wwPDB X-ray Structure Validation Summary Report (i)

Jan 14, 2024 – 01:02 am GMT

PDB ID	:	6HX7
Title	:	Crystal structure of human R180T variant of ORNITHINE AMINOTRANSFERASE at 1.8 Angstrom
Authors	:	Giardina, G.; Montioli, R.; Cellini, B.; Cutruzzola, F.; Borri Voltattorni, C.
Deposited on	:	2018-10-16
Resolution	:	1.80 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 (i)) were used in the production of this report:

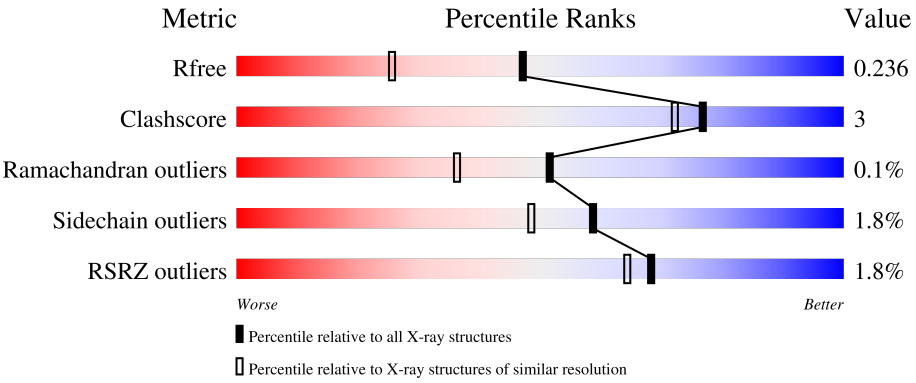
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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-RAY DIFFRACTION

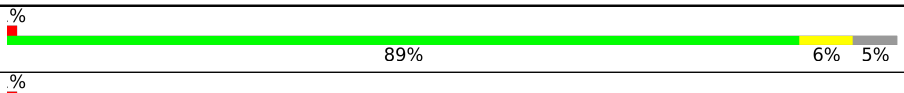
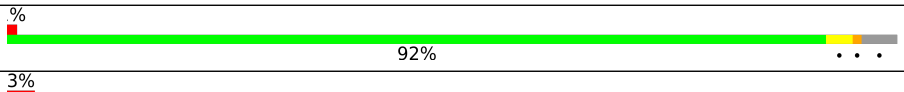
The reported resolution of this entry is 1.80 Å.

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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 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	A	415	
1	B	415	
1	C	415	

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
2	PLP	C	501	-	-	X	-

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 10446 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.

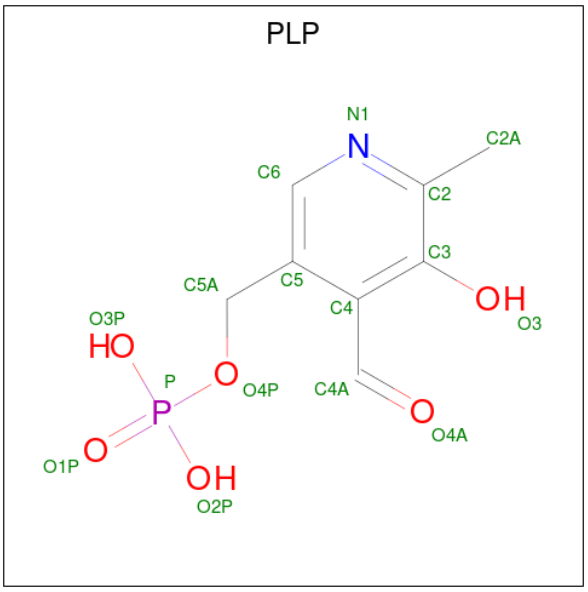
- Molecule 1 is a protein called Ornithine aminotransferase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	394	Total	C	N	O	S	0	7	0
			3065	1982	507	563	13			
1	B	399	Total	C	N	O	S	0	4	0
			3100	1996	519	571	14			
1	C	394	Total	C	N	O	S	0	0	0
			3036	1958	506	560	12			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	25	MET	-	initiating methionine	UNP P04181
A	180	THR	ARG	engineered mutation	UNP P04181
B	25	MET	-	initiating methionine	UNP P04181
B	180	THR	ARG	engineered mutation	UNP P04181
C	25	MET	-	initiating methionine	UNP P04181
C	180	THR	ARG	engineered mutation	UNP P04181

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: $C_8H_{10}NO_6P$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C N O P 15 8 1 5 1	0	0
2	B	1	Total C N O P 15 8 1 5 1	0	0
2	C	1	Total C N O P 15 8 1 5 1	0	0

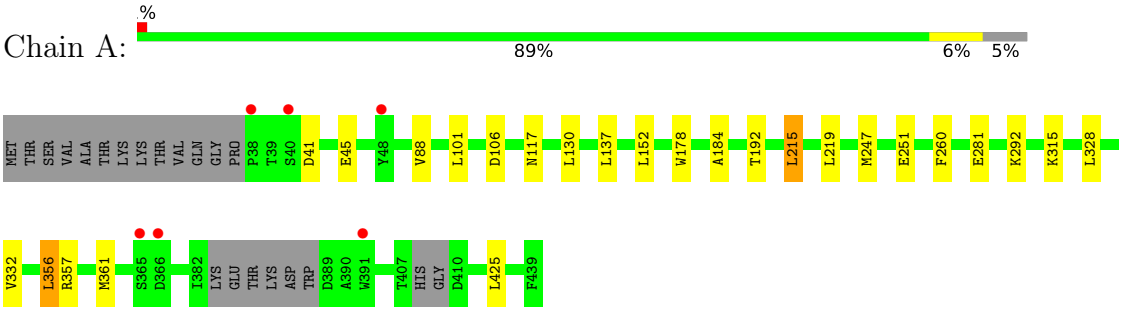
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	398	Total O 398 398	0	0
3	B	419	Total O 419 419	0	0
3	C	383	Total O 383 383	0	0

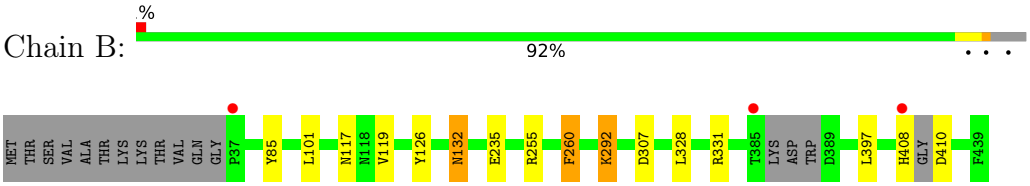
3 Residue-property plots (i)

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.

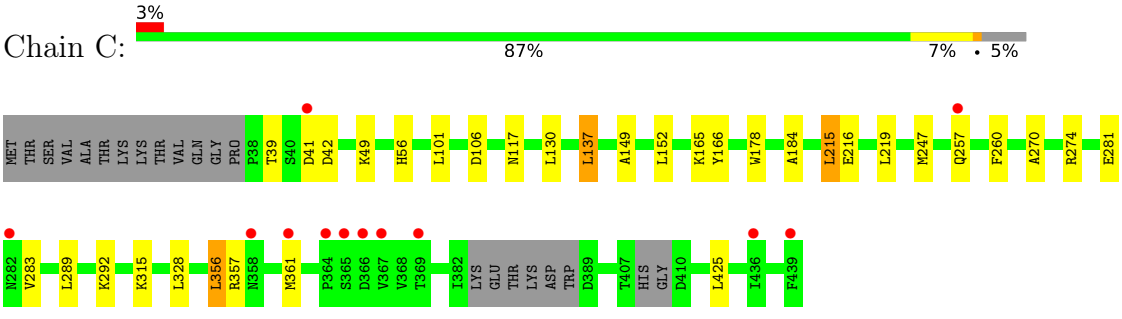
• Molecule 1: Ornithine aminotransferase, mitochondrial



• Molecule 1: Ornithine aminotransferase, mitochondrial



• Molecule 1: Ornithine aminotransferase, mitochondrial



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 1 2	Depositor
Cell constants a, b, c, α, β, γ	193.25Å 193.25Å 57.21Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.00 – 1.80 47.23 – 1.80	Depositor EDS
% Data completeness (in resolution range)	98.6 (45.00-1.80) 98.6 (47.23-1.80)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.93 (at 1.79Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.221 , 0.228 0.230 , 0.236	Depositor DCC
R_{free} test set	5358 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å^2)	11.1	Xtriage
Anisotropy	0.512	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 56.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.42$, $< L^2 > = 0.25$	Xtriage
Estimated twinning fraction	0.057 for -h,-k,l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	10446	wwPDB-VP
Average B, all atoms (Å^2)	16.0	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 77.07 % 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 9.1653e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: PLP

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	0.52	0/3154	0.65	0/4289
1	B	0.68	2/3178 (0.1%)	0.75	3/4319 (0.1%)
1	C	0.51	0/3104	0.65	2/4220 (0.0%)
All	All	0.58	2/9436 (0.0%)	0.68	5/12828 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	126	TYR	CG-CD2	-7.31	1.29	1.39
1	B	132	ASN	C-O	-6.13	1.11	1.23

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	307	ASP	CB-CG-OD1	6.03	123.73	118.30
1	C	137	LEU	CA-CB-CG	5.82	128.69	115.30
1	B	260	PHE	CB-CG-CD1	5.20	124.44	120.80
1	C	41	ASP	CB-CG-OD2	5.19	122.97	118.30
1	B	397	LEU	CA-CB-CG	5.18	127.22	115.30

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	3065	0	3063	17	0
1	B	3100	0	3079	16	1
1	C	3036	0	3012	21	0
2	A	15	0	6	4	0
2	B	15	0	6	5	0
2	C	15	0	6	6	0
3	A	398	0	0	4	2
3	B	419	0	0	5	2
3	C	383	0	0	5	3
All	All	10446	0	9172	54	8

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 3.

The worst 5 of 54 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:C:292:LYS:NZ	2:C:501:PLP:C4A	1.96	1.29
1:C:292:LYS:HZ1	2:C:501:PLP:C4A	1.53	1.17
1:B:292:LYS:NZ	2:B:501:PLP:C4A	2.17	1.08
1:B:292:LYS:HZ1	2:B:501:PLP:C4A	1.72	1.00
1:B:292:LYS:HZ2	2:B:501:PLP:C4A	1.89	0.84

The worst 5 of 8 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)
3:C:779:HOH:O	3:C:838:HOH:O[5_555]	1.88	0.32
3:B:971:HOH:O	3:B:979:HOH:O[4_555]	1.90	0.30
3:A:912:HOH:O	3:A:936:HOH:O[6_565]	1.94	0.26
1:B:132:ASN:OD1	1:B:132:ASN:OD1[4_554]	1.94	0.26
3:B:757:HOH:O	3:B:837:HOH:O[4_555]	2.04	0.16

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	395/415 (95%)	380 (96%)	15 (4%)	0	100 100
1	B	397/415 (96%)	381 (96%)	15 (4%)	1 (0%)	41 27
1	C	388/415 (94%)	372 (96%)	16 (4%)	0	100 100
All	All	1180/1245 (95%)	1133 (96%)	46 (4%)	1 (0%)	51 36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	292	LYS

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	322/347 (93%)	312 (97%)	10 (3%)	40 25
1	B	324/347 (93%)	323 (100%)	1 (0%)	92 91
1	C	316/347 (91%)	307 (97%)	9 (3%)	43 30
All	All	962/1041 (92%)	942 (98%)	20 (2%)	59 42

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	152	LEU
1	C	283	VAL
1	C	356	LEU
1	C	315	LYS
1	A	215[B]	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	56	HIS
1	B	164	GLN
1	C	257	GLN

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)

3 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	PLP	B	501	-	15,15,16	2.64	8 (53%)	20,22,23	2.29	8 (40%)
2	PLP	C	501	-	15,15,16	2.31	6 (40%)	20,22,23	2.20	7 (35%)
2	PLP	A	501	1	15,15,16	2.06	7 (46%)	20,22,23	1.90	6 (30%)

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	PLP	B	501	-	-	0/6/6/8	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PLP	C	501	-	-	0/6/6/8	0/1/1/1
2	PLP	A	501	1	-	0/6/6/8	0/1/1/1

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	PLP	C5-C4	5.06	1.46	1.40
2	C	501	PLP	C5-C4	4.89	1.45	1.40
2	B	501	PLP	C3-C2	4.67	1.45	1.40
2	A	501	PLP	C5-C4	4.42	1.45	1.40
2	B	501	PLP	C3-C4	4.20	1.48	1.40

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	501	PLP	C5A-C5-C6	4.99	127.58	119.37
2	A	501	PLP	C2A-C2-C3	-4.72	115.06	120.89
2	C	501	PLP	C5A-C5-C6	4.47	126.73	119.37
2	C	501	PLP	C2A-C2-C3	-3.82	116.17	120.89
2	A	501	PLP	C2A-C2-N1	3.80	125.10	117.67

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	PLP	5	0
2	C	501	PLP	6	0
2	A	501	PLP	4	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, 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	A	394/415 (94%)	0.04	6 (1%)	73	70	8, 17, 27, 43	0
1	B	399/415 (96%)	-0.29	3 (0%)	86	84	2, 9, 22, 40	0
1	C	394/415 (94%)	0.14	12 (3%)	50	44	9, 17, 31, 49	0
All	All	1187/1245 (95%)	-0.04	21 (1%)	68	64	2, 15, 28, 49	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	367	VAL	6.2
1	B	37	PRO	3.7
1	A	365	SER	3.6
1	C	364	PRO	3.4
1	C	41	ASP	2.9

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

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	PLP	C	501	15/16	0.95	0.11	10,15,19,27	0
2	PLP	A	501	15/16	0.96	0.10	11,14,24,27	0
2	PLP	B	501	15/16	0.97	0.10	2,5,19,22	0

6.5 Other polymers (i)

There are no such residues in this entry.