



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 04:12 pm BST

PDB ID : 5MFN
Title : Designed armadillo repeat protein YIIIM5AII
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Deposited on : 2016-11-18
Resolution : 2.80 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

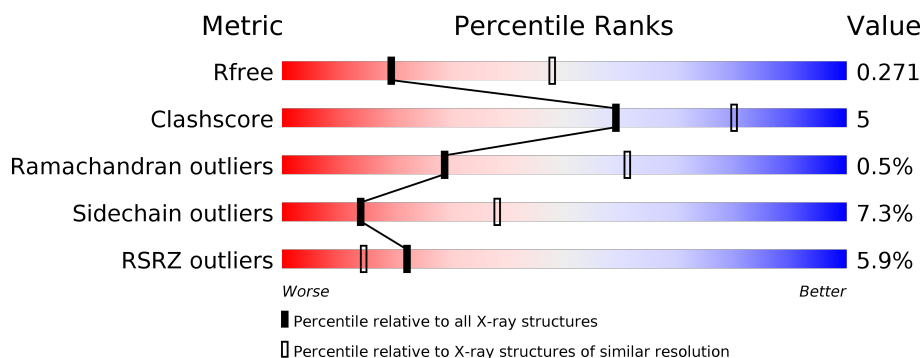
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 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	286	<div> <div>3%</div> <div> <div></div> <div>85%</div> <div>12%</div> <div>••</div> </div> </div>
1	B	286	<div> <div>9%</div> <div> <div></div> <div>78%</div> <div>16%</div> <div>••</div> </div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4170 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.

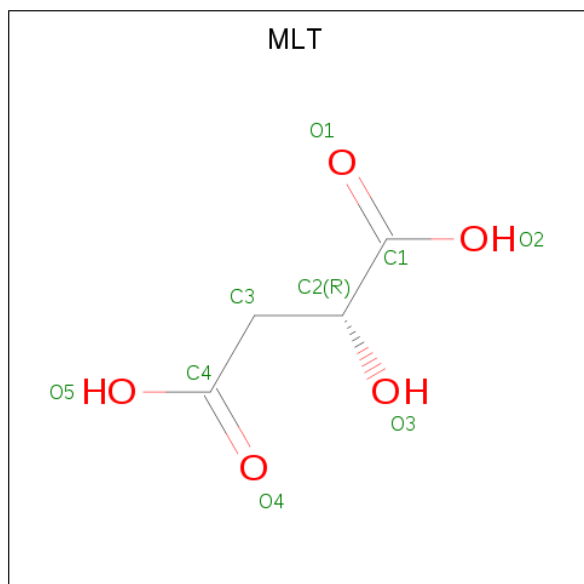
- Molecule 1 is a protein called YIIIM5AII.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	280	Total	C	N	O	S	0	0	0
			2075	1294	354	426	1			
1	B	278	Total	C	N	O	S	0	0	0
			2058	1283	351	423	1			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Ca	0	0
			2	2		
2	A	1	Total	Ca	0	0
			1	1		

- Molecule 3 is D-MALATE (three-letter code: MLT) (formula: C₄H₆O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			9	4	5		
3	B	1	Total	C	O	0	0
			9	4	5		

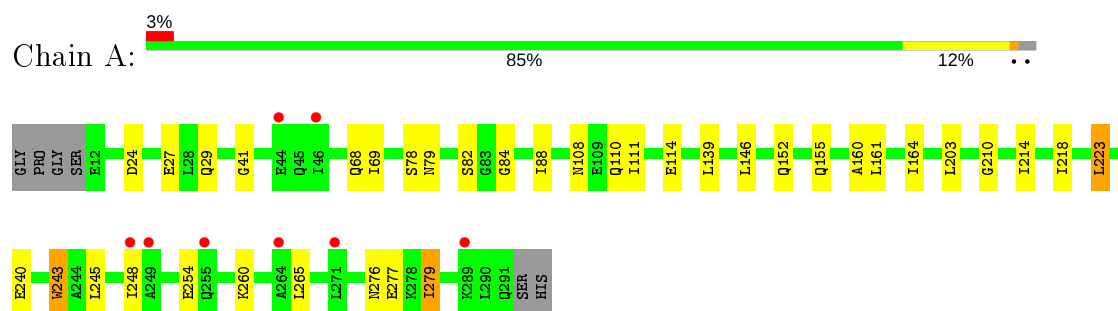
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	8	Total	O	0	0
			8	8		
4	B	8	Total	O	0	0
			8	8		

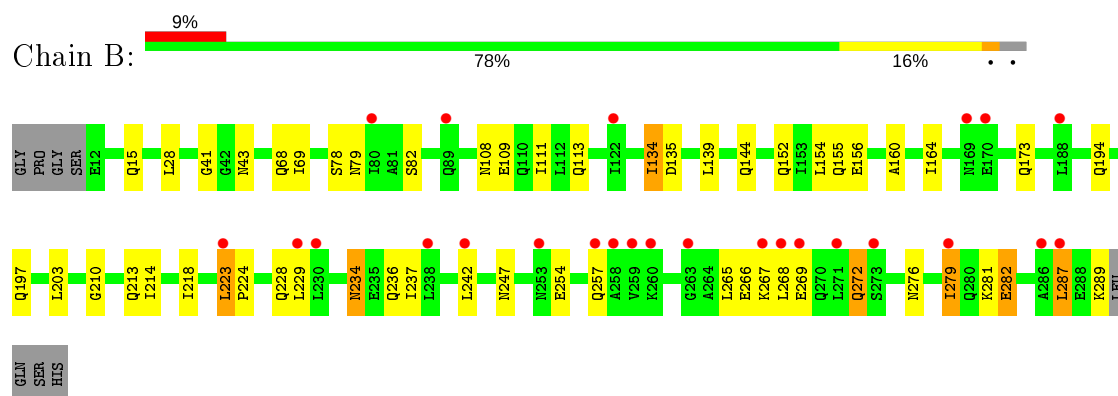
3 Residue-property plots [i](#)

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: YIIIM5AII



• Molecule 1: YIIIM5AII



4 Data and refinement statistics

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α , β , γ	142.55Å 142.55Å 142.12Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.66 – 2.80 46.66 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.66-2.80) 100.0 (46.66-2.80)	Depositor EDS
R_{merge}	0.26	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.20 (at 2.81Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.200 , 0.246 0.234 , 0.271	Depositor DCC
R_{free} test set	1029 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å ²)	85.4	Xtriage
Anisotropy	0.585	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 104.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4170	wwPDB-VP
Average B, all atoms (Å ²)	131.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.89% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.49	0/2097	0.68	0/2857
1	B	0.50	0/2080	0.70	0/2834
All	All	0.50	0/4177	0.69	0/5691

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2075	0	2087	18	0
1	B	2058	0	2068	24	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
3	A	9	0	4	0	0
3	B	9	0	4	1	0
4	A	8	0	0	0	0
4	B	8	0	0	0	0
All	All	4170	0	4163	39	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.

All (39) 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:144:GLN:HG3	3:B:303:MLT:H31	1.68	0.73
1:B:173:GLN:HE21	1:B:213:GLN:HE21	1.39	0.70
1:A:29:GLN:HG3	1:B:194:GLN:HG2	1.74	0.69
1:B:134:ILE:HG13	1:B:135:ASP:N	2.18	0.59
1:A:152:GLN:HE21	1:B:68:GLN:HA	1.68	0.59
1:A:79:ASN:O	1:A:82:SER:HB3	2.06	0.55
1:B:234:ASN:HD22	1:B:236:GLN:H	1.54	0.55
1:A:68:GLN:HA	1:B:152:GLN:HE21	1.74	0.51
1:B:109:GLU:O	1:B:113:GLN:HG3	2.10	0.51
1:A:260:LYS:HG2	1:A:265:LEU:HD21	1.93	0.51
1:B:229:LEU:HD22	1:B:237:ILE:CG2	2.42	0.49
1:B:210:GLY:O	1:B:214:ILE:HG12	2.13	0.48
1:A:210:GLY:O	1:A:214:ILE:HG12	2.14	0.48
1:A:160:ALA:O	1:A:164:ILE:HG12	2.15	0.47
1:B:269:GLU:HG2	1:B:287:LEU:HD11	1.96	0.47
1:B:160:ALA:O	1:B:164:ILE:HG12	2.15	0.46
1:A:218:ILE:HG23	1:A:223:LEU:HD11	1.98	0.46
1:B:79:ASN:O	1:B:82:SER:HB3	2.16	0.46
1:B:276:ASN:HD22	1:B:279:ILE:HG12	1.81	0.45
1:B:268:LEU:HG	1:B:287:LEU:HD12	1.99	0.45
1:B:242:LEU:HD13	1:B:282:GLU:HG2	1.99	0.45
1:A:218:ILE:HG12	1:A:223:LEU:HD21	1.97	0.44
1:A:139:LEU:HD21	1:A:164:ILE:HG21	1.99	0.44
1:B:224:PRO:O	1:B:228:GLN:HG3	2.17	0.44
1:B:218:ILE:HG12	1:B:223:LEU:HD21	1.99	0.43
1:A:110:GLN:HE21	1:A:114:GLU:HG2	1.84	0.42
1:A:108:ASN:HB3	1:A:111:ILE:HB	2.02	0.42
1:A:84:GLY:O	1:A:88:ILE:HG12	2.20	0.42
1:B:113:GLN:HG2	1:B:156:GLU:OE2	2.20	0.42
1:B:218:ILE:HG23	1:B:223:LEU:HD11	2.00	0.42
1:A:276:ASN:HD22	1:A:279:ILE:HD11	1.85	0.41
1:A:245:LEU:HA	1:A:248:ILE:HG12	2.01	0.41
1:B:108:ASN:HB3	1:B:111:ILE:HB	2.03	0.41
1:A:24:ASP:HB3	1:A:27:GLU:HB2	2.02	0.41
1:A:240:GLU:HA	1:A:243:TRP:HB2	2.02	0.41
1:B:234:ASN:HD22	1:B:236:GLN:N	2.19	0.41
1:B:269:GLU:O	1:B:272:GLN:HB2	2.20	0.41
1:A:146:LEU:HD21	1:A:161:LEU:HD12	2.03	0.41
1:B:139:LEU:HD21	1:B:164:ILE:HG21	2.03	0.41

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	278/286 (97%)	273 (98%)	4 (1%)	1 (0%)	34	66
1	B	276/286 (96%)	272 (99%)	2 (1%)	2 (1%)	22	53
All	All	554/572 (97%)	545 (98%)	6 (1%)	3 (0%)	29	61

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	41	GLY
1	B	41	GLY
1	B	279	ILE

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	220/224 (98%)	211 (96%)	9 (4%)	30	64
1	B	218/224 (97%)	195 (89%)	23 (11%)	6	20
All	All	438/448 (98%)	406 (93%)	32 (7%)	14	38

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	ILE
1	A	78	SER
1	A	155	GLN
1	A	203	LEU
1	A	223	LEU
1	A	243	TRP
1	A	254	GLU
1	A	277	GLU
1	A	279	ILE
1	B	15	GLN
1	B	28	LEU
1	B	43	ASN
1	B	69	ILE
1	B	78	SER
1	B	134	ILE
1	B	154	LEU
1	B	155	GLN
1	B	197	GLN
1	B	203	LEU
1	B	223	LEU
1	B	234	ASN
1	B	247	ASN
1	B	254	GLU
1	B	257	GLN
1	B	265	LEU
1	B	266	GLU
1	B	267	LYS
1	B	272	GLN
1	B	281	LYS
1	B	282	GLU
1	B	287	LEU
1	B	289	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	GLN
1	A	71	GLN
1	A	79	ASN
1	A	129	GLN
1	A	152	GLN
1	A	276	ASN
1	A	280	GLN

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Mol	Chain	Res	Type
1	B	15	GLN
1	B	71	GLN
1	B	129	GLN
1	B	152	GLN
1	B	173	GLN
1	B	186	GLN
1	B	234	ASN
1	B	247	ASN
1	B	274	HIS
1	B	276	ASN

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 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 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	$\# Z > 2$
3	MLT	B	303	-	2,8,8	1.14	0	3,10,10	1.53	1 (33%)
3	MLT	A	302	-	2,8,8	1.10	0	3,10,10	1.48	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
3	MLT	B	303	-	-	0/2/8/8	-
3	MLT	A	302	-	-	1/2/8/8	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	303	MLT	O3-C2-C3	2.63	114.27	108.50

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	302	MLT	O3-C2-C3-C4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	303	MLT	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, 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	280/286 (97%)	0.16	8 (2%) 51 41	75, 120, 176, 196	0
1	B	278/286 (97%)	0.45	25 (8%) 9 5	75, 135, 201, 214	0
All	All	558/572 (97%)	0.31	33 (5%) 22 14	75, 126, 192, 214	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	268	LEU	4.7
1	B	279	ILE	4.2
1	B	257	GLN	4.1
1	B	286	ALA	4.0
1	B	271	LEU	3.7
1	B	263	GLY	3.4
1	A	46	ILE	2.8
1	B	89	GLN	2.7
1	A	289	LYS	2.6
1	B	122	ILE	2.6
1	B	238	LEU	2.6
1	B	267	LYS	2.5
1	B	230	LEU	2.5
1	A	248	ILE	2.4
1	A	264	ALA	2.4
1	B	229	LEU	2.4
1	B	259	VAL	2.3
1	B	170	GLU	2.3
1	B	260	LYS	2.2
1	B	258	ALA	2.2
1	B	169	ASN	2.2
1	A	249	ALA	2.1
1	B	242	LEU	2.1
1	B	273	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	271	LEU	2.1
1	A	255	GLN	2.1
1	B	253	ASN	2.1
1	B	287	LEU	2.1
1	B	188	LEU	2.0
1	A	44	GLU	2.0
1	B	223	LEU	2.0
1	B	80	ILE	2.0
1	B	269	GLU	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. 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	B-factors(Å ²)	Q<0.9
3	MLT	B	303	9/9	0.62	0.27	101,106,108,109	0
3	MLT	A	302	9/9	0.92	0.21	87,94,97,101	0
2	CA	B	302	1/1	0.95	0.08	134,134,134,134	0
2	CA	A	301	1/1	0.97	0.10	129,129,129,129	0
2	CA	B	301	1/1	0.99	0.05	122,122,122,122	0

6.5 Other polymers [i](#)

There are no such residues in this entry.