



# wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 2LQW  
Title : Solution structure of phosphorylated CRKL  
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This is a wwPDB NMR 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/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

Cyrange : Kirchner and Güntert (2011)  
NmrClust : Kelley et al. (1996)  
MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : rb-20027457  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20027457

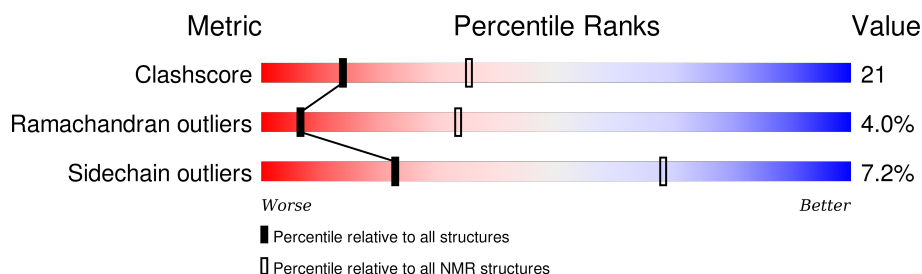
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 55%.

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)	NMR archive (#Entries)
Clashscore	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	303	<div> <div>42%</div> <div>26%</div> <div>•</div> <div>31%</div> </div>

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 10 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:4-A:104, A:125-A:180 (157)	0.46	10
2	A:238-A:247, A:254-A:295 (52)	0.50	1

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 4 clusters and 3 single-model clusters were found.

Cluster number	Models
1	9, 10, 11, 16, 17, 19, 20
2	1, 6, 8, 14
3	4, 13, 18
4	3, 7, 12
Single-model clusters	2; 5; 15

### 3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 4705 atoms, of which 2317 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Crk-like protein.

Mol	Chain	Residues	Atoms								Trace
1	A	303	Total	C	H	N	O	P	S		0
			4705	1504	2317	419	456	1	8		





## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 400 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CNS	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	2lqw_cs.str
Number of chemical shift lists	1
Total number of shifts	1949
Number of shifts mapped to atoms	1949
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	55%

No validations of the models with respect to experimental NMR restraints is performed at this time.

## 6 Model quality

### 6.1 Standard geometry

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

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 (average) 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	0.35±0.02	0±0/1745 (0.0±0.0%)	0.49±0.04	0±1/2366 (0.0±0.0%)
All	All	0.35	0/34900 (0.0%)	0.49	4/47320 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.8±1.1
All	All	0	16

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	57	ARG	N-CA-CB	-6.79	98.38	110.60	15	2
1	A	127	TYR	CB-CG-CD1	-5.65	117.61	121.00	9	1
1	A	68	ASN	N-CA-CB	5.09	119.76	110.60	15	1

There are no chirality outliers.

5 of 7 unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	169	ARG	Sidechain	10
1	A	68	ASN	Peptide	1
1	A	56	SER	Peptide	1

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	39	ARG	Sidechain	1
1	A	57	ARG	Sidechain	1

## 6.2 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 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.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1701	1681	1681	70±14
All	All	34020	33620	33620	1402

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 21.

5 of 693 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:142:LEU:HD11	1:A:165:ASN:HB2	1.09	1.24	13	14
1:A:242:ALA:HB1	1:A:259:GLU:HA	1.00	1.33	12	3
1:A:152:ILE:HD13	1:A:163:ALA:HB2	0.98	1.36	20	20
1:A:238:VAL:H	1:A:266:VAL:HG22	0.96	1.21	7	1
1:A:238:VAL:N	1:A:266:VAL:HG22	0.95	1.75	7	1

## 6.3 Torsion angles [i](#)

### 6.3.1 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 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	Percentiles	
1	A	209/303 (69%)	172±5 (82±2%)	29±5 (14±2%)	8±2 (4±1%)	6	33
All	All	4180/6060 (69%)	3431 (82%)	582 (14%)	167 (4%)	6	33

5 of 60 unique Ramachandran outliers are listed below. They are sorted by the frequency of

occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	126	GLU	15
1	A	55	ASN	9
1	A	74	GLY	9
1	A	9	SER	8
1	A	156	PRO	8

### 6.3.2 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 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	Percentiles
1	A	184/261 (70%)	171±3 (93±1%)	13±3 (7±1%)	23 68
All	All	3680/5220 (70%)	3416 (93%)	264 (7%)	23 68

5 of 90 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	146	LYS	19
1	A	172	MET	10
1	A	180	LYS	9
1	A	169	ARG	9
1	A	256	LEU	9

### 6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 6.4 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 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	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
1	PTR	A	207	1	13,16,17	0.51±0.02	0±0 (0±0%)

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	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
1	PTR	A	207	1	19,22,24	0.73±0.01	0±0 (0±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	PTR	A	207	1	-	0±0,9,11,13	0±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.

## 6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 6.7 Other polymers [i](#)

There are no such molecules in this entry.

## 6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 7 Chemical shift validation [i](#)

The completeness of assignment taking into account all chemical shift lists is 55% for the well-defined parts and 51% for the entire structure.

### 7.1 Chemical shift list 1

File name: 2lqw\_cs.str

Chemical shift list name: *assigned\_chem\_shift\_list\_1*

#### 7.1.1 Bookkeeping [i](#)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1949
Number of shifts mapped to atoms	1949
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	15

#### 7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	271	$0.12 \pm 0.09$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	245	$0.20 \pm 0.09$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	0	—	—
$^{15}\text{N}$	235	$0.18 \pm 0.27$	None needed ( $< 0.5$ ppm)

#### 7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 55%, i.e. 1484 atoms were assigned a chemical shift out of a possible 2688. 0 out of 33 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	709/1021 (69%)	328/406 (81%)	199/418 (48%)	182/197 (92%)
Sidechain	759/1421 (53%)	427/837 (51%)	332/508 (65%)	0/76 (0%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	16/246 (7%)	16/131 (12%)	0/106 (0%)	0/9 (0%)
Overall	1484/2688 (55%)	771/1374 (56%)	531/1032 (51%)	182/282 (65%)

#### 7.1.4 Statistically unusual chemical shifts ⓘ

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	1	MET	HE2	10.20	4.28 – -0.52	17.3
1	A	1	MET	HE1	10.20	4.28 – -0.52	17.3
1	A	1	MET	HE3	10.20	4.28 – -0.52	17.3
1	A	231	PRO	CD	42.81	55.31 – 45.41	-7.6
1	A	206	ALA	CA	40.20	63.07 – 43.27	-6.6
1	A	101	PRO	CA	53.31	71.13 – 55.53	-6.4
1	A	201	PRO	CA	53.89	71.13 – 55.53	-6.0
1	A	269	MET	HG3	0.14	4.30 – 0.50	-5.9
1	A	85	LEU	HD23	-0.74	2.14 – -0.66	-5.3
1	A	85	LEU	HD22	-0.74	2.14 – -0.66	-5.3
1	A	85	LEU	HD21	-0.74	2.14 – -0.66	-5.3
1	A	84	LEU	HA	1.92	6.66 – 1.96	-5.1
1	A	93	LEU	HD21	-0.67	2.14 – -0.66	-5.0
1	A	93	LEU	HD22	-0.67	2.14 – -0.66	-5.0
1	A	93	LEU	HD23	-0.67	2.14 – -0.66	-5.0

#### 7.1.5 Random Coil Index (RCI) plots ⓘ

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:

