Full wwPDB X-ray Structure Validation Report (i)

Oct 4, 2023 – 06:37 PM EDT

PDB ID	:	6PRV
Title	:	58nt RNA L11-binding domain from E. coli 23S rRNA
Authors	:	Conn, G.L.; Dunstan, M.S.
Deposited on	:	2019-07-11
Resolution	:	2.71 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 (i) 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 (i)) were used in the production of this report:

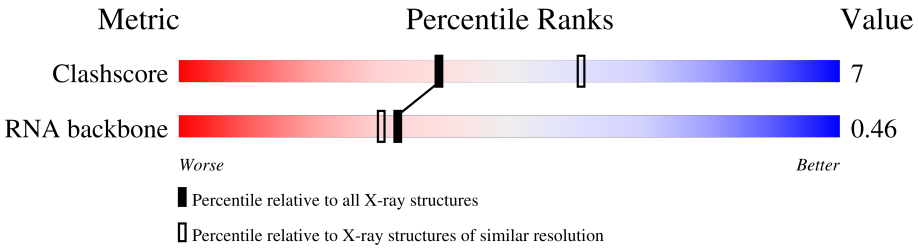
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance

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

The reported resolution of this entry is 2.71 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))
Clashscore	141614	3686 (2.74-2.70)
RNA backbone	3102	1067 (3.00-2.44)

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5027 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 23S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	58	Total 1250	C 555	N 226	O 409	P 60	0	0	0
1	B	58	Total 1250	C 555	N 226	O 409	P 60	0	0	0
1	C	58	Total 1250	C 555	N 226	O 409	P 60	0	0	0
1	D	58	Total 1250	C 555	N 226	O 409	P 60	0	0	0

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	9	Total 9	Mg 9	0	0
2	B	5	Total 5	Mg 5	0	0
2	C	6	Total 6	Mg 6	0	0
2	D	2	Total 2	Mg 2	0	0

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	K 1	0	0
3	B	1	Total 1	K 1	0	0
3	C	1	Total 1	K 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	2	Total O 2 2	0	0

SEQUENCE-PLOTS INFOmissingINFO

3 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	89.61Å 73.61Å 130.28Å 90.00° 100.96° 90.00°	Depositor
Resolution (Å)	39.36 – 2.71	Depositor
% Data completeness (in resolution range)	96.9 (39.36-2.71)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.96 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, R_{free}	0.204 , 0.260	Depositor
Wilson B-factor (Å^2)	78.6	Xtriage
Anisotropy	0.601	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.52$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5027	wwPDB-VP
Average B, all atoms (Å^2)	108.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.43% 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.

4 Model quality

4.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, MG, K

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	0.67	0/1363	1.19	4/2122 (0.2%)
1	B	0.49	0/1363	0.99	2/2122 (0.1%)
1	C	0.49	0/1363	1.04	1/2122 (0.0%)
1	D	0.40	0/1363	0.96	0/2122
All	All	0.52	0/5452	1.05	7/8488 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1069	A	O4'-C1'-N9	9.64	115.92	108.20
1	B	1069	A	O4'-C1'-N9	6.77	113.61	108.20
1	C	1069	A	P-O3'-C3'	5.72	126.57	119.70
1	A	1065	U	OP2-P-O3'	5.57	117.45	105.20
1	A	1091	G	N1-C2-N2	-5.55	111.20	116.20
1	A	1072	C	C6-N1-C2	-5.20	118.22	120.30
1	B	1074	G	C5-C6-O6	-5.12	125.53	128.60

There are no chirality outliers.

There are no planarity outliers.

4.2 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	1250	0	625	10	0
1	B	1250	0	625	12	1
1	C	1250	0	625	11	1
1	D	1250	0	624	17	0
2	A	9	0	0	0	0
2	B	5	0	0	0	0
2	C	6	0	0	0	0
2	D	2	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	B	2	0	0	0	0
All	All	5027	0	2499	50	1

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 7.

All (50) 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:1065:U:H3	1:C:1069:A:HO2'	1.05	0.93
1:B:1063:G:H1	1:B:1075:C:H42	1.34	0.76
1:D:1058:U:H2'	1:D:1059:G:H8	1.52	0.75
1:D:1081:U:H2'	1:D:1082:U:C6	2.28	0.69
1:D:1083:U:O2'	1:D:1085:A:N7	2.23	0.66
1:A:1056:G:H5"	1:A:1057:A:H5'	1.82	0.62
1:D:1058:U:H2'	1:D:1059:G:C8	2.32	0.62
1:D:1053:C:H2'	1:D:1054:A:H8	1.65	0.60
1:D:1053:C:H2'	1:D:1054:A:C8	2.37	0.60
1:D:1074:G:H2'	1:D:1075:C:H6	1.67	0.60
1:D:1074:G:H2'	1:D:1075:C:C6	2.39	0.58
1:B:1105:U:H2'	1:B:1106:G:C8	2.39	0.58
1:C:1074:G:H2'	1:C:1075:C:C6	2.39	0.57
1:B:1063:G:H1	1:B:1075:C:N4	2.00	0.57
1:C:1093:G:O2'	1:C:1098:A:N6	2.37	0.55
1:A:1065:U:H2'	1:A:1066:U:O4'	2.08	0.53
1:C:1056:G:H4'	1:C:1086:A:C8	2.44	0.52
1:C:1094:U:N3	1:C:1097:U:OP2	2.43	0.52
1:D:1059:G:H3'	1:D:1060:U:H2'	1.91	0.51
1:A:1082:U:H2'	1:A:1083:U:O4'	2.11	0.51
1:D:1092:C:H2'	1:D:1093:G:O4'	2.11	0.50
1:D:1064:C:H42	1:D:1074:G:H1	1.61	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1069:A:H4'	1:D:1070:A:H5"	1.95	0.48
1:B:1051:GTP:N3	1:B:1051:GTP:H2'	2.29	0.47
1:C:1056:G:H5"	1:C:1057:A:O4'	2.15	0.47
1:A:1056:G:N2	1:A:1102:C:C5	2.82	0.47
1:B:1062:G:H2'	1:B:1063:G:C8	2.50	0.47
1:A:1086:A:O2'	1:A:1103:A:N1	2.41	0.46
1:B:1064:C:H2'	1:B:1065:U:O4'	2.16	0.46
1:A:1077:A:N1	1:A:1088:A:O2'	2.40	0.46
1:C:1074:G:H2'	1:C:1075:C:H6	1.79	0.45
1:D:1059:G:N2	1:D:1060:U:O4	2.51	0.44
1:C:1094:U:O2'	1:C:1096:A:N7	2.42	0.44
1:D:1069:A:H5"	1:D:1070:A:C8	2.53	0.44
1:B:1095:A:H2'	1:B:1096:A:C8	2.53	0.43
1:A:1105:U:H2'	1:A:1106:G:C8	2.53	0.43
1:B:1056:G:H5"	1:B:1057:A:O4'	2.18	0.43
1:B:1056:G:H4'	1:B:1086:A:C8	2.53	0.43
1:D:1073:A:C4	1:D:1074:G:C8	3.07	0.42
1:C:1055:G:N3	1:C:1085:A:H2	2.17	0.42
1:A:1080:A:H2'	1:A:1081:U:H6	1.85	0.42
1:B:1070:A:H5'	1:B:1072:C:OP2	2.20	0.42
1:D:1052:C:H2'	1:D:1053:C:C6	2.56	0.41
1:C:1059:G:H2'	1:C:1060:U:C5	2.56	0.41
1:D:1080:A:H2'	1:D:1081:U:C6	2.56	0.41
1:C:1084:A:N3	1:C:1105:U:O2'	2.45	0.41
1:A:1095:A:H2'	1:A:1096:A:C8	2.56	0.40
1:A:1056:G:H4'	1:A:1086:A:C8	2.57	0.40
1:B:1062:G:H2'	1:B:1063:G:H8	1.86	0.40
1:B:1099:G:O2'	1:B:1100:C:H5'	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1108:U:O2'	1:C:1092:C:OP1[1_545]	2.14	0.06

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

There are no protein molecules in this entry.

4.3.2 Protein sidechains (i)

There are no protein molecules in this entry.

4.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	56/58 (96%)	9 (16%)	0
1	B	56/58 (96%)	5 (8%)	0
1	C	56/58 (96%)	7 (12%)	0
1	D	56/58 (96%)	14 (25%)	0
All	All	224/232 (96%)	35 (15%)	0

All (35) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	1060	U
1	A	1063	G
1	A	1064	C
1	A	1067	A
1	A	1070	A
1	A	1088	A
1	A	1090	A
1	A	1091	G
1	A	1097	U
1	B	1060	U
1	B	1070	A
1	B	1088	A
1	B	1090	A
1	B	1097	U
1	C	1060	U
1	C	1064	C
1	C	1070	A
1	C	1083	U
1	C	1088	A
1	C	1090	A
1	C	1108	U
1	D	1061	U
1	D	1064	C
1	D	1065	U
1	D	1069	A
1	D	1070	A
1	D	1084	A

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Mol	Chain	Res	Type
1	D	1087	G
1	D	1088	A
1	D	1089	A
1	D	1090	A
1	D	1097	U
1	D	1098	A
1	D	1101	U
1	D	1104	C

There are no RNA pucker outliers to report.

4.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry (i)

Of 25 ligands modelled in this entry, 25 are 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.

4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

5 Fit of model and data

5.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

5.2 Non-standard residues in protein, DNA, RNA chains

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

5.4 Ligands

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers

EDS failed to run properly - this section is therefore empty.