



wwPDB X-ray Structure Validation Summary Report

Mar 9, 2026 – 07:22 PM UTC

PDB ID : 3BSX / pdb_00003bsx
Title : Crystal Structure of Human Pumilio 1 in complex with Puf5 RNA
Authors : Gupta, Y.K.; Nair, D.T.; Wharton, R.P.; Aggarwal, A.K.
Deposited on : 2007-12-26
Resolution : 2.32 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  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](#) ) 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

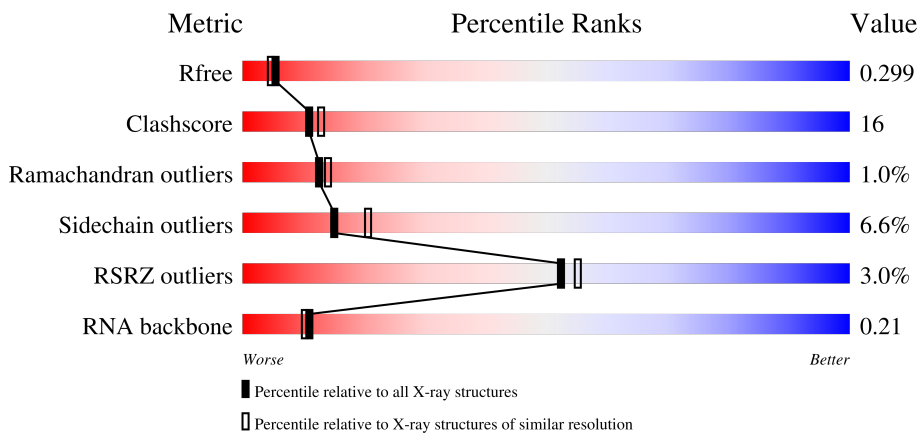
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

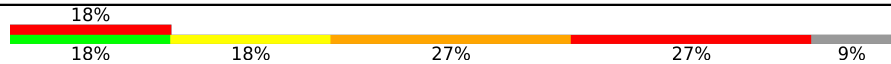

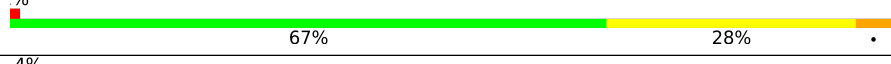

The reported resolution of this entry is 2.32 Å.

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	7754 (2.34-2.30)
Clashscore	190562	8383 (2.34-2.30)
Ramachandran outliers	187476	8303 (2.34-2.30)
Sidechain outliers	187428	8303 (2.34-2.30)
RSRZ outliers	180081	7760 (2.34-2.30)
RNA backbone	3983	1116 (2.64-2.00)

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 $\leq 5\%$. 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	C	11	
1	D	11	
2	A	343	
2	B	343	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6109 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 RNA chain called 5'-R(*UP*UP*GP*UP*AP*AP*UP*AP*UP*UP*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	C	10	Total 206	C 94	N 32	O 71	P 9	0	0	0
1	D	9	Total 186	C 85	N 30	O 63	P 8	0	0	0

- Molecule 2 is a protein called Pumilio homolog 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	A	341	Total 2749	C 1744	N 491	O 497	S 17	0	0	0
2	B	340	Total 2722	C 1727	N 489	O 489	S 17	0	0	0

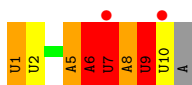
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	19	Total 19	O 19	0	0
3	D	12	Total 12	O 12	0	0
3	A	118	Total 118	O 118	0	0
3	B	97	Total 97	O 97	0	0

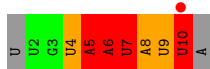
3 Residue-property plots [i](#)

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.

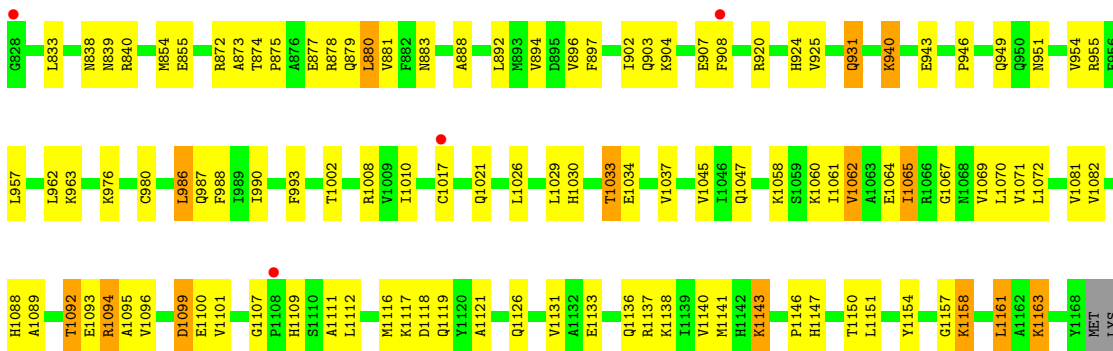
- Molecule 1: 5'-R(*UP*UP*GP*UP*AP*AP*UP*AP*UP*UP*A)-3'



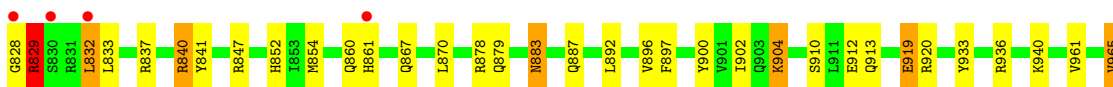
- Molecule 1: 5'-R(*UP*UP*GP*UP*AP*AP*UP*AP*UP*UP*A)-3'

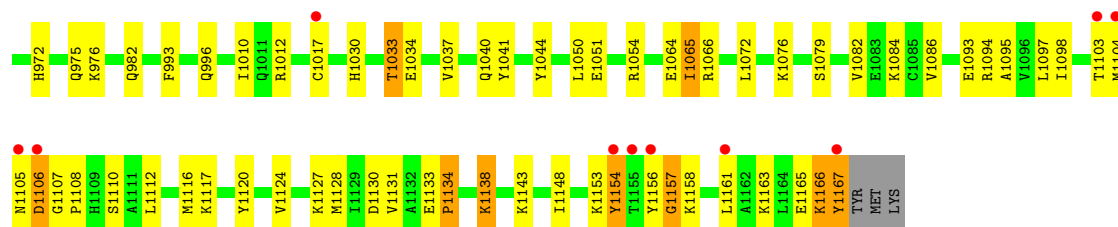


- Molecule 2: Pumilio homolog 1



- Molecule 2: Pumilio homolog 1





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	35.84Å 65.64Å 313.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.93 – 2.32 40.93 – 2.32	Depositor EDS
% Data completeness (in resolution range)	93.8 (40.93-2.32) 93.8 (40.93-2.32)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.66 (at 2.31Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.212 , 0.277 (Not available) , 0.299	Depositor DCC
R_{free} test set	3129 reflections (9.40%)	wwPDB-VP
Wilson B-factor (Å ²)	40.8	Xtrriage
Anisotropy	0.186	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 45.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6109	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.46% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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](#)

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	C	0.96	0/229	1.67	4/354 (1.1%)
1	D	1.21	2/207 (1.0%)	1.57	9/320 (2.8%)
2	A	0.98	2/2803 (0.1%)	1.12	2/3785 (0.1%)
2	B	0.91	2/2775 (0.1%)	1.08	0/3749
All	All	0.96	6/6014 (0.1%)	1.15	15/8208 (0.2%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	828	GLY	N-CA	8.21	1.58	1.45
2	B	965	VAL	CA-CB	5.92	1.61	1.54
1	D	10	U	O4'-C1'	5.35	1.50	1.42
2	A	1002	THR	CA-CB	5.35	1.62	1.53
1	D	4	U	C3'-O3'	5.24	1.50	1.42

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1107	GLY	CA-C-N	7.24	126.50	118.97
2	A	1107	GLY	C-N-CA	7.24	126.50	118.97
1	C	7	U	C4'-C3'-O3'	-7.23	102.15	113.00
1	C	1	U	P-O3'-C3'	7.01	130.72	120.20
1	D	7	U	P-O3'-C3'	6.94	130.61	120.20

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	C	206	0	106	4	0
1	D	186	0	96	12	0
2	A	2749	0	2742	89	0
2	B	2722	0	2712	93	0
3	A	118	0	0	20	0
3	B	97	0	0	26	0
3	C	19	0	0	0	0
3	D	12	0	0	3	0
All	All	6109	0	5656	190	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 16.

The worst 5 of 190 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)
2:B:975:GLN:HB3	3:B:202:HOH:O	1.34	1.22
2:A:904:LYS:HE2	3:A:93:HOH:O	1.36	1.22
2:A:1117:LYS:HA	3:A:138:HOH:O	1.45	1.16
2:A:1109:HIS:HB2	3:A:141:HOH:O	1.48	1.13
2:A:854:MET:HE3	2:A:888:ALA:HB3	1.33	1.09

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
2	A	339/343 (99%)	331 (98%)	7 (2%)	1 (0%)	36 45
2	B	338/343 (98%)	315 (93%)	17 (5%)	6 (2%)	6 5

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	677/686 (99%)	646 (95%)	24 (4%)	7 (1%)	12 14

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	839	ASN
2	B	1106	ASP
2	B	1166	LYS
2	B	840	ARG
2	B	1157	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
2	A	299/306 (98%)	278 (93%)	21 (7%)	14 18
2	B	294/306 (96%)	276 (94%)	18 (6%)	17 23
All	All	593/612 (97%)	554 (93%)	39 (7%)	15 21

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	940	LYS
2	B	1138	LYS
2	B	976	LYS
2	B	1065	ILE
2	B	1154	TYR

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

Mol	Chain	Res	Type
2	A	1126	GLN
2	B	858	GLN
2	B	1052	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	852	HIS
2	B	861	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C	10/11 (90%)	5 (50%)	3 (30%)
1	D	8/11 (72%)	5 (62%)	2 (25%)
All	All	18/22 (81%)	10 (55%)	5 (27%)

5 of 10 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C	2	U
1	C	5	A
1	C	7	U
1	C	8	A
1	C	9	U

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C	1	U
1	C	6	A
1	C	7	U
1	D	6	A
1	D	7	U

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](#)

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, 95th 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 ²)	Q<0.9
1	C	10/11 (90%)	0.61	2 (20%) 3 3	28, 44, 61, 68	0
1	D	9/11 (81%)	1.21	1 (11%) 10 11	36, 61, 79, 86	0
2	A	341/343 (99%)	-0.07	4 (1%) 76 78	21, 35, 60, 73	0
2	B	340/343 (99%)	0.23	14 (4%) 41 44	26, 41, 66, 79	0
All	All	700/708 (98%)	0.10	21 (3%) 52 55	21, 38, 64, 86	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	1106	ASP	5.3
2	B	1104	MET	4.5
2	B	1154	TYR	3.4
2	B	1167	TYR	3.2
2	B	1017	CYS	3.0

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.