



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 23, 2020 – 01:26 am BST

PDB ID : 6TYX  
Title : Structure of Ku80 von Willebrand domain S229A mutant complexed with XLF  
Ku Binding Motif  
Authors : Min, J.; Pedersen, L.C.  
Deposited on : 2019-08-09  
Resolution : 1.90 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](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 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

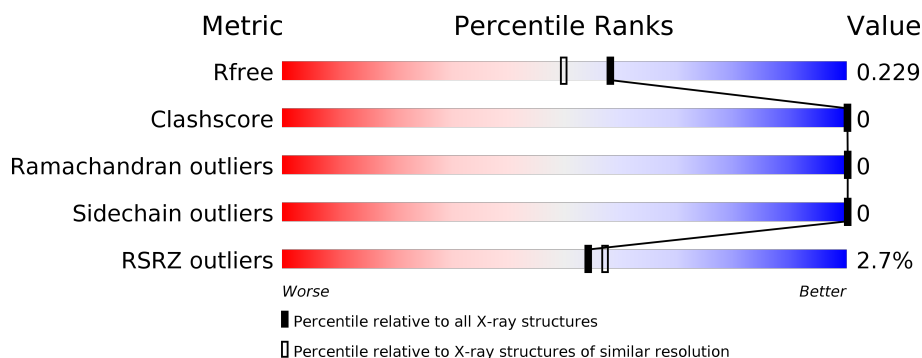
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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  $\geq 3$ , 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	231	<div> <div>2%</div> <div> <div></div> <div>91%</div> <div>9%</div> </div> </div>
1	B	231	<div> <div>3%</div> <div> <div></div> <div>94%</div> <div>6%</div> </div> </div>
2	C	18	<div> <div>28%</div> <div>72%</div> </div>
2	D	18	<div> <div>39%</div> <div>61%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6788 atoms, of which 3186 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 X-ray repair cross-complementing protein 5.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	211	Total	C	H	N	O	S	0	11	0
			3230	1061	1578	260	321	10			
1	B	216	Total	C	H	N	O	S	0	2	0
			3182	1053	1542	264	313	10			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MET	-	initiating methionine	UNP A0A1L8EVE5
A	-5	HIS	-	expression tag	UNP A0A1L8EVE5
A	-4	HIS	-	expression tag	UNP A0A1L8EVE5
A	-3	HIS	-	expression tag	UNP A0A1L8EVE5
A	-2	HIS	-	expression tag	UNP A0A1L8EVE5
A	-1	HIS	-	expression tag	UNP A0A1L8EVE5
A	0	HIS	-	expression tag	UNP A0A1L8EVE5
A	?	-	GLU	deletion	UNP A0A1L8EVE5
A	?	-	GLU	deletion	UNP A0A1L8EVE5
A	?	-	PHE	deletion	UNP A0A1L8EVE5
A	?	-	GLY	deletion	UNP A0A1L8EVE5
A	?	-	GLY	deletion	UNP A0A1L8EVE5
A	?	-	SER	deletion	UNP A0A1L8EVE5
A	?	-	SER	deletion	UNP A0A1L8EVE5
A	?	-	ASN	deletion	UNP A0A1L8EVE5
A	?	-	ASN	deletion	UNP A0A1L8EVE5
A	?	-	ARG	deletion	UNP A0A1L8EVE5
A	?	-	GLY	deletion	UNP A0A1L8EVE5
A	?	-	ASN	deletion	UNP A0A1L8EVE5
A	?	-	ALA	deletion	UNP A0A1L8EVE5
A	?	-	GLY	deletion	UNP A0A1L8EVE5
A	?	-	SER	deletion	UNP A0A1L8EVE5
A	?	-	SER	deletion	UNP A0A1L8EVE5
A	?	-	ASP	deletion	UNP A0A1L8EVE5
A	?	-	ARG	deletion	UNP A0A1L8EVE5

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A	190	SER	CYS	engineered mutation	UNP A0A1L8EVE5
A	229	ALA	SER	engineered mutation	UNP A0A1L8EVE5
B	-6	MET	-	initiating methionine	UNP A0A1L8EVE5
B	-5	HIS	-	expression tag	UNP A0A1L8EVE5
B	-4	HIS	-	expression tag	UNP A0A1L8EVE5
B	-3	HIS	-	expression tag	UNP A0A1L8EVE5
B	-2	HIS	-	expression tag	UNP A0A1L8EVE5
B	-1	HIS	-	expression tag	UNP A0A1L8EVE5
B	0	HIS	-	expression tag	UNP A0A1L8EVE5
B	?	-	GLU	deletion	UNP A0A1L8EVE5
B	?	-	GLU	deletion	UNP A0A1L8EVE5
B	?	-	PHE	deletion	UNP A0A1L8EVE5
B	?	-	GLY	deletion	UNP A0A1L8EVE5
B	?	-	GLY	deletion	UNP A0A1L8EVE5
B	?	-	SER	deletion	UNP A0A1L8EVE5
B	?	-	SER	deletion	UNP A0A1L8EVE5
B	?	-	ASN	deletion	UNP A0A1L8EVE5
B	?	-	ASN	deletion	UNP A0A1L8EVE5
B	?	-	ARG	deletion	UNP A0A1L8EVE5
B	?	-	GLY	deletion	UNP A0A1L8EVE5
B	?	-	ASN	deletion	UNP A0A1L8EVE5
B	?	-	ALA	deletion	UNP A0A1L8EVE5
B	?	-	GLY	deletion	UNP A0A1L8EVE5
B	?	-	SER	deletion	UNP A0A1L8EVE5
B	?	-	SER	deletion	UNP A0A1L8EVE5
B	?	-	ASP	deletion	UNP A0A1L8EVE5
B	?	-	ARG	deletion	UNP A0A1L8EVE5
B	190	SER	CYS	engineered mutation	UNP A0A1L8EVE5
B	229	ALA	SER	engineered mutation	UNP A0A1L8EVE5

- Molecule 2 is a protein called LYS-GLY-LEU-PHE-MET.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	5	Total	C	H	N	O	S	0	0
			69	25	33	5	5	1		0
2	D	7	Total	C	H	N	O		0	0
			76	29	33	7	7			0

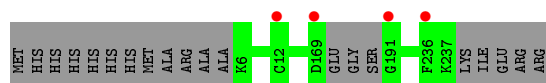
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	138	Total 141	O 141	0	3
3	B	89	Total 89	O 89	0	0
3	C	1	Total 1	O 1	0	0

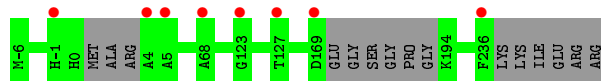
### 3 Residue-property plots [i](#)

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.

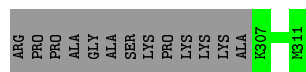
- Molecule 1: X-ray repair cross-complementing protein 5



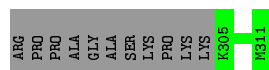
- Molecule 1: X-ray repair cross-complementing protein 5



- Molecule 2: LYS-GLY-LEU-PHE-MET



- Molecule 2: LYS-GLY-LEU-PHE-MET



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	44.80Å 71.61Å 74.60Å 90.00° 98.31° 90.00°	Depositor
Resolution (Å)	40.69 – 1.90 40.69 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.2 (40.69-1.90) 98.2 (40.69-1.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.27 (at 1.89Å)	Xtriage
Refinement program	PHENIX 1.10.1 _2155	Depositor
R, $R_{free}$	0.185 , 0.225 0.186 , 0.229	Depositor DCC
$R_{free}$ test set	1813 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	29.8	Xtriage
Anisotropy	0.218	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 57.4	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	0.96	EDS
Total number of atoms	6788	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.09% 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	0.31	0/1695	0.49	0/2298
1	B	0.29	0/1675	0.45	0/2269
2	C	0.26	0/36	0.47	0/46
2	D	0.31	0/43	0.64	0/57
All	All	0.30	0/3449	0.47	0/4670

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	1652	1578	1553	0	0
1	B	1640	1542	1536	0	0
2	C	36	33	33	0	0
2	D	43	33	33	0	0
3	A	141	0	0	0	0
3	B	89	0	0	0	0
3	C	1	0	0	0	0
All	All	3602	3186	3155	0	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 0.

There are no clashes within the asymmetric unit.



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	218/231 (94%)	213 (98%)	5 (2%)	0	100	100
1	B	212/231 (92%)	208 (98%)	4 (2%)	0	100	100
2	C	3/18 (17%)	3 (100%)	0	0	100	100
2	D	5/18 (28%)	5 (100%)	0	0	100	100
All	All	438/498 (88%)	429 (98%)	9 (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	175/203 (86%)	175 (100%)	0	100	100
1	B	168/203 (83%)	168 (100%)	0	100	100
2	C	3/13 (23%)	3 (100%)	0	100	100
2	D	2/13 (15%)	2 (100%)	0	100	100
All	All	348/432 (81%)	348 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some 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 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, 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	211/231 (91%)	-0.13	4 (1%) 66 69	18, 32, 69, 121	0
1	B	216/231 (93%)	0.09	8 (3%) 41 44	25, 47, 94, 124	0
2	C	5/18 (27%)	0.69	0 100 100	38, 48, 54, 110	0
2	D	7/18 (38%)	0.27	0 100 100	44, 57, 81, 88	0
All	All	439/498 (88%)	-0.01	12 (2%) 54 57	18, 41, 88, 124	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	236	PHE	4.2
1	A	12	CYS	4.1
1	B	123	GLY	3.7
1	B	127	THR	3.2
1	B	4	ALA	2.9

### 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.