Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 11:08 pm BST

PDB ID	:	5B1Z
Title	:	Crystal structure of Bcl-xL in complex with HBx-BH3 motif
Authors	:	Yuan, Y.A.
Deposited on	:	2015-12-22
Resolution	:	2.15 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 ⓘ symbol.

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

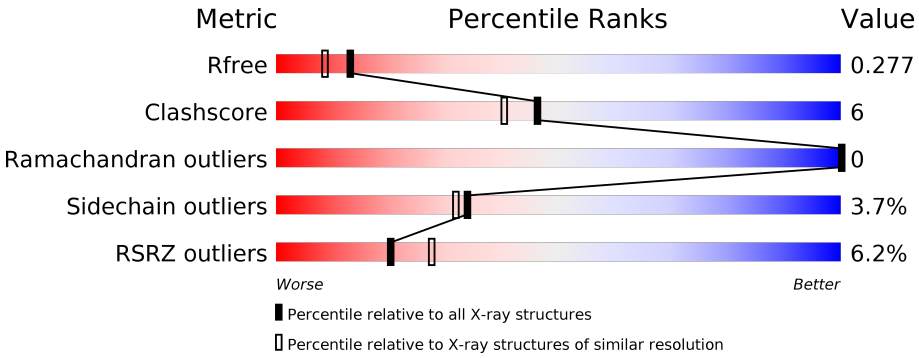
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.15 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	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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 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	153	7%, 84%, 8%, 6%
1	B	153	2%, 79%, 12%, 6%
2	C	23	22%, 48%, 22%, 30%
2	D	23	9%, 52%, 26%, 22%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2765 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 Bcl-2-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	144	Total	C	N	O	S	0	0	0
			1161	740	197	219	5			
1	B	144	Total	C	N	O	S	0	0	0
			1161	740	197	219	5			

There are 112 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	PHE	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	ASP	deletion	UNP Q07817
A	?	-	VAL	deletion	UNP Q07817
A	?	-	GLU	deletion	UNP Q07817
A	?	-	GLU	deletion	UNP Q07817
A	?	-	ASN	deletion	UNP Q07817
A	?	-	ARG	deletion	UNP Q07817
A	?	-	THR	deletion	UNP Q07817
A	?	-	GLU	deletion	UNP Q07817
A	?	-	ALA	deletion	UNP Q07817
A	?	-	PRO	deletion	UNP Q07817
A	?	-	GLU	deletion	UNP Q07817
A	?	-	GLY	deletion	UNP Q07817
A	?	-	THR	deletion	UNP Q07817
A	?	-	GLU	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	GLU	deletion	UNP Q07817
A	?	-	MET	deletion	UNP Q07817
A	?	-	GLU	deletion	UNP Q07817
A	?	-	THR	deletion	UNP Q07817
A	?	-	PRO	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	ALA	deletion	UNP Q07817
A	?	-	ILE	deletion	UNP Q07817

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ASN	deletion	UNP Q07817
A	?	-	GLY	deletion	UNP Q07817
A	?	-	ASN	deletion	UNP Q07817
A	?	-	PRO	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	TRP	deletion	UNP Q07817
A	?	-	HIS	deletion	UNP Q07817
A	?	-	LEU	deletion	UNP Q07817
A	?	-	ALA	deletion	UNP Q07817
A	?	-	ASP	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	PRO	deletion	UNP Q07817
A	?	-	ALA	deletion	UNP Q07817
A	?	-	VAL	deletion	UNP Q07817
A	?	-	ASN	deletion	UNP Q07817
A	?	-	GLY	deletion	UNP Q07817
A	?	-	ALA	deletion	UNP Q07817
A	?	-	THR	deletion	UNP Q07817
A	?	-	GLY	deletion	UNP Q07817
A	?	-	HIS	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	LEU	deletion	UNP Q07817
A	?	-	ASP	deletion	UNP Q07817
A	?	-	ALA	deletion	UNP Q07817
A	?	-	ARG	deletion	UNP Q07817
A	?	-	GLU	deletion	UNP Q07817
A	?	-	VAL	deletion	UNP Q07817
A	?	-	ILE	deletion	UNP Q07817
A	?	-	PRO	deletion	UNP Q07817
B	?	-	PHE	deletion	UNP Q07817
B	?	-	SER	deletion	UNP Q07817
B	?	-	ASP	deletion	UNP Q07817
B	?	-	VAL	deletion	UNP Q07817
B	?	-	GLU	deletion	UNP Q07817
B	?	-	GLU	deletion	UNP Q07817
B	?	-	ASN	deletion	UNP Q07817
B	?	-	ARG	deletion	UNP Q07817
B	?	-	THR	deletion	UNP Q07817
B	?	-	GLU	deletion	UNP Q07817
B	?	-	ALA	deletion	UNP Q07817

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	PRO	deletion	UNP Q07817
B	?	-	GLU	deletion	UNP Q07817
B	?	-	GLY	deletion	UNP Q07817
B	?	-	THR	deletion	UNP Q07817
B	?	-	GLU	deletion	UNP Q07817
B	?	-	SER	deletion	UNP Q07817
B	?	-	GLU	deletion	UNP Q07817
B	?	-	MET	deletion	UNP Q07817
B	?	-	GLU	deletion	UNP Q07817
B	?	-	THR	deletion	UNP Q07817
B	?	-	PRO	deletion	UNP Q07817
B	?	-	SER	deletion	UNP Q07817
B	?	-	ALA	deletion	UNP Q07817
B	?	-	ILE	deletion	UNP Q07817
B	?	-	ASN	deletion	UNP Q07817
B	?	-	GLY	deletion	UNP Q07817
B	?	-	ASN	deletion	UNP Q07817
B	?	-	PRO	deletion	UNP Q07817
B	?	-	SER	deletion	UNP Q07817
B	?	-	TRP	deletion	UNP Q07817
B	?	-	HIS	deletion	UNP Q07817
B	?	-	LEU	deletion	UNP Q07817
B	?	-	ALA	deletion	UNP Q07817
B	?	-	ASP	deletion	UNP Q07817
B	?	-	SER	deletion	UNP Q07817
B	?	-	PRO	deletion	UNP Q07817
B	?	-	ALA	deletion	UNP Q07817
B	?	-	VAL	deletion	UNP Q07817
B	?	-	ASN	deletion	UNP Q07817
B	?	-	GLY	deletion	UNP Q07817
B	?	-	ALA	deletion	UNP Q07817
B	?	-	THR	deletion	UNP Q07817
B	?	-	GLY	deletion	UNP Q07817
B	?	-	HIS	deletion	UNP Q07817
B	?	-	SER	deletion	UNP Q07817
B	?	-	SER	deletion	UNP Q07817
B	?	-	SER	deletion	UNP Q07817
B	?	-	LEU	deletion	UNP Q07817
B	?	-	ASP	deletion	UNP Q07817
B	?	-	ALA	deletion	UNP Q07817
B	?	-	ARG	deletion	UNP Q07817
B	?	-	GLU	deletion	UNP Q07817

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	VAL	deletion	UNP Q07817
B	?	-	ILE	deletion	UNP Q07817
B	?	-	PRO	deletion	UNP Q07817

- Molecule 2 is a protein called Peptide from Protein X.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	16	Total	C	N	O	0	0	0
			140	92	22	26			
2	D	18	Total	C	N	O	0	0	0
			152	100	24	28			

- Molecule 3 is water.

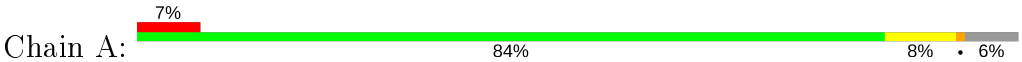
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	63	Total	O	0	0
			63	63		
3	B	78	Total	O	0	0
			78	78		
3	C	5	Total	O	0	0
			5	5		
3	D	5	Total	O	0	0
			5	5		

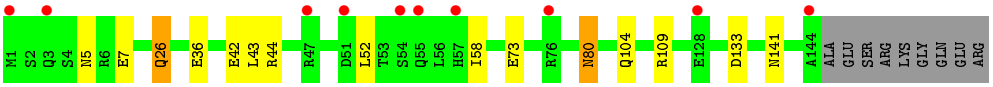
3 Residue-property plots (i)

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: Bcl-2-like protein 1

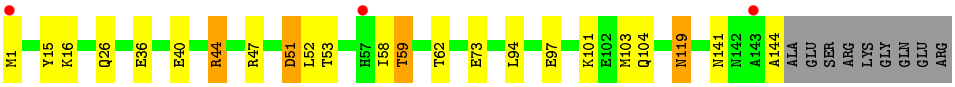
Chain A:





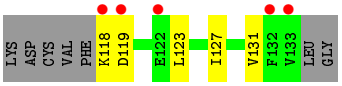
- Molecule 1: Bcl-2-like protein 1

Chain B:



- Molecule 2: Peptide from Protein X

Chain C:



- Molecule 2: Peptide from Protein X

Chain D:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	50.71Å 135.32Å 97.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.15 22.50 – 2.15	Depositor EDS
% Data completeness (in resolution range)	97.8 (50.00-2.15) 98.0 (22.50-2.15)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.06 (at 2.15Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.205 , 0.274 0.212 , 0.277	Depositor DCC
R_{free} test set	944 reflections (5.15%)	wwPDB-VP
Wilson B-factor (Å^2)	21.3	Xtriage
Anisotropy	0.421	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 48.3	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	0.93	EDS
Total number of atoms	2765	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.72% 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

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	0.78	1/1189 (0.1%)	0.84	3/1610 (0.2%)
1	B	0.84	0/1189	0.82	2/1610 (0.1%)
2	C	0.83	0/142	0.93	0/189
2	D	0.71	0/154	1.00	1/205 (0.5%)
All	All	0.80	1/2674 (0.0%)	0.85	6/3614 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	42	GLU	CD-OE1	-5.75	1.19	1.25

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	44	ARG	NE-CZ-NH1	6.59	123.60	120.30
1	A	80	ASN	CB-CA-C	-6.52	97.37	110.40
1	A	43	LEU	CA-CB-CG	5.47	127.88	115.30
1	A	109	ARG	NE-CZ-NH1	5.27	122.94	120.30
1	B	40	GLU	OE1-CD-OE2	5.06	129.37	123.30
2	D	134	LEU	CA-CB-CG	5.04	126.88	115.30

There are no chirality outliers.

There are no planarity outliers.

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	1161	0	1105	9	0
1	B	1161	0	1105	21	0
2	C	140	0	139	5	0
2	D	152	0	153	4	0
3	A	63	0	0	2	0
3	B	78	0	0	5	0
3	C	5	0	0	0	0
3	D	5	0	0	1	0
All	All	2765	0	2502	32	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 (32) 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:59:THR:HG21	3:B:268:HOH:O	1.72	0.88
1:B:104:GLN:NE2	3:B:201:HOH:O	1.94	0.86
1:A:5:ASN:HD22	1:B:119:ASN:ND2	1.88	0.71
1:A:5:ASN:HD22	1:B:119:ASN:HD22	1.37	0.70
1:B:36:GLU:OE1	1:B:141:ASN:ND2	2.26	0.69
2:C:123:LEU:HD23	2:C:127:ILE:HD11	1.76	0.67
1:A:73:GLU:OE2	2:C:118:LYS:HA	1.95	0.67
1:B:58:ILE:HD11	1:B:94:LEU:CD2	2.24	0.66
1:B:59:THR:HG22	1:B:62:THR:H	1.63	0.64
1:B:44:ARG:HD3	3:B:246:HOH:O	1.98	0.62
1:B:52:LEU:HD21	2:D:119:ASP:HB3	1.83	0.60
1:A:52:LEU:HD21	2:C:119:ASP:HB2	1.82	0.60
1:B:26:GLN:HG3	3:B:264:HOH:O	2.02	0.59
1:B:58:ILE:HD11	1:B:94:LEU:HD22	1.84	0.59
2:C:123:LEU:CD2	2:C:127:ILE:HD11	2.32	0.58
1:A:26:GLN:NE2	1:A:133:ASP:OD1	2.35	0.57
2:C:123:LEU:O	2:C:127:ILE:HG13	2.05	0.57
1:B:58:ILE:HD11	1:B:94:LEU:HD23	1.88	0.55
1:A:36:GLU:OE1	1:A:141:ASN:ND2	2.47	0.48
1:B:144:ALA:HB3	3:B:266:HOH:O	2.13	0.48
1:B:52:LEU:HD21	2:D:119:ASP:CB	2.43	0.48
1:B:44:ARG:NH2	2:D:130:LYS:HG3	2.30	0.46
1:A:80:ASN:ND2	3:A:202:HOH:O	2.47	0.45
1:B:73:GLU:HG2	3:D:204:HOH:O	2.18	0.43
1:B:47:ARG:O	1:B:51:ASP:HB2	2.18	0.42
1:B:59:THR:HB	1:B:62:THR:OG1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:ARG:HD3	3:A:248:HOH:O	2.19	0.41
1:B:101:LYS:HB2	1:B:103:MET:HE3	2.00	0.41
1:B:58:ILE:HD12	1:B:97:GLU:CD	2.41	0.41
2:D:122:GLU:O	2:D:126:GLU:HG3	2.21	0.41
1:B:15:TYR:CD2	1:B:16:LYS:HE2	2.55	0.40
1:A:58:ILE:HD13	1:A:58:ILE:HA	1.89	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	142/153 (93%)	139 (98%)	3 (2%)	0	100	100
1	B	142/153 (93%)	140 (99%)	2 (1%)	0	100	100
2	C	14/23 (61%)	14 (100%)	0	0	100	100
2	D	16/23 (70%)	14 (88%)	2 (12%)	0	100	100
All	All	314/352 (89%)	307 (98%)	7 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	121/128 (94%)	118 (98%)	3 (2%)	47	49
1	B	121/128 (94%)	116 (96%)	5 (4%)	30	29
2	C	15/21 (71%)	14 (93%)	1 (7%)	16	11
2	D	16/21 (76%)	15 (94%)	1 (6%)	18	13
All	All	273/298 (92%)	263 (96%)	10 (4%)	34	32

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	GLU
1	A	26	GLN
1	A	104	GLN
1	B	1	MET
1	B	51	ASP
1	B	53	THR
1	B	59	THR
1	B	119	ASN
2	C	131	VAL
2	D	131	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	GLN
1	A	104	GLN
1	B	119	ASN
1	B	127	GLN

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

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, 95^{th} 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	144/153 (94%)	0.20	10 (6%) 16 23	10, 29, 56, 74	0
1	B	144/153 (94%)	0.00	3 (2%) 63 71	11, 22, 42, 62	0
2	C	16/23 (69%)	1.63	5 (31%) 0 0	35, 45, 64, 77	0
2	D	18/23 (78%)	0.80	2 (11%) 5 7	33, 39, 51, 63	0
All	All	322/352 (91%)	0.22	20 (6%) 20 27	10, 27, 54, 77	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	118	LYS	6.1
2	C	118	LYS	5.0
1	A	144	ALA	4.3
2	C	122	GLU	4.3
1	B	57	HIS	3.4
1	A	76	ARG	3.4
2	C	119	ASP	3.4
1	A	55	GLN	3.1
1	A	51	ASP	3.1
1	A	1	MET	3.0
1	A	57	HIS	2.8
1	A	54	SER	2.7
1	A	128	GLU	2.7
1	B	143	ALA	2.6
2	C	133	VAL	2.3
1	A	3	GLN	2.3
1	A	47	ARG	2.2
1	B	1	MET	2.1
2	D	128	ARG	2.0
2	C	132	PHE	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.