



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 2, 2017 – 11:32 AM EST

PDB ID : 5G5S  
Title : Structure of the Argonaute protein from Methanocaldococcus janaschii  
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Deposited on : 2016-06-03  
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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20028442
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-20028442

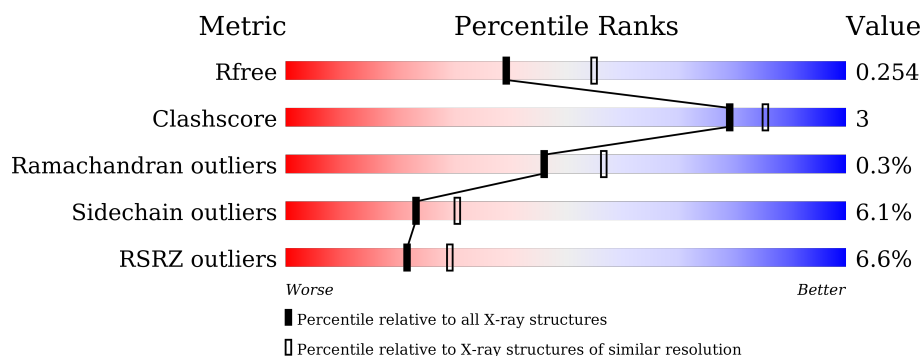
# 1 Overall quality at a glance

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	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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  $\geq 3$ , 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	A	715	<div> <div>6%</div> <div>83%</div> <div>12%</div> <div>..</div> </div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5570 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 ARGONAUTE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	692	5559	3629	892	1019	19	0	3	0

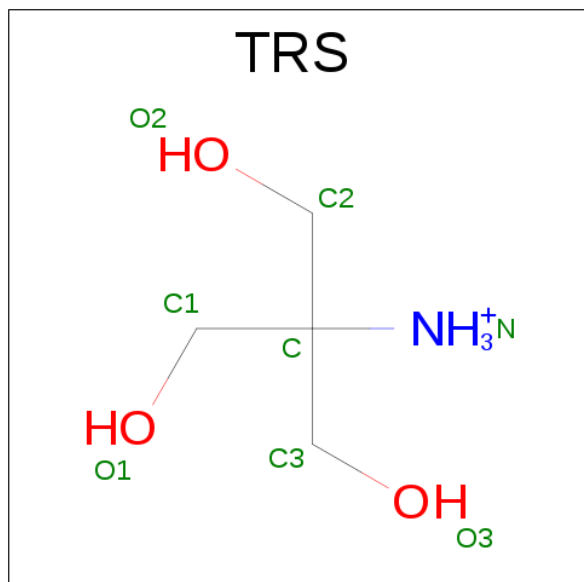
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	PHE	-	EXPRESSION TAG	UNP Q58717
A	0	THR	-	EXPRESSION TAG	UNP Q58717

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C<sub>4</sub>H<sub>12</sub>NO<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			8	4	1	3		

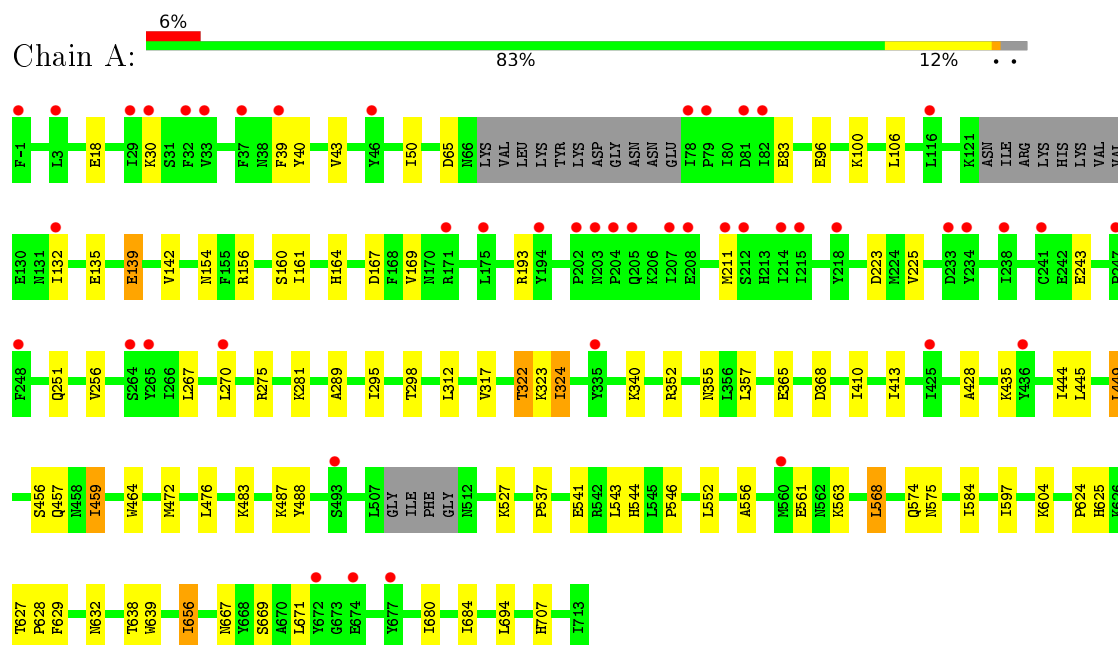
- Molecule 4 is water.

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

### 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: ARGONAUTE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	63.48Å 104.93Å 115.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.12 – 2.29 49.12 – 2.29	Depositor EDS
% Data completeness (in resolution range)	98.9 (49.12-2.29) 98.8 (49.12-2.29)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.14 (at 2.29Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, $R_{free}$	0.210 , 0.236 0.223 , 0.254	Depositor DCC
$R_{free}$ test set	1791 reflections (5.42%)	DCC
Wilson B-factor (Å <sup>2</sup> )	68.7	Xtriage
Anisotropy	0.275	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 72.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5570	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.43% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

### 5.1 Standard geometry

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

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	0.44	0/5697	0.68	0/7732

There are no bond length outliers.

There are no bond angle outliers.

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	A	5559	0	5331	38	0
2	A	1	0	0	0	0
3	A	8	0	12	0	0
4	A	2	0	0	0	0
All	All	5570	0	5343	38	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 3.

All (38) 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:164:HIS:CD2	1:A:251:GLN:HA	2.36	0.60
1:A:139:GLU:HG3	1:A:154:ASN:HB3	1.85	0.59
1:A:627:THR:HG22	1:A:628:PRO:HD2	1.89	0.55
1:A:322:THR:HG21	1:A:340:LYS:HE2	1.90	0.54
1:A:30:LYS:HB3	1:A:83:GLU:HB2	1.90	0.53
1:A:667:ASN:ND2	1:A:669:SER:H	2.08	0.52
1:A:627:THR:CG2	1:A:628:PRO:HD2	2.40	0.52
1:A:43:VAL:HG21	1:A:50:ILE:HG13	1.92	0.51
1:A:639:TRP:CZ3	1:A:656[A]:ILE:HG12	2.46	0.50
1:A:667:ASN:HD21	1:A:669:SER:HB2	1.76	0.50
1:A:40:TYR:HA	1:A:50:ILE:HD11	1.93	0.49
1:A:312:LEU:HB2	1:A:324:ILE:HG22	1.95	0.49
1:A:568:LEU:HG	1:A:597:ILE:HD12	1.95	0.48
1:A:544:HIS:CD2	1:A:546:PRO:HD2	2.50	0.47
1:A:487:LYS:HG2	1:A:527:LYS:HD2	1.97	0.46
1:A:680:ILE:HD12	1:A:684:ILE:HG23	1.98	0.46
1:A:275:ARG:HB2	1:A:629:PHE:CD1	2.51	0.45
1:A:39:PHE:CE2	1:A:50:ILE:HG12	2.51	0.45
1:A:537:PRO:HG2	1:A:541:GLU:HG3	1.99	0.45
1:A:267:LEU:HA	1:A:270:LEU:HD12	1.99	0.44
1:A:561:GLU:O	1:A:563:LYS:HG2	2.17	0.44
1:A:160:SER:HB3	1:A:256:VAL:HG22	1.99	0.44
1:A:457:GLN:HE21	1:A:483:LYS:HD2	1.82	0.44
1:A:459:ILE:HD12	1:A:464:TRP:HB2	2.00	0.44
1:A:457:GLN:NE2	1:A:483:LYS:HD2	2.32	0.44
1:A:132:ILE:HD11	1:A:161:ILE:HD13	2.00	0.44
1:A:410:ILE:HG21	1:A:444:ILE:HG22	2.00	0.44
1:A:552:LEU:HA	1:A:556:ALA:HB3	2.00	0.44
1:A:211:MET:HG2	1:A:225:VAL:HG11	2.00	0.43
1:A:445:LEU:O	1:A:449:LEU:HB2	2.18	0.43
1:A:164:HIS:CD2	1:A:167:ASP:H	2.36	0.43
1:A:476:LEU:HA	1:A:671:LEU:HD11	2.01	0.43
1:A:428:ALA:HB3	1:A:456:SER:HB3	2.01	0.42
1:A:487:LYS:NZ	1:A:707:HIS:O	2.53	0.42
1:A:459:ILE:HD11	1:A:472:MET:SD	2.60	0.41
1:A:604:LYS:HE3	1:A:632:ASN:OD1	2.21	0.40
1:A:289:ALA:HA	1:A:295:ILE:HD11	2.03	0.40
1:A:365:GLU:OE1	1:A:435:LYS:NZ	2.54	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	687/715 (96%)	662 (96%)	23 (3%)	2 (0%)	46 57

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	624	PRO
1	A	169	VAL

### 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	578/664 (87%)	541 (94%)	37 (6%)	22 28

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	GLU
1	A	65	ASP
1	A	96	GLU
1	A	100	LYS
1	A	106	LEU
1	A	135	GLU
1	A	139	GLU
1	A	142[A]	VAL
1	A	142[B]	VAL

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Mol	Chain	Res	Type
1	A	156	ARG
1	A	193	ARG
1	A	223	ASP
1	A	243	GLU
1	A	281	LYS
1	A	298	THR
1	A	317	VAL
1	A	322	THR
1	A	323	LYS
1	A	324	ILE
1	A	352	ARG
1	A	355	ASN
1	A	357	LEU
1	A	368	ASP
1	A	413	ILE
1	A	449	LEU
1	A	459	ILE
1	A	488	TYR
1	A	543	LEU
1	A	568	LEU
1	A	574	GLN
1	A	575	ASN
1	A	584	ILE
1	A	625	HIS
1	A	638	THR
1	A	656[A]	ILE
1	A	656[B]	ILE
1	A	694	LEU

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

Mol	Chain	Res	Type
1	A	203	ASN
1	A	457	GLN
1	A	667	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 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](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	TRS	A	1715	-	7,7,7	0.34	0	9,9,9	0.26	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	TRS	A	1715	-	-	0/9/9/9	0/0/0/0

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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	692/715 (96%)	0.42	46 (6%) 22 29	53, 88, 129, 160	1 (0%)

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	204	PRO	8.6
1	A	207	ILE	5.6
1	A	234	TYR	5.4
1	A	37	PHE	5.2
1	A	205	GLN	4.9
1	A	29	ILE	4.8
1	A	202	PRO	4.7
1	A	79	PRO	4.7
1	A	247	PRO	4.2
1	A	33	VAL	4.2
1	A	335	TYR	4.1
1	A	674	GLU	3.9
1	A	215	ILE	3.8
1	A	82	ILE	3.5
1	A	203	ASN	3.4
1	A	265	TYR	3.2
1	A	81	ASP	3.2
1	A	32	PHE	3.2
1	A	175	LEU	3.1
1	A	264	SER	2.9
1	A	214	ILE	2.8
1	A	3	LEU	2.8
1	A	212	SER	2.8
1	A	436	TYR	2.8
1	A	78	ILE	2.8
1	A	46	TYR	2.6
1	A	248	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	677	TYR	2.6
1	A	233	ASP	2.5
1	A	241	CYS	2.5
1	A	211	MET	2.5
1	A	238	ILE	2.4
1	A	218	TYR	2.4
1	A	208	GLU	2.4
1	A	171	ARG	2.4
1	A	-1	PHE	2.2
1	A	493	SER	2.2
1	A	39	PHE	2.2
1	A	116	LEU	2.2
1	A	194	TYR	2.2
1	A	560	MET	2.1
1	A	132	ILE	2.1
1	A	30	LYS	2.1
1	A	672	TYR	2.1
1	A	270	LEU	2.0
1	A	425	ILE	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	MG	A	1714	1/1	0.90	0.04	-3.20	87,87,87,87	0
3	TRS	A	1715	8/8	0.88	0.11	-	108,109,110,110	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.