



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 01:14 PM GMT

PDB ID : 4B3B  
Title : Humanised monomeric RadA in complex with FHTA tetrapeptide  
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Deposited on : 2012-07-23  
Resolution : 1.19 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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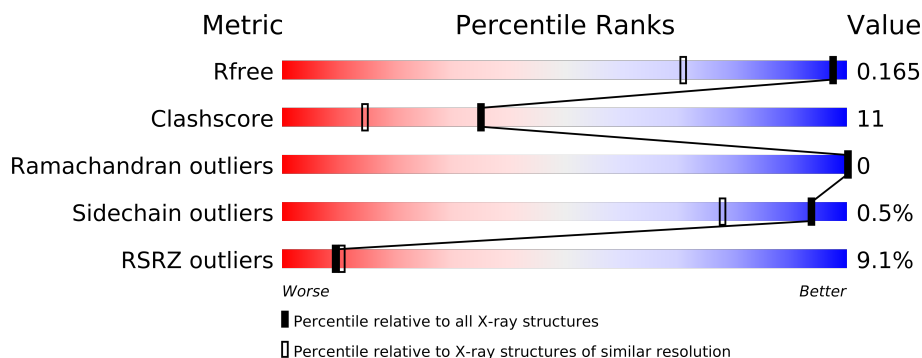
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.19 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	1038 (1.26-1.14)
Clashscore	79885	1158 (1.26-1.14)
Ramachandran outliers	78287	1106 (1.26-1.14)
Sidechain outliers	78261	1104 (1.26-1.14)
RSRZ outliers	66119	1038 (1.26-1.14)

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	231	
2	C	6	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4144 atoms, of which 1935 are hydrogens 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 DNA REPAIR AND RECOMBINATION PROTEIN RADA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	224	Total	C	H	N	O	S	0	22	0
			3754	1159	1906	340	344	5			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	MET	-	EXPRESSION TAG	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	ILE	ENGINEERED MUTATION	UNP O74036

- Molecule 2 is a protein called FHTA TETRAPEPTIDE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	6	Total	C	H	N	O	0	0	1
			66	24	29	7	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		

- Molecule 4 is water.

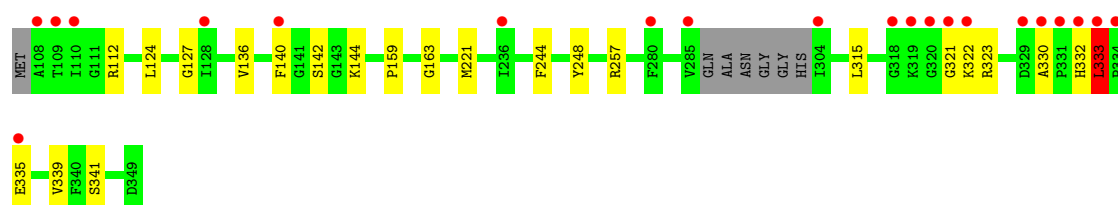
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	305	Total	O	0	0
			305	305		
4	C	14	Total	O	0	0
			14	14		

### 3 Residue-property plots i

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: DNA REPAIR AND RECOMBINATION PROTEIN RADA

Chain A: 



#### • Molecule 2: FHTA TETRAPEPTIDE

Chain C: 

There are no outlier residues recorded for this chain.

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	40.23Å 60.59Å 87.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	26.29 – 1.19 26.29 – 1.19	Depositor EDS
% Data completeness (in resolution range)	93.4 (26.29-1.19) 93.5 (26.29-1.19)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.07 (at 1.19Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.140 , 0.167 0.139 , 0.165	Depositor DCC
$R_{free}$ test set	3252 reflections (5.05%)	DCC
Wilson B-factor (Å <sup>2</sup> )	8.4	Xtriage
Anisotropy	0.257	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.50 , 51.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 64404 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	4144	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.83% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 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: PO4, ACE, NH2

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	0.46	0/1939	0.74	3/2609 (0.1%)
2	C	0.48	0/35	0.74	0/47
All	All	0.46	0/1974	0.74	3/2656 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	257	ARG	NE-CZ-NH1	9.55	125.07	120.30
1	A	257	ARG	NE-CZ-NH2	-7.53	116.54	120.30
1	A	333	LEU	CA-CB-CG	7.10	131.62	115.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 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	1848	1906	0	40	0
2	C	37	29	0	0	0
3	A	5	0	0	0	0
4	A	305	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	14	0	0	0	0
All	All	2209	1935	0	40	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 11.

All (40) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:140:PHE:CE1	1:A:140:PHE:HE2	0.93	1.63
1:A:140:PHE:HD1	1:A:140:PHE:CD2	0.93	1.62
1:A:248:TYR:CE2	1:A:248:TYR:HE1	0.93	1.61
1:A:248:TYR:CD1	1:A:248:TYR:HD2	0.93	1.61
1:A:244:PHE:HE2	1:A:244:PHE:CE1	0.93	1.61
1:A:244:PHE:HD1	1:A:244:PHE:CD2	0.93	1.60
1:A:140:PHE:HE1	1:A:140:PHE:CE2	0.93	1.60
1:A:140:PHE:CD1	1:A:140:PHE:HD2	0.93	1.60
1:A:244:PHE:CD1	1:A:244:PHE:HD2	0.93	1.57
1:A:248:TYR:CD2	1:A:248:TYR:HD1	0.93	1.56
1:A:248:TYR:CE1	1:A:248:TYR:HE2	0.93	1.56
1:A:244:PHE:HE1	1:A:244:PHE:CE2	0.93	1.56
1:A:136[B]:VAL:CG2	1:A:315[B]:LEU:HG	2.17	0.75
1:A:112[A]:ARG:NH1	1:A:127:GLY:O	2.22	0.72
1:A:332:HIS:CD2	1:A:333:LEU:CD1	2.80	0.65
1:A:332:HIS:CD2	1:A:333:LEU:HD12	2.35	0.61
1:A:136[B]:VAL:HG22	1:A:315[B]:LEU:CD1	2.31	0.60
1:A:142[B]:SER:O	1:A:323:ARG:HD2	2.04	0.57
1:A:332:HIS:NE2	1:A:333:LEU:HD12	2.18	0.57
1:A:136[B]:VAL:HG22	1:A:315[B]:LEU:HD12	1.87	0.57
1:A:332:HIS:CG	1:A:333:LEU:HD13	2.45	0.52
1:A:332:HIS:CD2	1:A:333:LEU:HD13	2.45	0.51
1:A:136[A]:VAL:HG13	1:A:144:LYS:HG2	1.91	0.51
1:A:136[B]:VAL:HG21	1:A:315[B]:LEU:HG	1.90	0.50
1:A:112[A]:ARG:NH1	1:A:124:LEU:O	2.43	0.50
1:A:142[A]:SER:O	1:A:315[A]:LEU:CD2	2.63	0.46
1:A:136[B]:VAL:CG2	1:A:315[B]:LEU:CG	2.92	0.46
1:A:322:LYS:HD2	1:A:339:VAL:HG13	1.98	0.46
1:A:159:PRO:HA	1:A:163:GLY:O	2.16	0.45
1:A:333:LEU:HD13	1:A:333:LEU:N	2.30	0.45
1:A:136[B]:VAL:CG2	1:A:315[B]:LEU:CD1	2.95	0.44
1:A:335:GLU:H	1:A:335:GLU:CD	2.20	0.44
1:A:321:GLY:O	1:A:341:SER:HA	2.18	0.43
1:A:142[A]:SER:O	1:A:315[A]:LEU:HD22	2.19	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:332:HIS:CG	1:A:333:LEU:CD1	3.01	0.42
1:A:322:LYS:HD2	1:A:339:VAL:CG1	2.50	0.41
1:A:330:ALA:HB2	1:A:333:LEU:HD11	2.02	0.41
1:A:335:GLU:N	1:A:335:GLU:CD	2.74	0.41
1:A:136[A]:VAL:CG1	1:A:144:LYS:HG2	2.51	0.41
1:A:221:MET:HE1	1:A:221:MET:HB2	1.94	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	242/231 (105%)	239 (99%)	3 (1%)	0	100	100
2	C	4/6 (67%)	4 (100%)	0	0	100	100
All	All	246/237 (104%)	243 (99%)	3 (1%)	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	202/189 (107%)	201 (100%)	1 (0%)	94	78
2	C	3/3 (100%)	3 (100%)	0	100	100
All	All	205/192 (107%)	204 (100%)	1 (0%)	94	78

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

Mol	Chain	Res	Type
1	A	333	LEU

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

Mol	Chain	Res	Type
1	A	199	HIS

### 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 ⓘ

1 ligand is 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	1350	-	4,4,4	0.36	0	6,6,6	0.31	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PO4	A	1350	-	-	0/0/0/0	0/0/0/0

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.

## 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	224/231 (96%)	0.49	21 (9%) 9 10	4, 9, 21, 41	2 (0%)
2	C	6/6 (100%)	0.25	0 100 100	10, 11, 14, 14	0
All	All	230/237 (97%)	0.49	21 (9%) 9 10	4, 10, 21, 41	2 (0%)

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	333	LEU	8.5
1	A	331	PRO	6.2
1	A	304	ILE	6.2
1	A	320	GLY	5.7
1	A	332	HIS	5.1
1	A	318	GLY	5.0
1	A	335	GLU	4.9
1	A	285	VAL	4.7
1	A	321	GLY	4.6
1	A	334	PRO	3.8
1	A	330	ALA	3.2
1	A	108	ALA	3.2
1	A	140	PHE	2.9
1	A	110	ILE	2.9
1	A	319	LYS	2.9
1	A	109	THR	2.7
1	A	128[A]	ILE	2.7
1	A	236	ILE	2.6
1	A	322	LYS	2.3
1	A	280	PHE	2.1
1	A	329	ASP	2.1

## 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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	PO4	A	1350	5/5	0.04	-1.39	8,8,9,9	0

## 6.5 Other polymers

There are no such residues in this entry.