



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:39 PM UTC

PDB ID : 5JEE / pdb\_00005jee  
Title : Apo-structure of humanised RadA-mutant humRadA26F  
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Deposited on : 2016-04-18  
Resolution : 1.49 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>.

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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 Phenix2.0  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

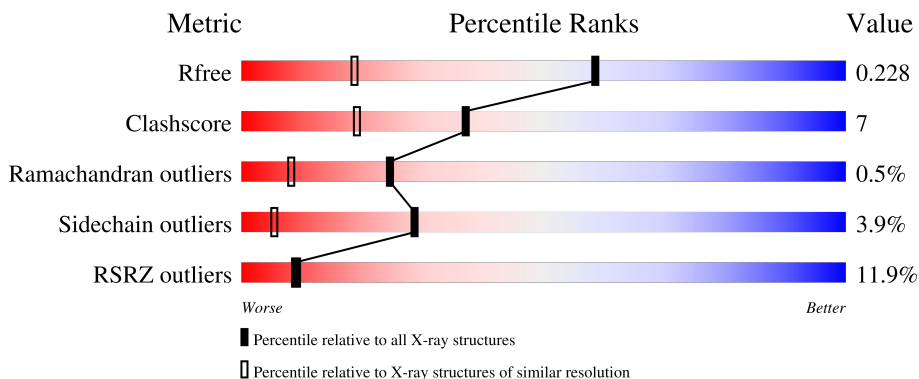
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.49 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))
$R_{free}$	180053	4037 (1.50-1.50)
Clashscore	190562	4235 (1.50-1.50)
Ramachandran outliers	187476	4153 (1.50-1.50)
Sidechain outliers	187428	4150 (1.50-1.50)
RSRZ outliers	180081	4039 (1.50-1.50)

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	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1834 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	218	1746	1093	315	332	6	0	7	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	MET	-	initiating methionine	UNP O74036
A	167	LYS	SER	engineered mutation	UNP O74036
A	168	ALA	VAL	engineered mutation	UNP O74036
A	169	MET	ILE	engineered mutation	UNP O74036
A	170	TYR	TRP	engineered mutation	UNP O74036
A	182	LEU	ILE	engineered mutation	UNP O74036
A	183	LEU	ARG	engineered mutation	UNP O74036
A	198	ASP	LYS	engineered mutation	UNP O74036
A	199	ASN	HIS	engineered mutation	UNP O74036
A	200	VAL	ILE	engineered mutation	UNP O74036
A	201	ALA	TYR	engineered mutation	UNP O74036
A	202	TYR	VAL	engineered mutation	UNP O74036
A	219	SER	GLU	engineered mutation	UNP O74036
A	221	MET	LYS	engineered mutation	UNP O74036
A	222	MET	ILE	engineered mutation	UNP O74036
A	?	-	ARG	deletion	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

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Chain	Residue	Modelled	Actual	Comment	Reference
A	293	ASN	ILE	engineered mutation	UNP O74036

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0

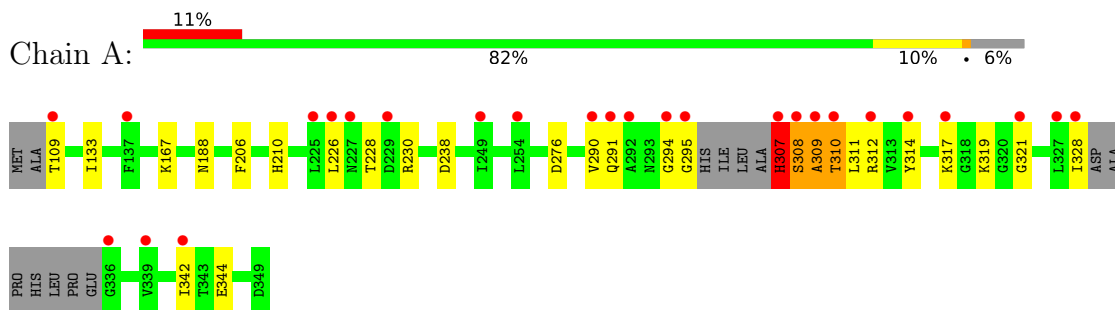
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	87	Total O 87 87	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: DNA repair and recombination protein RadA



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	50.58Å 50.60Å 74.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.13 – 1.49 37.13 – 1.49	Depositor EDS
% Data completeness (in resolution range)	99.2 (37.13-1.49) 99.2 (37.13-1.49)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.05 (at 1.49Å)	Xtrriage
Refinement program	BUSTER 2.10.0	Depositor
R, $R_{free}$	0.194 , 0.218 0.199 , 0.228	Depositor DCC
$R_{free}$ test set	1617 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	20.5	Xtrriage
Anisotropy	0.650	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 29.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.028 for k,h,-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	1834	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.62% 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: CA

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	0.78	1/1767 (0.1%)	1.24	11/2374 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	310	THR	CA-C	5.57	1.60	1.52

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	310	THR	CA-C-N	10.37	138.24	121.86
1	A	310	THR	C-N-CA	10.37	138.24	121.86
1	A	310	THR	N-CA-C	8.60	129.12	110.80
1	A	307	HIS	CA-C-N	8.53	137.83	121.54
1	A	307	HIS	C-N-CA	8.53	137.83	121.54
1	A	308	SER	N-CA-C	-7.22	95.41	110.80
1	A	238	ASP	CA-CB-CG	6.15	118.75	112.60
1	A	308	SER	CA-C-N	5.99	130.28	120.63
1	A	308	SER	C-N-CA	5.99	130.28	120.63
1	A	309	ALA	N-CA-C	5.98	120.11	112.34
1	A	276	ASP	CA-CB-CG	-5.41	107.19	112.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	307	HIS	Peptide

## 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	1746	0	1765	25	0
2	A	1	0	0	0	0
3	A	87	0	0	2	0
All	All	1834	0	1765	25	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.

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)
1:A:290:VAL:HG23	1:A:314[A]:TYR:CE1	2.04	0.92
1:A:290:VAL:HG23	1:A:314[A]:TYR:HE1	1.34	0.92
1:A:295:GLY:HA2	1:A:307:HIS:HE1	1.42	0.83
1:A:290:VAL:CG2	1:A:314[A]:TYR:CE1	2.66	0.79
1:A:294:GLY:HA3	1:A:295:GLY:C	2.10	0.76
1:A:295:GLY:HA2	1:A:307:HIS:CE1	2.21	0.75
1:A:295:GLY:CA	1:A:307:HIS:HE1	2.04	0.69
1:A:307:HIS:C	1:A:309:ALA:H	2.04	0.66
1:A:291:GLN:H	1:A:291:GLN:CD	2.05	0.65
1:A:206:PHE:H	1:A:210:HIS:HD2	1.45	0.64
1:A:307:HIS:HB3	1:A:312:ARG:HD2	1.80	0.62
1:A:314[B]:TYR:HB2	1:A:328:ILE:HD11	1.81	0.62
1:A:133:ILE:CG2	1:A:310:THR:HG22	2.31	0.61
1:A:307:HIS:C	1:A:309:ALA:N	2.60	0.58
1:A:133:ILE:HG22	1:A:310:THR:HG22	1.88	0.56
1:A:307:HIS:HD1	1:A:307:HIS:N	2.06	0.53
1:A:167:LYS:HG3	1:A:230:ARG:HG2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:ASN:ND2	1:A:344:GLU:HB3	2.26	0.50
1:A:314[A]:TYR:HB2	1:A:328:ILE:HD11	1.97	0.46
1:A:310:THR:HB	1:A:311:LEU:H	1.35	0.45
1:A:291:GLN:CD	1:A:291:GLN:N	2.76	0.44
1:A:307:HIS:N	1:A:307:HIS:ND1	2.66	0.43
1:A:210:HIS:HE1	3:A:524:HOH:O	2.00	0.43
1:A:291:GLN:NE2	3:A:503:HOH:O	2.50	0.41
1:A:133:ILE:HB	1:A:310:THR:HG22	2.02	0.41

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	219/231 (95%)	213 (97%)	5 (2%)	1 (0%)	24   8

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	321	GLY

### 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	185/188 (98%)	177 (96%)	8 (4%)	26 4

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	109	THR
1	A	226	LEU
1	A	228	THR
1	A	308	SER
1	A	317	LYS
1	A	319	LYS
1	A	342[A]	ILE
1	A	342[B]	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	165	ASN
1	A	210	HIS
1	A	211	GLN
1	A	289	GLN
1	A	307	HIS

### 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 oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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

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	218/231 (94%)	0.80	26 (11%) <b>9</b> <b>9</b>	10, 29, 60, 72	7 (3%)

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	226	LEU	5.5
1	A	328	ILE	4.8
1	A	292	ALA	4.6
1	A	309	ALA	4.4
1	A	109	THR	4.4
1	A	310	THR	4.1
1	A	249	ILE	4.0
1	A	225	LEU	4.0
1	A	227	ASN	3.9
1	A	342[A]	ILE	3.3
1	A	290	VAL	3.3
1	A	294	GLY	3.0
1	A	307	HIS	3.0
1	A	295	GLY	2.9
1	A	317	LYS	2.9
1	A	336	GLY	2.9
1	A	314[A]	TYR	2.5
1	A	327	LEU	2.5
1	A	291	GLN	2.5
1	A	308	SER	2.4
1	A	137	PHE	2.2
1	A	339	VAL	2.1
1	A	229	ASP	2.1
1	A	321	GLY	2.1
1	A	254	LEU	2.0
1	A	312	ARG	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 oligosaccharides 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(Å <sup>2</sup> )	Q<0.9
2	CA	A	401	1/1	0.98	0.11	36,36,36,36	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.