Full wwPDB X-ray Structure Validation Report (i)

Feb 19, 2016 – 09:20 PM GMT

PDB ID	:	4Z4E
Title	:	Human Argonaute2 Bound to t1-U Target RNA
Authors	:	Schirle, N.T.; MacRae, I.J.
Deposited on	:	2015-04-02
Resolution	:	1.80 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

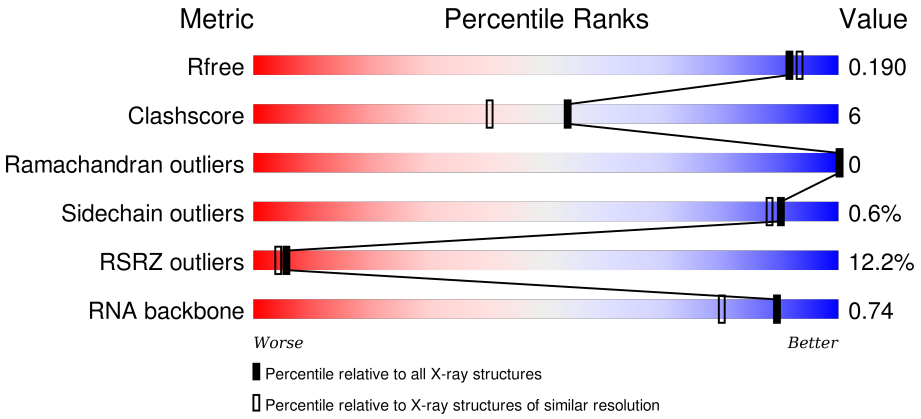
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026982
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20026982

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 1.80 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	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)
RNA backbone	2183	1044 (2.70-0.92)

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 >=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 <=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	859	12% 82% 11% 7%
2	B	21	10% 57% 33% 10%
3	D	11	82% 18%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	IPA	A	902	-	-	-	X
5	IPA	A	903	-	-	-	X
6	IPH	A	904	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7558 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 Protein argonaute-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	802	Total	C	N	O	S	0	0	0
			6429	4093	1157	1139	40			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	387	ASP	SER	engineered mutation	UNP Q9UKV8

- Molecule 2 is a RNA chain called RNA (5'-R(P*UP*UP*CP*AP*CP*AP*UP*UP*GP*CP *CP*CP*AP*AP*GP*UP*CP*UP*U)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	19	Total	C	N	O	P	0	0	0
			379	168	60	132	19			

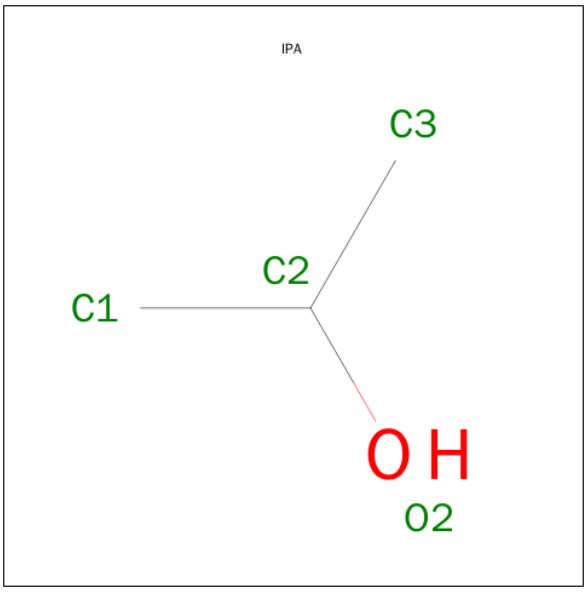
- Molecule 3 is a RNA chain called RNA (5'-R(*CP*AP*AP*UP*GP*UP*GP*AP*U)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	9	Total	C	N	O	P	0	0	0
			173	77	32	56	8			

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

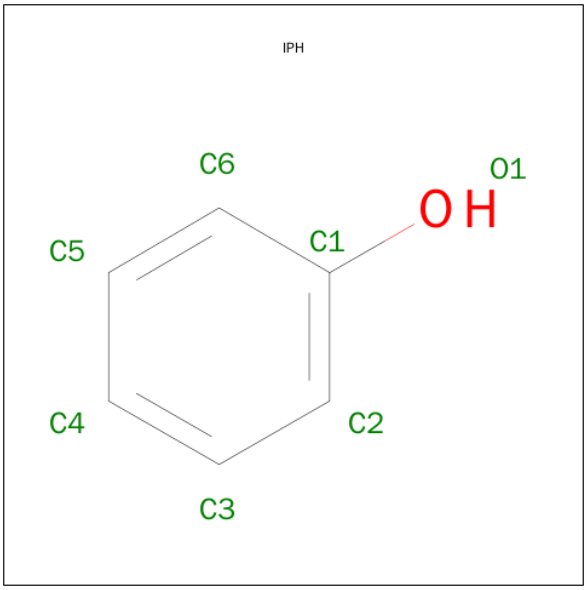
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		
4	A	1	Total	Mg	0	0
			1	1		
4	D	1	Total	Mg	0	0
			1	1		

- Molecule 5 is ISOPROPYL ALCOHOL (three-letter code: IPA) (formula: C_3H_8O).



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

- Molecule 6 is PHENOL (three-letter code: IPH) (formula: C_6H_6O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	6	1		
6	A	1	Total	C	O	0	0
			7	6	1		

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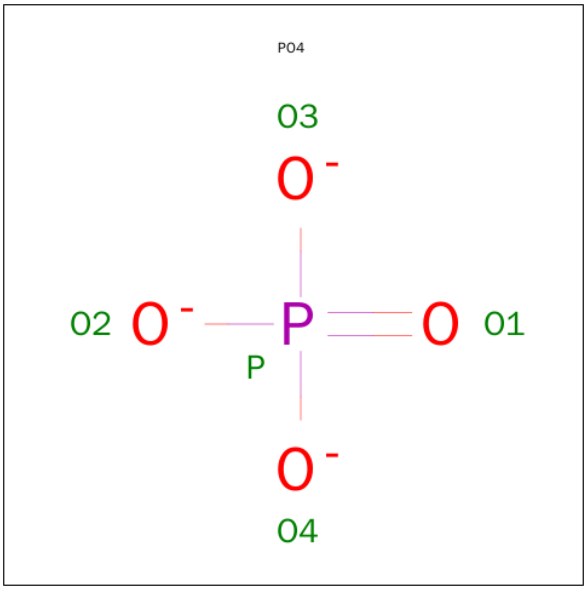
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 7 6 1	0	0
6	A	1	Total C O 7 6 1	0	0

- Molecule 7 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total O P 5 4 1	0	0

- Molecule 8 is water.

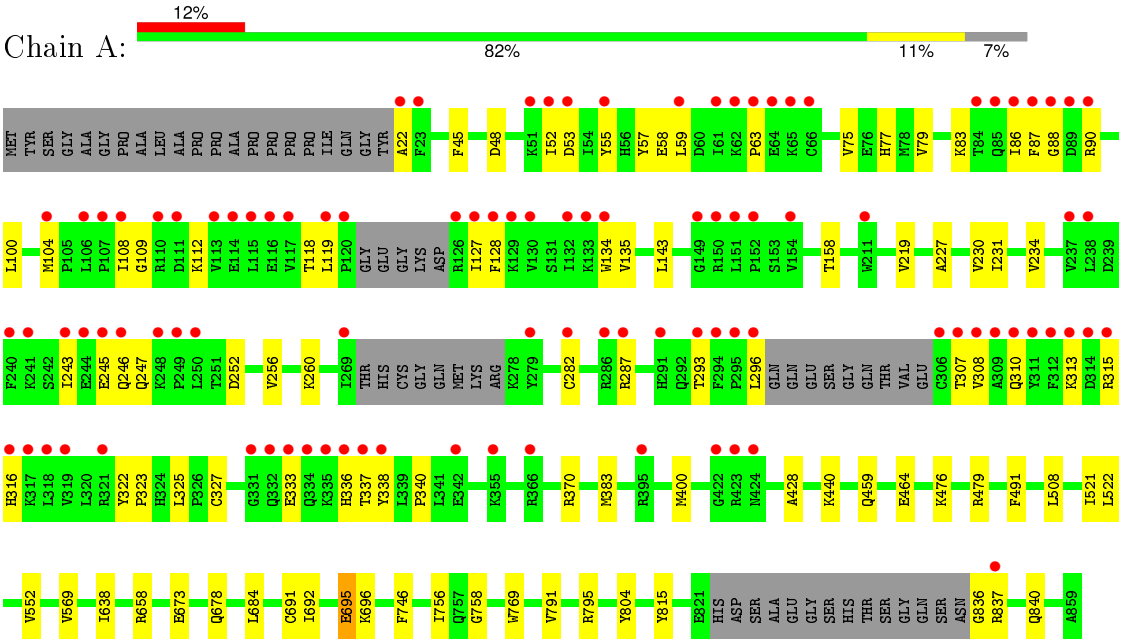
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	447	Total O 447 447	0	0
8	B	51	Total O 51 51	0	0
8	D	35	Total O 35 35	0	0

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.

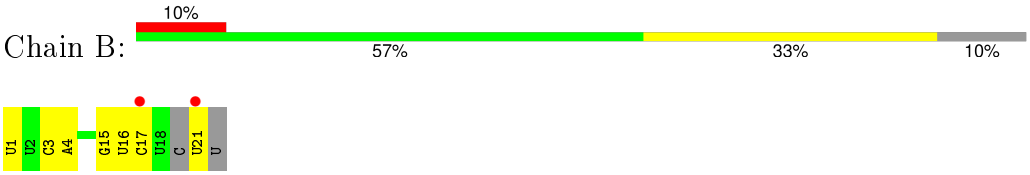
- Molecule 1: Protein argonaute-2

Chain A:



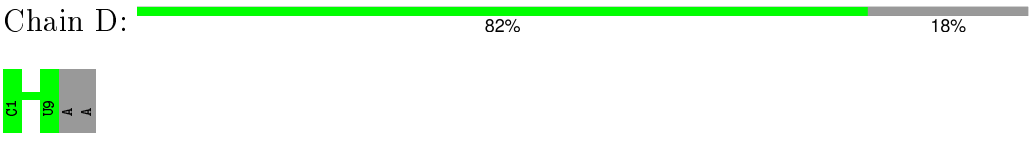
- Molecule 2: RNA (5'-R(P*UP*UP*CP*AP*CP*AP*UP*UP*GP*CP*CP*CP*AP*AP*GP*UP*CP*UP*U)-3')

Chain B:



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

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	55.65Å 116.84Å 69.74Å 90.00° 92.43° 90.00°	Depositor
Resolution (Å)	40.27 – 1.80 40.27 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.7 (40.27-1.80) 99.7 (40.27-1.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.05	Depositor
$< I/\sigma(I) >$ [1]	1.68 (at 1.79Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.158 , 0.185 0.163 , 0.190	Depositor DCC
R_{free} test set	4093 reflections (5.25%)	DCC
Wilson B-factor (Å^2)	21.6	Xtriage
Anisotropy	0.339	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 54.4	EDS
Estimated twinning fraction	0.036 for h,-k,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	0 of 82049 reflections	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	7558	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.08% 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, 0.375 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: PO4, MG, IPA, IPH

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	0.41	2/6581 (0.0%)	0.55	2/8906 (0.0%)
2	B	0.62	1/419 (0.2%)	0.81	0/645
3	D	0.40	0/193	0.72	0/300
All	All	0.43	3/7193 (0.0%)	0.58	2/9851 (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	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	U	OP3-P	-10.23	1.48	1.61
1	A	323	PRO	N-CD	5.35	1.55	1.47
1	A	340	PRO	N-CD	5.30	1.55	1.47

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	322	TYR	C-N-CD	5.37	139.68	128.40
1	A	522	LEU	C-N-CD	5.30	139.53	128.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	695	GLU	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	6429	0	6492	88	0
2	B	379	0	193	10	0
3	D	173	0	87	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	D	1	0	0	0	0
5	A	8	0	16	1	0
6	A	28	0	24	3	0
7	A	5	0	0	0	0
8	A	447	0	0	6	0
8	B	51	0	0	0	0
8	D	35	0	0	0	0
All	All	7558	0	6812	90	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 6.

All (90) 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:695:GLU:HG3	1:A:696:LYS:HB3	1.16	1.14
1:A:118:THR:HG22	1:A:127:ILE:HG22	1.37	1.04
1:A:86:ILE:CD1	1:A:87:PHE:CE2	2.40	1.03
1:A:695:GLU:CG	1:A:696:LYS:HB3	1.89	1.00
1:A:86:ILE:HD12	1:A:87:PHE:CE2	1.99	0.97
1:A:83:LYS:HG2	1:A:88:GLY:HA2	1.53	0.91
1:A:837:ARG:HD3	8:A:1002:HOH:O	1.73	0.89
1:A:90:ARG:HD3	1:A:104:MET:HB2	1.54	0.89
1:A:83:LYS:CG	1:A:88:GLY:HA2	2.03	0.89
1:A:86:ILE:HD12	1:A:87:PHE:CZ	2.09	0.87
1:A:227:ALA:H	5:A:902:IPA:H12	1.37	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:ILE:HG13	1:A:87:PHE:CD2	2.10	0.86
1:A:243:ILE:HD11	1:A:325:LEU:HD11	1.64	0.80
1:A:837:ARG:CD	8:A:1002:HOH:O	2.28	0.80
1:A:638:ILE:HD11	1:A:678:GLN:HG2	1.66	0.77
1:A:296:LEU:HG	1:A:296:LEU:O	1.83	0.77
1:A:336:HIS:HE1	2:B:21:U:H3	1.34	0.75
1:A:86:ILE:HD11	1:A:87:PHE:CE2	2.23	0.73
1:A:83:LYS:HA	1:A:86:ILE:O	1.91	0.70
1:A:336:HIS:ND1	2:B:21:U:O2	2.24	0.69
1:A:231:ILE:HG23	1:A:243:ILE:HD12	1.72	0.69
1:A:219:VAL:HG21	1:A:370:ARG:HH12	1.58	0.68
1:A:83:LYS:HG3	1:A:88:GLY:HA2	1.78	0.65
1:A:695:GLU:HG3	1:A:696:LYS:CB	2.10	0.65
1:A:459:GLN:NE2	1:A:464:GLU:OE2	2.31	0.64
1:A:55:TYR:HD2	1:A:134:TRP:CH2	2.16	0.63
1:A:219:VAL:HG21	1:A:370:ARG:NH1	2.15	0.61
1:A:86:ILE:HD11	1:A:87:PHE:HE2	1.66	0.59
1:A:22:ALA:HB3	1:A:684:LEU:HD23	1.85	0.58
1:A:296:LEU:HD13	2:B:21:U:C4	2.38	0.58
1:A:315:ARG:HG3	1:A:316:HIS:CD2	2.39	0.58
1:A:837:ARG:NE	8:A:1002:HOH:O	2.37	0.57
1:A:692:ILE:HD11	6:A:904:IPH:H4	1.86	0.57
1:A:307:THR:OG1	1:A:310:GLN:HB2	2.04	0.57
1:A:837:ARG:CZ	8:A:1002:HOH:O	2.52	0.56
1:A:55:TYR:HD2	1:A:134:TRP:CZ3	2.23	0.56
1:A:22:ALA:HB1	1:A:769:TRP:CH2	2.41	0.55
1:A:86:ILE:CG1	1:A:87:PHE:CE2	2.90	0.54
1:A:696:LYS:O	1:A:696:LYS:HG2	2.06	0.54
1:A:57:TYR:CE2	1:A:108:ILE:HD12	2.43	0.54
1:A:336:HIS:CE1	2:B:21:U:O2	2.61	0.54
1:A:691:CYS:HB2	6:A:904:IPH:H3	1.91	0.54
1:A:86:ILE:HG13	1:A:87:PHE:CE2	2.44	0.51
1:A:296:LEU:HD13	2:B:21:U:O4	2.11	0.51
1:A:370:ARG:O	1:A:758:GLY:HA2	2.11	0.51
1:A:22:ALA:HB3	1:A:684:LEU:CD2	2.40	0.51
1:A:428:ALA:HB2	1:A:440:LYS:HE2	1.93	0.50
1:A:45:PHE:CZ	1:A:383:MET:HG3	2.47	0.50
1:A:756:ILE:HD11	1:A:795:ARG:NH2	2.27	0.49
1:A:521:ILE:HD12	1:A:552:VAL:HG21	1.93	0.49
1:A:337:THR:HA	2:B:21:U:H1'	1.94	0.49
1:A:336:HIS:CE1	2:B:21:U:H3	2.22	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:3:C:H2'	2:B:4:A:C8	2.47	0.49
1:A:118:THR:HG22	1:A:127:ILE:CG2	2.26	0.49
1:A:77:HIS:ND1	1:A:119:LEU:HD12	2.29	0.48
1:A:246:GLN:HG3	1:A:247:GLN:N	2.29	0.48
1:A:22:ALA:HB1	1:A:769:TRP:CZ3	2.48	0.48
1:A:63:PRO:HD2	1:A:128:PHE:CD1	2.49	0.47
1:A:86:ILE:CG1	1:A:87:PHE:CD2	2.90	0.47
1:A:282:CYS:HB2	1:A:333:GLU:HG2	1.98	0.46
1:A:112:LYS:HB2	1:A:112:LYS:HE3	1.65	0.46
1:A:143:LEU:HB2	1:A:158:THR:HG21	1.99	0.45
1:A:692:ILE:CD1	6:A:904:IPH:H4	2.46	0.45
1:A:310:GLN:HA	1:A:313:LYS:HG3	1.99	0.45
1:A:246:GLN:HG3	1:A:247:GLN:H	1.82	0.45
1:A:296:LEU:O	1:A:296:LEU:CG	2.60	0.45
1:A:256:VAL:O	1:A:260:LYS:HG2	2.17	0.45
1:A:48:ASP:HB2	1:A:400:MET:HB2	1.99	0.45
1:A:58:GLU:HB2	1:A:135:VAL:HG21	1.99	0.44
1:A:308:VAL:HG11	1:A:327:CYS:SG	2.57	0.44
1:A:296:LEU:CD1	2:B:21:U:O4	2.65	0.44
1:A:230:VAL:O	1:A:234:VAL:HG23	2.18	0.44
1:A:336:HIS:O	1:A:338:TYR:CD2	2.70	0.43
1:A:86:ILE:O	1:A:87:PHE:HB2	2.18	0.43
1:A:491:PHE:CD1	1:A:508:LEU:HD21	2.53	0.43
1:A:476:LYS:HG3	1:A:479:ARG:NH2	2.33	0.43
1:A:52:ILE:HG22	1:A:53:ASP:O	2.18	0.43
1:A:336:HIS:O	1:A:338:TYR:CE2	2.71	0.43
1:A:569:VAL:HG21	1:A:791:VAL:HB	1.99	0.43
1:A:287:ARG:NH2	1:A:293:THR:H	2.16	0.43
1:A:90:ARG:HD3	1:A:104:MET:CB	2.36	0.43
1:A:673:GLU:HG3	8:A:1164:HOH:O	2.18	0.43
1:A:108:ILE:HG22	1:A:109:GLY:N	2.34	0.42
1:A:75:VAL:O	1:A:79:VAL:HG23	2.20	0.42
1:A:837:ARG:NH1	8:A:1002:HOH:O	2.53	0.41
1:A:836:GLY:O	1:A:840:GLN:HG2	2.20	0.41
1:A:658:ARG:HA	1:A:658:ARG:HD3	1.95	0.41
1:A:245:GLU:HA	1:A:246:GLN:HA	1.64	0.41
2:B:15:G:H2'	2:B:16:U:C6	2.56	0.41
1:A:59:LEU:CD1	1:A:100:LEU:HB2	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	792/859 (92%)	772 (98%)	20 (2%)	0	100 100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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	709/752 (94%)	705 (99%)	4 (1%)	90 88

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	252	ASP
1	A	746	PHE
1	A	804	TYR
1	A	815	TYR

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

Mol	Chain	Res	Type
1	A	291	HIS
1	A	316	HIS
1	A	324	HIS
1	A	336	HIS

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Mol	Chain	Res	Type
1	A	414	GLN
1	A	461	GLN
1	A	558	GLN
1	A	677	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	16/21 (76%)	1 (6%)	0
3	D	7/11 (63%)	0	0
All	All	23/32 (71%)	1 (4%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	17	C

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 10 ligands modelled in this entry, 3 are monoatomic - leaving 7 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	$\#\|Z\|>2$
5	IPA	A	902	-	3,3,3	0.54	0	3,3,3	0.32	0
5	IPA	A	903	-	3,3,3	0.55	0	3,3,3	0.26	0
6	IPH	A	904	-	7,7,7	0.45	0	8,8,8	0.29	0
6	IPH	A	905	-	7,7,7	0.35	0	8,8,8	0.29	0
6	IPH	A	906	-	7,7,7	0.48	0	8,8,8	0.27	0
6	IPH	A	907	-	7,7,7	0.42	0	8,8,8	0.30	0
7	PO4	A	908	-	4,4,4	1.04	0	6,6,6	0.23	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
5	IPA	A	902	-	-	0/0/0/0	0/0/0/0
5	IPA	A	903	-	-	0/0/0/0	0/0/0/0
6	IPH	A	904	-	-	0/0/0/0	0/1/1/1
6	IPH	A	905	-	-	0/0/0/0	0/1/1/1
6	IPH	A	906	-	-	0/0/0/0	0/1/1/1
6	IPH	A	907	-	-	0/0/0/0	0/1/1/1
7	PO4	A	908	-	-	0/0/0/0	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.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	902	IPA	1	0
6	A	904	IPH	3	0

5.7 Other polymers (i)

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^{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	802/859 (93%)	0.45	99 (12%) 5 4	12, 30, 91, 124	0
2	B	19/21 (90%)	-0.12	2 (10%) 8 6	14, 26, 131, 150	0
3	D	9/11 (81%)	-0.72	0 100 100	23, 23, 34, 90	0
All	All	830/891 (93%)	0.43	101 (12%) 5 4	12, 29, 92, 150	0

All (101) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	296	LEU	12.3
1	A	311	TYR	8.5
1	A	110	ARG	7.1
1	A	294	PHE	6.8
1	A	86	ILE	6.8
1	A	336	HIS	6.5
1	A	23	PHE	6.4
1	A	295	PRO	6.1
1	A	126	ARG	5.9
1	A	312	PHE	5.7
1	A	423	ARG	5.7
1	A	84	THR	5.4
1	A	319	VAL	5.3
1	A	293	THR	5.2
1	A	134	TRP	5.1
1	A	246	GLN	5.0
1	A	317	LYS	4.9
1	A	331	GLY	4.8
1	A	279	TYR	4.7
1	A	316	HIS	4.7
1	A	119	LEU	4.6
1	A	149	GLY	4.6
1	A	89	ASP	4.6

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Mol	Chain	Res	Type	RSRZ
1	A	338	TYR	4.5
1	A	318	LEU	4.5
1	A	117	VAL	4.4
1	A	108	ILE	4.3
1	A	282	CYS	4.1
1	A	334	GLN	4.1
1	A	151	LEU	4.1
1	A	52	ILE	4.1
1	A	65	LYS	4.0
1	A	248	LYS	4.0
1	A	333	GLU	4.0
1	A	291	HIS	3.9
1	A	342	GLU	3.8
1	A	315	ARG	3.8
1	A	307	THR	3.6
1	A	152	PRO	3.6
1	A	113	VAL	3.6
1	A	245	GLU	3.6
1	A	64	GLU	3.5
1	A	313	LYS	3.5
1	A	310	GLN	3.5
1	A	154	VAL	3.5
1	A	287	ARG	3.5
1	A	240	PHE	3.5
1	A	127	ILE	3.4
1	A	424	ASN	3.3
1	A	243	ILE	3.3
1	A	241	LYS	3.3
1	A	335	LYS	3.3
1	A	114	GLU	3.2
1	A	332	GLN	3.2
1	A	62	LYS	3.2
1	A	87	PHE	3.1
1	A	132	ILE	3.1
1	A	309	ALA	3.1
1	A	115	LEU	3.0
1	A	150	ARG	3.0
1	A	308	VAL	3.0
2	B	21	U	3.0
1	A	211	TRP	3.0
1	A	22	ALA	3.0
1	A	90	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	286	ARG	2.9
1	A	244	GLU	2.9
1	A	269	ILE	2.9
1	A	837	ARG	2.9
1	A	116	GLU	2.8
1	A	422	GLY	2.8
1	A	63	PRO	2.8
1	A	250	LEU	2.7
1	A	85	GLN	2.7
1	A	88	GLY	2.7
1	A	53	ASP	2.7
1	A	120	PRO	2.6
1	A	107	PRO	2.6
1	A	395	ARG	2.6
1	A	111	ASP	2.6
1	A	61	ILE	2.4
2	B	17	C	2.4
1	A	355	LYS	2.4
1	A	59	LEU	2.4
1	A	104	MET	2.3
1	A	133	LYS	2.3
1	A	314	ASP	2.3
1	A	238	LEU	2.2
1	A	66	CYS	2.2
1	A	249	PRO	2.2
1	A	337	THR	2.2
1	A	321	ARG	2.2
1	A	130	VAL	2.2
1	A	51	LYS	2.2
1	A	128	PHE	2.2
1	A	106	LEU	2.1
1	A	55	TYR	2.1
1	A	237	VAL	2.1
1	A	306	CYS	2.1
1	A	129	LYS	2.0
1	A	366	ARG	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^{th} 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^2)	Q<0.9
6	IPH	A	904	7/7	0.84	0.14	4.26	42,46,49,52	0
5	IPA	A	903	4/4	0.89	0.14	4.14	45,47,53,60	0
5	IPA	A	902	4/4	0.85	0.17	2.03	30,32,39,48	0
6	IPH	A	907	7/7	0.89	0.13	1.37	28,34,35,37	0
6	IPH	A	906	7/7	0.95	0.10	0.82	20,24,26,37	0
6	IPH	A	905	7/7	0.98	0.08	-0.38	24,25,29,39	0
4	MG	A	901	1/1	0.99	0.09	-0.74	14,14,14,14	0
4	MG	D	101	1/1	0.99	0.04	-	22,22,22,22	0
4	MG	B	101	1/1	0.98	0.10	-	33,33,33,33	0
7	PO4	A	908	5/5	0.81	0.46	-	118,119,119,119	0

6.5 Other polymers (i)

There are no such residues in this entry.