



Full wwPDB NMR Structure Validation Report ⓘ

Aug 2, 2016 – 10:10 PM EDT

PDB ID : 2N7D
Title : Solution structure of the UBL domain of human Ddi2
Authors : Siva, M.; Grantz Saskova, K.; Veverka, V.
Deposited on : 2015-09-08

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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 : unknown
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-20027939
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027939

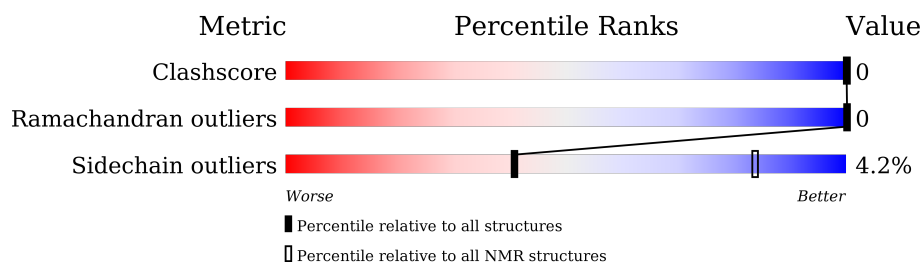
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 87%.

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	97	

2 Ensemble composition and analysis

This entry contains 40 models. Model 5 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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:100-A:176 (77)	0.28	5

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 5 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1522 atoms, of which 738 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Protein DDI1 homolog 2.

Mol	Chain	Residues	Atoms						Trace
1	A	97	Total	C	H	N	O	S	0
			1522	485	738	152	143	4	

There are 21 discrepancies between the modelled and reference sequences:

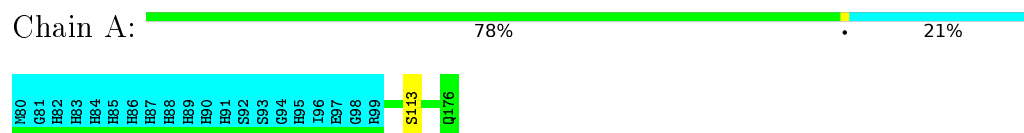
Chain	Residue	Modelled	Actual	Comment	Reference
A	80	MET	-	EXPRESSION TAG	UNP Q5TDH0
A	81	GLY	-	EXPRESSION TAG	UNP Q5TDH0
A	82	HIS	-	EXPRESSION TAG	UNP Q5TDH0
A	83	HIS	-	EXPRESSION TAG	UNP Q5TDH0
A	84	HIS	-	EXPRESSION TAG	UNP Q5TDH0
A	85	HIS	-	EXPRESSION TAG	UNP Q5TDH0
A	86	HIS	-	EXPRESSION TAG	UNP Q5TDH0
A	87	HIS	-	EXPRESSION TAG	UNP Q5TDH0
A	88	HIS	-	EXPRESSION TAG	UNP Q5TDH0
A	89	HIS	-	EXPRESSION TAG	UNP Q5TDH0
A	90	HIS	-	EXPRESSION TAG	UNP Q5TDH0
A	91	HIS	-	EXPRESSION TAG	UNP Q5TDH0
A	92	SER	-	EXPRESSION TAG	UNP Q5TDH0
A	93	SER	-	EXPRESSION TAG	UNP Q5TDH0
A	94	GLY	-	EXPRESSION TAG	UNP Q5TDH0
A	95	HIS	-	EXPRESSION TAG	UNP Q5TDH0
A	96	ILE	-	EXPRESSION TAG	UNP Q5TDH0
A	97	GLU	-	EXPRESSION TAG	UNP Q5TDH0
A	98	GLY	-	EXPRESSION TAG	UNP Q5TDH0
A	99	ARG	-	EXPRESSION TAG	UNP Q5TDH0
A	100	HIS	-	EXPRESSION TAG	UNP Q5TDH0

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: Protein DDI1 homolog 2

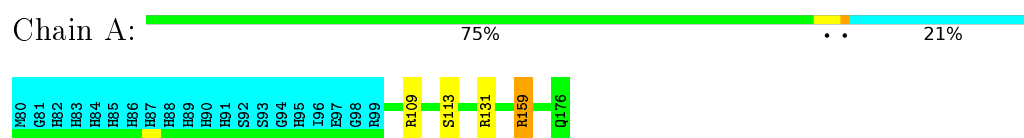


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

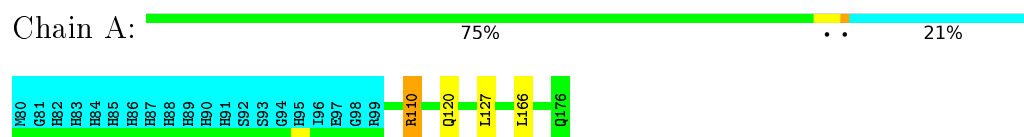
4.2.1 Score per residue for model 1

- Molecule 1: Protein DDI1 homolog 2



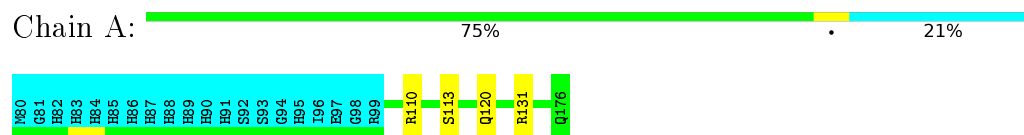
4.2.2 Score per residue for model 2

- Molecule 1: Protein DDI1 homolog 2



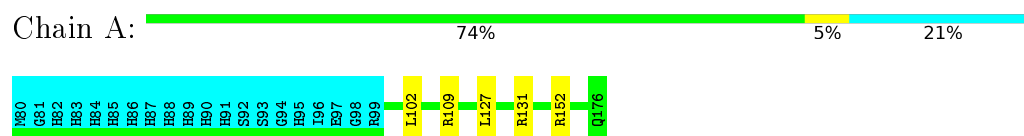
4.2.3 Score per residue for model 3

- Molecule 1: Protein DDI1 homolog 2



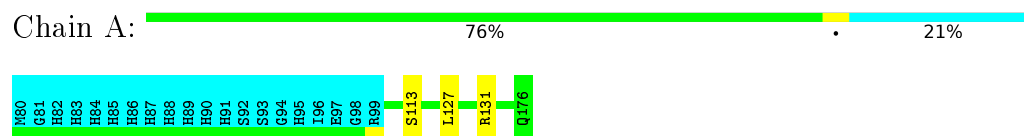
4.2.4 Score per residue for model 4

- Molecule 1: Protein DDI1 homolog 2



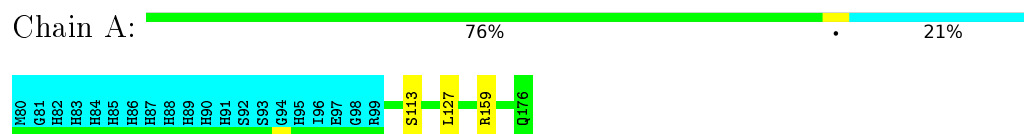
4.2.5 Score per residue for model 5 (medoid)

- Molecule 1: Protein DDI1 homolog 2



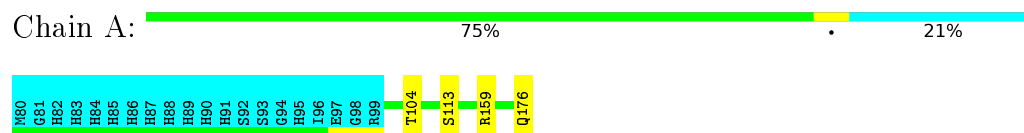
4.2.6 Score per residue for model 6

- Molecule 1: Protein DDI1 homolog 2



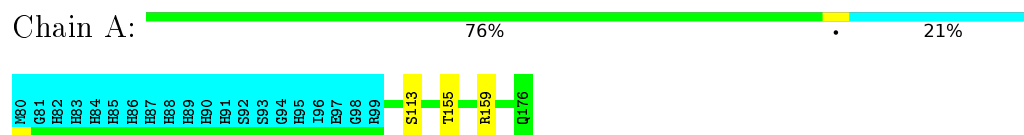
4.2.7 Score per residue for model 7

- Molecule 1: Protein DDI1 homolog 2



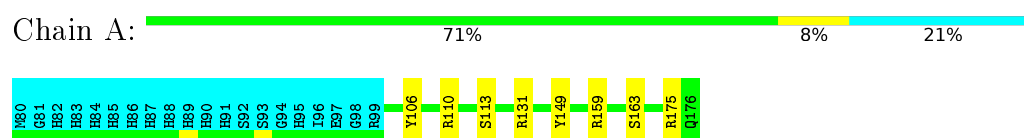
4.2.8 Score per residue for model 8

- Molecule 1: Protein DDI1 homolog 2



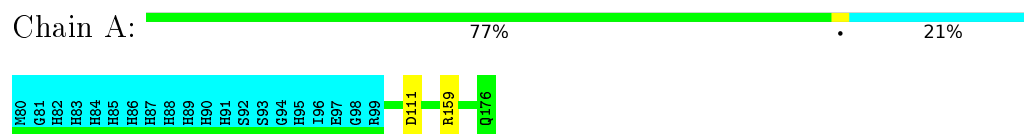
4.2.9 Score per residue for model 9

- Molecule 1: Protein DDI1 homolog 2



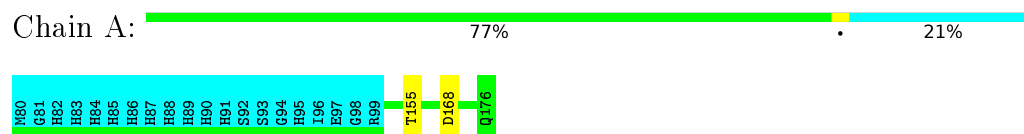
4.2.10 Score per residue for model 10

- Molecule 1: Protein DDI1 homolog 2



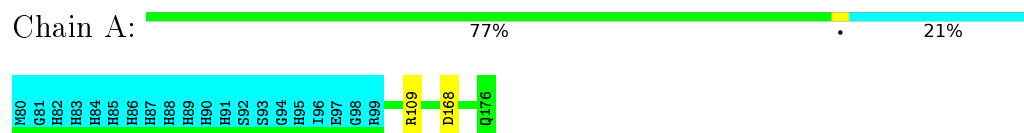
4.2.11 Score per residue for model 11

- Molecule 1: Protein DDI1 homolog 2



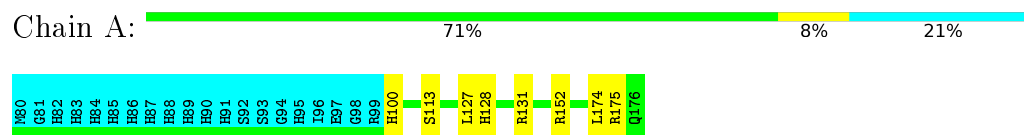
4.2.12 Score per residue for model 12

- Molecule 1: Protein DDI1 homolog 2



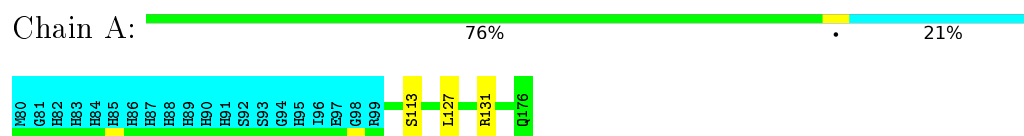
4.2.13 Score per residue for model 13

- Molecule 1: Protein DDI1 homolog 2



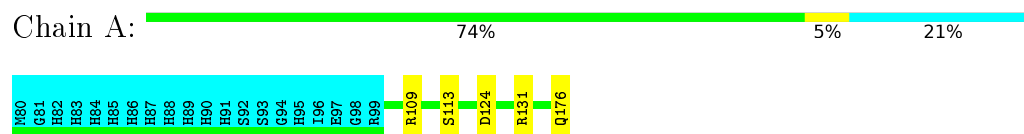
4.2.14 Score per residue for model 14

- Molecule 1: Protein DDI1 homolog 2



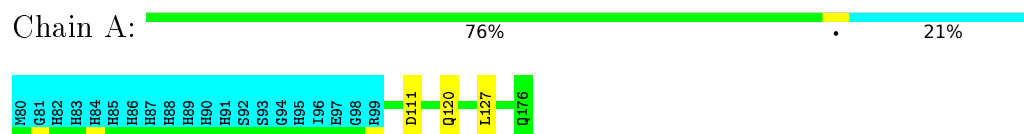
4.2.15 Score per residue for model 15

- Molecule 1: Protein DDI1 homolog 2



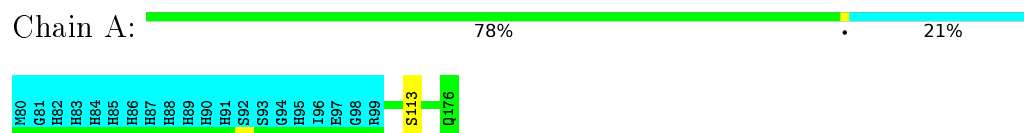
4.2.16 Score per residue for model 16

- Molecule 1: Protein DDI1 homolog 2



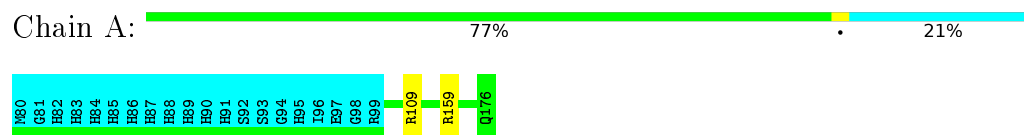
4.2.17 Score per residue for model 17

- Molecule 1: Protein DDI1 homolog 2



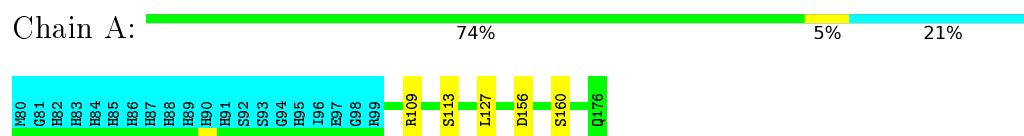
4.2.18 Score per residue for model 18

- Molecule 1: Protein DDI1 homolog 2



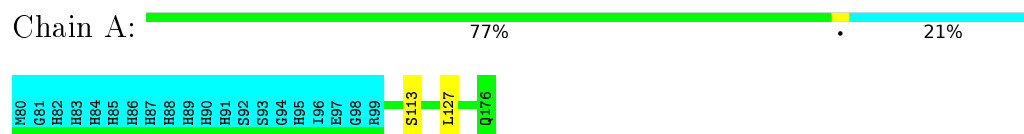
4.2.19 Score per residue for model 19

- Molecule 1: Protein DDI1 homolog 2



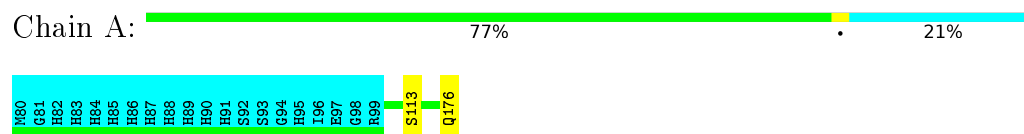
4.2.20 Score per residue for model 20

- Molecule 1: Protein DDI1 homolog 2



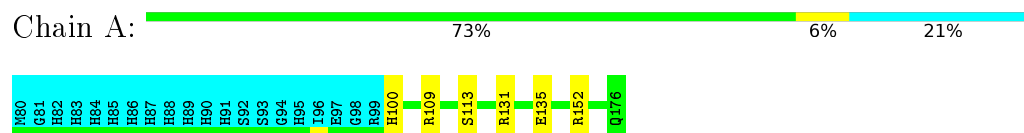
4.2.21 Score per residue for model 21

- Molecule 1: Protein DDI1 homolog 2



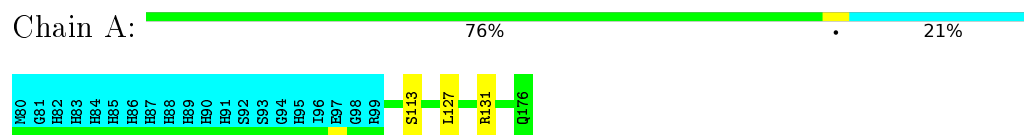
4.2.22 Score per residue for model 22

- Molecule 1: Protein DDI1 homolog 2



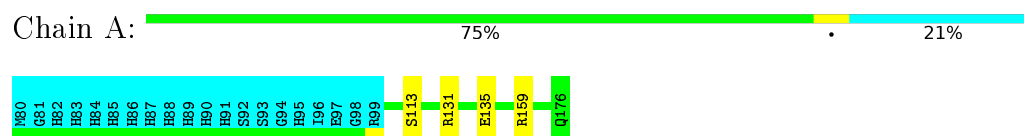
4.2.23 Score per residue for model 23

- Molecule 1: Protein DDI1 homolog 2



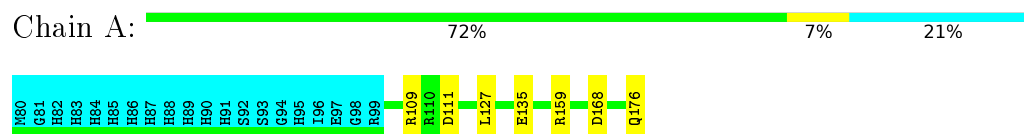
4.2.24 Score per residue for model 24

- Molecule 1: Protein DDI1 homolog 2



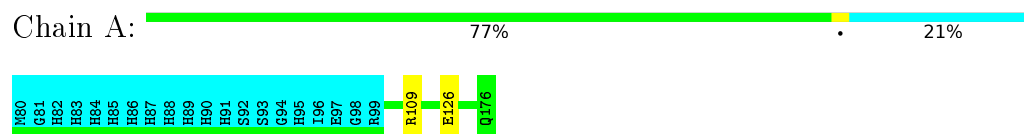
4.2.25 Score per residue for model 25

- Molecule 1: Protein DDI1 homolog 2



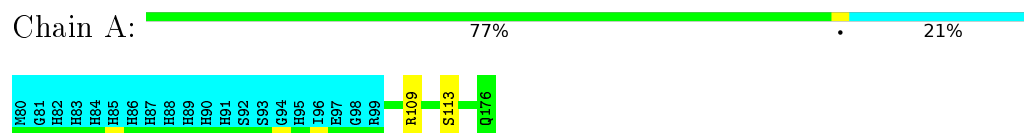
4.2.26 Score per residue for model 26

- Molecule 1: Protein DDI1 homolog 2



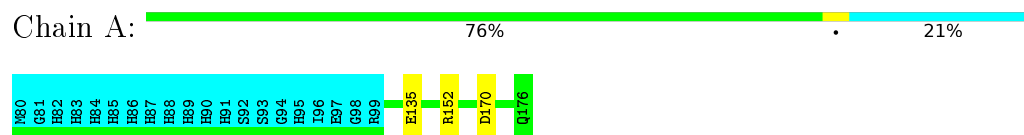
4.2.27 Score per residue for model 27

- Molecule 1: Protein DDI1 homolog 2



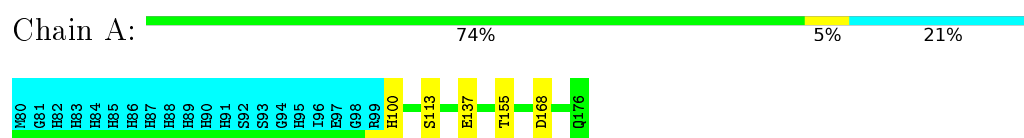
4.2.28 Score per residue for model 28

- Molecule 1: Protein DDI1 homolog 2



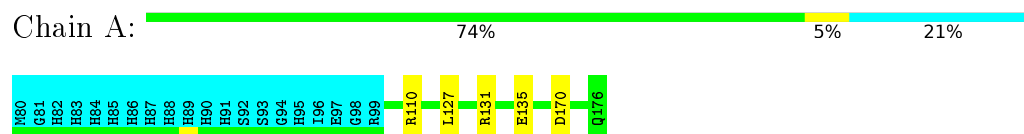
4.2.29 Score per residue for model 29

- Molecule 1: Protein DDI1 homolog 2



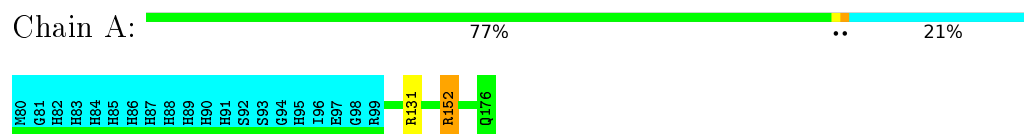
4.2.30 Score per residue for model 30

- Molecule 1: Protein DDI1 homolog 2



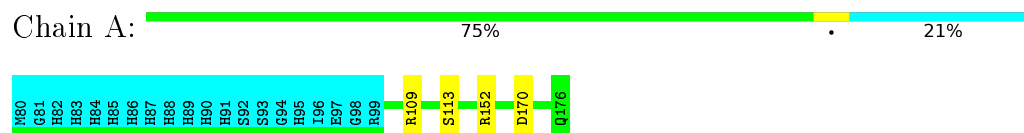
4.2.31 Score per residue for model 31

- Molecule 1: Protein DDI1 homolog 2



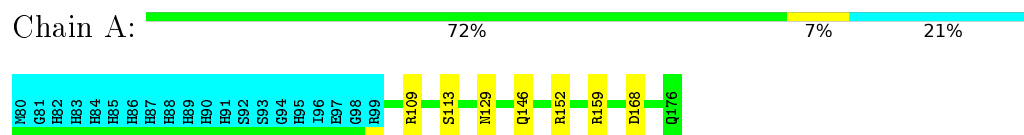
4.2.32 Score per residue for model 32

- Molecule 1: Protein DDI1 homolog 2



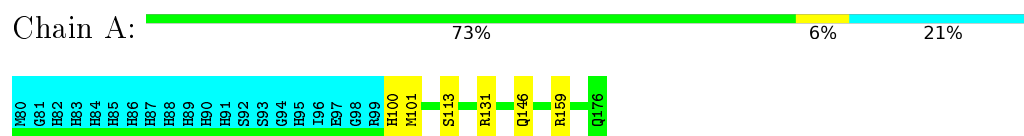
4.2.33 Score per residue for model 33

- Molecule 1: Protein DDI1 homolog 2



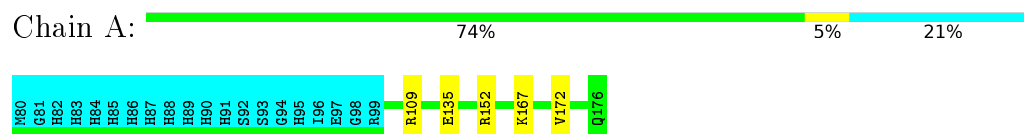
4.2.34 Score per residue for model 34

- Molecule 1: Protein DDI1 homolog 2



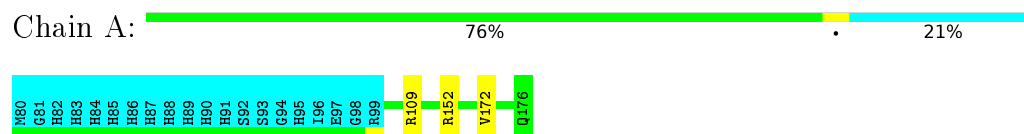
4.2.35 Score per residue for model 35

- Molecule 1: Protein DDI1 homolog 2



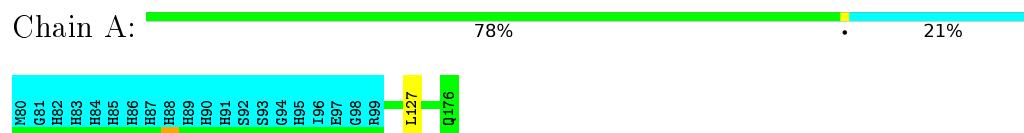
4.2.36 Score per residue for model 36

- Molecule 1: Protein DDI1 homolog 2



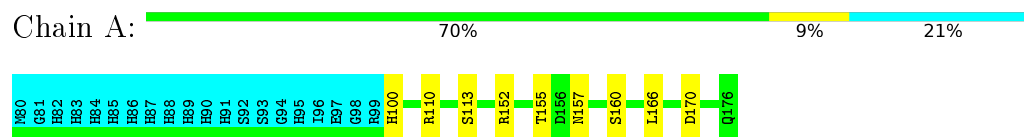
4.2.37 Score per residue for model 37

- Molecule 1: Protein DDI1 homolog 2



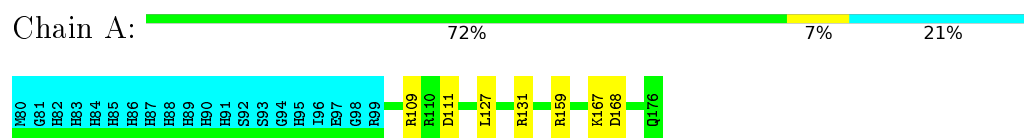
4.2.38 Score per residue for model 38

- Molecule 1: Protein DDI1 homolog 2



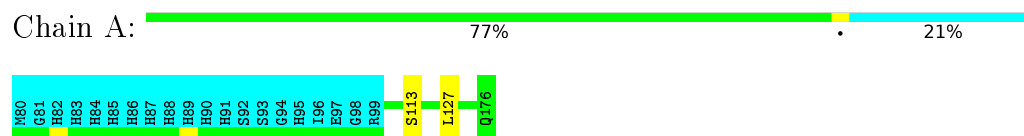
4.2.39 Score per residue for model 39

- Molecule 1: Protein DDI1 homolog 2



4.2.40 Score per residue for model 40

- Molecule 1: Protein DDI1 homolog 2



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 40 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

Software name	Classification	Version
YASARA	refinement	
CYANA	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	2n7d_cs.cif
Number of chemical shift lists	1
Total number of shifts	994
Number of shifts mapped to atoms	994
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	87%

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](#)

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±0.07	0±0/624 (0.0±0.0%)	0.74±0.05	1±1/844 (0.1±0.1%)
All	All	0.65	0/24960 (0.0%)	0.75	46/33760 (0.1%)

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	159	ARG	NE-CZ-NH1	9.20	124.90	120.30	9	12
1	A	109	ARG	NE-CZ-NH1	6.20	123.40	120.30	26	13
1	A	131	ARG	NE-CZ-NH1	6.16	123.38	120.30	9	5
1	A	152	ARG	NE-CZ-NH1	6.05	123.33	120.30	38	9
1	A	110	ARG	NE-CZ-NH1	5.88	123.24	120.30	9	5
1	A	175	ARG	NE-CZ-NH1	5.75	123.17	120.30	9	2

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
All	All	24560	24120	24080	-

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 -.

There are no clashes.

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	76/97 (78%)	74±1 (97±1%)	2±1 (3±1%)	0±0 (0±0%)	100	100
All	All	3040/3880 (78%)	2962 (97%)	78 (3%)	0 (0%)	100	100

There are no Ramachandran outliers.

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	68/85 (80%)	65±2 (96±2%)	3±2 (4±2%)	41	84
All	All	2720/3400 (80%)	2605 (96%)	115 (4%)	41	84

All 34 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	113	SER	24
1	A	127	LEU	15
1	A	131	ARG	10
1	A	168	ASP	6
1	A	135	GLU	6
1	A	100	HIS	5
1	A	155	THR	4
1	A	176	GLN	4
1	A	170	ASP	4
1	A	111	ASP	4

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Mol	Chain	Res	Type	Models (Total)
1	A	120	GLN	3
1	A	160	SER	2
1	A	146	GLN	2
1	A	109	ARG	2
1	A	172	VAL	2
1	A	167	LYS	2
1	A	152	ARG	2
1	A	166	LEU	2
1	A	126	GLU	1
1	A	110	ARG	1
1	A	128	HIS	1
1	A	124	ASP	1
1	A	149	TYR	1
1	A	159	ARG	1
1	A	101	MET	1
1	A	106	TYR	1
1	A	163	SER	1
1	A	157	ASN	1
1	A	174	LEU	1
1	A	129	ASN	1
1	A	156	ASP	1
1	A	137	GLU	1
1	A	102	LEU	1
1	A	104	THR	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation [i](#)

The completeness of assignment taking into account all chemical shift lists is 87% for the well-defined parts and 72% for the entire structure.

7.1 Chemical shift list 1

File name: 2n7d_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping [i](#)

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	994
Number of shifts mapped to atoms	994
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	82	0.37 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	78	0.18 ± 0.17	None needed (< 0.5 ppm)
$^{13}\text{C}'$	78	-0.25 ± 0.16	None needed (< 0.5 ppm)
^{15}N	78	0.04 ± 0.54	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 87%, i.e. 829 atoms were assigned a chemical shift out of a possible 953. 2 out of 18 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	375/381 (98%)	151/152 (99%)	150/154 (97%)	74/75 (99%)
Sidechain	421/500 (84%)	257/290 (89%)	159/186 (85%)	5/24 (21%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	33/72 (46%)	33/39 (85%)	0/30 (0%)	0/3 (0%)
Overall	829/953 (87%)	441/481 (92%)	309/370 (84%)	79/102 (77%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 72%, i.e. 876 atoms were assigned a chemical shift out of a possible 1211. 2 out of 18 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	397/481 (83%)	159/192 (83%)	160/194 (82%)	78/95 (82%)
Sidechain	446/581 (77%)	272/341 (80%)	169/213 (79%)	5/27 (19%)
Aromatic	33/149 (22%)	33/83 (40%)	0/52 (0%)	0/14 (0%)
Overall	876/1211 (72%)	464/616 (75%)	329/459 (72%)	83/136 (61%)

7.1.4 Statistically unusual chemical shifts [i](#)

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	137	GLU	HB2	0.86	3.08 – 0.98	-5.6
1	A	137	GLU	HB3	0.86	3.10 – 0.90	-5.2

7.1.5 Random Coil Index (RCI) plots [i](#)

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:

