Full wwPDB X-ray Structure Validation Report (i)

Aug 27, 2023 – 05:57 PM EDT

PDB ID	:	3HXM
Title	:	Structure of an argonaute complexed with guide DNA and target RNA duplex containing two mismatches.
Authors	:	Wang, Y.; Li, H.; Sheng, G.; Patel, D.J.
Deposited on	:	2009-06-21
Resolution	:	3.10 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:

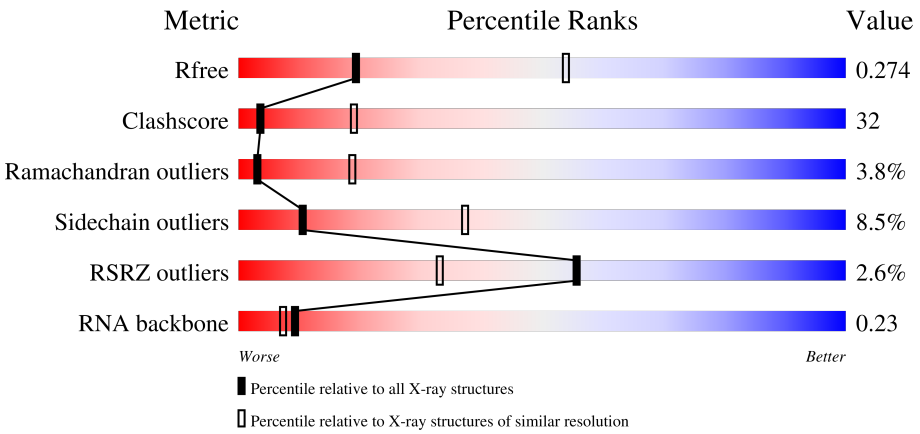
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 3.10 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	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)
RNA backbone	3102	1116 (3.40-2.80)

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	2%, 47%, 41%, 6%, 7%
2	C	21	10%, 14%, 33%, 10%, 5%, 38%
3	Y	20	5%, 10%, 15%, 20%, 55%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5225 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	637	4779	3053	887	833	6	2	0	0

- Molecule 2 is a DNA chain called DNA (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	C	13	258	120	48	77	13	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	Y	9	187	84	31	63	9	0	0	0

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

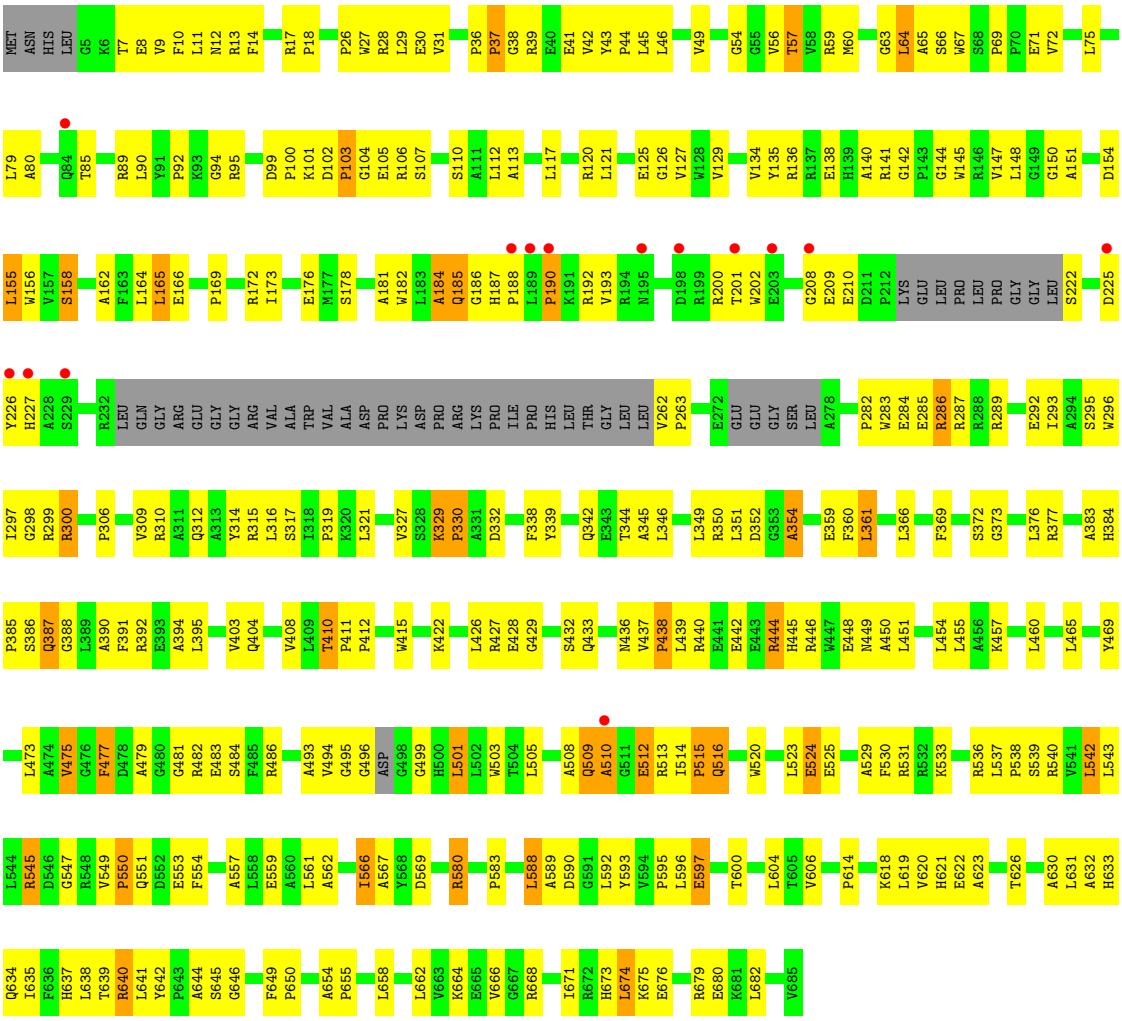
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
4	C	1	1	1	0	0

3 Residue-property plots (i)

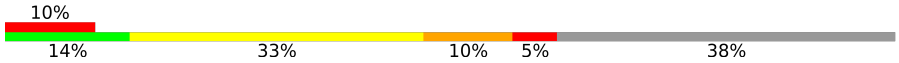
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

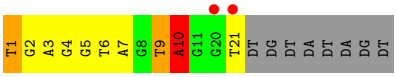
• Molecule 1: Argonaute

Chain A:



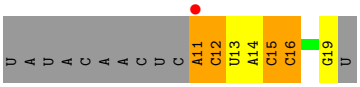
• Molecule 2: DNA (5'-D(P*TP*GP*AP*GP*GP*TP*AP*GP*TP*AP*GP*GP*TP*TP*GP*TP*AP*TP*AP*GP*T)-3')

Chain C: 



• Molecule 3: RNA (5'-R(*UP*AP*UP*AP*CP*AP*AP*CP*UP*CP*AP*CP*UP*AP*CP*CP*UP*CP*GP*U)-3')

Chain Y:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	121.84Å 118.87Å 59.19Å 90.00° 114.79° 90.00°	Depositor
Resolution (Å)	30.00 – 3.10 40.49 – 3.10	Depositor EDS
% Data completeness (in resolution range)	94.3 (30.00-3.10) 94.2 (40.49-3.10)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.37 (at 3.12Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.221 , 0.276 0.214 , 0.274	Depositor DCC
R_{free} test set	981 reflections (7.03%)	wwPDB-VP
Wilson B-factor (Å^2)	62.8	Xtriage
Anisotropy	0.399	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 61.1	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	0.91	EDS
Total number of atoms	5225	wwPDB-VP
Average B, all atoms (Å^2)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.69% 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	0.43	0/4888	0.75	4/6654 (0.1%)
2	C	1.02	1/288 (0.3%)	1.25	3/441 (0.7%)
3	Y	0.60	0/207	0.84	0/319
All	All	0.49	1/5383 (0.0%)	0.79	7/7414 (0.1%)

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
2	C	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1	DT	OP3-P	-6.91	1.52	1.61

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	103	PRO	CA-N-CD	-8.77	99.23	111.50
2	C	10	DA	N9-C1'-C2'	-6.74	99.80	112.60
2	C	9	DT	O4'-C1'-N1	6.34	112.44	108.00
1	A	481	GLY	N-CA-C	-5.85	98.48	113.10
1	A	190	PRO	N-CA-CB	5.85	110.31	103.30
1	A	674	LEU	N-CA-C	-5.20	96.96	111.00
2	C	1	DT	O5'-P-OP2	-5.11	101.10	105.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	10	DA	Sidechain

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	4779	0	4658	301	0
2	C	258	0	137	24	0
3	Y	187	0	98	10	0
4	C	1	0	0	0	0
All	All	5225	0	4893	320	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 32.

All (320) 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:103:PRO:HD2	1:A:104:GLY:H	1.10	1.11
1:A:327:VAL:HG23	1:A:332:ASP:HB2	1.30	1.10
1:A:531:ARG:HH11	1:A:537:LEU:HG	1.09	1.08
1:A:531:ARG:NH1	1:A:537:LEU:HG	1.77	0.98
1:A:121:LEU:HD22	1:A:134:VAL:HG21	1.47	0.96
1:A:621:HIS:ND1	1:A:631:LEU:HD11	1.81	0.95
1:A:226:TYR:CE2	2:C:21:DT:H2'	2.03	0.92
1:A:531:ARG:HH11	1:A:537:LEU:CG	1.83	0.91
1:A:505:LEU:HB2	1:A:675:LYS:NZ	1.89	0.88
1:A:103:PRO:HD2	1:A:104:GLY:N	1.87	0.86
1:A:469:TYR:HB3	1:A:634:GLN:NE2	1.93	0.84
2:C:21:DT:H2'	2:C:21:DT:O2	1.77	0.84
1:A:330:PRO:HB2	1:A:646:GLY:HA2	1.59	0.83
1:A:465:LEU:HG	1:A:641:LEU:HD21	1.60	0.83
1:A:440:ARG:HB3	1:A:442:GLU:OE2	1.80	0.82
1:A:222:SER:HB3	1:A:225:ASP:HB2	1.60	0.82
1:A:103:PRO:CD	1:A:104:GLY:H	1.93	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:540:ARG:HE	1:A:567:ALA:HB1	1.45	0.81
1:A:102:ASP:OD2	1:A:105:GLU:HG3	1.79	0.81
2:C:9:DT:H2"	2:C:10:DA:O5'	1.77	0.81
1:A:505:LEU:HB2	1:A:675:LYS:HZ3	1.46	0.80
1:A:316:LEU:HD11	1:A:593:TYR:CB	2.13	0.78
1:A:316:LEU:HD12	1:A:316:LEU:H	1.48	0.77
1:A:350:ARG:NH2	1:A:354:ALA:HB3	2.01	0.76
1:A:484:SER:HB2	1:A:553:GLU:OE2	1.85	0.76
1:A:496:GLY:HA3	1:A:499:GLY:N	2.01	0.76
2:C:2:DG:H2"	2:C:3:DA:O5'	1.85	0.76
1:A:444:ARG:HD2	1:A:448:GLU:OE2	1.85	0.76
1:A:469:TYR:HB3	1:A:634:GLN:HE21	1.49	0.76
1:A:600:THR:HG22	1:A:620:VAL:HG22	1.69	0.75
1:A:181:ALA:O	1:A:184:ALA:HB3	1.86	0.75
1:A:344:THR:CB	1:A:404:GLN:HE22	2.00	0.74
1:A:496:GLY:HA3	1:A:499:GLY:H	1.52	0.74
1:A:369:PHE:HA	1:A:372:SER:HB2	1.69	0.74
2:C:4:DG:H2'	2:C:5:DG:C8	2.23	0.73
1:A:455:LEU:HD22	1:A:460:LEU:HD22	1.70	0.72
1:A:479:ALA:O	1:A:482:ARG:NH2	2.22	0.72
1:A:316:LEU:HD11	1:A:593:TYR:HB2	1.71	0.72
1:A:8:GLU:OE2	1:A:310:ARG:HD3	1.89	0.71
1:A:226:TYR:HE2	2:C:21:DT:H2'	1.51	0.71
1:A:514:ILE:HG22	1:A:516:GLN:HG2	1.73	0.71
1:A:437:VAL:O	1:A:439:LEU:N	2.23	0.71
1:A:350:ARG:CZ	1:A:354:ALA:HB3	2.21	0.71
1:A:142:GLY:HA3	1:A:145:TRP:HE1	1.55	0.70
1:A:469:TYR:OH	1:A:637:HIS:HD2	1.74	0.70
1:A:640:ARG:HD2	1:A:640:ARG:N	2.05	0.70
1:A:351:LEU:HB2	1:A:410:THR:HB	1.74	0.70
2:C:4:DG:H2'	2:C:5:DG:H8	1.55	0.70
1:A:533:LYS:HD3	1:A:680:GLU:OE2	1.90	0.70
1:A:9:VAL:HG12	1:A:583:PRO:HA	1.72	0.70
1:A:501:LEU:HD11	1:A:682:LEU:HD11	1.74	0.69
1:A:135:TYR:CE2	1:A:172:ARG:HB2	2.28	0.69
1:A:226:TYR:CZ	2:C:21:DT:O2	2.45	0.69
1:A:501:LEU:CD1	1:A:682:LEU:HD11	2.24	0.68
1:A:442:GLU:C	1:A:444:ARG:H	1.96	0.67
1:A:103:PRO:CD	1:A:104:GLY:N	2.56	0.67
1:A:444:ARG:O	1:A:448:GLU:HG3	1.94	0.67
1:A:319:PRO:HG2	1:A:640:ARG:HD3	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:486:ARG:NH1	1:A:512:GLU:HB3	2.09	0.67
1:A:445:HIS:NE2	3:Y:19:G:OP1	2.23	0.67
1:A:512:GLU:O	1:A:513:ARG:HG3	1.94	0.67
1:A:545:ARG:NH1	1:A:622:GLU:OE1	2.27	0.67
1:A:314:TYR:O	1:A:592:LEU:HD12	1.94	0.67
1:A:483:GLU:C	1:A:549:VAL:HG12	2.15	0.66
1:A:147:VAL:HG22	1:A:173:ILE:HD13	1.78	0.66
1:A:136:ARG:HD3	1:A:293:ILE:HD13	1.77	0.66
1:A:147:VAL:HG22	1:A:173:ILE:CD1	2.26	0.66
1:A:559:GLU:O	1:A:562:ALA:HB3	1.95	0.66
1:A:449:ASN:ND2	1:A:645:SER:O	2.29	0.66
2:C:9:DT:C2'	2:C:10:DA:O5'	2.44	0.66
1:A:158:SER:HB3	1:A:162:ALA:H	1.61	0.65
1:A:369:PHE:CE1	1:A:376:LEU:HD13	2.32	0.65
1:A:46:LEU:HB3	1:A:59:ARG:HG3	1.77	0.65
1:A:671:ILE:CG2	1:A:674:LEU:CB	2.74	0.65
1:A:155:LEU:HD23	1:A:164:LEU:O	1.97	0.65
1:A:432:SER:O	1:A:457:LYS:HE2	1.96	0.65
1:A:538:PRO:O	1:A:566:ILE:HD13	1.97	0.65
1:A:549:VAL:O	1:A:550:PRO:O	2.14	0.64
1:A:141:ARG:HG3	1:A:142:GLY:H	1.62	0.64
1:A:345:ALA:H	1:A:404:GLN:HE21	1.46	0.64
1:A:523:LEU:HD21	1:A:561:LEU:HD11	1.79	0.63
1:A:540:ARG:NE	1:A:567:ALA:HB1	2.13	0.63
1:A:621:HIS:CE1	1:A:631:LEU:HD11	2.34	0.63
1:A:99:ASP:OD2	1:A:101:LYS:HB2	1.99	0.63
1:A:28:ARG:HG2	1:A:28:ARG:HH21	1.63	0.62
1:A:344:THR:HB	1:A:404:GLN:HE22	1.64	0.62
1:A:505:LEU:HD21	1:A:666:VAL:HG21	1.81	0.62
3:Y:11:A:H2'	3:Y:12:C:C6	2.35	0.62
1:A:315:ARG:HE	1:A:589:ALA:CB	2.13	0.62
1:A:536:ARG:NH1	1:A:536:ARG:HB3	2.14	0.62
1:A:226:TYR:CE2	2:C:21:DT:O2	2.53	0.62
1:A:327:VAL:CG2	1:A:332:ASP:HB2	2.20	0.61
1:A:315:ARG:HE	1:A:589:ALA:HB1	1.66	0.61
1:A:344:THR:HB	1:A:404:GLN:NE2	2.16	0.61
1:A:227:HIS:CE1	2:C:21:DT:H3'	2.36	0.60
1:A:539:SER:C	1:A:566:ILE:HD12	2.21	0.60
1:A:631:LEU:O	1:A:635:ILE:HG12	2.01	0.60
1:A:662:LEU:O	1:A:666:VAL:HG23	2.01	0.60
1:A:126:GLY:O	1:A:127:VAL:HG23	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:ARG:HG2	1:A:28:ARG:NH2	2.15	0.60
1:A:344:THR:HA	1:A:404:GLN:NE2	2.16	0.60
3:Y:12:C:H2'	3:Y:13:U:C6	2.37	0.59
1:A:505:LEU:HB2	1:A:675:LYS:HZ1	1.66	0.59
1:A:69:PRO:O	1:A:72:VAL:HG22	2.01	0.59
1:A:192:ARG:HA	1:A:202:TRP:O	2.03	0.59
1:A:129:VAL:HG22	1:A:134:VAL:HG22	1.85	0.59
1:A:140:ALA:HB3	1:A:147:VAL:HB	1.85	0.59
1:A:477:PHE:HZ	1:A:543:LEU:HD22	1.68	0.59
1:A:477:PHE:CZ	1:A:543:LEU:HD22	2.38	0.58
1:A:530:PHE:CD2	1:A:538:PRO:HD3	2.38	0.58
1:A:545:ARG:NH2	1:A:550:PRO:O	2.36	0.58
1:A:433:GLN:HG2	1:A:450:ALA:O	2.04	0.58
1:A:638:LEU:HD23	1:A:641:LEU:HD12	1.86	0.58
1:A:593:TYR:CZ	1:A:595:PRO:HG3	2.38	0.57
2:C:2:DG:H2"	2:C:3:DA:C5'	2.34	0.57
3:Y:12:C:O2'	3:Y:13:U:H5'	2.05	0.57
1:A:193:VAL:HG23	1:A:262:VAL:O	2.04	0.57
1:A:376:LEU:H	1:A:376:LEU:HD23	1.68	0.57
1:A:590:ASP:OD2	1:A:606:VAL:HA	2.04	0.57
1:A:227:HIS:CE1	2:C:21:DT:C3'	2.88	0.57
1:A:285:GLU:O	1:A:289:ARG:HG3	2.04	0.57
1:A:169:PRO:HD2	1:A:286:ARG:HH11	1.70	0.56
1:A:316:LEU:HD12	1:A:316:LEU:N	2.20	0.56
1:A:531:ARG:HD2	1:A:537:LEU:HD21	1.87	0.56
1:A:227:HIS:HE1	2:C:21:DT:H3'	1.71	0.56
1:A:640:ARG:HG3	1:A:649:PHE:CE2	2.40	0.56
1:A:316:LEU:HD11	1:A:593:TYR:HB3	1.88	0.56
1:A:621:HIS:ND1	1:A:631:LEU:CD1	2.64	0.56
2:C:6:DT:C2'	2:C:7:DA:O5'	2.54	0.56
1:A:600:THR:CG2	1:A:620:VAL:HG22	2.34	0.55
1:A:671:ILE:HG23	1:A:674:LEU:CB	2.36	0.55
1:A:384:HIS:H	1:A:387:GLN:CD	2.10	0.55
1:A:539:SER:O	1:A:566:ILE:HD12	2.06	0.55
1:A:639:THR:HG23	1:A:650:PRO:O	2.05	0.55
1:A:309:VAL:HG23	1:A:309:VAL:O	2.05	0.55
1:A:664:LYS:O	1:A:668:ARG:HD3	2.07	0.55
1:A:427:ARG:O	1:A:676:GLU:OE1	2.25	0.55
3:Y:15:C:H2'	3:Y:16:C:O4'	2.06	0.55
1:A:142:GLY:HA3	1:A:145:TRP:NE1	2.21	0.55
1:A:321:LEU:HD13	1:A:640:ARG:HB3	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:208:GLY:O	1:A:210:GLU:N	2.38	0.54
1:A:79:LEU:N	1:A:79:LEU:HD23	2.22	0.54
1:A:327:VAL:HG23	1:A:332:ASP:CB	2.21	0.54
1:A:494:VAL:HG22	1:A:501:LEU:HB3	1.89	0.54
1:A:127:VAL:CG1	1:A:134:VAL:HG13	2.38	0.54
1:A:344:THR:CG2	1:A:460:LEU:HD11	2.37	0.54
1:A:352:ASP:OD2	1:A:437:VAL:HG21	2.08	0.54
3:Y:11:A:H2'	3:Y:12:C:H6	1.72	0.53
1:A:596:LEU:HB3	1:A:597:GLU:OE2	2.08	0.53
1:A:344:THR:CB	1:A:404:GLN:NE2	2.68	0.53
1:A:387:GLN:HB3	1:A:390:ALA:HB3	1.91	0.53
1:A:422:LYS:O	1:A:426:LEU:HB2	2.08	0.53
1:A:484:SER:N	1:A:549:VAL:HG12	2.23	0.53
1:A:531:ARG:NH1	1:A:537:LEU:CG	2.55	0.53
1:A:645:SER:OG	1:A:646:GLY:N	2.41	0.53
1:A:13:ARG:HB2	1:A:309:VAL:CG2	2.38	0.53
1:A:29:LEU:HD12	1:A:29:LEU:N	2.25	0.52
1:A:226:TYR:OH	2:C:21:DT:O2	2.26	0.52
1:A:344:THR:CG2	1:A:404:GLN:HE22	2.22	0.52
1:A:411:PRO:O	1:A:412:PRO:C	2.45	0.52
1:A:531:ARG:NH1	1:A:537:LEU:CD1	2.72	0.52
1:A:384:HIS:CE1	1:A:385:PRO:HG2	2.45	0.52
1:A:138:GLU:HA	1:A:148:LEU:HD23	1.91	0.52
1:A:67:TRP:CE2	1:A:112:LEU:HD13	2.45	0.52
1:A:151:ALA:HB3	1:A:293:ILE:HG21	1.91	0.52
1:A:503:TRP:O	1:A:679:ARG:HD2	2.10	0.52
1:A:31:VAL:HG22	1:A:90:LEU:CD2	2.41	0.51
1:A:383:ALA:HA	1:A:387:GLN:OE1	2.10	0.51
1:A:102:ASP:OD1	1:A:103:PRO:CD	2.58	0.51
1:A:540:ARG:HH21	1:A:567:ALA:HB1	1.75	0.51
1:A:297:ILE:HG23	1:A:298:GLY:N	2.25	0.51
1:A:120:ARG:HG3	1:A:120:ARG:HH11	1.76	0.51
1:A:329:LYS:HD2	1:A:332:ASP:OD1	2.11	0.51
1:A:156:TRP:HE1	1:A:164:LEU:HD13	1.75	0.51
1:A:344:THR:CA	1:A:404:GLN:NE2	2.73	0.51
1:A:136:ARG:HD3	1:A:293:ILE:CD1	2.40	0.51
1:A:54:GLY:O	1:A:57:THR:HG23	2.12	0.50
1:A:344:THR:HG22	1:A:404:GLN:HE22	1.76	0.50
1:A:529:ALA:HB2	1:A:679:ARG:CZ	2.41	0.50
2:C:6:DT:H2"	2:C:7:DA:O5'	2.10	0.50
1:A:102:ASP:OD1	1:A:103:PRO:HD3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:PRO:HG2	1:A:72:VAL:HG22	1.92	0.50
1:A:469:TYR:OH	1:A:637:HIS:CD2	2.60	0.50
1:A:640:ARG:HG3	1:A:649:PHE:CD2	2.47	0.50
1:A:671:ILE:HG21	1:A:674:LEU:CB	2.41	0.50
1:A:41:GLU:C	1:A:44:PRO:HD2	2.31	0.50
1:A:69:PRO:HG2	1:A:72:VAL:HG13	1.94	0.50
1:A:12:ASN:OD1	1:A:580:ARG:N	2.45	0.50
1:A:117:LEU:HD22	1:A:155:LEU:HB2	1.94	0.50
1:A:503:TRP:HB2	1:A:662:LEU:HD22	1.94	0.49
1:A:14:PHE:HB3	1:A:306:PRO:HB2	1.92	0.49
1:A:550:PRO:HD2	1:A:553:GLU:OE2	2.12	0.49
1:A:437:VAL:O	1:A:438:PRO:C	2.48	0.49
1:A:293:ILE:O	1:A:297:ILE:HG22	2.12	0.49
1:A:626:THR:HG22	1:A:630:ALA:HB3	1.94	0.49
1:A:486:ARG:CZ	1:A:512:GLU:HB3	2.42	0.49
1:A:531:ARG:HH11	1:A:537:LEU:CD1	2.26	0.49
1:A:296:TRP:NE1	1:A:300:ARG:NH1	2.61	0.48
1:A:383:ALA:HB1	1:A:387:GLN:OE1	2.12	0.48
1:A:350:ARG:CZ	1:A:354:ALA:CB	2.91	0.48
1:A:110:SER:O	1:A:113:ALA:HB3	2.13	0.48
1:A:226:TYR:CE2	2:C:21:DT:C2'	2.87	0.48
1:A:10:PHE:HE1	1:A:310:ARG:HE	1.61	0.48
1:A:345:ALA:H	1:A:404:GLN:NE2	2.10	0.48
1:A:27:TRP:CE3	1:A:95:ARG:HG2	2.48	0.48
1:A:338:PHE:CD1	1:A:372:SER:OG	2.62	0.48
1:A:484:SER:HA	1:A:549:VAL:CG1	2.44	0.48
1:A:640:ARG:HA	1:A:649:PHE:CD2	2.49	0.48
1:A:56:VAL:HG12	1:A:56:VAL:O	2.13	0.48
1:A:580:ARG:NH2	2:C:7:DA:OP2	2.26	0.48
1:A:59:ARG:HA	1:A:64:LEU:HB3	1.95	0.47
1:A:283:TRP:CG	1:A:588:LEU:HD12	2.49	0.47
1:A:165:LEU:HD22	1:A:166:GLU:N	2.29	0.47
1:A:384:HIS:CG	1:A:385:PRO:HD2	2.50	0.47
3:Y:14:A:H2'	3:Y:15:C:C6	2.49	0.47
1:A:376:LEU:H	1:A:376:LEU:CD2	2.27	0.47
1:A:410:THR:O	1:A:436:ASN:HA	2.14	0.47
1:A:674:LEU:O	1:A:675:LYS:HD3	2.14	0.47
1:A:18:PRO:HA	1:A:162:ALA:HA	1.95	0.47
1:A:141:ARG:CG	1:A:142:GLY:H	2.24	0.47
1:A:178:SER:H	1:A:181:ALA:HB3	1.80	0.47
1:A:11:LEU:C	1:A:13:ARG:H	2.18	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:437:VAL:HG13	1:A:438:PRO:N	2.30	0.47
1:A:618:LYS:C	1:A:619:LEU:HD12	2.36	0.46
1:A:316:LEU:HD23	1:A:633:HIS:HA	1.96	0.46
1:A:193:VAL:HA	1:A:263:PRO:HA	1.96	0.46
1:A:495:GLY:O	1:A:499:GLY:HA2	2.15	0.46
1:A:477:PHE:CD1	1:A:477:PHE:N	2.83	0.46
1:A:154:ASP:HB3	1:A:166:GLU:HB3	1.96	0.46
1:A:295:SER:O	1:A:299:ARG:HB2	2.15	0.46
1:A:67:TRP:CD1	1:A:112:LEU:HD13	2.51	0.46
1:A:67:TRP:NE1	1:A:112:LEU:HD13	2.31	0.46
1:A:554:PHE:O	1:A:557:ALA:HB3	2.16	0.46
1:A:227:HIS:CE1	2:C:21:DT:O3'	2.68	0.46
1:A:391:PHE:O	1:A:394:ALA:HB3	2.16	0.46
1:A:465:LEU:HD11	1:A:637:HIS:O	2.16	0.46
1:A:141:ARG:HG3	1:A:142:GLY:N	2.29	0.45
1:A:282:PRO:HG2	1:A:285:GLU:HB3	1.98	0.45
1:A:37:PRO:HG2	1:A:38:GLY:H	1.80	0.45
1:A:342:GLN:NE2	1:A:404:GLN:OE1	2.50	0.45
1:A:514:ILE:CG2	1:A:516:GLN:HG2	2.44	0.45
1:A:540:ARG:HE	1:A:567:ALA:CB	2.22	0.45
1:A:69:PRO:HG2	1:A:72:VAL:CG2	2.47	0.45
1:A:121:LEU:HD22	1:A:134:VAL:CG2	2.32	0.45
1:A:29:LEU:N	1:A:29:LEU:CD1	2.80	0.45
1:A:80:ALA:HB2	1:A:85:THR:HG22	1.99	0.45
1:A:105:GLU:C	1:A:107:SER:N	2.69	0.45
1:A:316:LEU:H	1:A:316:LEU:CD1	2.24	0.45
1:A:345:ALA:HA	1:A:377:ARG:O	2.17	0.45
1:A:427:ARG:C	1:A:429:GLY:H	2.20	0.45
1:A:473:LEU:HD13	1:A:530:PHE:CD1	2.52	0.45
1:A:151:ALA:CB	1:A:293:ILE:HG21	2.47	0.44
1:A:386:SER:C	1:A:388:GLY:H	2.20	0.44
1:A:509:GLN:O	1:A:510:ALA:HB2	2.16	0.44
1:A:542:LEU:HD21	1:A:635:ILE:HD13	1.99	0.44
1:A:69:PRO:HG2	1:A:72:VAL:CG1	2.47	0.44
1:A:182:TRP:CZ2	1:A:187:HIS:CD2	3.06	0.44
1:A:383:ALA:CA	1:A:387:GLN:OE1	2.65	0.44
1:A:475:VAL:HB	1:A:493:ALA:HB2	1.98	0.44
1:A:484:SER:HA	1:A:549:VAL:HG12	1.99	0.44
1:A:13:ARG:HB2	1:A:309:VAL:HG22	1.99	0.44
1:A:45:LEU:O	1:A:49:VAL:HG23	2.17	0.44
1:A:442:GLU:C	1:A:444:ARG:N	2.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:542:LEU:HD21	1:A:635:ILE:CD1	2.48	0.44
1:A:144:GLY:C	1:A:176:GLU:HB2	2.39	0.43
1:A:127:VAL:HG11	1:A:134:VAL:HG13	2.01	0.43
1:A:184:ALA:O	1:A:185:GLN:C	2.56	0.43
1:A:283:TRP:CD1	1:A:588:LEU:HD12	2.54	0.43
1:A:43:TYR:HB2	1:A:44:PRO:HD3	2.00	0.43
1:A:60:MET:O	1:A:63:GLY:O	2.36	0.43
1:A:135:TYR:CZ	1:A:172:ARG:HB2	2.54	0.43
1:A:317:SER:O	1:A:637:HIS:HE1	2.01	0.43
1:A:619:LEU:HD12	1:A:619:LEU:N	2.33	0.43
1:A:540:ARG:NH2	1:A:567:ALA:HB1	2.34	0.43
1:A:392:ARG:HD3	1:A:428:GLU:OE2	2.19	0.42
1:A:75:LEU:HD22	1:A:90:LEU:HB2	2.01	0.42
1:A:359:GLU:HG2	1:A:360:PHE:N	2.35	0.42
1:A:515:PRO:HB3	1:A:553:GLU:OE1	2.20	0.42
2:C:3:DA:H2"	2:C:4:DG:O5'	2.20	0.42
1:A:169:PRO:HD2	1:A:286:ARG:NH1	2.32	0.42
1:A:361:LEU:HD12	1:A:361:LEU:HA	1.84	0.42
2:C:1:DT:H3'	2:C:2:DG:H3'	2.01	0.42
1:A:26:PRO:HB3	1:A:67:TRP:CD1	2.54	0.42
1:A:226:TYR:HE2	2:C:21:DT:C2'	2.27	0.42
1:A:654:ALA:O	1:A:658:LEU:HD12	2.20	0.42
1:A:551:GLN:C	1:A:553:GLU:H	2.23	0.42
1:A:638:LEU:HD13	1:A:655:PRO:HG2	2.02	0.42
1:A:135:TYR:CD1	1:A:135:TYR:N	2.88	0.42
1:A:551:GLN:C	1:A:553:GLU:N	2.72	0.42
1:A:569:ASP:HA	1:A:623:ALA:O	2.19	0.42
1:A:516:GLN:CD	1:A:516:GLN:H	2.23	0.42
1:A:57:THR:HG22	1:A:66:SER:OG	2.19	0.41
1:A:100:PRO:O	1:A:106:ARG:HB2	2.20	0.41
1:A:344:THR:CA	1:A:404:GLN:HE22	2.33	0.41
1:A:384:HIS:ND1	1:A:385:PRO:HG2	2.35	0.41
1:A:28:ARG:N	1:A:94:GLY:O	2.45	0.41
1:A:42:VAL:HG13	1:A:43:TYR:N	2.35	0.41
1:A:383:ALA:CB	1:A:387:GLN:OE1	2.68	0.41
1:A:520:TRP:O	1:A:524:GLU:HB3	2.20	0.41
1:A:395:LEU:HD12	1:A:428:GLU:HG3	2.03	0.41
1:A:536:ARG:HB3	1:A:536:ARG:CZ	2.50	0.41
1:A:673:HIS:O	1:A:675:LYS:N	2.53	0.41
1:A:545:ARG:HD2	1:A:554:PHE:CE1	2.55	0.41
1:A:200:ARG:O	1:A:201:THR:C	2.57	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:135:TYR:HA	1:A:150:GLY:HA3	2.02	0.41
1:A:13:ARG:HB2	1:A:309:VAL:HG21	2.02	0.41
1:A:444:ARG:NH2	3:Y:19:G:O3'	2.54	0.41
1:A:36:PRO:HA	1:A:37:PRO:HD2	1.73	0.41
1:A:296:TRP:O	1:A:300:ARG:HD3	2.20	0.41
1:A:446:ARG:CG	2:C:2:DG:C8	3.04	0.41
1:A:513:ARG:O	1:A:514:ILE:C	2.59	0.41
1:A:631:LEU:O	1:A:632:ALA:C	2.57	0.41
1:A:27:TRP:O	1:A:65:ALA:HA	2.21	0.40
1:A:642:TYR:CE2	1:A:644:ALA:HB3	2.56	0.40
1:A:387:GLN:O	1:A:390:ALA:HB3	2.21	0.40
1:A:473:LEU:HD22	1:A:538:PRO:HG3	2.03	0.40
1:A:604:LEU:HD11	1:A:614:PRO:HB2	2.03	0.40
1:A:349:LEU:HB3	1:A:408:VAL:HG22	2.04	0.40
3:Y:11:A:O2'	3:Y:12:C:OP1	2.36	0.40
3:Y:12:C:H2'	3:Y:13:U:H6	1.86	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	627/685 (92%)	521 (83%)	82 (13%)	24 (4%)	3 19

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	39	ARG
1	A	184	ALA
1	A	190	PRO
1	A	508	ALA
1	A	509	GLN

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Mol	Chain	Res	Type
1	A	510	ALA
1	A	550	PRO
1	A	185	GLN
1	A	339	TYR
1	A	354	ALA
1	A	597	GLU
1	A	387	GLN
1	A	438	PRO
1	A	158	SER
1	A	209	GLU
1	A	330	PRO
1	A	373	GLY
1	A	92	PRO
1	A	186	GLY
1	A	188	PRO
1	A	415	TRP
1	A	547	GLY
1	A	37	PRO
1	A	403	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	445/549 (81%)	407 (92%)	38 (8%)	10 37

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	THR
1	A	17	ARG
1	A	30	GLU
1	A	57	THR
1	A	64	LEU
1	A	71	GLU
1	A	89	ARG

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Mol	Chain	Res	Type
1	A	125	GLU
1	A	155	LEU
1	A	165	LEU
1	A	284	GLU
1	A	286	ARG
1	A	287	ARG
1	A	292	GLU
1	A	300	ARG
1	A	312	GLN
1	A	329	LYS
1	A	346	LEU
1	A	361	LEU
1	A	366	LEU
1	A	410	THR
1	A	444	ARG
1	A	451	LEU
1	A	454	LEU
1	A	475	VAL
1	A	477	PHE
1	A	501	LEU
1	A	512	GLU
1	A	515	PRO
1	A	516	GLN
1	A	524	GLU
1	A	525	GLU
1	A	542	LEU
1	A	545	ARG
1	A	566	ILE
1	A	580	ARG
1	A	588	LEU
1	A	640	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	GLN
1	A	342	GLN
1	A	404	GLN
1	A	449	ASN
1	A	607	HIS
1	A	634	GLN
1	A	637	HIS

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Mol	Chain	Res	Type
1	A	673	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	Y	9/20 (45%)	3 (33%)	1 (11%)

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	Y	12	C
3	Y	15	C
3	Y	16	C

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	Y	11	A

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	637/685 (92%)	-0.13	14 (2%)	62	41	38, 68, 113, 127	2 (0%)
2	C	13/21 (61%)	0.75	2 (15%)	2	1	48, 59, 130, 135	2 (15%)
3	Y	9/20 (45%)	0.28	1 (11%)	5	2	78, 90, 126, 132	0
All	All	659/726 (90%)	-0.10	17 (2%)	56	33	38, 69, 114, 135	4 (0%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	20	DG	5.6
2	C	21	DT	5.4
1	A	189	LEU	3.9
1	A	208	GLY	3.7
1	A	510	ALA	3.2
1	A	84	GLN	2.9
1	A	203	GLU	2.9
1	A	226	TYR	2.8
1	A	225	ASP	2.8
1	A	190	PRO	2.7
1	A	188	PRO	2.4
1	A	229	SER	2.3
1	A	227	HIS	2.2
1	A	195	ASN	2.1
3	Y	11	A	2.1
1	A	201	THR	2.1
1	A	198	ASP	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)

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	C	30	1/1	0.84	0.28	15,15,15,15	0

6.5 Other polymers (i)

There are no such residues in this entry.