



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 21, 2016 – 04:57 AM EDT

PDB ID : 5I9G
Title : Crystal structure of designed pentatricopeptide repeat protein dPPR-U8C2 in complex with its target RNA U8C2
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Deposited on : 2016-02-20
Resolution : 2.29 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
<http://wwpdb.org/validation/2016/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
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027257
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027257

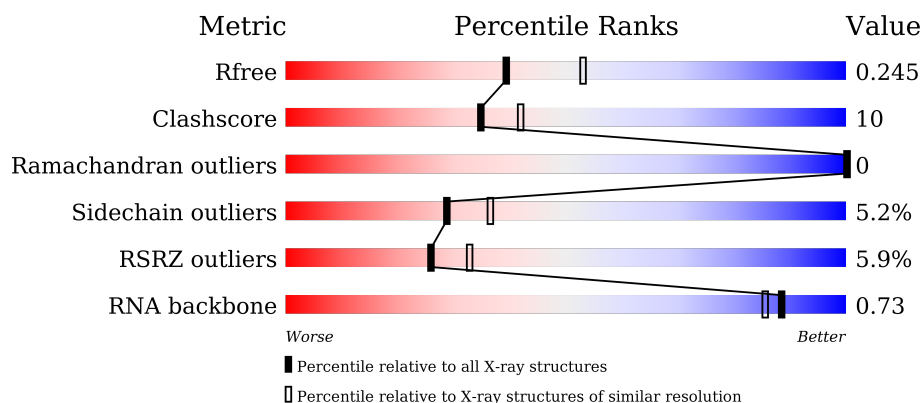
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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}	91344	5193 (2.30-2.26)
Clashscore	102246	5929 (2.30-2.26)
Ramachandran outliers	100387	5851 (2.30-2.26)
Sidechain outliers	100360	5850 (2.30-2.26)
RSRZ outliers	91569	5204 (2.30-2.26)
RNA backbone	2183	1000 (2.80-1.76)

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. 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	460	<div> <div>5%</div> <div>66%</div> <div>14%</div> <div>•</div> <div>18%</div> </div>
2	A	18	<div> <div>6%</div> <div>33%</div> <div>28%</div> <div>6%</div> <div>33%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3135 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 pentatricopeptide repeat protein dPPR-U8C2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	375	Total	C	N	O	S	0	0	0
			2860	1842	445	553	20			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	12	Total	C	N	O	P	0	0	0
			208	92	22	83	11			

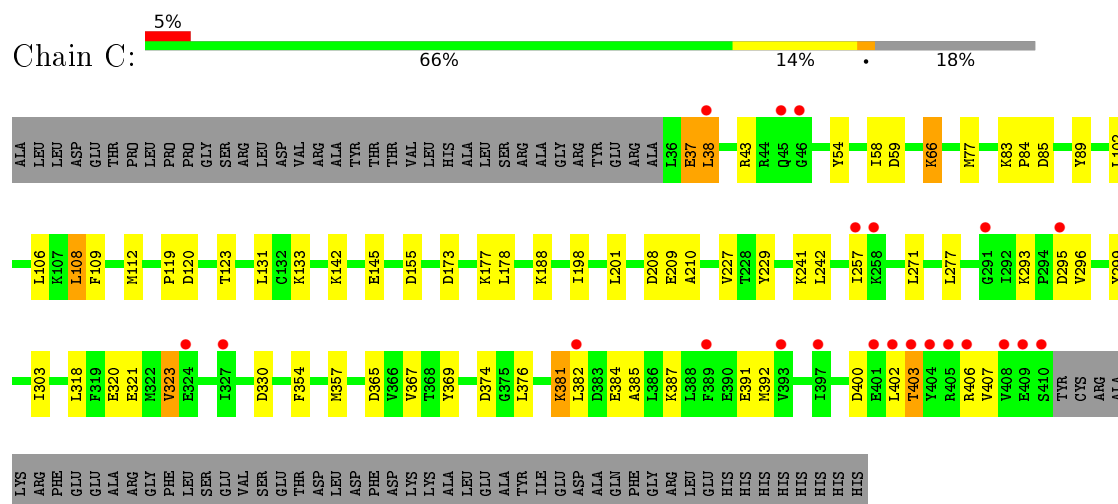
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	53	Total	O	0	0
			53	53		
3	A	14	Total	O	0	0
			14	14		

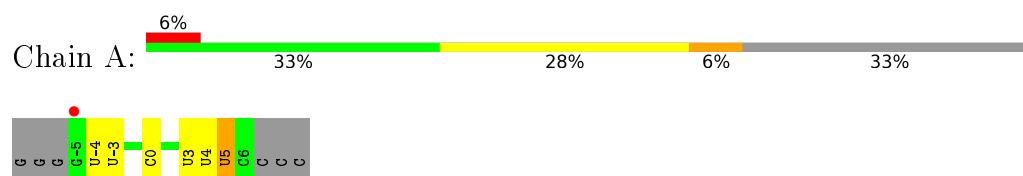
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: pentatricopeptide repeat protein dPPR-U8C2



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.43Å 84.78Å 94.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.67 – 2.29 39.86 – 2.29	Depositor EDS
% Data completeness (in resolution range)	97.5 (38.67-2.29) 95.3 (39.86-2.29)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.85 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.10.1 _2155: ???)	Depositor
R, R_{free}	0.225 , 0.247 0.223 , 0.245	Depositor DCC
R_{free} test set	887 reflections (4.84%)	DCC
Wilson B-factor (Å ²)	41.7	Xtriage
Anisotropy	0.191	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 61.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3135	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.55% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	C	0.74	0/2892	0.89	4/3892 (0.1%)
2	A	1.44	5/227 (2.2%)	0.83	0/349
All	All	0.81	5/3119 (0.2%)	0.89	4/4241 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	5	U	O3'-P	11.57	1.75	1.61
2	A	-3	U	O3'-P	-6.08	1.53	1.61
2	A	3	U	O3'-P	-5.63	1.54	1.61
2	A	-4	U	O3'-P	-5.38	1.54	1.61
2	A	4	U	O3'-P	-5.35	1.54	1.61

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	382	LEU	CA-CB-CG	-6.13	101.19	115.30
1	C	155	ASP	CB-CG-OD1	6.11	123.80	118.30
1	C	330	ASP	CB-CG-OD1	5.82	123.54	118.30
1	C	120	ASP	CB-CG-OD1	5.59	123.34	118.30

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	C	2860	0	2970	61	0
2	A	208	0	102	2	0
3	A	14	0	0	1	0
3	C	53	0	0	8	0
All	All	3135	0	3072	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:C:112:MET:SD	3:C:541:HOH:O	1.91	1.24
1:C:85:ASP:OD2	3:C:501:HOH:O	1.83	0.95
1:C:112:MET:HE3	1:C:123:THR:HG21	1.52	0.89
1:C:369:TYR:OH	3:C:502:HOH:O	1.93	0.86
1:C:89:TYR:HD1	1:C:108:LEU:HD23	1.38	0.85
1:C:112:MET:CE	1:C:123:THR:HG21	2.07	0.85
1:C:58:ILE:HD11	1:C:77:MET:HE3	1.60	0.83
1:C:83:LYS:O	3:C:503:HOH:O	1.99	0.78
1:C:295:ASP:CG	1:C:296:VAL:H	1.88	0.75
1:C:242:LEU:HD21	1:C:271:LEU:HD23	1.70	0.74
1:C:58:ILE:HD11	1:C:77:MET:CE	2.18	0.73
1:C:89:TYR:CD1	1:C:108:LEU:HD23	2.22	0.73
1:C:109:PHE:HD1	1:C:112:MET:HE1	1.54	0.73
1:C:89:TYR:HD1	1:C:108:LEU:CD2	2.03	0.71
1:C:299:TYR:HD1	1:C:318:LEU:HD23	1.57	0.69
1:C:391:GLU:OE2	3:C:502:HOH:O	2.10	0.69
1:C:321:GLU:OE1	3:C:504:HOH:O	2.10	0.69
1:C:303:ILE:HG13	1:C:318:LEU:HD22	1.74	0.68
1:C:38:LEU:HD13	1:C:38:LEU:C	2.13	0.68
1:C:299:TYR:HD1	1:C:318:LEU:CD2	2.07	0.68
1:C:201:LEU:HD13	1:C:209:GLU:HG3	1.76	0.67
1:C:365:ASP:OD2	3:C:505:HOH:O	2.12	0.67
1:C:89:TYR:CD1	1:C:108:LEU:CD2	2.80	0.64
1:C:38:LEU:HD22	1:C:38:LEU:O	1.97	0.64
1:C:295:ASP:CG	1:C:296:VAL:N	2.56	0.59
1:C:400:ASP:OD1	1:C:402:LEU:HB2	2.02	0.59
1:C:109:PHE:CD1	1:C:112:MET:CE	2.86	0.58
1:C:354:PHE:CD1	1:C:357:MET:HE3	2.39	0.57
1:C:198:ILE:HG23	1:C:210:ALA:HB1	1.86	0.56
1:C:109:PHE:HD1	1:C:112:MET:CE	2.19	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:112:MET:CE	1:C:119:PRO:HG3	2.36	0.55
1:C:354:PHE:CD1	1:C:357:MET:CE	2.89	0.55
1:C:188:LYS:O	3:C:506:HOH:O	2.18	0.53
1:C:37:GLU:OE2	1:C:37:GLU:HA	2.08	0.52
1:C:320:GLU:O	1:C:323:VAL:HG13	2.11	0.51
1:C:112:MET:HE1	1:C:123:THR:HG21	1.91	0.51
1:C:354:PHE:HA	1:C:357:MET:CE	2.41	0.50
1:C:112:MET:HE2	1:C:119:PRO:HG3	1.94	0.50
1:C:376:LEU:HB2	1:C:385:ALA:HB2	1.94	0.49
1:C:109:PHE:CD1	1:C:112:MET:HE1	2.40	0.49
1:C:392:MET:HE1	1:C:403:THR:HG21	1.95	0.49
1:C:54:TYR:O	1:C:58:ILE:HG13	2.14	0.48
1:C:173:ASP:O	1:C:177:LYS:HG2	2.13	0.48
1:C:83:LYS:HA	1:C:84:PRO:HD2	1.82	0.47
1:C:354:PHE:HA	1:C:357:MET:HE2	1.97	0.46
1:C:229:TYR:CE2	1:C:257:ILE:HD12	2.50	0.46
1:C:227:VAL:HG11	2:A:0:C:C2	2.51	0.46
1:C:354:PHE:HD1	1:C:357:MET:CE	2.27	0.45
1:C:66:LYS:HD3	1:C:66:LYS:HA	1.70	0.44
1:C:299:TYR:CD1	1:C:318:LEU:CD2	2.94	0.43
1:C:112:MET:HE3	1:C:119:PRO:HG3	2.00	0.43
1:C:102:LEU:HD21	1:C:131:LEU:HD23	2.01	0.43
1:C:106:LEU:HA	1:C:106:LEU:HD23	1.92	0.42
1:C:367:VAL:HG13	2:A:5:U:N1	2.33	0.42
1:C:374:ASP:OD1	1:C:406:ARG:NE	2.43	0.42
1:C:299:TYR:CD1	1:C:318:LEU:HD21	2.54	0.42
1:C:59:ASP:HB2	3:A:106:HOH:O	2.21	0.41
1:C:142:LYS:O	1:C:145:GLU:HG2	2.21	0.41
1:C:77:MET:HE2	1:C:77:MET:HB3	1.92	0.41
1:C:357:MET:HB3	1:C:357:MET:HE2	1.92	0.40
1:C:381:LYS:HD3	1:C:384:GLU:OE1	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	C	373/460 (81%)	353 (95%)	20 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	C	310/393 (79%)	294 (95%)	16 (5%)	29	36

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	37	GLU
1	C	38	LEU
1	C	43	ARG
1	C	66	LYS
1	C	108	LEU
1	C	133	LYS
1	C	178	LEU
1	C	208	ASP
1	C	241	LYS
1	C	277	LEU
1	C	293	LYS
1	C	323	VAL
1	C	381	LYS
1	C	387	LYS
1	C	403	THR
1	C	407	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	A	9/18 (50%)	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 carbohydrates 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 ⓘ

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, 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	375/460 (81%)	0.28	22 (5%)	26 33	27, 49, 79, 107	0
2	A	12/18 (66%)	-0.28	1 (8%)	14 19	40, 44, 73, 92	1 (8%)
All	All	387/478 (80%)	0.26	23 (5%)	26 33	27, 49, 79, 107	1 (0%)

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	408	VAL	5.6
1	C	401	GLU	4.9
1	C	410	SER	4.7
1	C	389	PHE	3.8
1	C	324	GLU	3.6
1	C	38	LEU	3.6
1	C	393	VAL	3.3
1	C	258	LYS	3.3
1	C	405	ARG	3.2
1	C	257	ILE	2.9
1	C	404	TYR	2.9
1	C	327	ILE	2.8
1	C	409	GLU	2.7
1	C	295	ASP	2.7
1	C	402	LEU	2.6
1	C	406	ARG	2.6
1	C	291	GLY	2.3
2	A	-5	G	2.2
1	C	382	LEU	2.2
1	C	403	THR	2.1
1	C	46	GLY	2.1
1	C	45	GLN	2.1
1	C	397	ILE	2.1

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 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.