



# Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 1FVR / pdb\_00001fvr  
Title : TIE2 KINASE DOMAIN  
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Deposited on : 2000-09-20  
Resolution : 2.20 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](mailto: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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0rc1  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

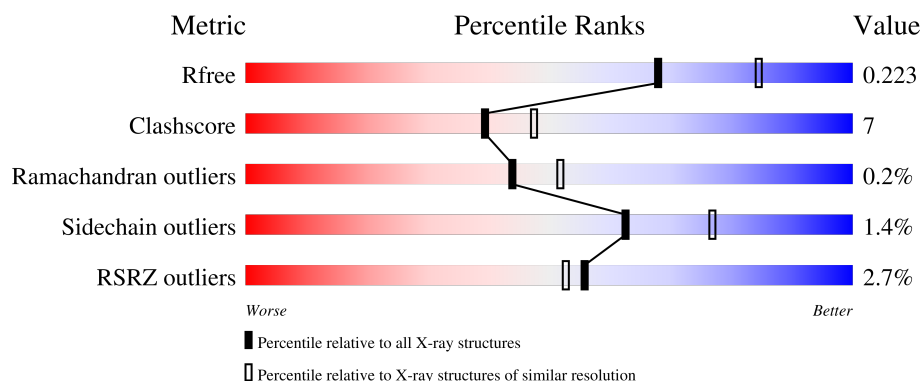
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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))
$R_{free}$	164625	5791 (2.20-2.20)
Clashscore	180529	6634 (2.20-2.20)
Ramachandran outliers	177936	6560 (2.20-2.20)
Sidechain outliers	177891	6561 (2.20-2.20)
RSRZ outliers	164620	5791 (2.20-2.20)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	327	
1	B	327	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5201 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 TYROSINE-PROTEIN KINASE TIE-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	299	Total	C	N	O	S	0	0	0
			2382	1524	402	442	14			
1	B	300	Total	C	N	O	S	0	0	0
			2378	1521	399	444	14			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	798	MET	-	expression tag	UNP Q02763
A	799	LYS	-	expression tag	UNP Q02763
A	800	LYS	-	expression tag	UNP Q02763
A	801	HIS	-	expression tag	UNP Q02763
A	802	HIS	-	expression tag	UNP Q02763
A	803	HIS	-	expression tag	UNP Q02763
A	804	HIS	-	expression tag	UNP Q02763
A	805	HIS	-	expression tag	UNP Q02763
A	806	HIS	-	expression tag	UNP Q02763
A	807	GLY	-	expression tag	UNP Q02763
B	798	MET	-	expression tag	UNP Q02763
B	799	LYS	-	expression tag	UNP Q02763
B	800	LYS	-	expression tag	UNP Q02763
B	801	HIS	-	expression tag	UNP Q02763
B	802	HIS	-	expression tag	UNP Q02763
B	803	HIS	-	expression tag	UNP Q02763
B	804	HIS	-	expression tag	UNP Q02763
B	805	HIS	-	expression tag	UNP Q02763
B	806	HIS	-	expression tag	UNP Q02763
B	807	GLY	-	expression tag	UNP Q02763

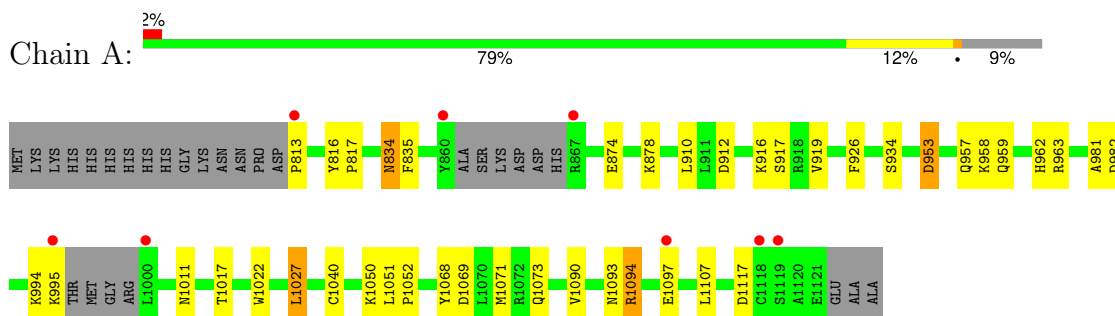
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	225	Total 225	O 225	0	0
2	B	216	Total 216	O 216	0	0

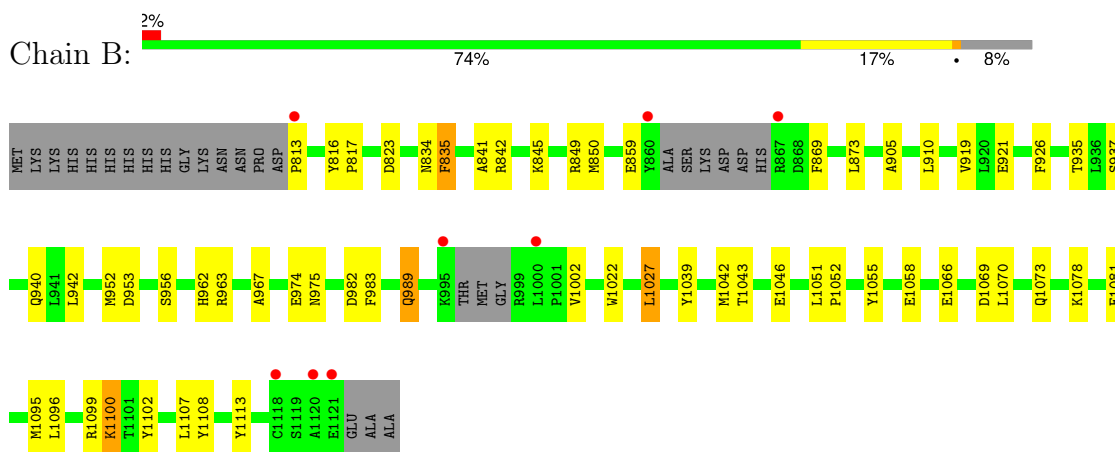
### 3 Residue-property plots

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: TYROSINE-PROTEIN KINASE TIE-2



#### • Molecule 1: TYROSINE-PROTEIN KINASE TIE-2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	66.49Å 92.89Å 70.80Å 90.00° 108.93° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 20.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.3 (20.00-2.20) 96.3 (20.00-2.20)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.00 (at 1.92Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.225 , 0.225 0.195 , 0.223	Depositor DCC
$R_{free}$ test set	4221 reflections (10.26%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	29.2	Xtriage
Anisotropy	0.264	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 41.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5201	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.50% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.39	0/2433	0.89	8/3295 (0.2%)
1	B	0.39	0/2429	0.90	13/3292 (0.4%)
All	All	0.39	0/4862	0.89	21/6587 (0.3%)

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1050	LYS	N-CA-C	6.67	118.64	111.36
1	B	982	ASP	N-CA-C	6.42	119.10	110.88
1	B	813	PRO	N-CA-CB	6.26	109.89	103.00
1	A	813	PRO	N-CA-CB	6.17	109.79	103.00
1	B	1107	LEU	N-CA-C	6.04	117.54	111.07
1	B	1108	TYR	CB-CA-C	-5.89	109.79	116.63
1	A	982	ASP	N-CA-C	5.86	118.38	110.88
1	A	953	ASP	N-CA-C	-5.65	105.04	111.14
1	A	835	PHE	N-CA-C	-5.61	106.39	113.18
1	B	835	PHE	N-CA-C	-5.48	106.55	113.18
1	B	953	ASP	N-CA-C	-5.43	105.44	111.36
1	B	841	ALA	N-CA-C	5.38	115.64	108.38
1	A	1107	LEU	N-CA-C	5.27	116.70	111.07
1	A	1011	ASN	N-CA-C	5.25	116.81	111.14
1	B	905	ALA	CA-C-N	5.23	125.03	119.28
1	B	905	ALA	C-N-CA	5.23	125.03	119.28
1	B	1070	LEU	N-CA-C	-5.19	105.54	111.14
1	A	910	LEU	N-CA-C	5.18	116.93	111.28
1	B	935	THR	N-CA-C	-5.13	106.97	113.18
1	B	910	LEU	N-CA-C	5.12	116.86	111.28
1	B	1002	VAL	N-CA-C	5.03	116.36	110.62

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	2382	0	2327	23	0
1	B	2378	0	2310	39	0
2	A	225	0	0	3	0
2	B	216	0	0	2	0
All	All	5201	0	4637	62	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 7.

All (62) 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:845:LYS:HB3	1:B:850:MET:HE3	1.55	0.87
1:B:937:SER:H	1:B:940:GLN:HE21	1.15	0.87
1:A:1017:THR:HG22	2:A:51:HOH:O	1.78	0.81
1:B:1039:TYR:HB3	1:B:1042:MET:HE3	1.64	0.77
1:B:1095:MET:HE2	1:B:1102:TYR:CD2	2.21	0.76
1:B:1066:GLU:HB3	1:B:1095:MET:HE3	1.71	0.73
1:B:919:VAL:HG21	1:B:926:PHE:HD2	1.55	0.72
1:B:937:SER:H	1:B:940:GLN:NE2	1.88	0.71
1:B:1069:ASP:O	1:B:1073:GLN:HG3	1.93	0.69
1:B:1078:LYS:HB2	1:B:1081:GLU:CG	2.25	0.66
1:B:1042:MET:HE2	2:B:108:HOH:O	1.97	0.65
1:B:1051:LEU:HB2	1:B:1052:PRO:HD3	1.78	0.65
1:B:1078:LYS:HB2	1:B:1081:GLU:HG3	1.80	0.63
1:B:842:ARG:HH21	1:B:850:MET:HA	1.63	0.63
1:A:919:VAL:HG21	1:A:926:PHE:HD2	1.65	0.62
1:B:1066:GLU:HB3	1:B:1095:MET:CE	2.29	0.62
1:B:1043:THR:OG1	1:B:1046:GLU:HG3	2.01	0.61
1:A:1093:ASN:O	1:A:1097:GLU:HG2	2.01	0.60
1:A:919:VAL:HG21	1:A:926:PHE:CD2	2.38	0.59
1:A:994:LYS:O	1:A:995:LYS:CB	2.51	0.58
1:A:1069:ASP:O	1:A:1073:GLN:HG3	2.04	0.57
1:B:919:VAL:HG21	1:B:926:PHE:CD2	2.39	0.57
1:B:823:ASP:O	1:B:849:ARG:NH2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:816:TYR:HB3	1:A:817:PRO:HA	1.85	0.56
1:A:1051:LEU:HB2	1:A:1052:PRO:HD3	1.87	0.55
1:B:859:GLU:HG2	1:B:869:PHE:CZ	2.42	0.55
1:B:1078:LYS:HB2	1:B:1081:GLU:HG2	1.89	0.55
1:B:989:GLN:NE2	2:B:121:HOH:O	2.42	0.52
1:B:1099:ARG:O	1:B:1100:LYS:O	2.28	0.51
1:A:953:ASP:O	1:A:957:GLN:HG2	2.11	0.50
1:B:1039:TYR:CB	1:B:1042:MET:HE3	2.37	0.50
1:B:816:TYR:HB3	1:B:817:PRO:HA	1.93	0.50
1:A:1027:LEU:O	1:A:1027:LEU:HD12	2.11	0.49
1:B:1066:GLU:CB	1:B:1095:MET:HE3	2.40	0.49
1:A:1040:CYS:SG	1:A:1117:ASP:HB2	2.52	0.49
1:A:1017:THR:HG21	2:A:62:HOH:O	2.12	0.48
1:B:1027:LEU:C	1:B:1027:LEU:HD13	2.38	0.48
1:B:942:LEU:HB2	1:B:1096:LEU:HD21	1.96	0.47
1:A:962:HIS:O	1:A:963:ARG:HB2	2.14	0.47
1:B:842:ARG:HH21	1:B:850:MET:CA	2.28	0.47
1:B:967:ALA:N	1:B:1027:LEU:HD23	2.29	0.47
1:B:873:LEU:O	1:B:873:LEU:HD23	2.15	0.46
1:A:874:GLU:O	1:A:878:LYS:HG2	2.16	0.46
1:B:1066:GLU:CG	1:B:1095:MET:HE3	2.46	0.46
1:A:1017:THR:CG2	2:A:62:HOH:O	2.65	0.45
1:B:1042:MET:HE1	1:B:1055:TYR:HE1	1.83	0.44
1:A:834:ASN:ND2	1:A:981:ALA:HB1	2.33	0.43
1:B:962:HIS:O	1:B:963:ARG:HB2	2.17	0.43
1:A:1068:TYR:O	1:A:1071:MET:HB2	2.18	0.43
1:A:1090:VAL:O	1:A:1094:ARG:HG2	2.18	0.43
1:B:921:GLU:HG3	1:B:1113:TYR:HE2	1.83	0.43
1:A:1022:TRP:CD1	1:A:1022:TRP:C	2.97	0.43
1:A:912:ASP:OD1	1:A:916:LYS:HE2	2.19	0.42
1:B:1022:TRP:CD1	1:B:1022:TRP:C	2.97	0.42
1:B:1042:MET:HE1	1:B:1055:TYR:CE1	2.54	0.42
1:A:917:SER:O	1:A:934:SER:HA	2.19	0.42
1:B:835:PHE:CD2	1:B:983:PHE:HB2	2.55	0.41
1:B:974:GLU:O	1:B:975:ASN:HB2	2.20	0.41
1:A:834:ASN:C	1:A:834:ASN:HD22	2.27	0.41
1:A:958:LYS:O	1:A:959:GLN:HB2	2.20	0.41
1:B:952:MET:O	1:B:956:SER:HB2	2.21	0.41
1:B:1100:LYS:HD3	1:B:1102:TYR:CZ	2.56	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	293/327 (90%)	285 (97%)	8 (3%)	0	100	100
1	B	294/327 (90%)	284 (97%)	9 (3%)	1 (0%)	37	42
All	All	587/654 (90%)	569 (97%)	17 (3%)	1 (0%)	44	52

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1100	LYS

### 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	250/280 (89%)	247 (99%)	3 (1%)	67	80
1	B	249/280 (89%)	245 (98%)	4 (2%)	58	73
All	All	499/560 (89%)	492 (99%)	7 (1%)	62	77

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	834	ASN
1	A	1027	LEU
1	A	1094	ARG
1	B	834	ASN
1	B	989	GLN

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Mol	Chain	Res	Type
1	B	1027	LEU
1	B	1058	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	834	ASN
1	A	930	ASN
1	A	989	GLN
1	A	1053	GLN
1	B	834	ASN
1	B	940	GLN
1	B	975	ASN
1	B	989	GLN
1	B	1053	GLN
1	B	1073	GLN
1	B	1093	ASN

### 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 oligosaccharides 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 ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	299/327 (91%)	-0.15	8 (2%) 56 53	19, 31, 52, 66	0
1	B	300/327 (91%)	-0.09	8 (2%) 56 53	20, 31, 53, 68	0
All	All	599/654 (91%)	-0.12	16 (2%) 56 53	19, 31, 53, 68	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	813	PRO	4.8
1	A	867	ARG	3.7
1	B	867	ARG	3.0
1	A	1119	SER	2.9
1	B	860	TYR	2.7
1	B	1121	GLU	2.7
1	B	1000	LEU	2.7
1	A	1118	CYS	2.6
1	A	860	TYR	2.4
1	B	1120	ALA	2.4
1	A	1000	LEU	2.4
1	A	813	PRO	2.3
1	B	995	LYS	2.3
1	A	995	LYS	2.2
1	A	1097	GLU	2.1
1	B	1118	CYS	2.1

### 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.