Full wwPDB X-ray Structure Validation Report ⓘ

Jun 30, 2022 – 10:03 AM EDT

PDB ID	:	7R8G
Title	:	Crystal structure of Pseudooceanicola lipolyticus Argonaute bound to 5' OH guide DNA
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Deposited on	:	2021-06-26
Resolution	:	2.50 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

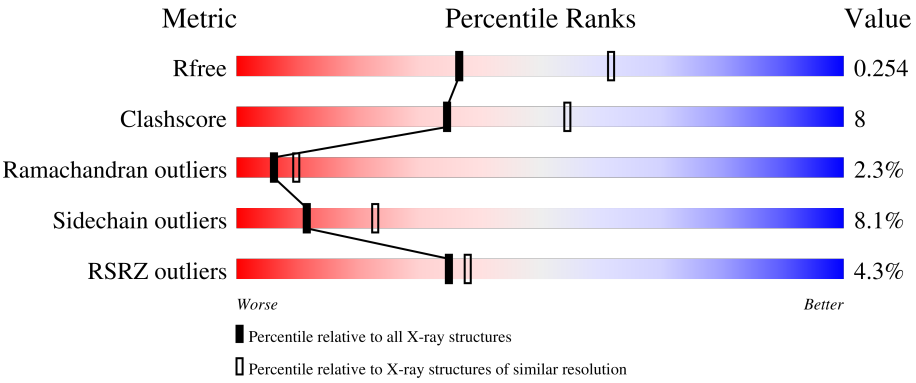
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.29
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.29

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 <=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	789	4% 72% 22%
2	T	17	53% 35% 12%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6336 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	769	6029	3832	1071	1098	28	0	0	0

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

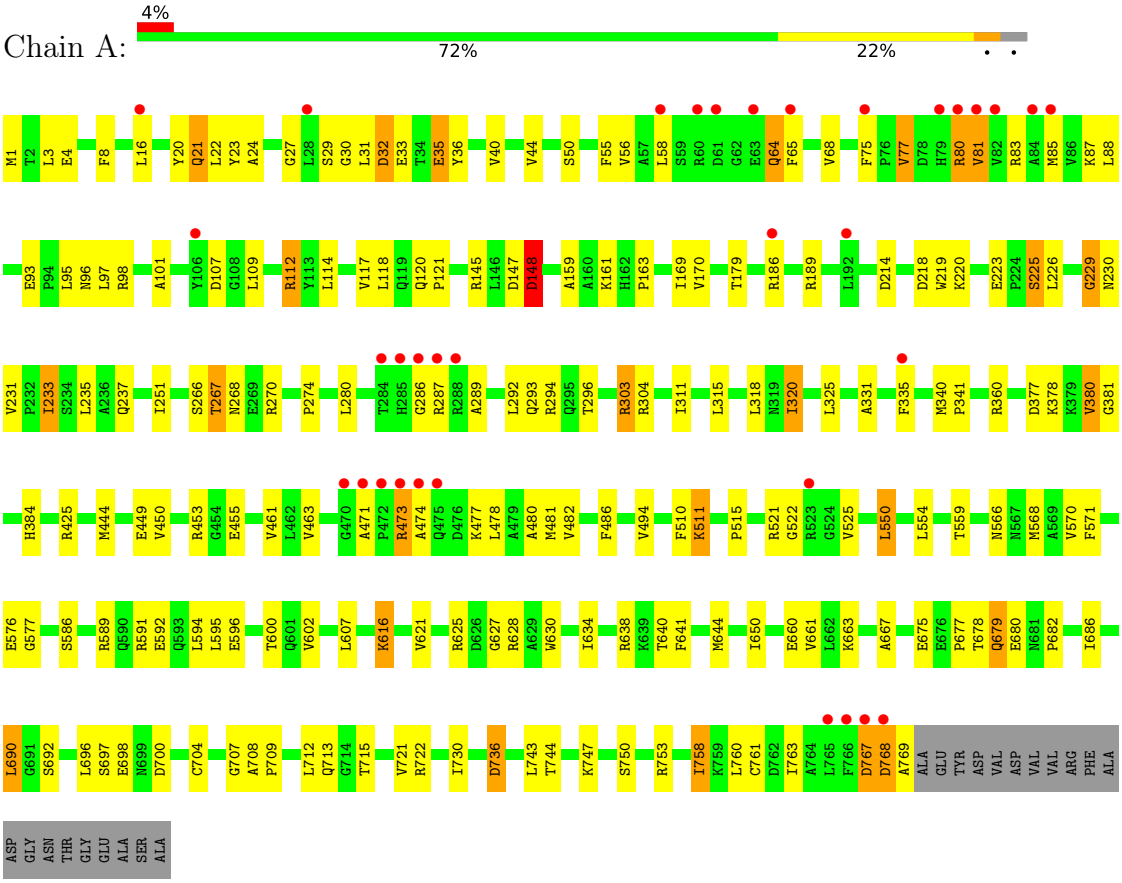
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	T	15	307	146	58	88	15	0	0	0

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: Argonaute

Chain A:



• Molecule 2: DNA (5'-D(*TP*AP*CP*TP*GP*CP*AP*CP*AP*GP*GP*TP*GP*AP*CP*GP *A)-3')

Chain T:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, α, β, γ	200.60Å 200.60Å 200.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.86 – 2.50 44.86 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (44.86-2.50) 100.0 (44.86-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.44 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.211 , 0.254 0.211 , 0.254	Depositor DCC
R_{free} test set	2003 reflections (4.31%)	wwPDB-VP
Wilson B-factor (Å^2)	75.1	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 53.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.023 for -l,-k,-h	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	6336	wwPDB-VP
Average B, all atoms (Å^2)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.04% 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.

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	A	0.44	0/6163	0.68	1/8337 (0.0%)
2	T	1.11	0/343	1.00	0/524
All	All	0.50	0/6506	0.70	1/8861 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	576	GLU	C-N-CA	-5.48	110.80	122.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	577	GLY	Peptide
1	A	707	GLY	Peptide

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	6029	0	6060	103	0
2	T	307	0	170	5	0
All	All	6336	0	6230	104	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 8.

All (104) 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:32:ASP:HB2	1:A:35:GLU:HB2	1.69	0.74
1:A:16:LEU:HD22	1:A:325:LEU:HD21	1.70	0.73
1:A:554:LEU:HD22	1:A:736:ASP:HB3	1.72	0.70
1:A:628:ARG:HH12	2:T:13:DT:H5'	1.55	0.70
1:A:566:ASN:ND2	1:A:768:ASP:OD2	2.25	0.68
1:A:678:THR:O	1:A:680:GLU:N	2.29	0.65
1:A:56:VAL:HG22	1:A:112:ARG:HD2	1.77	0.65
1:A:179:THR:HG23	1:A:280:LEU:O	1.99	0.63
1:A:595:LEU:H	1:A:595:LEU:HD12	1.66	0.61
1:A:229:GLY:O	1:A:231:VAL:N	2.35	0.60
1:A:621:VAL:HG11	1:A:641:PHE:CZ	2.36	0.59
1:A:117:VAL:HB	1:A:320:ILE:HG21	1.83	0.59
1:A:293:GLN:O	1:A:296:THR:HG22	2.02	0.59
1:A:663:LYS:O	1:A:753:ARG:NH2	2.37	0.58
1:A:145:ARG:HH12	1:A:148:ASP:H	1.51	0.58
1:A:107:ASP:OD2	1:A:161:LYS:NZ	2.31	0.57
1:A:478:LEU:O	1:A:482:VAL:HG23	2.03	0.57
1:A:286:GLY:HA2	1:A:473:ARG:HD2	1.86	0.57
1:A:589:ARG:HB2	1:A:595:LEU:HD11	1.88	0.56
1:A:23:TYR:HD2	1:A:88:LEU:HB3	1.72	0.55
1:A:634:ILE:O	1:A:638:ARG:HG3	2.06	0.55
1:A:554:LEU:HD22	1:A:736:ASP:CB	2.37	0.54
1:A:121:PRO:HG2	1:A:318:LEU:HD22	1.90	0.53
1:A:747:LYS:HD3	1:A:750:SER:HB3	1.91	0.53
1:A:377:ASP:HB3	1:A:380:VAL:HG13	1.91	0.52
1:A:449:GLU:O	1:A:453:ARG:HG3	2.10	0.52
1:A:303:ARG:NH1	2:T:7:DC:OP1	2.43	0.52
1:A:3:LEU:HD11	1:A:692:SER:HB3	1.91	0.52
1:A:117:VAL:HA	1:A:120:GLN:HG3	1.92	0.52
1:A:591:ARG:HG2	1:A:592:GLU:HG3	1.91	0.52
1:A:294:ARG:NH1	1:A:713:GLN:HG3	2.25	0.51
1:A:708:ALA:HB3	1:A:709:PRO:HD3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4:GLU:OE2	1:A:304:ARG:HD2	2.11	0.50
1:A:677:PRO:HB3	1:A:682:PRO:O	2.12	0.50
1:A:566:ASN:HB2	1:A:768:ASP:HB2	1.93	0.50
1:A:380:VAL:HG22	1:A:381:GLY:N	2.27	0.50
1:A:690:LEU:O	1:A:704:CYS:O	2.30	0.50
1:A:219:TRP:HB2	1:A:225:SER:HB3	1.93	0.49
1:A:27:GLY:HA2	1:A:85:MET:O	2.13	0.49
1:A:616:LYS:O	1:A:616:LYS:HG2	2.12	0.49
1:A:235:LEU:HD21	1:A:274:PRO:HD3	1.93	0.49
1:A:22:LEU:HG	1:A:95:LEU:HD11	1.94	0.49
1:A:77:VAL:HG13	1:A:88:LEU:O	2.13	0.49
1:A:21:GLN:O	1:A:68:VAL:HG12	2.14	0.48
1:A:31:LEU:HG	1:A:36:TYR:CG	2.48	0.48
1:A:36:TYR:OH	1:A:64:GLN:HG3	2.14	0.48
1:A:675:GLU:HB2	1:A:686:ILE:HD13	1.96	0.47
1:A:40:VAL:O	1:A:44:VAL:HG23	2.15	0.47
1:A:444:MET:HG3	1:A:481:MET:CE	2.44	0.47
1:A:697:SER:OG	1:A:698:GLU:N	2.48	0.46
1:A:75:PHE:O	1:A:77:VAL:HG23	2.13	0.46
1:A:661:VAL:HG11	1:A:758:ILE:HD11	1.98	0.46
1:A:97:LEU:H	1:A:97:LEU:HD22	1.80	0.46
1:A:627:GLY:O	1:A:660:GLU:HG2	2.16	0.46
1:A:114:LEU:HD23	1:A:159:ALA:HB1	1.96	0.46
1:A:266:SER:OG	2:T:16:DC:OP1	2.25	0.46
1:A:289:ALA:HB1	1:A:292:LEU:HB2	1.98	0.46
1:A:55:PHE:CE2	1:A:68:VAL:HG23	2.51	0.45
1:A:29:SER:O	1:A:31:LEU:N	2.50	0.45
1:A:700:ASP:OD2	1:A:722:ARG:HG3	2.16	0.45
1:A:311:ILE:HD13	1:A:315:LEU:HD12	1.99	0.45
1:A:315:LEU:HD22	1:A:318:LEU:HD11	1.98	0.45
1:A:24:ALA:O	1:A:88:LEU:HA	2.17	0.45
1:A:311:ILE:CD1	1:A:315:LEU:HD12	2.47	0.45
1:A:568:MET:HE2	1:A:769:ALA:H	1.82	0.45
1:A:163:PRO:HD3	1:A:696:LEU:HD22	1.98	0.45
1:A:449:GLU:HG3	1:A:453:ARG:NH1	2.32	0.45
1:A:58:LEU:O	1:A:65:PHE:HB2	2.18	0.44
1:A:267:THR:O	1:A:267:THR:OG1	2.31	0.44
1:A:20:TYR:CD2	1:A:109:LEU:HD12	2.52	0.44
1:A:189:ARG:NH2	1:A:218:ASP:OD1	2.51	0.44
1:A:219:TRP:CB	1:A:225:SER:HB3	2.48	0.44
1:A:571:PHE:CD1	1:A:602:VAL:HG11	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:170:VAL:HG21	1:A:667:ALA:HB1	1.99	0.43
1:A:120:GLN:OE1	2:T:15:DA:N6	2.52	0.43
1:A:340:MET:SD	1:A:360:ARG:NH1	2.91	0.43
1:A:644:MET:HB2	1:A:650:ILE:HD13	2.00	0.43
1:A:600:THR:HA	1:A:640:THR:OG1	2.19	0.43
1:A:287:ARG:NH2	1:A:289:ALA:HB2	2.34	0.42
1:A:87:LYS:HD3	1:A:88:LEU:N	2.34	0.42
1:A:450:VAL:HG22	1:A:453:ARG:NH2	2.34	0.42
1:A:550:LEU:HD13	1:A:743:LEU:HD21	2.00	0.42
1:A:480:ALA:HA	1:A:767:ASP:HB3	2.00	0.42
1:A:744:THR:HG21	1:A:750:SER:O	2.18	0.42
1:A:594:LEU:HD23	1:A:594:LEU:HA	1.90	0.42
1:A:511:LYS:HE2	1:A:511:LYS:HB3	1.76	0.42
1:A:482:VAL:O	1:A:486:PHE:HB2	2.20	0.41
1:A:8:PHE:CE2	1:A:331:ALA:HB2	2.55	0.41
1:A:32:ASP:HB2	1:A:35:GLU:CB	2.46	0.41
1:A:214:ASP:OD2	1:A:270:ARG:NH1	2.53	0.41
1:A:233:ILE:HG23	1:A:237:GLN:HB3	2.03	0.41
1:A:287:ARG:HE	1:A:287:ARG:HB3	1.76	0.41
1:A:630:TRP:O	1:A:634:ILE:HD12	2.20	0.41
1:A:80:ARG:HB3	1:A:81:VAL:H	1.43	0.41
1:A:118:LEU:O	1:A:121:PRO:HD2	2.21	0.41
1:A:23:TYR:O	1:A:65:PHE:HA	2.21	0.41
1:A:453:ARG:NE	1:A:455:GLU:OE2	2.41	0.41
1:A:722:ARG:HG3	1:A:722:ARG:HH11	1.86	0.41
1:A:570:VAL:HG11	1:A:761:CYS:HA	2.03	0.40
1:A:220:LYS:HE3	1:A:223:GLU:OE1	2.21	0.40
1:A:22:LEU:HD23	1:A:22:LEU:HA	1.80	0.40
1:A:117:VAL:HB	1:A:320:ILE:CG2	2.48	0.40
1:A:607:LEU:HD12	1:A:607:LEU:HA	1.88	0.40
2:T:4:DC:H2"	2:T:5:DT:H5'	2.03	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	767/789 (97%)	698 (91%)	51 (7%)	18 (2%)	6 10

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	77	VAL
1	A	30	GLY
1	A	81	VAL
1	A	522	GLY
1	A	80	ARG
1	A	230	ASN
1	A	471	ALA
1	A	679	GLN
1	A	64	GLN
1	A	83	ARG
1	A	93	GLU
1	A	101	ALA
1	A	148	ASP
1	A	229	GLY
1	A	474	ALA
1	A	33	GLU
1	A	147	ASP
1	A	525	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	642/659 (97%)	590 (92%)	52 (8%)	11 23

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET

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Mol	Chain	Res	Type
1	A	21	GLN
1	A	32	ASP
1	A	35	GLU
1	A	50	SER
1	A	96	ASN
1	A	98	ARG
1	A	112	ARG
1	A	148	ASP
1	A	169	ILE
1	A	186	ARG
1	A	225	SER
1	A	226	LEU
1	A	233	ILE
1	A	251	ILE
1	A	267	THR
1	A	268	ASN
1	A	303	ARG
1	A	320	ILE
1	A	335	PHE
1	A	341	PRO
1	A	378	LYS
1	A	380	VAL
1	A	384	HIS
1	A	425	ARG
1	A	461	VAL
1	A	463	VAL
1	A	473	ARG
1	A	477	LYS
1	A	494	VAL
1	A	510	PHE
1	A	511	LYS
1	A	515	PRO
1	A	521	ARG
1	A	550	LEU
1	A	559	THR
1	A	586	SER
1	A	596	GLU
1	A	616	LYS
1	A	625	ARG
1	A	679	GLN
1	A	690	LEU
1	A	712	LEU

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Mol	Chain	Res	Type
1	A	715	THR
1	A	721	VAL
1	A	730	ILE
1	A	736	ASP
1	A	758	ILE
1	A	760	LEU
1	A	763	ILE
1	A	767	ASP
1	A	768	ASP

Sometimes 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 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)

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^{th} 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	769/789 (97%)	0.20	34 (4%) 34 37	47, 78, 128, 174	0
2	T	15/17 (88%)	-0.31	0 100 100	66, 78, 135, 143	0
All	All	784/806 (97%)	0.19	34 (4%) 35 38	47, 78, 129, 174	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	472	PRO	15.6
1	A	471	ALA	12.5
1	A	473	ARG	12.4
1	A	474	ALA	7.7
1	A	285	HIS	7.4
1	A	766	PHE	6.9
1	A	475	GLN	6.8
1	A	470	GLY	6.6
1	A	81	VAL	5.9
1	A	284	THR	5.5
1	A	286	GLY	5.0
1	A	288	ARG	4.7
1	A	765	LEU	4.0
1	A	523	ARG	3.8
1	A	28	LEU	3.7
1	A	768	ASP	3.4
1	A	767	ASP	3.3
1	A	84	ALA	3.1
1	A	60	ARG	2.9
1	A	85	MET	2.7
1	A	61	ASP	2.7
1	A	16	LEU	2.7
1	A	287	ARG	2.6
1	A	106	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	80	ARG	2.6
1	A	58	LEU	2.6
1	A	65	PHE	2.5
1	A	79	HIS	2.5
1	A	82	VAL	2.4
1	A	335	PHE	2.4
1	A	192	LEU	2.3
1	A	63	GLU	2.2
1	A	186	ARG	2.2
1	A	75	PHE	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 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.