



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 3, 2021 – 08:04 PM EST

PDB ID : 6OON
Title : Human Argonaute4 bound to guide RNA
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Deposited on : 2019-04-23
Resolution : 1.90 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	:	2.17.1
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)	:	2.17.1

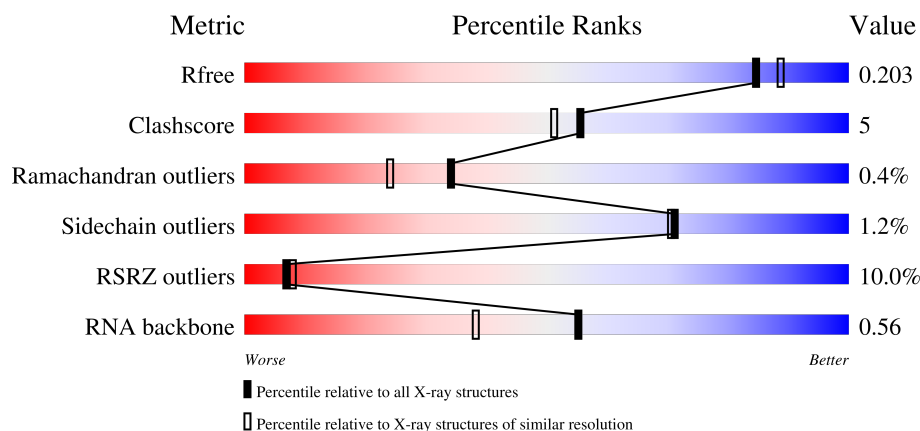
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)
RNA backbone	3102	1013 (2.42-1.38)

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	863	<div> <div>9%</div> <div> <div></div> <div>81%</div> <div>10%</div> <div>9%</div> </div> </div>
2	B	12	<div> <div>25%</div> <div> <div></div> <div>58%</div> <div>42%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7021 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 Protein argonaute-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	785	Total	C	N	O	S	8	5	0
			6314	4026	1126	1118	44			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q9HCK5
A	0	SER	-	expression tag	UNP Q9HCK5

- Molecule 2 is a RNA chain called RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*AP*UP*U)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	12	Total	C	N	O	P	0	0	0
			243	108	49	74	12			

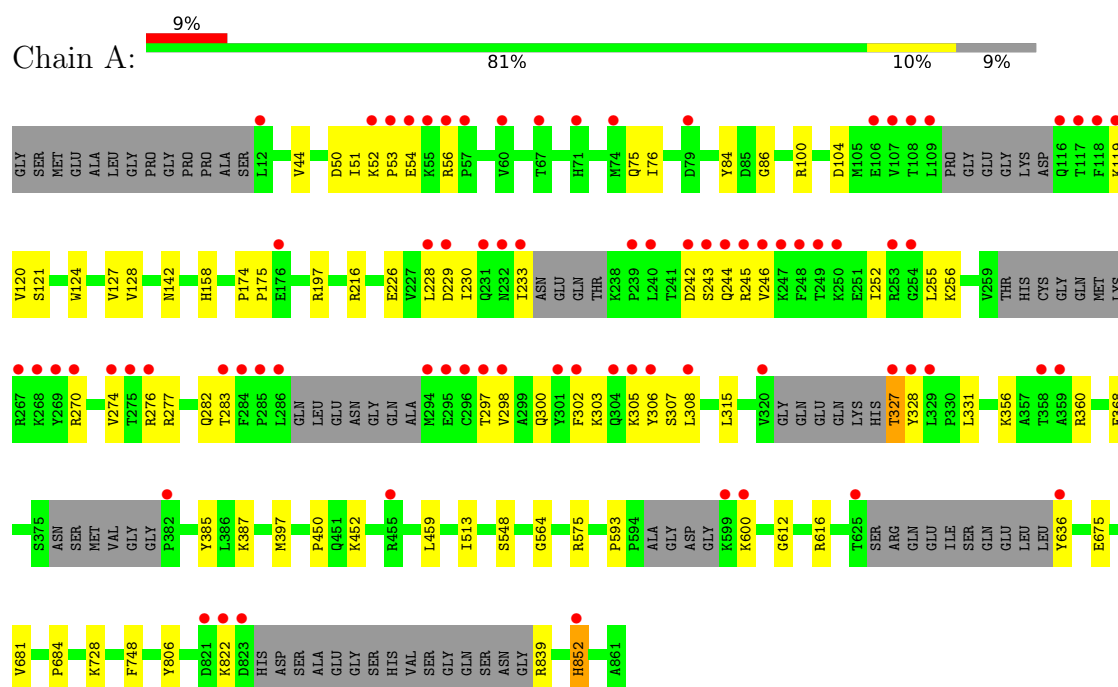
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	452	Total	O	0	0
			452	452		
3	B	12	Total	O	0	0
			12	12		

3 Residue-property plots [i](#)

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: Protein argonaute-4



• Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*UP*U)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	213.98Å 68.01Å 83.27Å 90.00° 102.68° 90.00°	Depositor
Resolution (Å)	49.08 – 1.90 49.08 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.9 (49.08-1.90) 98.9 (49.08-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 1.90Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.171 , 0.202 0.173 , 0.203	Depositor DCC
R_{free} test set	4550 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	27.8	Xtriage
Anisotropy	0.200	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 56.4	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	0.96	EDS
Total number of atoms	7021	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.86% 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	0.39	0/6466	0.55	0/8754
2	B	0.86	1/271 (0.4%)	0.90	0/414
All	All	0.42	1/6737 (0.0%)	0.57	0/9168

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	A	OP3-P	-11.89	1.46	1.61

There are no bond angle outliers.

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	6314	0	6385	64	0
2	B	243	0	121	6	0
3	A	452	0	0	3	0
3	B	12	0	0	0	0
All	All	7021	0	6506	66	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 5.

All (66) 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:452:LYS:HD2	1:A:452:LYS:H	1.38	0.87
1:A:283:THR:HG22	1:A:297:THR:HG22	1.67	0.74
1:A:450:PRO:HB2	1:A:452:LYS:HD3	1.68	0.74
1:A:452:LYS:H	1:A:452:LYS:CD	2.03	0.71
1:A:51:ILE:HG12	1:A:120:VAL:HG12	1.76	0.67
1:A:100:ARG:HG2	1:A:100:ARG:HH11	1.58	0.67
1:A:298:VAL:HG13	1:A:302:PHE:HE2	1.63	0.64
1:A:216:ARG:NH2	1:A:226:GLU:OE2	2.34	0.61
1:A:245:ARG:HH12	1:A:274:VAL:HB	1.66	0.61
1:A:243:SER:HA	1:A:246:VAL:HG12	1.83	0.60
1:A:360:ARG:NH1	1:A:368:GLU:OE2	2.34	0.60
1:A:327:THR:N	2:B:21:U:HO2'	2.00	0.59
1:A:228:LEU:O	1:A:230:ILE:HG13	2.02	0.59
1:A:197:ARG:NH2	1:A:675:GLU:OE2	2.36	0.58
1:A:459:LEU:HD21	1:A:513:ILE:HD11	1.84	0.58
1:A:245:ARG:NH1	1:A:274:VAL:HB	2.20	0.57
1:A:104:ASP:CG	1:A:119:LYS:HZ3	2.11	0.54
2:B:7:A:H2'	2:B:8:A:C8	2.43	0.53
1:A:245:ARG:HE	1:A:276:ARG:HG2	1.74	0.53
1:A:459:LEU:HD21	1:A:513:ILE:CD1	2.38	0.53
1:A:256:LYS:HE2	1:A:270:ARG:HH22	1.72	0.53
2:B:7:A:H2'	2:B:8:A:H8	1.74	0.53
1:A:100:ARG:HH11	1:A:100:ARG:CG	2.24	0.50
1:A:283:THR:HA	1:A:297:THR:HA	1.93	0.50
1:A:52:LYS:HA	1:A:53:PRO:C	2.31	0.50
1:A:142:ASN:OD1	1:A:142:ASN:N	2.45	0.49
1:A:298:VAL:HG13	1:A:302:PHE:CE2	2.46	0.49
1:A:277:ARG:NH2	1:A:283:THR:H	2.11	0.48
1:A:277:ARG:NH2	1:A:283:THR:OG1	2.46	0.48
1:A:277:ARG:NE	1:A:282:GLN:HA	2.28	0.48
1:A:564:GLY:HA2	1:A:616:ARG:CZ	2.43	0.48
1:A:300:GLN:HA	1:A:303:LYS:HE2	1.97	0.46
1:A:303:LYS:HA	1:A:308:LEU:H	1.81	0.46
1:A:233:ILE:HD12	1:A:233:ILE:O	2.15	0.46
1:A:228:LEU:HD13	1:A:244:GLN:HB3	1.98	0.46
1:A:305:LYS:HB2	1:A:306:TYR:HD1	1.81	0.45
1:A:564:GLY:HA2	1:A:616:ARG:NH2	2.31	0.45
1:A:53:PRO:HG2	1:A:56:ARG:HE	1.82	0.45
1:A:104:ASP:CB	1:A:119:LYS:HZ3	2.29	0.45
1:A:397:MET:HB3	1:A:397:MET:HE2	1.72	0.45
1:A:636:TYR:N	3:A:916:HOH:O	2.49	0.45
1:A:452:LYS:HD2	1:A:452:LYS:N	2.20	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:307:SER:O	1:A:307:SER:OG	2.28	0.44
1:A:104:ASP:OD1	1:A:119:LYS:NZ	2.49	0.44
1:A:852:HIS:O	1:A:852:HIS:ND1	2.49	0.43
1:A:681:VAL:O	1:A:684:PRO:HD2	2.18	0.43
1:A:728:LYS:HG3	3:A:925:HOH:O	2.19	0.43
1:A:75:GLN:HG2	1:A:76:ILE:HG12	2.01	0.43
1:A:84:TYR:CE2	1:A:86:GLY:HA2	2.54	0.43
1:A:256:LYS:NZ	2:B:15:A:OP2	2.48	0.43
1:A:124:TRP:HZ2	1:A:127:VAL:HG23	1.85	0.42
1:A:174:PRO:HA	1:A:175:PRO:HD3	1.87	0.42
1:A:356:LYS:HE2	1:A:356:LYS:HB2	1.68	0.42
1:A:593:PRO:HG2	1:A:600:LYS:O	2.19	0.42
1:A:252:ILE:HD12	1:A:255:LEU:HD12	2.01	0.42
1:A:575:ARG:NH1	1:A:612:GLY:O	2.53	0.42
1:A:44:VAL:CG2	1:A:128:VAL:HB	2.49	0.42
1:A:245:ARG:NE	1:A:276:ARG:HG2	2.35	0.42
1:A:53:PRO:HG3	1:A:56:ARG:HH21	1.85	0.41
1:A:158:HIS:CD2	1:A:385:TYR:CZ	3.09	0.41
1:A:50:ASP:HB3	1:A:121:SER:HB2	2.03	0.40
1:A:315:LEU:HD13	1:A:331:LEU:HD12	2.03	0.40
1:A:616:ARG:NH1	3:A:930:HOH:O	2.54	0.40
1:A:327:THR:N	2:B:21:U:H1'	2.37	0.40
1:A:328:TYR:H	2:B:21:U:H4'	1.85	0.40
1:A:256:LYS:HZ3	1:A:270:ARG:HH12	1.70	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	770/863 (89%)	746 (97%)	21 (3%)	3 (0%)	34 24

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	54	GLU
1	A	242	ASP
1	A	822	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	699/752 (93%)	691 (99%)	8 (1%)	73 73

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	229	ASP
1	A	327	THR
1	A	387	LYS
1	A	548	SER
1	A	748	PHE
1	A	806	TYR
1	A	839	ARG
1	A	852	HIS

Sometimes 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	B	8/12 (66%)	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	15:A	O3'	20:U	P	17.02

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	A	785/863 (90%)	0.37	77 (9%) 7 8	17, 38, 98, 142	0
2	B	12/12 (100%)	0.55	3 (25%) 0 0	33, 48, 125, 133	0
All	All	797/875 (91%)	0.38	80 (10%) 7 8	17, 38, 98, 142	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	306	TYR	10.4
1	A	294	MET	8.1
1	A	382	PRO	7.6
1	A	296	CYS	6.7
1	A	274	VAL	6.3
1	A	286	LEU	6.3
1	A	240	LEU	6.1
1	A	12	LEU	6.1
1	A	71	HIS	5.9
1	A	109	LEU	5.7
1	A	636	TYR	5.3
1	A	284	PHE	4.8
1	A	116	GLN	4.7
1	A	301	TYR	4.6
1	A	304	GLN	4.5
1	A	228	LEU	4.3
1	A	74	MET	4.2
1	A	246	VAL	4.2
1	A	245	ARG	4.1
1	A	119	LYS	4.1
1	A	117	THR	4.0
1	A	247	LYS	3.9
1	A	57	PRO	3.8
1	A	320	VAL	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	231	GLN	3.8
1	A	297	THR	3.8
1	A	302	PHE	3.8
1	A	267	ARG	3.7
1	A	107	VAL	3.6
1	A	327	THR	3.5
1	A	285	PRO	3.4
1	A	328	TYR	3.4
1	A	599	LYS	3.3
1	A	108	THR	3.3
1	A	248	PHE	3.2
1	A	55	LYS	3.2
1	A	249	THR	3.2
1	A	244	GLN	3.1
1	A	233	ILE	3.1
1	A	308	LEU	3.0
1	A	79	ASP	3.0
1	A	822	LYS	3.0
1	A	455	ARG	2.9
2	B	9	A	2.9
1	A	329	LEU	2.9
1	A	823	ASP	2.9
1	A	305	LYS	2.9
1	A	359	ALA	2.9
1	A	56	ARG	2.8
1	A	243	SER	2.8
1	A	106	GLU	2.8
1	A	283	THR	2.7
1	A	118	PHE	2.7
1	A	242	ASP	2.7
1	A	232	ASN	2.7
1	A	298	VAL	2.6
1	A	54	GLU	2.6
1	A	176	GLU	2.5
1	A	625	THR	2.5
1	A	250	LYS	2.5
1	A	270	ARG	2.5
1	A	276	ARG	2.5
1	A	295	GLU	2.5
1	A	67	THR	2.4
1	A	52	LYS	2.4
1	A	53	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	275	THR	2.3
1	A	358	THR	2.2
2	B	20	U	2.2
1	A	269	TYR	2.2
1	A	229	ASP	2.1
2	B	15	A	2.1
1	A	253	ARG	2.1
1	A	821	ASP	2.1
1	A	254	GLY	2.1
1	A	60	VAL	2.1
1	A	239	PRO	2.1
1	A	268	LYS	2.1
1	A	600	LYS	2.1
1	A	852	HIS	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 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.