



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 01:50 AM UTC

PDB ID : 8B6U / pdb_00008b6u
Title : Mpf2Ba1 monomer
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Deposited on : 2022-09-27
Resolution : 2.13 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 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
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

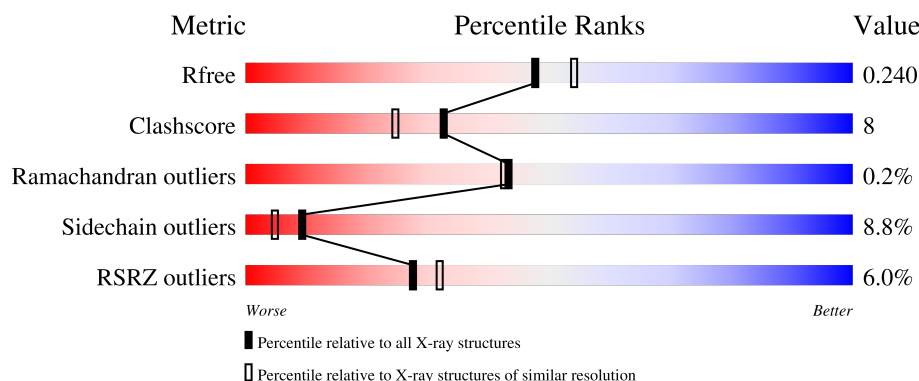
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.13 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	3689 (2.16-2.12)
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)
RSRZ outliers	180081	3691 (2.16-2.12)

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 $\leq 5\%$. 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	483	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7541 atoms, of which 3626 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 Mpf2Ba1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	481	Total	C	H	N	O	S	244	0	0
			7356	2362	3626	636	723	9			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	79	LEU	ILE	conflict	UNP A0A4Y8SM08
A	90	PHE	TYR	conflict	UNP A0A4Y8SM08
A	98	LEU	ILE	conflict	UNP A0A4Y8SM08
A	309	SER	ASN	conflict	UNP A0A4Y8SM08
A	320	PHE	TYR	conflict	UNP A0A4Y8SM08
A	332	PHE	TYR	conflict	UNP A0A4Y8SM08
A	338	PHE	TYR	conflict	UNP A0A4Y8SM08
A	345	LEU	ILE	conflict	UNP A0A4Y8SM08
A	433	PHE	TYR	conflict	UNP A0A4Y8SM08
A	452	LEU	ILE	conflict	UNP A0A4Y8SM08

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

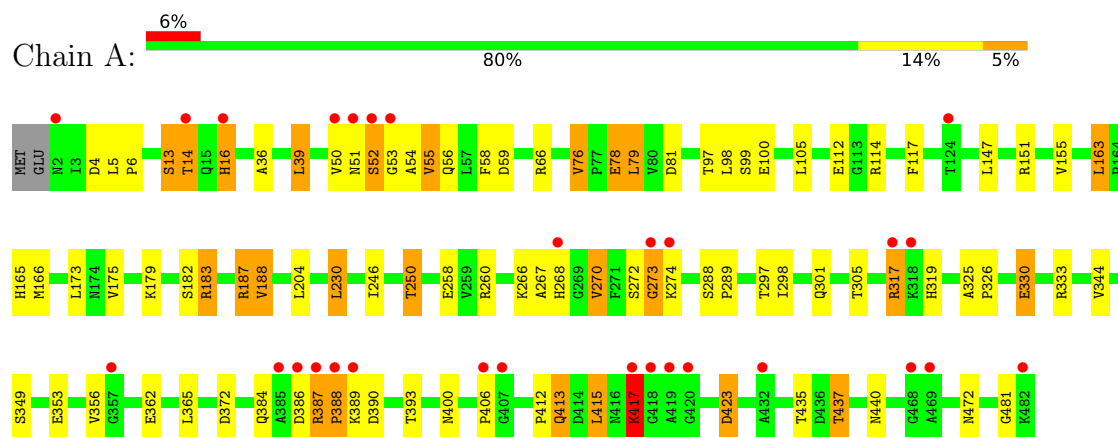
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	184	Total	O	0	0
			184	184		

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: Mpf2Ba1



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	127.60Å 127.60Å 116.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	57.13 – 2.13 57.13 – 2.13	Depositor EDS
% Data completeness (in resolution range)	99.3 (57.13-2.13) 99.2 (57.13-2.13)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.8.0352	Depositor
R, R_{free}	0.209 , 0.241 0.208 , 0.240	Depositor DCC
R_{free} test set	2602 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	29.1	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 33.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7541	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% 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: MG

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	0.73	0/3815	1.26	24/5177 (0.5%)

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	8

There are no bond length outliers.

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	117	PHE	CA-C-N	-15.53	99.10	122.86
1	A	117	PHE	C-N-CA	-15.53	99.10	122.86
1	A	117	PHE	O-C-N	-10.87	110.60	122.12
1	A	51	ASN	CB-CA-C	8.90	125.84	109.46
1	A	16	HIS	CB-CA-C	8.28	122.64	111.14
1	A	356	VAL	O-C-N	-7.40	114.54	121.94
1	A	268	HIS	N-CA-C	-7.24	99.73	110.23
1	A	268	HIS	CA-C-N	-6.87	112.52	123.31
1	A	268	HIS	C-N-CA	-6.87	112.52	123.31
1	A	14	THR	CA-CB-OG1	-6.63	99.65	109.60
1	A	187	ARG	CA-C-N	-6.51	116.26	123.16
1	A	187	ARG	C-N-CA	-6.51	116.26	123.16
1	A	423	ASP	CA-CB-CG	6.51	119.11	112.60
1	A	258	GLU	CB-CG-CD	6.35	123.40	112.60
1	A	188	VAL	N-CA-CB	5.91	116.48	111.64
1	A	188	VAL	CB-CA-C	5.86	116.27	111.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	78	GLU	CB-CA-C	-5.63	101.11	110.68
1	A	81	ASP	CB-CA-C	5.54	118.89	109.53
1	A	76	VAL	N-CA-CB	-5.14	104.02	111.21
1	A	112	GLU	CB-CG-CD	5.12	121.31	112.60
1	A	390	ASP	CB-CA-C	5.10	118.15	109.53
1	A	356	VAL	CA-C-N	-5.08	108.85	121.60
1	A	356	VAL	C-N-CA	-5.08	108.85	121.60
1	A	353	GLU	CB-CG-CD	5.06	121.20	112.60

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	183	ARG	Sidechain
1	A	272	SER	Peptide
1	A	273	GLY	Peptide
1	A	317	ARG	Sidechain
1	A	406	PRO	Peptide
1	A	417	LYS	Peptide
1	A	472	ASN	Peptide
1	A	53	GLY	Peptide

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	3730	3626	3617	58	0
2	A	1	0	0	0	0
3	A	184	0	0	3	0
All	All	3915	3626	3617	58	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 8.

All (58) 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:387:ARG:HB2	1:A:388:PRO:O	1.55	1.04
1:A:301:GLN:NE2	1:A:305:THR:HG21	1.87	0.90
1:A:56:GLN:HE21	1:A:58:PHE:H	1.18	0.84
1:A:387:ARG:CB	1:A:388:PRO:O	2.25	0.83
1:A:440:ASN:HD22	1:A:481:GLY:H	1.26	0.82
1:A:301:GLN:HE21	1:A:305:THR:HG21	1.45	0.80
1:A:36:ALA:HA	1:A:39:LEU:HD22	1.67	0.77
1:A:440:ASN:ND2	1:A:481:GLY:H	1.83	0.77
1:A:59:ASP:HB2	1:A:163:LEU:HD13	1.68	0.74
1:A:97:THR:HG23	1:A:100:GLU:H	1.55	0.71
1:A:4:ASP:O	1:A:250:THR:HG21	1.91	0.69
1:A:437:THR:HG22	3:A:698:HOH:O	1.97	0.64
1:A:79:LEU:HD11	1:A:155:VAL:HG21	1.81	0.62
1:A:267:ALA:O	1:A:270:VAL:HG13	2.01	0.60
1:A:387:ARG:N	1:A:388:PRO:HA	2.15	0.60
1:A:165:HIS:CE1	1:A:166:MET:HE2	2.40	0.57
1:A:4:ASP:O	1:A:250:THR:CG2	2.53	0.57
1:A:151:ARG:HH11	1:A:151:ARG:HG2	1.73	0.54
1:A:365:LEU:HD23	1:A:415:LEU:HG	1.90	0.52
1:A:412:PRO:HD2	1:A:413:GLN:HE22	1.74	0.51
1:A:97:THR:HG22	1:A:100:GLU:HB2	1.93	0.51
1:A:79:LEU:HD11	1:A:155:VAL:CG2	2.41	0.50
1:A:372:ASP:OD2	1:A:417:LYS:HD2	2.11	0.50
1:A:400:ASN:ND2	1:A:423:ASP:H	2.10	0.49
1:A:97:THR:CG2	1:A:100:GLU:H	2.25	0.49
1:A:344:VAL:HB	1:A:413:GLN:HG2	1.95	0.48
1:A:412:PRO:HD2	1:A:413:GLN:NE2	2.28	0.48
1:A:400:ASN:HD21	1:A:423:ASP:H	1.62	0.47
1:A:393:THR:HG22	1:A:437:THR:CG2	2.44	0.47
1:A:230:LEU:O	1:A:273:GLY:HA3	2.14	0.47
1:A:330:GLU:CD	1:A:333:ARG:HH11	2.22	0.47
1:A:151:ARG:HG2	1:A:298:ILE:HD11	1.96	0.47
1:A:344:VAL:HB	1:A:413:GLN:CG	2.44	0.46
1:A:16:HIS:CE1	1:A:52:SER:HA	2.50	0.46
1:A:330:GLU:OE1	1:A:333:ARG:HD3	2.15	0.46
1:A:393:THR:CG2	1:A:437:THR:CG2	2.93	0.46
1:A:5:LEU:HB3	1:A:230:LEU:HD13	1.98	0.46
1:A:147:LEU:HD12	1:A:289:PRO:HB3	1.98	0.46
1:A:246:ILE:O	1:A:250:THR:HG23	2.16	0.46
1:A:55:VAL:HG12	1:A:166:MET:HE3	1.97	0.45
1:A:151:ARG:HG2	1:A:151:ARG:NH1	2.31	0.45
1:A:39:LEU:HG	1:A:54:ALA:HB1	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:59:ASP:CB	1:A:163:LEU:HD13	2.41	0.43
1:A:66:ARG:HH11	1:A:78:GLU:HA	1.83	0.43
1:A:325:ALA:HB3	1:A:326:PRO:HD3	2.01	0.43
1:A:6:PRO:HD3	1:A:250:THR:HG22	2.00	0.43
1:A:55:VAL:CG1	1:A:166:MET:HE1	2.49	0.42
1:A:56:GLN:HE21	1:A:58:PHE:N	2.00	0.42
1:A:182:SER:OG	1:A:319:HIS:HE1	2.03	0.42
1:A:393:THR:CG2	1:A:437:THR:HG23	2.50	0.41
1:A:97:THR:HG22	1:A:100:GLU:CG	2.50	0.41
1:A:13:SER:HB2	1:A:260:ARG:HE	1.85	0.41
1:A:183:ARG:HD3	1:A:187:ARG:NH1	2.36	0.41
1:A:97:THR:HG22	1:A:100:GLU:CB	2.51	0.41
1:A:297:THR:HG23	3:A:664:HOH:O	2.21	0.41
1:A:317:ARG:NH1	3:A:628:HOH:O	2.53	0.41
1:A:387:ARG:N	1:A:388:PRO:CA	2.83	0.41
1:A:389:LYS:HD2	1:A:389:LYS:N	2.36	0.41

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	479/483 (99%)	464 (97%)	14 (3%)	1 (0%)	43	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	388	PRO

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	400/403 (99%)	365 (91%)	35 (9%)	9 5

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	SER
1	A	14	THR
1	A	39	LEU
1	A	50	VAL
1	A	52	SER
1	A	55	VAL
1	A	76	VAL
1	A	79	LEU
1	A	98	LEU
1	A	99	SER
1	A	105	LEU
1	A	114	ARG
1	A	163	LEU
1	A	173	LEU
1	A	175	VAL
1	A	179	LYS
1	A	188	VAL
1	A	204	LEU
1	A	230	LEU
1	A	250	THR
1	A	266	LYS
1	A	270	VAL
1	A	274	LYS
1	A	288	SER
1	A	330	GLU
1	A	349	SER
1	A	362	GLU
1	A	384	GLN
1	A	386	ASP
1	A	387	ARG

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Mol	Chain	Res	Type
1	A	413	GLN
1	A	415	LEU
1	A	417	LYS
1	A	435	THR
1	A	437	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	GLN
1	A	56	GLN
1	A	83	GLN
1	A	84	GLN
1	A	85	ASN
1	A	102	GLN
1	A	143	GLN
1	A	165	HIS
1	A	174	ASN
1	A	254	ASN
1	A	257	GLN
1	A	301	GLN
1	A	319	HIS
1	A	341	GLN
1	A	384	GLN
1	A	400	ASN
1	A	413	GLN
1	A	440	ASN

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

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

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	481/483 (99%)	0.03	29 (6%)	27 32	16, 30, 52, 84	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	388	PRO	6.2
1	A	52	SER	5.3
1	A	51	ASN	4.0
1	A	419	ALA	3.7
1	A	387	ARG	3.6
1	A	53	GLY	3.4
1	A	14	THR	3.3
1	A	357	GLY	3.1
1	A	268	HIS	3.1
1	A	50	VAL	3.1
1	A	385	ALA	3.0
1	A	469	ALA	3.0
1	A	418	GLY	2.9
1	A	389	LYS	2.9
1	A	317	ARG	2.9
1	A	2	ASN	2.9
1	A	417	LYS	2.8
1	A	407	GLY	2.7
1	A	273	GLY	2.7
1	A	468	GLY	2.7
1	A	420	GLY	2.7
1	A	386	ASP	2.6
1	A	482	LYS	2.5
1	A	16	HIS	2.4
1	A	318	LYS	2.2
1	A	432	ALA	2.1
1	A	406	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	124	THR	2.0
1	A	274	LYS	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 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, 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($\text{\AA}^2$)	Q<0.9
2	MG	A	501	1/1	0.99	0.05	22,22,22,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.