Full wwPDB NMR Structure Validation Report (i)

Jun 11, 2024 – 07:04 PM EDT

PDB ID	:	2JVO
BMRB ID	:	15485
Title	:	Segmental isotope labeling of Npl3
Authors	:	Skrisovska, L.; Allain, F.H.-T.
Deposited on	:	2007-09-24

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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

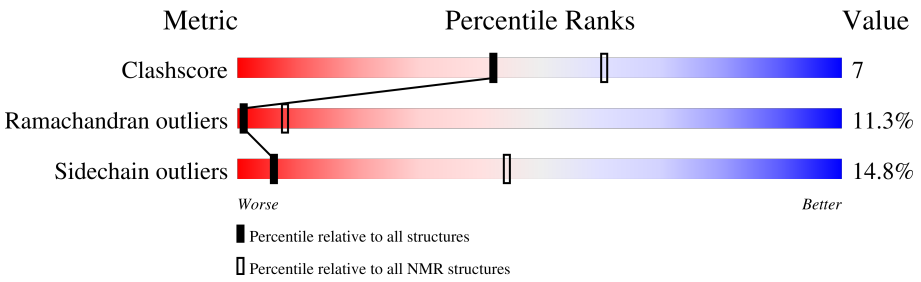
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
SOLUTION NMR

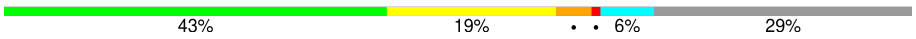
The overall completeness of chemical shifts assignment is 83%.

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

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	108	

2 Ensemble composition and analysis (i)

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:30-A:100 (71)	0.43	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 3 clusters. No single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1208 atoms, of which 598 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Nucleolar protein 3.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	77	1208	397	598	96	116	1	0

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP Q01560
A	2	GLY	-	expression tag	UNP Q01560
A	3	SER	-	expression tag	UNP Q01560
A	4	SER	-	expression tag	UNP Q01560
A	5	HIS	-	expression tag	UNP Q01560
A	6	HIS	-	expression tag	UNP Q01560
A	7	HIS	-	expression tag	UNP Q01560
A	8	HIS	-	expression tag	UNP Q01560
A	9	HIS	-	expression tag	UNP Q01560
A	10	HIS	-	expression tag	UNP Q01560
A	11	SER	-	expression tag	UNP Q01560
A	12	SER	-	expression tag	UNP Q01560
A	13	GLY	-	expression tag	UNP Q01560
A	14	LEU	-	expression tag	UNP Q01560
A	15	VAL	-	expression tag	UNP Q01560
A	16	PRO	-	expression tag	UNP Q01560
A	17	ARG	-	expression tag	UNP Q01560
A	18	GLY	-	expression tag	UNP Q01560
A	19	SER	-	expression tag	UNP Q01560
A	20	HIS	-	expression tag	UNP Q01560
A	21	MET	-	expression tag	UNP Q01560
A	22	HIS	-	expression tag	UNP Q01560

4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide 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: Nucleolar protein 3

Chain A: 43% 19% • • 6% 29%

MET GLY SER SER HIS HIS HIS HIS HIS HIS SER SER GLY LEU VAL PRO ARG GLY SER HIS MET HIS HIS ARG GLN GLU GLY E28 L29 S30 N31 T32 R33 L34 F35 V36 R37 P38 F39 M58 K59 E60 V61 K62 I63 L64 N65 F69 V70 E71 F72 E73 E74 K80 V85

A91 L95 E96 V97 V98 Y99 S100 K101 L102 P103 A104 LYS ARG TYR ARG

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: Nucleolar protein 3

Chain A: 44% 18% • • 6% 29%

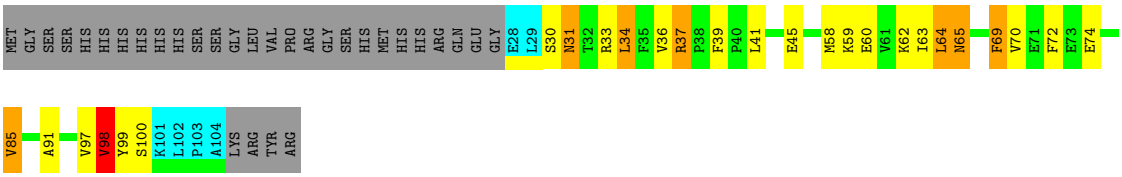
MET GLY SER SER HIS HIS HIS HIS HIS HIS SER SER GLY LEU VAL PRO ARG GLY SER HIS MET HIS HIS ARG GLN GLU GLY E28 L29 S30 N31 T32 R33 L34 F35 V36 R37 P38 F39 P40 L41 M58 K59 E60 V61 K62 I63 L64 N65 F69 V70 E71 F72 E73 E74 K80

V85 A91 V98 Y99 S100 K101 L102 P103 A104 LYS ARG TYR ARG

4.2.2 Score per residue for model 2

• Molecule 1: Nucleolar protein 3

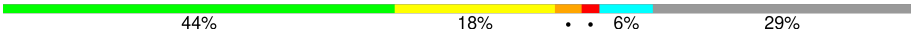
Chain A: 42% 17% 6% • 6% 29%

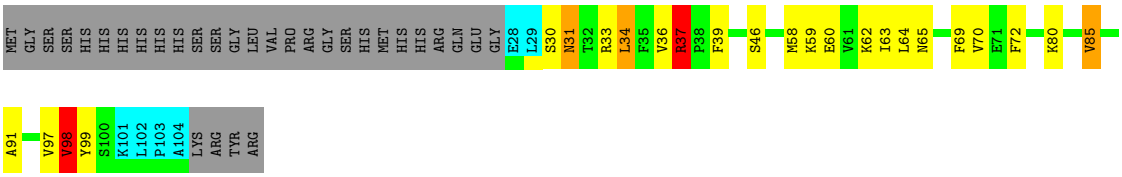


4.2.3 Score per residue for model 3

- Molecule 1: Nucleolar protein 3

Chain A:

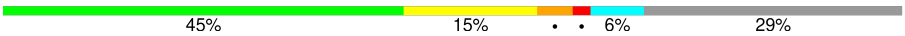


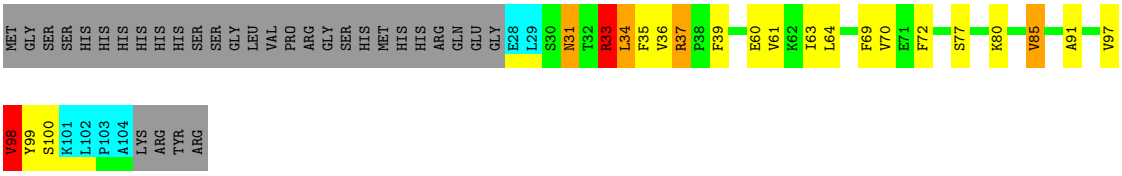


4.2.4 Score per residue for model 4

- Molecule 1: Nucleolar protein 3

Chain A:

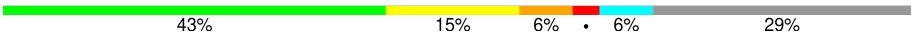


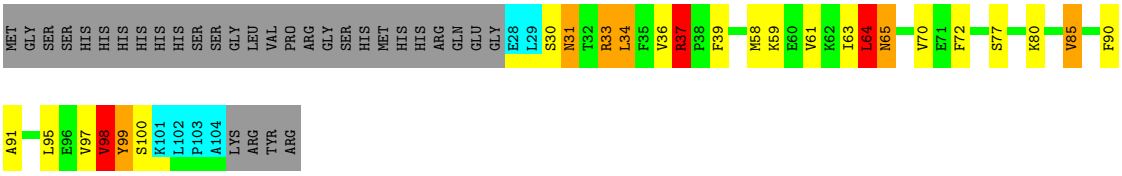


4.2.5 Score per residue for model 5

- Molecule 1: Nucleolar protein 3

Chain A:





4.2.6 Score per residue for model 6

- Molecule 1: Nucleolar protein 3

Chain A: 44% 16% 6% • 6% 29%

MET GLY SER SER HIS HIS HIS HIS HIS HIS HIS SER SER GLY LEU VAL PRO ARG GLY SER HIS MET HIS HIS ARG GLN GLU GLY E28 L29 S30 N31 T32 R33 L34 F35 V36 R37 P38 F39 P40 Q44 M58 K59 E60 V61 K62 I63 L64 N65 F69 V70 E71 F72 E73 E74 V85

A91 V97 V98 Y99 S100 K101 L102 P103 A104 LYS ARG TYR ARG

4.2.7 Score per residue for model 7

- Molecule 1: Nucleolar protein 3

Chain A: 43% 19% • • 6% 29%

MET GLY SER SER HIS HIS HIS HIS HIS HIS HIS SER SER GLY LEU VAL PRO ARG GLY SER HIS MET HIS HIS ARG GLN GLU GLY E28 L29 S30 N31 T32 R33 L34 F35 V36 R37 P38 F39 Q44 F52 F55 K59 E60 V61 K62 I63 L64 F69 V70 E71 F72 E73 E74

V85 F90 A91 L95 E96 V97 V98 Y99 S100 K101 L102 P103 A104 LYS ARG TYR ARG

4.2.8 Score per residue for model 8

- Molecule 1: Nucleolar protein 3

Chain A: 43% 19% • • 6% 29%

MET GLY SER SER HIS HIS HIS HIS HIS HIS HIS SER SER GLY LEU VAL PRO ARG GLY SER HIS MET HIS HIS ARG GLN GLU GLY E28 L29 S30 N31 T32 R33 L34 R37 P38 F39 P40 L41 L48 K59 E60 V61 K62 I63 L64 N65 F69 V70 E71 F72 E73 E74 K80

V85 A91 V97 V98 Y99 S100 K101 L102 P103 A104 LYS ARG TYR ARG

4.2.9 Score per residue for model 9

- Molecule 1: Nucleolar protein 3

Chain A: 41% 19% • • 6% 29%

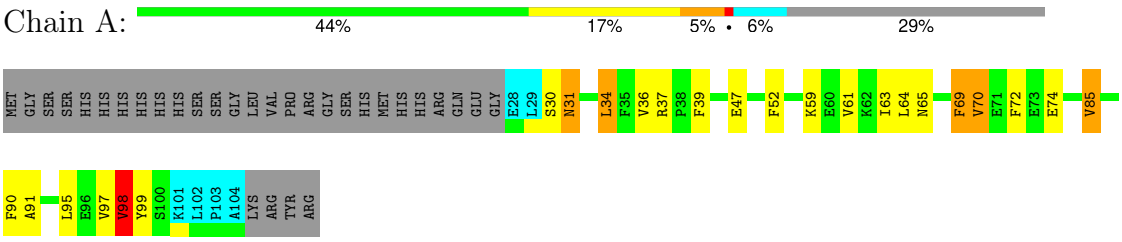
MET GLY SER SER HIS HIS HIS HIS HIS HIS HIS SER SER GLY LEU VAL PRO ARG GLY SER HIS MET HIS HIS ARG GLN GLU GLY E28 L29 S30 N31 T32 R33 L34 R37 P38 F39 P40 L41 E45 L48 M58 K59 E60 V61 K62 I63 L64 N65 F69 V70 E71 F72 S77

V85 K88 A91 N92 Q93 P94 L95 V98 Y99 S100 K101 L102 P103 A104 LYS ARG TYR ARG

4.2.10 Score per residue for model 10

- Molecule 1: Nucleolar protein 3

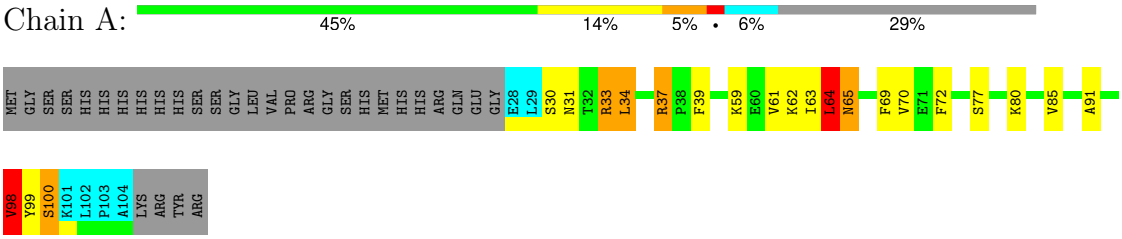
Chain A:



4.2.11 Score per residue for model 11

- Molecule 1: Nucleolar protein 3

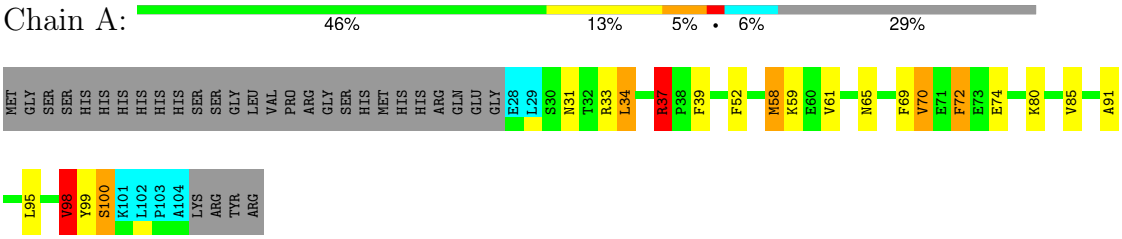
Chain A:



4.2.12 Score per residue for model 12

- Molecule 1: Nucleolar protein 3

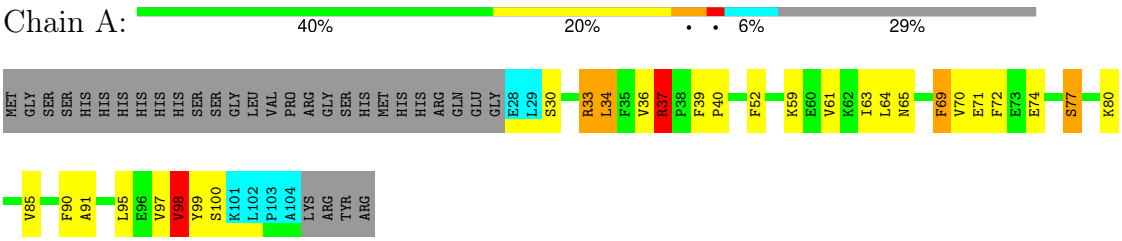
Chain A:



4.2.13 Score per residue for model 13

- Molecule 1: Nucleolar protein 3

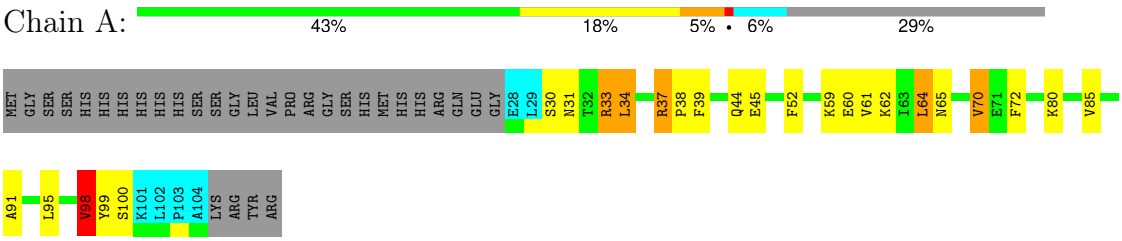
Chain A:



4.2.14 Score per residue for model 14

- Molecule 1: Nucleolar protein 3

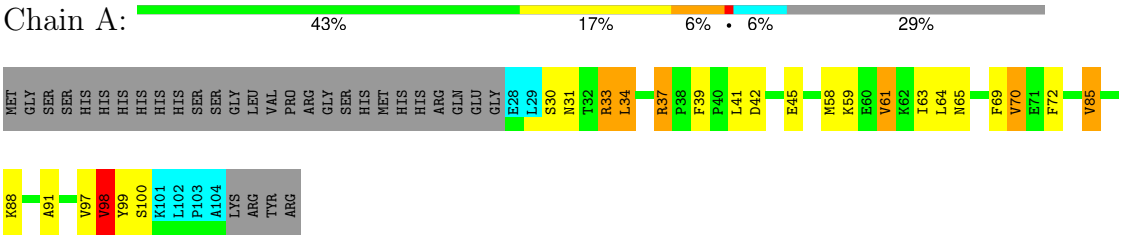
Chain A:



4.2.15 Score per residue for model 15

- Molecule 1: Nucleolar protein 3

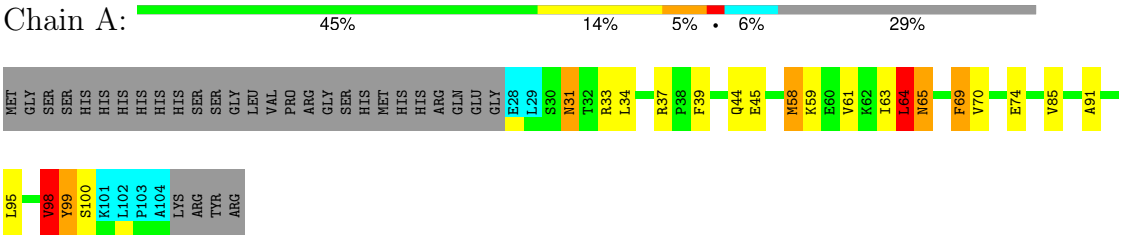
Chain A:



4.2.16 Score per residue for model 16

- Molecule 1: Nucleolar protein 3

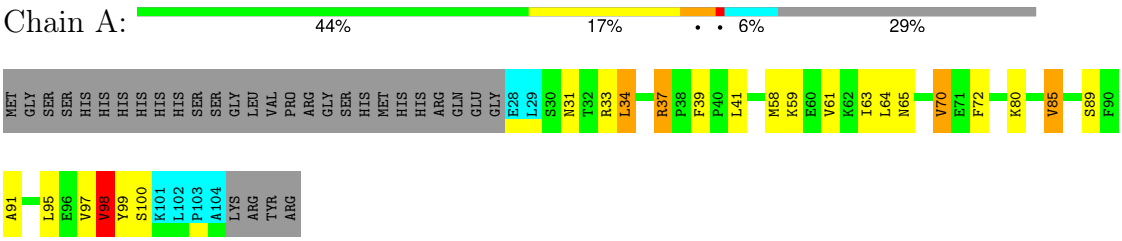
Chain A:



4.2.17 Score per residue for model 17

- Molecule 1: Nucleolar protein 3

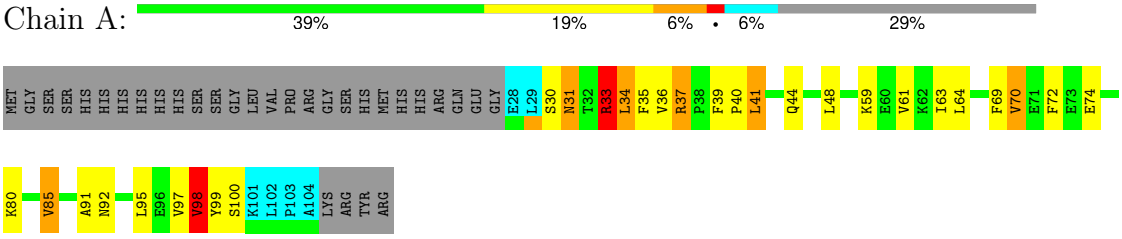
Chain A:



4.2.18 Score per residue for model 18

- Molecule 1: Nucleolar protein 3

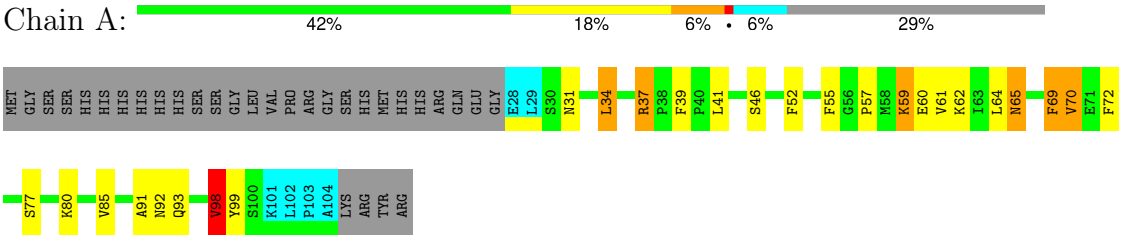
Chain A:



4.2.19 Score per residue for model 19

- Molecule 1: Nucleolar protein 3

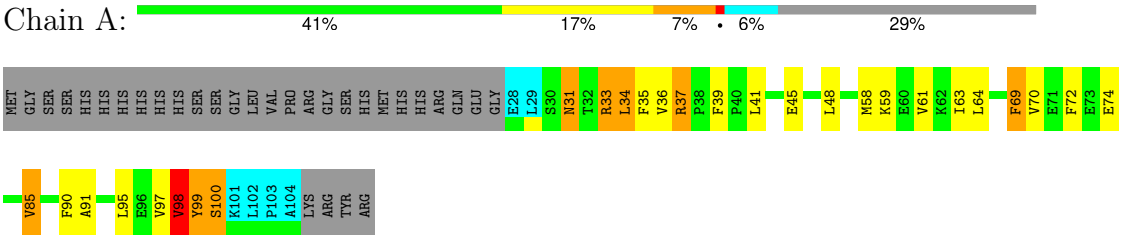
Chain A:



4.2.20 Score per residue for model 20

- Molecule 1: Nucleolar protein 3

Chain A:



5 Refinement protocol and experimental data overview (i)

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	**Classification**	**Version**
ATNOS/CANDID	structure calculation	

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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	823
Number of shifts mapped to atoms	823
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	83%

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	0.75±0.01	0±0/579 (0.0± 0.0%)	1.35±0.04	5±1/784 (0.6± 0.2%)
All	All	0.75	0/11580 (0.0%)	1.35	99/15680 (0.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.2±0.4
All	All	0	5

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(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	33	ARG	NE-CZ-NH1	12.76	126.68	120.30	4	15
1	A	37	ARG	NE-CZ-NH1	11.84	126.22	120.30	7	17
1	A	70	VAL	CG1-CB-CG2	-8.45	97.37	110.90	18	20
1	A	98	VAL	CA-CB-CG1	7.95	122.82	110.90	17	20
1	A	36	VAL	CA-CB-CG1	7.36	121.94	110.90	4	11
1	A	33	ARG	CD-NE-CZ	6.90	133.26	123.60	13	3
1	A	33	ARG	NE-CZ-NH2	-6.77	116.92	120.30	7	2
1	A	37	ARG	CD-NE-CZ	5.65	131.51	123.60	7	1
1	A	64	LEU	CB-CG-CD1	5.52	120.39	111.00	16	1
1	A	64	LEU	CB-CG-CD2	5.43	120.23	111.00	5	2
1	A	99	TYR	CB-CG-CD2	-5.30	117.82	121.00	16	2
1	A	99	TYR	C-N-CA	5.26	134.85	121.70	20	1
1	A	64	LEU	C-N-CA	5.25	134.83	121.70	11	1
1	A	98	VAL	CG1-CB-CG2	5.20	119.21	110.90	10	2
1	A	37	ARG	NH1-CZ-NH2	-5.02	113.88	119.40	11	1

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
1	A	33	ARG	Sidechain	2
1	A	52	PHE	Sidechain	2
1	A	72	PHE	Sidechain	1

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	564	545	545	8±2
All	All	11280	10900	10900	160

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 7.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:34:LEU:HD21	1:A:72:PHE:CE2	0.73	2.19	18	19
1:A:98:VAL:HG13	1:A:99:TYR:H	0.72	1.44	15	15
1:A:85:VAL:HG13	1:A:97:VAL:HG21	0.61	1.71	20	13
1:A:41:LEU:H	1:A:41:LEU:HD22	0.58	1.59	18	7
1:A:98:VAL:CG1	1:A:99:TYR:H	0.57	2.13	20	5
1:A:63:ILE:C	1:A:64:LEU:HD12	0.54	2.23	10	15
1:A:34:LEU:HD21	1:A:72:PHE:CZ	0.53	2.39	5	8
1:A:64:LEU:HD13	1:A:69:PHE:CE1	0.52	2.40	10	9
1:A:48:LEU:CD1	1:A:63:ILE:HD11	0.51	2.35	9	2
1:A:31:ASN:HA	1:A:99:TYR:CD1	0.49	2.43	2	9
1:A:33:ARG:HB3	1:A:100:SER:HB3	0.48	1.84	1	10
1:A:52:PHE:CE2	1:A:70:VAL:HG21	0.48	2.43	19	3
1:A:98:VAL:HG13	1:A:99:TYR:N	0.47	2.23	18	10
1:A:64:LEU:HD13	1:A:69:PHE:CE2	0.47	2.44	4	1
1:A:33:ARG:C	1:A:34:LEU:HD13	0.47	2.30	14	3
1:A:63:ILE:C	1:A:64:LEU:HD22	0.47	2.29	5	1
1:A:95:LEU:HB3	1:A:97:VAL:HG23	0.46	1.88	18	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:48:LEU:HD12	1:A:63:ILE:HD11	0.45	1.86	18	2
1:A:72:PHE:CD2	1:A:77:SER:HB3	0.45	2.46	9	1
1:A:77:SER:HA	1:A:80:LYS:CE	0.45	2.42	5	4
1:A:33:ARG:CB	1:A:100:SER:HB3	0.45	2.41	6	3
1:A:90:PHE:HB2	1:A:95:LEU:HD21	0.44	1.88	20	5
1:A:33:ARG:HB3	1:A:100:SER:HB2	0.43	1.88	14	1
1:A:52:PHE:HA	1:A:55:PHE:CE2	0.43	2.48	19	1
1:A:77:SER:HA	1:A:80:LYS:HE3	0.43	1.90	11	2
1:A:52:PHE:CZ	1:A:70:VAL:HG21	0.43	2.49	10	1
1:A:59:LYS:HE2	1:A:72:PHE:C	0.43	2.33	19	1
1:A:37:ARG:H	1:A:38:PRO:HD3	0.42	1.75	14	1
1:A:33:ARG:HE	1:A:71:GLU:CD	0.41	2.18	13	1
1:A:72:PHE:CG	1:A:77:SER:HB2	0.41	2.50	13	1
1:A:34:LEU:HD23	1:A:70:VAL:HB	0.41	1.92	8	2
1:A:35:PHE:HB2	1:A:100:SER:HB2	0.41	1.93	18	1
1:A:61:VAL:HG13	1:A:70:VAL:HG22	0.40	1.94	15	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	71/108 (66%)	54±1 (76±2%)	9±1 (13±2%)	8±1 (11±1%)	1 8
All	All	1420/2160 (66%)	1074 (76%)	186 (13%)	160 (11%)	1 8

All 15 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	37	ARG	20
1	A	91	ALA	20
1	A	98	VAL	20
1	A	61	VAL	18
1	A	85	VAL	18
1	A	65	ASN	16

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Mol	Chain	Res	Type	Models (Total)
1	A	58	MET	11
1	A	31	ASN	10
1	A	100	SER	10
1	A	30	SER	9
1	A	40	PRO	3
1	A	41	LEU	2
1	A	42	ASP	1
1	A	89	SER	1
1	A	57	PRO	1

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	61/93 (66%)	52±2 (85±4%)	9±2 (15±4%)	6 44
All	All	1220/1860 (66%)	1039 (85%)	181 (15%)	6 44

All 30 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	34	LEU	20
1	A	39	PHE	20
1	A	59	LYS	19
1	A	69	PHE	16
1	A	98	VAL	12
1	A	74	GLU	11
1	A	31	ASN	9
1	A	80	LYS	8
1	A	37	ARG	7
1	A	45	GLU	6
1	A	60	GLU	6
1	A	62	LYS	6
1	A	64	LEU	5
1	A	65	ASN	5
1	A	44	GLN	5
1	A	95	LEU	4

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Mol	Chain	Res	Type	Models (Total)
1	A	58	MET	3
1	A	46	SER	2
1	A	35	PHE	2
1	A	70	VAL	2
1	A	88	LYS	2
1	A	93	GLN	2
1	A	92	ASN	2
1	A	30	SER	1
1	A	55	PHE	1
1	A	47	GLU	1
1	A	40	PRO	1
1	A	77	SER	1
1	A	33	ARG	1
1	A	41	LEU	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 monosaccharides 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 83% for the well-defined parts and 78% for the entire structure.

7.1 Chemical shift list 1

File name: working_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	823
Number of shifts mapped to atoms	823
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 ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	67	1.79 ± 0.18	Should be applied
$^{13}C_{\beta}$	67	1.87 ± 0.19	Should be applied
$^{13}C'$	0	—	None (insufficient data)
^{15}N	67	6.05 ± 0.52	Should be applied

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 83%, i.e. 802 atoms were assigned a chemical shift out of a possible 966. 0 out of 12 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	265/349 (76%)	135/141 (96%)	66/142 (46%)	64/66 (97%)
Sidechain	474/521 (91%)	324/338 (96%)	144/167 (86%)	6/16 (38%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	63/96 (66%)	41/48 (85%)	22/47 (47%)	0/1 (0%)
Overall	802/966 (83%)	500/527 (95%)	232/356 (65%)	70/83 (84%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 78%, i.e. 823 atoms were assigned a chemical shift out of a possible 1053. 0 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	273/377 (72%)	139/152 (91%)	67/154 (44%)	67/71 (94%)
Sidechain	487/580 (84%)	333/377 (88%)	148/186 (80%)	6/17 (35%)
Aromatic	63/96 (66%)	41/48 (85%)	22/47 (47%)	0/1 (0%)
Overall	823/1053 (78%)	513/577 (89%)	237/387 (61%)	73/89 (82%)

7.1.4 Statistically unusual chemical shifts (i)

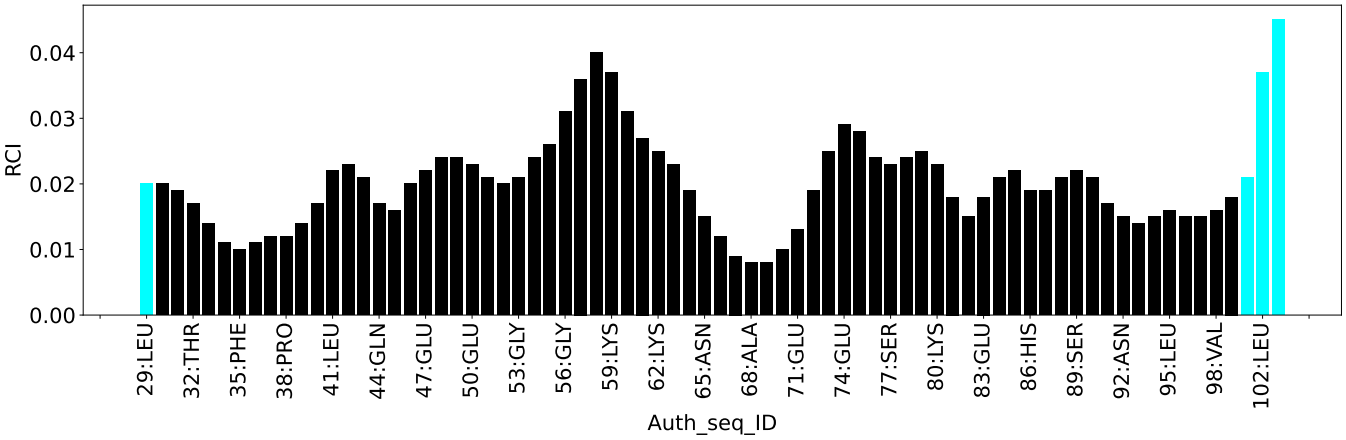
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	29	LEU	CD1	16.09	16.71 – 32.55	-5.4
1	A	38	PRO	CG	21.46	21.69 – 32.72	-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.If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:


RCI
0.00
0.01
0.02
0.03
0.04
29:LEU
32:THR
35:PHE
38:PRO
41:LEU
44:GLN
47:GLU
50:GLU
53:GLY
56:GLY
59:LYS
62:LYS
65:ASN
68:ALA
71:GLU
74:GLU
77:SER
80:LYS
83:GLU
86:HIS
89:SER
92:ASN
95:LEU
98:VAL
102:LEU
Auth_seq_ID