



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 5IWW  
Title : Crystal structure of RNA editing factor of designer PLS-type PPR/9R protein in complex with MORF9/RIP9  
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Deposited on : unknown  
Resolution : 2.65 Å(reported)

This is a wwPDB X-ray 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/XrayValidationReportHelp>

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:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
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)	:	rb-20030345

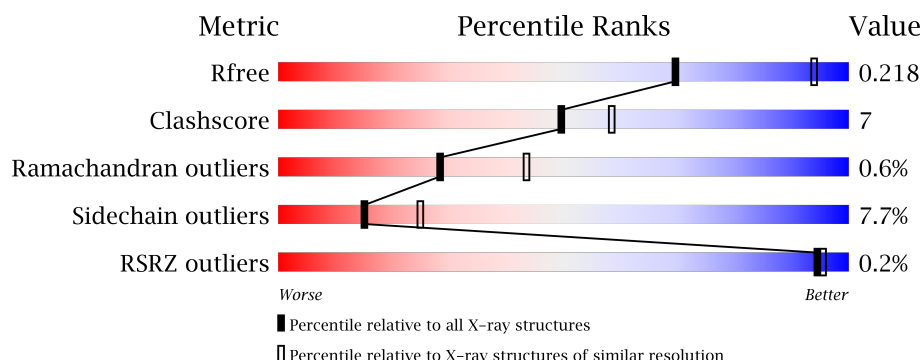
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*



The reported resolution of this entry is 2.65 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	3491 (2.70-2.62)
Clashscore	112137	1026 (2.68-2.64)
Ramachandran outliers	110173	1010 (2.68-2.64)
Sidechain outliers	110143	1010 (2.68-2.64)
RSRZ outliers	101464	3511 (2.70-2.62)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	133	
1	B	133	
1	C	133	
2	D	347	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4987 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 Multiple organellar RNA editing factor 9, chloroplastic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	110	Total	C	N	O	S	0	0	0
			871	559	132	174	6			
1	B	110	Total	C	N	O	S	0	0	0
			871	559	132	174	6			
1	C	108	Total	C	N	O	S	0	0	0
			857	551	130	170	6			

There are 39 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	74	MET	-	initiating methionine	UNP Q9LPZ1
A	85	SER	CYS	engineered mutation	UNP Q9LPZ1
A	187	SER	CYS	engineered mutation	UNP Q9LPZ1
A	197	LEU	-	expression tag	UNP Q9LPZ1
A	198	GLU	-	expression tag	UNP Q9LPZ1
A	199	HIS	-	expression tag	UNP Q9LPZ1
A	200	HIS	-	expression tag	UNP Q9LPZ1
A	201	HIS	-	expression tag	UNP Q9LPZ1
A	202	HIS	-	expression tag	UNP Q9LPZ1
A	203	HIS	-	expression tag	UNP Q9LPZ1
A	204	HIS	-	expression tag	UNP Q9LPZ1
A	205	HIS	-	expression tag	UNP Q9LPZ1
A	206	HIS	-	expression tag	UNP Q9LPZ1
B	74	MET	-	initiating methionine	UNP Q9LPZ1
B	85	SER	CYS	engineered mutation	UNP Q9LPZ1
B	187	SER	CYS	engineered mutation	UNP Q9LPZ1
B	197	LEU	-	expression tag	UNP Q9LPZ1
B	198	GLU	-	expression tag	UNP Q9LPZ1
B	199	HIS	-	expression tag	UNP Q9LPZ1
B	200	HIS	-	expression tag	UNP Q9LPZ1
B	201	HIS	-	expression tag	UNP Q9LPZ1
B	202	HIS	-	expression tag	UNP Q9LPZ1
B	203	HIS	-	expression tag	UNP Q9LPZ1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	204	HIS	-	expression tag	UNP Q9LPZ1
B	205	HIS	-	expression tag	UNP Q9LPZ1
B	206	HIS	-	expression tag	UNP Q9LPZ1
C	74	MET	-	initiating methionine	UNP Q9LPZ1
C	85	SER	CYS	engineered mutation	UNP Q9LPZ1
C	187	SER	CYS	engineered mutation	UNP Q9LPZ1
C	197	LEU	-	expression tag	UNP Q9LPZ1
C	198	GLU	-	expression tag	UNP Q9LPZ1
C	199	HIS	-	expression tag	UNP Q9LPZ1
C	200	HIS	-	expression tag	UNP Q9LPZ1
C	201	HIS	-	expression tag	UNP Q9LPZ1
C	202	HIS	-	expression tag	UNP Q9LPZ1
C	203	HIS	-	expression tag	UNP Q9LPZ1
C	204	HIS	-	expression tag	UNP Q9LPZ1
C	205	HIS	-	expression tag	UNP Q9LPZ1
C	206	HIS	-	expression tag	UNP Q9LPZ1

- Molecule 2 is a protein called PLS9-PPR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	300	Total 2332	C 1501	N 368	O 446	S 17	0	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	18	Total 18	O 18	0	0
3	B	9	Total 9	O 9	0	0
3	C	8	Total 8	O 8	0	0
3	D	21	Total 21	O 21	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 64	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	103.19Å 103.19Å 149.15Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	51.59 – 2.65 76.66 – 2.65	Depositor EDS
% Data completeness (in resolution range)	98.3 (51.59-2.65) 95.4 (76.66-2.65)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.03 (at 2.65Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, $R_{free}$	0.180 , 0.221 0.176 , 0.218	Depositor DCC
$R_{free}$ test set	1211 reflections (4.86%)	DCC
Wilson B-factor (Å <sup>2</sup> )	54.4	Xtriage
Anisotropy	0.326	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 39.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.055 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4987	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.19% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical 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	0.39	0/893	0.57	0/1214
1	B	0.39	0/893	0.58	0/1214
1	C	0.43	0/879	0.58	0/1194
2	D	0.43	0/2367	0.59	0/3178
All	All	0.42	0/5032	0.58	0/6800

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	871	0	842	7	0
1	B	871	0	842	9	0
1	C	857	0	828	11	0
2	D	2332	0	2379	43	0
3	A	18	0	0	2	0
3	B	9	0	0	2	0
3	C	8	0	0	0	0
3	D	21	0	0	1	0
All	All	4987	0	4891	66	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 7.

The worst 5 of 66 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:188:THR:O	3:A:301:HOH:O	1.83	0.97
1:B:85:SER:HA	3:B:301:HOH:O	1.62	0.96
2:D:265:ALA:HB2	2:D:298:MET:HA	1.49	0.92
1:B:164:ASP:O	3:B:301:HOH:O	2.01	0.79
1:C:171:ASN:ND2	1:C:171:ASN:O	2.26	0.67

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	108/133 (81%)	106 (98%)	2 (2%)	0	100	100
1	B	108/133 (81%)	104 (96%)	4 (4%)	0	100	100
1	C	106/133 (80%)	100 (94%)	5 (5%)	1 (1%)	20	31
2	D	298/347 (86%)	286 (96%)	9 (3%)	3 (1%)	18	28
All	All	620/746 (83%)	596 (96%)	20 (3%)	4 (1%)	28	43

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	181	ASN
2	D	304	LEU
2	D	313	ASP
2	D	292	TYR



### 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	98/121 (81%)	91 (93%)	7 (7%)	17	27
1	B	98/121 (81%)	91 (93%)	7 (7%)	17	27
1	C	96/121 (79%)	88 (92%)	8 (8%)	13	20
2	D	254/297 (86%)	234 (92%)	20 (8%)	14	23
All	All	546/660 (83%)	504 (92%)	42 (8%)	15	25

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	171	ASN
2	D	32	LYS
2	D	283	SER
1	C	173	ASP
1	C	181	ASN

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

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 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 [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<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	110/133 (82%)	-0.11	0 <span>100</span> <span>100</span>	41, 51, 76, 100	0
1	B	110/133 (82%)	-0.08	1 (0%) <span>84</span> <span>84</span>	45, 57, 94, 115	0
1	C	108/133 (81%)	-0.15	0 <span>100</span> <span>100</span>	46, 62, 102, 122	0
2	D	300/347 (86%)	-0.09	0 <span>100</span> <span>100</span>	41, 57, 87, 110	0
All	All	628/746 (84%)	-0.10	1 (0%) <span>94</span> <span>95</span>	41, 57, 94, 122	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	167	ILE	2.2

### 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.