Full wwPDB X-ray Structure Validation Report (i)

Aug 27, 2023 – 02:23 PM EDT

PDB ID	:	3HJF
Title	:	Crystal structure of T. thermophilus Argonaute E546 mutant protein complexed with DNA guide strand and 15-nt RNA target strand
Authors	:	Wang, Y.; Li, H.; Sheng, G.; Patel, D.J.
Deposited on	:	2009-05-21
Resolution	:	3.06 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 (1)) were used in the production of this report:

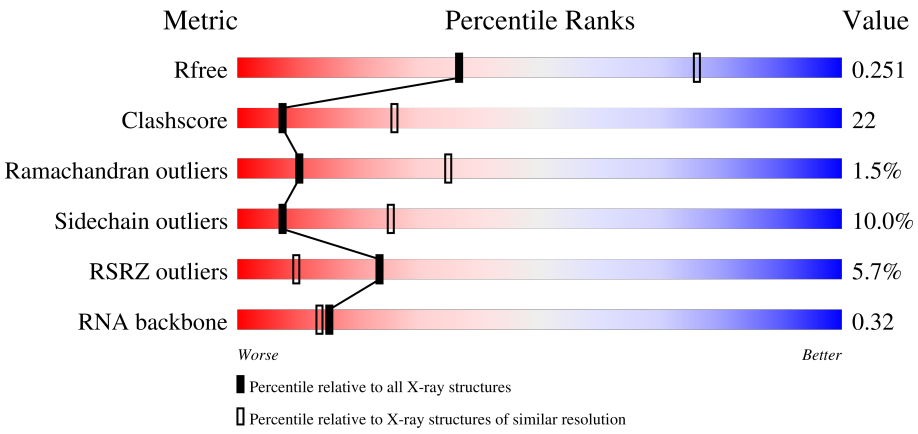
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 3.06 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	1754 (3.10-3.02)
Clashscore	141614	1864 (3.10-3.02)
Ramachandran outliers	138981	1794 (3.10-3.02)
Sidechain outliers	138945	1793 (3.10-3.02)
RSRZ outliers	127900	1713 (3.10-3.02)
RNA backbone	3102	1036 (3.32-2.80)

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 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	685	6% 60% 32% 5% •
2	X	21	43% 38% 19%
3	Y	15	20% 67% 13%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 5511 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	665	4872	3107	918	842	5	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	546	GLU	ASP	engineered mutation	UNP Q746M7

- Molecule 2 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
			Total	C	N	O	P			
2	X	17	342	160	62	103	17	0	0	0

- Molecule 3 is a RNA chain called 5'-R(*CP*AP*AP*CP*CP*UP*AP*CP*UP*AP*CP*CP*UP*CP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	Y	15	287	129	47	97	14	0	0	0

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

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

- Molecule 5 is water.

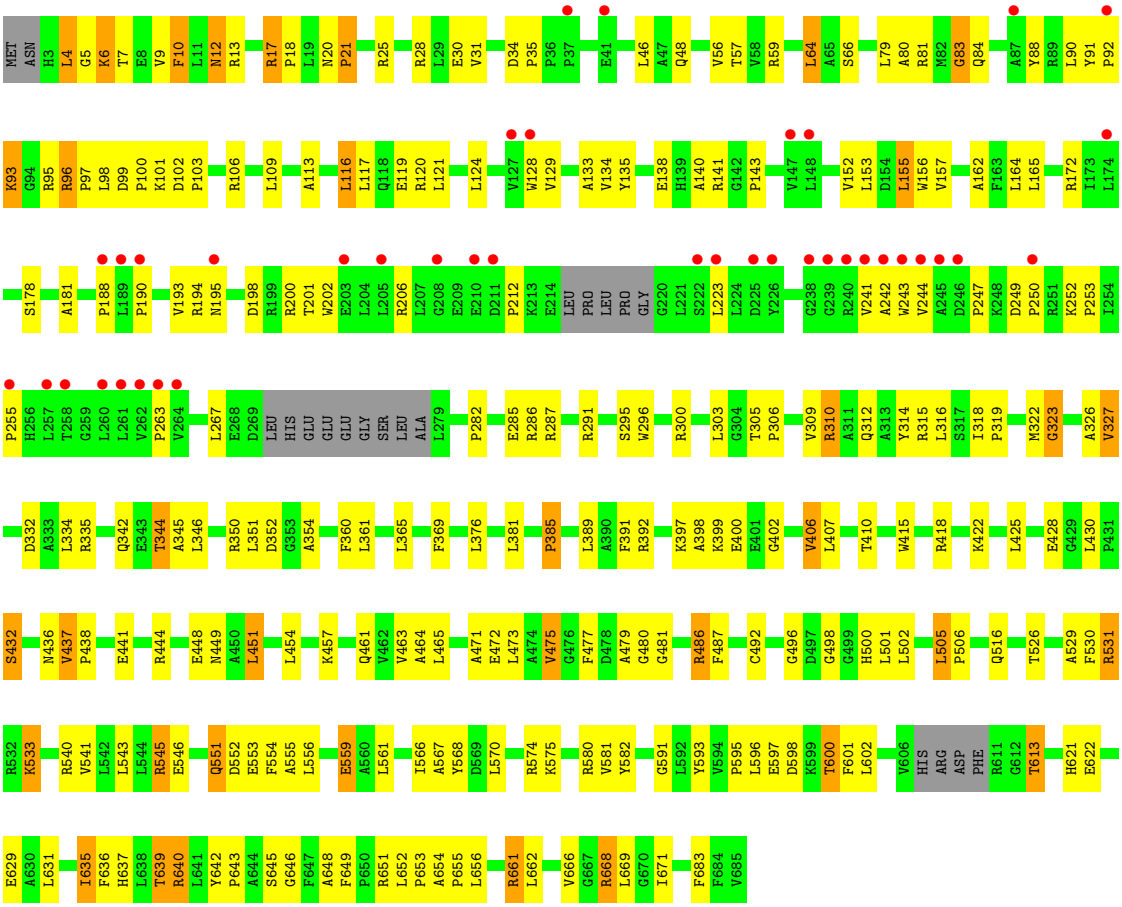
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	8	8	8	0	0
			Total	O		
5	Y	1	1	1	0	0

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.

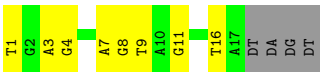
• Molecule 1: Argonaute

Chain A: 6% 60% 32% 5%



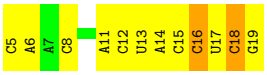
• Molecule 2: 5'-D(P*TP*GP*AP*GP*GP*TP*AP*GP*TP*AP*GP*GP*TP*TP*GP*TP*AP*TP*AP*GP*T)-3'

Chain X: 43% 38% 19%



• Molecule 3: 5'-R(*CP*AP*AP*CP*CP*UP*AP*CP*UP*AP*CP*CP*UP*CP*G)-3'

Chain Y: 20% 67% 13%



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	111.87Å 111.87Å 177.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.55 – 3.06 43.55 – 3.06	Depositor EDS
% Data completeness (in resolution range)	96.3 (43.55-3.06) 99.1 (43.55-3.06)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.21 (at 3.06Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.202 , 0.255 0.198 , 0.251	Depositor DCC
R_{free} test set	1112 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	88.0	Xtriage
Anisotropy	0.257	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 69.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	5511	wwPDB-VP
Average B, all atoms (Å^2)	97.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.44% 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 (i)

5.1 Standard geometry (i)

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	0.45	0/4979	0.66	6/6780 (0.1%)
2	X	0.97	1/383 (0.3%)	1.49	4/591 (0.7%)
3	Y	0.67	0/318	1.15	0/492
All	All	0.51	1/5680 (0.0%)	0.79	10/7863 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	X	1	DT	OP3-P	-11.98	1.46	1.61

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	385	PRO	CA-N-CD	-7.82	100.56	111.50
2	X	11	DG	O4'-C1'-N9	6.84	112.79	108.00
2	X	1	DT	OP1-P-OP2	-6.68	109.58	119.60
2	X	16	DT	O4'-C1'-N1	6.18	112.33	108.00
1	A	263	PRO	N-CA-CB	6.05	110.56	103.30
1	A	212	PRO	N-CA-CB	5.99	110.49	103.30
1	A	247	PRO	N-CA-CB	5.96	110.45	103.30
1	A	250	PRO	N-CA-CB	5.92	110.41	103.30
1	A	143	PRO	N-CA-CB	5.89	110.37	103.30
2	X	1	DT	N3-C4-O4	5.05	122.93	119.90

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	4872	0	4664	215	0
2	X	342	0	182	6	0
3	Y	287	0	148	14	0
4	X	1	0	0	0	0
5	A	8	0	0	0	0
5	Y	1	0	0	0	0
All	All	5511	0	4994	233	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 22.

All (233) 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:4:LEU:CD1	1:A:5:GLY:N	1.69	1.56
1:A:4:LEU:HD12	1:A:5:GLY:N	1.14	1.40
1:A:4:LEU:HD13	1:A:5:GLY:N	1.62	1.10
1:A:639:THR:HG22	1:A:640:ARG:HE	1.18	1.03
1:A:4:LEU:HB3	1:A:315:ARG:O	1.56	1.03
1:A:661:ARG:HG2	1:A:661:ARG:HH21	1.32	0.91
1:A:13:ARG:HB2	1:A:309:VAL:HG11	1.54	0.90
1:A:9:VAL:HG11	1:A:581:VAL:HG13	1.56	0.87
1:A:188:PRO:O	1:A:190:PRO:HD3	1.75	0.85
1:A:4:LEU:HD12	1:A:5:GLY:CA	2.07	0.84
1:A:639:THR:CG2	1:A:640:ARG:HE	1.90	0.83
1:A:661:ARG:HH21	1:A:661:ARG:CG	1.92	0.83
1:A:621:HIS:ND1	1:A:631:LEU:HD11	1.94	0.83
1:A:645:SER:HB2	1:A:648:ALA:O	1.78	0.82
1:A:327:VAL:HG23	1:A:332:ASP:HB2	1.60	0.82
1:A:342:GLN:O	1:A:344:THR:HG22	1.80	0.82
1:A:117:LEU:HD22	1:A:155:LEU:HB2	1.61	0.81
1:A:636:PHE:O	1:A:639:THR:HB	1.81	0.81
3:Y:11:A:H2'	3:Y:12:C:H6	1.46	0.80
1:A:9:VAL:HG13	1:A:582:TYR:O	1.81	0.80
1:A:639:THR:HG22	1:A:640:ARG:NE	1.97	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:6:LYS:HD3	1:A:312:GLN:NE2	1.98	0.77
1:A:124:LEU:HD22	1:A:300:ARG:HH21	1.47	0.77
1:A:178:SER:H	1:A:181:ALA:HB3	1.50	0.77
1:A:597:GLU:HG2	1:A:598:ASP:H	1.48	0.76
1:A:593:TYR:CZ	1:A:595:PRO:HG3	2.19	0.76
1:A:178:SER:N	1:A:181:ALA:HB3	2.02	0.75
1:A:385:PRO:HD3	1:A:391:PHE:CE1	2.22	0.73
1:A:48:GLN:HE21	1:A:79:LEU:HD11	1.53	0.73
1:A:540:ARG:HB2	1:A:567:ALA:HB3	1.70	0.73
1:A:13:ARG:HB2	1:A:309:VAL:CG1	2.18	0.72
1:A:465:LEU:H	1:A:498:GLY:HA2	1.55	0.71
1:A:315:ARG:HH11	1:A:316:LEU:H	1.38	0.71
3:Y:11:A:H2'	3:Y:12:C:C6	2.25	0.70
1:A:350:ARG:NH2	1:A:354:ALA:HB3	2.08	0.69
1:A:101:LYS:O	1:A:103:PRO:HD3	1.93	0.69
1:A:121:LEU:HD22	1:A:134:VAL:HG21	1.74	0.68
1:A:13:ARG:O	1:A:309:VAL:HG12	1.93	0.67
1:A:492:CYS:SG	1:A:526:THR:HG23	2.36	0.66
3:Y:6:A:H8	3:Y:6:A:H5"	1.58	0.66
1:A:109:LEU:HB3	1:A:157:VAL:HG21	1.78	0.66
1:A:327:VAL:CG2	1:A:332:ASP:HB2	2.26	0.66
1:A:661:ARG:HG2	1:A:661:ARG:NH2	2.09	0.65
1:A:116:LEU:HD21	1:A:120:ARG:NE	2.12	0.65
1:A:295:SER:HA	1:A:306:PRO:HG2	1.78	0.64
1:A:286:ARG:HD2	1:A:613:THR:HG21	1.78	0.63
1:A:621:HIS:CE1	1:A:631:LEU:HD11	2.33	0.63
1:A:99:ASP:OD2	1:A:101:LYS:HB2	1.98	0.62
1:A:471:ALA:HB2	1:A:540:ARG:HG2	1.82	0.62
1:A:574:ARG:HD3	3:Y:8:C:OP1	2.00	0.61
1:A:385:PRO:HD3	1:A:391:PHE:CZ	2.35	0.61
1:A:323:GLY:H	1:A:327:VAL:HG12	1.66	0.61
1:A:531:ARG:HD3	1:A:531:ARG:C	2.22	0.60
1:A:17:ARG:HD2	1:A:303:LEU:HA	1.84	0.60
3:Y:6:A:H5"	3:Y:6:A:C8	2.36	0.60
1:A:10:PHE:HB3	1:A:310:ARG:HB3	1.84	0.60
1:A:319:PRO:HG2	1:A:640:ARG:HD3	1.82	0.60
1:A:475:VAL:HG22	1:A:477:PHE:CE1	2.37	0.60
1:A:640:ARG:HA	1:A:649:PHE:CD2	2.36	0.59
1:A:344:THR:CG2	1:A:369:PHE:CE2	2.84	0.59
1:A:575:LYS:HB3	1:A:651:ARG:NH2	2.18	0.59
1:A:465:LEU:N	1:A:498:GLY:HA2	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:VAL:HG21	1:A:46:LEU:HD11	1.85	0.58
1:A:345:ALA:HB3	1:A:402:GLY:O	2.03	0.58
1:A:30:GLU:CB	1:A:93:LYS:HD3	2.33	0.58
1:A:316:LEU:HB2	1:A:591:GLY:O	2.03	0.58
3:Y:14:A:H2'	3:Y:15:C:H6	1.68	0.57
1:A:195:ASN:O	1:A:198:ASP:O	2.23	0.57
1:A:551:GLN:O	1:A:552:ASP:HB2	2.03	0.57
1:A:97:PRO:O	1:A:98:LEU:HD12	2.05	0.56
1:A:344:THR:CG2	1:A:369:PHE:HE2	2.18	0.56
1:A:172:ARG:HD2	2:X:9:DT:OP1	2.04	0.56
1:A:621:HIS:ND1	1:A:631:LEU:CD1	2.68	0.55
3:Y:14:A:H2'	3:Y:15:C:C6	2.41	0.55
1:A:516:GLN:OE1	1:A:555:ALA:HB3	2.07	0.55
1:A:4:LEU:CD1	1:A:5:GLY:CA	2.76	0.54
1:A:323:GLY:H	1:A:327:VAL:CG1	2.20	0.54
3:Y:16:C:H2'	3:Y:16:C:O2	2.06	0.54
1:A:501:LEU:O	1:A:502:LEU:HD23	2.06	0.54
1:A:116:LEU:HD21	1:A:120:ARG:HE	1.71	0.54
1:A:296:TRP:CZ2	1:A:300:ARG:HD3	2.42	0.54
1:A:13:ARG:C	1:A:309:VAL:HG12	2.27	0.54
1:A:59:ARG:HA	1:A:64:LEU:HB3	1.89	0.54
1:A:461:GLN:NE2	1:A:463:VAL:O	2.36	0.54
1:A:193:VAL:HG22	1:A:194:ARG:H	1.73	0.53
1:A:315:ARG:NH1	1:A:316:LEU:H	2.05	0.53
1:A:344:THR:HG21	1:A:369:PHE:CE2	2.44	0.53
1:A:480:GLY:HA2	1:A:486:ARG:HG3	1.90	0.53
1:A:56:VAL:HG12	1:A:56:VAL:O	2.09	0.52
1:A:113:ALA:HB1	1:A:155:LEU:HD13	1.92	0.52
3:Y:18:C:HO2'	3:Y:19:G:P	2.32	0.52
1:A:155:LEU:HD22	1:A:164:LEU:O	2.09	0.52
1:A:546:GLU:OE2	1:A:575:LYS:HE2	2.10	0.52
1:A:345:ALA:O	1:A:346:LEU:HD12	2.09	0.52
1:A:25:ARG:HA	1:A:97:PRO:HA	1.92	0.52
1:A:57:THR:HG22	1:A:66:SER:OG	2.10	0.51
1:A:464:ALA:HB1	1:A:498:GLY:HA3	1.92	0.51
1:A:287:ARG:O	1:A:291:ARG:HG3	2.10	0.51
1:A:516:GLN:HB3	1:A:556:LEU:HG	1.92	0.51
2:X:7:DA:H2"	2:X:8:DG:H8	1.75	0.51
1:A:48:GLN:NE2	1:A:79:LEU:HD11	2.22	0.51
1:A:206:ARG:O	1:A:242:ALA:HA	2.10	0.51
1:A:80:ALA:HA	1:A:84:GLN:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:575:LYS:HB3	1:A:651:ARG:HH22	1.76	0.51
1:A:129:VAL:HG22	1:A:134:VAL:HG22	1.93	0.51
1:A:598:ASP:O	1:A:600:THR:HG22	2.11	0.51
1:A:410:THR:N	1:A:437:VAL:HG23	2.25	0.51
1:A:415:TRP:CZ3	1:A:668:ARG:HG2	2.46	0.51
1:A:350:ARG:CZ	1:A:354:ALA:HB3	2.41	0.50
1:A:286:ARG:HG2	1:A:582:TYR:OH	2.11	0.50
1:A:437:VAL:HG12	1:A:438:PRO:CD	2.42	0.50
1:A:437:VAL:HG12	1:A:438:PRO:N	2.26	0.50
1:A:34:ASP:HA	1:A:35:PRO:C	2.31	0.50
1:A:287:ARG:HH22	1:A:291:ARG:HH11	1.58	0.50
1:A:392:ARG:NH2	1:A:428:GLU:OE2	2.45	0.49
1:A:418:ARG:CZ	1:A:422:LYS:HZ3	2.24	0.49
1:A:457:LYS:HG2	1:A:683:PHE:HA	1.95	0.49
1:A:640:ARG:HG3	1:A:649:PHE:CE2	2.46	0.49
1:A:193:VAL:HG12	1:A:202:TRP:O	2.11	0.49
1:A:444:ARG:HG2	1:A:448:GLU:OE2	2.12	0.49
1:A:18:PRO:HA	1:A:162:ALA:HA	1.93	0.49
1:A:410:THR:O	1:A:436:ASN:HA	2.12	0.49
1:A:496:GLY:O	1:A:498:GLY:N	2.46	0.49
1:A:480:GLY:CA	1:A:486:ARG:HG3	2.43	0.49
1:A:629:GLU:H	1:A:629:GLU:CD	2.16	0.49
1:A:381:LEU:HD21	1:A:398:ALA:HB2	1.94	0.48
1:A:135:TYR:CE2	1:A:172:ARG:HB2	2.48	0.48
1:A:193:VAL:O	1:A:201:THR:HA	2.13	0.48
1:A:287:ARG:NH2	1:A:291:ARG:HD2	2.28	0.48
1:A:46:LEU:HD23	1:A:59:ARG:CD	2.43	0.48
1:A:437:VAL:HG12	1:A:438:PRO:HD3	1.96	0.48
1:A:596:LEU:HD11	1:A:602:LEU:HD21	1.96	0.48
2:X:8:DG:H3'	2:X:9:DT:H71	1.96	0.48
1:A:465:LEU:O	1:A:498:GLY:HA2	2.14	0.47
1:A:133:ALA:HB2	1:A:152:VAL:HG22	1.95	0.47
3:Y:18:C:O2'	3:Y:19:G:P	2.71	0.47
1:A:64:LEU:HD21	1:A:90:LEU:CD1	2.44	0.47
1:A:140:ALA:O	1:A:141:ARG:HG2	2.15	0.47
1:A:642:TYR:HA	1:A:643:PRO:HD3	1.60	0.47
1:A:140:ALA:C	1:A:141:ARG:HG2	2.35	0.47
1:A:479:ALA:HA	1:A:487:PHE:O	2.14	0.47
1:A:12:ASN:H	1:A:12:ASN:HD22	1.62	0.47
1:A:344:THR:HG23	1:A:369:PHE:CE2	2.50	0.47
1:A:593:TYR:CE2	1:A:629:GLU:HG3	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:661:ARG:CG	1:A:661:ARG:NH2	2.61	0.47
1:A:350:ARG:C	1:A:351:LEU:HD23	2.35	0.47
1:A:6:LYS:HD3	1:A:312:GLN:HE22	1.80	0.46
1:A:473:LEU:HD11	1:A:526:THR:HG22	1.97	0.46
3:Y:6:A:H8	3:Y:6:A:C5'	2.26	0.46
1:A:506:PRO:HG2	1:A:666:VAL:HG21	1.97	0.46
1:A:399:LYS:HD3	1:A:430:LEU:HD21	1.98	0.46
1:A:477:PHE:HB2	1:A:545:ARG:HG2	1.97	0.46
1:A:529:ALA:O	1:A:533:LYS:HG2	2.15	0.46
1:A:322:MET:SD	1:A:326:ALA:HA	2.55	0.46
1:A:481:GLY:O	1:A:486:ARG:HD2	2.15	0.46
1:A:415:TRP:HZ3	1:A:668:ARG:HG2	1.81	0.46
1:A:12:ASN:HD22	1:A:12:ASN:N	2.14	0.45
1:A:295:SER:HA	1:A:306:PRO:CG	2.45	0.45
1:A:13:ARG:HH11	1:A:156:TRP:HZ2	1.64	0.45
1:A:6:LYS:HG2	1:A:314:TYR:CE1	2.52	0.45
1:A:635:ILE:HG23	1:A:653:PRO:HG3	1.99	0.45
1:A:561:LEU:HD22	1:A:566:ILE:HB	1.98	0.45
2:X:3:DA:H2'	2:X:4:DG:C8	2.52	0.45
1:A:473:LEU:HB3	1:A:541:VAL:HG12	1.98	0.45
1:A:64:LEU:HD22	1:A:64:LEU:H	1.82	0.45
1:A:116:LEU:HD22	1:A:120:ARG:HG3	1.99	0.45
1:A:561:LEU:HD13	1:A:568:TYR:HB3	1.99	0.45
1:A:425:LEU:HD12	1:A:432:SER:HB3	1.99	0.44
1:A:28:ARG:HD3	1:A:96:ARG:HG3	1.98	0.44
1:A:64:LEU:HD21	1:A:90:LEU:HD12	1.98	0.44
1:A:88:TYR:CD2	1:A:90:LEU:CD2	3.01	0.44
1:A:243:TRP:HA	1:A:255:PRO:HA	1.98	0.44
1:A:451:LEU:HD12	1:A:451:LEU:HA	1.74	0.44
1:A:597:GLU:HB3	1:A:600:THR:HG23	2.00	0.44
3:Y:17:U:H2'	3:Y:18:C:C6	2.52	0.44
1:A:319:PRO:HG3	1:A:637:HIS:CD2	2.52	0.44
1:A:399:LYS:HD3	1:A:430:LEU:CD2	2.48	0.44
1:A:351:LEU:HD23	1:A:351:LEU:N	2.33	0.43
1:A:28:ARG:NH1	1:A:93:LYS:NZ	2.66	0.43
1:A:129:VAL:HG12	1:A:129:VAL:O	2.16	0.43
1:A:287:ARG:NH2	1:A:291:ARG:HH11	2.16	0.43
1:A:397:LYS:O	1:A:400:GLU:HB3	2.18	0.43
1:A:593:TYR:OH	1:A:595:PRO:HG3	2.19	0.43
1:A:449:ASN:OD1	1:A:646:GLY:HA3	2.19	0.43
1:A:46:LEU:HD23	1:A:59:ARG:HD2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Y:12:C:H2'	3:Y:12:C:O2	2.19	0.43
1:A:334:LEU:HD23	1:A:334:LEU:HA	1.84	0.43
1:A:90:LEU:CD2	1:A:90:LEU:N	2.82	0.43
1:A:545:ARG:HD2	1:A:553:GLU:OE2	2.18	0.43
1:A:20:ASN:HB2	1:A:21:PRO:HD2	2.01	0.42
1:A:352:ASP:HB3	1:A:437:VAL:HG21	2.01	0.42
1:A:100:PRO:HA	1:A:106:ARG:HB2	2.01	0.42
1:A:318:ILE:H	1:A:318:ILE:HG13	1.62	0.42
1:A:6:LYS:O	1:A:7:THR:OG1	2.27	0.42
1:A:138:GLU:CB	1:A:141:ARG:HH21	2.31	0.42
1:A:305:THR:HA	1:A:306:PRO:HD3	1.74	0.42
1:A:545:ARG:HG3	1:A:554:PHE:CZ	2.55	0.42
1:A:540:ARG:NH2	1:A:567:ALA:HB1	2.34	0.42
1:A:102:ASP:OD2	1:A:102:ASP:C	2.58	0.42
1:A:406:VAL:HG23	1:A:407:LEU:O	2.19	0.42
1:A:472:GLU:HB3	1:A:530:PHE:HE1	1.84	0.42
1:A:282:PRO:O	1:A:285:GLU:N	2.51	0.42
1:A:119:GLU:HA	1:A:119:GLU:OE2	2.19	0.42
1:A:295:SER:CA	1:A:306:PRO:HG2	2.47	0.42
1:A:389:LEU:HD23	1:A:389:LEU:HA	1.77	0.42
1:A:471:ALA:CB	1:A:540:ARG:HG2	2.49	0.42
1:A:121:LEU:HD13	1:A:134:VAL:CG2	2.50	0.42
1:A:193:VAL:HG22	1:A:194:ARG:N	2.34	0.42
1:A:593:TYR:HE2	1:A:629:GLU:HG3	1.84	0.42
1:A:135:TYR:N	1:A:135:TYR:CD1	2.88	0.41
1:A:95:ARG:C	1:A:96:ARG:HG2	2.41	0.41
1:A:128:TRP:HZ3	1:A:172:ARG:HG2	1.84	0.41
1:A:318:ILE:HA	1:A:319:PRO:HD3	1.93	0.41
1:A:360:PHE:CG	1:A:441:GLU:HG2	2.55	0.41
2:X:7:DA:C2	2:X:8:DG:C6	3.08	0.41
1:A:315:ARG:NH1	1:A:316:LEU:O	2.53	0.41
1:A:344:THR:O	1:A:376:LEU:HD12	2.19	0.41
2:X:7:DA:H2"	2:X:8:DG:C8	2.54	0.41
1:A:133:ALA:CB	1:A:152:VAL:HG22	2.51	0.41
1:A:501:LEU:C	1:A:502:LEU:HD23	2.41	0.41
1:A:540:ARG:HA	1:A:567:ALA:O	2.20	0.41
3:Y:13:U:H2'	3:Y:14:A:C8	2.55	0.41
1:A:90:LEU:N	1:A:90:LEU:HD22	2.35	0.41
1:A:654:ALA:HB3	1:A:655:PRO:HD3	2.03	0.41
1:A:360:PHE:CD1	1:A:441:GLU:HG2	2.56	0.41
1:A:361:LEU:O	1:A:365:LEU:HD12	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:601:PHE:HD2	1:A:602:LEU:O	2.04	0.41
1:A:81:ARG:C	1:A:83:GLY:N	2.75	0.40
1:A:194:ARG:HA	1:A:200:ARG:O	2.21	0.40
1:A:505:LEU:HD22	1:A:671:ILE:HD11	2.04	0.40
1:A:252:LYS:HA	1:A:253:PRO:HD3	1.84	0.40
1:A:91:TYR:HA	1:A:92:PRO:HD3	1.87	0.40
1:A:559:GLU:OE1	1:A:559:GLU:O	2.39	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	657/685 (96%)	581 (88%)	66 (10%)	10 (2%)	10 35

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	249	ASP
1	A	223	LEU
1	A	244	VAL
1	A	6	LYS
1	A	83	GLY
1	A	267	LEU
1	A	323	GLY
1	A	241	VAL
1	A	21	PRO
1	A	635	ILE

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	428/549 (78%)	385 (90%)	43 (10%)	7 25

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	10	PHE
1	A	12	ASN
1	A	17	ARG
1	A	64	LEU
1	A	93	LYS
1	A	96	ARG
1	A	116	LEU
1	A	153	LEU
1	A	155	LEU
1	A	165	LEU
1	A	310	ARG
1	A	327	VAL
1	A	335	ARG
1	A	344	THR
1	A	406	VAL
1	A	432	SER
1	A	437	VAL
1	A	451	LEU
1	A	454	LEU
1	A	475	VAL
1	A	486	ARG
1	A	500	HIS
1	A	505	LEU
1	A	531	ARG
1	A	533	LYS
1	A	543	LEU
1	A	545	ARG
1	A	551	GLN
1	A	559	GLU

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Mol	Chain	Res	Type
1	A	570	LEU
1	A	580	ARG
1	A	600	THR
1	A	613	THR
1	A	622	GLU
1	A	639	THR
1	A	640	ARG
1	A	652	LEU
1	A	656	LEU
1	A	661	ARG
1	A	662	LEU
1	A	668	ARG
1	A	669	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	ASN
1	A	48	GLN
1	A	118	GLN
1	A	312	GLN
1	A	404	GLN
1	A	509	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	Y	13/15 (86%)	1 (7%)	2 (15%)

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	Y	16	C

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	Y	5	C
3	Y	18	C

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)

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, 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	665/685 (97%)	-0.10	40 (6%) 21 9	49, 85, 207, 242	0
2	X	17/21 (80%)	-0.30	0 100 100	72, 99, 181, 205	0
3	Y	15/15 (100%)	-0.61	0 100 100	72, 103, 138, 148	0
All	All	697/721 (96%)	-0.12	40 (5%) 23 10	49, 86, 206, 242	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	148	LEU	4.6
1	A	245	ALA	4.6
1	A	205	LEU	4.3
1	A	211	ASP	4.2
1	A	239	GLY	3.8
1	A	263	PRO	3.7
1	A	244	VAL	3.7
1	A	241	VAL	3.6
1	A	258	THR	3.4
1	A	37	PRO	3.4
1	A	243	TRP	3.3
1	A	261	LEU	3.2
1	A	189	LEU	3.0
1	A	210	GLU	3.0
1	A	128	TRP	3.0
1	A	250	PRO	3.0
1	A	260	LEU	2.9
1	A	242	ALA	2.8
1	A	222	SER	2.8
1	A	262	VAL	2.7
1	A	147	VAL	2.6
1	A	257	LEU	2.5
1	A	226	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	41	GLU	2.5
1	A	188	PRO	2.5
1	A	255	PRO	2.4
1	A	195	ASN	2.4
1	A	87	ALA	2.4
1	A	208	GLY	2.3
1	A	190	PRO	2.3
1	A	203	GLU	2.2
1	A	223	LEU	2.2
1	A	92	PRO	2.2
1	A	127	VAL	2.2
1	A	238	GLY	2.1
1	A	246	ASP	2.1
1	A	225	ASP	2.1
1	A	240	ARG	2.1
1	A	264	VAL	2.1
1	A	174	LEU	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)

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. The B-factors column lists the minimum, median, 95th 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	B-factors(Å^2)	Q<0.9
4	MG	X	22	1/1	0.97	0.29	65,65,65,65	0

6.5 Other polymers (i)

There are no such residues in this entry.