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P R O T E I N   D A T A   B A N K

wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 06:52 PM GMT

PDB ID	:	4MXV
Title	:	Structure of Lymphotoxin alpha bound to anti-LTa Fab
Authors	:	Yin, J.P.; Hymowitz, S.G.
Deposited on	:	2013-09-26
Resolution	:	3.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) symbol.

The following versions of software and data (see references (i)) 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 (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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.
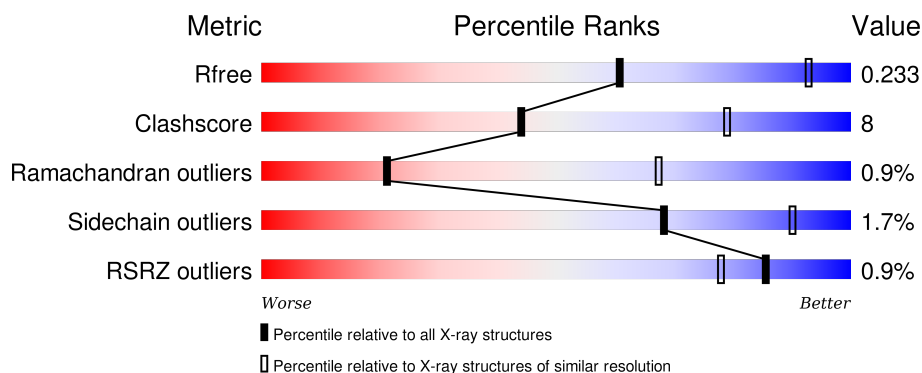
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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. 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	157	64% 22% • 13%
1	B	157	64% 23% • 13%
1	D	157	64% 19% • 16%
2	E	211	84% 15%
2	L	211	80% 19% •

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Mol	Chain	Length	Quality of chain
2	X	211	83% 16%
3	F	213	90% 9%
3	H	213	3% 85% 15%
3	Y	213	82% 17%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 12881 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 Lymphotoxin-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	137	Total	C	N	O	S	0	0	0
			1075	700	177	196	2			
1	B	137	Total	C	N	O	S	0	0	0
			1072	697	177	196	2			
1	D	132	Total	C	N	O	S	0	0	0
			1029	669	171	187	2			

There are 39 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	15	ALA	-	EXPRESSION TAG	UNP P01374
A	16	ASP	-	EXPRESSION TAG	UNP P01374
A	17	LEU	-	EXPRESSION TAG	UNP P01374
A	18	GLY	-	EXPRESSION TAG	UNP P01374
A	19	SER	-	EXPRESSION TAG	UNP P01374
A	20	ASP	-	EXPRESSION TAG	UNP P01374
A	21	TYR	-	EXPRESSION TAG	UNP P01374
A	22	LYS	-	EXPRESSION TAG	UNP P01374
A	23	ASP	-	EXPRESSION TAG	UNP P01374
A	24	ASP	-	EXPRESSION TAG	UNP P01374
A	25	ASP	-	EXPRESSION TAG	UNP P01374
A	26	ASP	-	EXPRESSION TAG	UNP P01374
A	27	LYS	-	EXPRESSION TAG	UNP P01374
B	15	ALA	-	EXPRESSION TAG	UNP P01374
B	16	ASP	-	EXPRESSION TAG	UNP P01374
B	17	LEU	-	EXPRESSION TAG	UNP P01374
B	18	GLY	-	EXPRESSION TAG	UNP P01374
B	19	SER	-	EXPRESSION TAG	UNP P01374
B	20	ASP	-	EXPRESSION TAG	UNP P01374
B	21	TYR	-	EXPRESSION TAG	UNP P01374
B	22	LYS	-	EXPRESSION TAG	UNP P01374
B	23	ASP	-	EXPRESSION TAG	UNP P01374
B	24	ASP	-	EXPRESSION TAG	UNP P01374

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Chain	Residue	Modelled	Actual	Comment	Reference
B	25	ASP	-	EXPRESSION TAG	UNP P01374
B	26	ASP	-	EXPRESSION TAG	UNP P01374
B	27	LYS	-	EXPRESSION TAG	UNP P01374
D	15	ALA	-	EXPRESSION TAG	UNP P01374
D	16	ASP	-	EXPRESSION TAG	UNP P01374
D	17	LEU	-	EXPRESSION TAG	UNP P01374
D	18	GLY	-	EXPRESSION TAG	UNP P01374
D	19	SER	-	EXPRESSION TAG	UNP P01374
D	20	ASP	-	EXPRESSION TAG	UNP P01374
D	21	TYR	-	EXPRESSION TAG	UNP P01374
D	22	LYS	-	EXPRESSION TAG	UNP P01374
D	23	ASP	-	EXPRESSION TAG	UNP P01374
D	24	ASP	-	EXPRESSION TAG	UNP P01374
D	25	ASP	-	EXPRESSION TAG	UNP P01374
D	26	ASP	-	EXPRESSION TAG	UNP P01374
D	27	LYS	-	EXPRESSION TAG	UNP P01374

- Molecule 2 is a protein called anti-Lymphotoxin alpha antibody light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	211	Total 1622	C 1015	N 273	O 329	S 5	0	0	0
2	L	211	Total 1622	C 1015	N 273	O 329	S 5	0	0	0
2	X	211	Total 1622	C 1015	N 273	O 329	S 5	0	0	0

- Molecule 3 is a protein called anti-Lymphotoxin alpha antibody heavy chain.

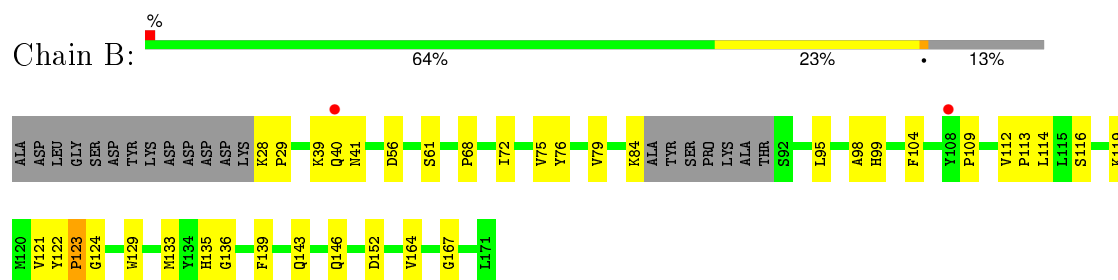| Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	213	Total 1613	C 1028	N 269	O 310	S 6	0	0	0
3	H	213	Total 1613	C 1028	N 269	O 310	S 6	0	0	0
3	Y	213	Total 1613	C 1028	N 269	O 310	S 6	0	0	0

3 Residue-property plots ⓘ

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.
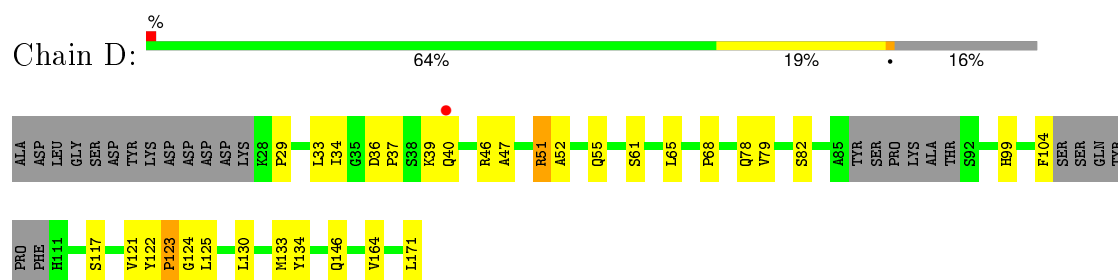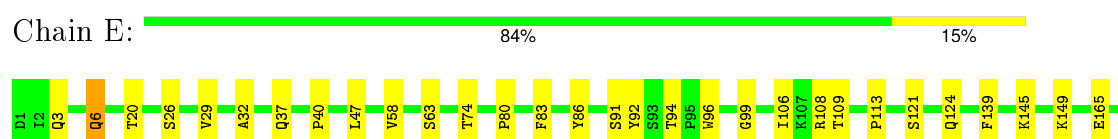
- Molecule 1: Lymphotoxin-alpha

Chain A:

- Molecule 1: Lymphotoxin-alpha

Chain B:

- Molecule 1: Lymphotoxin-alpha

Chain D:

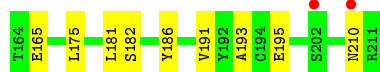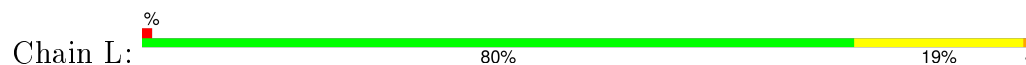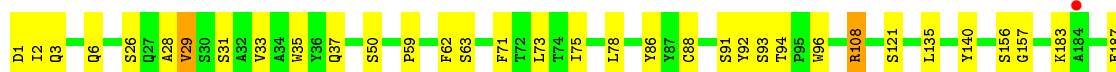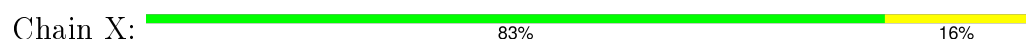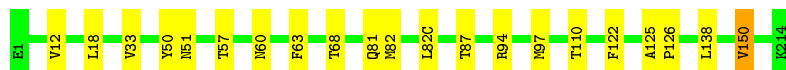- Molecule 2: anti-Lymphotoxin alpha antibody light chain

Chain E:

- Molecule 2: anti-Lymphotoxin alpha antibody light chain
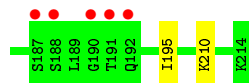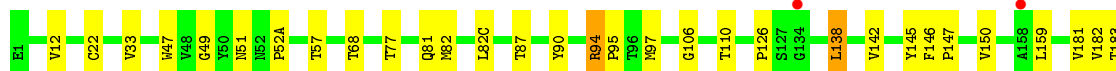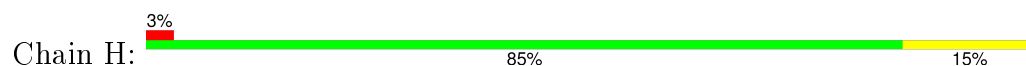
Chain L:

- Molecule 2: anti-Lymphotoxin alpha antibody light chain

Chain X:

- Molecule 3: anti-Lymphotoxin alpha antibody heavy chain

Chain F:

- Molecule 3: anti-Lymphotoxin alpha antibody heavy chain

Chain H:

- Molecule 3: anti-Lymphotoxin alpha antibody heavy chain

Chain Y:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	209.85Å 209.85Å 130.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.80 – 3.20 29.80 – 3.20	Depositor EDS
% Data completeness (in resolution range)	96.8 (29.80-3.20) 96.8 (29.80-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	4.13 (at 3.18Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.177 , 0.235 0.175 , 0.233	Depositor DCC
R_{free} test set	2796 reflections (5.98%)	DCC
Wilson B-factor (Å^2)	61.1	Xtriage
Anisotropy	0.005	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 40.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$<|L|> = 0.48, <L^2> = 0.31$	Xtriage
Outliers	0 of 46763 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	12881	wwPDB-VP
Average B, all atoms (Å^2)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.89% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1] Intensities estimated from amplitudes.

[2] Theoretical values of $<|L|>$, $<L^2>$ 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	0.46	0/1110	0.65	0/1512
1	B	0.45	0/1106	0.67	0/1505
1	D	0.50	0/1060	0.65	0/1442
2	E	0.45	0/1659	0.61	0/2255
2	L	0.42	0/1659	0.57	0/2255
2	X	0.48	0/1659	0.63	0/2255
3	F	0.43	0/1657	0.63	0/2261
3	H	0.39	0/1657	0.58	0/2261
3	Y	0.47	0/1657	0.66	1/2261 (0.0%)
All	All	0.45	0/13224	0.62	1/18007 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	Y	178	LEU	CA-CB-CG	5.37	127.65	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	1075	0	1040	21	0
1	B	1072	0	1033	24	0
1	D	1029	0	1001	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	1622	0	1573	23	0
2	L	1622	0	1573	35	0
2	X	1622	0	1573	27	0
3	F	1613	0	1576	15	0
3	H	1613	0	1576	27	0
3	Y	1613	0	1576	29	0
All	All	12881	0	12521	203	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 8.

The worst 5 of 203 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)
3:H:195:ILE:HG12	3:H:210:LYS:HG2	1.39	1.04
2:X:135:LEU:HD22	3:Y:181:VAL:HG11	1.49	0.94
3:H:159:LEU:HD21	3:H:182:VAL:HG21	1.54	0.86
3:H:145:TYR:CE1	3:H:150:VAL:HG23	2.12	0.84
3:Y:126:PRO:HG3	3:Y:138:LEU:HB3	1.62	0.80

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	133/157 (85%)	123 (92%)	6 (4%)	4 (3%)	5	35
1	B	133/157 (85%)	121 (91%)	8 (6%)	4 (3%)	5	35
1	D	126/157 (80%)	116 (92%)	6 (5%)	4 (3%)	5	33
2	E	209/211 (99%)	196 (94%)	13 (6%)	0	100	100
2	L	209/211 (99%)	196 (94%)	12 (6%)	1 (0%)	34	78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	X	209/211 (99%)	197 (94%)	11 (5%)	1 (0%)	34	78
3	F	209/213 (98%)	197 (94%)	12 (6%)	0	100	100
3	H	209/213 (98%)	197 (94%)	12 (6%)	0	100	100
3	Y	209/213 (98%)	198 (95%)	11 (5%)	0	100	100
All	All	1646/1743 (94%)	1541 (94%)	91 (6%)	14 (1%)	21	67

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	121	VAL
1	B	109	PRO
1	B	123	PRO
1	D	123	PRO
1	A	40	GLN

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	119/135 (88%)	117 (98%)	2 (2%)	68	90
1	B	118/135 (87%)	115 (98%)	3 (2%)	55	86
1	D	113/135 (84%)	111 (98%)	2 (2%)	66	89
2	E	185/185 (100%)	182 (98%)	3 (2%)	70	91
2	L	185/185 (100%)	183 (99%)	2 (1%)	80	94
2	X	185/185 (100%)	182 (98%)	3 (2%)	70	91
3	F	179/179 (100%)	177 (99%)	2 (1%)	80	94
3	H	179/179 (100%)	176 (98%)	3 (2%)	68	90
3	Y	179/179 (100%)	175 (98%)	4 (2%)	60	87
All	All	1442/1497 (96%)	1418 (98%)	24 (2%)	68	90

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	94	ARG
2	L	155	GLN
3	Y	148	GLU
3	F	150	VAL
2	L	26	SER

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

Mol	Chain	Res	Type
1	B	135	HIS
3	F	82(A)	ASN
2	L	137	ASN
3	Y	171	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 (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	137/157 (87%)	-0.29	1 (0%)	89	83	17, 36, 88, 127	0
1	B	137/157 (87%)	-0.23	2 (1%)	76	63	19, 43, 96, 137	0
1	D	132/157 (84%)	-0.26	1 (0%)	87	80	15, 36, 92, 115	0
2	E	211/211 (100%)	-0.36	0	100	100	23, 48, 77, 105	0
2	L	211/211 (100%)	-0.17	3 (1%)	78	65	29, 59, 87, 101	0
2	X	211/211 (100%)	-0.43	1 (0%)	91	87	17, 36, 71, 86	0
3	F	213/213 (100%)	-0.28	0	100	100	18, 42, 68, 100	0
3	H	213/213 (100%)	0.06	7 (3%)	50	35	28, 65, 108, 138	0
3	Y	213/213 (100%)	-0.42	0	100	100	12, 33, 71, 96	0
All	All	1678/1743 (96%)	-0.26	15 (0%)	85	78	12, 45, 87, 138	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	H	191	THR	4.2
3	H	187	SER	3.0
3	H	134	GLY	3.0
2	L	210	ASN	2.9
1	D	40	GLN	2.4

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.