



# Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 07:54 PM GMT

PDB ID : 4L6U  
Title : Crystal structure of AF1868: Cmr1 subunit of the Cmr RNA silencing complex  
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Deposited on : 2013-06-12  
Resolution : 2.50 Å(reported)

This is a full wwPDB validation 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/ValidationPDFNotes.html>

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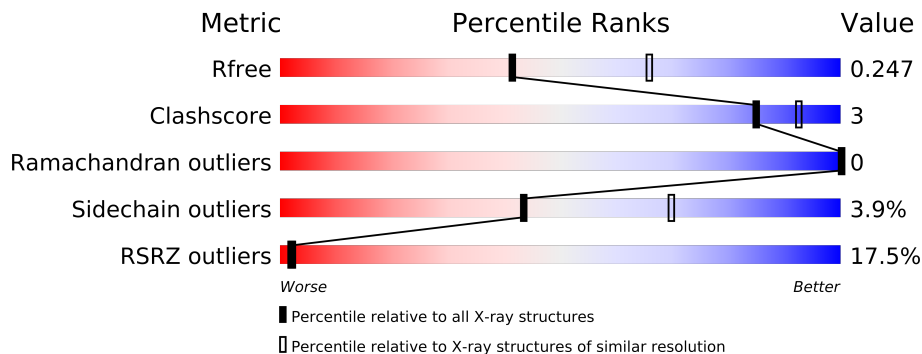
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.50 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))
$R_{free}$	66092	2784 (2.50-2.50)
Clashscore	79885	3562 (2.50-2.50)
Ramachandran outliers	78287	3480 (2.50-2.50)
Sidechain outliers	78261	3482 (2.50-2.50)
RSRZ outliers	66119	2785 (2.50-2.50)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	329	
1	B	329	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4638 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Putative uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	299	Total	C	N	O	S	0	0	0
			2369	1533	397	428	11			
1	B	288	Total	C	N	O	S	0	0	0
			2264	1464	374	414	12			

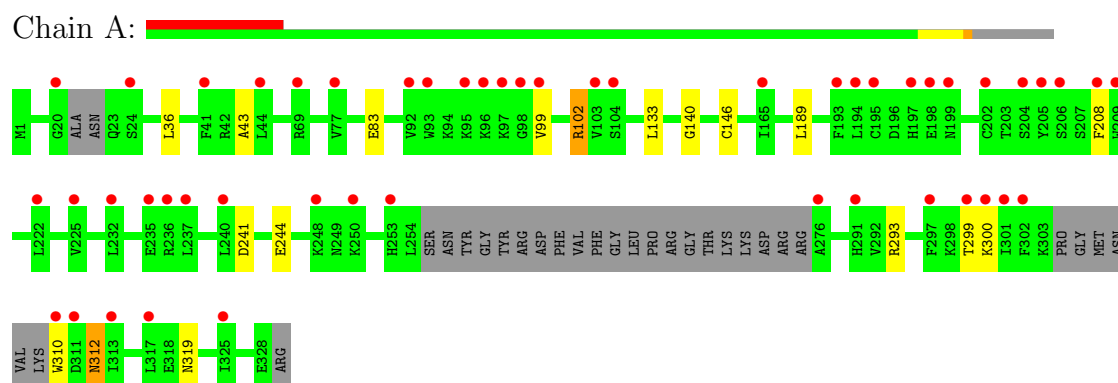
- Molecule 2 is water.

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

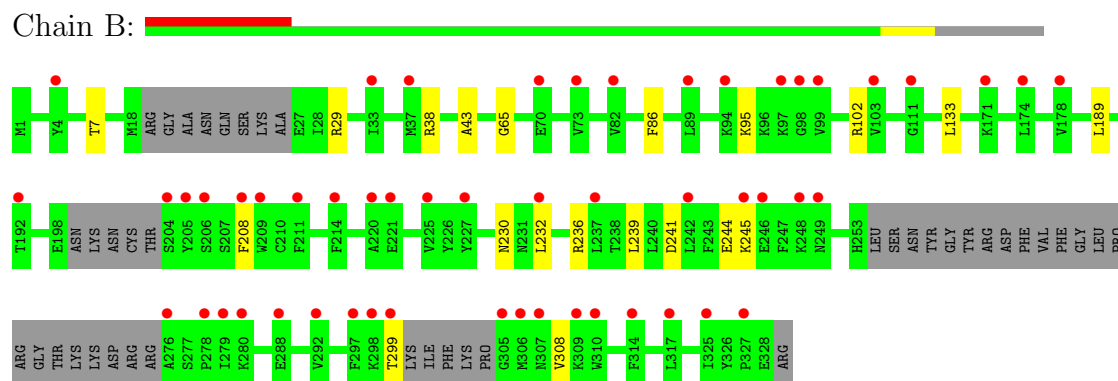
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Putative uncharacterized protein



#### • Molecule 1: Putative uncharacterized protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.69Å 64.16Å 79.28Å 90.00° 93.79° 90.00°	Depositor
Resolution (Å)	79.10 – 2.50 79.10 – 2.50	Depositor EDS
% Data completeness (in resolution range)	96.4 (79.10-2.50) 81.4 (79.10-2.50)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.41 (at 2.51Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, $R_{free}$	0.230 , 0.253 0.233 , 0.247	Depositor DCC
$R_{free}$ test set	1317 reflections (5.40%)	DCC
Wilson B-factor (Å <sup>2</sup> )	65.5	Xtriage
Anisotropy	0.479	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 88.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 24295 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	4638	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	109.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.50% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

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	0/2416	0.38	0/3253
1	B	0.24	0/2308	0.42	0/3114
All	All	0.23	0/4724	0.40	0/6367

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Close contacts

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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2369	0	0	6	0
1	B	2264	0	0	7	0
2	A	4	0	0	0	0
2	B	1	0	0	0	0
All	All	4638	0	0	13	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 3.

All (13) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:232:LEU:O	1:B:245:LYS:NZ	2.18	0.76

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:102:ARG:NH2	1:B:244:GLU:OE2	2.25	0.69
1:A:140:GLY:O	1:A:293:ARG:NH2	2.31	0.63
1:B:102:ARG:NH1	1:B:241:ASP:OD1	2.36	0.58
1:B:38:ARG:NH2	1:B:65:GLY:O	2.38	0.57
1:A:299:THR:OG1	1:A:300:LYS:N	2.39	0.56
1:A:312:ASN:OD1	1:A:312:ASN:N	2.39	0.55
1:A:102:ARG:NH1	1:A:241:ASP:OD1	2.43	0.51
1:B:299:THR:O	1:B:299:THR:OG1	2.31	0.48
1:B:43:ALA:O	1:B:208:PHE:N	2.50	0.44
1:B:230:ASN:OD1	1:B:230:ASN:N	2.49	0.44
1:A:43:ALA:O	1:A:208:PHE:N	2.52	0.42
1:A:102:ARG:NH2	1:A:244:GLU:OE2	2.54	0.41

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	289/329 (88%)	277 (96%)	12 (4%)	0	100	100
1	B	278/329 (84%)	265 (95%)	13 (5%)	0	100	100
All	All	567/658 (86%)	542 (96%)	25 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	251/292 (86%)	241 (96%)	10 (4%)	42	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	239/292 (82%)	230 (96%)	9 (4%)	44	71
All	All	490/584 (84%)	471 (96%)	19 (4%)	43	70

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	LEU
1	A	83	GLU
1	A	99	VAL
1	A	102	ARG
1	A	133	LEU
1	A	146	CYS
1	A	189	LEU
1	A	310	TRP
1	A	312	ASN
1	A	319	ASN
1	B	7	THR
1	B	29	ARG
1	B	86	PHE
1	B	95	LYS
1	B	133	LEU
1	B	189	LEU
1	B	236	ARG
1	B	239	LEU
1	B	308	VAL

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

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 5.7 Other polymers ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	299/329 (90%)	1.36	50 (16%) 2 2	59, 99, 180, 235	0
1	B	288/329 (87%)	1.34	53 (18%) 2 2	57, 100, 182, 230	0
All	All	587/658 (89%)	1.35	103 (17%) 2 2	57, 99, 182, 235	0

All (103) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	98	GLY	15.5
1	B	204	SER	11.8
1	B	305	GLY	11.5
1	A	301	ILE	11.4
1	A	205	TYR	10.8
1	A	194	LEU	10.1
1	A	302	PHE	8.1
1	A	208	PHE	7.7
1	A	195	CYS	7.6
1	B	306	MET	7.3
1	A	310	TRP	7.1
1	B	307	ASN	7.0
1	B	276	ALA	6.8
1	B	310	TRP	6.7
1	B	97	LYS	5.7
1	B	205	TYR	5.7
1	A	97	LYS	5.7
1	A	96	LYS	5.5
1	B	208	PHE	5.4
1	B	192	THR	5.3
1	B	248	LYS	5.3
1	B	299	THR	5.0
1	A	202	CYS	5.0
1	B	245	LYS	5.0

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Mol	Chain	Res	Type	RSRZ
1	A	299	THR	4.9
1	A	325	ILE	4.9
1	B	209	TRP	4.5
1	A	103	VAL	4.3
1	A	276	ALA	4.2
1	A	69	ARG	4.1
1	A	317	LEU	4.1
1	B	242	LEU	4.0
1	A	253	HIS	4.0
1	B	249	ASN	4.0
1	A	209	TRP	4.0
1	B	298	LYS	4.0
1	A	235	GLU	4.0
1	B	237	LEU	3.9
1	A	225	VAL	3.9
1	A	206	SER	3.9
1	B	325	ILE	3.9
1	B	227	TYR	3.9
1	A	291	HIS	3.8
1	B	309	LYS	3.7
1	A	240	LEU	3.7
1	A	300	LYS	3.6
1	B	278	PRO	3.6
1	A	198	GLU	3.6
1	A	99	VAL	3.5
1	A	193	PHE	3.5
1	A	92	VAL	3.5
1	B	174	LEU	3.5
1	B	171	LYS	3.4
1	A	24	SER	3.4
1	B	280	LYS	3.3
1	B	279	ILE	3.3
1	A	197	HIS	3.3
1	A	311	ASP	3.2
1	A	236	ARG	3.1
1	A	165	ILE	3.1
1	B	178	VAL	3.0
1	B	4	TYR	3.0
1	B	327	PRO	2.9
1	A	44	LEU	2.8
1	B	314	PHE	2.8
1	B	103	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	89	LEU	2.7
1	A	313	ILE	2.7
1	B	33	ILE	2.6
1	B	206	SER	2.6
1	A	248	LYS	2.5
1	A	104	SER	2.5
1	B	82	VAL	2.5
1	B	98	GLY	2.5
1	B	232	LEU	2.5
1	B	214	PHE	2.4
1	B	220	ALA	2.4
1	B	221	GLU	2.4
1	B	246	GLU	2.4
1	A	77	VAL	2.4
1	B	111	GLY	2.4
1	A	41	PHE	2.4
1	A	222	LEU	2.4
1	B	317	LEU	2.3
1	A	93	TRP	2.3
1	B	37	MET	2.3
1	A	237	LEU	2.2
1	B	225	VAL	2.2
1	A	250	LYS	2.2
1	A	20	GLY	2.2
1	B	297	PHE	2.2
1	B	288	GLU	2.1
1	B	211	PHE	2.1
1	A	204	SER	2.1
1	B	73	VAL	2.1
1	B	99	VAL	2.1
1	B	292	VAL	2.1
1	A	297	PHE	2.1
1	B	70	GLU	2.1
1	A	95	LYS	2.1
1	B	94	LYS	2.1
1	A	199	ASN	2.0
1	A	232	LEU	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

There are no ligands in this entry.

### 6.5 Other polymers ⓘ

There are no such residues in this entry.