



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 8, 2025 – 12:10 PM JST

PDB ID : 9IP6 / pdb\_00009ip6  
Title : The complex of rice immune receptor RGA5-HMA8 with rice blast effector protein AVR1-CO39  
Authors : Zhang, X.; Liu, J.  
Deposited on : 2024-07-10  
Resolution : 2.63 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)

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<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>.

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

MolProbity : 4-5-2 with Phenix2.0rc1  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.44

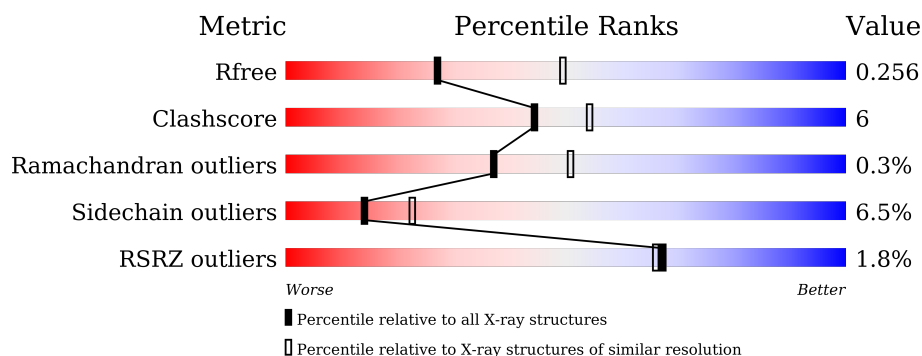
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.63 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))
$R_{free}$	164625	1851 (2.66-2.62)
Clashscore	180529	1953 (2.66-2.62)
Ramachandran outliers	177936	1929 (2.66-2.62)
Sidechain outliers	177891	1929 (2.66-2.62)
RSRZ outliers	164620	1850 (2.66-2.62)

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 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	A	84	<div> <div>71%</div> <div>15%</div> <div>13%</div> </div>
1	B	84	<div> <div>74%</div> <div>13%</div> <div>12%</div> </div>
1	E	84	<div> <div>5%</div> <div>63%</div> <div>21%</div> <div>13%</div> </div>
2	C	70	<div> <div>%</div> <div>64%</div> <div>23%</div> <div>13%</div> </div>
2	D	70	<div> <div>%</div> <div>79%</div> <div>9%</div> <div>13%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2677 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 Disease resistance protein RGA5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	73	Total	C	N	O	S	0	0	0
			543	342	100	97	4			
1	B	74	Total	C	N	O	S	0	0	0
			552	347	102	99	4			
1	E	73	Total	C	N	O	S	0	0	0
			548	345	101	98	4			

There are 33 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	986	MET	-	initiating methionine	UNP F7J0N2
A	987	SER	-	expression tag	UNP F7J0N2
A	988	HIS	-	expression tag	UNP F7J0N2
A	989	HIS	-	expression tag	UNP F7J0N2
A	990	HIS	-	expression tag	UNP F7J0N2
A	991	HIS	-	expression tag	UNP F7J0N2
A	992	HIS	-	expression tag	UNP F7J0N2
A	993	HIS	-	expression tag	UNP F7J0N2
A	994	SER	-	expression tag	UNP F7J0N2
A	995	MET	-	expression tag	UNP F7J0N2
A	1016	LEU	MET	conflict	UNP F7J0N2
B	986	MET	-	initiating methionine	UNP F7J0N2
B	987	SER	-	expression tag	UNP F7J0N2
B	988	HIS	-	expression tag	UNP F7J0N2
B	989	HIS	-	expression tag	UNP F7J0N2
B	990	HIS	-	expression tag	UNP F7J0N2
B	991	HIS	-	expression tag	UNP F7J0N2
B	992	HIS	-	expression tag	UNP F7J0N2
B	993	HIS	-	expression tag	UNP F7J0N2
B	994	SER	-	expression tag	UNP F7J0N2
B	995	MET	-	expression tag	UNP F7J0N2
B	1016	LEU	MET	conflict	UNP F7J0N2
E	986	MET	-	initiating methionine	UNP F7J0N2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	987	SER	-	expression tag	UNP F7J0N2
E	988	HIS	-	expression tag	UNP F7J0N2
E	989	HIS	-	expression tag	UNP F7J0N2
E	990	HIS	-	expression tag	UNP F7J0N2
E	991	HIS	-	expression tag	UNP F7J0N2
E	992	HIS	-	expression tag	UNP F7J0N2
E	993	HIS	-	expression tag	UNP F7J0N2
E	994	SER	-	expression tag	UNP F7J0N2
E	995	MET	-	expression tag	UNP F7J0N2
E	1016	LEU	MET	conflict	UNP F7J0N2

- Molecule 2 is a protein called AVR1-CO39 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	61	Total	C	N	O	S	0	0	0
			499	317	82	98	2			
2	D	61	Total	C	N	O	S	0	0	0
			499	317	82	98	2			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	21	MET	-	initiating methionine	UNP Q8J180
C	83	LEU	-	expression tag	UNP Q8J180
C	84	GLU	-	expression tag	UNP Q8J180
C	85	HIS	-	expression tag	UNP Q8J180
C	86	HIS	-	expression tag	UNP Q8J180
C	87	HIS	-	expression tag	UNP Q8J180
C	88	HIS	-	expression tag	UNP Q8J180
C	89	HIS	-	expression tag	UNP Q8J180
C	90	HIS	-	expression tag	UNP Q8J180
D	21	MET	-	initiating methionine	UNP Q8J180
D	83	LEU	-	expression tag	UNP Q8J180
D	84	GLU	-	expression tag	UNP Q8J180
D	85	HIS	-	expression tag	UNP Q8J180
D	86	HIS	-	expression tag	UNP Q8J180
D	87	HIS	-	expression tag	UNP Q8J180
D	88	HIS	-	expression tag	UNP Q8J180
D	89	HIS	-	expression tag	UNP Q8J180
D	90	HIS	-	expression tag	UNP Q8J180

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	7	Total 7	O 7	0	0
3	C	12	Total 12	O 12	0	0
3	B	4	Total 4	O 4	0	0
3	D	12	Total 12	O 12	0	0
3	E	1	Total 1	O 1	0	0

### 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: Disease resistance protein RGA5

Chain A: 



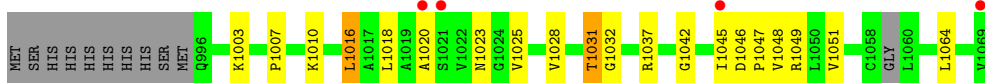
- Molecule 1: Disease resistance protein RGA5

Chain B: 



- Molecule 1: Disease resistance protein RGA5

Chain E: 




- Molecule 2: AVR1-CO39 protein

Chain C: 



- Molecule 2: AVR1-CO39 protein

Chain D: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	40.60Å 126.81Å 47.23Å 90.00° 110.74° 90.00°	Depositor
Resolution (Å)	35.72 – 2.63 35.72 – 2.63	Depositor EDS
% Data completeness (in resolution range)	98.5 (35.72-2.63) 98.5 (35.72-2.63)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.40 (at 2.65Å)	Xtriage
Refinement program	PHENIX (1.18.2_3874: ???)	Depositor
R, $R_{free}$	0.185 , 0.257 0.187 , 0.256	Depositor DCC
$R_{free}$ test set	11985 reflections (9.94%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.6	Xtriage
Anisotropy	0.715	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 50.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	2677	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.96% 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	0.33	0/545	0.52	0/733
1	B	0.32	0/554	0.56	0/745
1	E	0.23	0/549	0.44	0/737
2	C	0.36	0/511	0.53	0/696
2	D	0.35	0/511	0.61	0/696
All	All	0.32	0/2670	0.54	0/3607

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	543	0	598	5	0
1	B	552	0	606	5	1
1	E	548	0	602	11	0
2	C	499	0	469	9	1
2	D	499	0	469	3	0
3	A	7	0	0	0	0
3	B	4	0	0	0	0
3	C	12	0	0	0	0
3	D	12	0	0	1	0
3	E	1	0	0	1	0
All	All	2677	0	2744	32	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 6.

All (32) 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:E:1046:ASP:HB3	1:E:1049:ARG:HG2	1.59	0.83
1:E:1037:ARG:NH1	3:E:1101:HOH:O	2.28	0.66
2:D:54:LYS:O	3:D:101:HOH:O	2.17	0.59
2:C:49:THR:HG22	2:C:54:LYS:HD3	1.85	0.58
1:E:1016:LEU:HG	1:E:1028:VAL:HG12	1.86	0.57
2:C:30:ARG:NH2	2:C:51:GLU:OE1	2.38	0.57
1:A:1024:GLY:O	1:A:1042:GLY:HA3	2.08	0.54
2:C:44:ARG:HB3	2:C:59:GLU:HA	1.89	0.54
1:B:996:GLN:HE21	1:B:996:GLN:N	2.06	0.53
2:C:32:LYS:HE3	2:C:33:ASP:OD1	2.08	0.53
1:E:1031:THR:HG22	1:E:1032:GLY:H	1.76	0.50
2:D:40:TYR:CZ	2:D:50:ILE:HG23	2.47	0.49
1:E:1020:ALA:HA	1:E:1025:VAL:HG11	1.95	0.49
1:A:997:ARG:NH2	1:A:1026:ASP:OD2	2.46	0.49
1:B:1051:VAL:HG21	1:B:1063:LEU:HG	1.94	0.48
1:A:1051:VAL:HG21	1:A:1063:LEU:HB2	1.95	0.47
2:C:67:ILE:HD12	2:C:73:VAL:HG22	1.96	0.47
2:C:50:ILE:HD12	2:C:55:VAL:HG21	1.98	0.46
1:E:1046:ASP:CB	1:E:1049:ARG:HG2	2.39	0.45
2:C:32:LYS:HD2	2:C:32:LYS:HA	1.64	0.44
1:E:1047:PRO:O	1:E:1051:VAL:HG23	2.18	0.44
1:E:1016:LEU:HG	1:E:1028:VAL:CG1	2.47	0.43
1:B:1016:LEU:HB3	2:D:39:ILE:HD13	2.01	0.43
2:C:59:GLU:H	2:C:59:GLU:CD	2.27	0.43
1:E:1037:ARG:HE	1:E:1064:LEU:HD22	1.84	0.43
1:B:1024:GLY:O	1:B:1042:GLY:HA3	2.19	0.42
1:E:1003:LYS:HE2	1:E:1003:LYS:HB3	1.76	0.42
1:B:1042:GLY:HA3	1:B:1045:ILE:HD11	2.01	0.41
2:C:30:ARG:NH2	2:C:70:ASP:OD2	2.53	0.41
1:A:1014:LYS:HE3	1:A:1014:LYS:HB3	1.74	0.41
1:E:1042:GLY:HA3	1:E:1045:ILE:HD11	2.02	0.41
1:A:1005:HIS:HB2	1:A:1060:LEU:HB3	2.03	0.41

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)
2:C:80:SER:OG	1:B:1056:GLU:OE2[1_656]	2.10	0.10

## 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	71/84 (84%)	70 (99%)	1 (1%)	0	100	100
1	B	72/84 (86%)	68 (94%)	4 (6%)	0	100	100
1	E	69/84 (82%)	68 (99%)	0	1 (1%)	9	12
2	C	59/70 (84%)	58 (98%)	1 (2%)	0	100	100
2	D	59/70 (84%)	56 (95%)	3 (5%)	0	100	100
All	All	330/392 (84%)	320 (97%)	9 (3%)	1 (0%)	37	51

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	1007	PRO

### 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	60/71 (84%)	56 (93%)	4 (7%)	13	21
1	B	61/71 (86%)	56 (92%)	5 (8%)	9	14
1	E	61/71 (86%)	55 (90%)	6 (10%)	6	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	55/64 (86%)	53 (96%)	2 (4%)	30	47
2	D	55/64 (86%)	53 (96%)	2 (4%)	30	47
All	All	292/341 (86%)	273 (94%)	19 (6%)	14	22

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

Mol	Chain	Res	Type
1	A	1006	MET
1	A	1011	SER
1	A	1049	ARG
1	A	1068	LEU
2	C	25	ASP
2	C	71	ARG
1	B	996	GLN
1	B	998	THR
1	B	1014	LYS
1	B	1018	LEU
1	B	1053	LEU
2	D	23	TRP
2	D	35	ASP
1	E	1010	LYS
1	E	1016	LEU
1	E	1018	LEU
1	E	1023	ASN
1	E	1031	THR
1	E	1048	VAL

Sometimes 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 molecules 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 [i](#)

There are no oligosaccharides 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	73/84 (86%)	-0.55	0	100 100	32, 43, 59, 77	0
1	B	74/84 (88%)	-0.41	0	100 100	34, 44, 65, 85	0
1	E	73/84 (86%)	0.57	4 (5%)	32 30	55, 77, 99, 111	0
2	C	61/70 (87%)	-0.36	1 (1%)	70 69	34, 43, 61, 68	0
2	D	61/70 (87%)	-0.38	1 (1%)	70 69	33, 41, 57, 63	0
All	All	342/392 (87%)	-0.22	6 (1%)	67 66	32, 46, 90, 111	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	1020	ALA	2.8
1	E	1045	ILE	2.6
2	D	82	TYR	2.5
1	E	1069	VAL	2.1
1	E	1021	SER	2.1
2	C	82	TYR	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 oligosaccharides 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.