



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 2, 2023 – 11:39 PM EDT

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 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 types of validation reports are described at

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

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

MolProbity : **FAILED**
Xtrriage (Phenix) : 1.13
EDS : **FAILED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

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 1.90 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition [i](#)

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	
			Total	C	H	N	O				S
1	A	211	3230	1061	1578	260	321	10	0	11	0
1	B	216	3182	1053	1542	264	313	10	0	2	0

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	0
			69	25	33	5	5	1			
2	D	7	Total	C	H	N	O		0	0	0
			76	29	33	7	7				

- 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

MolProbity and EDS failed to run properly - this section is therefore empty.

3 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	44.80Å 71.61Å 74.60Å 90.00° 98.31° 90.00°	Depositor
Resolution (Å)	40.69 – 1.90	Depositor
% Data completeness (in resolution range)	98.2 (40.69-1.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.27 (at 1.89Å)	Xtrriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.185 , 0.225	Depositor
Wilson B-factor (Å ²)	29.8	Xtrriage
Anisotropy	0.218	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	6788	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtrriage'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.*

¹ Intensities estimated from amplitudes.

² 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.

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

4.6 Ligand geometry [i](#)

There are no ligands in this entry.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues

There are no chain breaks in this entry.

5 Fit of model and data

5.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

5.2 Non-standard residues in protein, DNA, RNA chains

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

5.4 Ligands

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers

EDS failed to run properly - this section is therefore empty.