



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 03:28 am GMT

PDB ID : 5AMR
Title : Structure of the La Crosse Bunyavirus polymerase in complex with the 3' viral RNA
Authors : Reguera, J.; Gerlach, P.; Cusack, S.
Deposited on : 2015-03-12
Resolution : 2.57 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

<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
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

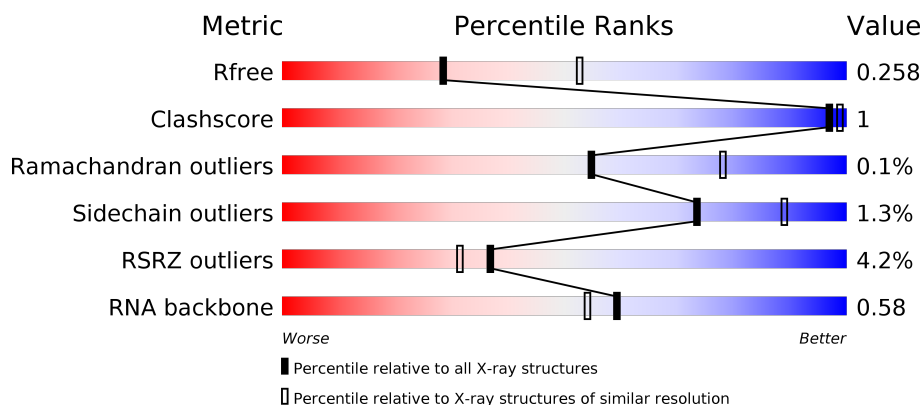
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.57 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	2899 (2.60-2.56)
Clashscore	112137	3268 (2.60-2.56)
Ramachandran outliers	110173	3218 (2.60-2.56)
Sidechain outliers	110143	3218 (2.60-2.56)
RSRZ outliers	101464	2907 (2.60-2.56)
RNA backbone	2435	1007 (2.98-2.18)

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 ≥ 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	2264	<div> <div>3%</div> <div>70%</div> <div>27%</div> </div>
2	B	16	<div> <div>75%</div> <div>25%</div> </div>
3	C	8	<div> <div>75%</div> <div>13%</div> <div>13%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 14163 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 POLYMERASE L.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1657	Total	C	N	O	S	0	0	0
			13571	8701	2256	2525	89			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	EXPRESSION TAG	UNP A5HC98

- Molecule 2 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	16	Total	C	N	O	P	0	0	0
			334	151	56	112	15			

- Molecule 3 is a RNA chain called RNA.

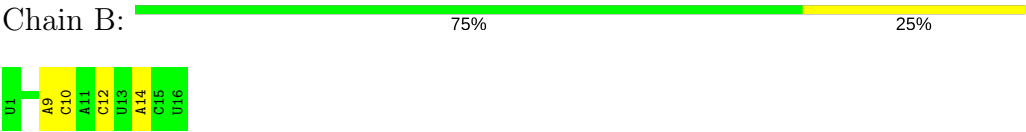
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	8	Total	C	N	O	P	0	0	0
			166	76	31	52	7			

- Molecule 4 is water.

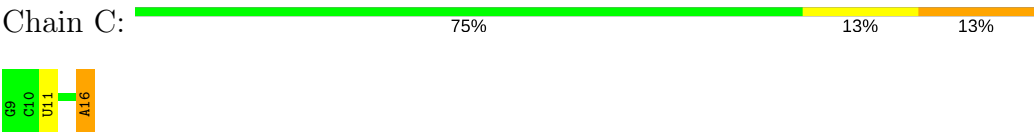
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	87	Total	O	0	0
			87	87		
4	B	1	Total	O	0	0
			1	1		
4	C	4	Total	O	0	0
			4	4		

ASP	ALA	LYS	THR
ASN	PHE	CYS	LYS
ILE	THR	PHE	LYS
ASN	PHE	MET	LEU
GLY	SER	GLY	LYS
LEU	ASN	PRO	GLY
GLU	GLY	ILE	GLY
PHE	PHE	THR	GLY
LEU	ILE	ARG	ARG
SER	SER	ILE	ASN
ASP	PRO	ILE	ASN
ASP	GLU	TRP	ILE
PRO	ASN	VAL	GLU
MET	LEU	VAL	ASN
ASN	GLY	MET	THR
ASN	CYS	PHE	THR
THR	LEU	ARG	ILE
THR	GLU	GLY	ASN
GLY	GLY	PHE	ILE
GLU	ALA	ILE	THR
ALA	VAL	ASN	PRO
ILE	VAL	SER	GLY
ILE	SER	LEU	THR
HIS	LEU	PRO	GLY
SER	ILE	GLY	THR
THR	LYS	THR	ASN
PRO	LEU	ASP	THR
ILE	LEU	LYS	ILE
ILE	LYS	ILE	LYS
PHE	THR	THR	ASN
ASN	ASN	PRO	THR
ILE	ILE	TRP	TRP
TYR	TYR	ASN	ASN
LYS	LYS	VAL	PHE
ARG	VAL	THR	LYS
GLY	ILE	GLY	LYS
GLU	ASP	ASN	CYS
ARG	LYS	PHE	ILE
HIS	CYS	LYS	ALA
THR	ILE	LYS	LEU
THR	HIS	LYS	ILE
TYR	TYR	CYS	ILE
ARG	ARG	ILE	ALA
ASN	ASN	LEU	ALA
ALA	ALA	ILE	LYS
LYS	LYS	ILE	ASN
LEU	ASN	SER	GLY
LEU	MET	LYS	MET
ILE	ASP	PHE	ASP
GLU	HIS	GLU	HIS
GLU	ARG	THR	MET
ARG	GLN	THR	GLU
LYS	HIS	ARG	TYR
THR	SER	ASP	HIS
LYS	PHE	PHE	SER
ILE	ASP	SER	PHE
PHE	GLU	GLU	ASP
GLU	VAL	PHE	GLU
GLU	PRO	PHE	VAL

● Molecule 2: RNA



● Molecule 3: RNA



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	102.00Å 140.70Å 162.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.66 – 2.57 48.66 – 2.57	Depositor EDS
% Data completeness (in resolution range)	95.3 (48.66-2.57) 94.7 (48.66-2.57)	Depositor EDS
R_{merge}	0.01	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 2.58Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.204 , 0.252 0.209 , 0.258	Depositor DCC
R_{free} test set	3533 reflections (4.97%)	DCC
Wilson B-factor (Å ²)	54.5	Xtriage
Anisotropy	0.568	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14163	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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	0.23	0/13841	0.36	0/18649
2	B	0.19	0/372	0.71	0/577
3	C	0.18	0/185	0.69	0/286
All	All	0.23	0/14398	0.38	0/19512

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	13571	0	13652	27	0
2	B	334	0	172	1	0
3	C	166	0	89	2	0
4	A	87	0	0	10	0
4	B	1	0	0	0	0
4	C	4	0	0	2	0
All	All	14163	0	13913	30	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 1.

All (30) 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:A:334:ILE:O	4:A:3025:HOH:O	1.81	0.96
1:A:501:GLU:OE1	4:A:3037:HOH:O	1.82	0.95
1:A:741:TYR:OH	4:A:3046:HOH:O	2.05	0.73
4:A:3080:HOH:O	2:B:12:C:OP1	2.07	0.73
1:A:917:GLU:OE2	4:A:3054:HOH:O	2.10	0.68
3:C:16:A:O3'	4:C:3004:HOH:O	2.11	0.68
3:C:11:U:OP1	4:C:3001:HOH:O	2.13	0.67
1:A:992:GLU:OE1	4:A:3066:HOH:O	2.13	0.65
1:A:1614:ARG:NH1	1:A:1702:THR:OG1	2.36	0.59
1:A:932:GLN:OE1	4:A:3057:HOH:O	2.18	0.54
1:A:20:CYS:SG	1:A:181:LYS:NZ	2.80	0.54
1:A:214:MET:HE3	1:A:1075:TRP:HE1	1.70	0.54
1:A:457:MET:HE3	1:A:681:LEU:HD12	1.90	0.53
1:A:776:GLU:OE2	1:A:780:ASN:ND2	2.43	0.52
1:A:736:VAL:HG22	1:A:740:GLU:HB2	1.93	0.50
1:A:1490:ASN:OD1	4:A:3082:HOH:O	2.20	0.47
1:A:917:GLU:OE1	4:A:3053:HOH:O	2.21	0.46
1:A:1374:VAL:HG22	1:A:1592:ILE:HD12	1.97	0.46
1:A:1068:ASP:OD1	1:A:1069:VAL:N	2.48	0.45
1:A:64:PRO:O	4:A:3004:HOH:O	2.21	0.45
1:A:195:LYS:HG3	1:A:196:THR:HG23	1.99	0.44
1:A:515:MET:HE3	1:A:518:ILE:HB	1.99	0.44
1:A:178:PHE:CZ	1:A:182:VAL:HG21	2.54	0.43
1:A:817:LEU:HD13	1:A:984:LEU:HD11	2.02	0.42
1:A:1507:PHE:CZ	1:A:1511:ILE:HD11	2.55	0.42
1:A:229:ASN:O	1:A:229:ASN:OD1	2.39	0.41
1:A:1740:TYR:CD2	1:A:1744:ILE:HD11	2.56	0.40
1:A:63:ARG:HB3	1:A:66:VAL:HG23	2.03	0.40
1:A:966:GLU:OE1	1:A:966:GLU:N	2.45	0.40
1:A:1673:GLU:O	1:A:1677:GLY:N	2.52	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	1629/2264 (72%)	1567 (96%)	60 (4%)	2 (0%)	55 78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	707	ARG
1	A	1234	CYS

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	1535/2087 (74%)	1515 (99%)	20 (1%)	73 89

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	92	ASP
1	A	93	TYR
1	A	250	ASP
1	A	339	THR
1	A	379	MET
1	A	446	ASP
1	A	556	THR
1	A	597	ASP
1	A	602	GLN
1	A	666	VAL
1	A	732	PHE
1	A	820	ARG
1	A	843	CYS
1	A	987	ASP
1	A	1062	SER
1	A	1138	LEU
1	A	1313	GLN
1	A	1392	ASN
1	A	1554	ARG

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Mol	Chain	Res	Type
1	A	1606	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	15/16 (93%)	3 (20%)	0
3	C	7/8 (87%)	1 (14%)	0
All	All	22/24 (91%)	4 (18%)	0

All (4) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	9	A
2	B	10	C
2	B	14	A
3	C	16	A

There are no RNA pucker outliers to report.

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

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, 95th 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 ²)	Q<0.9
1	A	1657/2264 (73%)	0.31	71 (4%) 36 30	36, 62, 111, 145	0
2	B	16/16 (100%)	-0.62	0 100 100	49, 57, 62, 66	0
3	C	8/8 (100%)	-0.94	0 100 100	55, 62, 72, 73	0
All	All	1681/2288 (73%)	0.29	71 (4%) 37 31	36, 62, 111, 145	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1039	LEU	6.6
1	A	1745	LEU	6.4
1	A	1436	GLY	5.8
1	A	1042	ILE	5.6
1	A	1544	LEU	5.5
1	A	714	TYR	5.3
1	A	1743	GLN	4.7
1	A	1432	PHE	4.4
1	A	1643	THR	4.3
1	A	1655	PHE	4.3
1	A	872	ARG	4.3
1	A	708	ASP	4.0
1	A	184	HIS	4.0
1	A	1654	GLU	3.9
1	A	1625	LEU	3.8
1	A	1545	GLY	3.8
1	A	719	LYS	3.7
1	A	1650	VAL	3.7
1	A	183	ALA	3.6
1	A	1367	VAL	3.4
1	A	1635	PRO	3.4
1	A	1651	HIS	3.4
1	A	1699	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	707	ARG	3.3
1	A	866	VAL	3.3
1	A	1371	ARG	3.2
1	A	1040	GLY	3.1
1	A	1384	TRP	3.1
1	A	1649	LEU	3.0
1	A	1368	MET	3.0
1	A	1661	LEU	3.0
1	A	1653	LYS	2.9
1	A	1364	TYR	2.9
1	A	722	LYS	2.9
1	A	851	LYS	2.8
1	A	895	MET	2.8
1	A	1634	ASN	2.7
1	A	1657	GLU	2.7
1	A	1698	TYR	2.7
1	A	862	LYS	2.7
1	A	1621	HIS	2.6
1	A	1043	GLU	2.6
1	A	1044	LYS	2.6
1	A	1045	LEU	2.6
1	A	1741	LEU	2.6
1	A	1576	TYR	2.5
1	A	859	LYS	2.5
1	A	1375	VAL	2.5
1	A	1644	GLU	2.5
1	A	720	GLY	2.4
1	A	1406	ASP	2.4
1	A	425	LYS	2.4
1	A	1378	ILE	2.4
1	A	723	ASP	2.4
1	A	1637	ILE	2.4
1	A	761	HIS	2.3
1	A	1633	ASN	2.3
1	A	1659	THR	2.3
1	A	65	GLU	2.3
1	A	1565	LEU	2.3
1	A	855	LEU	2.2
1	A	1696	TYR	2.2
1	A	434	ASP	2.2
1	A	1744	ILE	2.2
1	A	873	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	19	ALA	2.1
1	A	869	ARG	2.1
1	A	1647	ARG	2.1
1	A	1528	TYR	2.1
1	A	1692	TYR	2.0
1	A	706	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 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.