

Full wwPDB X-ray Structure Validation Report (i)

Apr 8, 2024 – 01:00 PM EDT

PDB ID : 8G90

Title: LaM domain of human LARP1 in complex with Sp phosphorothicate isomer

of AAAAA(SRA) RNA

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Deposited on : 2023-02-20

Resolution : 1.20 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.orgA 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:

 $Mol Probity \quad : \quad 4.02b\text{--}467$

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.36.1

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)

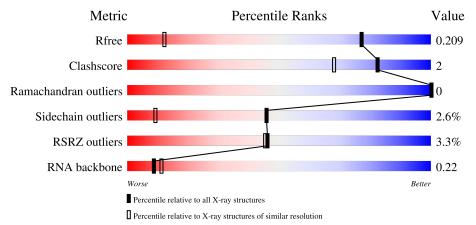
Validation Pipeline (wwPDB-VP) : 2.36.1

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 1.20 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	Similar resolution		
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$		
R_{free}	130704	1223 (1.22-1.18)		
Clashscore	141614	1286 (1.22-1.18)		
Ramachandran outliers	138981	1240 (1.22-1.18)		
Sidechain outliers	138945	1239 (1.22-1.18)		
RSRZ outliers	127900	1200 (1.22-1.18)		
RNA backbone	3102	1000 (2.34-0.62)		

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	99	2%	82%		6% • 11%	
2	В	6	17%	50%	17%	33%	



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 927 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 Isoform 2 of La-related protein 1.

\mathbf{Mol}	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	88	Total 737	C 481	N 126	O 129	S 1	0	2	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference	
A	312	MET	-	initiating methionine	UNP Q6PKG0-3	
A	313	GLY	-	expression tag	UNP Q6PKG0-3	
A	314	SER	-	expression tag	UNP Q6PKG0-3	
A	315	SER	-	expression tag	UNP Q6PKG0-3	
A	316	HIS	-	expression tag	UNP Q6PKG0-3	
A	317	HIS	-	expression tag	UNP Q6PKG0-3	
A	318	HIS	-	expression tag	UNP Q6PKG0-3	
A	319	HIS	-	expression tag	UNP Q6PKG0-3	
A	320	HIS	-	expression tag	UNP Q6PKG0-3	
A	321	HIS	-	expression tag	UNP Q6PKG0-3	
A	322	SER	-	expression tag	UNP Q6PKG0-3	

• Molecule 2 is a RNA chain called RNA (5'-R(*AP*AP*AP*AP*AP*(SRA))-3').

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace			
2	В	4	Total 75	C 35	N 15	O 21	P 3	S 1	0	0	0

• Molecule 3 is water.

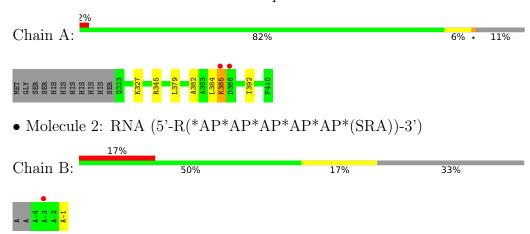
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	106	Total O 106 106	0	0
3	В	9	Total O 9 9	0	0



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: Isoform 2 of La-related protein 1





4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 21 21 21	Depositor	
Cell constants	36.95Å 46.65Å 59.28Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	26.02 - 1.20	Depositor	
rtesolution (A)	26.02 - 1.20	EDS	
% Data completeness	94.9 (26.02-1.20)	Depositor	
(in resolution range)	94.9 (26.02-1.20)	EDS	
R_{merge}	(Not available)	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	2.50 (at 1.20Å)	Xtriage	
Refinement program	PHENIX 1.19_4092	Depositor	
D D.	0.192 , 0.210	Depositor	
R, R_{free}	0.191 , 0.209	DCC	
R_{free} test set	1550 reflections (5.00%)	wwPDB-VP	
Wilson B-factor (Å ²)	12.5	Xtriage	
Anisotropy	0.219	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.38, 47.3	EDS	
L-test for twinning ²	$ < L >=0.50, < L^2>=0.33$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
F_o, F_c correlation	0.96	EDS	
Total number of atoms	927	wwPDB-VP	
Average B, all atoms (Å ²)	19.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.97% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

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

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		
MIOI		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.28	0/756	0.61	0/1020	
2	В	0.24	0/59	0.68	0/90	
All	All	0.28	0/815	0.62	0/1110	

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	737	0	745	4	0
2	В	75	0	39	0	0
3	A	106	0	0	0	0
3	В	9	0	0	0	0
All	All	927	0	784	4	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 (4) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	$egin{array}{ll} ext{Interatomic} \ ext{distance} & (ext{Å}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$	
1:A:327[A]:LYS:HG3	1:A:379:LEU:HD11	1.81	0.61	
1:A:384:LEU:HB2	1:A:392:ILE:HD11	1.88	0.54	
1:A:382:ALA:O	1:A:385:LYS:HG3	2.08	0.52	
1:A:327[A]:LYS:HG3	1:A:379:LEU:CD1	2.45	0.47	

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	88/99 (89%)	86 (98%)	2 (2%)	0	100 100	П

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	78/92 (85%)	76 (97%)	2 (3%)	46 9

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	345	ARG
1	A	385	LYS



Sometimes 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	В	2/6 (33%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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

1 non-standard protein/DNA/RNA residue is 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	Dec	Link	B	ond leng	gths	В	ond ang	les
MIOI	туре	Chain	Res	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SRA	В	-1	2	18,24,25	4.04	10 (55%)	18,35,38	2.81	6 (33%)

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	\mathbf{Rings}
2	SRA	В	-1	2	-	0/3/25/26	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(A)
2	В	-1	SRA	C2'-C3'	-9.85	1.26	1.53
2	В	-1	SRA	O4'-C1'	6.97	1.50	1.41
2	В	-1	SRA	O4'-C4'	-6.77	1.29	1.45
2	В	-1	SRA	C2'-C1'	5.26	1.61	1.53

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Mol	Chain	Res	Type	Atoms	${f Z}$	$\operatorname{Observed}(\text{\AA})$	$Ideal(\AA)$
2	В	-1	SRA	C3'-C4'	5.03	1.65	1.53
2	В	-1	SRA	C6-N6	3.44	1.46	1.34
2	В	-1	SRA	O2'-C2'	3.32	1.50	1.43
2	В	-1	SRA	C2-N3	2.65	1.36	1.32
2	В	-1	SRA	C5-C4	-2.41	1.34	1.40
2	В	-1	SRA	O3'-C3'	2.29	1.48	1.43

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
2	В	-1	SRA	C5-C6-N6	7.00	130.98	120.35
2	В	-1	SRA	N3-C2-N1	-5.14	120.65	128.68
2	В	-1	SRA	N6-C6-N1	-4.49	109.26	118.57
2	В	-1	SRA	C3'-C2'-C1'	4.26	107.39	100.98
2	В	-1	SRA	O4'-C1'-C2'	-3.10	102.40	106.93
2	В	-1	SRA	C1'-N9-C4	-2.86	121.61	126.64

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 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	<RSRZ $>$	# RSRZ > 2	$OWAB(A^2)$	Q < 0.9
1	A	88/99 (88%)	0.74	2 (2%) 60 59	10, 15, 31, 35	0
2	В	3/6 (50%)	3.68	1 (33%) 0 1	21, 21, 27, 71	0
All	All	91/105 (86%)	0.84	3 (3%) 46 45	10, 15, 31, 71	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	В	-3	A	9.2
1	A	386	ASP	2.7
1	A	385	LYS	2.0

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

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. The B-factors column lists the minimum, median, 95^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
2	SRA	В	-1	22/23	0.94	0.11	13,17,20,26	0

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.

