

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	181	GLU	-	expression tag	UNP E2RZS2
А	182	THR	-	expression tag	UNP E2RZS2
А	183	GLY	-	expression tag	UNP E2RZS2
А	482	ARG	LEU	engineered mutation	UNP E2RZS2
А	102	HIS	ASN	engineered mutation	UNP Q9GJT3
А	108	TYR	ARG	engineered mutation	UNP Q9GJT3
А	141	GLY	-	expression tag	UNP Q9GJT3
А	142	THR	-	expression tag	UNP Q9GJT3
А	143	LYS	-	expression tag	UNP Q9GJT3
А	144	HIS	-	expression tag	UNP Q9GJT3
А	145	HIS	-	expression tag	UNP Q9GJT3
А	146	HIS	-	expression tag	UNP Q9GJT3
А	147	HIS	-	expression tag	UNP Q9GJT3
А	148	HIS	-	expression tag	UNP Q9GJT3
А	149	HIS	-	expression tag	UNP Q9GJT3
В	181	GLU	-	expression tag	UNP E2RZS2
В	182	THR	-	expression tag	UNP E2RZS2
В	183	GLY	-	expression tag	UNP E2RZS2
В	482	ARG	LEU	engineered mutation	UNP E2RZS2
В	102	HIS	ASN	engineered mutation	UNP Q9GJT3
В	108	TYR	ARG	engineered mutation	UNP Q9GJT3

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Chain	Residue	Modelled	Actual	Comment	Reference
В	141	GLY	-	expression tag	UNP Q9GJT3
В	142	THR	-	expression tag	UNP Q9GJT3
В	143	LYS	_	expression tag	UNP Q9GJT3
В	144	HIS	_	expression tag	UNP Q9GJT3
В	145	HIS	_	expression tag	UNP Q9GJT3
В	146	HIS	-	expression tag	UNP Q9GJT3
В	147	HIS	-	expression tag	UNP Q9GJT3
В	148	HIS	-	expression tag	UNP Q9GJT3
В	149	HIS	-	expression tag	UNP Q9GJT3
С	181	GLU	-	expression tag	UNP E2RZS2
С	182	THR	-	expression tag	UNP E2RZS2
С	183	GLY	-	expression tag	UNP E2RZS2
С	482	ARG	LEU	engineered mutation	UNP E2RZS2
С	102	HIS	ASN	engineered mutation	UNP Q9GJT3
С	108	TYR	ARG	engineered mutation	UNP Q9GJT3
С	141	GLY	-	expression tag	UNP Q9GJT3
С	142	THR	-	expression tag	UNP Q9GJT3
С	143	LYS	-	expression tag	UNP Q9GJT3
С	144	HIS	-	expression tag	UNP Q9GJT3
С	145	HIS	-	expression tag	UNP Q9GJT3
С	146	HIS	-	expression tag	UNP Q9GJT3
С	147	HIS	-	expression tag	UNP Q9GJT3
С	148	HIS	-	expression tag	UNP Q9GJT3
С	149	HIS	-	expression tag	UNP Q9GJT3
D	181	GLU	-	expression tag	UNP E2RZS2
D	182	THR	-	expression tag	UNP E2RZS2
D	183	GLY	-	expression tag	UNP E2RZS2
D	482	ARG	LEU	engineered mutation	UNP E2RZS2
D	102	HIS	ASN	engineered mutation	UNP Q9GJT3
D	108	TYR	ARG	engineered mutation	UNP Q9GJT3
D	141	GLY	-	expression tag	UNP Q9GJT3
D	142	THR	-	expression tag	UNP Q9GJT3
D	143	LYS	-	expression tag	UNP Q9GJT3
D	144	HIS	-	expression tag	UNP Q9GJT3
D	145	HIS	-	expression tag	UNP Q9GJT3
D	146	HIS	-	expression tag	UNP Q9GJT3
D	147	HIS	-	expression tag	UNP Q9GJT3
D	148	HIS	-	expression tag	UNP Q9GJT3
D	149	HIS	-	expression tag	UNP Q9GJT3

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• Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	
2	А	1	Total C N O	0	0	
		1	14 8 1 5	Ŭ	0	
2	В	1	Total C N O	0	0	
		1	14 8 1 5	0	0	
2	В	1	Total C N O	0	0	
2		I	14 8 1 5	0	0	
2	C	C	1	Total C N O	0	0
2	U	I	14 8 1 5	0	0	
2	С	1	Total C N O	0	0	
	1	14 8 1 5	0	0		
2	П	1	Total C N O	0	0	
		L	14 8 1 5		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: Hemagglutinin,LINKER,CDw150









# 178 178 181 181 181 181 181 181 182 183 184 184 184 184 185 185 186 186 192 192 193 193 193 193 193 193 193 193 193 193 193 193 193 193 193 193 193 193 1107 1107 1107 1107 1107 1107 1107 1107 1107 1107 1107 1107 1113

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# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	187.71Å 170.07Å 110.68Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $117.28^{\circ}$ $90.00^{\circ}$	Depositor
Bosolution(A)	19.97 - 3.15	Depositor
Resolution (A)	19.96 - 3.16	EDS
% Data completeness	99.1 (19.97-3.15)	Depositor
(in resolution range)	99.2 (19.96-3.16)	EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.59 (at 3.15 \text{\AA})$	Xtriage
Refinement program	CNS 1.3	Depositor
P. P.	0.231 , $0.292$	Depositor
$n, n_{free}$	0.232 , $0.292$	DCC
$R_{free}$ test set	2644 reflections $(5.04%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	71.0	Xtriage
Anisotropy	0.367	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.31, 63.5	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.47, < L^2>=0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	16313	wwPDB-VP
Average B, all atoms $(Å^2)$	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 19.25% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: 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).

Mal	Chain	Bond lengths		Bond angles		
		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.49	0/4155	0.74	2/5646~(0.0%)	
1	В	0.44	0/4243	0.71	2/5763~(0.0%)	
1	С	0.46	0/4151	0.71	1/5638~(0.0%)	
1	D	0.41	0/4083	0.66	0/5545	
All	All	0.45	0/16632	0.70	5/22592~(0.0%)	

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	С	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	В	48	THR	N-CA-C	-6.29	94.02	111.00
1	С	132	CYS	CA-CB-SG	-6.03	103.15	114.00
1	А	48	THR	N-CA-C	-5.52	96.09	111.00
1	В	92	LEU	N-CA-C	-5.35	96.54	111.00
1	А	92	LEU	N-CA-C	-5.34	96.58	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	С	541	TYR	Sidechain



### 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	А	4053	0	4023	288	0
1	В	4141	0	4119	297	0
1	С	4051	0	4024	313	0
1	D	3984	0	3964	350	0
2	А	14	0	13	0	0
2	В	28	0	26	0	0
2	С	28	0	26	1	0
2	D	14	0	13	1	0
All	All	16313	0	16208	1224	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 38.

The worst 5 of 1224 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:85:GLU:HG2	1:A:86:ALA:H	1.09	1.16
1:A:236:LYS:HB3	1:A:237:PRO:HD2	1.30	1.14
1:D:503:GLU:HB2	1:D:76:ASN:HD22	1.05	1.09
1:A:60:ILE:HG22	1:A:61:HIS:H	1.13	1.08
1:A:540:TYR:HE1	1:A:568:VAL:HG21	1.22	1.04

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	P	erc	entile	es
1	А	509/559~(91%)	416 (82%)	62 (12%)	31 (6%)		1	10	
1	В	520/559~(93%)	412 (79%)	86 (16%)	22 (4%)		3	17	
1	С	504/559~(90%)	407 (81%)	67~(13%)	30 (6%)		1	10	
1	D	492/559~(88%)	389~(79%)	70 (14%)	33~(7%)		1	8	
All	All	2025/2236~(91%)	1624 (80%)	285 (14%)	116 (6%)		1	12	

5 of 116 Ramachandran outliers are listed below:

Mol	Chain	$\mathbf{Res}$	Type
1	А	311	GLN
1	А	389	LYS
1	А	439	SER
1	А	490	ALA
1	А	494	CYS

#### 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	А	457/489~(94%)	403 (88%)	54 (12%)	5	21		
1	В	468/489~(96%)	433 (92%)	35~(8%)	13	42		
1	С	457/489~(94%)	400 (88%)	57 (12%)	4	19		
1	D	449/489~(92%)	419 (93%)	30 (7%)	16	47		
All	All	1831/1956 (94%)	1655 (90%)	176 (10%)	8	29		

5 of 176 residues with a non-rotameric sidechain are listed below:

Mol	Chain	$\mathbf{Res}$	Type
1	С	449	ASN
1	С	102	HIS
1	С	464	LEU
1	С	589	GLU
1	D	232	TYR



Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 58 such sidechains are listed below:

Mol	Chain	$\mathbf{Res}$	Type
1	С	384	GLN
1	D	102	HIS
1	С	37	GLN
1	D	76	ASN
1	D	593	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 monosaccharides in this entry.

#### 5.6 Ligand geometry (i)

6 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).

Mal	Mal Turna Chain P		Deg Lini		Bo	Bond lengths			Bond angles		
INIOI	туре	ype Chain	nes	$\operatorname{Kes}   \operatorname{Link}$	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2	
2	NAG	С	801	1	14,14,15	0.81	0	17,19,21	0.57	0	
2	NAG	D	901	1	14,14,15	0.93	1 (7%)	17,19,21	0.83	0	
2	NAG	В	901	1	14,14,15	0.57	0	17,19,21	0.86	1 (5%)	
2	NAG	В	801	1	14,14,15	1.02	1 (7%)	17,19,21	0.82	1 (5%)	
2	NAG	С	901	1	14,14,15	0.72	0	17,19,21	0.80	0	
2	NAG	А	901	1	14,14,15	0.88	1 (7%)	17,19,21	1.26	3 (17%)	



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	С	801	1	-	4/6/23/26	0/1/1/1
2	NAG	D	901	1	-	6/6/23/26	0/1/1/1
2	NAG	В	901	1	-	4/6/23/26	0/1/1/1
2	NAG	В	801	1	-	4/6/23/26	0/1/1/1
2	NAG	С	901	1	-	2/6/23/26	0/1/1/1
2	NAG	А	901	1	-	4/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
2	В	801	NAG	C1-C2	3.13	1.57	1.52
2	D	901	NAG	C1-C2	2.19	1.55	1.52
2	А	901	NAG	C4-C5	2.16	1.57	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
2	А	901	NAG	C3-C4-C5	2.99	115.58	110.24
2	А	901	NAG	C2-N2-C7	-2.47	119.39	122.90
2	В	901	NAG	C2-N2-C7	-2.31	119.62	122.90
2	А	901	NAG	O5-C1-C2	-2.14	107.91	111.29
2	В	801	NAG	C3-C4-C5	-2.03	106.61	110.24

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	А	901	NAG	C8-C7-N2-C2
2	А	901	NAG	O7-C7-N2-C2
2	В	801	NAG	C8-C7-N2-C2
2	В	801	NAG	O7-C7-N2-C2
2	С	801	NAG	C8-C7-N2-C2

There are no ring outliers.

2 monomers are involved in 2 short contacts:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	901	NAG	1	0
2	С	901	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 (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,  $95^{th}$  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	А	515/559~(92%)	-0.28	7 (1%) 75 63	33, 57, 97, 115	0
1	В	526/559~(94%)	-0.14	18 (3%) 45 28	38, 66, 109, 122	0
1	С	514/559~(91%)	-0.18	9 (1%) 68 55	39, 66, 101, 118	0
1	D	504/559~(90%)	-0.10	10 (1%) 65 50	49, 75, 114, 130	0
All	All	2059/2236~(92%)	-0.17	44 (2%) 63 49	33, 67, 108, 130	0

The worst 5 of 44 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	314	GLY	4.3
1	С	590	SER	4.2
1	В	589	GLU	4.0
1	В	313	SER	3.8
1	D	313	SER	3.8

### 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 monosaccharides 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,  $95^{th}$  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	$B-factors(Å^2)$	Q<0.9
2	NAG	D	901	14/15	0.66	0.47	$95,\!98,\!103,\!105$	0
2	NAG	С	801	14/15	0.67	0.50	90,94,98,98	0
2	NAG	В	801	14/15	0.70	0.44	89,91,93,93	0
2	NAG	С	901	14/15	0.77	0.36	94,97,99,99	0
2	NAG	В	901	14/15	0.83	0.27	100,102,104,104	0
2	NAG	А	901	14/15	0.85	0.28	88,90,91,91	0

# 6.5 Other polymers (i)

There are no such residues in this entry.

