Full wwPDB X-ray Structure Validation Report (i)

Nov 21, 2023 – 01:46 AM JST

PDB ID	:	7EA1
Title	:	Crystal Structure of Spindlin1 bound to SPINDOC Docpep2
Authors	:	Zhao, F.; Li, H.
Deposited on	:	2021-03-05
Resolution	:	2.70 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:

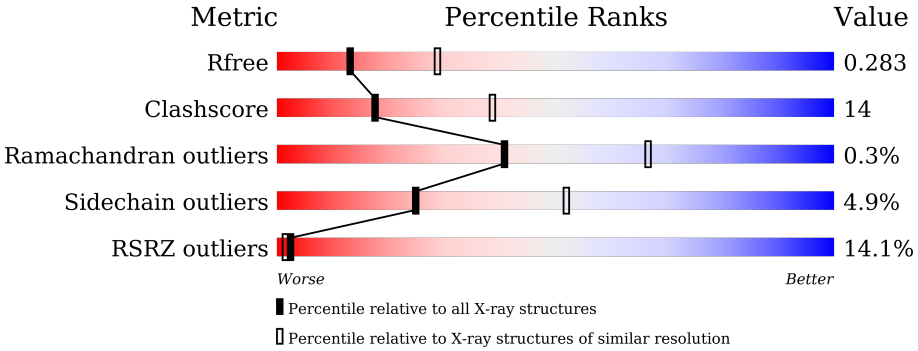
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	215	5%, 74%, 19%, 7%
1	C	215	19%, 55%, 28%, •, 14%
2	B	12	33%, 25%, 17%, 58%
2	D	12	8%, 8%, 83%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3188 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 Spindlin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	200	1622	1034	271	308	9	0	1	0
1	C	184	1486	951	246	281	8	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	48	GLY	-	expression tag	UNP Q9Y657
A	49	SER	-	expression tag	UNP Q9Y657
C	48	GLY	-	expression tag	UNP Q9Y657
C	49	SER	-	expression tag	UNP Q9Y657

- Molecule 2 is a protein called Peptide from Spindlin interactor and repressor of chromatin-binding protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	5	47	29	13	5	0	0	0
2	D	2	20	12	6	2	0	0	0

- Molecule 3 is water.

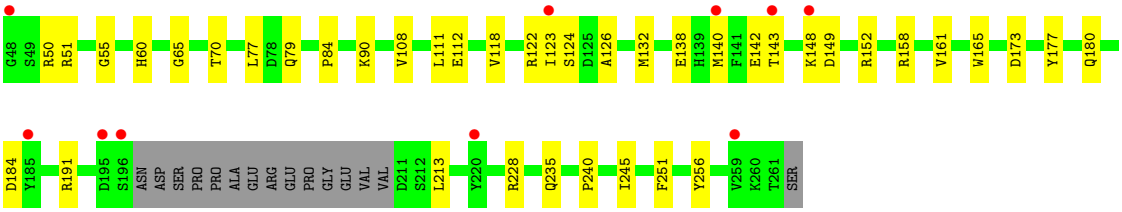
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	10	10	10	0	0
3	C	3	3	3	0	0

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.

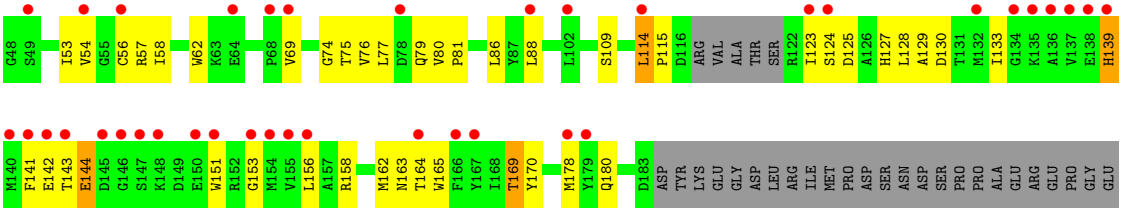
• Molecule 1: Spindlin-1

Chain A:



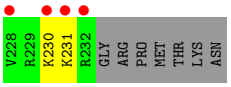
• Molecule 1: Spindlin-1

Chain C:



• Molecule 2: Peptide from Spindlin interactor and repressor of chromatin-binding protein

Chain B:



• Molecule 2: Peptide from Spindlin interactor and repressor of chromatin-binding protein

Chain D:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	83.80Å 136.90Å 42.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.36 – 2.70 40.36 – 2.69	Depositor EDS
% Data completeness (in resolution range)	99.3 (40.36-2.70) 99.5 (40.36-2.69)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.14 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.14_3247	Depositor
R, R_{free}	0.254 , 0.286 0.252 , 0.283	Depositor DCC
R_{free} test set	669 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å^2)	66.1	Xtriage
Anisotropy	0.718	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 64.5	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	3188	wwPDB-VP
Average B, all atoms (Å^2)	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.01% 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	0.39	0/1663	0.56	0/2250
1	C	0.38	0/1520	0.61	0/2056
2	B	0.21	0/46	0.54	0/57
2	D	0.22	0/19	0.44	0/22
All	All	0.38	0/3248	0.58	0/4385

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 (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	1622	0	1577	26	1
1	C	1486	0	1445	62	0
2	B	47	0	60	1	0
2	D	20	0	25	1	0
3	A	10	0	0	0	0
3	C	3	0	0	0	0
All	All	3188	0	3107	86	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 14.

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:C:58:ILE:HD11	1:C:76:VAL:CG1	1.99	0.93
1:A:123:ILE:HG12	1:A:158:ARG:HH22	1.35	0.91
1:C:234:HIS:NE2	1:C:236:VAL:HG13	1.86	0.90
1:C:143:THR:HG22	1:C:144:GLU:HG3	1.56	0.87
1:C:234:HIS:NE2	1:C:236:VAL:CG1	2.41	0.83
1:C:77:LEU:HD23	1:C:88:LEU:O	1.80	0.81
1:A:138:GLU:HG3	1:A:191:ARG:HH11	1.45	0.81
1:C:241:SER:HB2	1:C:259:VAL:HG23	1.63	0.79
1:A:122:ARG:HG2	1:A:122:ARG:HH21	1.49	0.77
1:C:58:ILE:HA	1:C:114:LEU:HD22	1.68	0.75
1:C:234:HIS:CD2	1:C:236:VAL:HG13	2.23	0.74
1:A:142:GLU:OE1	1:A:142:GLU:N	2.19	0.72
1:A:173:ASP:OD2	1:A:177:TYR:OH	2.10	0.70
1:C:77:LEU:HD23	1:C:77:LEU:H	1.58	0.69
1:C:58:ILE:HD11	1:C:76:VAL:HG11	1.75	0.67
1:C:141:PHE:HZ	2:D:229:ARG:HH11	1.42	0.67
1:A:122:ARG:HG2	1:A:122:ARG:NH2	2.10	0.66
2:B:230:LYS:HG3	1:C:211:ASP:HB2	1.76	0.66
1:C:58:ILE:HD11	1:C:76:VAL:HG13	1.78	0.65
1:C:54:VAL:HA	1:C:76:VAL:HG23	1.79	0.65
1:C:58:ILE:CD1	1:C:76:VAL:CG1	2.75	0.64
1:C:54:VAL:HA	1:C:76:VAL:CG2	2.28	0.63
1:C:153:GLY:HA3	1:C:170:TYR:HA	1.82	0.62
1:C:77:LEU:HD23	1:C:77:LEU:N	2.16	0.60
1:C:241:SER:HB2	1:C:259:VAL:CG2	2.31	0.60
1:C:58:ILE:N	1:C:74:GLY:O	2.25	0.59
1:C:123:ILE:HG22	1:C:123:ILE:O	2.01	0.59
1:C:234:HIS:NE2	1:C:236:VAL:HG12	2.19	0.58
1:C:56:CYS:HB2	1:C:114:LEU:HB2	1.85	0.57
1:C:142:GLU:HG2	1:C:142:GLU:O	2.04	0.57
1:C:250:ASP:OD1	1:C:251:PHE:N	2.38	0.56
1:C:58:ILE:HD13	1:C:114:LEU:HD21	1.89	0.54
1:C:123:ILE:HG22	1:C:125:ASP:OD1	2.07	0.53
1:C:77:LEU:N	1:C:77:LEU:CD2	2.71	0.53
1:C:237:GLU:N	1:C:237:GLU:OE2	2.42	0.53
1:A:77:LEU:HD11	1:A:90:LYS:HB2	1.91	0.51
1:C:56:CYS:HB2	1:C:114:LEU:HD12	1.92	0.50
1:C:133:ILE:HG22	1:C:238:ALA:HB2	1.91	0.50
1:A:122:ARG:NH2	1:A:122:ARG:CG	2.72	0.50
1:C:77:LEU:CD2	1:C:88:LEU:O	2.57	0.50
1:A:213:LEU:H	1:A:213:LEU:HD23	1.77	0.50
1:C:77:LEU:HD23	1:C:88:LEU:C	2.33	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:139:HIS:O	1:C:151:TRP:N	2.39	0.49
1:C:162:MET:HB3	1:C:165:TRP:CD1	2.48	0.48
1:C:242:VAL:HA	1:C:256:TYR:O	2.12	0.48
1:A:55:GLY:HA2	1:A:161:VAL:HG11	1.95	0.48
1:C:250:ASP:OD2	1:C:254:TYR:OH	2.32	0.47
1:A:60:HIS:CG	1:A:108:VAL:HG13	2.49	0.47
1:C:53:ILE:HG13	1:C:76:VAL:HG21	1.96	0.47
1:C:123:ILE:O	1:C:125:ASP:OD1	2.32	0.47
1:C:127:HIS:O	1:C:158:ARG:NH1	2.49	0.46
1:C:129:ALA:HB2	1:C:158:ARG:NH2	2.31	0.46
1:C:243:TYR:CD1	1:C:258:LEU:HD12	2.50	0.46
1:C:62:TRP:H	1:C:69:VAL:HG13	1.81	0.46
1:C:129:ALA:HB2	1:C:158:ARG:HH22	1.80	0.45
1:A:50:ARG:O	1:A:51:ARG:HG3	2.16	0.45
1:A:70:THR:HG21	1:C:213:LEU:HD13	1.98	0.45
1:C:130:ASP:N	1:C:130:ASP:OD1	2.48	0.45
1:C:169:THR:OG1	1:C:170:TYR:N	2.50	0.45
1:C:163:ASN:OD1	1:C:163:ASN:N	2.49	0.45
1:A:143:THR:HG23	1:A:149:ASP:HB2	1.99	0.44
1:C:260:LYS:HZ2	1:C:260:LYS:HB3	1.83	0.44
1:A:245:ILE:HD12	1:A:256:TYR:HD2	1.82	0.44
1:C:57:ARG:NH1	1:C:75:THR:OG1	2.51	0.44
1:C:245:ILE:HD13	1:C:256:TYR:HD1	1.83	0.44
1:A:123:ILE:HG21	1:A:126:ALA:HA	2.00	0.43
1:C:77:LEU:CD2	1:C:88:LEU:C	2.87	0.43
1:C:229:THR:OG1	1:C:248:ASP:OD2	2.34	0.43
1:A:138:GLU:OE1	1:A:152:ARG:HD3	2.18	0.43
1:A:123:ILE:H	1:A:123:ILE:HG13	1.41	0.43
1:A:79:GLN:NE2	1:A:84:PRO:O	2.34	0.43
1:A:235:GLN:NE2	1:A:240:PRO:O	2.46	0.43
1:C:80:VAL:HG21	1:C:86:LEU:HD22	1.99	0.42
1:C:133:ILE:HG23	1:C:156:LEU:O	2.19	0.42
1:A:60:HIS:HB3	1:A:111:LEU:HA	2.02	0.42
1:C:242:VAL:HG12	1:C:257:ASP:HB3	2.01	0.42
1:C:58:ILE:CD1	1:C:76:VAL:HG13	2.45	0.42
1:C:164:THR:O	1:C:180:GLN:HB2	2.20	0.41
1:A:65:GLY:HA3	1:C:260:LYS:HB3	2.02	0.41
1:C:58:ILE:CG1	1:C:76:VAL:HG13	2.51	0.41
1:A:140:MET:SD	1:A:148:LYS:HB3	2.60	0.41
1:A:165:TRP:CE2	1:A:180:GLN:HG3	2.56	0.40
1:C:156:LEU:HD13	1:C:244:PHE:CE1	2.55	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:55:GLY:O	1:A:118:VAL:HG13	2.21	0.40
1:A:123:ILE:HG21	1:A:158:ARG:HH12	1.86	0.40
1:C:79:GLN:HG3	1:C:81:PRO:HD3	2.04	0.40

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:112:GLU:OE2	1:A:122:ARG:NH1[2_554]	1.99	0.21

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	197/215 (92%)	189 (96%)	8 (4%)	0	100	100
1	C	178/215 (83%)	161 (90%)	16 (9%)	1 (1%)	25	50
2	B	3/12 (25%)	1 (33%)	2 (67%)	0	100	100
All	All	378/442 (86%)	351 (93%)	26 (7%)	1 (0%)	41	66

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	115	PRO

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	177/189 (94%)	172 (97%)	5 (3%)	43	73
1	C	162/189 (86%)	151 (93%)	11 (7%)	16	36
2	B	5/11 (46%)	4 (80%)	1 (20%)	1	3
2	D	2/11 (18%)	2 (100%)	0	100	100
All	All	346/400 (86%)	329 (95%)	17 (5%)	25	52

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

Mol	Chain	Res	Type
1	A	124	SER
1	A	132	MET
1	A	184	ASP
1	A	228	ARG
1	A	251	PHE
2	B	231	LYS
1	C	109	SER
1	C	114	LEU
1	C	124	SER
1	C	128	LEU
1	C	139	HIS
1	C	144	GLU
1	C	169	THR
1	C	178	MET
1	C	220	TYR
1	C	237	GLU
1	C	251	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	200/215 (93%)	0.38	10 (5%) 28 27	41, 66, 143, 217	0
1	C	184/215 (85%)	1.31	41 (22%) 0 0	58, 122, 187, 225	0
2	B	5/12 (41%)	3.40	4 (80%) 0 0	136, 157, 170, 177	0
2	D	2/12 (16%)	1.05	0 100 100	134, 134, 134, 154	0
All	All	391/454 (86%)	0.86	55 (14%) 2 1	41, 90, 179, 225	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	136	ALA	10.2
1	C	146	GLY	9.7
1	C	141	PHE	9.2
1	C	147	SER	7.8
1	C	56	CYS	7.1
1	C	166	PHE	6.4
1	C	137	VAL	5.7
1	C	156	LEU	5.2
1	C	140	MET	5.1
2	B	228	VAL	4.9
2	B	232	ARG	4.5
1	C	167	TYR	4.4
1	C	145	ASP	4.1
1	C	262	SER	4.1
1	C	142	GLU	4.0
1	A	123	ILE	3.9
1	C	148	LYS	3.8
1	C	164	THR	3.5
1	C	134	GLY	3.4
1	C	102	LEU	3.4
1	C	143	THR	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	179	TYR	3.3
1	C	49	SER	3.2
1	C	178	MET	3.1
1	A	143	THR	3.1
1	A	148	LYS	3.1
1	C	154	MET	3.0
1	A	48	GLY	3.0
1	C	68	PRO	3.0
2	B	230	LYS	2.9
1	C	150	GLU	2.9
2	B	231	LYS	2.9
1	C	151	TRP	2.9
1	C	132	MET	2.9
1	C	210	VAL	2.8
1	A	220	TYR	2.8
1	C	138	GLU	2.8
1	C	211	ASP	2.6
1	C	88	LEU	2.6
1	C	78	ASP	2.5
1	C	155	VAL	2.5
1	C	124	SER	2.4
1	C	135	LYS	2.4
1	A	259	VAL	2.4
1	C	54	VAL	2.4
1	A	195	ASP	2.3
1	C	139	HIS	2.3
1	C	64	GLU	2.3
1	C	153	GLY	2.3
1	A	185	TYR	2.2
1	A	196	SER	2.2
1	C	123	ILE	2.2
1	C	69	VAL	2.1
1	C	114	LEU	2.1
1	A	140	MET	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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.