



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 05:22 PM BST

PDB ID : 1RCK
Title : THE THREE DIMENSIONAL STRUCTURE OF GUANINE-SPECIFIC RIBONUCLEASE F1 IN SOLUTION DETERMINED BY NMR SPECTROSCOPY AND DISTANCE GEOMETRY
Authors : Nakai, T.; Yoshikawa, W.; Nakamura, H.; Yoshida, H.
Deposited on : 1994-08-08

This is a Full wwPDB NMR 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/NMRValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

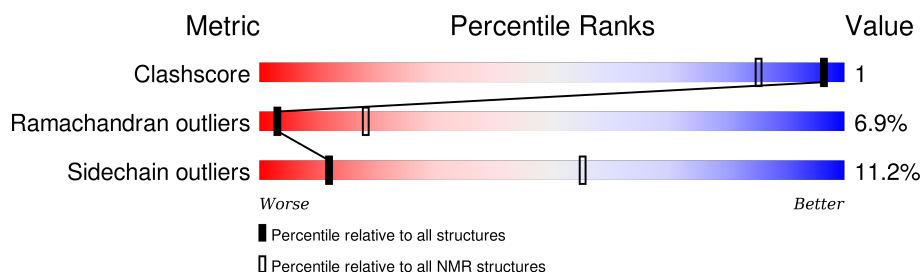
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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)	NMR archive (#Entries)
Clashscore	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	106	 89% 9% ..

2 Ensemble composition and analysis

This entry contains 42 models. Model 31 is the overall representative, medoid model (most similar to other models).

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:2-A:106 (105)	0.98	31

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 7 clusters and 1 single-model cluster was found.

Cluster number	Models
1	2, 3, 8, 9, 10, 11, 12, 14, 15, 19, 20, 23, 27, 30, 31, 32, 36, 38, 40, 41, 42
2	4, 7, 17, 21, 22, 24, 28, 33, 34, 37
3	18, 29
4	6, 26
5	5, 39
6	1, 13
7	16, 35
Single-model clusters	25

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1446 atoms, of which 673 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called RIBONUCLEASE F1.

Mol	Chain	Residues	Atoms						Trace
1	A	106	Total	C	H	N	O	S	0
			1446	470	673	131	168	4	

There are 2 discrepancies between the modelled and reference sequences:

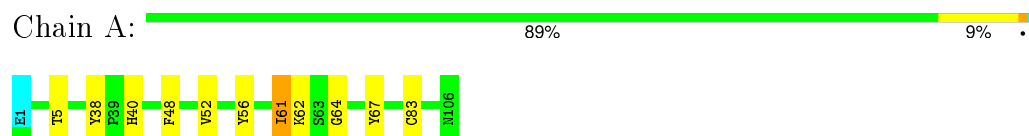
Chain	Residue	Modelled	Actual	Comment	Reference
A	32	THR	SER	CONFLICT	UNP P10282
A	36	SER	THR	CONFLICT	UNP P10282

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: RIBONUCLEASE F1

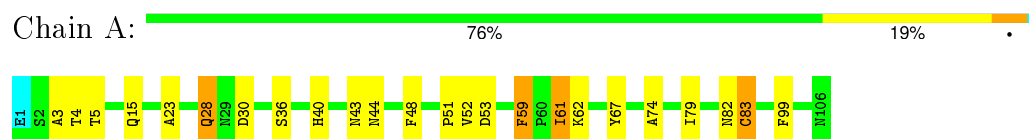


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

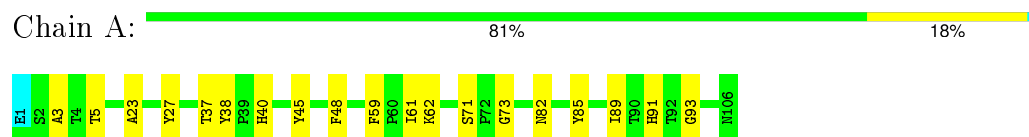
4.2.1 Score per residue for model 1

- Molecule 1: RIBONUCLEASE F1



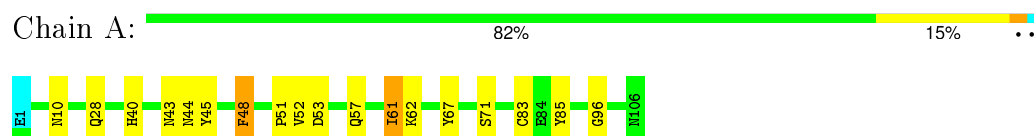
4.2.2 Score per residue for model 2

- Molecule 1: RIBONUCLEASE F1



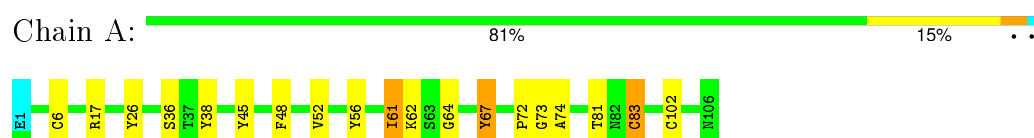
4.2.3 Score per residue for model 3

- Molecule 1: RIBONUCLEASE F1



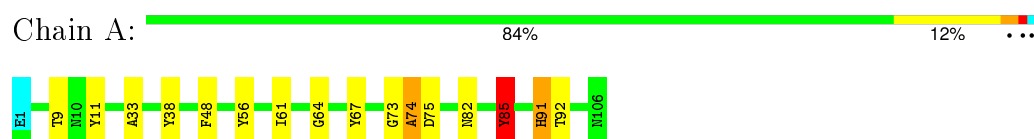
4.2.4 Score per residue for model 4

- Molecule 1: RIBONUCLEASE F1



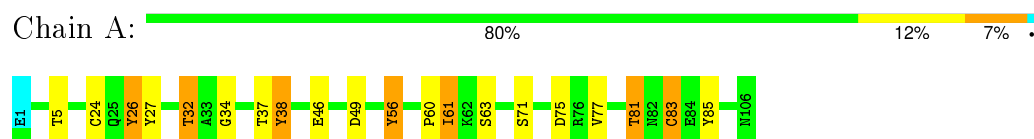
4.2.5 Score per residue for model 5

- Molecule 1: RIBONUCLEASE F1



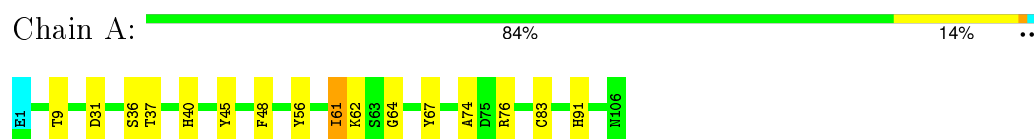
4.2.6 Score per residue for model 6

- Molecule 1: RIBONUCLEASE F1



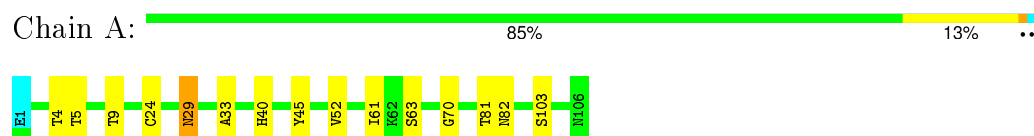
4.2.7 Score per residue for model 7

- Molecule 1: RIBONUCLEASE F1



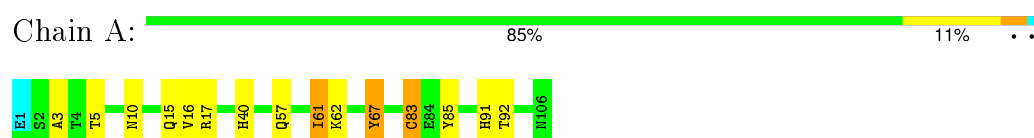
4.2.8 Score per residue for model 8

- Molecule 1: RIBONUCLEASE F1



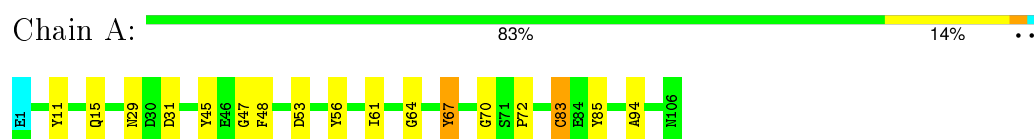
4.2.9 Score per residue for model 9

- Molecule 1: RIBONUCLEASE F1



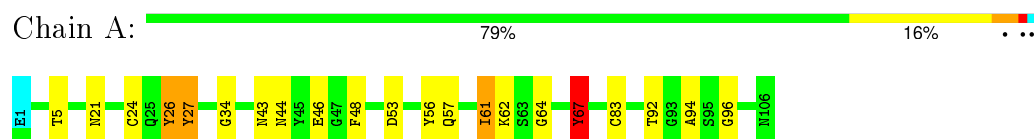
4.2.10 Score per residue for model 10

- Molecule 1: RIBONUCLEASE F1



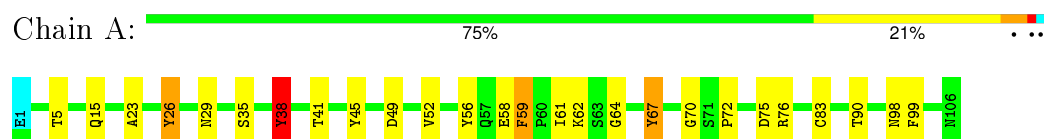
4.2.11 Score per residue for model 11

- Molecule 1: RIBONUCLEASE F1



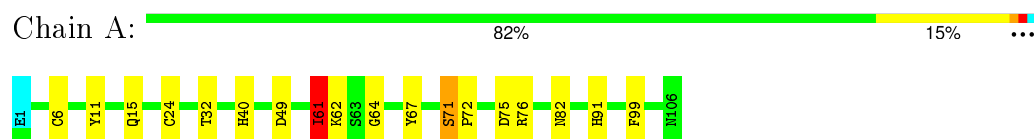
4.2.12 Score per residue for model 12

- Molecule 1: RIBONUCLEASE F1



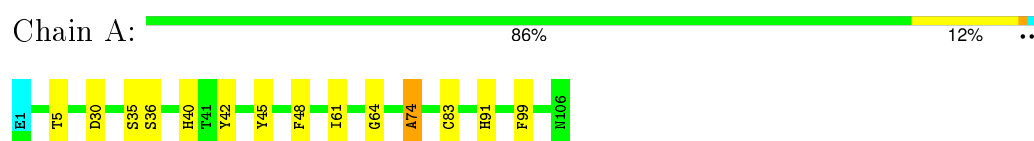
4.2.13 Score per residue for model 13

- Molecule 1: RIBONUCLEASE F1



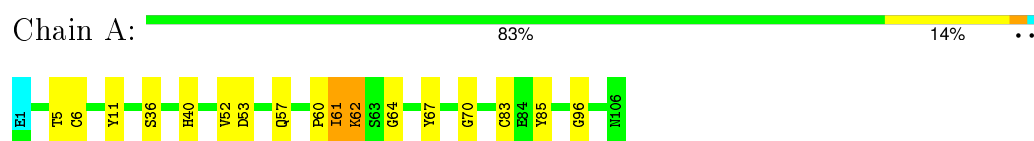
4.2.14 Score per residue for model 14

- Molecule 1: RIBONUCLEASE F1



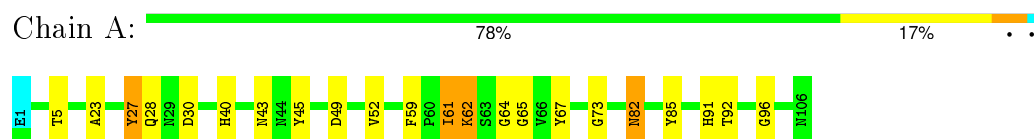
4.2.15 Score per residue for model 15

- Molecule 1: RIBONUCLEASE F1



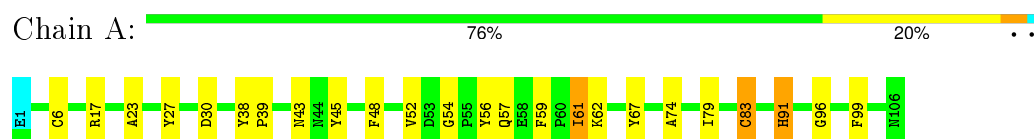
4.2.16 Score per residue for model 16

- Molecule 1: RIBONUCLEASE F1



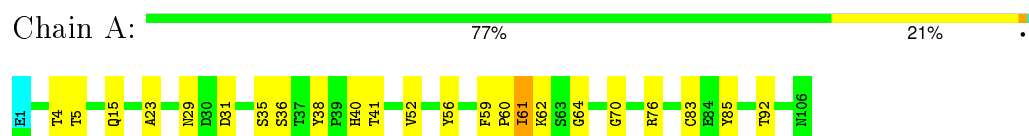
4.2.17 Score per residue for model 17

- Molecule 1: RIBONUCLEASE F1



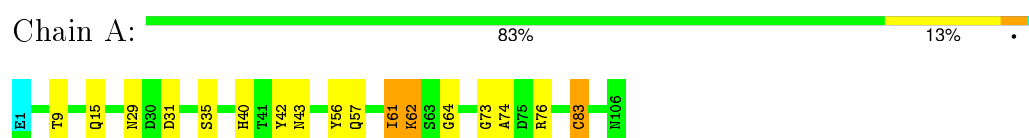
4.2.18 Score per residue for model 18

- Molecule 1: RIBONUCLEASE F1



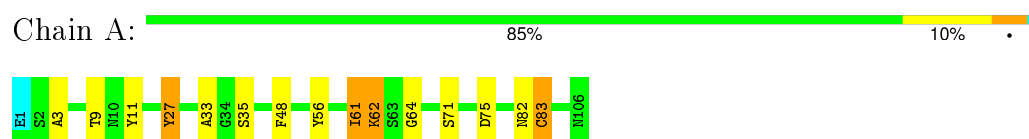
4.2.19 Score per residue for model 19

- Molecule 1: RIBONUCLEASE F1



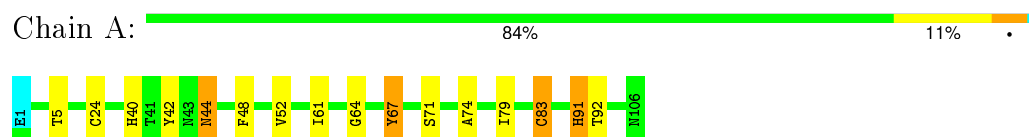
4.2.20 Score per residue for model 20

- Molecule 1: RIBONUCLEASE F1



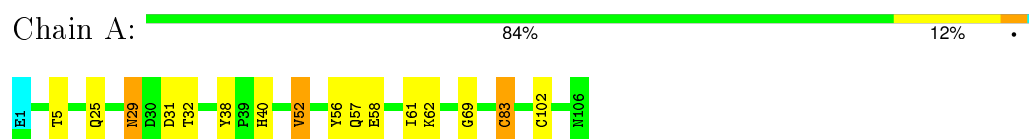
4.2.21 Score per residue for model 21

- Molecule 1: RIBONUCLEASE F1



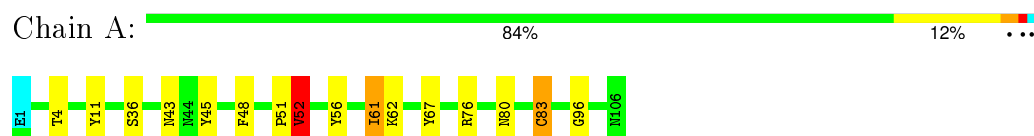
4.2.22 Score per residue for model 22

- Molecule 1: RIBONUCLEASE F1



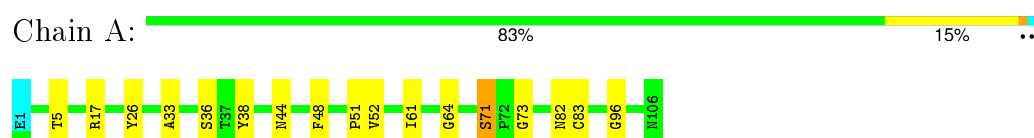
4.2.23 Score per residue for model 23

- Molecule 1: RIBONUCLEASE F1



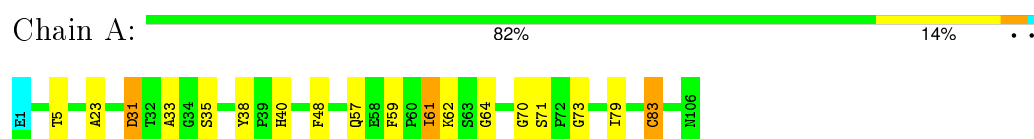
4.2.24 Score per residue for model 24

- Molecule 1: RIBONUCLEASE F1



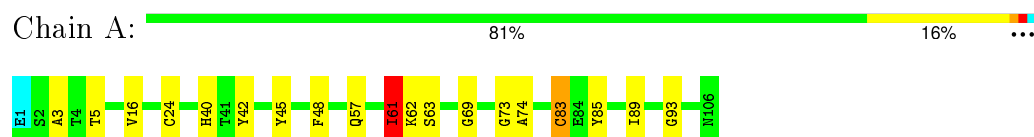
4.2.25 Score per residue for model 25

- Molecule 1: RIBONUCLEASE F1



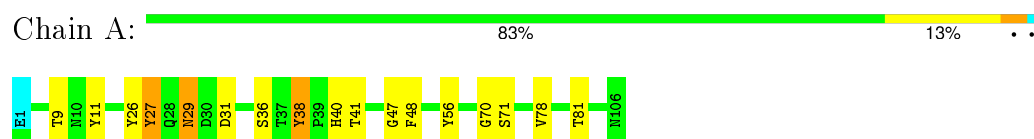
4.2.26 Score per residue for model 26

- Molecule 1: RIBONUCLEASE F1



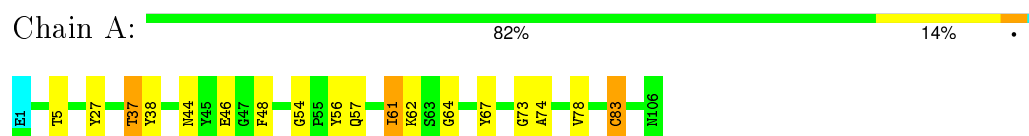
4.2.27 Score per residue for model 27

- Molecule 1: RIBONUCLEASE F1



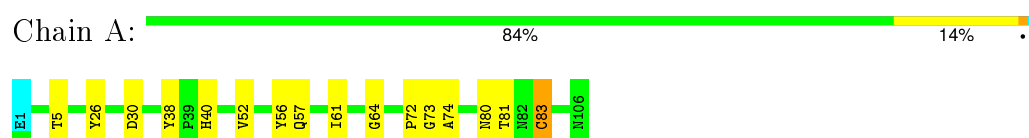
4.2.28 Score per residue for model 28

- Molecule 1: RIBONUCLEASE F1



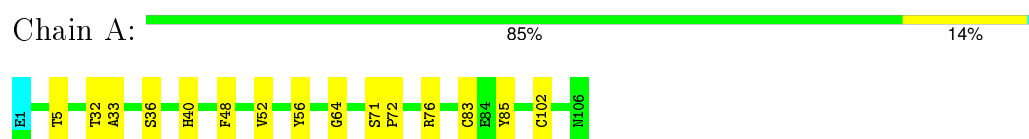
4.2.29 Score per residue for model 29

- Molecule 1: RIBONUCLEASE F1



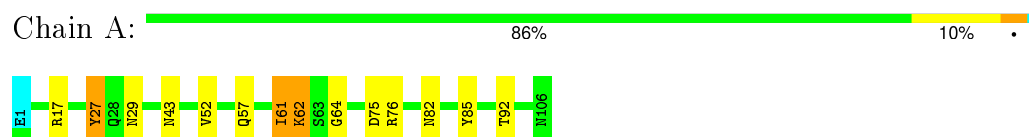
4.2.30 Score per residue for model 30

- Molecule 1: RIBONUCLEASE F1



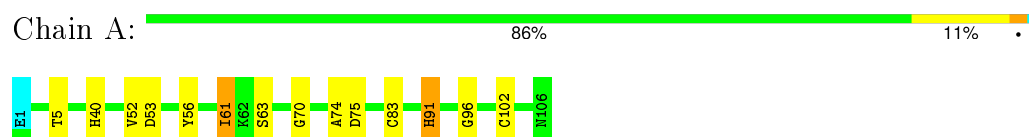
4.2.31 Score per residue for model 31 (medoid)

- Molecule 1: RIBONUCLEASE F1



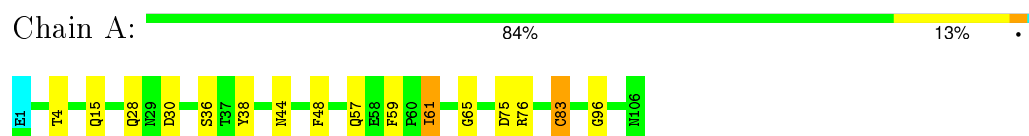
4.2.32 Score per residue for model 32

- Molecule 1: RIBONUCLEASE F1



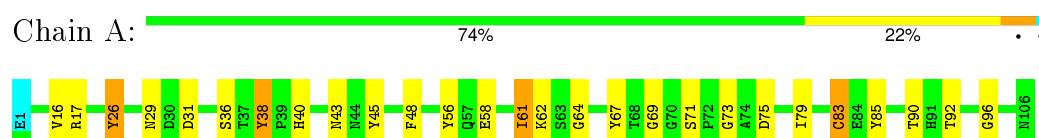
4.2.33 Score per residue for model 33

- Molecule 1: RIBONUCLEASE F1



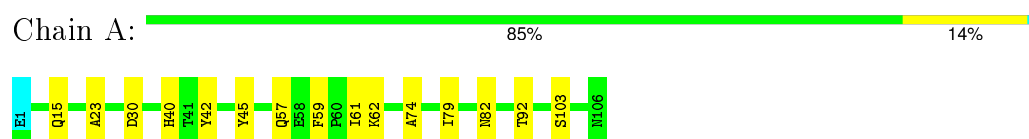
4.2.34 Score per residue for model 34

- Molecule 1: RIBONUCLEASE F1



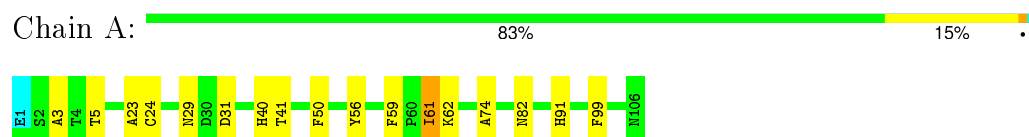
4.2.35 Score per residue for model 35

- Molecule 1: RIBONUCLEASE F1



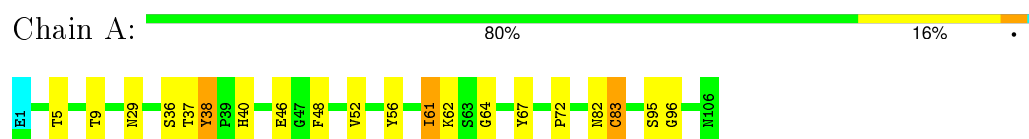
4.2.36 Score per residue for model 36

- Molecule 1: RIBONUCLEASE F1



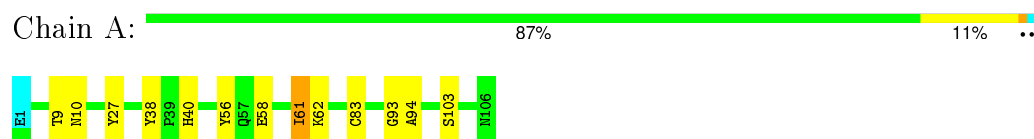
4.2.37 Score per residue for model 37

- Molecule 1: RIBONUCLEASE F1



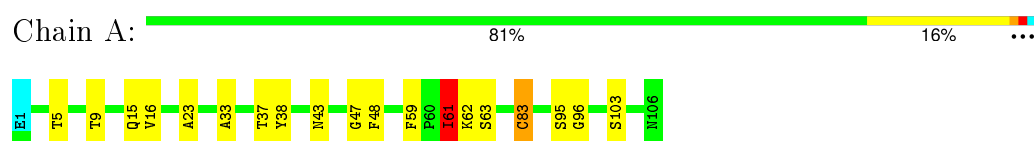
4.2.38 Score per residue for model 38

- Molecule 1: RIBONUCLEASE F1



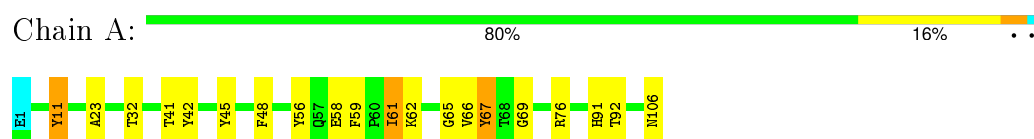
4.2.39 Score per residue for model 39

- Molecule 1: RIBONUCLEASE F1



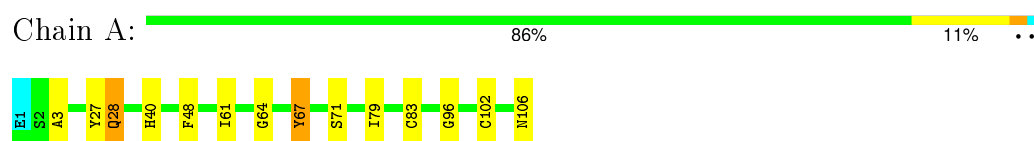
4.2.40 Score per residue for model 40

- Molecule 1: RIBONUCLEASE F1



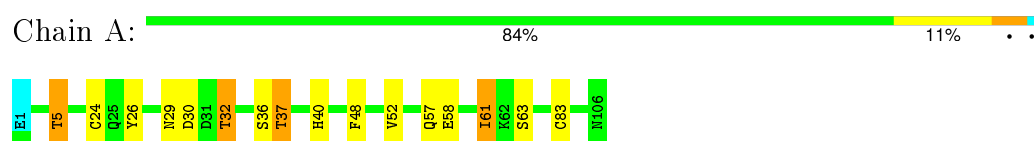
4.2.41 Score per residue for model 41

- Molecule 1: RIBONUCLEASE F1



4.2.42 Score per residue for model 42

- Molecule 1: RIBONUCLEASE F1



5 Refinement protocol and experimental data overview ⓘ

Of the ? calculated structures, 42 were deposited, based on the following criterion: ?.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
EMBOSS	refinement	
PRESTO	refinement	

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality [i](#)

6.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PCA

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 (average) 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	0.64±0.01	0±0/784 (0.0±0.0%)	1.04±0.05	2±1/1070 (0.2±0.1%)
All	All	0.64	0/32928 (0.0%)	1.04	83/44940 (0.2%)

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	61	ILE	CA-CB-CG1	9.69	129.40	111.00	26	31
1	A	27	TYR	CB-CG-CD1	-8.61	115.83	121.00	11	2
1	A	61	ILE	CA-CB-CG2	8.53	127.96	110.90	37	4
1	A	38	TYR	CB-CG-CD1	-8.01	116.19	121.00	6	3
1	A	26	TYR	CB-CG-CD2	-7.56	116.47	121.00	12	5
1	A	56	TYR	CA-CB-CG	7.54	127.72	113.40	6	2
1	A	27	TYR	CB-CG-CD2	-6.88	116.87	121.00	16	4
1	A	26	TYR	CA-CB-CG	6.65	126.03	113.40	34	4
1	A	82	ASN	N-CA-C	-6.49	93.49	111.00	31	2
1	A	40	HIS	CB-CA-C	-5.82	98.76	110.40	19	1
1	A	91	HIS	N-CA-CB	5.54	120.58	110.60	5	5
1	A	85	TYR	CB-CG-CD1	-5.46	117.72	121.00	5	1
1	A	27	TYR	C-N-CA	5.38	135.15	121.70	41	1
1	A	26	TYR	CB-CG-CD1	5.37	124.22	121.00	34	2
1	A	38	TYR	CB-CG-CD2	5.35	124.21	121.00	6	2
1	A	28	GLN	CB-CA-C	5.33	121.07	110.40	1	1
1	A	58	GLU	N-CA-CB	-5.30	101.06	110.60	34	2
1	A	40	HIS	CA-CB-CG	5.26	122.53	113.60	19	1
1	A	27	TYR	CA-CB-CG	5.22	123.31	113.40	16	2
1	A	5	THR	CA-CB-CG2	-5.16	105.17	112.40	42	1
1	A	80	ASN	C-N-CA	5.15	134.57	121.70	29	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	67	TYR	CB-CG-CD2	-5.14	117.91	121.00	41	3
1	A	60	PRO	C-N-CA	5.08	134.41	121.70	6	1
1	A	48	PHE	CB-CG-CD2	-5.05	117.27	120.80	3	1
1	A	5	THR	N-CA-C	-5.04	97.38	111.00	37	1

There are no chirality outliers.

There are no planarity outliers.

6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	765	667	667	2±1
All	All	32130	28014	28014	67

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 1.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:74:ALA:CB	1:A:91:HIS:HB2	0.65	2.21	32	4
1:A:74:ALA:HB2	1:A:91:HIS:HB2	0.61	1.72	32	1
1:A:23:ALA:HB2	1:A:59:PHE:CD2	0.59	2.31	12	4
1:A:37:THR:C	1:A:38:TYR:CD1	0.57	2.78	6	2
1:A:56:TYR:CZ	1:A:78:VAL:HG12	0.55	2.36	27	1
1:A:23:ALA:HB2	1:A:59:PHE:CG	0.54	2.38	35	5
1:A:38:TYR:CD1	1:A:38:TYR:N	0.53	2.75	37	3
1:A:38:TYR:C	1:A:38:TYR:CD1	0.53	2.82	12	1
1:A:61:ILE:CG1	1:A:62:LYS:H	0.49	2.20	1	20
1:A:37:THR:O	1:A:38:TYR:CD1	0.49	2.65	39	1
1:A:16:VAL:CG1	1:A:85:TYR:CE2	0.49	2.96	26	1
1:A:85:TYR:C	1:A:85:TYR:CD1	0.48	2.87	5	1
1:A:91:HIS:NE2	1:A:99:PHE:CE2	0.45	2.84	36	1
1:A:57:GLN:O	1:A:78:VAL:HG13	0.45	2.11	28	1
1:A:23:ALA:HB2	1:A:59:PHE:CD1	0.45	2.47	16	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:91:HIS:CD2	1:A:99:PHE:CZ	0.45	3.05	17	1
1:A:16:VAL:HG13	1:A:85:TYR:CE2	0.45	2.47	9	1
1:A:37:THR:C	1:A:38:TYR:CG	0.44	2.91	37	1
1:A:74:ALA:HB1	1:A:91:HIS:HB2	0.44	1.89	14	3
1:A:37:THR:HG23	1:A:40:HIS:CE1	0.44	2.48	42	1
1:A:38:TYR:CD2	1:A:60:PRO:HD3	0.43	2.47	18	1
1:A:61:ILE:CG2	1:A:62:LYS:N	0.43	2.82	13	1
1:A:11:TYR:N	1:A:11:TYR:CD1	0.42	2.87	40	1
1:A:74:ALA:HB1	1:A:91:HIS:CB	0.42	2.44	14	1
1:A:61:ILE:HG23	1:A:62:LYS:N	0.42	2.30	39	2
1:A:52:VAL:CG1	1:A:80:ASN:ND2	0.42	2.83	23	1
1:A:27:TYR:C	1:A:27:TYR:CD1	0.41	2.94	27	1
1:A:71:SER:CB	1:A:72:PRO:CD	0.41	2.98	13	1
1:A:61:ILE:HG13	1:A:77:VAL:HG13	0.41	1.91	6	1
1:A:27:TYR:CD2	1:A:57:GLN:HG3	0.41	2.50	28	1
1:A:27:TYR:CD2	1:A:57:GLN:CG	0.40	3.05	28	1

6.3 Torsion angles [i](#)

6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	104/106 (98%)	73±4 (71±4%)	23±4 (23±4%)	7±2 (7±2%)	3	18
All	All	4368/4452 (98%)	3084 (71%)	984 (23%)	300 (7%)	3	18

All 45 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	83	CYS	32
1	A	64	GLY	23
1	A	36	SER	14
1	A	52	VAL	14
1	A	96	GLY	13
1	A	67	TYR	13

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Mol	Chain	Res	Type	Models (Total)
1	A	71	SER	12
1	A	29	ASN	11
1	A	73	GLY	11
1	A	74	ALA	9
1	A	82	ASN	9
1	A	70	GLY	8
1	A	92	THR	8
1	A	30	ASP	8
1	A	3	ALA	7
1	A	43	ASN	7
1	A	33	ALA	7
1	A	31	ASP	6
1	A	35	SER	6
1	A	72	PRO	6
1	A	63	SER	6
1	A	53	ASP	6
1	A	44	ASN	5
1	A	32	THR	4
1	A	69	GLY	4
1	A	45	TYR	4
1	A	51	PRO	4
1	A	61	ILE	4
1	A	38	TYR	4
1	A	46	GLU	3
1	A	65	GLY	3
1	A	103	SER	3
1	A	93	GLY	3
1	A	49	ASP	3
1	A	94	ALA	3
1	A	47	GLY	3
1	A	34	GLY	2
1	A	54	GLY	2
1	A	48	PHE	2
1	A	95	SER	2
1	A	81	THR	2
1	A	41	THR	1
1	A	39	PRO	1
1	A	28	GLN	1
1	A	66	VAL	1

6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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	79/79 (100%)	70±2 (89±3%)	9±2 (11±3%)	12	55
All	All	3318/3318 (100%)	2948 (89%)	370 (11%)	12	55

All 56 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	40	HIS	25
1	A	48	PHE	24
1	A	5	THR	23
1	A	56	TYR	21
1	A	83	CYS	19
1	A	57	GLN	14
1	A	67	TYR	13
1	A	45	TYR	11
1	A	85	TYR	11
1	A	76	ARG	10
1	A	15	GLN	10
1	A	62	LYS	10
1	A	75	ASP	9
1	A	9	THR	9
1	A	38	TYR	9
1	A	27	TYR	8
1	A	24	CYS	8
1	A	61	ILE	8
1	A	11	TYR	8
1	A	79	ILE	7
1	A	52	VAL	7
1	A	26	TYR	6
1	A	17	ARG	6
1	A	42	TYR	6
1	A	28	GLN	5
1	A	102	CYS	5
1	A	4	THR	5
1	A	58	GLU	4
1	A	32	THR	4

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Mol	Chain	Res	Type	Models (Total)
1	A	31	ASP	4
1	A	29	ASN	4
1	A	99	PHE	4
1	A	91	HIS	4
1	A	6	CYS	4
1	A	41	THR	4
1	A	37	THR	4
1	A	81	THR	4
1	A	44	ASN	3
1	A	59	PHE	3
1	A	10	ASN	3
1	A	43	ASN	3
1	A	89	ILE	2
1	A	106	ASN	2
1	A	90	THR	2
1	A	92	THR	2
1	A	16	VAL	2
1	A	82	ASN	2
1	A	21	ASN	1
1	A	46	GLU	1
1	A	103	SER	1
1	A	71	SER	1
1	A	50	PHE	1
1	A	60	PRO	1
1	A	49	ASP	1
1	A	25	GLN	1
1	A	98	ASN	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds 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 is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is

considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
1	PCA	A	1	1	7,8,9	1.75±0.02	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of 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 angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
1	PCA	A	1	1	9,10,12	1.08±0.25	0±0 (0±1%)

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
1	PCA	A	1	1	-	0±0,0,11,13	0±0,1,1,1

There are no bond-length outliers.

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	1	PCA	CB-CA-C	7.27	123.59	112.80	5	1

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided