



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:53 PM GMT

PDB ID : 4N47  
Title : Structure of Thermus thermophilus Argonaute bound to guide DNA and 12-mer target DNA  
Authors : Sheng, G.; Zhao, H.; Wang, J.; Rao, Y.; Wang, Y.  
Deposited on : 2013-10-08  
Resolution : 2.82 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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

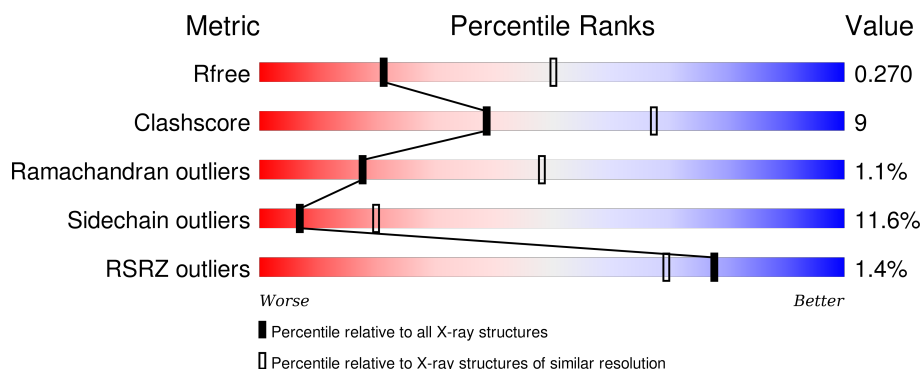
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.82 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	2676 (2.84-2.80)
Clashscore	102246	3124 (2.84-2.80)
Ramachandran outliers	100387	3072 (2.84-2.80)
Sidechain outliers	100360	3074 (2.84-2.80)
RSRZ outliers	91569	2690 (2.84-2.80)

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	685	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 10%, orange 10%, yellow 73%, green 15%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>73%</span> <span>21%</span> <span>• •</span> </div> </div>
2	D	12	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 42%, yellow 58%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>42%</span> <span>58%</span> </div> </div>
3	C	21	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 29%, yellow 33%, orange 5%, grey 33%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>29%</span> <span>33%</span> <span>5%</span> <span>33%</span> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5542 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
1	A	666	Total	C	N	O	S	0	0	0
			5008	3214	921	868	5			

- Molecule 2 is a DNA chain called 5'-D(\*CP\*CP\*TP\*AP\*CP\*TP\*AP\*CP\*CP\*TP\*CP\*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	12	Total	C	N	O	P	0	0	0
			235	114	39	71	11			

- Molecule 3 is a DNA chain called 5'-D(P\*TP\*GP\*AP\*GP\*GP\*TP\*AP\*GP\*TP\*AP\*GP\*GP\*TP\*TP\*GP\*TP\*AP\*TP\*AP\*GP\*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	14	Total	C	N	O	P	0	0	0
			298	140	58	86	14			

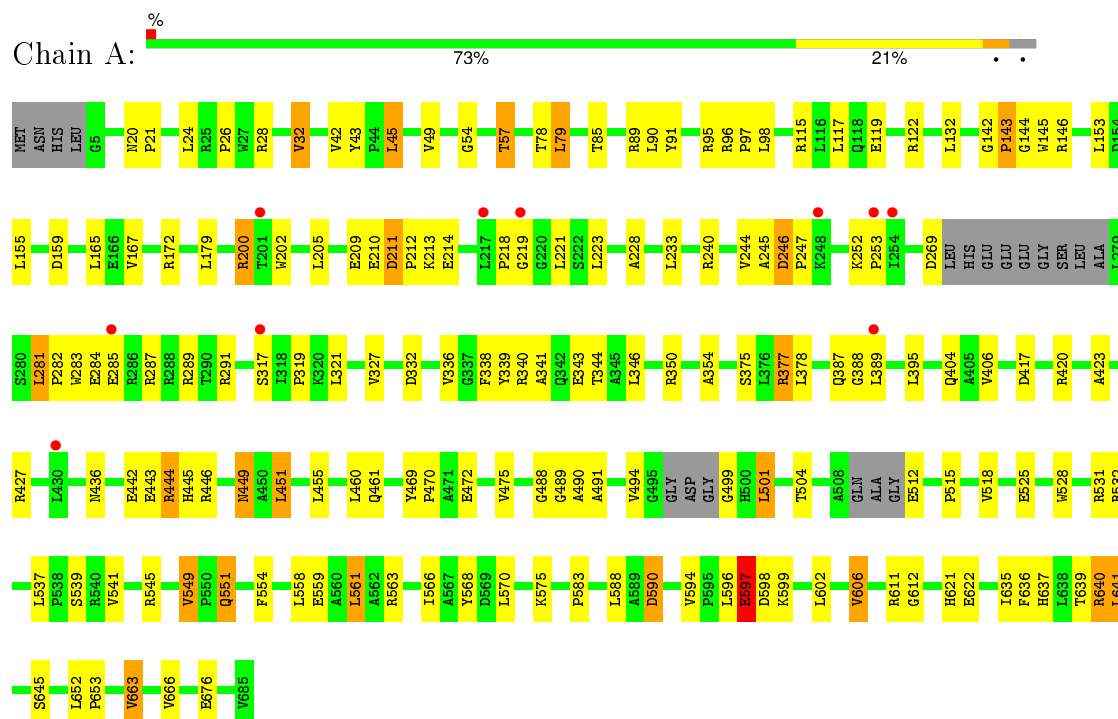
- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

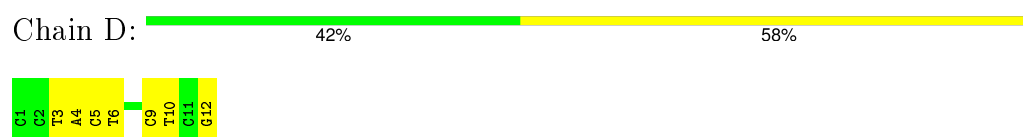
### 3 Residue-property plots

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.

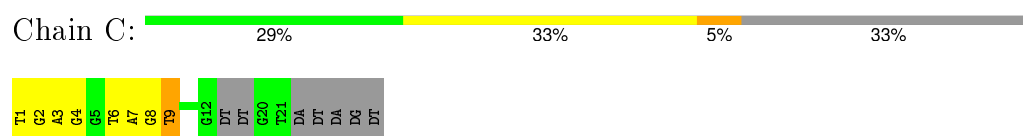
#### • Molecule 1: Argonaute



#### • Molecule 2: 5'-D(\*CP\*CP\*TP\*AP\*CP\*TP\*AP\*CP\*CP\*TP\*CP\*G)-3'



#### • Molecule 3: 5'-D(P\*TP\*GP\*AP\*GP\*GP\*TP\*AP\*GP\*TP\*AP\*GP\*GP\*TP\*TP\*GP\*TP\*AP\*TP\*AP\*GP\*T)-3'



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	58.89Å 110.55Å 124.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.33 – 2.82 47.93 – 2.82	Depositor EDS
% Data completeness (in resolution range)	98.1 (38.33-2.82) 98.1 (47.93-2.82)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.34 (at 2.81Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, $R_{free}$	0.192 , 0.264 0.191 , 0.270	Depositor DCC
$R_{free}$ test set	1004 reflections (5.09%)	DCC
Wilson B-factor (Å <sup>2</sup> )	66.2	Xtriage
Anisotropy	0.343	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 61.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 19738 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5542	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: 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	0.34	0/5129	0.50	4/6993 (0.1%)
2	D	0.52	0/261	1.21	0/399
3	C	0.83	1/334 (0.3%)	1.14	1/512 (0.2%)
All	All	0.39	1/5724 (0.0%)	0.62	5/7904 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1	DT	OP3-P	-10.75	1.48	1.61

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	515	PRO	N-CA-CB	6.05	110.56	103.30
1	A	143	PRO	N-CA-CB	5.88	110.36	103.30
3	C	9	DT	O4'-C4'-C3'	-5.84	102.16	104.50
1	A	79	LEU	CA-CB-CG	5.33	127.55	115.30
1	A	281	LEU	CA-CB-CG	5.19	127.23	115.30

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	A	5008	0	4880	87	0
2	D	235	0	137	5	0
3	C	298	0	160	6	0
4	A	1	0	0	0	0
All	All	5542	0	5177	95	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 9.

All (95) 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:344:THR:HG21	1:A:460:LEU:HD11	1.55	0.89
2:D:9:DC:H2"	2:D:10:DT:H5"	1.66	0.77
1:A:319:PRO:HG2	1:A:640:ARG:HD3	1.67	0.75
1:A:282:PRO:HD2	1:A:285:GLU:OE1	1.88	0.73
1:A:590:ASP:OD2	2:D:12:DG:N1	2.19	0.72
1:A:590:ASP:N	1:A:590:ASP:OD1	2.21	0.72
1:A:115:ARG:NH2	1:A:119:GLU:OE1	2.22	0.72
1:A:417:ASP:OD1	1:A:420:ARG:NH1	2.21	0.72
1:A:639:THR:HG22	1:A:640:ARG:HE	1.54	0.71
1:A:211:ASP:C	1:A:211:ASP:OD1	2.29	0.70
1:A:561:LEU:HD13	1:A:566:ILE:HB	1.72	0.69
1:A:596:LEU:C	1:A:597:GLU:HG3	2.15	0.67
1:A:200:ARG:NH2	1:A:246:ASP:OD1	2.29	0.67
1:A:575:LYS:HE2	1:A:652:LEU:HD11	1.78	0.66
1:A:211:ASP:OD1	1:A:213:LYS:N	2.27	0.66
1:A:531:ARG:HE	1:A:537:LEU:HD21	1.62	0.65
1:A:545:ARG:HH21	1:A:549:VAL:HG12	1.62	0.64
1:A:597:GLU:OE2	1:A:598:ASP:N	2.30	0.64
1:A:340:ARG:HB2	1:A:461:GLN:HB3	1.82	0.61
1:A:635:ILE:HG23	1:A:653:PRO:HG3	1.83	0.60
1:A:387:GLN:O	1:A:389:LEU:N	2.34	0.59
1:A:343:GLU:HG3	1:A:375:SER:HB3	1.84	0.58
1:A:636:PHE:O	1:A:639:THR:HB	2.04	0.58
1:A:442:GLU:O	1:A:444:ARG:N	2.34	0.57
2:D:3:DT:H2'	2:D:4:DA:H8	1.69	0.57
1:A:89:ARG:NH1	1:A:90:LEU:O	2.38	0.57
1:A:461:GLN:NE2	1:A:499:GLY:O	2.38	0.56
1:A:377:ARG:NH1	1:A:378:LEU:H	2.03	0.56
1:A:545:ARG:NH2	1:A:549:VAL:O	2.39	0.56
1:A:436:ASN:O	1:A:446:ARG:NH2	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:490:ALA:HB3	1:A:663:VAL:HG12	1.88	0.56
2:D:3:DT:H2'	2:D:4:DA:C8	2.41	0.55
1:A:606:VAL:HG13	1:A:611:ARG:HH22	1.71	0.55
1:A:327:VAL:CG2	1:A:332:ASP:HB2	2.37	0.55
1:A:449:ASN:ND2	1:A:645:SER:O	2.40	0.55
1:A:488:GLY:HA2	1:A:518:VAL:HG11	1.89	0.54
1:A:45:LEU:O	1:A:49:VAL:HG23	2.07	0.54
1:A:561:LEU:HD12	1:A:568:TYR:HB3	1.89	0.54
1:A:283:TRP:CZ3	1:A:583:PRO:HD2	2.43	0.53
1:A:20:ASN:HB2	1:A:21:PRO:HD2	1.88	0.53
1:A:528:TRP:O	1:A:532:ARG:HG2	2.10	0.52
1:A:455:LEU:HD22	1:A:460:LEU:HD22	1.91	0.52
1:A:159:ASP:OD2	1:A:159:ASP:N	2.43	0.52
1:A:142:GLY:O	1:A:144:GLY:N	2.43	0.51
1:A:205:LEU:HD11	1:A:245:ALA:HB2	1.92	0.51
1:A:319:PRO:HG3	1:A:637:HIS:CD2	2.45	0.51
1:A:599:LYS:HB3	1:A:621:HIS:HB3	1.93	0.50
1:A:327:VAL:HG23	1:A:332:ASP:HB2	1.92	0.50
1:A:95:ARG:O	1:A:97:PRO:HD3	2.12	0.49
1:A:558:LEU:HD22	1:A:568:TYR:CE2	2.47	0.49
1:A:338:PHE:HD2	1:A:341:ALA:HB2	1.78	0.48
1:A:583:PRO:HD3	1:A:588:LEU:HD13	1.93	0.48
1:A:32:VAL:HG21	1:A:91:TYR:HE2	1.78	0.48
1:A:228:ALA:HB2	1:A:233:LEU:HD12	1.94	0.48
1:A:211:ASP:HA	1:A:212:PRO:HD3	1.56	0.47
1:A:54:GLY:O	1:A:57:THR:HG23	2.14	0.47
1:A:494:VAL:HG22	1:A:501:LEU:HB3	1.96	0.47
3:C:6:DT:H2''	3:C:7:DA:H5''	1.97	0.47
1:A:377:ARG:HH11	1:A:377:ARG:HA	1.79	0.47
1:A:343:GLU:N	1:A:343:GLU:OE1	2.40	0.46
1:A:491:ALA:HB3	1:A:504:THR:OG1	2.15	0.46
3:C:3:DA:H2''	3:C:4:DG:C8	2.51	0.45
1:A:211:ASP:OD2	1:A:214:GLU:HG2	2.17	0.45
1:A:339:TYR:CD2	1:A:340:ARG:HG2	2.52	0.45
1:A:594:VAL:HB	1:A:602:LEU:HB2	1.99	0.45
1:A:445:HIS:O	1:A:449:ASN:HB2	2.17	0.44
1:A:472:GLU:OE1	1:A:539:SER:OG	2.30	0.44
1:A:210:GLU:N	1:A:210:GLU:OE2	2.41	0.44
1:A:142:GLY:HA3	1:A:145:TRP:CE2	2.53	0.44
1:A:117:LEU:HD23	1:A:132:LEU:HD22	1.99	0.44
1:A:446:ARG:HG3	3:C:2:DG:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:42:VAL:HG13	1:A:43:TYR:CD1	2.54	0.43
3:C:7:DA:H2'	3:C:8:DG:C8	2.54	0.43
1:A:172:ARG:NH1	3:C:9:DT:OP1	2.45	0.43
1:A:423:ALA:O	1:A:427:ARG:HG3	2.19	0.43
1:A:551:GLN:OE1	1:A:622:GLU:HB3	2.19	0.43
2:D:5:DC:H2'	2:D:6:DT:C6	2.55	0.42
1:A:469:TYR:HA	1:A:470:PRO:HD3	1.92	0.42
1:A:153:LEU:HD22	1:A:167:VAL:HG22	2.01	0.42
1:A:246:ASP:HA	1:A:247:PRO:HD3	1.86	0.42
1:A:494:VAL:HG11	1:A:641:LEU:HD23	2.02	0.42
1:A:559:GLU:HB3	1:A:563:ARG:HH21	1.85	0.42
1:A:451:LEU:HD12	1:A:451:LEU:HA	1.86	0.42
1:A:641:LEU:HD12	1:A:641:LEU:HA	1.78	0.42
1:A:115:ARG:HD2	1:A:115:ARG:HA	1.83	0.41
1:A:554:PHE:O	1:A:558:LEU:HG	2.20	0.41
3:C:3:DA:H2''	3:C:4:DG:H8	1.84	0.41
1:A:45:LEU:HD12	1:A:45:LEU:HA	1.84	0.41
1:A:350:ARG:NH2	1:A:354:ALA:HB3	2.35	0.41
1:A:26:PRO:HD2	1:A:96:ARG:O	2.21	0.41
1:A:24:LEU:O	1:A:97:PRO:HA	2.21	0.40
1:A:42:VAL:HG13	1:A:43:TYR:HD1	1.86	0.40
1:A:252:LYS:HA	1:A:253:PRO:HD3	1.74	0.40
1:A:202:TRP:HA	1:A:247:PRO:HD3	2.03	0.40
1:A:281:LEU:O	1:A:612:GLY:HA2	2.21	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	658/685 (96%)	615 (94%)	36 (6%)	7 (1%)	17 48

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	218	PRO
1	A	388	GLY
1	A	443	GLU
1	A	597	GLU
1	A	219	GLY
1	A	489	GLY
1	A	143	PRO

### 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	466/549 (85%)	412 (88%)	54 (12%)	<b>7</b> <b>20</b>

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	ARG
1	A	32	VAL
1	A	45	LEU
1	A	57	THR
1	A	78	THR
1	A	79	LEU
1	A	85	THR
1	A	98	LEU
1	A	122	ARG
1	A	146	ARG
1	A	155	LEU
1	A	165	LEU
1	A	179	LEU
1	A	200	ARG
1	A	209	GLU
1	A	211	ASP
1	A	221	LEU
1	A	223	LEU

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Mol	Chain	Res	Type
1	A	240	ARG
1	A	244	VAL
1	A	246	ASP
1	A	269	ASP
1	A	284	GLU
1	A	287	ARG
1	A	289	ARG
1	A	291	ARG
1	A	317	SER
1	A	321	LEU
1	A	336	VAL
1	A	346	LEU
1	A	377	ARG
1	A	395	LEU
1	A	404	GLN
1	A	406	VAL
1	A	444	ARG
1	A	449	ASN
1	A	451	LEU
1	A	475	VAL
1	A	501	LEU
1	A	512	GLU
1	A	525	GLU
1	A	541	VAL
1	A	549	VAL
1	A	551	GLN
1	A	561	LEU
1	A	570	LEU
1	A	590	ASP
1	A	597	GLU
1	A	606	VAL
1	A	640	ARG
1	A	641	LEU
1	A	663	VAL
1	A	666	VAL
1	A	676	GLU

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

### 5.3.3 RNA [i](#)

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 1 ligands modelled in this entry, 1 is 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.

### 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, 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	666/685 (97%)	-0.21	10 (1%) 76 68	29, 63, 106, 144	0
2	D	12/12 (100%)	-0.71	0 100 100	51, 55, 66, 68	0
3	C	14/21 (66%)	-0.38	0 100 100	37, 43, 96, 105	0
All	All	692/718 (96%)	-0.22	10 (1%) 78 69	29, 62, 106, 144	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	253	PRO	5.1
1	A	219	GLY	3.5
1	A	254	ILE	3.4
1	A	201	THR	2.7
1	A	389	LEU	2.7
1	A	430	LEU	2.4
1	A	217	LEU	2.1
1	A	285	GLU	2.0
1	A	248	LYS	2.0
1	A	317	SER	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( $\text{\AA}^2$ )	Q<0.9
4	MG	A	701	1/1	0.95	0.08	-2.54	75,75,75,75	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.