Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 02:37 am BST

PDB ID	:	3Q0S
Title	:	Crystal structure of the PUMILIO-homology domain from Human PUMILIO2 in complex with erk2 NRE
Authors	:	Lu, G.; Hall, T.M.T.
Deposited on	:	2010-12-15
Resolution	:	2.00 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see references ⓘ) were used in the production of this report:

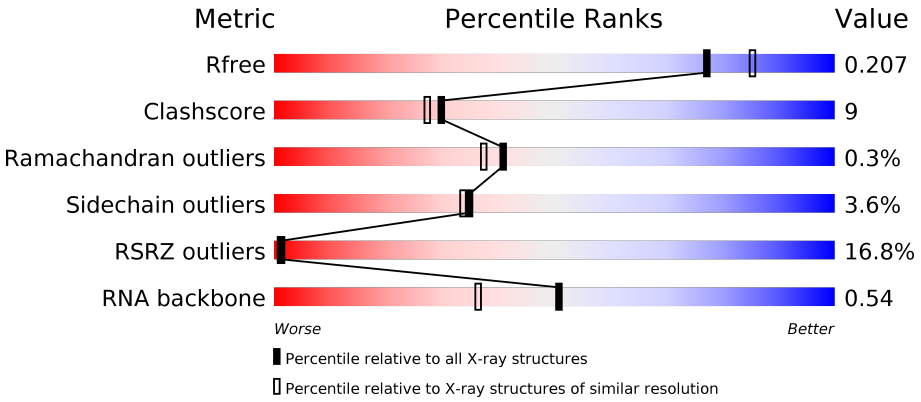
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)
RNA backbone	3102	1079 (2.50-1.50)

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 on 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	A	351	17% 77% 18%
2	B	8	88% 13%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3083 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 Pumilio homolog 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	343	Total	C	N	O	S	0	0	0
			2783	1760	502	503	18			

- Molecule 2 is a RNA chain called 5'-R(UP*GP*UP*AP*CP*AP*UP*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	8	Total	C	N	O	P	0	0	0
			164	75	27	55	7			

- Molecule 3 is water.

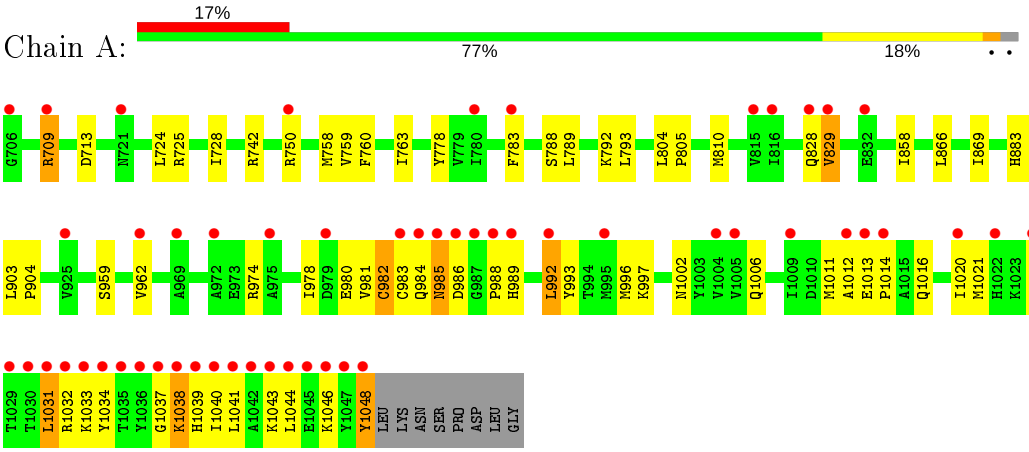
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	128	Total	O	0	0
			128	128		
3	B	8	Total	O	0	0
			8	8		

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 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.

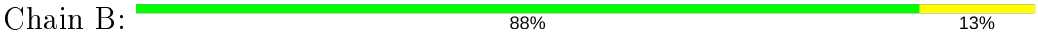
- Molecule 1: Pumilio homolog 2

Chain A:



- Molecule 2: 5'-R(UP*GP*UP*AP*CP*AP*UP*C)-3'

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	115.40Å 45.36Å 97.80Å 90.00° 125.26° 90.00°	Depositor
Resolution (Å)	24.00 – 2.00 24.03 – 2.00	Depositor EDS
% Data completeness (in resolution range)	92.4 (24.00-2.00) 98.8 (24.03-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.33 (at 1.99Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.4_6)	Depositor
R, R_{free}	0.207 , 0.249 0.212 , 0.207	Depositor DCC
R_{free} test set	1404 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	39.2	Xtriage
Anisotropy	0.725	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 55.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	0.013 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	3083	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.77% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	A	0.33	0/2835	0.47	1/3820 (0.0%)
2	B	0.53	0/182	1.08	0/281
All	All	0.34	0/3017	0.54	1/4101 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	985	ASN	CB-CA-C	-8.02	94.36	110.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2783	0	2807	54	0
2	B	164	0	87	1	0
3	A	128	0	0	1	0
3	B	8	0	0	0	0
All	All	3083	0	2894	54	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 9.

All (54) 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:742:ARG:HG3	3:A:111:HOH:O	1.78	0.82
1:A:724:LEU:HD21	1:A:759:VAL:CG2	2.20	0.70
1:A:1013:GLU:HB3	1:A:1014:PRO:HD2	1.75	0.69
1:A:793:LEU:HD22	1:A:829:VAL:HG21	1.75	0.67
1:A:980:GLU:O	1:A:984:GLN:HG3	1.94	0.67
1:A:978:ILE:O	1:A:982:CYS:HB3	1.99	0.63
1:A:1044:LEU:HD23	1:A:1048:TYR:HB3	1.81	0.62
1:A:804:LEU:HB3	1:A:805:PRO:HD3	1.82	0.62
1:A:996:MET:HB3	1:A:1031:LEU:HD11	1.82	0.62
1:A:793:LEU:CD2	1:A:829:VAL:HG21	2.31	0.60
1:A:1021:MET:SD	1:A:1044:LEU:HG	2.44	0.57
1:A:866:LEU:HD22	1:A:869:ILE:HD12	1.87	0.57
1:A:996:MET:SD	1:A:1031:LEU:HD11	2.46	0.56
1:A:789:LEU:HD23	1:A:789:LEU:C	2.27	0.56
1:A:1032:ARG:O	1:A:1038:LYS:HE3	2.06	0.54
1:A:725:ARG:O	1:A:728:ILE:HG13	2.08	0.54
1:A:789:LEU:HD23	1:A:789:LEU:O	2.06	0.54
1:A:760:PHE:HA	1:A:763:ILE:HG12	1.90	0.53
1:A:1002:ASN:O	1:A:1006:GLN:HG3	2.09	0.52
1:A:1043:LYS:HA	1:A:1046:LYS:HE2	1.90	0.52
1:A:1048:TYR:HD2	1:A:1048:TYR:H	1.56	0.52
1:A:883:HIS:CG	1:A:884:PRO:HD2	2.46	0.50
1:A:989:HIS:CE1	1:A:1027:HIS:HE1	2.29	0.50
1:A:1025:ARG:N	1:A:1026:PRO:HD2	2.27	0.50
1:A:992:LEU:O	1:A:996:MET:HG3	2.14	0.48
1:A:903:LEU:HB3	1:A:904:PRO:CD	2.44	0.48
1:A:1037:GLY:C	1:A:1039:HIS:H	2.17	0.47
1:A:709:ARG:NH1	1:A:713:ASP:OD1	2.48	0.47
1:A:750:ARG:O	1:A:750:ARG:HG2	2.16	0.46
1:A:988:PRO:HG2	1:A:989:HIS:H	1.80	0.46
1:A:981:VAL:O	1:A:992:LEU:HD13	2.16	0.46
1:A:788:SER:O	1:A:792:LYS:HG3	2.18	0.44
1:A:980:GLU:O	1:A:984:GLN:CG	2.62	0.43
1:A:1044:LEU:HD23	1:A:1048:TYR:CB	2.47	0.43
1:A:760:PHE:HB2	1:A:783:PHE:CE1	2.54	0.43
1:A:1020:ILE:O	1:A:1024:ILE:HG13	2.19	0.43
1:A:993:TYR:HA	1:A:996:MET:HE2	2.01	0.43
1:A:959:SER:HA	1:A:962:VAL:HG12	2.02	0.42
1:A:1012:ALA:HB1	1:A:1016:GLN:HB3	2.01	0.42
1:A:724:LEU:HD23	1:A:724:LEU:O	2.19	0.42
1:A:985:ASN:ND2	1:A:986:ASP:H	2.17	0.42
1:A:724:LEU:HD21	1:A:759:VAL:HG22	1.99	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:974:ARG:HD2	1:A:1011:MET:HB3	2.02	0.41
1:A:858:ILE:HA	1:A:866:LEU:CD1	2.50	0.41
1:A:1038:LYS:C	1:A:1041:LEU:HG	2.41	0.41
1:A:997:LYS:HE3	1:A:1034:TYR:CZ	2.56	0.41
1:A:778:TYR:CE2	2:B:8:C:C4	3.09	0.41
1:A:793:LEU:HD22	1:A:829:VAL:CG2	2.46	0.41
1:A:997:LYS:HB2	1:A:997:LYS:HE2	1.74	0.41
1:A:1013:GLU:CB	1:A:1014:PRO:HD2	2.46	0.41
1:A:1033:LYS:HB2	1:A:1033:LYS:NZ	2.35	0.41
1:A:1031:LEU:HA	1:A:1031:LEU:HD23	1.91	0.41
1:A:1013:GLU:HB3	1:A:1014:PRO:CD	2.47	0.40
1:A:997:LYS:HE3	1:A:1034:TYR:OH	2.21	0.40

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	341/351 (97%)	328 (96%)	12 (4%)	1 (0%)	41 37

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1038	LYS

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	307/314 (98%)	296 (96%)	11 (4%)	35 34

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	709	ARG
1	A	758	MET
1	A	810	MET
1	A	828	GLN
1	A	829	VAL
1	A	982	CYS
1	A	983	CYS
1	A	992	LEU
1	A	1031	LEU
1	A	1040	ILE
1	A	1048	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	723	GLN
1	A	761	ASN
1	A	769	GLN
1	A	781	GLN
1	A	985	ASN
1	A	989	HIS
1	A	999	GLN
1	A	1027	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	7/8 (87%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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

There are no ligands in this entry.

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^{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	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	343/351 (97%)	1.05	59 (17%) 1 1	27, 45, 126, 168	0
2	B	8/8 (100%)	-0.58	0 100 100	39, 41, 55, 78	0
All	All	351/359 (97%)	1.01	59 (16%) 1 1	27, 45, 126, 168	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	989	HIS	14.4
1	A	1046	LYS	11.9
1	A	1037	GLY	11.8
1	A	1047	TYR	11.8
1	A	986	ASP	11.1
1	A	985	ASN	10.2
1	A	1044	LEU	9.3
1	A	984	GLN	8.8
1	A	1029	THR	8.4
1	A	1039	HIS	7.8
1	A	987	GLY	7.5
1	A	1040	ILE	7.4
1	A	1041	LEU	7.1
1	A	1033	LYS	7.0
1	A	1030	THR	6.9
1	A	1042	ALA	6.6
1	A	1048	TYR	6.5
1	A	972	ALA	6.1
1	A	1034	TYR	5.8
1	A	1031	LEU	5.8
1	A	706	GLY	5.7
1	A	1032	ARG	5.6
1	A	1045	GLU	5.4
1	A	1005	VAL	5.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	1035	THR	4.6
1	A	1004	VAL	4.6
1	A	1038	LYS	4.6
1	A	979	ASP	4.4
1	A	1025	ARG	4.4
1	A	1013	GLU	4.2
1	A	988	PRO	4.1
1	A	983	CYS	3.8
1	A	750	ARG	3.5
1	A	1024	ILE	3.4
1	A	828	GLN	3.1
1	A	1014	PRO	2.8
1	A	962	VAL	2.7
1	A	1028	ILE	2.6
1	A	815	VAL	2.6
1	A	992	LEU	2.5
1	A	721	ASN	2.5
1	A	780	ILE	2.5
1	A	1022	HIS	2.5
1	A	1020	ILE	2.5
1	A	995	MET	2.4
1	A	1012	ALA	2.4
1	A	829	VAL	2.3
1	A	889	VAL	2.3
1	A	816	ILE	2.3
1	A	925	VAL	2.2
1	A	1043	LYS	2.2
1	A	1036	TYR	2.2
1	A	783	PHE	2.2
1	A	709	ARG	2.1
1	A	832	GLU	2.1
1	A	890	ILE	2.1
1	A	975	ALA	2.0
1	A	1009	ILE	2.0
1	A	969	ALA	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 carbohydrates 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.