



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 4, 2024 – 06:34 pm GMT

PDB ID : 5FOW  
Title : HUMANISED MONOMERIC RADA IN COMPLEX WITH WHTA  
TETRAPEPTIDE  
Authors : Scott, D.E.; Marsh, M.; Blundell, T.L.; Abell, C.; Hyvonen, M.  
Deposited on : 2015-11-26  
Resolution : 1.80 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

<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 : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
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) : 2.36

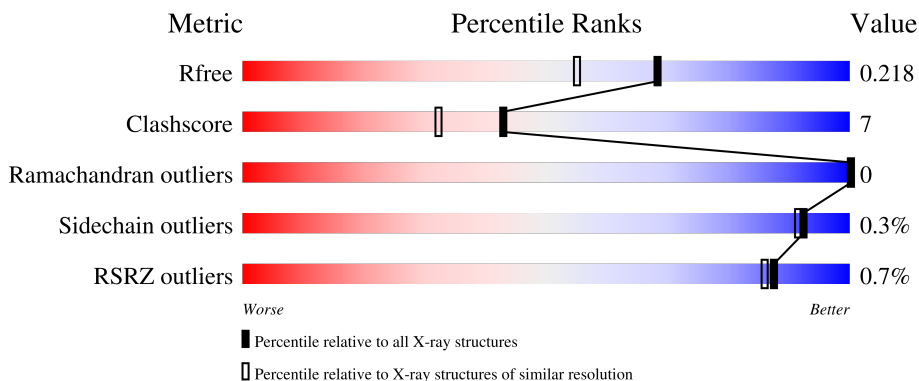
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	231	 88% 8%
1	C	231	 79% 15% 6%
2	E	6	 100%
2	F	6	 67% 33%

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4151 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 DNA repair and recombination protein RadA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	222	1751	1101	321	325	4	0	3	0
1	C	217	1713	1075	314	320	4	0	3	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	MET	-	initiating methionine	UNP O74036
A	169	MET	ILE	engineered mutation	UNP O74036
A	201	ALA	TYR	engineered mutation	UNP O74036
A	202	TYR	VAL	engineered mutation	UNP O74036
A	221	MET	LYS	engineered mutation	UNP O74036
A	300	ASN	ARG	engineered mutation	UNP O74036
A	?	-	PRO	deletion	UNP O74036
A	?	-	ASP	deletion	UNP O74036
A	?	-	ALA	deletion	UNP O74036
A	?	-	PHE	deletion	UNP O74036
A	?	-	PHE	deletion	UNP O74036
A	?	-	GLY	deletion	UNP O74036
A	?	-	ASP	deletion	UNP O74036
A	?	-	PRO	deletion	UNP O74036
A	?	-	THR	deletion	UNP O74036
A	?	-	ARG	deletion	UNP O74036
A	?	-	PRO	deletion	UNP O74036
A	?	-	ILE	deletion	UNP O74036
C	107	MET	-	initiating methionine	UNP O74036
C	169	MET	ILE	engineered mutation	UNP O74036
C	201	ALA	TYR	engineered mutation	UNP O74036
C	202	TYR	VAL	engineered mutation	UNP O74036
C	221	MET	LYS	engineered mutation	UNP O74036
C	300	ASN	ARG	engineered mutation	UNP O74036
C	?	-	PRO	deletion	UNP O74036

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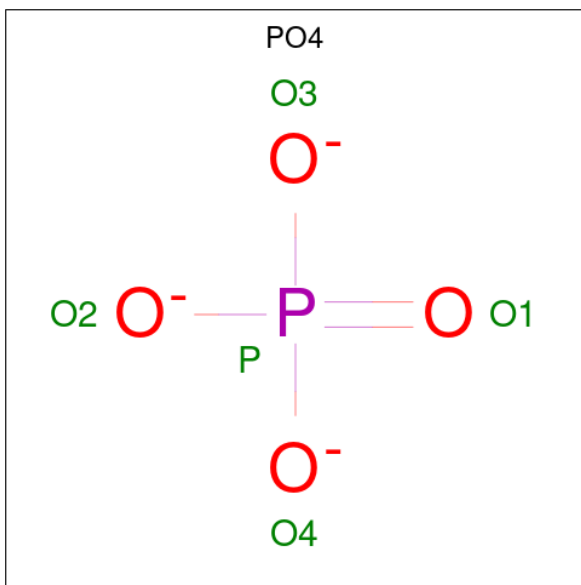
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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	ASP	deletion	UNP O74036
C	?	-	ALA	deletion	UNP O74036
C	?	-	PHE	deletion	UNP O74036
C	?	-	PHE	deletion	UNP O74036
C	?	-	GLY	deletion	UNP O74036
C	?	-	ASP	deletion	UNP O74036
C	?	-	PRO	deletion	UNP O74036
C	?	-	THR	deletion	UNP O74036
C	?	-	ARG	deletion	UNP O74036
C	?	-	PRO	deletion	UNP O74036
C	?	-	ILE	deletion	UNP O74036

- Molecule 2 is a protein called WHTA PEPTIDE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	6	Total	C	N	O	0	0	1
			40	26	8	6			
2	F	6	Total	C	N	O	0	0	1
			40	26	8	6			

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	O	P	0	0
			5	4	1		


- Molecule 4 is water.

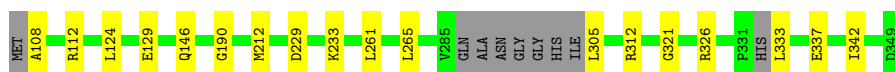
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	300	Total	O	0	0
			300	300		
4	C	275	Total	O	0	0
			275	275		
4	E	11	Total	O	0	0
			11	11		
4	F	11	Total	O	0	0
			11	11		

### 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.

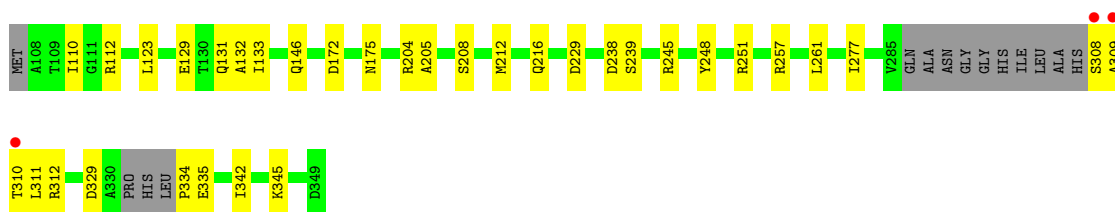
- Molecule 1: DNA repair and recombination protein RadA

Chain A:  88% 8%



- Molecule 1: DNA repair and recombination protein RadA

Chain C:  79% 15% 6%



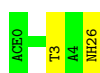
- Molecule 2: WHTA PEPTIDE

Chain E:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: WHTA PEPTIDE

Chain F:  67% 33%



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	40.48Å 87.60Å 61.94Å 90.00° 92.37° 90.00°	Depositor
Resolution (Å)	33.23 – 1.80 43.80 – 1.80	Depositor EDS
% Data completeness (in resolution range)	95.7 (33.23-1.80) 95.7 (43.80-1.80)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.49 (at 1.79Å)	Xtrriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.183 , 0.218 0.185 , 0.218	Depositor DCC
$R_{free}$ test set	1980 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	12.7	Xtrriage
Anisotropy	0.820	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 45.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.159 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4151	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.93% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ACE, NH2, PO4

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	0.34	0/1784	0.53	0/2401
1	C	0.33	0/1744	0.51	0/2343
2	E	0.23	0/39	0.42	0/54
2	F	0.34	0/39	0.46	0/54
All	All	0.34	0/3606	0.52	0/4852

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	1751	0	1797	18	0
1	C	1713	0	1757	30	0
2	E	40	0	32	0	0
2	F	40	0	32	1	0
3	A	5	0	0	0	0
3	C	5	0	0	0	0
4	A	300	0	0	10	6
4	C	275	0	0	17	7
4	E	11	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	F	11	0	0	0	0
All	All	4151	0	3618	49	8

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 49 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:305:LEU:N	4:A:501:HOH:O	1.92	1.01
1:A:333:LEU:N	4:A:502:HOH:O	1.94	1.00
1:C:311:LEU:N	4:C:501:HOH:O	1.93	0.99
1:A:108:ALA:N	4:A:503:HOH:O	1.99	0.95
1:C:131:GLN:N	4:C:503:HOH:O	2.02	0.91

The worst 5 of 8 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)
4:A:689:HOH:O	4:C:746:HOH:O[1_556]	1.89	0.31
4:A:569:HOH:O	4:C:693:HOH:O[2_645]	1.96	0.24
4:C:603:HOH:O	4:C:740:HOH:O[2_644]	2.04	0.16
4:A:765:HOH:O	4:C:732:HOH:O[1_556]	2.05	0.15
4:C:705:HOH:O	4:C:740:HOH:O[2_644]	2.05	0.15

## 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	219/231 (95%)	218 (100%)	1 (0%)	0	100   100
1	C	214/231 (93%)	213 (100%)	1 (0%)	0	100   100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	4/6 (67%)	4 (100%)	0	0	100	100
2	F	4/6 (67%)	4 (100%)	0	0	100	100
All	All	441/474 (93%)	439 (100%)	2 (0%)	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	A	186/189 (98%)	186 (100%)	0	100	100
1	C	182/189 (96%)	181 (100%)	1 (0%)	88	87
2	E	3/3 (100%)	3 (100%)	0	100	100
2	F	3/3 (100%)	3 (100%)	0	100	100
All	All	374/384 (97%)	373 (100%)	1 (0%)	92	91

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	261	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	227	ASN

### 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](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or 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 length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	PO4	A	401	-	4,4,4	0.76	0	6,6,6	0.55	0
3	PO4	C	401	-	4,4,4	0.76	0	6,6,6	0.56	0

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.

No monomer is involved in short contacts.

## 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	222/231 (96%)	-0.35	0 <b>100</b> <b>100</b>	6, 14, 27, 39	0
1	C	217/231 (93%)	-0.30	3 (1%) 75 72	6, 14, 31, 42	0
2	E	4/6 (66%)	-0.53	0 <b>100</b> <b>100</b>	11, 17, 19, 20	0
2	F	4/6 (66%)	-0.19	0 <b>100</b> <b>100</b>	10, 18, 23, 23	0
All	All	447/474 (94%)	-0.32	3 (0%) 87 86	6, 14, 30, 42	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	308	SER	3.4
1	C	310	THR	2.3
1	C	309	ALA	2.0

### 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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	PO4	C	401	5/5	0.98	0.06	12,12,12,14	0
3	PO4	A	401	5/5	0.99	0.05	11,13,13,16	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.