



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 12, 2024 – 05:58 PM EDT

PDB ID : 3H3D  
Title : Drosophila Pumilio RNA binding domain (Puf domain)  
Authors : Edwards, T.A.; Aggarwal, A.K.; Wharton, R.P.  
Deposited on : 2009-04-16  
Resolution : 2.30 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
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
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)	:	2.36.2

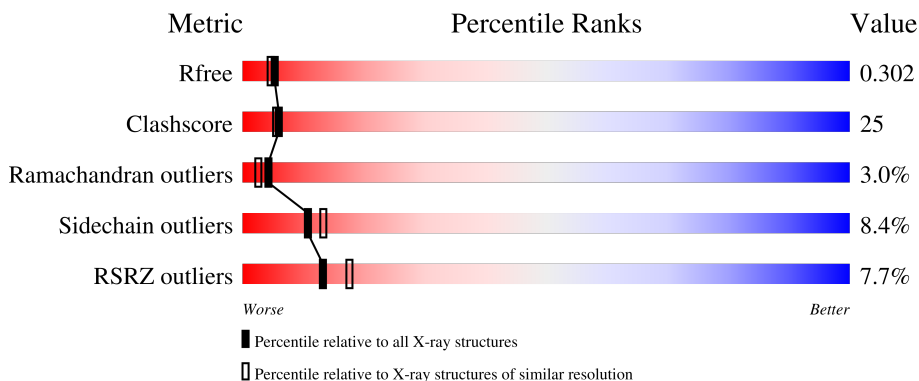
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*



The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	X	323	
1	Y	323	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5344 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 Maternal protein pumilio.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	X	313	Total	C	N	O	S	0	0	0
			2501	1577	438	469	17			
1	Y	314	Total	C	N	O	S	0	0	0
			2508	1581	442	468	17			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	-2	GLY	-	expression tag	UNP P25822
X	-1	SER	-	expression tag	UNP P25822
X	0	HIS	-	expression tag	UNP P25822
X	1	MET	-	expression tag	UNP P25822
X	315	LYS	PRO	SEE REMARK 999	UNP P25822
X	316	ASN	HIS	SEE REMARK 999	UNP P25822
Y	312	GLY	-	expression tag	UNP P25822
Y	313	SER	-	expression tag	UNP P25822
Y	314	HIS	-	expression tag	UNP P25822
Y	315	MET	-	expression tag	UNP P25822
Y	629	LYS	PRO	SEE REMARK 999	UNP P25822
Y	630	ASN	HIS	SEE REMARK 999	UNP P25822

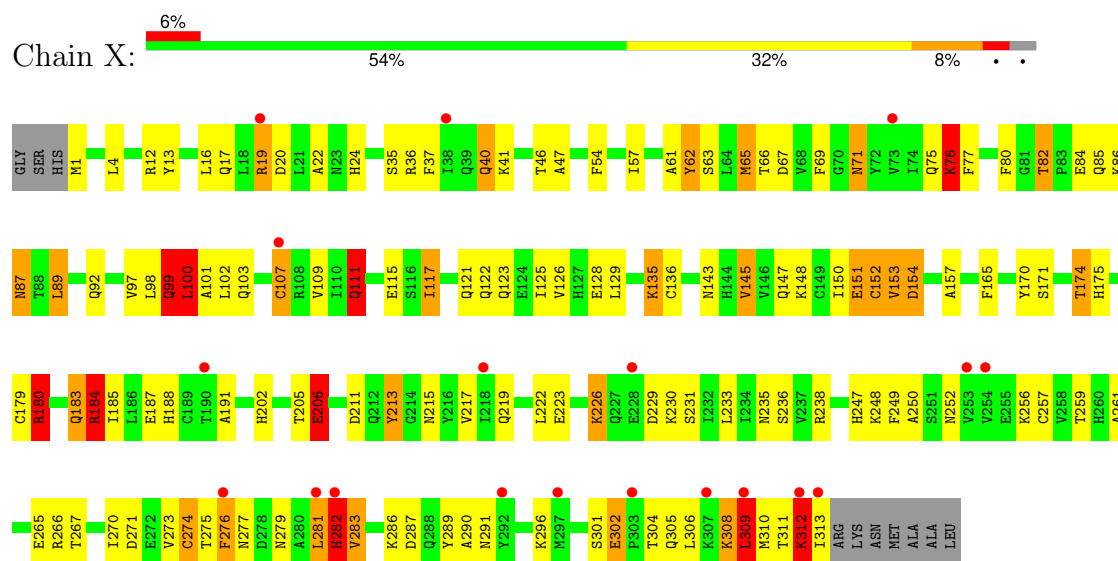
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	X	179	Total	O	0	0
			179	179		
2	Y	156	Total	O	0	0
			156	156		

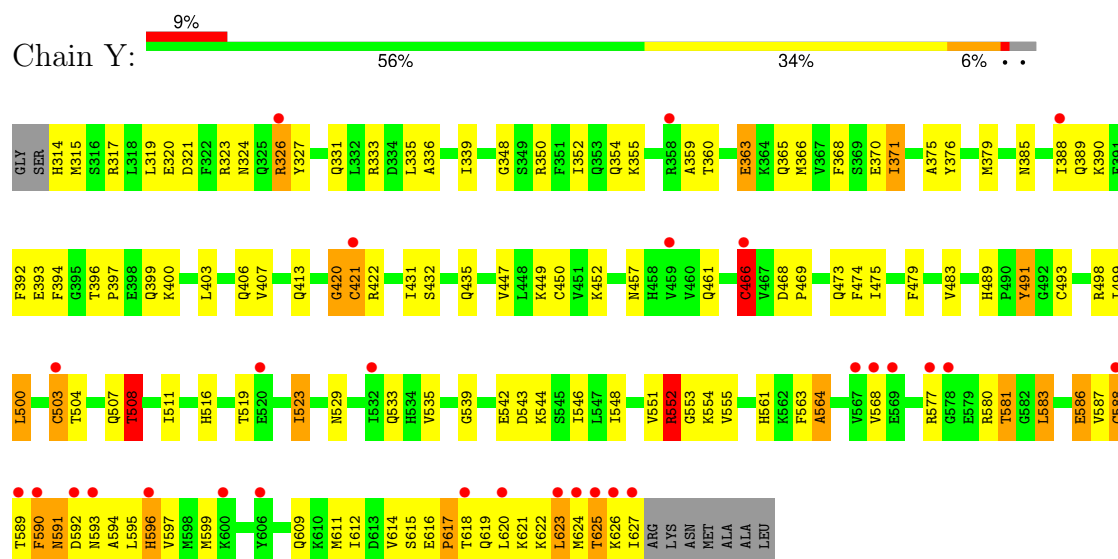
### 3 Residue-property plots

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: Maternal protein pumilio



#### • Molecule 1: Maternal protein pumilio



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	94.58Å 94.58Å 229.27Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.78 – 2.30 19.78 – 2.30	Depositor EDS
% Data completeness (in resolution range)	95.3 (19.78-2.30) 94.6 (19.78-2.30)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.01 (at 2.30Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.252 , 0.298 0.252 , 0.302	Depositor DCC
$R_{free}$ test set	2440 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	37.2	Xtriage
Anisotropy	0.006	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 68.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.079 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	5344	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% 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

### 5.1 Standard geometry

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	X	1.68	22/2544 (0.9%)	1.28	25/3435 (0.7%)
1	Y	1.50	16/2551 (0.6%)	1.25	9/3444 (0.3%)
All	All	1.59	38/5095 (0.7%)	1.26	34/6879 (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	X	0	1

The worst 5 of 38 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	X	107	CYS	CB-SG	36.44	2.44	1.82
1	Y	466	CYS	CB-SG	18.19	2.13	1.82
1	X	107	CYS	CA-CB	15.43	1.87	1.53
1	Y	421	CYS	CA-CB	14.30	1.85	1.53
1	X	183	GLN	CD-NE2	13.38	1.66	1.32

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Y	421	CYS	CA-CB-SG	19.74	149.53	114.00
1	X	107	CYS	CA-CB-SG	19.57	149.22	114.00
1	Y	421	CYS	N-CA-CB	16.31	139.96	110.60
1	X	136	CYS	CA-CB-SG	-11.20	93.84	114.00
1	X	107	CYS	N-CA-CB	11.15	130.66	110.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	X	309	LEU	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	X	2501	0	2491	115	0
1	Y	2508	0	2497	139	0
2	X	179	0	0	10	0
2	Y	156	0	0	12	0
All	All	5344	0	4988	249	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 25.

The worst 5 of 249 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:X:183:GLN:CG	1:X:183:GLN:CB	1.77	1.56
1:X:111:GLN:CD	1:X:111:GLN:CG	1.75	1.54
1:Y:421:CYS:N	1:Y:421:CYS:CA	1.70	1.53
1:X:107:CYS:CA	1:X:107:CYS:CB	1.87	1.51
1:Y:421:CYS:CA	1:Y:421:CYS:CB	1.85	1.49

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	X	311/323 (96%)	288 (93%)	12 (4%)	11 (4%)	3	2
1	Y	312/323 (97%)	282 (90%)	22 (7%)	8 (3%)	5	4
All	All	623/646 (96%)	570 (92%)	34 (6%)	19 (3%)	4	2

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	X	180	ARG
1	X	282	HIS
1	X	312	LYS
1	Y	590	PHE
1	Y	617	PRO

### 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	X	279/289 (96%)	251 (90%)	28 (10%)	7	9
1	Y	279/289 (96%)	260 (93%)	19 (7%)	16	21
All	All	558/578 (96%)	511 (92%)	47 (8%)	11	13

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Y	320	GLU
1	Y	450	CYS
1	Y	326	ARG
1	Y	371	ILE
1	Y	508	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	X	247	HIS

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Mol	Chain	Res	Type
1	Y	338	HIS
1	Y	561	HIS
1	X	305	GLN
1	Y	353	GLN

### 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<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	X	313/323 (96%)	0.42	19 (6%) 21 27	17, 39, 70, 87	0
1	Y	314/323 (97%)	0.48	29 (9%) 9 12	19, 42, 73, 97	0
All	All	627/646 (97%)	0.45	48 (7%) 13 17	17, 41, 72, 97	0

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	X	276	PHE	8.9
1	Y	593	ASN	8.0
1	Y	590	PHE	4.9
1	Y	624	MET	4.3
1	Y	577	ARG	4.1

### 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 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.