



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 11:59 PM UTC

PDB ID : 5KVY / pdb_00005kvy
Title : CRYSTAL STRUCTURE OF THE TWO TANDEM RRM DOMAINS OF PUF60 BOUND TO A PORTION OF AN ADML PRE-MRNA 3' SPLICE SITE ANALOG
Authors : Hsiao, H.-H.; Crichlow, G.V.; Albright, R.A.; Murphy, J.W.; Lolis, E.J.; Brad-dock, D.T.
Deposited on : 2016-07-15
Resolution : 1.95 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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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
Xtriage (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

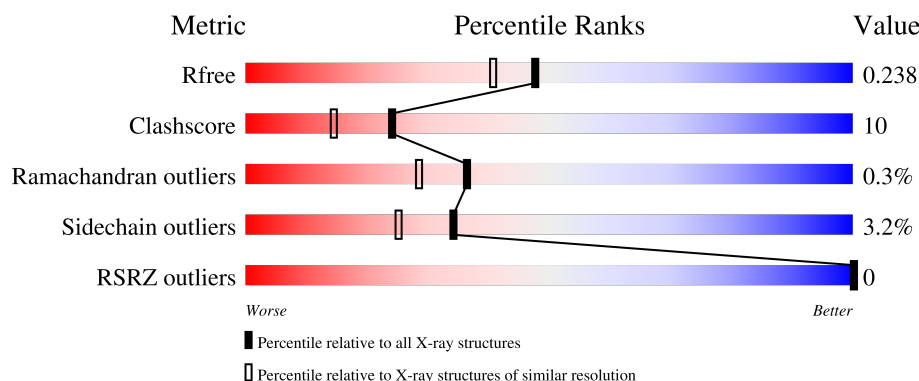
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	A	216	 71% 18% • 10%
1	B	216	 66% 23% • 10%
2	C	30	 7% 17% • 73%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3314 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 Poly(U)-binding-splicing factor PUF60.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	195	Total	C	N	O	S	0	0	0
			1501	951	258	285	7			
1	B	195	Total	C	N	O	S	0	0	0
			1504	951	260	286	7			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	101	GLY	-	expression tag	UNP Q9UHX1
A	102	SER	-	expression tag	UNP Q9UHX1
A	103	HIS	-	expression tag	UNP Q9UHX1
A	104	MET	-	expression tag	UNP Q9UHX1
A	105	ALA	-	expression tag	UNP Q9UHX1
A	106	SER	-	expression tag	UNP Q9UHX1
A	107	MET	-	expression tag	UNP Q9UHX1
A	108	THR	-	expression tag	UNP Q9UHX1
A	109	GLY	-	expression tag	UNP Q9UHX1
A	110	GLY	-	expression tag	UNP Q9UHX1
A	111	GLN	-	expression tag	UNP Q9UHX1
A	112	GLN	-	expression tag	UNP Q9UHX1
A	113	MET	-	expression tag	UNP Q9UHX1
A	114	GLY	-	expression tag	UNP Q9UHX1
A	115	ARG	-	expression tag	UNP Q9UHX1
A	116	GLY	-	expression tag	UNP Q9UHX1
A	117	SER	-	expression tag	UNP Q9UHX1
A	123	GLY	ARG	engineered mutation	UNP Q9UHX1
A	129	SER	CYS	engineered mutation	UNP Q9UHX1
A	255	ALA	CYS	engineered mutation	UNP Q9UHX1
B	101	GLY	-	expression tag	UNP Q9UHX1
B	102	SER	-	expression tag	UNP Q9UHX1
B	103	HIS	-	expression tag	UNP Q9UHX1
B	104	MET	-	expression tag	UNP Q9UHX1
B	105	ALA	-	expression tag	UNP Q9UHX1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	106	SER	-	expression tag	UNP Q9UHX1
B	107	MET	-	expression tag	UNP Q9UHX1
B	108	THR	-	expression tag	UNP Q9UHX1
B	109	GLY	-	expression tag	UNP Q9UHX1
B	110	GLY	-	expression tag	UNP Q9UHX1
B	111	GLN	-	expression tag	UNP Q9UHX1
B	112	GLN	-	expression tag	UNP Q9UHX1
B	113	MET	-	expression tag	UNP Q9UHX1
B	114	GLY	-	expression tag	UNP Q9UHX1
B	115	ARG	-	expression tag	UNP Q9UHX1
B	116	GLY	-	expression tag	UNP Q9UHX1
B	117	SER	-	expression tag	UNP Q9UHX1
B	123	GLY	ARG	engineered mutation	UNP Q9UHX1
B	129	SER	CYS	engineered mutation	UNP Q9UHX1
B	255	ALA	CYS	engineered mutation	UNP Q9UHX1

- Molecule 2 is a DNA chain called DNA (30-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	8	Total	C	N	O	P	0	0	2
			89	37	11	35	6			

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	116	Total	O	0	0
			116	116		
4	B	101	Total	O	0	0
			101	101		
4	C	2	Total	O	0	0
			2	2		

4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	62.44Å 62.44Å 83.33Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 1.95 30.00 – 2.03	Depositor EDS
% Data completeness (in resolution range)	94.2 (30.00-1.95) 94.5 (30.00-2.03)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 2.03Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.196 , 0.232 0.202 , 0.238	Depositor DCC
R_{free} test set	998 reflections (4.53%)	wwPDB-VP
Wilson B-factor (Å ²)	31.0	Xtriage
Anisotropy	0.042	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 34.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.020 for -h,-k,l 0.329 for h,-h-k,-l 0.026 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	3314	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.14% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section:
CL

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	0.43	0/1530	0.89	1/2063 (0.0%)
1	B	0.41	0/1533	0.89	1/2066 (0.0%)
2	C	1.53	6/96 (6.2%)	1.22	1/147 (0.7%)
All	All	0.49	6/3159 (0.2%)	0.90	3/4276 (0.1%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	16	DC	O3'-P	6.16	1.62	1.56
2	C	18	DG	O3'-P	5.85	1.62	1.56
2	C	27	DU	O3'-P	5.62	1.61	1.56
2	C	17	DU	O3'-P	5.43	1.61	1.56
2	C	29	DU	O3'-P	5.37	1.61	1.56
2	C	28	DU	O3'-P	5.13	1.61	1.56

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	18	DG	N9-C1'-C2'	-6.95	103.07	113.50
1	B	117	SER	N-CA-C	-5.23	103.63	110.53
1	A	287	MET	N-CA-C	5.18	119.75	113.38

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	A	1501	0	1477	27	0
1	B	1504	0	1487	34	0
2	C	89	0	41	1	0
3	A	1	0	0	0	0
4	A	116	0	0	1	0
4	B	101	0	0	2	0
4	C	2	0	0	0	0
All	All	3314	0	3005	61	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 10.

All (61) 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:152:PHE:HZ	1:A:190:MET:HE3	1.33	0.92
1:B:146:ARG:HH11	1:B:146:ARG:HB3	1.36	0.87
1:A:152:PHE:CZ	1:A:190:MET:HE3	2.10	0.87
1:A:115:ARG:HB3	1:A:217:GLN:HG2	1.62	0.81
1:B:146:ARG:HB3	1:B:146:ARG:NH1	1.97	0.78
1:A:184:GLN:O	1:A:188:GLU:HG3	1.92	0.70
1:B:251:LYS:HE3	1:B:275:GLU:OE2	1.91	0.70
1:A:234:HIS:HB3	1:A:237:LEU:CD2	2.23	0.68
1:B:168:LYS:HE2	1:B:169:HIS:H	1.59	0.67
1:A:138:TYR:CE1	1:A:139:GLU:HG2	2.34	0.61
1:B:242:ILE:HG22	1:B:272:ILE:HD11	1.86	0.58
1:A:307:MET:HB3	1:A:310:LEU:HD22	1.87	0.56
1:A:244:SER:O	1:A:247:GLU:HG2	2.06	0.56
1:A:212:GLN:HB3	1:A:213:PRO:HD3	1.86	0.56
1:A:137:TYR:HB3	1:A:140:LEU:HG	1.87	0.55
1:B:137:TYR:HA	1:B:198:ARG:CZ	2.36	0.55
1:B:184:GLN:O	1:B:188:GLU:HG3	2.06	0.55
1:B:155:ILE:HD12	1:B:175:VAL:CG1	2.37	0.54
1:B:210:GLN:HG2	1:B:210:GLN:O	2.06	0.53
1:A:207:ASN:CG	1:A:208:ILE:N	2.63	0.53
1:A:161:SER:HB2	1:A:170:LYS:HB2	1.91	0.52
1:B:246:PHE:HB3	1:B:274:TYR:OH	2.08	0.52
1:B:239:ASP:OD1	1:B:259:ARG:NH2	2.41	0.51
1:B:154:PRO:HG2	1:B:178:GLU:OE2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:ARG:HB3	1:A:217:GLN:CG	2.37	0.50
1:B:122:GLN:HG2	4:B:496:HOH:O	2.13	0.48
1:A:179:VAL:HG13	1:A:181:GLU:OE1	2.12	0.48
1:A:216:ASP:O	1:A:220:GLU:HG3	2.14	0.48
1:A:207:ASN:HB3	2:C:18:DG:O6	2.14	0.47
1:B:253:LYS:HE3	1:B:275:GLU:HA	1.95	0.47
1:B:149:PHE:HB3	1:B:177:TYR:OH	2.15	0.47
1:A:288:ASN:O	1:A:289:LEU:HB2	2.15	0.47
1:B:301:LYS:HG3	1:B:302:ALA:N	2.29	0.47
1:B:137:TYR:CE2	1:B:139:GLU:HB2	2.50	0.46
1:B:142:GLU:HG3	1:B:160:MET:HG3	1.96	0.46
1:B:190:MET:O	1:B:193:VAL:HG22	2.16	0.46
1:A:217:GLN:HG3	1:A:221:GLU:OE2	2.15	0.46
1:B:238:SER:N	1:B:241:ASP:OD2	2.47	0.45
1:B:167:MET:O	1:B:168:LYS:HG2	2.16	0.45
1:B:138:TYR:HB2	1:B:168:LYS:NZ	2.32	0.45
1:B:185:LEU:HD21	1:B:300:GLY:HA3	1.99	0.45
1:B:150:ALA:N	1:B:151:PRO:CD	2.80	0.44
1:B:258:ALA:HB1	1:B:267:LYS:HE2	1.99	0.44
1:B:140:LEU:HD22	1:B:144:THR:HG21	2.00	0.44
1:B:161:SER:HB2	1:B:170:LYS:HB2	1.98	0.44
1:B:307:MET:HB3	1:B:310:LEU:HG	2.00	0.44
1:A:150:ALA:N	1:A:151:PRO:CD	2.81	0.44
1:A:234:HIS:HB3	1:A:237:LEU:HD22	1.99	0.43
1:A:115:ARG:HA	4:A:552:HOH:O	2.19	0.42
1:B:241:ASP:O	1:B:245:VAL:HG23	2.20	0.42
1:B:191:ASN:HB3	4:B:418:HOH:O	2.19	0.42
1:B:137:TYR:HB3	1:B:140:LEU:HG	2.02	0.42
1:B:190:MET:HA	1:B:190:MET:HE2	2.01	0.41
1:A:142:GLU:H	1:A:142:GLU:CD	2.26	0.41
1:A:194:MET:HE3	1:A:197:GLY:HA2	2.02	0.41
1:B:115:ARG:HD3	1:B:115:ARG:HA	1.94	0.41
1:A:179:VAL:CG1	1:A:181:GLU:OE1	2.70	0.40
1:A:241:ASP:O	1:A:245:VAL:HG23	2.21	0.40
1:A:152:PHE:CE2	1:A:190:MET:HG2	2.56	0.40
1:A:179:VAL:HG13	1:A:180:PRO:HD2	2.03	0.40
1:B:137:TYR:HA	1:B:198:ARG:NE	2.36	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	191/216 (88%)	189 (99%)	1 (0%)	1 (0%)	24	16
1	B	191/216 (88%)	189 (99%)	2 (1%)	0	100	100
All	All	382/432 (88%)	378 (99%)	3 (1%)	1 (0%)	36	28

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	207	ASN

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	155/171 (91%)	149 (96%)	6 (4%)	28	18
1	B	157/171 (92%)	153 (98%)	4 (2%)	42	34
All	All	312/342 (91%)	302 (97%)	10 (3%)	34	25

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	115	ARG
1	A	146	ARG
1	A	164	SER
1	A	179	VAL
1	A	235	GLN

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Mol	Chain	Res	Type
1	A	309	LEU
1	B	139	GLU
1	B	146	ARG
1	B	160	MET
1	B	195	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	122	GLN
1	A	235	GLN
1	B	281	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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 [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	A	195/216 (90%)	-1.32	0 100 100	21, 31, 46, 56	0
1	B	195/216 (90%)	-1.31	0 100 100	22, 31, 44, 55	0
2	C	2/30 (6%)	-0.69	0 100 100	62, 62, 62, 83	0
All	All	392/462 (84%)	-1.31	0 100 100	21, 32, 45, 83	0

There are no RSRZ outliers to report.

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, 95th 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 ²)	Q<0.9
3	CL	A	401	1/1	0.99	0.05	46,46,46,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.