

# Full wwPDB X-ray Structure Validation Report (i)

#### Mar 9, 2024 – 09:08 AM EST

PDB ID : 3JSB

Title : Crystal structure of the N-terminal domain of the Lymphocytic Choriomenin-

gitis Virus L protein

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Deposited on : 2009-09-10

Resolution : 2.13 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 (i) 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 (1)) were used in the production of this report:

 $\begin{array}{ccc} & Mol Probity & : & 4.02b\text{-}467 \\ & Xtriage \text{ (Phenix)} & : & 1.13 \end{array}$ 

EDS: 2.36

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

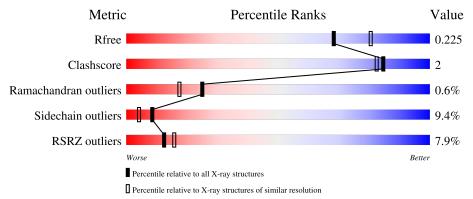
Validation Pipeline (wwPDB-VP) : 2.36

## 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 2.13 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{\rm A})}) \end{array}$
$R_{free}$	130704	2523 (2.16-2.12)
Clashscore	141614	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)
RSRZ outliers	127900	2485 (2.16-2.12)

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 >=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 <=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	204	73%	11%		15%
1	В	204	81%		13%	6 • 5%



## 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3259 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 RNA-directed RNA polymerase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	۸	173	Total	С	N	О	S	0	6	0
1	A	173	1420	901	237	271	11	U	O	0
1	D	194	Total	С	N	О	S	0	2	0
1	Б	194	1586	1008	262	306	10	0	3	

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	UNP P14240
A	-6	LYS	-	expression tag	UNP P14240
A	-5	HIS	-	expression tag	UNP P14240
A	-4	HIS	-	expression tag	UNP P14240
A	-3	HIS	-	expression tag	UNP P14240
A	-2	HIS	-	expression tag	UNP P14240
A	-1	HIS	-	expression tag	UNP P14240
A	0	HIS	-	expression tag	UNP P14240
A	107	THR	SER	engineered mutation	UNP P14240
A	173	ASP	ASN	engineered mutation	UNP P14240
В	-7	MET	-	initiating methionine	UNP P14240
В	-6	LYS	-	expression tag	UNP P14240
В	-5	HIS	-	expression tag	UNP P14240
В	-4	HIS	-	expression tag	UNP P14240
В	-3	HIS	_	expression tag	UNP P14240
В	-2	HIS	-	expression tag	UNP P14240
В	-1	HIS	-	expression tag	UNP P14240
В	0	HIS	-	expression tag	UNP P14240
В	107	THR	SER	engineered mutation	UNP P14240
В	173	ASP	ASN	engineered mutation	UNP P14240

• Molecule 2 is water.



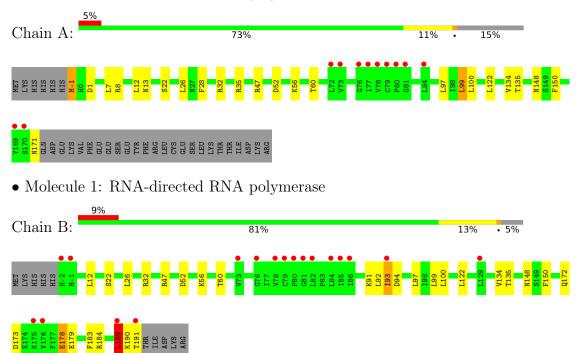
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	125	Total O 125 125	0	0
2	В	127	Total O 128 128	0	1



## 3 Residue-property plots (i)

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: RNA-directed RNA polymerase





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants	145.01Å 159.35Å 52.62Å	Donositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.59 - 2.13	Depositor
Resolution (A)	42.59 - 2.13	EDS
% Data completeness	97.9 (42.59-2.13)	Depositor
(in resolution range)	98.0 (42.59-2.13)	EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	0.04	Depositor
$< I/\sigma(I) > 1$	2.72 (at 2.14Å)	Xtriage
Refinement program	BUSTER 2.11.0	Depositor
D D.	0.199 , 0.222	Depositor
$R, R_{free}$	0.199 , $0.225$	DCC
$R_{free}$ test set	1698 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.8	Xtriage
Anisotropy	0.232	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.35, 61.7	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.48, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3259	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.68% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

## 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	Mol Chain		lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.51	0/1459	0.68	0/1969	
1	В	0.50	0/1621	0.70	0/2187	
All	All	0.50	0/3080	0.69	0/4156	

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	1420	0	1432	8	0
1	В	1586	0	1575	8	0
2	A	125	0	0	1	0
2	В	128	0	0	0	0
All	All	3259	0	3007	14	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 2.

All (14) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	$egin{aligned}  ext{Clash} \  ext{overlap } ( ext{Å}) \end{aligned}$	
1:B:189:LEU:O	1:B:191:THR:HB	1.96	0.65	

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Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	Clash overlap (Å)
1:A:148:ASN:HD22	1:A:150:PHE:H	1.49	0.61
1:B:148:ASN:HD22	1:B:150:PHE:H	1.50	0.59
1:A:52:ASP:O	1:A:56:LYS:HG2	2.10	0.50
1:A:22:SER:HB3	1:B:22:SER:HB3	1.94	0.49
1:A:-1:HIS:HD2	1:A:1:ASP:H	1.62	0.48
1:B:178:GLU:HG3	1:B:183:PHE:CE2	2.50	0.47
1:B:91:LYS:HG2	1:B:93:ILE:HG12	1.99	0.45
1:A:8[A]:ARG:NH2	2:A:261:HOH:O	2.51	0.43
1:B:52:ASP:O	1:B:56:LYS:HG3	2.19	0.42
1:B:184:ARG:HE	1:B:184:ARG:HB3	1.70	0.42
1:A:7:LEU:HB3	1:A:28:PHE:HZ	1.85	0.42
1:A:13:ASN:HD21	1:B:32:ARG:HH11	1.67	0.41
1:A:99:LEU:HD12	1:A:99:LEU:HA	1.97	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	Perce	ntiles
1	A	177/204 (87%)	173 (98%)	4 (2%)	0	100	100
1	В	194/204~(95%)	191 (98%)	1 (0%)	2 (1%)	15	8
All	All	371/408 (91%)	364 (98%)	5 (1%)	2 (0%)	25	22

#### All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	189	LEU
1	В	93	ILE



#### 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	165/190 (87%)	151 (92%)	14 (8%)	10 6	
1	В	182/190 (96%)	164 (90%)	18 (10%)	8 3	
All	All	347/380 (91%)	315 (91%)	32 (9%)	8 4	

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-1	HIS
1	A	12	LEU
1	A	26	LEU
1	A	32	ARG
1	A	35	ARG
1	A	47	ARG
1	A	60	THR
1	A A A	97	LEU
1	A	99	LEU
1		100	LEU
1	A	122	LEU
1	A A	134	VAL
1	A	135	THR
1	A	171	ASN
1	В	12	LEU
1	В	26	LEU
1	В	47	ARG
1	В	60	THR
1	В	92	LEU
1	В	94	ASP
1	В	97	LEU
1	В	99	LEU
1	В	100	LEU
1	В	122	LEU
1	В	134	VAL
1	В	135	THR
1	В	172	GLN

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Mol	Chain	Res	Type
1	В	173	ASP
1	В	178	GLU
1	В	179	GLU
1	В	189	LEU
1	В	190	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	-1	HIS
1	A	13	ASN
1	A	27	ASN
1	A	148	ASN
1	В	27	ASN
1	В	63	HIS
1	В	148	ASN
1	В	171	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 monosaccharides 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,  $95^{th}$  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	$\langle { m RSRZ} \rangle$	#RSRZ>	>2	$OWAB(Å^2)$	Q < 0.9
1	A	173/204 (84%)	0.39	11 (6%) 19	24	32, 51, 105, 133	0
1	В	194/204~(95%)	0.50	18 (9%) 8	11	33, 58, 100, 123	2 (1%)
All	All	367/408 (89%)	0.45	29 (7%) 12	16	32, 55, 100, 133	2 (0%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	78	VAL	8.0
1	В	80	PRO	7.9
1	A	78	VAL	6.9
1	A	169	TYR	6.8
1	A	80	PRO	5.9
1	В	84	LEU	5.0
1	В	79	CYS	4.9
1	В	81	GLY	4.6
1	A	76	GLY	4.6
1	В	175	LYS	4.4
1	В	176	VAL	3.7
1	A	77	ILE	3.7
1	A	84	LEU	3.6
1	В	73	VAL	3.6
1	В	-2	HIS	3.4
1	В	76	GLY	3.2
1	В	85	ILE	3.2
1	В	191	THR	3.1
1	A	72	LEU	2.9
1	В	93	ILE	2.8
1	A	81	GLY	2.8
1	В	-1	HIS	2.8
1	A	170	SER	2.5
1	A	79	CYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	73	VAL	2.3
1	В	189	LEU	2.2
1	В	86	ILE	2.1
1	В	82	LEU	2.1
1	В	129	LEU	2.0

## 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.

