



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 16, 2017 – 02:12 PM EDT

PDB ID : 3CWV
Title : Crystal structure of B-subunit of the DNA gyrase from *Myxococcus xanthus*
Authors : Ramagopal, U.A.; Toro, R.; Meyer, A.J.; Burley, S.K.; Almo, S.C.; New York
SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : unknown
Resolution : 1.95 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

<http://wwpdb.org/validation/2016/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)	:	1.9-1692
EDS	:	rb-20030345
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030345

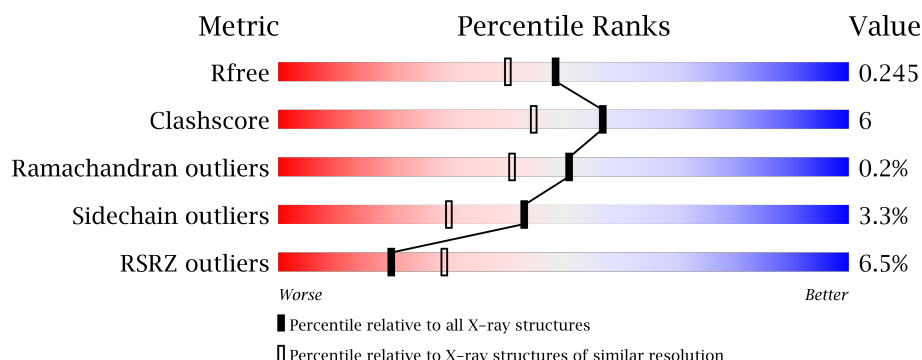
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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}	100719	2004 (1.96-1.96)
Clashscore	112137	2136 (1.96-1.96)
Ramachandran outliers	110173	2117 (1.96-1.96)
Sidechain outliers	110143	2117 (1.96-1.96)
RSRZ outliers	101464	2018 (1.96-1.96)

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. 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	369	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="width: 100%; height: 10px; background-color: green;"></div> <div style="width: 100%; height: 10px; background-color: yellow;"></div> <div style="width: 100%; height: 10px; background-color: grey;"></div> <div style="display: flex; justify-content: space-between; font-size: 0.8em;"> 11% 84% 10% • 5% </div> </div>
1	B	369	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="width: 100%; height: 10px; background-color: green;"></div> <div style="width: 100%; height: 10px; background-color: yellow;"></div> <div style="width: 100%; height: 10px; background-color: grey;"></div> <div style="display: flex; justify-content: space-between; font-size: 0.8em;"> 11% 69% 14% • 16% </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5479 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 DNA gyrase, B subunit, truncated.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	349	Total	C	N	O	S	0	1	0
			2704	1711	502	479	12			
1	B	311	Total	C	N	O	S	0	3	0
			2430	1540	448	429	13			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	EXPRESSION TAG	UNP Q1CZR7
A	1	SER	-	EXPRESSION TAG	UNP Q1CZR7
A	2	LEU	-	EXPRESSION TAG	UNP Q1CZR7
A	361	GLU	-	EXPRESSION TAG	UNP Q1CZR7
A	362	GLY	-	EXPRESSION TAG	UNP Q1CZR7
A	363	HIS	-	EXPRESSION TAG	UNP Q1CZR7
A	364	HIS	-	EXPRESSION TAG	UNP Q1CZR7
A	365	HIS	-	EXPRESSION TAG	UNP Q1CZR7
A	366	HIS	-	EXPRESSION TAG	UNP Q1CZR7
A	367	HIS	-	EXPRESSION TAG	UNP Q1CZR7
A	368	HIS	-	EXPRESSION TAG	UNP Q1CZR7
B	0	MET	-	EXPRESSION TAG	UNP Q1CZR7
B	1	SER	-	EXPRESSION TAG	UNP Q1CZR7
B	2	LEU	-	EXPRESSION TAG	UNP Q1CZR7
B	361	GLU	-	EXPRESSION TAG	UNP Q1CZR7
B	362	GLY	-	EXPRESSION TAG	UNP Q1CZR7
B	363	HIS	-	EXPRESSION TAG	UNP Q1CZR7
B	364	HIS	-	EXPRESSION TAG	UNP Q1CZR7
B	365	HIS	-	EXPRESSION TAG	UNP Q1CZR7
B	366	HIS	-	EXPRESSION TAG	UNP Q1CZR7
B	367	HIS	-	EXPRESSION TAG	UNP Q1CZR7
B	368	HIS	-	EXPRESSION TAG	UNP Q1CZR7

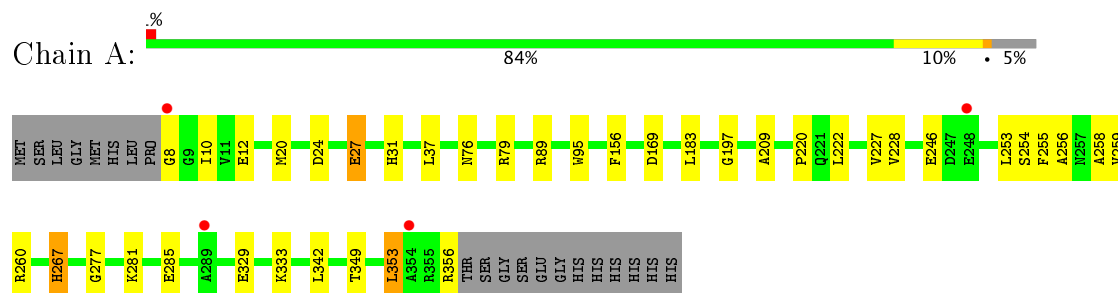
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	270	Total 270	O 270	0	0
2	B	75	Total 75	O 75	0	0

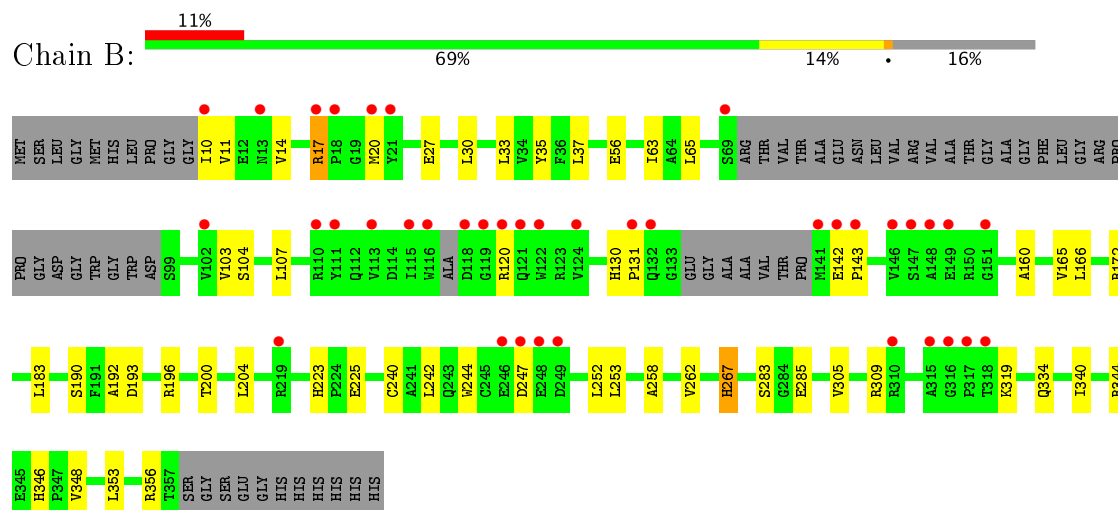
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: DNA gyrase, B subunit, truncated



- Molecule 1: DNA gyrase, B subunit, truncated



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	160.61Å 57.80Å 119.44Å 90.00° 127.23° 90.00°	Depositor
Resolution (Å)	40.00 – 1.95 40.01 – 1.95	Depositor EDS
% Data completeness (in resolution range)	97.8 (40.00-1.95) 97.8 (40.01-1.95)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 1.95Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.209 , 0.247 0.207 , 0.245	Depositor DCC
R_{free} test set	3170 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	34.2	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 49.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5479	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.36% 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 [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	0.60	0/2770	0.69	2/3767 (0.1%)
1	B	0.44	0/2489	0.56	0/3376
All	All	0.53	0/5259	0.63	2/7143 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	24	ASP	CB-CG-OD1	6.57	124.22	118.30
1	A	20	MET	CG-SD-CE	-5.24	91.82	100.20

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	2704	0	2683	23	0
1	B	2430	0	2423	36	0
2	A	270	0	0	1	0
2	B	75	0	0	3	0
All	All	5479	0	5106	58	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 (58) 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:A:31:HIS:HE1	1:A:169:ASP:H	1.26	0.83
1:B:14:VAL:HG12	1:B:107:LEU:HD11	1.61	0.82
1:A:31:HIS:CE1	1:A:169:ASP:H	2.09	0.69
1:A:27:GLU:O	1:A:31:HIS:HD2	1.78	0.67
1:B:334:GLN:NE2	2:B:435:HOH:O	2.27	0.67
1:A:227:VAL:HG13	1:A:342:LEU:HD11	1.78	0.65
1:A:76:ASN:HD21	1:A:95:TRP:H	1.45	0.64
1:B:223:HIS:HE1	1:B:244:TRP:H	1.46	0.62
1:B:160:ALA:HA	1:B:166:LEU:HD21	1.83	0.61
1:B:33:LEU:HD22	1:B:104:SER:HA	1.82	0.61
1:B:283:SER:HB3	1:B:353:LEU:HD22	1.85	0.58
1:B:223:HIS:HD2	1:B:225:GLU:O	1.86	0.58
1:B:27:GLU:HA	1:B:165:VAL:HG11	1.86	0.58
1:B:223:HIS:CE1	1:B:244:TRP:H	2.22	0.58
1:B:183:LEU:HD13	1:B:258:ALA:HA	1.86	0.57
1:A:349:THR:HG22	1:A:353:LEU:HD12	1.87	0.57
1:B:10:ILE:HG23	1:B:11:VAL:N	2.20	0.57
1:B:130:HIS:NE2	2:B:404:HOH:O	2.26	0.56
1:B:103:VAL:O	1:B:107:LEU:HD13	2.05	0.56
1:B:30:LEU:HD22	1:B:165:VAL:HG13	1.86	0.56
1:B:165:VAL:HG13	1:B:165:VAL:O	2.07	0.53
1:A:197:GLY:HA3	1:B:204:LEU:HD23	1.91	0.52
1:A:255:PHE:CE1	1:A:260:ARG:HG3	2.44	0.52
1:A:183:LEU:HD13	1:A:258:ALA:HA	1.92	0.52
1:A:267:HIS:H	1:A:267:HIS:CD2	2.28	0.52
1:B:340:ILE:O	1:B:344:ARG:HG3	2.11	0.50
1:B:142:GLU:HB3	1:B:143:PRO:HD2	1.94	0.49
1:A:277:GLY:O	1:A:281:LYS:HG3	2.13	0.49
1:B:37:LEU:HB3	1:B:65:LEU:HD22	1.93	0.48
1:B:165:VAL:O	1:B:165:VAL:CG1	2.61	0.47
1:A:254:SER:HB2	1:A:267:HIS:CE1	2.50	0.47
1:B:10:ILE:O	1:B:14:VAL:HG23	2.15	0.46
1:A:8:GLY:N	1:A:12:GLU:H	2.14	0.46
1:B:35:TYR:OH	1:B:172[B]:ARG:NE	2.49	0.46
1:A:329:GLU:OE2	1:A:333:LYS:HE3	2.14	0.46
1:A:222:LEU:HD21	1:A:246:GLU:HB3	1.97	0.45
1:B:190:SER:HA	1:B:200:THR:O	2.16	0.45
1:A:10:ILE:CD1	1:A:89[B]:ARG:HH22	2.29	0.45
1:B:262:VAL:HG22	2:B:391:HOH:O	2.17	0.45
1:B:107:LEU:N	1:B:107:LEU:HD12	2.33	0.43
1:B:10:ILE:CG2	1:B:11:VAL:N	2.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:10:ILE:HG23	1:B:11:VAL:H	1.82	0.43
1:B:14:VAL:CG1	1:B:107:LEU:HD11	2.42	0.43
1:B:346:HIS:ND1	1:B:348:VAL:HG12	2.34	0.43
1:A:256:ALA:O	1:A:259:VAL:HG22	2.20	0.42
1:A:209:ALA:HB2	1:A:228:VAL:CG1	2.50	0.42
1:B:17:ARG:O	1:B:17:ARG:HG2	2.20	0.42
1:B:309:ARG:HA	1:B:309:ARG:HD3	1.86	0.41
1:B:56:GLU:HG2	1:B:192:ALA:HB3	2.02	0.41
1:B:240[A]:CYS:SG	1:B:242:LEU:HD11	2.60	0.41
1:A:76:ASN:HD21	1:A:95:TRP:N	2.14	0.41
1:B:193:ASP:OD2	1:B:196:ARG:HD3	2.19	0.41
1:B:10:ILE:CG2	1:B:11:VAL:H	2.34	0.41
1:A:220:PRO:HG2	1:A:246:GLU:HG3	2.02	0.41
1:A:79:ARG:NH2	2:A:413:HOH:O	2.53	0.41
1:B:267:HIS:HB3	1:B:305[B]:VAL:HG21	2.03	0.41
1:A:27:GLU:O	1:A:31:HIS:CD2	2.67	0.40
1:A:37:LEU:HD12	1:A:156:PHE:HE2	1.86	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	348/369 (94%)	344 (99%)	4 (1%)	0	100	100
1	B	306/369 (83%)	295 (96%)	10 (3%)	1 (0%)	44	33
All	All	654/738 (89%)	639 (98%)	14 (2%)	1 (0%)	51	41

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	131	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	274/291 (94%)	268 (98%)	6 (2%)	57	49
1	B	251/291 (86%)	240 (96%)	11 (4%)	33	18
All	All	525/582 (90%)	508 (97%)	17 (3%)	43	31

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	GLU
1	A	253	LEU
1	A	267	HIS
1	A	285	GLU
1	A	353	LEU
1	A	356	ARG
1	B	17	ARG
1	B	20	MET
1	B	63	ILE
1	B	120	ARG
1	B	247	ASP
1	B	252	LEU
1	B	253	LEU
1	B	267	HIS
1	B	285	GLU
1	B	319	LYS
1	B	356	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	HIS
1	A	76	ASN
1	A	239	GLN
1	A	267	HIS
1	A	311	GLN

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Mol	Chain	Res	Type
1	B	32	HIS
1	B	221	GLN
1	B	223	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 carbohydrates 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 ⓘ

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	349/369 (94%)	-0.09	4 (1%) 80 86	20, 32, 54, 70	0
1	B	311/369 (84%)	0.51	39 (12%) 4 7	27, 49, 78, 98	0
All	All	660/738 (89%)	0.20	43 (6%) 20 29	20, 40, 73, 98	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	124	VAL	9.0
1	B	122	TRP	6.6
1	B	120	ARG	5.6
1	A	289	ALA	5.0
1	A	8	GLY	4.7
1	B	118	ASP	4.4
1	B	316	GLY	4.2
1	A	248	GLU	3.7
1	B	116	TRP	3.6
1	B	121	GLN	3.5
1	B	119	GLY	3.4
1	B	131	PRO	3.4
1	B	148	ALA	3.3
1	B	249	ASP	3.3
1	B	111	TYR	3.3
1	B	132	GLN	3.3
1	B	147	SER	3.1
1	B	115	ILE	3.0
1	B	21	TYR	3.0
1	A	354	ALA	3.0
1	B	141	MET	3.0
1	B	247	ASP	3.0
1	B	18	PRO	2.9
1	B	142	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	149	GLU	2.9
1	B	315	ALA	2.8
1	B	219	ARG	2.7
1	B	143	PRO	2.7
1	B	110	ARG	2.7
1	B	310	ARG	2.6
1	B	113	VAL	2.6
1	B	10	ILE	2.6
1	B	318	THR	2.6
1	B	248	GLU	2.5
1	B	246	GLU	2.4
1	B	146	VAL	2.3
1	B	20	MET	2.2
1	B	69	SER	2.2
1	B	317	PRO	2.2
1	B	102	VAL	2.2
1	B	13	ASN	2.1
1	B	17	ARG	2.1
1	B	151	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 carbohydrates 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.