



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 01:09 pm GMT

PDB ID : 2RJF  
Title : Crystal structure of L3MBTL1 in complex with H4K20Me2 (residues 12-30), orthorhombic form I  
Authors : Allali-Hassani, A.; Liu, Y.; Herzanych, N.; Ouyang, H.; Mackenzie, F.; Crombet, L.; Loppnau, P.; Kozieradzki, I.; Vedadi, M.; Weigelt, J.; Sundstrom, M.; Arrowsmith, C.H.; Edwards, A.M.; Bochkarev, A.; Min, J.R.; Structural Genomics Consortium (SGC)  
Deposited on : 2007-10-14  
Resolution : 2.05 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

<http://wwpdb.org/validation/2016/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
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

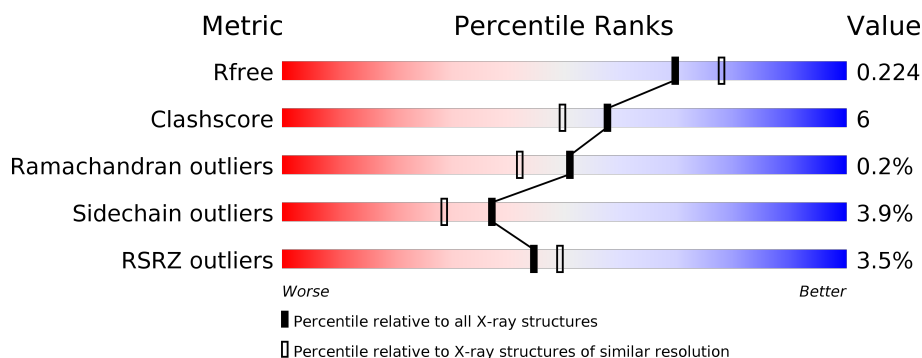
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.05 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))
$R_{free}$	100719	1316 (2.04-2.04)
Clashscore	112137	1394 (2.04-2.04)
Ramachandran outliers	110173	1383 (2.04-2.04)
Sidechain outliers	110143	1383 (2.04-2.04)
RSRZ outliers	101464	1319 (2.04-2.04)

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. 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	331	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>13%</div> <div>• 5%</div> </div> </div>
1	C	331	<div> <div>3%</div> <div> <div></div> <div>80%</div> <div>13%</div> <div>• 5%</div> </div> </div>
1	E	331	<div> <div>5%</div> <div> <div></div> <div>79%</div> <div>14%</div> <div>• 5%</div> </div> </div>
2	B	20	<div> <div>5%</div> <div> <div></div> <div>30%</div> <div>20%</div> <div>50%</div> </div> </div>
2	D	20	<div> <div>10%</div> <div> <div></div> <div>40%</div> <div>5%</div> <div>55%</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8413 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 Lethal(3)malignant brain tumor-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	315	Total	C	N	O	S	0	0	0
			2556	1645	434	465	12			
1	C	315	Total	C	N	O	S	0	0	0
			2556	1645	434	465	12			
1	E	315	Total	C	N	O	S	0	0	0
			2556	1645	434	465	12			

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	10	Total	C	N	O	0	0	0
			87	54	20	13			
2	D	9	Total	C	N	O	0	0	0
			85	51	22	12			

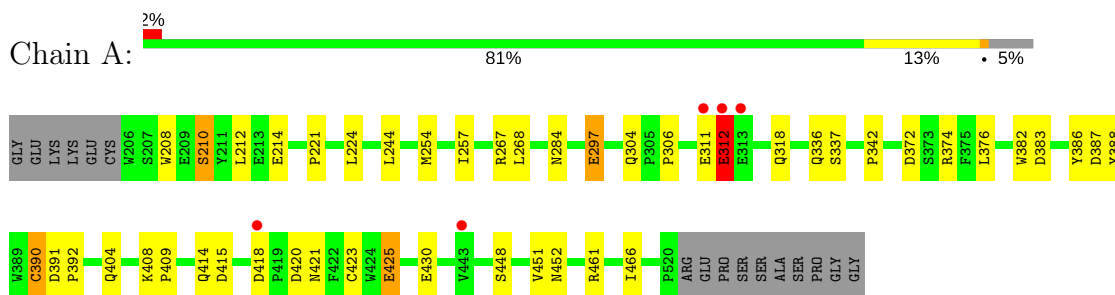
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	221	Total	O	0	0
			221	221		
3	B	7	Total	O	0	0
			7	7		
3	C	186	Total	O	0	0
			186	186		
3	D	8	Total	O	0	0
			8	8		
3	E	151	Total	O	0	0
			151	151		

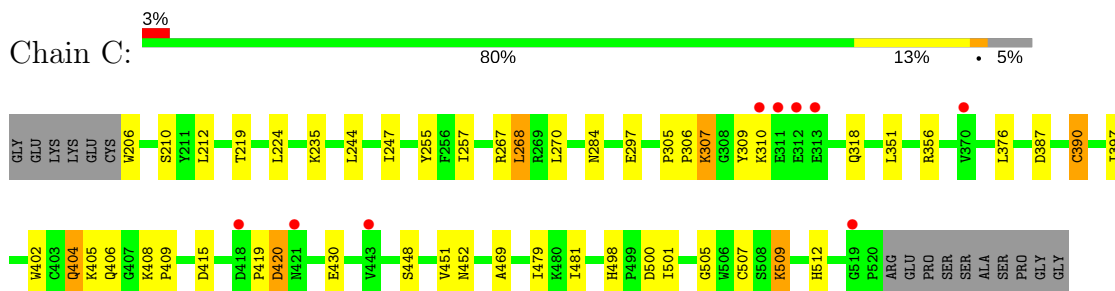
### 3 Residue-property plots [i](#)

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.

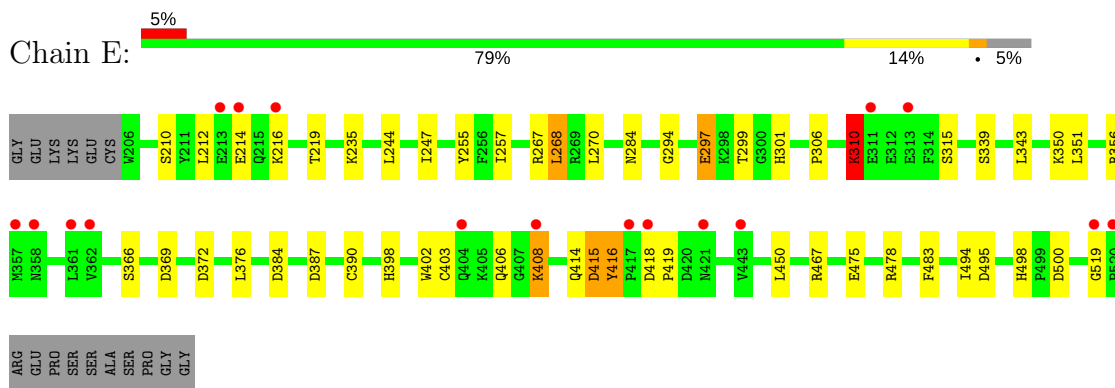
- Molecule 1: Lethal(3)malignant brain tumor-like protein



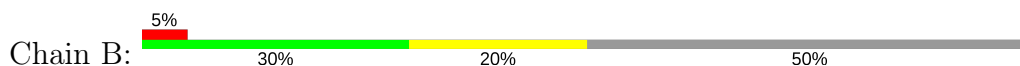
- Molecule 1: Lethal(3)malignant brain tumor-like protein



- Molecule 1: Lethal(3)malignant brain tumor-like protein

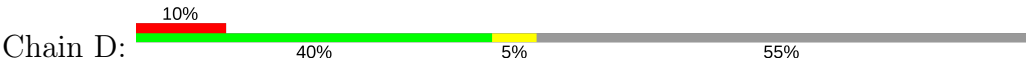


- Molecule 2: Histone H4





● Molecule 2: Histone H4



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.46Å 117.81Å 132.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.65 – 2.05 39.64 – 2.05	Depositor EDS
% Data completeness (in resolution range)	97.3 (39.65-2.05) 97.3 (39.64-2.05)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.33 (at 2.05Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.179 , 0.225 0.179 , 0.224	Depositor DCC
$R_{free}$ test set	4370 reflections (5.33%)	DCC
Wilson B-factor (Å <sup>2</sup> )	35.1	Xtriage
Anisotropy	0.009	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 43.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	8413	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MLY

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	1.09	7/2656 (0.3%)	0.88	4/3631 (0.1%)
1	C	1.04	6/2656 (0.2%)	0.82	2/3631 (0.1%)
1	E	0.97	5/2656 (0.2%)	0.79	2/3631 (0.1%)
2	B	1.12	0/76	1.02	0/101
2	D	0.99	0/74	1.05	0/97
All	All	1.03	18/8118 (0.2%)	0.84	8/11091 (0.1%)

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	310	LYS	CE-NZ	16.36	1.90	1.49
1	C	307	LYS	CE-NZ	15.97	1.89	1.49
1	C	390	CYS	CB-SG	-11.35	1.62	1.82
1	A	390	CYS	CB-SG	-8.55	1.67	1.82
1	A	297	GLU	CG-CD	7.33	1.62	1.51

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	307	LYS	CD-CE-NZ	-9.55	89.73	111.70
1	E	310	LYS	CD-CE-NZ	-8.72	91.65	111.70
1	A	374	ARG	NE-CZ-NH2	-7.16	116.72	120.30
1	E	450	LEU	CA-CB-CG	5.67	128.33	115.30
1	C	356	ARG	NE-CZ-NH2	-5.56	117.52	120.30

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	2556	0	2390	25	0
1	C	2556	0	2390	31	0
1	E	2556	0	2390	28	0
2	B	87	0	90	4	0
2	D	85	0	90	1	0
3	A	221	0	0	3	0
3	B	7	0	0	0	0
3	C	186	0	0	3	0
3	D	8	0	0	0	0
3	E	151	0	0	2	0
All	All	8413	0	7350	85	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.

The worst 5 of 85 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:C:307:LYS:CE	1:C:307:LYS:NZ	1.89	1.36
1:E:310:LYS:CE	1:E:310:LYS:NZ	1.90	1.34
1:C:257:ILE:HD12	1:C:306:PRO:HD3	1.58	0.85
1:E:301:HIS:HE1	1:E:369:ASP:OD1	1.64	0.80
1:C:420:ASP:HA	3:C:827:HOH:O	1.89	0.72

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	313/331 (95%)	307 (98%)	5 (2%)	1 (0%)	44	35
1	C	313/331 (95%)	307 (98%)	6 (2%)	0	100	100
1	E	313/331 (95%)	305 (97%)	7 (2%)	1 (0%)	44	35
2	B	7/20 (35%)	6 (86%)	1 (14%)	0	100	100
2	D	6/20 (30%)	6 (100%)	0	0	100	100
All	All	952/1033 (92%)	931 (98%)	19 (2%)	2 (0%)	51	42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	519	GLY
1	A	312	GLU

### 5.3.2 Protein sidechains ⓘ

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	278/290 (96%)	267 (96%)	11 (4%)	36	27
1	C	278/290 (96%)	267 (96%)	11 (4%)	36	27
1	E	278/290 (96%)	267 (96%)	11 (4%)	36	27
2	B	8/15 (53%)	8 (100%)	0	100	100
2	D	8/15 (53%)	8 (100%)	0	100	100
All	All	850/900 (94%)	817 (96%)	33 (4%)	37	29

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	268	LEU
1	C	404	GLN
1	E	351	LEU
1	C	310	LYS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	318	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	414	GLN
1	E	498	HIS
1	E	284	ASN
1	C	233	HIS
1	C	498	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	MLY	B	20	2	10,10,11	1.01	1 (10%)	8,11,13	1.17	1 (12%)
2	MLY	D	20	2	10,10,11	1.15	1 (10%)	8,11,13	0.84	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MLY	B	20	2	-	0/7/9/11	0/0/0/0
2	MLY	D	20	2	-	0/7/9/11	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	20	MLY	CA-C	2.15	1.53	1.50
2	B	20	MLY	CA-C	2.16	1.53	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	20	MLY	CH2-NZ-CH1	-2.02	104.30	109.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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 ⓘ

### 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<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	315/331 (95%)	-0.14	5 (1%) 72 75	11, 22, 33, 49	0
1	C	315/331 (95%)	-0.05	9 (2%) 52 58	12, 24, 35, 47	0
1	E	315/331 (95%)	0.13	17 (5%) 26 29	13, 33, 43, 48	0
2	B	9/20 (45%)	0.60	1 (11%) 6 6	32, 43, 52, 53	0
2	D	8/20 (40%)	0.66	2 (25%) 1 0	34, 40, 52, 55	0
All	All	962/1033 (93%)	-0.01	34 (3%) 44 49	11, 25, 42, 55	0

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	520	PRO	7.2
1	E	519	GLY	5.0
1	A	443	VAL	4.3
1	C	443	VAL	4.1
1	C	311	GLU	4.0

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	MLY	D	20	11/12	0.96	0.08	-	24,29,33,33	0
2	MLY	B	20	11/12	0.97	0.06	-	26,30,33,33	0

### 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.