



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2018 – 11:28 pm GMT

PDB ID : 1MC1  
Title : BETA-LACTAM SYNTHETASE WITH PRODUCT (DGPC), AMP AND PPI  
Authors : Miller, M.T.; Bachmann, B.O.; Townsend, C.A.; Rosenzweig, A.C.  
Deposited on : 2002-08-04  
Resolution : 2.16 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

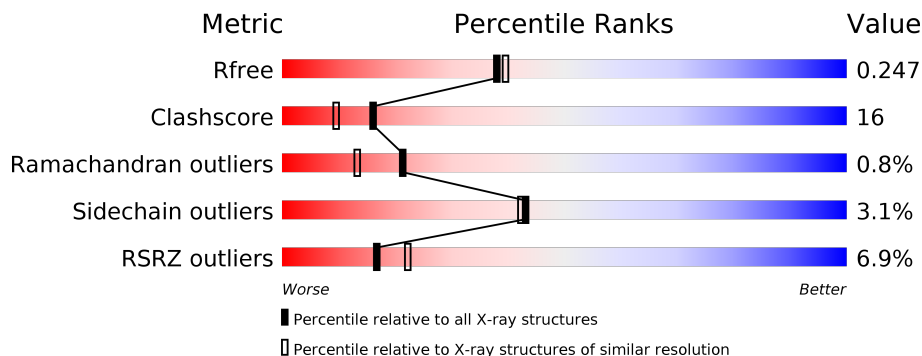
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.16 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	1287 (2.16-2.16)
Clashscore	122126	1390 (2.16-2.16)
Ramachandran outliers	120053	1368 (2.16-2.16)
Sidechain outliers	120020	1367 (2.16-2.16)
RSRZ outliers	108989	1262 (2.16-2.16)

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	513	<div> <div>8%</div> <div>68%</div> <div>24%</div> <div>• • •</div> </div>
1	B	513	<div> <div>6%</div> <div>72%</div> <div>23%</div> <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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	AMP	A	702	-	-	X	-
5	PCX	B	706	-	-	X	-

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 7946 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.

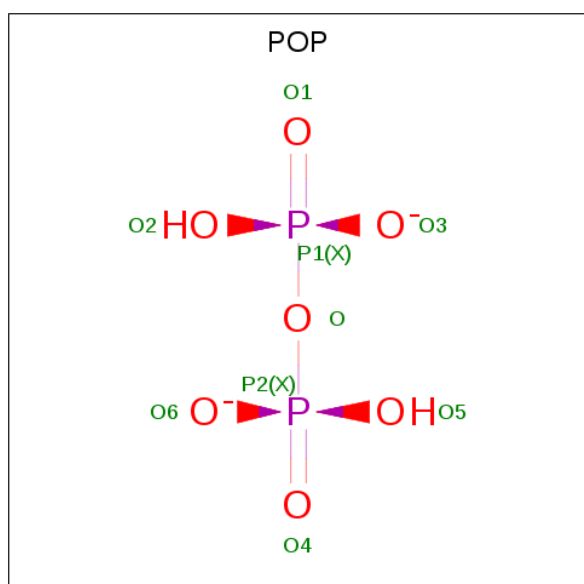
- Molecule 1 is a protein called BETA-LACTAM SYNTHETASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	491	Total	C	N	O	S	0	0	0
			3693	2305	678	702	8			
1	B	498	Total	C	N	O	S	0	0	0
			3748	2339	692	709	8			

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

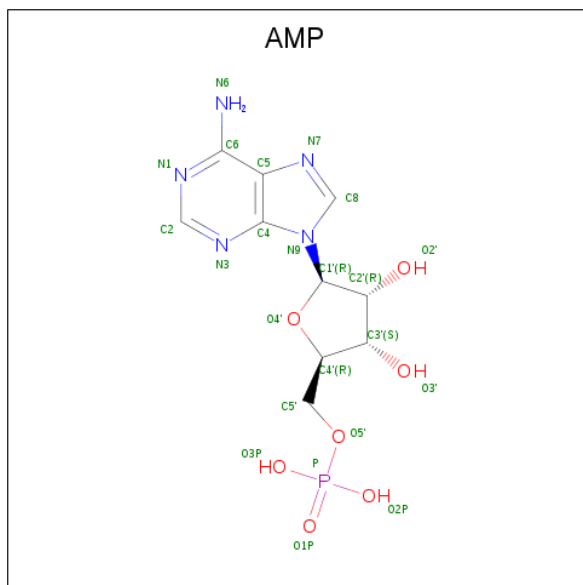
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Mg	0	0
			2	2		
2	A	2	Total	Mg	0	0
			2	2		

- Molecule 3 is PYROPHOSPHATE 2- (three-letter code: POP) (formula:  $\text{H}_2\text{O}_7\text{P}_2$ ).



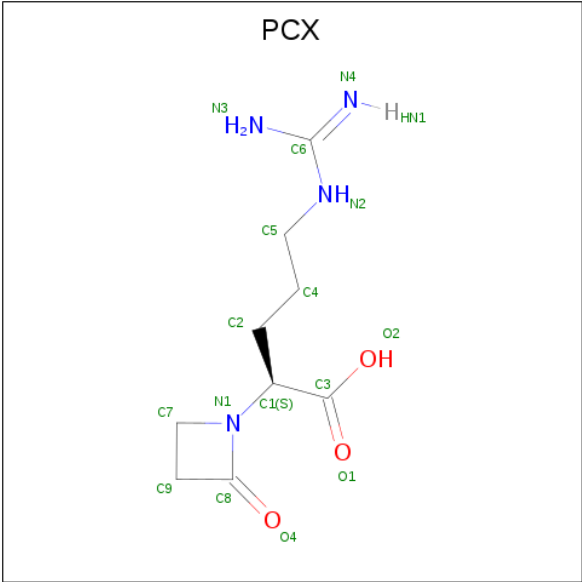
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			9	7	2		
3	B	1	Total	O	P	0	0
			9	7	2		

- Molecule 4 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula:  $C_{10}H_{14}N_5O_7P$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0
			23	10	5	7	1	0
4	B	1	Total	C	N	O	P	0
			23	10	5	7	1	0

- Molecule 5 is DEOXYGUANIDINOPROCLAVAMINIC ACID (three-letter code: PCX) (formula:  $C_9H_{16}N_4O_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			16	9	4	3		
5	B	1	Total	C	N	O	0	0
			16	9	4	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	175	Total	O	0	0
			175	175		
6	B	230	Total	O	0	0
			230	230		



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	61.04Å 96.57Å 80.91Å 90.00° 90.54° 90.00°	Depositor
Resolution (Å)	29.10 – 2.16 29.10 – 2.00	Depositor EDS
% Data completeness (in resolution range)	94.7 (29.10-2.16) 94.6 (29.10-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.00 (at 2.00Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.208 , 0.247 0.208 , 0.247	Depositor DCC
$R_{free}$ test set	4350 reflections (6.86%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	21.6	Xtriage
Anisotropy	0.549	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 54.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.053 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	7946	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.04% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: AMP, PCX, MG, POP

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	0.51	4/3765 (0.1%)	0.87	19/5136 (0.4%)
1	B	0.41	1/3824 (0.0%)	0.74	8/5219 (0.2%)
All	All	0.46	5/7589 (0.1%)	0.81	27/10355 (0.3%)

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	9
1	B	1	5
All	All	1	14

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	169	GLY	CA-C	-6.76	1.41	1.51
1	A	169	GLY	N-CA	-6.73	1.35	1.46
1	A	468	ASP	N-CA	6.52	1.59	1.46
1	A	445	GLY	C-O	6.07	1.33	1.23
1	B	23	ALA	N-CA	5.26	1.56	1.46

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	170	PHE	C-N-CD	12.67	155.00	128.40
1	A	169	GLY	N-CA-C	11.90	142.85	113.10
1	A	69	ALA	C-N-CD	11.84	153.26	128.40
1	B	23	ALA	O-C-N	-11.46	99.32	121.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	469	ARG	O-C-N	-10.71	105.57	122.70

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	22	ARG	CA

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	174	ASP	Sidechain
1	A	42	GLY	Mainchain,Peptide
1	A	44	ARG	Mainchain
1	A	445	GLY	Mainchain
1	A	70	PRO	Mainchain

## 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	3693	0	3680	128	2
1	B	3748	0	3742	102	1
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	9	0	0	0	0
3	B	9	0	0	1	0
4	A	23	0	12	13	0
4	B	23	0	12	3	0
5	A	16	0	14	5	0
5	B	16	0	14	8	0
6	A	175	0	0	3	0
6	B	230	0	0	7	0
All	All	7946	0	7474	233	2

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 16.

The worst 5 of 233 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)
4:A:702:AMP:O3P	5:A:703:PCX:H9C1	1.14	1.32
1:A:149:PRO:CD	1:A:170:PHE:CZ	2.20	1.23
1:A:149:PRO:CD	1:A:170:PHE:CE1	2.30	1.15
1:A:149:PRO:HD3	1:A:170:PHE:CE1	1.80	1.15
1:A:326:TYR:CE2	1:A:447:HIS:CE1	2.44	1.05

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:420:GLY:O	1:B:359:ARG:NE[1_655]	2.10	0.10
1:A:44:ARG:NE	1:A:276:ASP:OD1[1_455]	2.10	0.10

## 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	485/513 (94%)	461 (95%)	18 (4%)	6 (1%)	14	7
1	B	494/513 (96%)	474 (96%)	18 (4%)	2 (0%)	36	31
All	All	979/1026 (95%)	935 (96%)	36 (4%)	8 (1%)	21	13

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	42	GLY
1	A	90	PRO
1	A	111	LEU
1	B	111	LEU
1	B	339	GLY

### 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	383/395 (97%)	373 (97%)	10 (3%)	49	51
1	B	388/395 (98%)	374 (96%)	14 (4%)	38	36
All	All	771/790 (98%)	747 (97%)	24 (3%)	43	42

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	13	LEU
1	B	143	LEU
1	B	426	LEU
1	B	85	LEU
1	B	101	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	164	HIS
1	B	186	GLN
1	B	381	ASN
1	B	41	GLN
1	B	358	HIS

### 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 [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 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	POP	A	701	2	8,8,8	1.40	1 (12%)	9,13,13	1.01	0
4	AMP	A	702	2	22,25,25	2.09	6 (27%)	23,38,38	1.86	5 (21%)
5	PCX	A	703	-	11,16,16	10.00	4 (36%)	7,21,21	3.62	1 (14%)
3	POP	B	704	2	8,8,8	1.49	2 (25%)	9,13,13	0.79	0
4	AMP	B	705	2	22,25,25	2.15	6 (27%)	23,38,38	1.81	5 (21%)
5	PCX	B	706	-	11,16,16	6.72	3 (27%)	7,21,21	4.16	1 (14%)

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	POP	A	701	2	-	0/6/6/6	0/0/0/0
4	AMP	A	702	2	-	0/6/26/26	0/3/3/3
5	PCX	A	703	-	-	0/10/24/24	0/1/1/1
3	POP	B	704	2	-	0/6/6/6	0/0/0/0
4	AMP	B	705	2	-	0/6/26/26	0/3/3/3
5	PCX	B	706	-	-	0/10/24/24	0/1/1/1

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	703	PCX	C1-N1	-31.24	1.02	1.47
5	B	706	PCX	C1-N1	-19.88	1.18	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	703	PCX	C7-C9	-7.54	1.42	1.54
5	B	706	PCX	C7-C9	-7.16	1.42	1.54
5	A	703	PCX	C7-N1	-6.90	1.40	1.48

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	706	PCX	C7-N1-C8	-10.89	87.61	95.75
5	A	703	PCX	C7-N1-C8	-9.48	88.66	95.75
4	A	702	AMP	N3-C2-N1	-4.57	124.95	128.86
4	B	705	AMP	N3-C2-N1	-4.31	125.17	128.86
4	B	705	AMP	C4'-O4'-C1'	2.16	112.08	109.83

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	702	AMP	13	0
5	A	703	PCX	5	0
3	B	704	POP	1	0
4	B	705	AMP	3	0
5	B	706	PCX	8	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	491/513 (95%)	0.35	39 (7%)	12 17	10, 25, 46, 59	0
1	B	498/513 (97%)	0.24	29 (5%)	23 30	13, 23, 42, 60	0
All	All	989/1026 (96%)	0.30	68 (6%)	17 22	10, 24, 45, 60	0

The worst 5 of 68 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	22	ARG	9.4
1	B	93	PRO	7.0
1	A	91	ALA	6.7
1	A	170	PHE	6.7
1	B	23	ALA	6.3

### 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
4	AMP	B	705	23/23	0.59	0.32	41,46,60,61	0
5	PCX	A	703	16/16	0.80	0.20	39,46,49,51	0
5	PCX	B	706	16/16	0.81	0.19	23,31,37,39	0
4	AMP	A	702	23/23	0.84	0.19	26,39,49,50	0
2	MG	A	603	1/1	0.89	0.13	35,35,35,35	0
2	MG	B	605	1/1	0.89	0.07	29,29,29,29	0
2	MG	B	602	1/1	0.92	0.06	38,38,38,38	0
2	MG	A	601	1/1	0.93	0.14	32,32,32,32	0
3	POP	A	701	9/9	0.95	0.10	23,27,30,31	0
3	POP	B	704	9/9	0.97	0.08	19,20,22,23	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.