



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 25, 2024 – 02:49 AM EDT

PDB ID : 6G11  
Title : Complex of rice blast (*Magnaporthe oryzae*) effector protein AVR-PikE with the HMA domain of Pikp-1 from rice (*Oryza sativa*)  
Authors : De la Concepcion, J.C.; Franceschetti, M.; Banfield, M.J.  
Deposited on : 2018-03-20  
Resolution : 1.90 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.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	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)	:	2.37.1

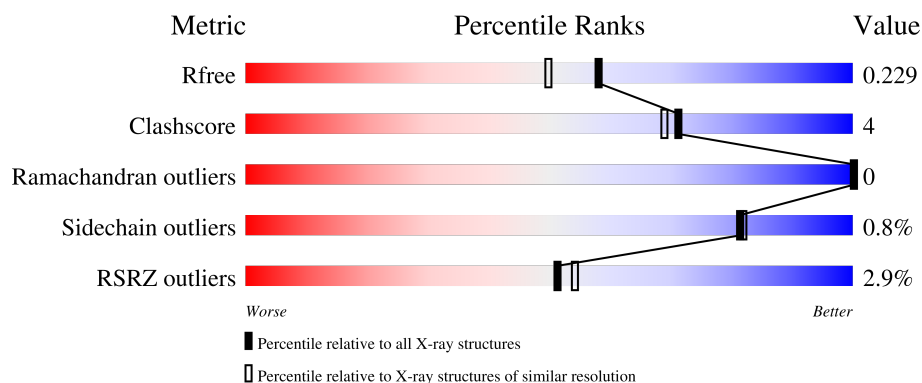
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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))
$R_{free}$	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	C	93	<div> <div>0%</div> <div>85%</div> <div>12%</div> </div>
1	F	93	<div> <div>87%</div> <div>12%</div> </div>
2	A	80	<div> <div>2%</div> <div>78%</div> <div>10%</div> <div>12%</div> </div>
2	B	80	<div> <div>5%</div> <div>82%</div> <div>9%</div> <div>9%</div> </div>
2	D	80	<div> <div>4%</div> <div>79%</div> <div>6%</div> <div>12%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	E	80	<div> <div></div> <div>4%</div> <div>80%</div> <div>11%</div> <div>9%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3712 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 AVR-Pik protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	82	Total	C	N	O	S	0	0	0
			665	427	114	118	6			
1	F	82	Total	C	N	O	S	0	0	0
			665	427	114	118	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	21	MET	-	initiating methionine	UNP C4B8C2
F	21	MET	-	initiating methionine	UNP C4B8C2

- Molecule 2 is a protein called Resistance protein Pikp-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	70	Total	C	N	O	S	0	1	0
			518	329	91	95	3			
2	B	73	Total	C	N	O	S	0	7	0
			561	352	100	106	3			
2	D	70	Total	C	N	O	S	0	1	0
			518	329	91	95	3			
2	E	73	Total	C	N	O	S	0	8	0
			555	349	98	105	3			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	184	GLY	-	expression tag	UNP E9KPB5
A	185	PRO	-	expression tag	UNP E9KPB5
B	184	GLY	-	expression tag	UNP E9KPB5
B	185	PRO	-	expression tag	UNP E9KPB5
D	184	GLY	-	expression tag	UNP E9KPB5
D	185	PRO	-	expression tag	UNP E9KPB5

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
E	184	GLY	-	expression tag	UNP E9KPB5
E	185	PRO	-	expression tag	UNP E9KPB5

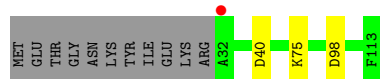
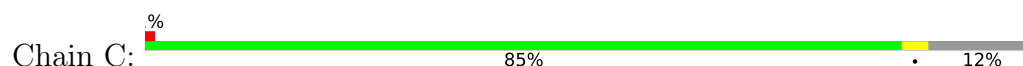
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	70	Total	O	0	0
			70	70		
3	A	24	Total	O	0	0
			24	24		
3	B	39	Total	O	0	1
			40	40		
3	F	42	Total	O	0	1
			43	43		
3	D	14	Total	O	0	0
			14	14		
3	E	38	Total	O	0	1
			39	39		

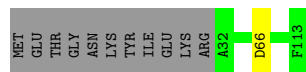
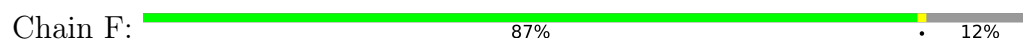
### 3 Residue-property plots [i](#)

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.

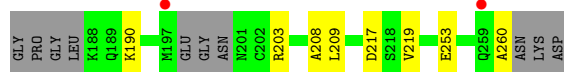
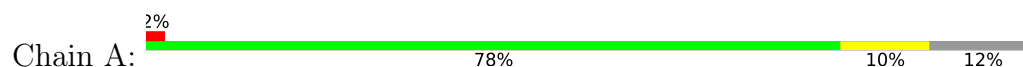
- Molecule 1: AVR-Pik protein



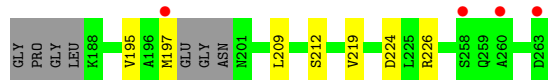
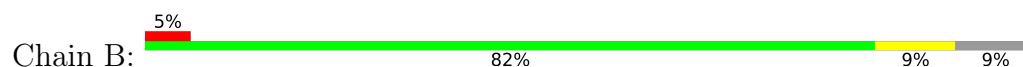
- Molecule 1: AVR-Pik protein



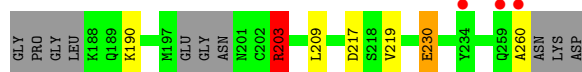
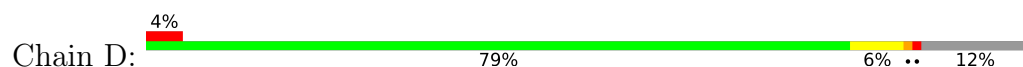
- Molecule 2: Resistance protein Pknp-1



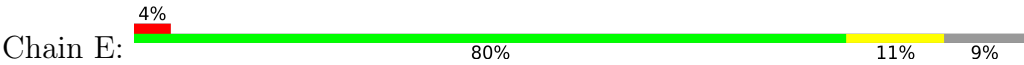
- Molecule 2: Resistance protein Pknp-1



- Molecule 2: Resistance protein Pknp-1



- Molecule 2: Resistance protein Pknp-1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.20Å 80.18Å 105.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.29 – 1.90 40.09 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.29-1.90) 100.0 (40.09-1.90)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.73 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.209 , 0.224 0.217 , 0.229	Depositor DCC
$R_{free}$ test set	2178 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.2	Xtriage
Anisotropy	0.878	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 48.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3712	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 39.14 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.3163e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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

### 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	C	0.72	0/689	0.84	1/933 (0.1%)
1	F	0.67	0/689	0.80	0/933
2	A	0.76	0/521	0.90	0/697
2	B	0.72	0/561	0.86	1/750 (0.1%)
2	D	0.72	1/521 (0.2%)	0.87	1/697 (0.1%)
2	E	0.70	0/558	0.87	1/746 (0.1%)
All	All	0.71	1/3539 (0.0%)	0.85	4/4756 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	230	GLU	CD-OE1	5.27	1.31	1.25

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	203	ARG	NE-CZ-NH1	6.05	123.32	120.30
2	B	224	ASP	CB-CG-OD1	5.52	123.27	118.30
1	C	40	ASP	CB-CG-OD1	5.12	122.91	118.30
2	E	224	ASP	CB-CG-OD1	5.11	122.90	118.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-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 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	C	665	0	623	1	0
1	F	665	0	623	1	0
2	A	518	0	574	8	0
2	B	561	0	609	9	0
2	D	518	0	574	8	0
2	E	555	0	606	9	0
3	A	24	0	0	1	0
3	B	40	0	0	0	0
3	C	70	0	0	0	1
3	D	14	0	0	1	0
3	E	39	0	0	0	1
3	F	43	0	0	0	0
All	All	3712	0	3609	25	1

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 4.

All (25) 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)
2:A:253:GLU:HG2	3:A:323:HOH:O	2.02	0.58
2:A:190:LYS:HB2	2:A:260:ALA:HB2	1.87	0.56
2:D:219[A]:VAL:CG1	2:E:219:VAL:HG22	2.38	0.54
2:A:219[A]:VAL:CG2	2:B:219:VAL:HG22	2.40	0.52
1:F:66:ASP:OD2	2:E:228:LYS:HE3	2.10	0.52
2:D:230:GLU:OE2	3:D:301:HOH:O	2.19	0.49
2:D:190:LYS:HB2	2:D:260:ALA:HB2	1.95	0.48
2:B:195:VAL:HG23	2:B:197:MET:CE	2.44	0.48
2:D:219[A]:VAL:HG12	2:E:219:VAL:CG2	2.44	0.48
2:D:217:ASP:OD1	2:E:226:ARG:NH2	2.43	0.48
2:A:219[A]:VAL:HG22	2:B:219:VAL:CG2	2.44	0.47
2:A:219[A]:VAL:HG22	2:B:219:VAL:HG22	1.96	0.46
2:B:195:VAL:HG23	2:B:197:MET:SD	2.56	0.45
2:E:195:VAL:HG23	2:E:197:MET:SD	2.56	0.45
2:A:217:ASP:OD1	2:B:226:ARG:NH2	2.47	0.45
2:B:209:LEU:C	2:B:209:LEU:HD23	2.37	0.44
2:A:209:LEU:C	2:A:209:LEU:HD23	2.39	0.43
2:D:209:LEU:C	2:D:209:LEU:HD23	2.39	0.43
2:E:225:LEU:N	2:E:225:LEU:HD12	2.34	0.43
2:D:219[A]:VAL:HG12	2:E:219:VAL:HG22	2.00	0.42
2:E:209:LEU:C	2:E:209:LEU:HD23	2.40	0.42
2:A:208:ALA:HB2	2:B:212:SER:HB3	2.03	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:228:LYS:HE2	2:E:255:LEU:CD1	2.51	0.40
2:B:195:VAL:HG23	2:B:197:MET:HE2	2.03	0.40
1:C:98:ASP:OD2	2:D:203:ARG:HB2	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:253:HOH:O	3:E:327:HOH:O[4_545]	2.16	0.04

## 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	C	80/93 (86%)	79 (99%)	1 (1%)	0	100	100
1	F	80/93 (86%)	79 (99%)	1 (1%)	0	100	100
2	A	67/80 (84%)	66 (98%)	1 (2%)	0	100	100
2	B	72/80 (90%)	71 (99%)	1 (1%)	0	100	100
2	D	67/80 (84%)	66 (98%)	1 (2%)	0	100	100
2	E	72/80 (90%)	70 (97%)	2 (3%)	0	100	100
All	All	438/506 (87%)	431 (98%)	7 (2%)	0	100	100

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	C	73/83 (88%)	72 (99%)	1 (1%)	67	65
1	F	73/83 (88%)	73 (100%)	0	100	100
2	A	57/63 (90%)	56 (98%)	1 (2%)	59	55
2	B	62/63 (98%)	62 (100%)	0	100	100
2	D	57/63 (90%)	56 (98%)	1 (2%)	59	55
2	E	62/63 (98%)	62 (100%)	0	100	100
All	All	384/418 (92%)	381 (99%)	3 (1%)	81	82

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	75	LYS
2	A	203	ARG
2	D	203	ARG

Sometimes 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

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 [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	C	82/93 (88%)	-0.28	1 (1%) 79 81	21, 28, 44, 56	0
1	F	82/93 (88%)	-0.11	0 100 100	24, 35, 54, 64	0
2	A	70/80 (87%)	-0.02	2 (2%) 51 54	25, 34, 65, 76	0
2	B	73/80 (91%)	0.07	4 (5%) 25 28	23, 32, 62, 78	4 (5%)
2	D	70/80 (87%)	0.13	3 (4%) 35 38	24, 37, 64, 70	0
2	E	73/80 (91%)	0.43	3 (4%) 37 40	24, 30, 56, 87	5 (6%)
All	All	450/506 (88%)	0.03	13 (2%) 51 54	21, 33, 62, 87	9 (2%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	260[A]	ALA	4.4
2	D	234	TYR	4.2
2	D	260	ALA	4.0
2	B	263[A]	ASP	3.1
2	D	259	GLN	2.9
2	E	197	MET	2.9
2	A	259	GLN	2.8
2	A	197	MET	2.7
2	E	258[A]	SER	2.6
2	E	263[A]	ASP	2.5
2	B	258[A]	SER	2.4
2	B	197	MET	2.3
1	C	32	ALA	2.1

### 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 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.