



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 8, 2023 – 10:59 AM EDT

PDB ID : 6EEN
Title : Crystal structure of a designer Pentatrigo Peptide RNA binding protein, bound to a complex RNA target and featuring an infinite superhelix and microheterogeneity.
Authors : Schmidberger, J.W.; Bond, C.S.
Deposited on : 2018-08-15
Resolution : 2.01 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

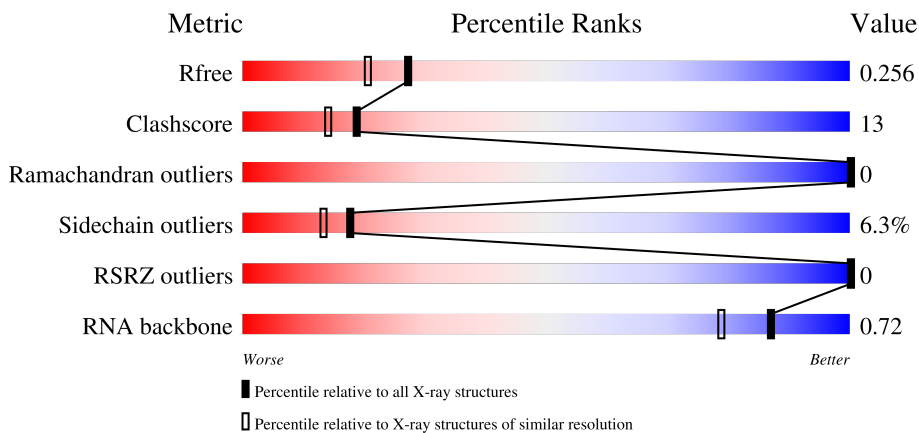
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.01 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.



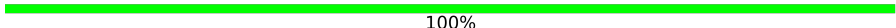
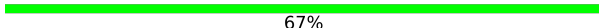
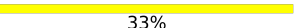
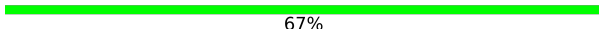
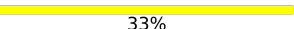
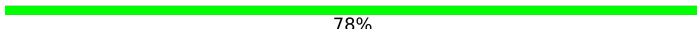
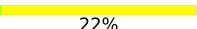
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)
RNA backbone	3102	1079 (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 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	315	 79% 19%
2	B	315	 79% 18%
3	C	315	 75% 24%
4	D	315	 79% 19%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	F	9	 100%
6	G	9	 67%  33%
7	H	9	 67%  33%
8	I	9	 78%  22%

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 10755 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 Designer Pentatricopeptide Protein dPPR10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	315	2444	1563	392	480	9	0	315	0

- Molecule 2 is a protein called Designer Pentatricopeptide Protein dPPR10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	315	2453	1563	401	480	9	0	315	0

- Molecule 3 is a protein called Designer Pentatricopeptide Protein dPPR10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	315	2444	1563	401	471	9	0	315	0

- Molecule 4 is a protein called Designer Pentatricopeptide Protein dPPR10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	315	2435	1554	401	471	9	0	315	0

- Molecule 5 is a RNA chain called RNA (5'-R(P*GP*GP*GP*GP*GP*GP*GP*GP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
5	F	9	207	90	45	63	9	0	9	0

- Molecule 6 is a RNA chain called RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*U)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
6	G	9	180	81	18	72	9	0	9	0

- Molecule 7 is a RNA chain called RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*A)-3').

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
			Total	C	N	O				P
7	H	9	198	90	45	54	9	0	9	0

- Molecule 8 is a RNA chain called RNA (5'-R(P*CP*CP*CP*CP*CP*CP*CP*C)-3').

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
			Total	C	N	O				P
8	I	9	180	81	27	63	9	0	9	0

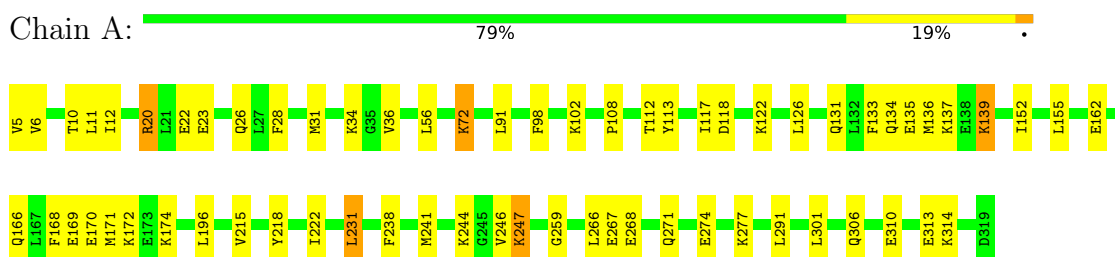
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	87	Total	O	0	0
			87	87		
9	B	35	Total	O	0	0
			35	35		
9	C	31	Total	O	0	0
			31	31		
9	D	25	Total	O	0	0
			25	25		
9	F	16	Total	O	0	0
			16	16		
9	G	1	Total	O	0	0
			1	1		
9	H	16	Total	O	0	0
			16	16		
9	I	3	Total	O	0	0
			3	3		

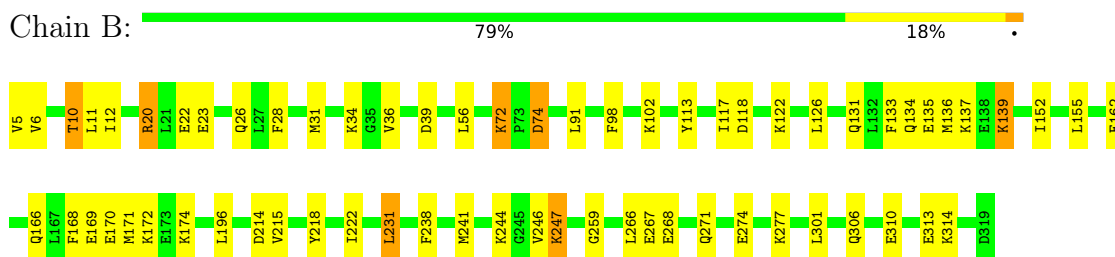
3 Residue-property plots

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.

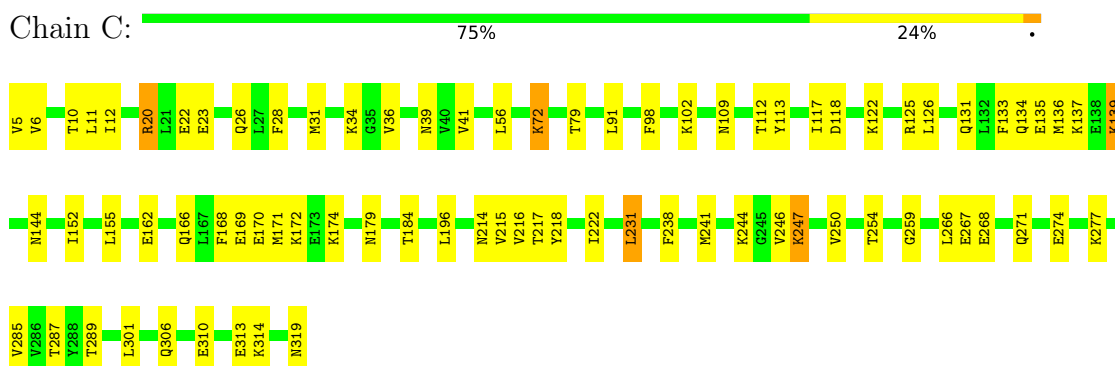
- Molecule 1: Designer Pentatricopeptide Protein dPPR10



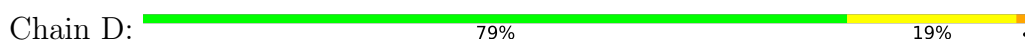
- Molecule 2: Designer Pentatricopeptide Protein dPPR10

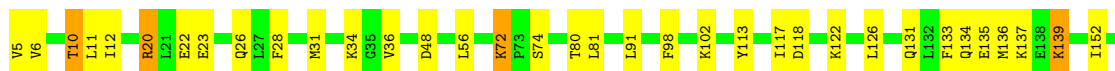


- Molecule 3: Designer Pentatricopeptide Protein dPPR10



- Molecule 4: Designer Pentatricopeptide Protein dPPR10



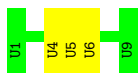


- Molecule 5: RNA (5'-R(P*GP*GP*GP*GP*GP*GP*GP*GP*G)-3')

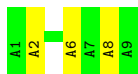


There are no outlier residues recorded for this chain.

- Molecule 6: RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*U)-3')



- Molecule 7: RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*A)-3')



- Molecule 8: RNA (5'-R(P*CP*CP*CP*CP*CP*CP*CP*CP*C)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	43.35Å 51.65Å 51.97Å 118.12° 97.21° 96.00°	Depositor
Resolution (Å)	44.92 – 2.01 44.92 – 2.01	Depositor EDS
% Data completeness (in resolution range)	97.0 (44.92-2.01) 97.0 (44.92-2.01)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 2.01Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.183 , 0.248 0.192 , 0.256	Depositor DCC
R_{free} test set	1207 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	26.9	Xtrriage
Anisotropy	0.660	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 35.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.055 for -h,-l,-k	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10755	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.61% 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	A	0.76	2/2470 (0.1%)	0.80	0/3323
2	B	0.81	3/2479 (0.1%)	0.84	0/3332
3	C	0.77	2/2470 (0.1%)	0.82	0/3323
4	D	0.79	3/2461 (0.1%)	0.81	0/3305
5	F	0.21	0/233	0.59	0/365
6	G	1.56	2/197 (1.0%)	1.20	1/302 (0.3%)
7	H	0.71	0/224	0.81	0/347
8	I	1.12	1/197 (0.5%)	1.05	0/302
All	All	0.80	13/10731 (0.1%)	0.83	1/14599 (0.0%)

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
3	C	0	1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	313[A]	GLU	CD-OE2	6.75	1.33	1.25
2	B	313[B]	GLU	CD-OE2	6.74	1.33	1.25
6	G	5[B]	U	P-OP2	-6.69	1.37	1.49
3	C	313[C]	GLU	CD-OE2	6.68	1.32	1.25
4	D	313[D]	GLU	CD-OE2	6.68	1.32	1.25

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	G	6[B]	U	C5'-C4'-O4'	5.16	115.29	109.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	125[C]	ARG	Sidechain

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	2444	0	2503	63	0
2	B	2453	0	2484	64	0
3	C	2444	0	2509	75	0
4	D	2435	0	2493	63	0
5	F	207	0	69	0	0
6	G	180	0	72	0	0
7	H	198	0	79	3	0
8	I	180	0	74	1	0
9	A	87	0	0	13	0
9	B	35	0	0	4	0
9	C	31	0	0	4	0
9	D	25	0	0	0	0
9	F	16	0	0	7	0
9	G	1	0	0	0	0
9	H	16	0	0	3	0
9	I	3	0	0	0	0
All	All	10755	0	10283	267	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 13.

The worst 5 of 267 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:28[A]:PHE:HA	1:A:31[A]:MET:HE2	1.33	1.10
4:D:28[D]:PHE:HA	4:D:31[D]:MET:HE2	1.33	1.10
2:B:28[B]:PHE:HA	2:B:31[B]:MET:HE2	1.33	1.10
3:C:28[C]:PHE:HA	3:C:31[C]:MET:HE2	1.33	1.10
1:A:215[A]:VAL:HG23	9:B:422:HOH:O	1.52	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	
1	A	313/315 (99%)	300 (96%)	13 (4%)	0	100	100
2	B	313/315 (99%)	302 (96%)	11 (4%)	0	100	100
3	C	313/315 (99%)	301 (96%)	12 (4%)	0	100	100
4	D	313/315 (99%)	303 (97%)	10 (3%)	0	100	100
All	All	1252/1260 (99%)	1206 (96%)	46 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	260/261 (100%)	244 (94%)	16 (6%)	18	13
2	B	260/261 (100%)	243 (94%)	17 (6%)	17	12
3	C	260/261 (100%)	244 (94%)	16 (6%)	18	13
4	D	260/261 (100%)	243 (94%)	17 (6%)	17	12
All	All	1040/1044 (100%)	974 (94%)	66 (6%)	18	13

5 of 66 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	137[D]	LYS
4	D	172[D]	LYS
4	D	306[D]	GLN
2	B	137[B]	LYS
2	B	134[B]	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	99[C]	GLN
4	D	64[D]	GLN
3	C	166[C]	GLN
3	C	306[C]	GLN
4	D	99[D]	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	F	8/9 (88%)	0	0
6	G	8/9 (88%)	0	0
7	H	8/9 (88%)	0	0
8	I	8/9 (88%)	0	0
All	All	32/36 (88%)	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 [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, 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	315/315 (100%)	-0.58	0 100 100	18, 31, 52, 67	315 (100%)
2	B	315/315 (100%)	-0.59	0 100 100	15, 30, 51, 67	315 (100%)
3	C	315/315 (100%)	-0.59	0 100 100	17, 30, 52, 67	315 (100%)
4	D	315/315 (100%)	-0.60	0 100 100	15, 30, 52, 67	315 (100%)
5	F	9/9 (100%)	-1.03	0 100 100	24, 31, 50, 57	9 (100%)
6	G	9/9 (100%)	-1.07	0 100 100	20, 23, 26, 29	9 (100%)
7	H	9/9 (100%)	-1.12	0 100 100	22, 26, 43, 46	9 (100%)
8	I	9/9 (100%)	-1.10	0 100 100	21, 24, 29, 32	9 (100%)
All	All	1296/1296 (100%)	-0.60	0 100 100	15, 30, 52, 67	1296 (100%)

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 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.