



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 07:45 AM GMT

PDB ID : 2FPN
Title : The crystal structure of the ywmB protein from Bacillus subtilis
Authors : Zhang, R.; Wu, R.; Moy, S.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2006-01-16
Resolution : 2.49 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>

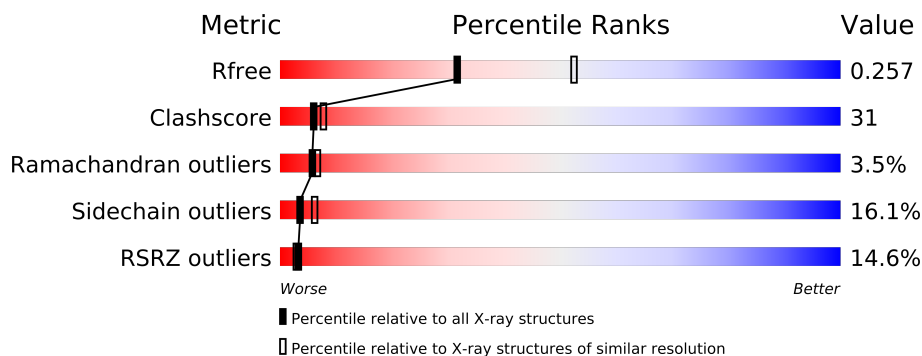
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.49 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	216	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1753 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 ywmB.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	205	Total	C	N	O	S	Se	0	0	0
			1700	1080	287	325	1	7			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	MSE	MET	MODIFIED RESIDUE	GB 2636202
A	11	MSE	MET	MODIFIED RESIDUE	GB 2636202
A	60	MSE	MET	MODIFIED RESIDUE	GB 2636202
A	98	MSE	MET	MODIFIED RESIDUE	GB 2636202
A	139	MSE	MET	MODIFIED RESIDUE	GB 2636202
A	182	MSE	MET	MODIFIED RESIDUE	GB 2636202
A	188	MSE	MET	MODIFIED RESIDUE	GB 2636202
A	199	MSE	MET	MODIFIED RESIDUE	GB 2636202

- Molecule 2 is water.

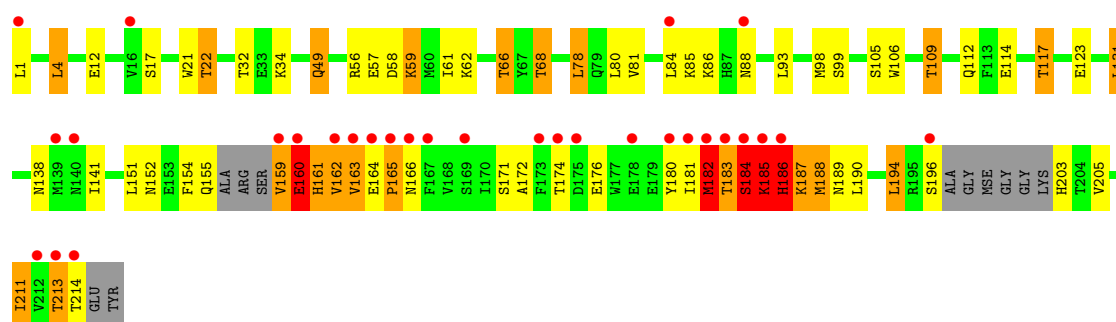
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	53	Total	O	0	0
			53	53		

3 Residue-property plots i

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: ywmB

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	88.79Å 50.86Å 81.26Å 90.00° 96.49° 90.00°	Depositor
Resolution (Å)	80.85 – 2.49 40.37 – 2.49	Depositor EDS
% Data completeness (in resolution range)	96.4 (80.85-2.49) 96.4 (40.37-2.49)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 2.48Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.242 , 0.281 0.258 , 0.257	Depositor DCC
R_{free} test set	625 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	51.5	Xtriage
Anisotropy	0.250	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	2 of 12430 reflections (0.016%)	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	1753	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.01% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	1.04	4/1725 (0.2%)	0.84	4/2319 (0.2%)

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	3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	182	MSE	CG-SE	32.03	3.04	1.95
1	A	188	MSE	CG-SE	13.13	2.40	1.95
1	A	182	MSE	SE-CE	7.14	2.37	1.95
1	A	188	MSE	SE-CE	7.08	2.37	1.95

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	182	MSE	CB-CG-SE	-16.72	62.55	112.70
1	A	182	MSE	CG-SE-CE	-16.20	63.26	98.90
1	A	131	LEU	CA-CB-CG	5.79	128.61	115.30
1	A	188	MSE	CG-SE-CE	-5.72	86.32	98.90

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	160	GLU	Peptide
1	A	185	LYS	Peptide

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Mol	Chain	Res	Type	Group
1	A	186	HIS	Peptide

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	1700	0	1687	105	0
2	A	53	0	0	9	0
All	All	1753	0	1687	105	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 31.

All (105) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:162:VAL:O	1:A:163:VAL:HG23	1.14	1.27
1:A:188:MSE:SE	1:A:188:MSE:CE	2.37	1.23
1:A:182:MSE:CE	1:A:182:MSE:SE	2.37	1.23
1:A:182:MSE:SE	1:A:182:MSE:HB2	1.88	1.22
1:A:188:MSE:CG	1:A:188:MSE:SE	2.40	1.20
1:A:151:LEU:CD2	1:A:159:VAL:HG11	1.73	1.19
1:A:151:LEU:HD21	1:A:159:VAL:CG1	1.78	1.11
1:A:162:VAL:HG13	1:A:163:VAL:N	1.64	1.10
1:A:151:LEU:HD11	1:A:159:VAL:HG13	1.38	1.06
1:A:185:LYS:HG3	1:A:185:LYS:O	1.51	1.05
1:A:151:LEU:HD11	1:A:159:VAL:CG1	1.87	1.04
1:A:162:VAL:O	1:A:163:VAL:CG2	2.03	1.04
1:A:162:VAL:CG1	1:A:163:VAL:N	2.24	1.00
1:A:155:GLN:HB2	1:A:174:THR:CG2	1.92	1.00
1:A:185:LYS:O	1:A:186:HIS:CD2	2.17	0.97
1:A:155:GLN:HB2	1:A:174:THR:HG21	1.46	0.96
1:A:182:MSE:CB	1:A:182:MSE:SE	2.70	0.90
1:A:182:MSE:CG	2:A:254:HOH:O	2.21	0.88
1:A:151:LEU:CD1	1:A:159:VAL:CG1	2.52	0.86
1:A:49:GLN:H	1:A:49:GLN:HE21	1.20	0.86

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:180:TYR:CE2	1:A:182:MSE:SE	2.79	0.86
1:A:151:LEU:HD21	1:A:159:VAL:HG11	0.88	0.86
1:A:180:TYR:HE2	1:A:182:MSE:SE	2.10	0.83
1:A:185:LYS:O	1:A:186:HIS:CG	2.31	0.83
1:A:68:THR:HG22	2:A:229:HOH:O	1.80	0.82
1:A:182:MSE:HG2	2:A:254:HOH:O	1.80	0.81
1:A:162:VAL:HG13	1:A:163:VAL:H	1.43	0.80
1:A:154:PHE:O	1:A:155:GLN:CG	2.30	0.79
1:A:154:PHE:O	1:A:155:GLN:CB	2.31	0.79
1:A:182:MSE:HG3	2:A:254:HOH:O	1.82	0.78
1:A:151:LEU:CD2	1:A:159:VAL:CG1	2.46	0.77
1:A:159:VAL:C	1:A:171:SER:O	2.25	0.75
1:A:188:MSE:HE2	1:A:211:ILE:HG22	1.67	0.75
1:A:185:LYS:CG	1:A:185:LYS:O	2.30	0.74
1:A:151:LEU:CD1	1:A:159:VAL:HG12	2.19	0.72
1:A:184:SER:O	1:A:185:LYS:C	2.32	0.69
1:A:159:VAL:O	1:A:160:GLU:CB	2.40	0.68
1:A:155:GLN:HB2	1:A:174:THR:HG22	1.72	0.68
1:A:196:SER:HA	1:A:203:HIS:CD2	2.29	0.67
1:A:159:VAL:O	1:A:160:GLU:CG	2.42	0.67
1:A:154:PHE:O	1:A:155:GLN:HB2	1.94	0.66
1:A:155:GLN:CB	1:A:174:THR:CG2	2.71	0.66
1:A:58:ASP:HB3	1:A:59:LYS:HE3	1.77	0.66
1:A:32:THR:HG22	1:A:34:LYS:H	1.61	0.65
1:A:154:PHE:O	1:A:155:GLN:HG3	1.94	0.65
1:A:49:GLN:NE2	1:A:49:GLN:H	1.92	0.65
1:A:159:VAL:HA	1:A:171:SER:O	1.98	0.64
1:A:160:GLU:HA	1:A:161:HIS:ND1	2.13	0.64
1:A:159:VAL:O	1:A:160:GLU:HG2	1.99	0.63
1:A:188:MSE:CE	1:A:211:ILE:HG22	2.28	0.62
1:A:21:TRP:HB3	1:A:131:LEU:HD13	1.81	0.62
1:A:155:GLN:CB	1:A:174:THR:HG22	2.29	0.61
1:A:159:VAL:CA	1:A:171:SER:O	2.49	0.60
1:A:159:VAL:O	1:A:160:GLU:HB3	2.02	0.59
1:A:66:THR:HG22	2:A:233:HOH:O	2.01	0.59
1:A:180:TYR:CD2	1:A:182:MSE:SE	3.06	0.59
1:A:105:SER:O	1:A:109:THR:HG23	2.03	0.58
1:A:49:GLN:HE21	1:A:49:GLN:N	1.96	0.58
1:A:160:GLU:HA	1:A:161:HIS:CE1	2.39	0.57
1:A:183:THR:O	1:A:184:SER:C	2.44	0.56
1:A:160:GLU:HG3	1:A:171:SER:HB2	1.88	0.56
1:A:182:MSE:CG	1:A:182:MSE:SE	3.04	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:78:LEU:HD22	1:A:93:LEU:HD11	1.88	0.56
1:A:183:THR:OG1	1:A:184:SER:N	2.35	0.55
1:A:164:GLU:HB3	1:A:165:PRO:HD2	1.89	0.55
1:A:22:THR:HG23	2:A:219:HOH:O	2.07	0.55
1:A:181:ILE:HD11	1:A:211:ILE:CG2	2.38	0.54
1:A:160:GLU:N	1:A:171:SER:O	2.41	0.54
1:A:86:LYS:HD2	1:A:88:ASN:O	2.08	0.53
1:A:185:LYS:C	1:A:186:HIS:CG	2.77	0.52
1:A:194:LEU:HD13	1:A:205:VAL:HG22	1.91	0.52
1:A:194:LEU:CD1	1:A:205:VAL:HG22	2.40	0.52
1:A:98:MSE:HG3	2:A:236:HOH:O	2.10	0.51
1:A:182:MSE:CE	1:A:182:MSE:CG	2.89	0.50
1:A:187:LYS:HB2	2:A:254:HOH:O	2.11	0.49
1:A:154:PHE:C	1:A:155:GLN:HG3	2.32	0.49
1:A:180:TYR:HA	1:A:189:ASN:HB3	1.94	0.49
1:A:160:GLU:CD	1:A:171:SER:HB2	2.33	0.49
1:A:186:HIS:HB2	1:A:187:LYS:H	1.58	0.48
1:A:162:VAL:HG13	1:A:163:VAL:CA	2.42	0.47
1:A:32:THR:HG22	1:A:34:LYS:N	2.29	0.47
1:A:151:LEU:HD13	1:A:159:VAL:HG12	1.96	0.47
1:A:188:MSE:HB2	1:A:188:MSE:HE3	1.97	0.46
1:A:159:VAL:N	1:A:172:ALA:HA	2.31	0.46
1:A:160:GLU:CG	1:A:171:SER:HB2	2.46	0.46
1:A:21:TRP:CE2	1:A:99:SER:HB3	2.51	0.45
1:A:174:THR:C	1:A:176:GLU:H	2.18	0.45
1:A:181:ILE:HD11	1:A:211:ILE:HG23	1.98	0.45
1:A:66:THR:HB	2:A:217:HOH:O	2.16	0.45
1:A:114:GLU:O	1:A:117:THR:HB	2.17	0.44
1:A:151:LEU:CG	1:A:159:VAL:CG1	2.96	0.44
1:A:138:ASN:O	1:A:141:ILE:HG22	2.18	0.44
1:A:188:MSE:CB	1:A:188:MSE:SE	3.12	0.44
1:A:162:VAL:HG12	1:A:163:VAL:N	2.27	0.43
1:A:62:LYS:HG3	1:A:81:VAL:HG22	2.00	0.43
1:A:160:GLU:HG3	1:A:171:SER:O	2.19	0.43
1:A:160:GLU:HA	1:A:161:HIS:CG	2.54	0.42
1:A:59:LYS:HG3	1:A:85:LYS:HD3	2.01	0.42
1:A:56:ARG:NH2	1:A:84:LEU:HD11	2.34	0.42
1:A:213:THR:HB	1:A:214:THR:H	1.72	0.42
1:A:152:ASN:C	1:A:154:PHE:N	2.73	0.42
1:A:196:SER:C	1:A:203:HIS:HD2	2.22	0.41
1:A:182:MSE:N	1:A:182:MSE:SE	3.03	0.41
1:A:4:LEU:HD13	1:A:106:TRP:HE3	1.86	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:159:VAL:C	1:A:160:GLU:CG	2.89	0.41

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	199/216 (92%)	181 (91%)	11 (6%)	7 (4%)	6 7

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	160	GLU
1	A	163	VAL
1	A	186	HIS
1	A	185	LYS
1	A	184	SER
1	A	165	PRO
1	A	162	VAL

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	192/190 (101%)	161 (84%)	31 (16%)	3 6

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

Mol	Chain	Res	Type
1	A	1	LEU
1	A	4	LEU
1	A	12	GLU
1	A	17	SER
1	A	22	THR
1	A	49	GLN
1	A	57	GLU
1	A	59	LYS
1	A	61	ILE
1	A	66	THR
1	A	68	THR
1	A	78	LEU
1	A	80	LEU
1	A	109	THR
1	A	112	GLN
1	A	117	THR
1	A	123	GLU
1	A	159	VAL
1	A	160	GLU
1	A	161	HIS
1	A	166	ASN
1	A	182	MSE
1	A	183	THR
1	A	184	SER
1	A	185	LYS
1	A	186	HIS
1	A	187	LYS
1	A	190	LEU
1	A	194	LEU
1	A	211	ILE
1	A	213	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	GLN
1	A	97	GLN
1	A	122	GLN
1	A	144	GLN
1	A	152	ASN
1	A	166	ASN
1	A	203	HIS

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 ⓘ

There are no ligands in this entry.

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	205/216 (94%)	0.95	30 (14%) 3 3	8, 27, 65, 73	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	214	THR	5.1
1	A	183	THR	5.0
1	A	184	SER	5.0
1	A	159	VAL	4.8
1	A	175	ASP	4.3
1	A	163	VAL	4.2
1	A	185	LYS	4.1
1	A	166	ASN	3.9
1	A	140	ASN	3.8
1	A	84	LEU	3.8
1	A	212	VAL	3.7
1	A	173	PHE	3.3
1	A	167	PHE	3.2
1	A	162	VAL	3.1
1	A	213	THR	2.8
1	A	169	SER	2.7
1	A	160	GLU	2.7
1	A	178	GLU	2.7
1	A	182	MSE	2.6
1	A	180	TYR	2.5
1	A	181	ILE	2.5
1	A	186	HIS	2.5
1	A	88	ASN	2.4
1	A	196	SER	2.4
1	A	164	GLU	2.4
1	A	139	MSE	2.2
1	A	16	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	174	THR	2.1
1	A	165	PRO	2.1
1	A	1	LEU	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 ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.