



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 11:14 PM GMT

PDB ID : 3SPA
Title : Crystal Structure of Human Mitochondrial RNA Polymerase
Authors : Ringel, R.; Sologub, M.; Morozov, Y.I.; Litonin, D.; Cramer, P.; Temiakov, D.
Deposited on : 2011-07-01
Resolution : 2.50 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

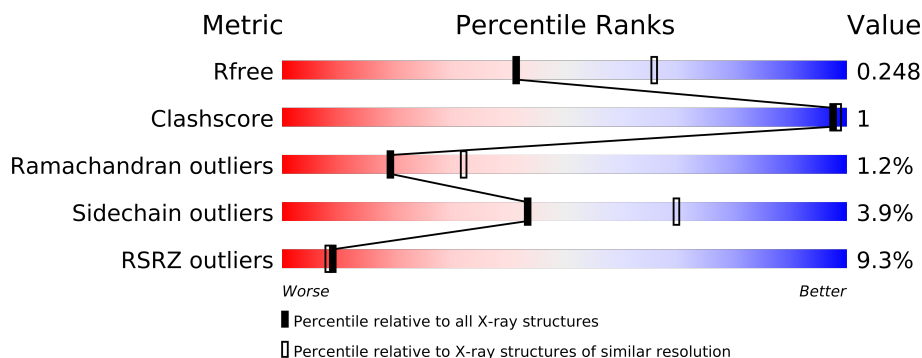
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.50 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}	66092	2784 (2.50-2.50)
Clashscore	79885	3562 (2.50-2.50)
Ramachandran outliers	78287	3480 (2.50-2.50)
Sidechain outliers	78261	3482 (2.50-2.50)
RSRZ outliers	66119	2785 (2.50-2.50)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	1134	
2	B	9	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	GOL	A	2	-	X
4	CL	A	1231	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7666 atoms, of which 0 are hydrogen and 0 are deuterium.

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 DNA-directed RNA polymerase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	941	Total	C	N	O	S	0	7	0
			7454	4745	1345	1315	49			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	97	MET	-	EXPRESSION TAG	UNP O00411
A	98	GLY	-	EXPRESSION TAG	UNP O00411
A	99	HIS	-	EXPRESSION TAG	UNP O00411
A	100	HIS	-	EXPRESSION TAG	UNP O00411
A	101	HIS	-	EXPRESSION TAG	UNP O00411
A	102	HIS	-	EXPRESSION TAG	UNP O00411
A	103	HIS	-	EXPRESSION TAG	UNP O00411
A	104	HIS	-	EXPRESSION TAG	UNP O00411
A	555	ALA	GLU	ENGINEERED MUTATION	UNP O00411

- Molecule 2 is a protein called Nonamer peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	9	Total	C	N	O	0	0	0
			45	27	9	9			

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).

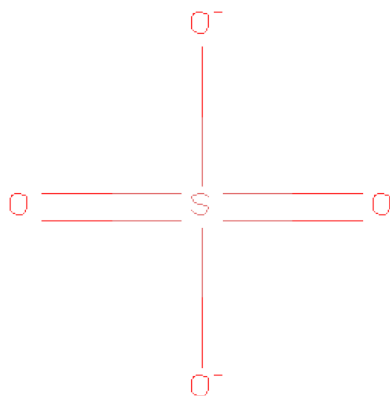


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	5	Total	Cl	0	0
			5	5		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		

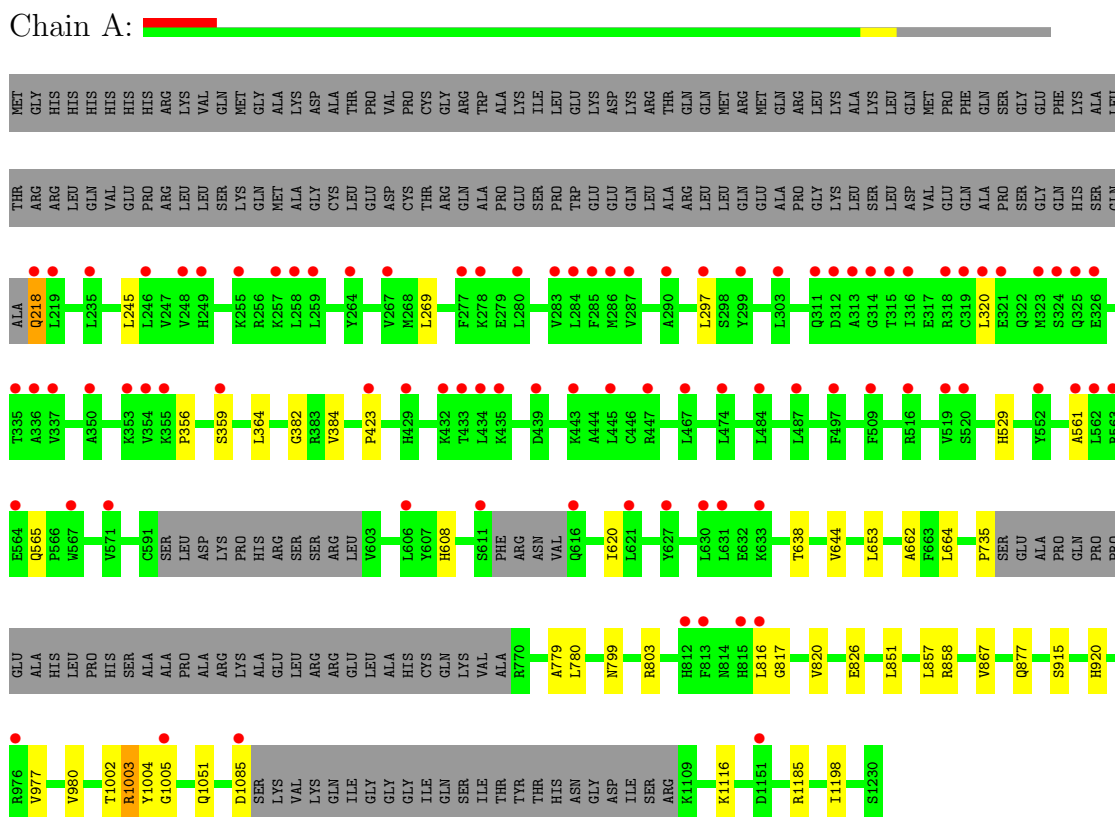
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	145	Total	O	0	0
			145	145		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: DNA-directed RNA polymerase, mitochondrial



- Molecule 2: Nonamer peptide

Chain B: 

There are no outlier residues recorded for this chain.

4 Data and refinement statistics

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, α , β , γ	211.26 Å 211.26 Å 60.46 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	58.13 – 2.50 58.13 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (58.13-2.50) 99.8 (58.13-2.50)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 2.51 Å)	Xtriage
Refinement program	BUSTER 2.11.1	Depositor
R, R_{free}	0.185 , 0.231 0.211 , 0.248	Depositor DCC
R_{free} test set	2346 reflections (5.05%)	DCC
Wilson B-factor (Å ²)	61.3	Xtriage
Anisotropy	0.549	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 64.5	EDS
Estimated twinning fraction	0.013 for -k,-h,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 46505 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7666	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, SO4, CL

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	0.47	0/7651	0.69	3/10383 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	356	PRO	N-CA-CB	6.00	110.50	103.30
1	A	735	PRO	N-CA-CB	5.57	109.98	103.30
1	A	1085	ASP	CB-CG-OD2	5.18	122.96	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7454	0	4	6	0
2	B	45	0	11	0	0
3	A	12	0	16	3	0
4	A	5	0	0	0	0
5	A	5	0	0	0	0
6	A	145	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	7666	0	31	6	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 1.

All (6) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:218:GLN:HG3	1:A:218:GLN:O	1.77	0.78
1:A:1051[B]:GLN:NE2	6:A:1295:HOH:O	2.33	0.61
1:A:218:GLN:CG	1:A:218:GLN:O	2.49	0.56
1:A:826:GLU:OE2	3:A:2:GOL:H12	2.18	0.43
1:A:779:ALA:CB	3:A:1:GOL:H32	2.49	0.42
1:A:820:VAL:CG1	3:A:1:GOL:H2	2.51	0.40

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	938/1134 (83%)	891 (95%)	36 (4%)	11 (1%)	19	32

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	359	SER
1	A	561	ALA
1	A	816	LEU
1	A	817	GLY
1	A	1002	THR
1	A	1003	ARG
1	A	382	GLY
1	A	662	ALA
1	A	565	GLN

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Mol	Chain	Res	Type
1	A	1005	GLY
1	A	423	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	795/982 (81%)	764 (96%)	31 (4%)	43	70

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	218	GLN
1	A	245	LEU
1	A	269	LEU
1	A	297	LEU
1	A	320	LEU
1	A	364	LEU
1	A	384	VAL
1	A	529	HIS
1	A	608	HIS
1	A	620	ILE
1	A	638	THR
1	A	644	VAL
1	A	653	LEU
1	A	664	LEU
1	A	780	LEU
1	A	799	ASN
1	A	803	ARG
1	A	851	LEU
1	A	857	LEU
1	A	858	ARG
1	A	867	VAL
1	A	877	GLN
1	A	915	SER
1	A	920	HIS
1	A	977	VAL
1	A	980	VAL

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Mol	Chain	Res	Type
1	A	1003	ARG
1	A	1004	TYR
1	A	1116	LYS
1	A	1185	ARG
1	A	1198	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains 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 8 ligands modelled in this entry, 5 are monoatomic - leaving 3 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	GOL	A	1	-	5,5,5	0.66	0	5,5,5	1.04	0
5	SO4	A	1233	-	4,4,4	1.01	0	6,6,6	0.49	0
3	GOL	A	2	-	5,5,5	0.44	0	5,5,5	0.49	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	GOL	A	1	-	-	0/4/4/4	0/0/0/0
5	SO4	A	1233	-	-	0/0/0/0	0/0/0/0
3	GOL	A	2	-	-	0/4/4/4	0/0/0/0

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.

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	941/1134 (82%)	0.69	88 (9%) 9 8	43, 82, 144, 194	0
2	B	0/9	-	-	-	-
All	All	941/1143 (82%)	0.69	88 (9%) 9 8	43, 82, 144, 194	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	563	ARG	8.5
1	A	562	LEU	8.2
1	A	815	HIS	7.9
1	A	285	PHE	6.7
1	A	323	MET	5.9
1	A	258	LEU	5.9
1	A	567	TRP	5.8
1	A	325	GLN	5.7
1	A	324	SER	5.3
1	A	218	GLN	5.3
1	A	359	SER	5.1
1	A	336	ALA	5.0
1	A	1085	ASP	4.6
1	A	290	ALA	4.3
1	A	326	GLU	4.2
1	A	297	LEU	3.9
1	A	283	VAL	3.9
1	A	249	HIS	3.7
1	A	353	LYS	3.7
1	A	316	ILE	3.6
1	A	259	LEU	3.6
1	A	246	LEU	3.5
1	A	1151	ASP	3.4
1	A	287	VAL	3.4
1	A	278	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	312	ASP	3.4
1	A	355	LYS	3.3
1	A	812	HIS	3.1
1	A	434	LEU	3.1
1	A	813	PHE	3.1
1	A	264	TYR	3.1
1	A	284	LEU	3.0
1	A	248	VAL	3.0
1	A	467	LEU	3.0
1	A	631	LEU	3.0
1	A	255	LYS	3.0
1	A	350	ALA	3.0
1	A	321	GLU	3.0
1	A	630	LEU	2.9
1	A	311	GLN	2.9
1	A	564	GLU	2.8
1	A	432	LYS	2.8
1	A	320	LEU	2.8
1	A	267	VAL	2.8
1	A	520	SER	2.7
1	A	286	MET	2.7
1	A	439	ASP	2.7
1	A	611	SER	2.7
1	A	571	VAL	2.6
1	A	616	GLN	2.6
1	A	433	THR	2.6
1	A	497	PHE	2.6
1	A	219	LEU	2.6
1	A	314	GLY	2.6
1	A	429	HIS	2.5
1	A	447	ARG	2.5
1	A	303	LEU	2.5
1	A	816	LEU	2.5
1	A	633	LYS	2.4
1	A	561	ALA	2.4
1	A	606	LEU	2.4
1	A	423	PRO	2.4
1	A	509	PHE	2.3
1	A	1005	GLY	2.3
1	A	474	LEU	2.3
1	A	318	ARG	2.3
1	A	335	THR	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	235	LEU	2.2
1	A	277	PHE	2.2
1	A	315	THR	2.2
1	A	484	LEU	2.2
1	A	337	VAL	2.2
1	A	280	LEU	2.2
1	A	976	ARG	2.2
1	A	435	LYS	2.2
1	A	443	LYS	2.2
1	A	516	ARG	2.2
1	A	319	CYS	2.2
1	A	487	LEU	2.2
1	A	445	LEU	2.1
1	A	257	LYS	2.1
1	A	299	TYR	2.1
1	A	552	TYR	2.1
1	A	354	VAL	2.1
1	A	313	ALA	2.1
1	A	627	TYR	2.1
1	A	621	LEU	2.0
1	A	519	VAL	2.0

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	CL	A	1231	1/1	0.24	5.08	113,113,113,113	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	GOL	A	2	6/6	0.30	3.98	107,108,109,109	0
3	GOL	A	1	6/6	0.26	1.79	85,86,86,87	0
5	SO4	A	1233	5/5	0.16	1.08	73,77,79,80	0
4	CL	A	3	1/1	0.17	0.55	122,122,122,122	0
4	CL	A	4	1/1	0.21	0.48	121,121,121,121	0
4	CL	A	1232	1/1	0.15	-0.85	102,102,102,102	0
4	CL	A	5	1/1	0.12	-2.47	97,97,97,97	0

6.5 Other polymers ⓘ

There are no such residues in this entry.