



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:55 AM GMT

PDB ID : 2ES3
Title : Crystal Structure of Thrombospondin-1 N-terminal Domain in P1 Form at 1.85Å Resolution
Authors : Tan, K.; Wang, J.; Lawler, J.
Deposited on : 2005-10-25
Resolution : 1.85 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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

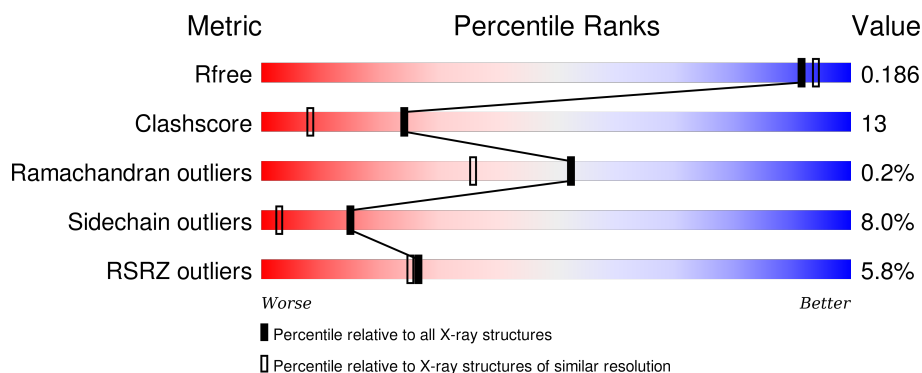
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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}	91344	1745 (1.86-1.86)
Clashscore	102246	1898 (1.86-1.86)
Ramachandran outliers	100387	1875 (1.86-1.86)
Sidechain outliers	100360	1875 (1.86-1.86)
RSRZ outliers	91569	1747 (1.86-1.86)

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	209	<div> <div>6%</div> <div>78%</div> <div>18%</div> <div>• •</div> </div>
1	B	209	<div> <div>6%</div> <div>75%</div> <div>22%</div> <div>•</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3471 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 Thrombospondin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	209	Total	C	N	O	S	0	0	0
			1609	1009	288	308	4			
1	B	208	Total	C	N	O	S	0	0	0
			1605	1007	287	307	4			

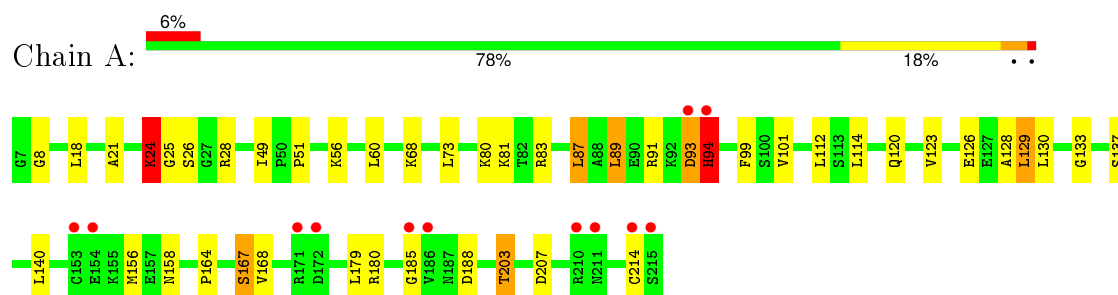
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	133	Total	O	0	0
			133	133		
2	B	124	Total	O	0	0
			124	124		

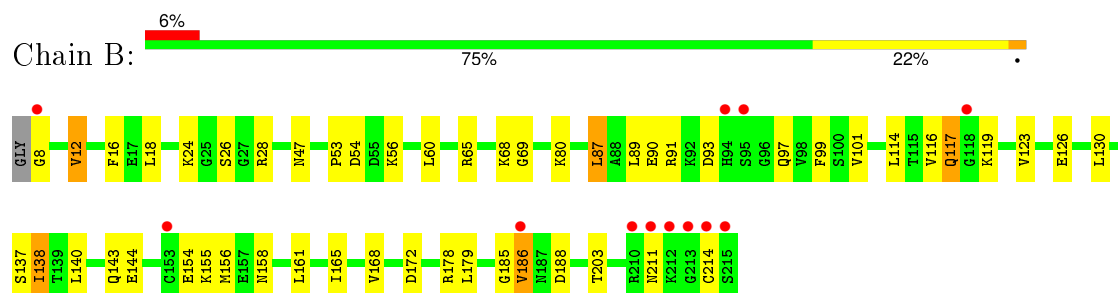
3 Residue-property plots [i](#)

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 ($\text{RSRZ} > 2$). 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: Thrombospondin-1



• Molecule 1: Thrombospondin-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	40.02Å 41.71Å 59.99Å 73.63° 89.59° 75.73°	Depositor
Resolution (Å)	24.43 – 1.85 23.51 – 1.85	Depositor EDS
% Data completeness (in resolution range)	94.7 (24.43-1.85) 86.3 (23.51-1.85)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.68 (at 1.85Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.187 , 0.250 0.190 , 0.186	Depositor DCC
R_{free} test set	1436 reflections (5.19%)	DCC
Wilson B-factor (Å ²)	20.6	Xtriage
Anisotropy	0.132	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 54.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 29111 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3471	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.08% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0.86	0/1632	0.91	1/2202 (0.0%)
1	B	0.84	1/1628 (0.1%)	0.95	2/2197 (0.1%)
All	All	0.85	1/3260 (0.0%)	0.93	3/4399 (0.1%)

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 (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	16	PHE	CE2-CZ	5.12	1.47	1.37

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	138	ILE	CG1-CB-CG2	5.21	122.86	111.40
1	A	24	LYS	C-N-CA	-5.08	111.63	122.30
1	B	54	ASP	CB-CG-OD1	5.01	122.81	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	133	GLY	Peptide
1	A	93	ASP	Peptide
1	A	94	HIS	Peptide

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	1609	0	1629	44	1
1	B	1605	0	1626	43	1
2	A	133	0	0	17	0
2	B	124	0	0	18	0
All	All	3471	0	3255	84	1

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 13.

All (84) 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)
2:A:336:HOH:O	1:B:68:LYS:HG3	1.58	1.02
1:B:143:GLN:HG3	2:B:275:HOH:O	1.60	1.01
1:A:114:LEU:HD22	1:A:168:VAL:HG21	1.41	1.00
1:A:99:PHE:HD1	1:A:114:LEU:HD23	1.30	0.96
1:B:119:LYS:HE3	2:B:276:HOH:O	1.67	0.94
1:B:47:ASN:HB3	2:B:272:HOH:O	1.69	0.92
1:A:24:LYS:NZ	1:A:26:SER:O	2.05	0.89
1:A:18:LEU:HD22	1:A:56:LYS:HD3	1.54	0.88
1:A:214:CYS:HA	2:A:302:HOH:O	1.74	0.86
1:A:137:SER:HB2	2:A:327:HOH:O	1.76	0.85
1:B:178:ARG:HD3	2:B:305:HOH:O	1.80	0.81
1:A:99:PHE:CD1	1:A:114:LEU:HD23	2.16	0.79
1:A:164:PRO:O	1:A:167:SER:HB2	1.82	0.78
1:B:154:GLU:HG3	1:B:155:LYS:HB2	1.67	0.75
1:B:126:GLU:HG2	2:B:262:HOH:O	1.89	0.72
1:B:155:LYS:CE	2:B:294:HOH:O	2.39	0.70
1:A:128:ALA:HA	2:A:335:HOH:O	1.92	0.69
1:A:114:LEU:HD22	1:A:168:VAL:CG2	2.19	0.69
1:B:90:GLU:HG3	2:B:323:HOH:O	1.92	0.69
1:A:89:LEU:CD1	1:A:179:LEU:HD13	2.24	0.68
1:A:156:MET:CE	1:A:158:ASN:HD21	2.08	0.66
1:B:117:GLN:HE21	1:B:119:LYS:HE2	1.62	0.65
1:B:155:LYS:HE3	2:B:294:HOH:O	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:ARG:HD2	2:A:277:HOH:O	1.97	0.64
1:B:18:LEU:HD22	1:B:56:LYS:HD3	1.78	0.64
1:A:123:VAL:HG23	2:A:227:HOH:O	1.98	0.63
1:A:24:LYS:HD2	1:A:25:GLY:H	1.64	0.62
1:B:178:ARG:NH1	2:B:316:HOH:O	2.32	0.61
1:A:99:PHE:CD1	1:A:114:LEU:CD2	2.84	0.61
1:A:83:ARG:HD2	1:A:188:ASP:OD1	2.00	0.61
1:A:129:LEU:N	2:A:335:HOH:O	2.35	0.59
1:B:126:GLU:CG	2:B:262:HOH:O	2.47	0.59
1:A:203:THR:HG22	1:A:207:ASP:HB2	1.84	0.59
1:B:97:GLN:HE22	1:B:185:GLY:H	1.50	0.58
1:B:91:ARG:NH1	1:B:93:ASP:OD2	2.37	0.58
2:A:336:HOH:O	1:B:68:LYS:CG	2.30	0.58
1:A:8:GLY:HA3	2:A:319:HOH:O	2.03	0.57
1:B:156:MET:CE	1:B:158:ASN:HD21	2.17	0.57
1:A:114:LEU:CD2	1:A:168:VAL:HG21	2.24	0.56
1:A:24:LYS:HZ3	1:A:49:ILE:HA	1.71	0.55
1:A:156:MET:HE2	1:A:158:ASN:HD21	1.71	0.55
1:B:24:LYS:HE3	2:B:306:HOH:O	2.05	0.55
1:A:94:HIS:HE1	2:A:326:HOH:O	1.88	0.55
1:A:89:LEU:HD22	1:A:99:PHE:HB3	1.89	0.54
1:A:156:MET:HE3	1:A:158:ASN:HD21	1.73	0.54
1:A:21:ALA:HA	1:A:24:LYS:HG3	1.89	0.53
1:B:53:PRO:HD2	1:B:56:LYS:HD2	1.91	0.53
1:A:112:LEU:HB2	2:A:309:HOH:O	2.08	0.53
1:A:128:ALA:CA	2:A:335:HOH:O	2.55	0.52
1:B:156:MET:HE3	1:B:158:ASN:HD21	1.72	0.52
1:B:186:VAL:HG22	2:B:286:HOH:O	2.08	0.52
1:B:89:LEU:HD12	1:B:179:LEU:HD13	1.92	0.52
1:A:81:LYS:HE3	2:A:341:HOH:O	2.09	0.52
1:A:87:LEU:HD23	1:A:101:VAL:HB	1.92	0.51
1:B:24:LYS:HE2	2:B:334:HOH:O	2.10	0.51
1:A:128:ALA:C	2:A:335:HOH:O	2.49	0.51
1:B:89:LEU:CD1	1:B:179:LEU:HD13	2.41	0.51
1:B:87:LEU:CD2	1:B:101:VAL:HB	2.42	0.49
1:B:116:VAL:HG22	1:B:168:VAL:CG2	2.42	0.49
1:A:83:ARG:NH2	1:B:161:LEU:O	2.44	0.49
1:B:186:VAL:CG2	2:B:286:HOH:O	2.62	0.48
1:B:8:GLY:N	2:B:318:HOH:O	2.45	0.48
1:B:99:PHE:HD1	1:B:114:LEU:HD23	1.78	0.48
1:B:60:LEU:HD23	1:B:60:LEU:C	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:LEU:CD2	1:A:101:VAL:HB	2.45	0.47
1:A:126:GLU:OE2	1:B:144:GLU:OE2	2.32	0.47
1:A:129:LEU:HD21	2:A:318:HOH:O	2.15	0.47
1:A:51:PRO:HB3	1:A:180:ARG:HD3	1.97	0.47
1:A:24:LYS:HZ1	1:A:49:ILE:HG12	1.81	0.46
1:B:168:VAL:HG13	2:B:291:HOH:O	2.16	0.45
1:B:123:VAL:HG11	1:B:161:LEU:HD23	1.98	0.45
1:A:24:LYS:HD2	1:A:25:GLY:N	2.32	0.44
1:A:120:GLN:H	1:B:156:MET:CE	2.30	0.44
1:B:69:GLY:HA2	1:B:165:ILE:HG21	1.98	0.44
1:A:203:THR:HG22	1:A:207:ASP:CB	2.47	0.44
1:B:117:GLN:NE2	1:B:119:LYS:HE2	2.30	0.43
1:B:185:GLY:HA3	1:B:188:ASP:HB2	1.99	0.43
1:A:21:ALA:HA	1:A:24:LYS:CG	2.48	0.43
1:B:89:LEU:HD22	1:B:99:PHE:HB3	2.01	0.43
1:B:80:LYS:HG2	2:B:245:HOH:O	2.19	0.42
1:B:90:GLU:CG	2:B:323:HOH:O	2.60	0.42
1:A:94:HIS:CE1	2:A:326:HOH:O	2.67	0.41
1:A:68:LYS:HG3	2:A:293:HOH:O	2.21	0.41
1:B:65:ARG:NH1	1:B:65:ARG:HG3	2.35	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:LYS:O	1:B:12:VAL:O[1_554]	1.87	0.33

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	207/209 (99%)	199 (96%)	7 (3%)	1 (0%)	34 17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	206/209 (99%)	198 (96%)	8 (4%)	0	100	100
All	All	413/418 (99%)	397 (96%)	15 (4%)	1 (0%)	52	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	185	GLY

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	176/176 (100%)	162 (92%)	14 (8%)	15	3
1	B	176/176 (100%)	162 (92%)	14 (8%)	15	3
All	All	352/352 (100%)	324 (92%)	28 (8%)	15	3

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	LYS
1	A	28	ARG
1	A	60	LEU
1	A	73	LEU
1	A	80	LYS
1	A	87	LEU
1	A	89	LEU
1	A	93	ASP
1	A	94	HIS
1	A	129	LEU
1	A	130	LEU
1	A	140	LEU
1	A	167	SER
1	A	203	THR
1	B	12	VAL

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Mol	Chain	Res	Type
1	B	26	SER
1	B	28	ARG
1	B	87	LEU
1	B	117	GLN
1	B	130	LEU
1	B	137	SER
1	B	138	ILE
1	B	140	LEU
1	B	172	ASP
1	B	186	VAL
1	B	203	THR
1	B	211	ASN
1	B	214	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	78	GLN
1	A	97	GLN
1	A	121	HIS
1	A	158	ASN
1	A	196	ASN
1	B	78	GLN
1	B	97	GLN
1	B	117	GLN
1	B	120	GLN
1	B	121	HIS
1	B	158	ASN
1	B	196	ASN

5.3.3 RNA ⓘ

There are no RNA molecules 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 [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	209/209 (100%)	0.13	12 (5%)	27 26	13, 22, 40, 55	0
1	B	208/209 (99%)	0.09	12 (5%)	26 25	12, 21, 36, 57	0
All	All	417/418 (99%)	0.11	24 (5%)	26 25	12, 21, 38, 57	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	214	CYS	7.3
1	B	186	VAL	6.6
1	B	215	SER	5.6
1	A	215	SER	5.0
1	A	94	HIS	3.7
1	B	211	ASN	3.6
1	A	186	VAL	3.5
1	B	94	HIS	3.4
1	A	93	ASP	3.2
1	A	214	CYS	3.2
1	B	213	GLY	3.0
1	A	154	GLU	2.9
1	A	172	ASP	2.9
1	A	171	ARG	2.7
1	B	153	CYS	2.7
1	A	211	ASN	2.7
1	B	210	ARG	2.7
1	B	8	GLY	2.4
1	B	212	LYS	2.3
1	A	153	CYS	2.3
1	B	95	SER	2.2
1	B	118	GLY	2.1
1	A	210	ARG	2.0
1	A	185	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.