



Full wwPDB NMR Structure Validation Report ⓘ

Feb 13, 2017 – 02:27 am GMT

PDB ID : 2YUD
Title : Solution structure of the YTH domain in YTH domain-containing protein 1 (Putative splicing factor YT521)
Authors : He, F.; Muto, Y.; Inoue, M.; Kigawa, T.; Shirouzu, M.; Tarada, T.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2007-04-06

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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
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : trunk28760
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

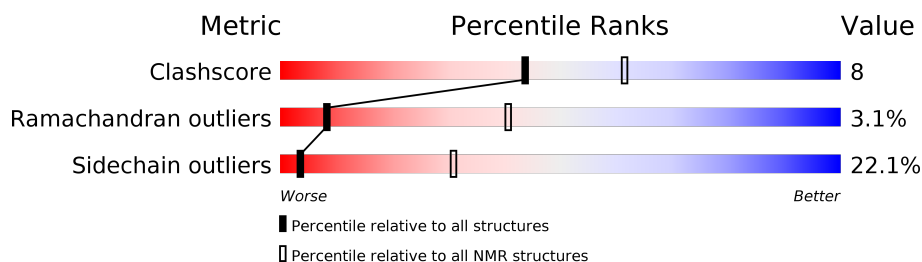
1 Overall quality at a glance

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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	180	

2 Ensemble composition and analysis

This entry contains 20 models. Model 1 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:16-A:75, A:79-A:91, A:96-A:178 (156)	0.19	1

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 2 clusters and 7 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2867 atoms, of which 1443 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called YTH domain-containing protein 1.

Mol	Chain	Residues	Atoms						Trace
1	A	180	Total	C	H	N	O	S	0
			2867	906	1443	261	251	6	

There are 7 discrepancies between the modelled and reference sequences:

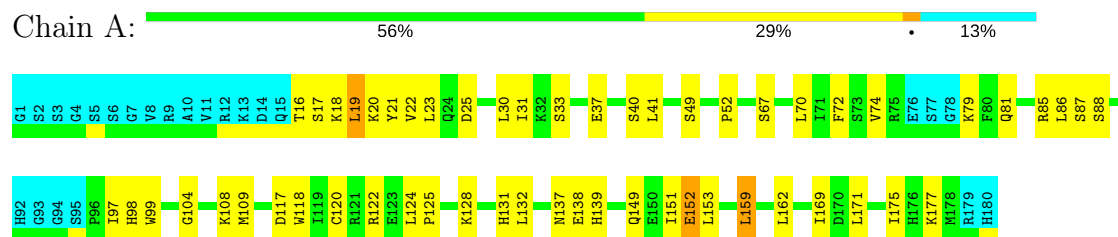
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	EXPRESSION TAG	UNP Q96MU7
A	2	SER	-	EXPRESSION TAG	UNP Q96MU7
A	3	SER	-	EXPRESSION TAG	UNP Q96MU7
A	4	GLY	-	EXPRESSION TAG	UNP Q96MU7
A	5	SER	-	EXPRESSION TAG	UNP Q96MU7
A	6	SER	-	EXPRESSION TAG	UNP Q96MU7
A	7	GLY	-	EXPRESSION TAG	UNP Q96MU7

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: YTH domain-containing protein 1

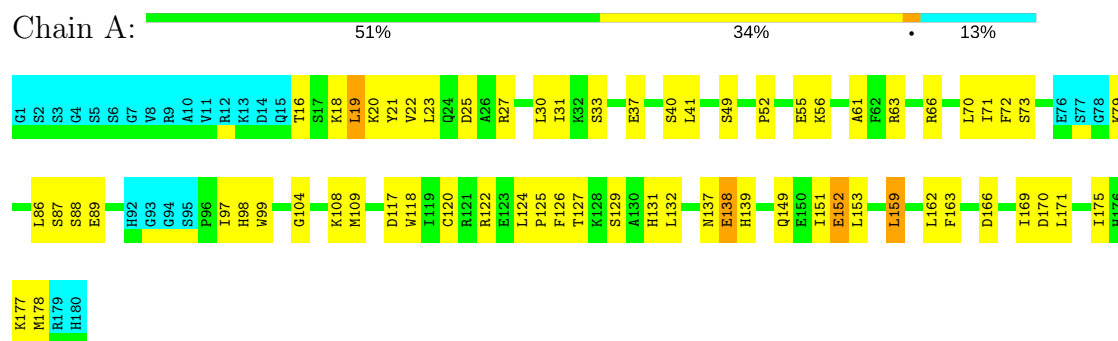


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

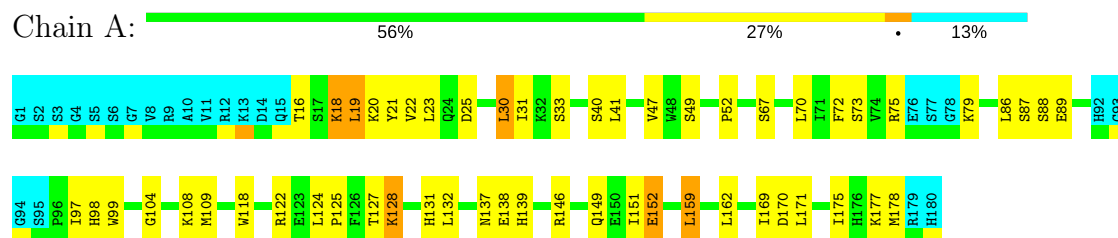
4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: YTH domain-containing protein 1



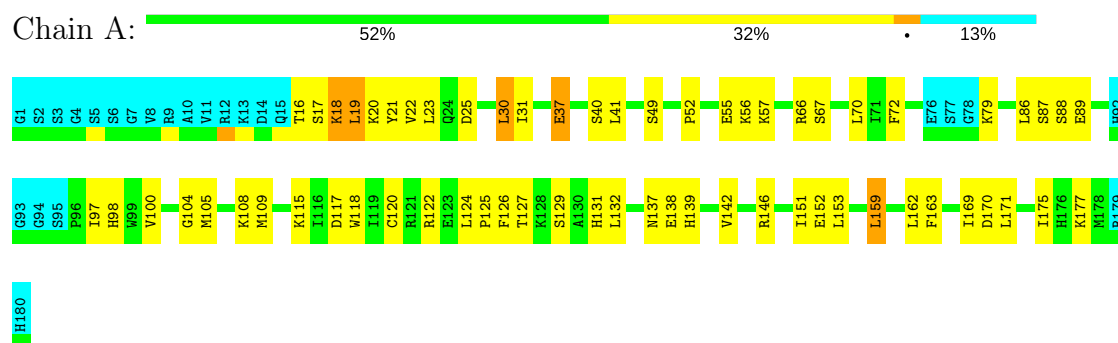
4.2.2 Score per residue for model 2

- Molecule 1: YTH domain-containing protein 1



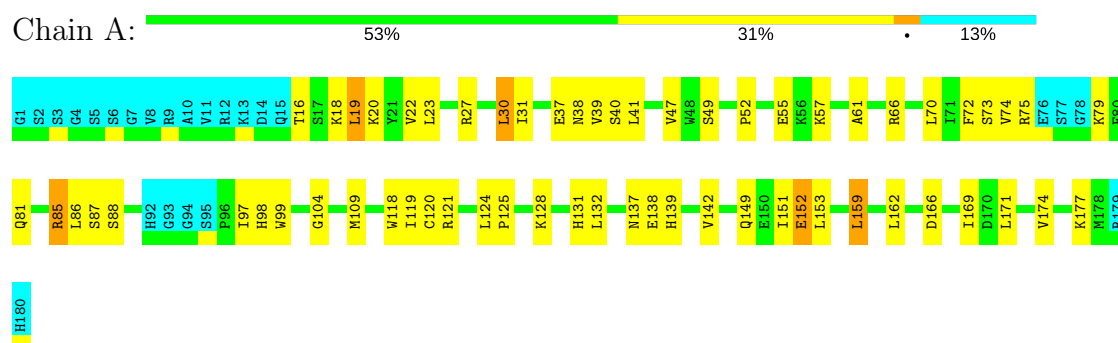
4.2.3 Score per residue for model 3

- Molecule 1: YTH domain-containing protein 1



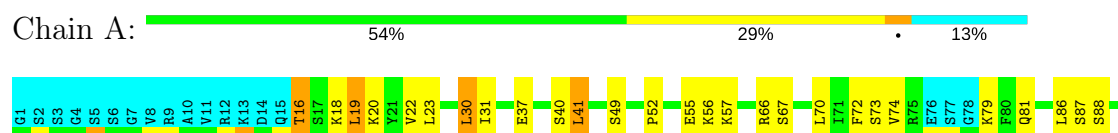
4.2.4 Score per residue for model 4

- Molecule 1: YTH domain-containing protein 1



4.2.5 Score per residue for model 5

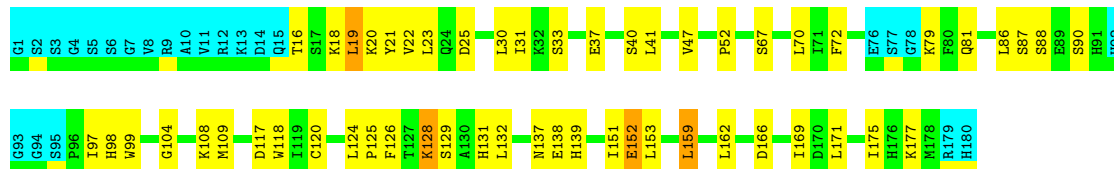
- Molecule 1: YTH domain-containing protein 1





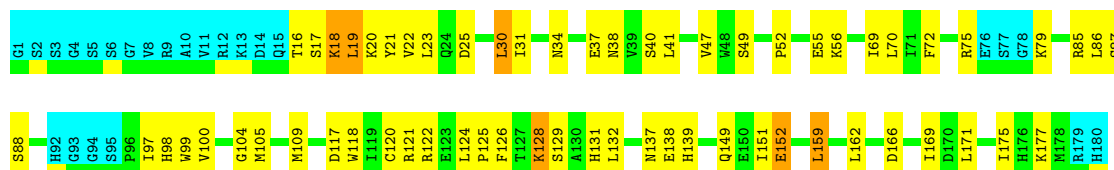
4.2.6 Score per residue for model 6

- Molecule 1: YTH domain-containing protein 1



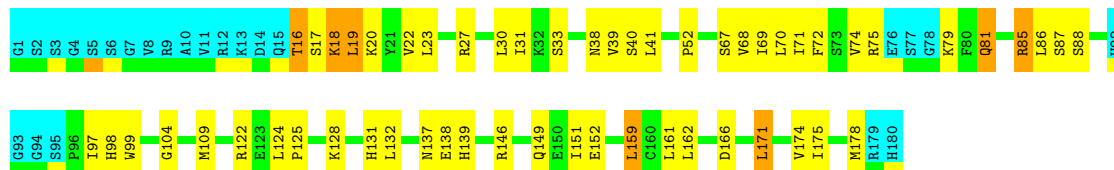
4.2.7 Score per residue for model 7

- Molecule 1: YTH domain-containing protein 1



4.2.8 Score per residue for model 8

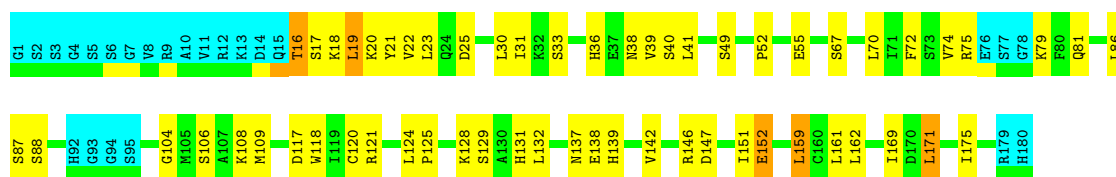
- Molecule 1: YTH domain-containing protein 1



4.2.9 Score per residue for model 9

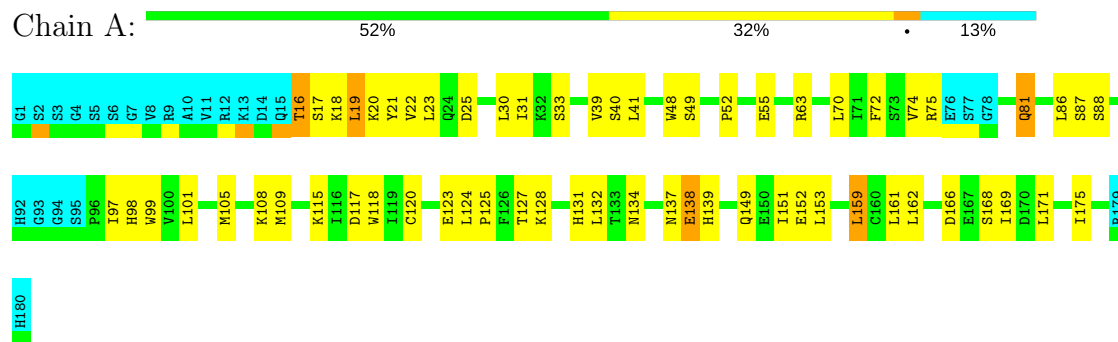
- Molecule 1: YTH domain-containing protein 1





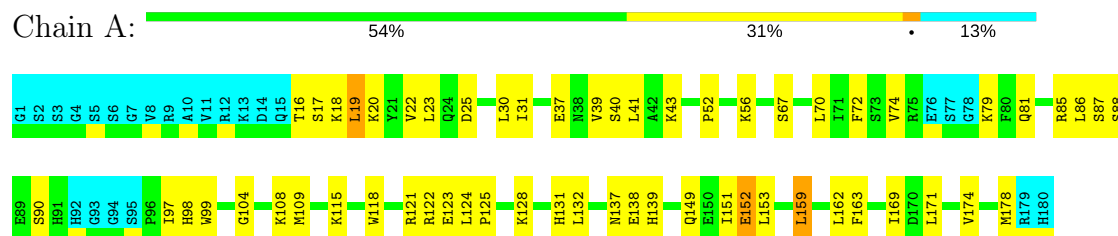
4.2.10 Score per residue for model 10

- Molecule 1: YTH domain-containing protein 1



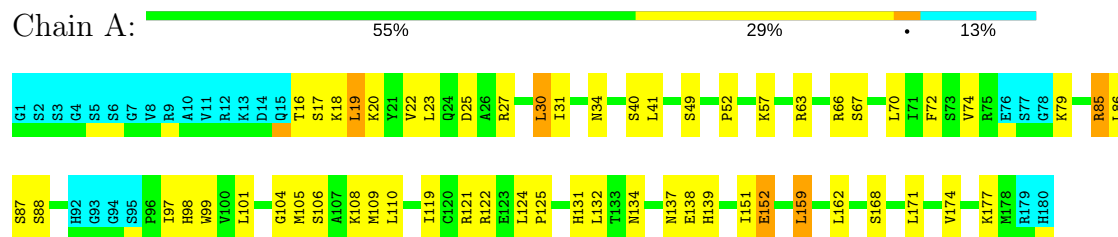
4.2.11 Score per residue for model 11

- Molecule 1: YTH domain-containing protein 1



4.2.12 Score per residue for model 12

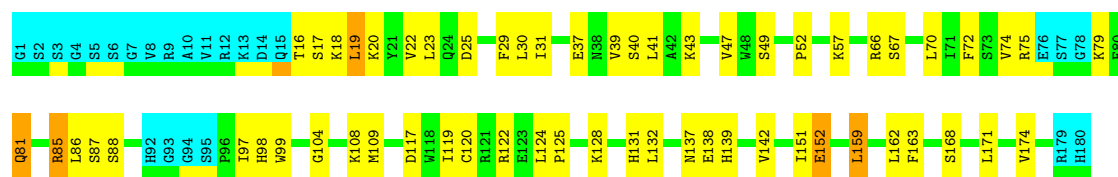
- Molecule 1: YTH domain-containing protein 1



4.2.13 Score per residue for model 13

- Molecule 1: YTH domain-containing protein 1

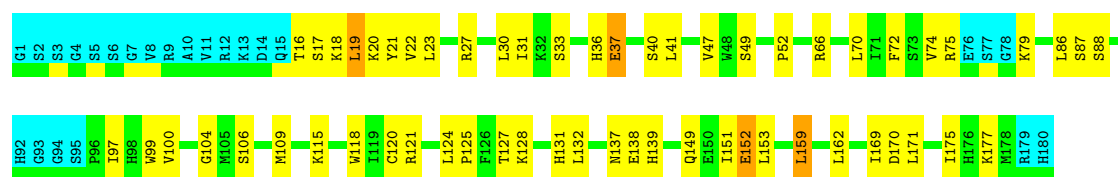
Chain A: 54% 30% • 13%



4.2.14 Score per residue for model 14

- Molecule 1: YTH domain-containing protein 1

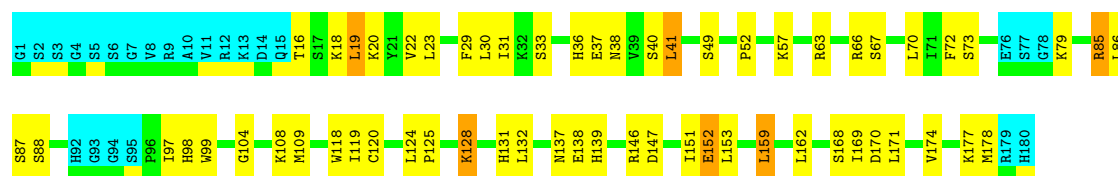
Chain A:  54% 30% 2% 13%



4.2.15 Score per residue for model 15

- Molecule 1: YTH domain-containing protein 1

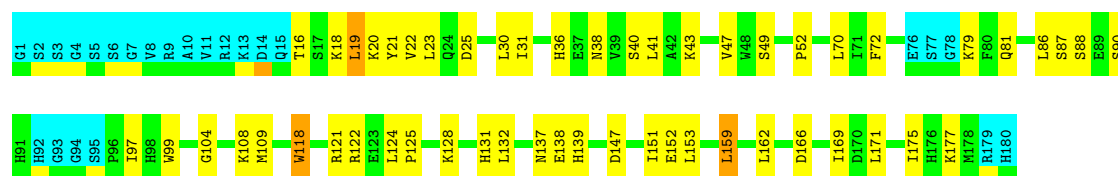
Chain A:  53% 30% • 13%



4.2.16 Score per residue for model 16

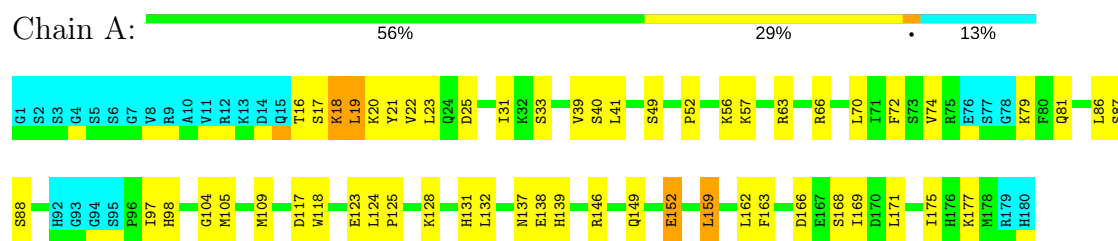
- Molecule 1: YTH domain-containing protein 1

Chain A:  57% 28% • 13%



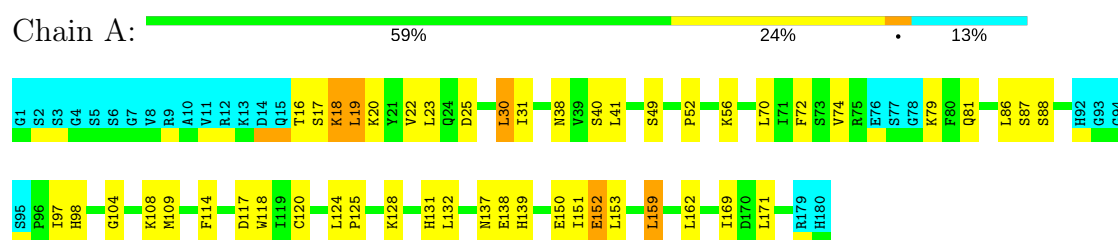
4.2.17 Score per residue for model 17

- Molecule 1: YTH domain-containing protein 1



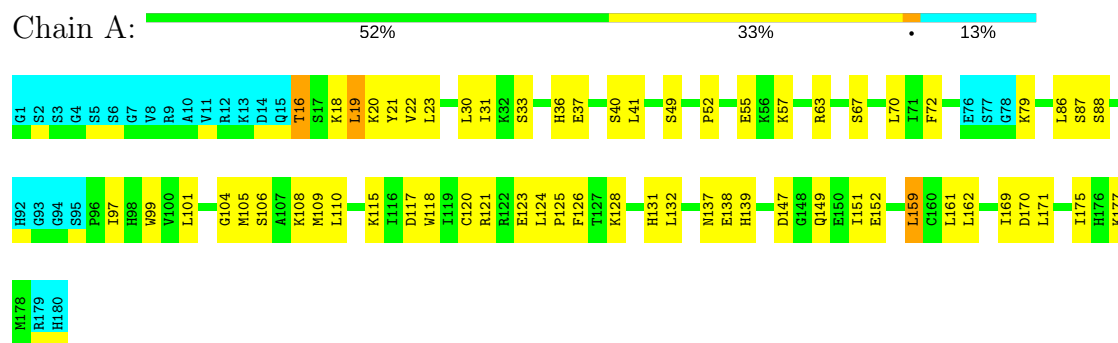
4.2.18 Score per residue for model 18

- Molecule 1: YTH domain-containing protein 1



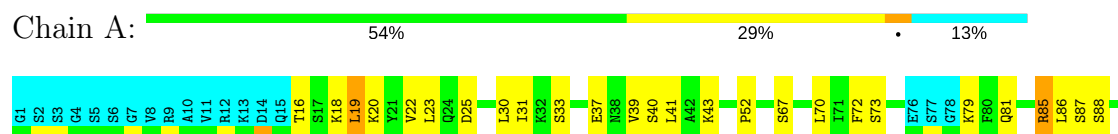
4.2.19 Score per residue for model 19

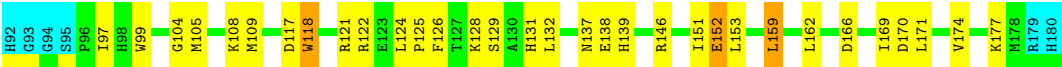
- Molecule 1: YTH domain-containing protein 1



4.2.20 Score per residue for model 20

- Molecule 1: YTH domain-containing protein 1





5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations, target function*.

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

Software name	Classification	Version
CYANA	structure solution	2.1
CYANA	refinement	2.1

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](#)

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

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	1257	1288	1288	20±3
All	All	25140	25760	25760	407

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 8.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:30:LEU:HD13	1:A:151:ILE:HD11	0.83	1.49	16	3
1:A:70:LEU:HD11	1:A:86:LEU:HD13	0.78	1.55	15	20
1:A:52:PRO:HD3	1:A:109:MET:O	0.68	1.89	15	20
1:A:18:LYS:O	1:A:22:VAL:HG13	0.64	1.93	19	20
1:A:37:GLU:OE1	1:A:100:VAL:HG11	0.63	1.94	14	1
1:A:70:LEU:HD11	1:A:86:LEU:CD1	0.63	2.24	9	15
1:A:39:VAL:HG11	1:A:81:GLN:HG2	0.63	1.69	20	1
1:A:132:LEU:HD12	1:A:159:LEU:HD23	0.62	1.70	10	20
1:A:31:ILE:HD11	1:A:72:PHE:CG	0.62	2.30	2	17
1:A:19:LEU:O	1:A:22:VAL:HG22	0.62	1.95	13	20
1:A:118:TRP:O	1:A:169:ILE:HD13	0.61	1.96	16	17
1:A:31:ILE:HD11	1:A:72:PHE:CD2	0.60	2.32	19	19
1:A:30:LEU:HB2	1:A:151:ILE:HD11	0.60	1.74	8	14
1:A:39:VAL:HG11	1:A:81:GLN:HG3	0.59	1.73	11	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:30:LEU:CG	1:A:151:ILE:HD11	0.58	2.29	12	5
1:A:36:HIS:CE1	1:A:74:VAL:HG11	0.56	2.35	14	1
1:A:30:LEU:HG	1:A:151:ILE:HD11	0.56	1.77	12	2
1:A:39:VAL:HG11	1:A:81:GLN:CG	0.56	2.30	17	6
1:A:124:LEU:HD22	1:A:125:PRO:HD2	0.55	1.78	8	20
1:A:21:TYR:CE1	1:A:175:ILE:HG23	0.54	2.37	7	11
1:A:85:ARG:HG2	1:A:119:ILE:HD11	0.54	1.79	4	4
1:A:37:GLU:HB3	1:A:100:VAL:HG11	0.54	1.80	7	3
1:A:30:LEU:HD13	1:A:151:ILE:CD1	0.54	2.29	16	3
1:A:47:VAL:HG23	1:A:99:TRP:CH2	0.54	2.38	16	7
1:A:41:LEU:CD2	1:A:97:ILE:HD13	0.53	2.32	11	10
1:A:159:LEU:HA	1:A:162:LEU:HD12	0.53	1.81	11	20
1:A:41:LEU:HD21	1:A:97:ILE:CD1	0.52	2.33	14	7
1:A:27:ARG:HD3	1:A:61:ALA:HB1	0.52	1.82	4	2
1:A:132:LEU:HD12	1:A:159:LEU:CD2	0.52	2.35	3	20
1:A:68:VAL:O	1:A:69:ILE:HD13	0.52	2.05	8	1
1:A:29:PHE:HB2	1:A:70:LEU:HD23	0.51	1.83	15	2
1:A:69:ILE:HD13	1:A:85:ARG:HG3	0.51	1.83	7	1
1:A:118:TRP:O	1:A:169:ILE:HG21	0.50	2.07	14	1
1:A:97:ILE:HD11	1:A:99:TRP:CD2	0.49	2.43	19	11
1:A:105:MET:HE1	1:A:110:LEU:HD21	0.49	1.85	19	2
1:A:101:LEU:HD13	1:A:105:MET:HG2	0.49	1.84	10	1
1:A:85:ARG:CZ	1:A:174:VAL:HG13	0.48	2.39	11	7
1:A:16:THR:CG2	1:A:161:LEU:HD22	0.48	2.38	10	4
1:A:39:VAL:HG11	1:A:81:GLN:HB3	0.48	1.86	9	2
1:A:41:LEU:HD21	1:A:97:ILE:HD13	0.48	1.85	17	2
1:A:101:LEU:HD13	1:A:105:MET:CE	0.48	2.38	19	2
1:A:105:MET:CE	1:A:110:LEU:HD21	0.47	2.40	12	2
1:A:30:LEU:CB	1:A:151:ILE:HD11	0.47	2.38	7	4
1:A:71:ILE:HD12	1:A:151:ILE:HD12	0.47	1.86	8	1
1:A:16:THR:HG22	1:A:161:LEU:HD22	0.47	1.85	8	3
1:A:97:ILE:HD11	1:A:99:TRP:CE3	0.46	2.45	11	10
1:A:30:LEU:CD1	1:A:151:ILE:HD11	0.46	2.34	16	1
1:A:70:LEU:CD1	1:A:86:LEU:HD13	0.46	2.36	12	2
1:A:37:GLU:CB	1:A:100:VAL:HG11	0.46	2.39	7	1
1:A:124:LEU:HD23	1:A:163:PHE:HA	0.45	1.87	13	5
1:A:142:VAL:HG11	1:A:159:LEU:CD2	0.45	2.42	13	4
1:A:124:LEU:HD11	1:A:128:LYS:HB2	0.45	1.88	14	14
1:A:101:LEU:HD13	1:A:105:MET:HE1	0.44	1.88	19	2
1:A:134:ASN:HD21	1:A:151:ILE:HG23	0.43	1.73	12	1
1:A:86:LEU:HD11	1:A:114:PHE:CD1	0.42	2.50	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:19:LEU:HG	1:A:171:LEU:HD11	0.42	1.92	20	1
1:A:142:VAL:HG11	1:A:159:LEU:HD21	0.41	1.91	9	1
1:A:31:ILE:HD13	1:A:48:TRP:NE1	0.41	2.31	10	1
1:A:31:ILE:HD11	1:A:72:PHE:CE2	0.41	2.51	10	1
1:A:18:LYS:HB3	1:A:175:ILE:HD11	0.41	1.93	8	1
1:A:166:ASP:OD2	1:A:169:ILE:HD12	0.40	2.17	10	1
1:A:30:LEU:HD12	1:A:71:ILE:HB	0.40	1.93	1	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	156/180 (87%)	131±3 (84±2%)	20±3 (13±2%)	5±1 (3±0%)	8	41
All	All	3120/3600 (87%)	2626 (84%)	397 (13%)	97 (3%)	8	41

All 7 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	138	GLU	20
1	A	131	HIS	20
1	A	137	ASN	20
1	A	104	GLY	19
1	A	152	GLU	14
1	A	89	GLU	2
1	A	118	TRP	2

6.3.2 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 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	139/156 (89%)	108±3 (78±2%)	31±3 (22±2%)	3	31
All	All	2780/3120 (89%)	2167 (78%)	613 (22%)	3	31

All 63 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	19	LEU	20
1	A	88	SER	20
1	A	139	HIS	20
1	A	159	LEU	20
1	A	40	SER	20
1	A	87	SER	20
1	A	16	THR	20
1	A	23	LEU	20
1	A	152	GLU	20
1	A	20	LYS	20
1	A	79	LYS	19
1	A	49	SER	16
1	A	171	LEU	16
1	A	98	HIS	15
1	A	108	LYS	15
1	A	177	LYS	14
1	A	25	ASP	14
1	A	153	LEU	12
1	A	120	CYS	12
1	A	67	SER	12
1	A	117	ASP	11
1	A	122	ARG	11
1	A	149	GLN	11
1	A	17	SER	11
1	A	33	SER	11
1	A	37	GLU	10
1	A	121	ARG	10
1	A	166	ASP	9
1	A	66	ARG	9
1	A	57	LYS	8
1	A	75	ARG	8
1	A	146	ARG	8
1	A	55	GLU	8
1	A	30	LEU	7
1	A	38	ASN	7
1	A	81	GLN	7

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Mol	Chain	Res	Type	Models (Total)
1	A	170	ASP	7
1	A	128	LYS	7
1	A	56	LYS	7
1	A	129	SER	6
1	A	127	THR	6
1	A	178	MET	6
1	A	63	ARG	6
1	A	18	LYS	6
1	A	73	SER	6
1	A	85	ARG	6
1	A	126	PHE	6
1	A	168	SER	6
1	A	115	LYS	5
1	A	41	LEU	5
1	A	147	ASP	4
1	A	36	HIS	4
1	A	105	MET	4
1	A	123	GLU	4
1	A	43	LYS	4
1	A	106	SER	4
1	A	27	ARG	3
1	A	90	SER	3
1	A	138	GLU	2
1	A	34	ASN	2
1	A	150	GLU	1
1	A	134	ASN	1
1	A	89	GLU	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

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