

Full wwPDB NMR Structure Validation Report (i)

May 29, 2020 - 10:25 am BST

PDB ID	:	1LIR
Title	:	LQ2 FROM LEIURUS QUINQUESTRIATUS, NMR, 22 STRUCTURES
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Deposited on	:	1998-04-02

This is a Full wwPDB NMR 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/NMRValidationReportHelp with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

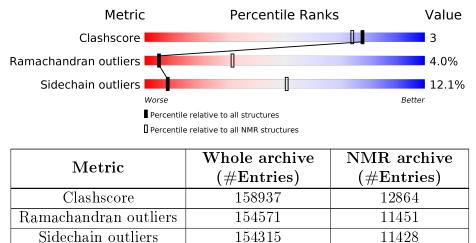
Cyrange	:	Kirchner and Güntert (2011)
$\operatorname{NmrClust}$:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	$v_1n_11_5_13_A$ (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
${ m ShiftChecker}$:	2.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $SOLUTION \ NMR$

The overall completeness of chemical shifts assignment was not calculated.

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.



The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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%

Mol	Chain	Length	Quality of chain					
1	А	37	65%	14%	5%	16%		



2 Ensemble composition and analysis (i)

This entry contains 22 models. Model 10 is the overall representative, medoid model (most similar to other models).

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues								
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model					
1	A:5-A:35 (31)	0.16	10					

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 2 clusters and 1 single-model cluster was found.

Cluster number	Models
1	$ \begin{array}{c} 1, \ 2, \ 3, \ 4, \ 5, \ 7, \ 8, \ 10, \ 11, \ 12, \ 13, \ 14, \ 15, \ 16, \ 17, \ 18, \\ 19, \ 22 \end{array} $
2	9, 20, 21
Single-model clusters	6



3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 580 atoms, of which 282 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called LQ2.

Mol	Chain	Residues	Atoms					Trace	
1	Λ	27	Total	С	Η	Ν	Ο	S	0
1 A	57	580	177	282	59	55	7	0	



4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

• Molecule 1: LQ2

Chain A:	65%	14% 5%	16%
	R25 R34 S37 S37 S37		

4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

 \bullet Molecule 1: LQ2



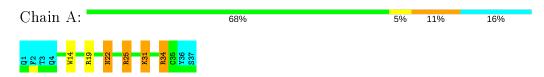
4.2.2 Score per residue for model 2





4.2.3 Score per residue for model 3

 \bullet Molecule 1: LQ2



4.2.4 Score per residue for model 4

 \bullet Molecule 1: LQ2

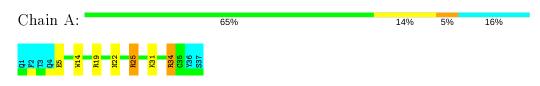
Chain A:			_	_										
Unam A:						62%			14%	;	5%	•	16%	
						_								
5 <mark>5 3 3 5</mark>	M14 R10	R25	K31 K32	C33 R34	C35 Y36	S 37								

4.2.5 Score per residue for model 5

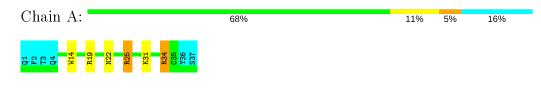
 \bullet Molecule 1: LQ2

Chain A:					57%	22	% 5%	16%
C13 C13 C13 C13 C13 C13 C13 C13 C13 C13	W14 R19	N22	R25 <mark>626</mark> K27	N30 K31	R34 C35 Y36 S37			

4.2.6 Score per residue for model 6



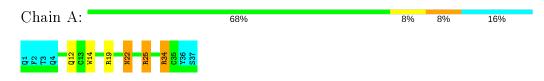
- 4.2.7 Score per residue for model 7
- \bullet Molecule 1: LQ2





4.2.8 Score per residue for model 8

 \bullet Molecule 1: LQ2



4.2.9 Score per residue for model 9

 \bullet Molecule 1: LQ2

Chain A:				54%	24%	5%	16%
Q1 73 74 012 012 012 013 014 014 014	K18 R19	N22 P26	R25 G26 K27	K31 K34 C35 Y36 S37			

4.2.10 Score per residue for model 10 (medoid)

 \bullet Molecule 1: LQ2

Chain A:	49%	30%	5%	16%
Q 1 F 2 C 7 C 7 C 7 C 7 C 7 C 7 C 7 C 7 C 7 C 7	414 K19 K19 K27 K27 K27 K27 K23 K23 K23 K23 K23 K23 K27 K27 K27 K27 K27 K27 K27 K27 K27 K27			

4.2.11 Score per residue for model 11

 \bullet Molecule 1: LQ2



4.2.12 Score per residue for model 12





4.2.13 Score per residue for model 13

 \bullet Molecule 1: LQ2



4.2.14 Score per residue for model 14

 \bullet Molecule 1: LQ2



4.2.15 Score per residue for model 15

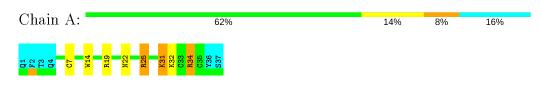
 \bullet Molecule 1: LQ2

Chain A:	57%	22%	••	16%
01 13 13 13 13 13 13 13 13 13 13 13 13 13	H14 H14 H21 H21 H21 H21 H21 H21 H21 H21 H21 H21			

4.2.16 Score per residue for model 16



- 4.2.17 Score per residue for model 17
- \bullet Molecule 1: LQ2





4.2.18 Score per residue for model 18

 \bullet Molecule 1: LQ2



4.2.19 Score per residue for model 19

 \bullet Molecule 1: LQ2



4.2.20 Score per residue for model 20

 \bullet Molecule 1: LQ2

Chain A:	62%	19%	•	16%
Q1 F2 Q4 B5 R19 R19	N22 825 837 837 837 837 837			

4.2.21 Score per residue for model 21

 \bullet Molecule 1: LQ2



4.2.22 Score per residue for model 22

Chain A:	57%	19%	8%	16%
다. 13 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	C33 R34 036 1736 S37			



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *distance geometry*.

Of the 22 calculated structures, 22 were deposited, based on the following criterion: LEAST RESTRAINT VIOLATION.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
DIANA	structure solution	
X-PLOR	structure solution	
X-PLOR	refinement	

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

COVALENT-GEOMETRY INFOmissingINFO

5.1 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 each 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 averaged over the ensemble.

Ν	Лоl	Chain	Non-H	H(model)	H(added)	Clashes
	1	А	244	238	238	1±1
1	All	All	5368	5236	5236	31

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 3.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Moo	dels
Atom-1	Atom-2	Clash(A)		Worst	Total
1:A:20:LEU:HB3	1:A:21:HIS:CD2	0.53	2.39	16	1
1:A:25:ARG:HD2	1:A:25:ARG:N	0.51	2.21	19	5
1:A:22:ASN:HD22	1:A:22:ASN:H	0.50	1.49	22	1
1:A:22:ASN:ND2	1:A:22:ASN:H	0.48	2.06	22	1
1:A:22:ASN:ND2	1:A:22:ASN:N	0.46	2.63	22	1
1:A:24:ASN:H	1:A:25:ARG:HE	0.46	1.54	10	1
1:A:22:ASN:N	1:A:22:ASN:ND2	0.45	2.64	4	1
1:A:24:ASN:H	1:A:25:ARG:CZ	0.45	2.25	2	1
1:A:7:CYS:SG	1:A:32:LYS:O	0.45	2.75	15	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Moo	dels
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:A:25:ARG:CD	1:A:25:ARG:N	0.45	2.79	19	2
1:A:17:CYS:SG	1:A:33:CYS:SG	0.44	3.16	14	2
1:A:13:CYS:SG	1:A:27:LYS:O	0.44	2.76	9	2
1:A:17:CYS:SG	1:A:26:GLY:HA3	0.44	2.53	1	1
1:A:25:ARG:N	1:A:25:ARG:HD2	0.42	2.29	7	3
1:A:26:GLY:C	1:A:27:LYS:HD3	0.40	2.37	1	1
1:A:34:ARG:HD3	1:A:35:CYS:N	0.40	2.31	10	1

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5.2 Torsion angles (i)

5.2.1 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 PDB entries followed by that with respect to all NMR entries. 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	P	erce	entiles
1	А	31/37~(84%)	26 ± 1 (82 $\pm3\%$)	$4\pm1~(14\pm3\%)$	1±0 (4±1%)		5	31
All	All	682/814 (84%)	561 (82%)	94 (14%)	27 (4%)		5	31

All 3 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	А	22	ASN	22
1	А	31	LYS	4
1	А	30	ASN	1

5.2.2 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 PDB entries followed by that with respect to all NMR entries. 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	P	erc	entiles
1	А	29/34~(85%)	$26 \pm 1 \ (88 \pm 4\%)$	$4\pm1~(12\pm4\%)$		8	51
All	All	638/748~(85%)	561 (88%)	77 (12%)		8	51



I	Mol	Chain	\mathbf{Res}	Type	Models (Total)
	1	А	31	LYS	16
	1	А	34	ARG	14
	1	А	25	ARG	13
	1	А	5	GLU	12
	1	А	22	ASN	8
	1	А	12	GLN	5
	1	А	27	LYS	5
	1	А	18	LYS	3
	1	А	20	LEU	1

All 9 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

5.2.3 RNA (i)

There are no RNA molecules in this entry.

5.3 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 for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds 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 is the number of standard deviations the observed value is removed from the expected value. A bond length with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Tuno	Chain	Dog	Link		Bond leng	gths
	туре	Chain	nes	Link	Counts	RMSZ	#Z>2
1	PCA	А	1	1	7,8,9	1.01 ± 0.04	$0\pm0~(0\pm0\%)$

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of 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 angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Tuno	Chain	Dog	Link	Bond angles		
	туре	Chain	nes	Link	Counts	RMSZ	#Z>2
1	PCA	А	1	1	$9,\!10,\!12$	$1.11 {\pm} 0.07$	$0{\pm}0~(0{\pm}0\%)$



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
1	PCA	А	1	1	-	$0\pm0,0,11,13$	$0{\pm}0{,}1{,}1{,}1$

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.4 Carbohydrates (i)

There are no carbohydrates in this entry.

5.5 Ligand geometry (i)

There are no ligands in this entry.

5.6 Other polymers (i)

There are no such molecules in this entry.

5.7 Polymer linkage issues (i)

There are no chain breaks in this entry.



6 Chemical shift validation (i)

No chemical shift data were provided

