



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 6P3J
Title : Crystal structure of LigU
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Deposited on : 2019-05-23
Resolution : 2.02 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
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
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)	:	2.13.1

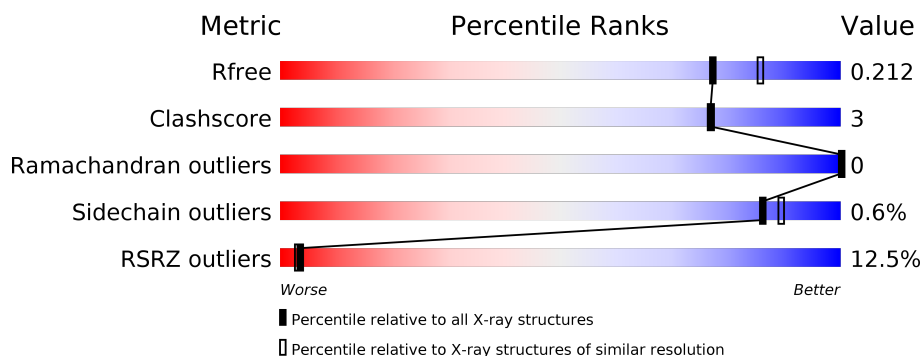
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.02 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	10434 (2.04-2.00)
Clashscore	141614	11643 (2.04-2.00)
Ramachandran outliers	138981	11493 (2.04-2.00)
Sidechain outliers	138945	11492 (2.04-2.00)
RSRZ outliers	127900	10220 (2.04-2.00)

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	365	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 98%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 2px auto;"> % 90% 6% </div> </div>
1	B	365	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 23%, orange 1%, yellow 1%, green 88%, grey 8%);"></div> <div style="display: flex; justify-content: space-between; width: 88%; margin: 2px auto;"> 23% 88% 9% </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5380 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 (4E)-oxalomesaconate Delta-isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	353	Total	C	N	O	S	0	5	0
			2575	1605	445	505	20			
1	B	352	Total	C	N	O	S	0	2	0
			2569	1598	455	496	20			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	358	LEU	-	expression tag	UNP Q0KJL4
A	359	GLU	-	expression tag	UNP Q0KJL4
A	360	HIS	-	expression tag	UNP Q0KJL4
A	361	HIS	-	expression tag	UNP Q0KJL4
A	362	HIS	-	expression tag	UNP Q0KJL4
A	363	HIS	-	expression tag	UNP Q0KJL4
A	364	HIS	-	expression tag	UNP Q0KJL4
A	365	HIS	-	expression tag	UNP Q0KJL4
B	358	LEU	-	expression tag	UNP Q0KJL4
B	359	GLU	-	expression tag	UNP Q0KJL4
B	360	HIS	-	expression tag	UNP Q0KJL4
B	361	HIS	-	expression tag	UNP Q0KJL4
B	362	HIS	-	expression tag	UNP Q0KJL4
B	363	HIS	-	expression tag	UNP Q0KJL4
B	364	HIS	-	expression tag	UNP Q0KJL4
B	365	HIS	-	expression tag	UNP Q0KJL4

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total 2	Ca 2	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total 1	Na 1	0	0

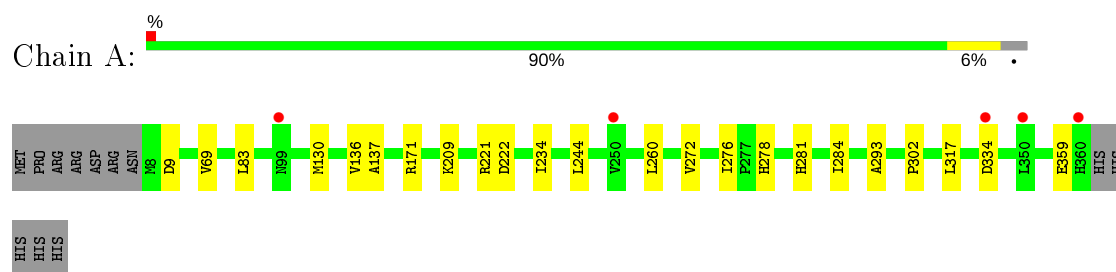
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	120	Total 120	O 120	0	0
5	B	104	Total 104	O 104	0	0

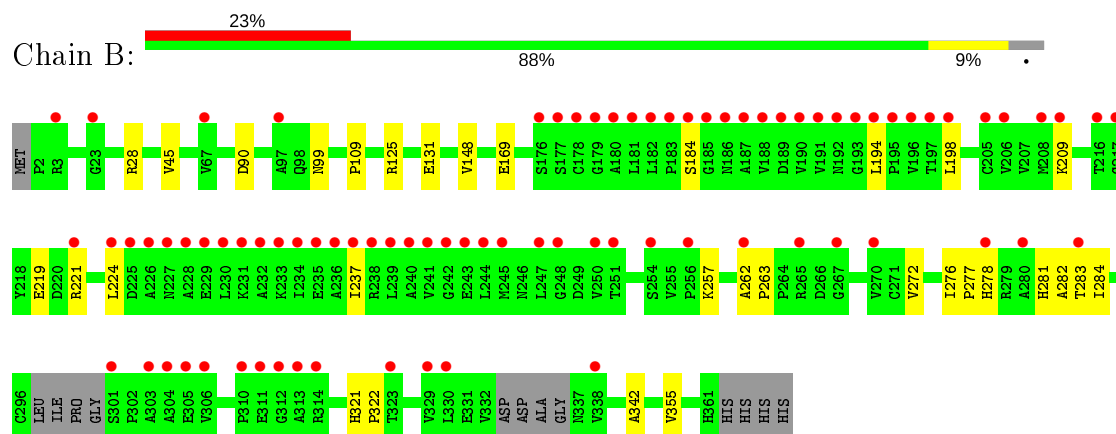
3 Residue-property plots [i](#)

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: (4E)-oxalomesaconate Delta-isomerase



- Molecule 1: (4E)-oxalomesaconate Delta-isomerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	62.78 Å 67.36 Å 161.07 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.99 – 2.02 41.99 – 2.02	Depositor EDS
% Data completeness (in resolution range)	97.9 (41.99-2.02) 97.9 (41.99-2.02)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.30 (at 2.01 Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, R_{free}	0.186 , 0.212 0.186 , 0.212	Depositor DCC
R_{free} test set	2003 reflections (4.48%)	wwPDB-VP
Wilson B-factor (Å ²)	44.3	Xtriage
Anisotropy	0.293	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 53.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5380	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% 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: NA, CA, 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	0.26	0/2616	0.46	0/3563
1	B	0.26	0/2609	0.46	0/3546
All	All	0.26	0/5225	0.46	0/7109

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	2575	0	2574	12	0
1	B	2569	0	2576	19	0
2	A	5	0	0	0	0
2	B	4	0	0	0	0
3	B	2	0	0	0	0
4	B	1	0	0	0	0
5	A	120	0	0	1	0
5	B	104	0	0	1	0
All	All	5380	0	5150	31	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 3.

All (31) 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:272:VAL:HG11	1:B:284:ILE:HD12	1.75	0.69
1:A:9:ASP:HB3	1:A:359:GLU:HG2	1.77	0.66
1:A:272:VAL:HG11	1:A:284:ILE:HD12	1.80	0.63
1:A:136:VAL:HG13	1:A:171:ARG:HG3	1.80	0.62
1:B:221:ARG:HD3	1:B:282:ALA:HA	1.87	0.57
1:B:283:THR:OG1	1:B:284:ILE:N	2.36	0.57
1:A:221:ARG:NH2	1:A:222[B]:ASP:OD1	2.39	0.56
1:B:45:VAL:HG13	1:B:355:VAL:HG21	1.89	0.54
1:A:209:LYS:HG3	1:A:302:PRO:HB3	1.90	0.54
1:B:125:ARG:NH2	5:B:503:HOH:O	2.41	0.53
1:A:276:ILE:HG21	1:A:281:HIS:HD2	1.75	0.52
1:B:257:LYS:HD2	1:B:276:ILE:HG22	1.89	0.52
1:B:194:LEU:HD23	1:B:194:LEU:H	1.76	0.51
1:B:184:SER:HB3	1:B:198:LEU:HD12	1.92	0.51
1:A:234[A]:ILE:HD11	1:A:260:LEU:HD11	1.93	0.50
1:B:277:PRO:HG2	1:B:278:HIS:CE1	2.47	0.50
1:B:209:LYS:HZ3	1:B:263:PRO:HD3	1.76	0.49
1:B:169:GLU:HG2	1:B:342:ALA:HB2	1.97	0.46
1:B:28[B]:ARG:NH2	1:B:131:GLU:OE1	2.49	0.45
1:A:69:VAL:HB	1:A:83:LEU:HB3	1.98	0.45
1:B:209:LYS:HZ2	1:B:262:ALA:HA	1.82	0.44
1:A:130:MET:HE2	1:A:137:ALA:HB2	1.99	0.44
1:A:244:LEU:HA	1:A:244:LEU:HD23	1.92	0.42
1:A:293:ALA:HB1	1:A:317:LEU:HD12	2.01	0.42
1:B:219:GLU:HB2	1:B:224:LEU:HG	2.02	0.42
1:A:278:HIS:HD2	5:A:612:HOH:O	2.03	0.42
1:B:281:HIS:HD2	1:B:283:THR:H	1.68	0.41
1:B:194:LEU:HD21	1:B:237:ILE:HD11	2.02	0.41
1:B:321:HIS:HB2	1:B:322:PRO:HD2	2.02	0.41
1:B:209:LYS:NZ	1:B:263:PRO:HD3	2.36	0.40
1:B:109:PRO:HB3	1:B:148:VAL:HG11	2.02	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	356/365 (98%)	347 (98%)	9 (2%)	0	100	100
1	B	348/365 (95%)	334 (96%)	14 (4%)	0	100	100
All	All	704/730 (96%)	681 (97%)	23 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	273/280 (98%)	272 (100%)	1 (0%)	91	93
1	B	272/280 (97%)	269 (99%)	3 (1%)	73	77
All	All	545/560 (97%)	541 (99%)	4 (1%)	86	87

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	334	ASP
1	B	90[A]	ASP
1	B	90[B]	ASP
1	B	99	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	281	HIS

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](#)

Of 12 ligands modelled in this entry, 12 are 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 [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	353/365 (96%)	0.26	5 (1%) 75 74	33, 51, 78, 135	0
1	B	352/365 (96%)	1.27	83 (23%) 0 0	33, 61, 122, 147	0
All	All	705/730 (96%)	0.76	88 (12%) 3 3	33, 54, 112, 147	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	194	LEU	10.4
1	B	178	CYS	8.7
1	B	191	VAL	8.3
1	B	226	ALA	6.5
1	B	241	VAL	6.4
1	B	234	ILE	6.1
1	B	186	ASN	6.0
1	B	188	VAL	5.7
1	B	177	SER	5.4
1	B	176	SER	5.3
1	B	196	VAL	5.3
1	B	250	VAL	5.0
1	B	185	GLY	5.0
1	B	193	GLY	5.0
1	B	267	GLY	4.9
1	B	247	LEU	4.7
1	B	232	ALA	4.6
1	B	221	ARG	4.4
1	B	179	GLY	4.4
1	B	236	ALA	4.3
1	B	198	LEU	4.2
1	B	237	ILE	4.2
1	B	184	SER	4.1
1	B	187	ALA	4.1

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Mol	Chain	Res	Type	RSRZ
1	B	224	LEU	4.1
1	A	360	HIS	4.0
1	B	245	MET	4.0
1	B	240	ALA	3.9
1	B	230	LEU	3.9
1	B	280	ALA	3.8
1	B	262	ALA	3.8
1	B	189	ASP	3.7
1	B	242	GLY	3.7
1	B	243	GLU	3.5
1	B	278	HIS	3.5
1	B	228	ALA	3.5
1	B	244	LEU	3.5
1	B	3	ARG	3.4
1	B	283	THR	3.4
1	B	248	GLY	3.3
1	B	303	ALA	3.3
1	B	338	VAL	3.3
1	B	225	ASP	3.2
1	B	311	GLU	3.2
1	B	312	GLY	3.2
1	B	238	ARG	3.2
1	B	330	LEU	3.1
1	B	265	ARG	3.1
1	B	239	LEU	3.1
1	B	195	PRO	3.1
1	B	181	LEU	3.1
1	B	304	ALA	3.0
1	B	310	PRO	3.0
1	B	182	LEU	3.0
1	B	251	THR	2.9
1	B	235	GLU	2.9
1	B	254	SER	2.9
1	B	306	VAL	2.7
1	B	208	MET	2.7
1	B	323	THR	2.7
1	B	216	THR	2.7
1	B	233	LYS	2.7
1	B	314	ARG	2.6
1	B	305	GLU	2.6
1	B	256	PRO	2.5
1	B	183	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	180	ALA	2.4
1	B	217	GLY	2.4
1	B	301	SER	2.4
1	B	190	VAL	2.3
1	B	227	ASN	2.3
1	B	97	ALA	2.3
1	B	205	CYS	2.3
1	B	231	LYS	2.2
1	B	206	VAL	2.2
1	A	99[A]	ASN	2.2
1	A	334	ASP	2.2
1	B	329	VAL	2.2
1	B	209	LYS	2.1
1	B	313	ALA	2.1
1	B	67	VAL	2.1
1	B	197	THR	2.1
1	B	192	ASN	2.1
1	B	229	GLU	2.0
1	B	270	VAL	2.0
1	A	350	LEU	2.0
1	A	250	VAL	2.0
1	B	23	GLY	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 monosaccharides 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
2	CL	B	406	1/1	0.81	0.24	88,88,88,88	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	CL	B	404	1/1	0.91	0.17	67,67,67,67	0
4	NA	B	407	1/1	0.93	0.11	52,52,52,52	0
2	CL	A	405	1/1	0.94	0.11	67,67,67,67	0
2	CL	A	401	1/1	0.95	0.16	66,66,66,66	0
2	CL	B	405	1/1	0.95	0.25	70,70,70,70	0
2	CL	A	404	1/1	0.96	0.12	67,67,67,67	0
2	CL	A	402	1/1	0.96	0.15	61,61,61,61	0
3	CA	B	402	1/1	0.99	0.10	38,38,38,38	0
2	CL	B	403	1/1	0.99	0.09	48,48,48,48	0
2	CL	A	403	1/1	0.99	0.11	49,49,49,49	0
3	CA	B	401	1/1	0.99	0.08	40,40,40,40	0

6.5 Other polymers ⓘ

There are no such residues in this entry.