

# wwPDB X-ray Structure Validation Summary Report (i)

#### Oct 14, 2023 – 08:22 PM EDT

PDB ID	:	8EM9
Title	:	Human PU.1 ETS-Domain (165-270) Bound to $d(AATAGGAGAAGTAGGG)$
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Deposited on		
Resolution	:	2.34  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 A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

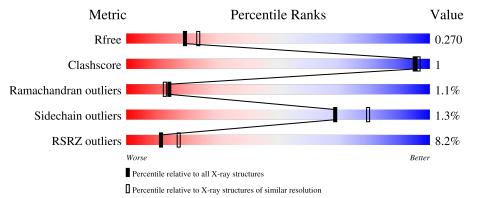
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 2.34 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	$2096 \ (2.36-2.32)$
Clashscore	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (2.36-2.32)
RSRZ outliers	127900	2067 (2.36-2.32)

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 >=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 <=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	С	16	100%	
2	D	16	94%	6%
3	F	106	9% 80% 5%	15%



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# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2516 atoms, of which 1113 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 DNA chain called DNA (5'-D(\*AP\*AP\*TP\*AP\*GP\*GP\*AP\*GP\*AP\*AP\*GP\*AP\*AP\*GP\*TP\*AP\*GP\*GP\*G)-3').

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
1	С	16	Total 518	C 160	H 180	N 74	O 89	Р 15	0	0	0

• Molecule 2 is a DNA chain called DNA (5'-D(\*TP\*CP\*CP\*CP\*TP\*AP\*CP\*TP\*TP\*CP\* TP\*CP\*CP\*TP\*A)-3').

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace			
2	D	16	Total 469	C 144	Н 172	N 43	O 95	Р 15	0	0	0

• Molecule 3 is a protein called Transcription factor PU.1.

Mol	Chain	Residues		Atoms				ZeroOcc	AltConf	Trace	
3	F	90	Total 1505	C 479	Н 761	N 136	0 126	${ m S} { m 3}$	8	1	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	С	14	Total         O           14         14	0	0
4	D	4	Total O 4 4	0	0
4	F	6	Total O 6 6	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 (5'-D(\*AP\*AP\*TP\*AP\*GP\*GP\*AP\*GP\*AP\*GP\*AP\*GP\*TP\*AP\*GP\*GP\*G)-3')

Chain C: 100% There are no outlier residues recorded for this chain.

• Molecule 2: DNA (5'-D(\*TP\*CP\*CP\*CP\*TP\*AP\*CP\*TP\*TP\*CP\*TP\*CP\*CP\*TP\*A)-3')

Chain D:	94%		6%
T18 C24 T33			
• Molecul	e 3: Transcription factor PU.1		
Chain F:	9%80%	5%	15%
GLY SER LYS LYS K169 K169 B134	N190         N190           D195         0195           P199         0195           P200         7200           P201         7200           P201         7200           P201         7200           P202         7200           P203         7200           P204         7200           P205         4231           P205         240           P205         255           P10         255           P10         255           P10         255           P10         255           P10         255           P10         P10           P11         P10		



# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32	Depositor
Cell constants	46.18Å 46.18Å 90.99Å	Derresiter
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	24.17 - 2.34	Depositor
Resolution (A)	24.17 - 2.34	EDS
% Data completeness	99.7 (24.17-2.34)	Depositor
(in resolution range)	99.7(24.17-2.34)	EDS
R <sub>merge</sub>	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.74 (at 2.33Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
D D	0.223 , $0.270$	Depositor
$R, R_{free}$	0.221 , $0.270$	DCC
$R_{free}$ test set	928 reflections $(10.17\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	52.6	Xtriage
Anisotropy	0.246	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.30, $35.8$	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.51, < L^2 > = 0.35$	Xtriage
	0.018 for -h,-k,l	
Estimated twinning fraction	0.055 for h,-h-k,-l	Xtriage
	0.035 for -k,-h,-l	
$\mathbf{F}_o, \mathbf{F}_c$ correlation	0.94	EDS
Total number of atoms	2516	wwPDB-VP
Average B, all atoms $(Å^2)$	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.82% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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		
	Ullaili	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	С	0.51	0/383	0.82	0/592	
2	D	0.56	0/328	1.01	0/502	
3	F	0.25	0/762	0.47	0/1014	
All	All	0.41	0/1473	0.73	0/2108	

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	С	338	180	180	0	0
2	D	297	172	172	1	0
3	F	744	761	763	3	0
4	С	14	0	0	0	0
4	D	4	0	0	0	0
4	F	6	0	0	0	0
All	All	1403	1113	1115	3	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 1.

All (3) 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)
3:F:255:GLU:OE1	3:F:255:GLU:N	2.29	0.63
3:F:240:GLU:N	3:F:240:GLU:OE1	2.36	0.55
2:D:24:DC:OP2	3:F:235:TYR:OH	2.24	0.47

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
3	F	89/106~(84%)	87~(98%)	1 (1%)	1 (1%)	14 13

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	F	184	ASP

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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.

Mo	Chain	Analysed	Rotameric	Outliers	Percentiles
3	F	76/90 (84%)	75~(99%)	1 (1%)	69 79

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

Mol	Chain	Res	Type
3	F	242	LYS



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 (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,  $95^{th}$  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	$\langle RSRZ \rangle$	$\# RSRZ {>}2$	$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q < 0.9
1	С	16/16~(100%)	-0.21	0 100 100	53, 62, 111, 114	0
2	D	16/16~(100%)	0.14	0 100 100	40, 75, 113, 121	0
3	F	90/106~(84%)	0.67	10 (11%) 5 9	40, 61, 104, 113	3 (3%)
All	All	122/138~(88%)	0.49	10 (8%) 11 17	40, 63, 107, 121	3(2%)

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	256	VAL	3.3
3	F	201	PHE	3.1
3	F	195	ASP	3.0
3	F	231	ALA	2.6
3	F	255	GLU	2.4

## 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.

