Full wwPDB X-ray Structure Validation Report (i)

Jun 23, 2024 – 05:54 AM EDT

PDB ID	:	6FV8
Title	:	Dimer structure of the MATE family multidrug resistance transporter Aq_128 from Aquifex aeolicus in the outward-facing state
Authors	:	Zhao, J.; Safarian, S.; Thielmann, Y.; Xie, H.; Wang, J.; Michel, H.
Deposited on	:	2018-03-01
Resolution	:	3.00 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 (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 (1)) were used in the production of this report:

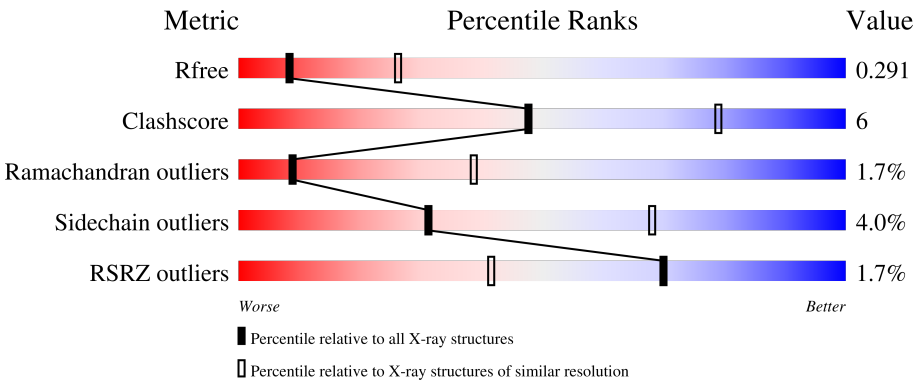
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

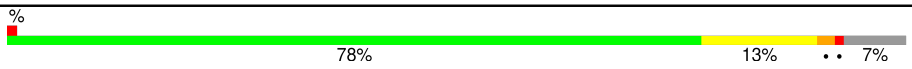
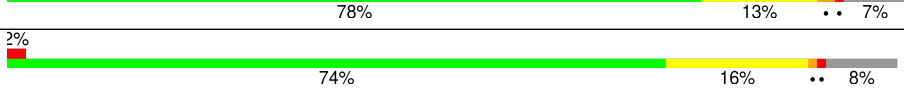
The reported resolution of this entry is 3.00 Å.

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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 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	472	
1	B	472	

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 6908 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 Aq128.

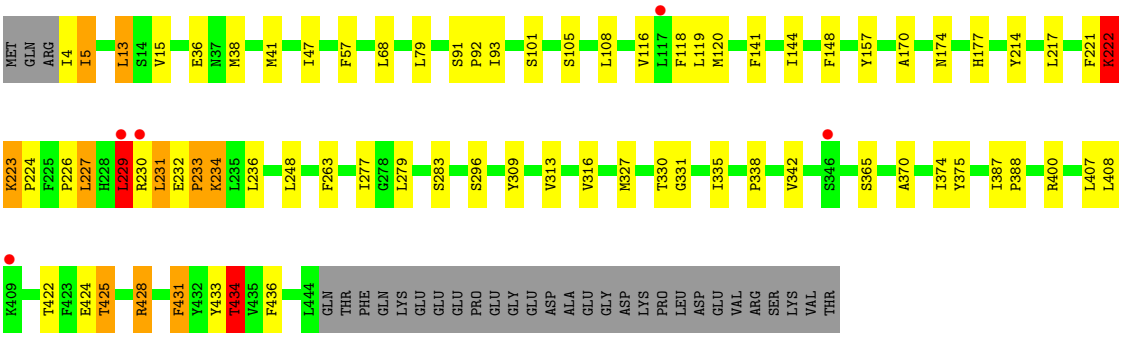
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	441	3470	2344	537	575	14	0	0	0
1	B	436	3438	2319	534	571	14	0	0	0

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.

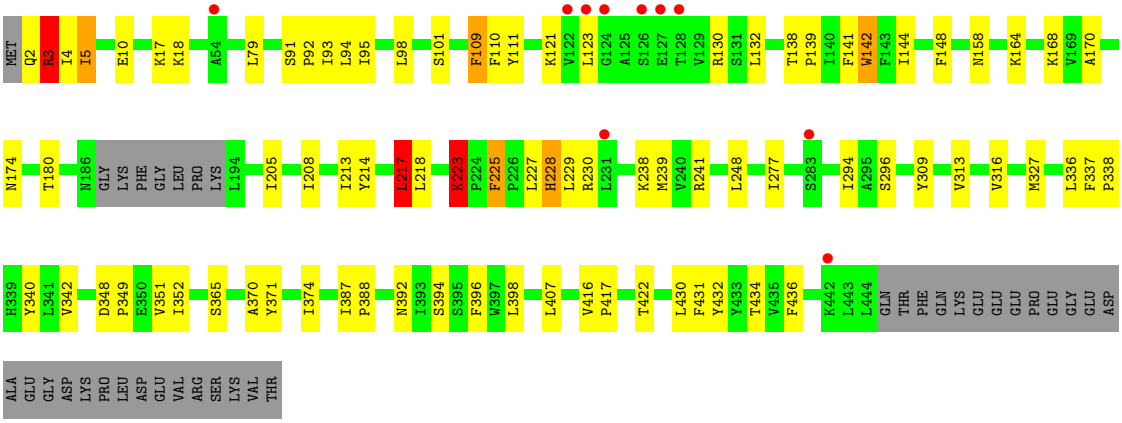
- Molecule 1: Aq128

Chain A:



- Molecule 1: Aq128

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	80.10Å 73.60Å 101.80Å 90.00° 99.80° 90.00°	Depositor
Resolution (Å)	19.93 – 3.00 19.93 – 3.00	Depositor EDS
% Data completeness (in resolution range)	98.9 (19.93-3.00) 99.0 (19.93-3.00)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.96 (at 2.98Å)	Xtriage
Refinement program	PHENIX (1.14_3260: ???)	Depositor
R, R_{free}	0.265 , 0.287 0.268 , 0.291	Depositor DCC
R_{free} test set	1166 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	82.4	Xtriage
Anisotropy	0.211	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 55.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	6908	wwPDB-VP
Average B, all atoms (Å^2)	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.60% of the height of the origin peak. No significant pseudotranslation is detected.*

[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 (i)

5.1 Standard geometry (i)

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	0/3571	0.43	2/4857 (0.0%)
1	B	0.25	0/3536	0.40	1/4809 (0.0%)
All	All	0.26	0/7107	0.41	3/9666 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	227	LEU	CA-CB-CG	6.50	130.25	115.30
1	A	222	LYS	C-N-CA	5.80	136.20	121.70
1	B	217	LEU	CA-CB-CG	5.45	127.83	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	3470	0	3627	41	0
1	B	3438	0	3588	46	0
All	All	6908	0	7215	86	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 6.

All (86) 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:214:TYR:O	1:B:223:LYS:NZ	2.13	0.81
1:B:327:MET:HG3	1:B:370:ALA:HB2	1.72	0.71
1:A:327:MET:HG3	1:A:370:ALA:HB2	1.71	0.71
1:B:238:LYS:HD2	1:B:241:ARG:HH21	1.54	0.70
1:A:365:SER:HB3	1:A:422:THR:HG23	1.72	0.69
1:B:109:PHE:O	1:B:111:TYR:N	2.25	0.69
1:B:95:ILE:HD11	1:B:230:ARG:HG2	1.75	0.69
1:A:400:ARG:HB2	1:A:424:GLU:HG3	1.75	0.68
1:A:425:THR:O	1:A:425:THR:OG1	2.13	0.67
1:B:121:LYS:HG2	1:B:130:ARG:HH12	1.59	0.66
1:A:36:GLU:OE2	1:A:177:HIS:ND1	2.24	0.66
1:B:79:LEU:HB3	1:B:93:ILE:HD13	1.78	0.65
1:A:141:PHE:HA	1:A:144:ILE:HG13	1.78	0.65
1:A:170:ALA:O	1:A:174:ASN:ND2	2.32	0.62
1:A:229:LEU:HD13	1:A:229:LEU:H	1.66	0.61
1:B:365:SER:HB3	1:B:422:THR:HG23	1.83	0.61
1:A:231:LEU:HB2	1:A:233:PRO:HD3	1.82	0.60
1:A:223:LYS:CG	1:A:224:PRO:HD2	2.34	0.57
1:B:10:GLU:OE2	1:B:18:LYS:NZ	2.39	0.56
1:A:222:LYS:HG2	1:A:226:PRO:HB3	1.86	0.56
1:A:101:SER:HB2	1:A:148:PHE:HB3	1.88	0.55
1:B:227:LEU:HG	1:B:228:HIS:H	1.71	0.55
1:A:13:LEU:H	1:A:13:LEU:HD22	1.71	0.55
1:B:170:ALA:O	1:B:174:ASN:ND2	2.28	0.54
1:A:316:VAL:HG21	1:A:436:PHE:CZ	2.43	0.54
1:B:316:VAL:HG21	1:B:436:PHE:CZ	2.44	0.52
1:B:213:ILE:HG23	1:B:217:LEU:HD11	1.92	0.52
1:A:263:PHE:HD2	1:A:408:LEU:HD12	1.74	0.51
1:B:79:LEU:HD12	1:B:239:MET:HG2	1.94	0.50
1:A:79:LEU:HB3	1:A:93:ILE:HD13	1.94	0.49
1:A:223:LYS:HG2	1:A:224:PRO:HD2	1.94	0.49
1:B:277:ILE:HG21	1:B:342:VAL:HG13	1.94	0.49
1:A:277:ILE:HG21	1:A:342:VAL:HG13	1.94	0.48
1:A:279:LEU:O	1:A:283:SER:N	2.44	0.48
1:A:331:GLY:O	1:A:335:ILE:HG12	2.13	0.48
1:A:296:SER:HB3	1:A:374:ILE:HD12	1.95	0.48
1:B:205:ILE:HA	1:B:208:ILE:HG12	1.96	0.47
1:B:101:SER:HB2	1:B:148:PHE:HB3	1.97	0.47
1:A:375:TYR:CE2	1:A:433:TYR:HB2	2.50	0.47
1:B:95:ILE:HA	1:B:98:LEU:HB2	1.95	0.46
1:A:431:PHE:O	1:A:434:THR:OG1	2.34	0.46
1:B:349:PRO:HA	1:B:352:ILE:HD12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:LEU:C	1:A:223:LYS:HG3	2.36	0.46
1:B:180:THR:HG21	1:B:205:ILE:HD12	1.98	0.46
1:B:338:PRO:O	1:B:342:VAL:HG23	2.15	0.45
1:B:392:ASN:ND2	1:B:432:TYR:OH	2.49	0.45
1:B:223:LYS:HA	1:B:223:LYS:HD2	1.52	0.45
1:A:214:TYR:O	1:A:223:LYS:NZ	2.34	0.44
1:B:348:ASP:HB3	1:B:351:VAL:HG23	1.99	0.44
1:A:38:MET:HA	1:A:41:MET:HE2	2.00	0.44
1:A:105:SER:HB2	1:A:144:ILE:HG22	1.99	0.44
1:B:158:ASN:HD22	1:B:294:ILE:HG21	1.82	0.44
1:B:164:LYS:O	1:B:168:LYS:HG2	2.17	0.44
1:B:3:ARG:HG2	1:B:5:ILE:HG22	1.99	0.44
1:A:68:LEU:HD12	1:A:108:LEU:HD11	1.99	0.44
1:B:371:TYR:HA	1:B:374:ILE:HG22	2.00	0.44
1:A:424:GLU:OE2	1:A:428:ARG:NH1	2.51	0.43
1:B:91:SER:OG	1:B:92:PRO:HD3	2.19	0.43
1:B:218:LEU:HG	1:B:223:LYS:HG2	1.99	0.43
1:B:392:ASN:O	1:B:396:PHE:HB2	2.19	0.43
1:A:221:PHE:O	1:A:223:LYS:N	2.52	0.43
1:A:248:LEU:HG	1:B:248:LEU:HD11	1.99	0.43
1:A:91:SER:OG	1:A:92:PRO:HD3	2.19	0.43
1:A:316:VAL:HG21	1:A:436:PHE:HZ	1.82	0.43
1:A:327:MET:HA	1:A:330:THR:HB	2.00	0.43
1:B:309:TYR:O	1:B:313:VAL:HG23	2.19	0.43
1:B:296:SER:HB3	1:B:374:ILE:HD12	2.01	0.42
1:B:316:VAL:HG21	1:B:436:PHE:HZ	1.84	0.42
1:A:309:TYR:O	1:A:313:VAL:HG23	2.20	0.42
1:B:139:PRO:HA	1:B:142:TRP:HB2	2.01	0.42
1:A:157:TYR:CE1	1:A:223:LYS:HE2	2.55	0.42
1:B:79:LEU:HD23	1:B:79:LEU:HA	1.90	0.42
1:B:387:ILE:HB	1:B:388:PRO:HD3	2.02	0.42
1:B:94:LEU:HB2	1:B:225:PHE:CZ	2.55	0.41
1:B:228:HIS:HB3	1:B:229:LEU:H	1.50	0.41
1:A:4:ILE:O	1:A:5:ILE:HB	2.20	0.41
1:B:337:PHE:HB3	1:B:340:TYR:HB2	2.01	0.41
1:A:116:VAL:HA	1:A:120:MET:HB2	2.01	0.41
1:B:141:PHE:HA	1:B:144:ILE:HD11	2.01	0.41
1:B:394:SER:O	1:B:398:LEU:HG	2.20	0.41
1:B:336:LEU:C	1:B:338:PRO:HD3	2.41	0.41
1:A:400:ARG:HB2	1:A:424:GLU:CG	2.48	0.41
1:A:387:ILE:HB	1:A:388:PRO:HD3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:PHE:HB3	1:A:120:MET:SD	2.61	0.41
1:B:132:LEU:HD23	1:B:132:LEU:HA	1.93	0.40
1:B:416:VAL:HB	1:B:417:PRO:HD3	2.04	0.40

There are no symmetry-related clashes.

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	439/472 (93%)	409 (93%)	21 (5%)	9 (2%)	7 33
1	B	432/472 (92%)	403 (93%)	23 (5%)	6 (1%)	11 43
All	All	871/944 (92%)	812 (93%)	44 (5%)	15 (2%)	9 39

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	222	LYS
1	A	223	LYS
1	A	434	THR
1	B	110	PHE
1	B	228	HIS
1	A	229	LEU
1	B	123	LEU
1	B	434	THR
1	A	5	ILE
1	B	3	ARG
1	A	234	LYS
1	A	338	PRO
1	B	223	LYS
1	A	233	PRO
1	A	47	ILE

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	375/403 (93%)	359 (96%)	16 (4%)	29	66
1	B	372/403 (92%)	358 (96%)	14 (4%)	33	69
All	All	747/806 (93%)	717 (96%)	30 (4%)	31	68

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	LEU
1	A	15	VAL
1	A	118	PHE
1	A	119	LEU
1	A	227	LEU
1	A	229	LEU
1	A	230	ARG
1	A	231	LEU
1	A	232	GLU
1	A	234	LYS
1	A	236	LEU
1	A	407	LEU
1	A	425	THR
1	A	428	ARG
1	A	431	PHE
1	A	434	THR
1	B	2	GLN
1	B	3	ARG
1	B	4	ILE
1	B	5	ILE
1	B	17	LYS
1	B	109	PHE
1	B	138	THR
1	B	142	TRP
1	B	217	LEU
1	B	223	LYS
1	B	225	PHE

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Mol	Chain	Res	Type
1	B	407	LEU
1	B	430	LEU
1	B	431	PHE

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

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)

There are no ligands in this entry.

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, 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	441/472 (93%)	-0.22	5 (1%)	80	56	46, 73, 110, 133	0
1	B	436/472 (92%)	-0.12	10 (2%)	60	31	47, 76, 126, 153	0
All	All	877/944 (92%)	-0.17	15 (1%)	70	41	46, 75, 120, 153	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	117	LEU	5.0
1	B	128	THR	3.2
1	B	124	GLY	3.1
1	B	283	SER	2.9
1	B	231	LEU	2.9
1	B	127	GLU	2.7
1	B	126	SER	2.5
1	A	346	SER	2.5
1	A	409	LYS	2.4
1	B	123	LEU	2.2
1	B	442	LYS	2.2
1	A	230	ARG	2.1
1	B	122	VAL	2.1
1	A	229	LEU	2.1
1	B	54	ALA	2.1

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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.