



Full wwPDB NMR Structure Validation Report ⓘ

May 28, 2020 – 11:55 pm BST

PDB ID : 2MJH
Title : Solution structure of the GLD-1 RNA-binding domain in complex with RNA
Authors : Daubner, G.M.; Allain, F.H.-T.
Deposited on : 2014-01-09

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

<https://www.wwpdb.org/validation/2017/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
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : 2.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

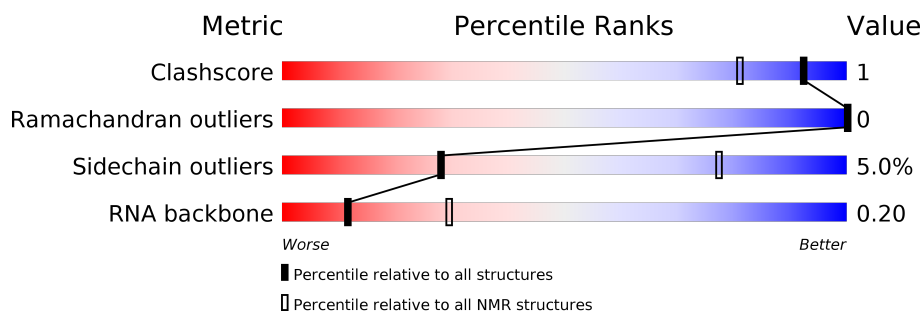
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR



The overall completeness of chemical shifts assignment is 66%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428
RNA backbone	4643	676

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	142	
2	B	10	

2 Ensemble composition and analysis

This entry contains 20 models. Model 13 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:201-A:246, A:274-A:305, A:317-A:327 (89)	0.20	13

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 4 clusters. No single-model clusters were found.

Cluster number	Models
1	4, 6, 9, 12, 16, 17, 18, 19
2	7, 10, 11, 14, 15
3	3, 5, 13, 20
4	1, 2, 8

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 2581 atoms, of which 1255 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Female germline-specific tumor suppressor gld-1.

Mol	Chain	Residues	Atoms						Trace
1	A	142	Total	C	H	N	O	S	0
			2270	702	1147	201	212	8	

- Molecule 2 is a RNA chain called 5'-CUACUCAUAU-3'.

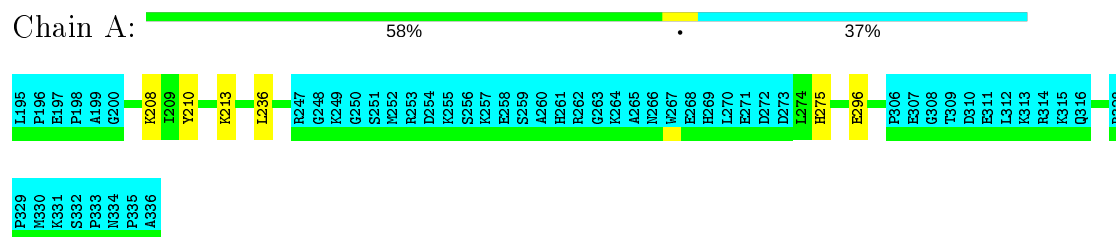
Mol	Chain	Residues	Atoms						Trace
2	B	10	Total	C	H	N	O	P	0
			311	93	108	32	69	9	

4 Residue-property plots [i](#)

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: Female germline-specific tumor suppressor gld-1



- Molecule 2: 5'-CUACUCAUAU-3'

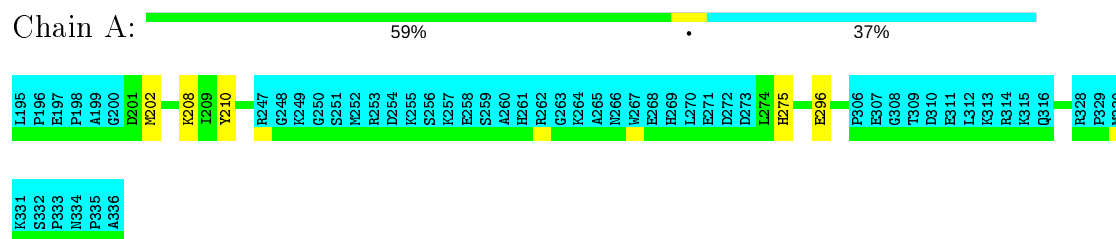


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Female germline-specific tumor suppressor gld-1

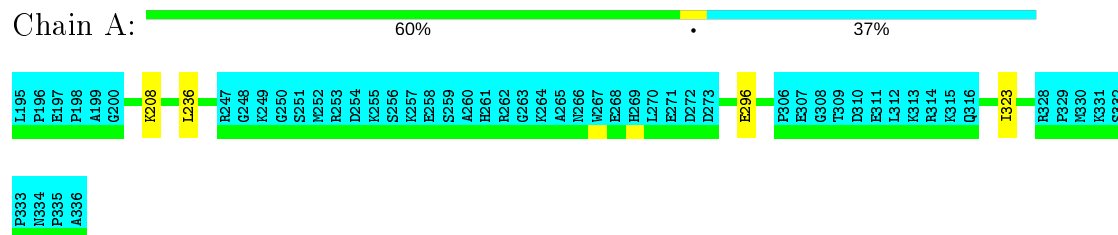


- Molecule 2: 5'-CUACUCAUAU-3'



4.2.2 Score per residue for model 2

- Molecule 1: Female germline-specific tumor suppressor gld-1

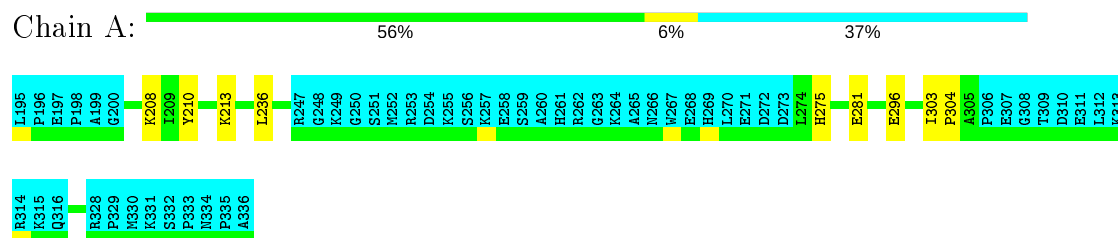


- Molecule 2: 5'-CUACUCAUAU-3'

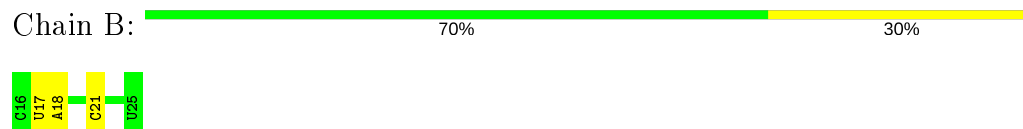


4.2.3 Score per residue for model 3

- Molecule 1: Female germline-specific tumor suppressor gld-1

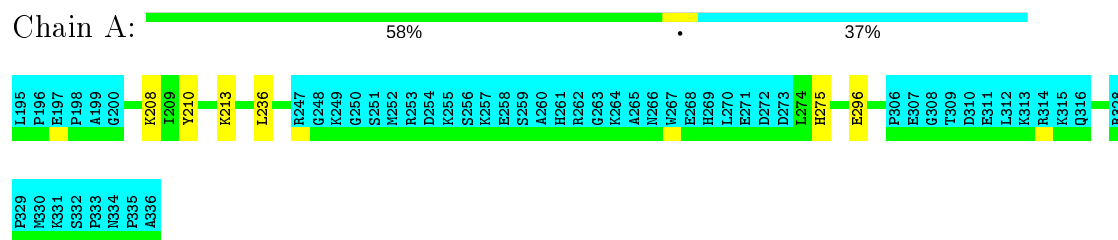


- Molecule 2: 5'-CUACUCAUAU-3'

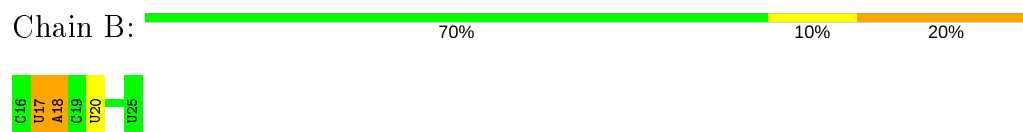


4.2.4 Score per residue for model 4

- Molecule 1: Female germline-specific tumor suppressor gld-1

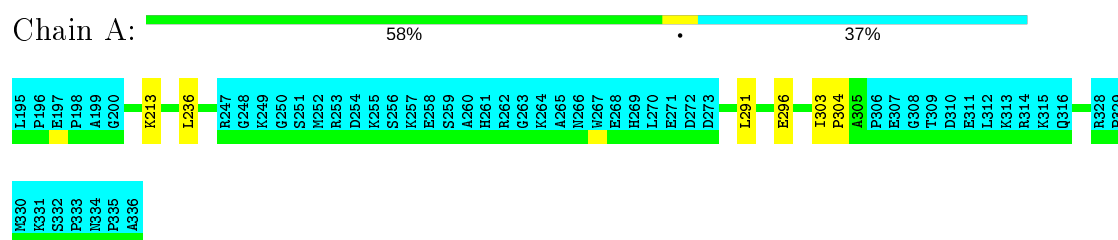


- Molecule 2: 5'-CUACUCAUUAU-3'



4.2.5 Score per residue for model 5

- Molecule 1: Female germline-specific tumor suppressor gld-1

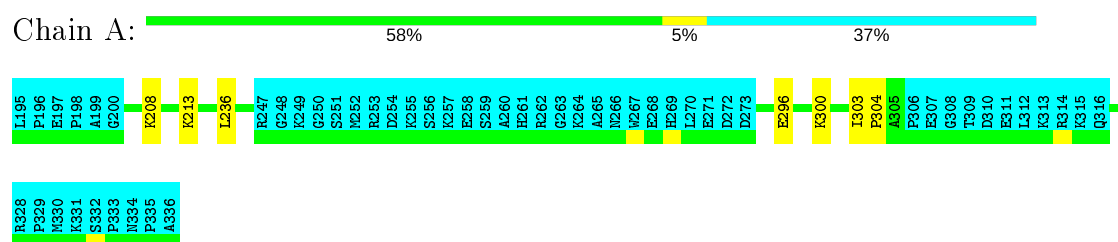


- Molecule 2: 5'-CUACUCAUUAU-3'



4.2.6 Score per residue for model 6

- Molecule 1: Female germline-specific tumor suppressor gld-1



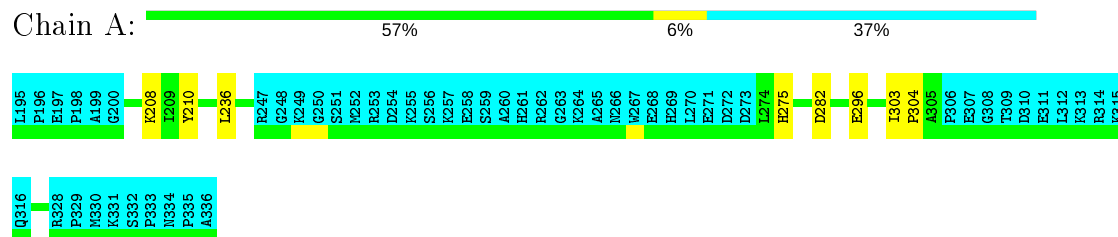
- Molecule 2: 5'-CUACUCAUUAU-3'



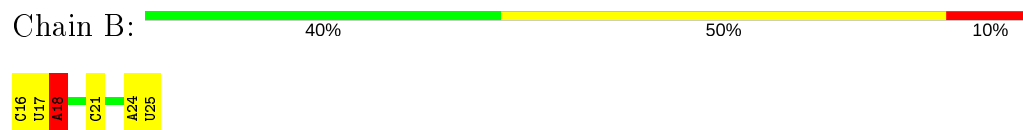


4.2.7 Score per residue for model 7

- Molecule 1: Female germline-specific tumor suppressor gld-1

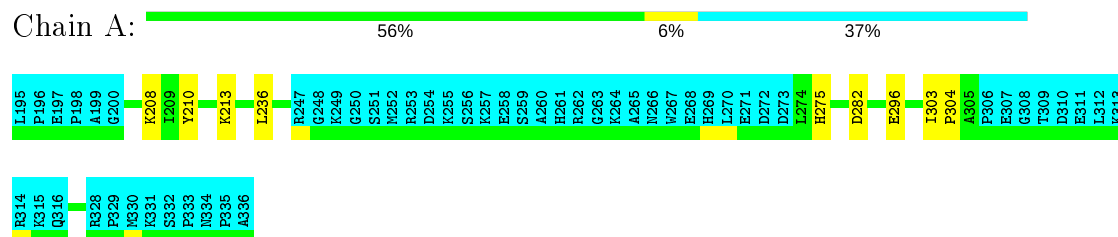


- Molecule 2: 5'-CUACUCAU-3'

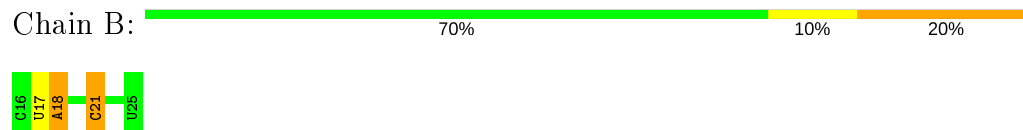


4.2.8 Score per residue for model 8

- Molecule 1: Female germline-specific tumor suppressor gld-1



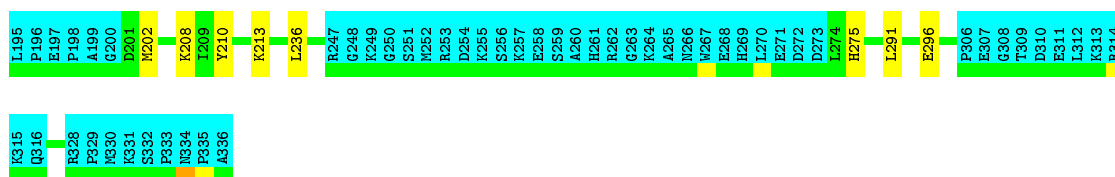
- Molecule 2: 5'-CUACUCAU-3'



4.2.9 Score per residue for model 9

- Molecule 1: Female germline-specific tumor suppressor gld-1



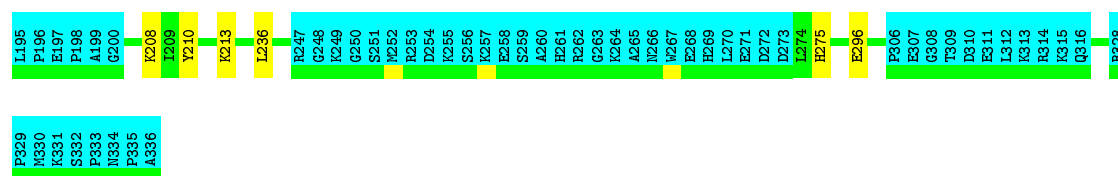


- Molecule 2: 5'-CUACUCAUUAU-3'

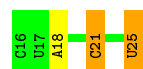


4.2.10 Score per residue for model 10

- Molecule 1: Female germline-specific tumor suppressor gld-1

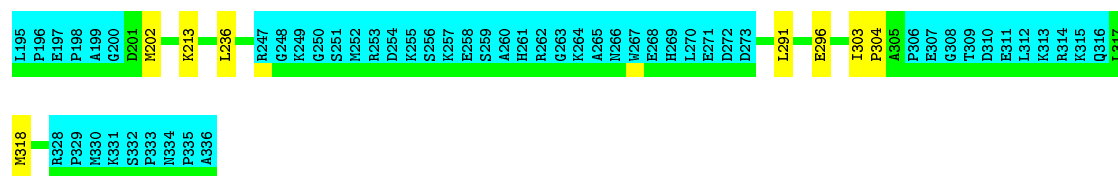


- Molecule 2: 5'-CUACUCAUUAU-3'



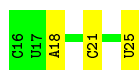
4.2.11 Score per residue for model 11

- Molecule 1: Female germline-specific tumor suppressor gld-1



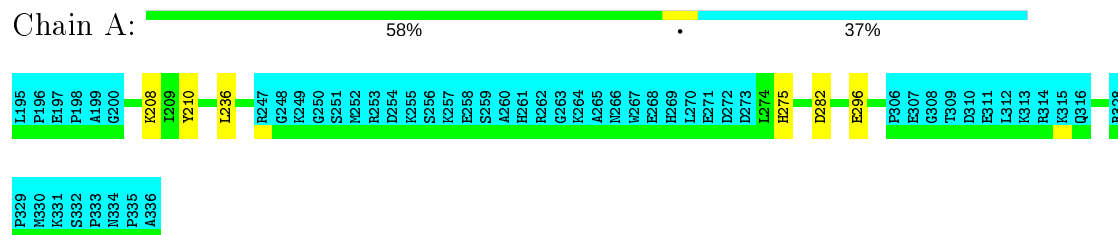
- Molecule 2: 5'-CUACUCAUUAU-3'





4.2.12 Score per residue for model 12

- Molecule 1: Female germline-specific tumor suppressor gld-1

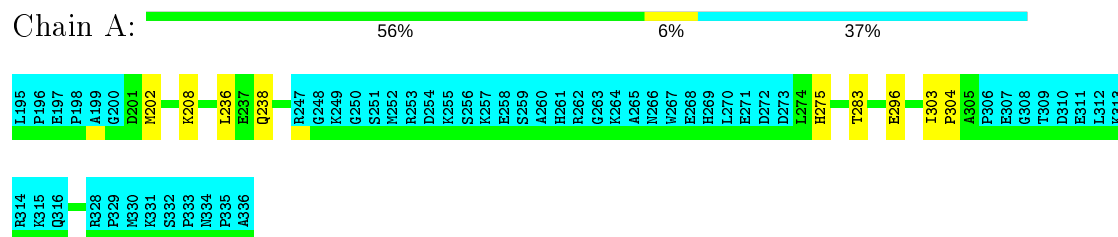


- Molecule 2: 5'-CUACUCAUAU-3'



4.2.13 Score per residue for model 13 (medoid)

- Molecule 1: Female germline-specific tumor suppressor gld-1



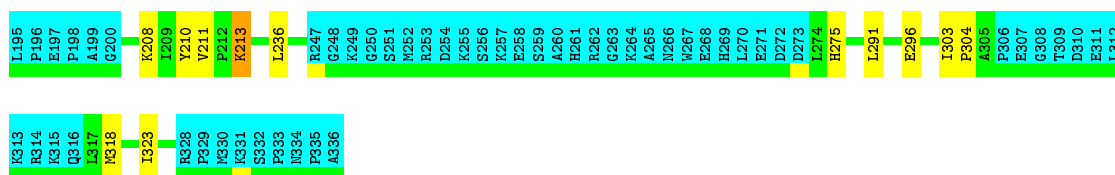
- Molecule 2: 5'-CUACUCAUAU-3'



4.2.14 Score per residue for model 14

- Molecule 1: Female germline-specific tumor suppressor gld-1





- Molecule 2: 5'-CUACUCAUAU-3'

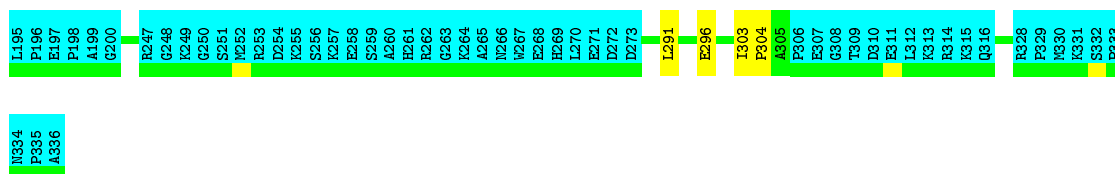
Chain B: 80% 20%



4.2.15 Score per residue for model 15

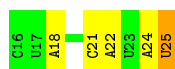
- Molecule 1: Female germline-specific tumor suppressor gld-1

Chain A: 60% 37%



- Molecule 2: 5'-CUACUCAUAU-3'

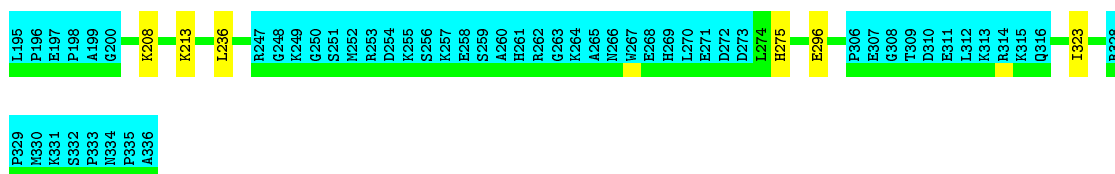
Chain B: 50% 40% 10%



4.2.16 Score per residue for model 16

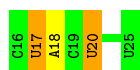
- Molecule 1: Female germline-specific tumor suppressor gld-1

Chain A: 58% 37%



- Molecule 2: 5'-CUACUCAUAU-3'

Chain B: 70% 10% 20%



4.2.17 Score per residue for model 17

- Molecule 1: Female germline-specific tumor suppressor gld-1

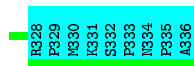
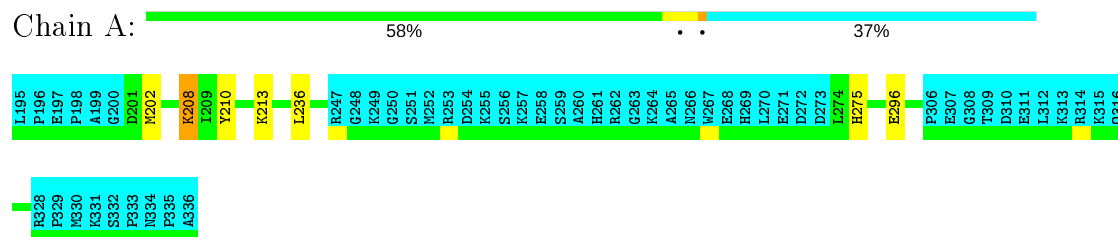


- Molecule 2: 5'-CUACUCAUAU-3'

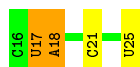


4.2.18 Score per residue for model 18

- Molecule 1: Female germline-specific tumor suppressor gld-1



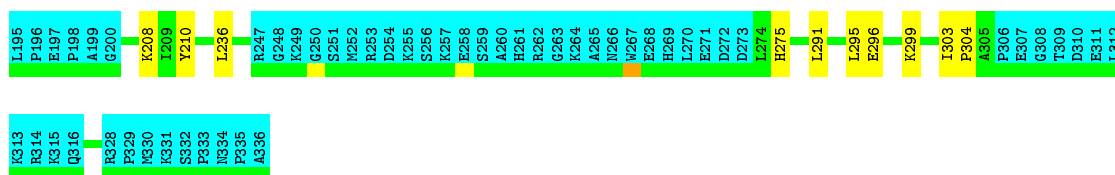
- Molecule 2: 5'-CUACUCAUAU-3'



4.2.19 Score per residue for model 19

- Molecule 1: Female germline-specific tumor suppressor gld-1





- Molecule 2: 5'-CUACUCAUUAU-3'

Chain B: 40% 60%



4.2.20 Score per residue for model 20

- Molecule 1: Female germline-specific tumor suppressor gld-1

Chain A: 60% 37%



- Molecule 2: 5'-CUACUCAUUAU-3'

Chain B: 90% 10%



5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 250 calculated structures, 20 were deposited, based on the following criterion: *Lowest energy and NOE violations*.

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

Software name	Classification	Version
AMBER	refinement	9
CYANA	structure solution	3.0

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 6 of this report.

Chemical shift file(s)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	1386
Number of shifts mapped to atoms	1386
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	66%

No validations of the models with respect to experimental NMR restraints is performed at this time.

COVALENT-GEOMETRY INFOmissingINFO

5.1 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 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	706	737	737	2±1
2	B	203	108	108	0±0
All	All	18180	16900	16900	48

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:208:LYS:HE2	1:A:210:TYR:CE2	0.62	2.30	9	5
1:A:208:LYS:HE3	1:A:275:HIS:CD2	0.55	2.36	10	10
1:A:208:LYS:HE2	1:A:210:TYR:CE1	0.50	2.42	8	6
1:A:208:LYS:HE2	1:A:210:TYR:CZ	0.47	2.45	9	2
1:A:208:LYS:HE3	1:A:275:HIS:CG	0.46	2.45	9	3
1:A:208:LYS:HE2	1:A:275:HIS:CD2	0.46	2.46	13	2
2:B:25:U:H5''	2:B:25:U:C6	0.44	2.47	10	1
2:B:18:A:H5'	2:B:19:C:C5	0.44	2.48	13	1
1:A:211:VAL:O	1:A:213:LYS:HE3	0.43	2.14	14	1
1:A:303:ILE:N	1:A:304:PRO:CD	0.43	2.80	7	10
2:B:18:A:H2'	2:B:18:A:N3	0.42	2.30	7	2
2:B:18:A:N3	2:B:18:A:H2'	0.41	2.30	18	3
2:B:24:A:H3'	2:B:25:U:C5'	0.41	2.46	15	1
1:A:295:LEU:C	1:A:295:LEU:HD12	0.41	2.37	19	1

5.2 Torsion angles ⓘ

5.2.1 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 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	89/142 (63%)	84±1 (94±1%)	5±1 (6±1%)	0±0 (0±0%)	100	100
All	All	1780/2840 (63%)	1672 (94%)	108 (6%)	0 (0%)	100	100

There are no Ramachandran outliers.

5.2.2 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	79/123 (64%)	75±1 (95±1%)	4±1 (5±1%)	28	77
All	All	1580/2460 (64%)	1501 (95%)	79 (5%)	28	77

All 14 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	296	GLU	20
1	A	236	LEU	18
1	A	213	LYS	11
1	A	202	MET	6
1	A	291	LEU	6
1	A	208	LYS	5
1	A	323	ILE	3
1	A	282	ASP	3
1	A	318	MET	2
1	A	281	GLU	1
1	A	299	LYS	1
1	A	300	LYS	1
1	A	238	GLN	1
1	A	275	HIS	1

5.2.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
2	B	10/10 (100%)	3±1 (28±9%)	1±1 (14±10%)	0.20±0.06
All	All	184/200 (92%)	55 (30%)	27 (15%)	0.20

The overall RNA backbone suiteness is 0.20.

All unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	B	18	A	20
2	B	17	U	12
2	B	25	U	8
2	B	21	C	4
2	B	22	A	4
2	B	20	U	4
2	B	23	U	2
2	B	19	C	1

All unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	B	18	A	19
2	B	16	C	4

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Mol	Chain	Res	Type	Models (Total)
2	B	24	A	2
2	B	22	A	1
2	B	19	C	1

5.3 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.4 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.5 Ligand geometry [i](#)

There are no ligands in this entry.

5.6 Other polymers [i](#)

There are no such molecules in this entry.

5.7 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 66% for the well-defined parts and 66% for the entire structure.

6.1 Chemical shift list 1

File name: input_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

6.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1386
Number of shifts mapped to atoms	1386
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	3

6.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	121	2.33 ± 0.17	Should be applied
$^{13}\text{C}_\beta$	108	2.74 ± 0.06	Should be applied
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	127	-0.35 ± 0.19	None needed (< 0.5 ppm)

6.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 66%, i.e. 866 atoms were assigned a chemical shift out of a possible 1303. 13 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	337/437 (77%)	174/174 (100%)	78/178 (44%)	85/85 (100%)
Sidechain	426/629 (68%)	246/366 (67%)	169/238 (71%)	11/25 (44%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	48/55 (87%)	24/29 (83%)	24/24 (100%)	0/2 (0%)
Overall	866/1303 (66%)	499/671 (74%)	271/510 (53%)	96/122 (79%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 66%, i.e. 1301 atoms were assigned a chemical shift out of a possible 1976. 14 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	514/690 (74%)	266/274 (97%)	121/284 (43%)	127/132 (96%)
Sidechain	665/1022 (65%)	412/604 (68%)	237/368 (64%)	16/50 (32%)
Aromatic	67/82 (82%)	34/43 (79%)	32/33 (97%)	1/6 (17%)
Overall	1301/1976 (66%)	767/1023 (75%)	390/755 (52%)	144/198 (73%)

6.1.4 Statistically unusual chemical shifts ⓘ

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	304	PRO	HG2	0.22	3.48 – 0.38	-5.5
1	A	212	PRO	CB	25.42	37.79 – 25.89	-5.4
2	B	23	U	H3'	3.67	5.29 – 3.69	-5.1

6.1.5 Random Coil Index (RCI) plots ⓘ

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:

