



Full wwPDB NMR Structure Validation Report ⓘ

Mar 3, 2022 – 08:51 AM EST

PDB ID : 2JPS
Title : NAB2 N-terminal domain
Authors : Grant, R.; Marshall, N.J.; Yang, J.; Fasken, M.; Kelly, S.; Harreman, M.T.;
Neuhaus, D.; Corbett, A.H.; Stewart, M.
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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:

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	:	2.27
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

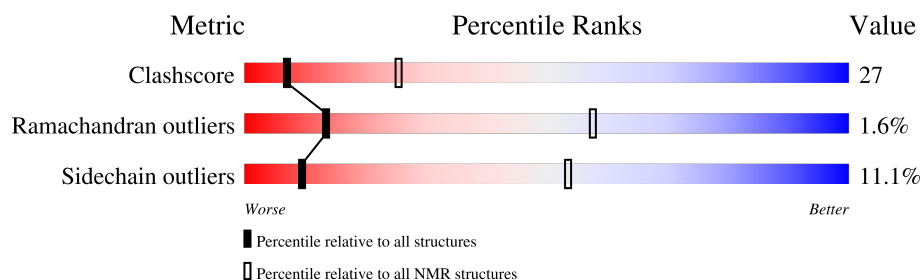
1 Overall quality at a glance

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	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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	105	

2 Ensemble composition and analysis

This entry contains 45 models. Model 4 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:3-A:22, A:27-A:95 (89)	0.24	4

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 10 single-model clusters were found.

Cluster number	Models
1	3, 4, 9, 10, 11, 15, 19, 27, 33
2	13, 17, 30, 32, 35, 40
3	5, 6, 12, 14, 25
4	18, 24, 26, 28, 38
5	7, 8, 16, 21
6	20, 29, 41, 44
7	1, 2
Single-model clusters	22; 23; 31; 34; 36; 37; 39; 42; 43; 45

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1608 atoms, of which 804 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Nuclear polyadenylated RNA-binding protein NAB2.

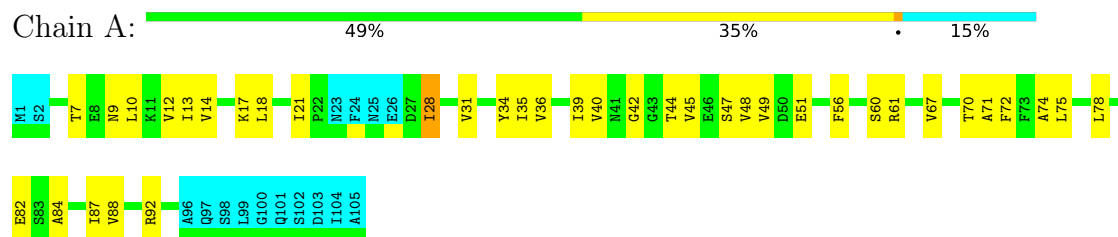
Mol	Chain	Residues	Atoms						Trace
1	A	105	Total	C	H	N	O	S	0
			1608	506	804	129	166	3	

4 Residue-property plots

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: Nuclear polyadenylated RNA-binding protein NAB2

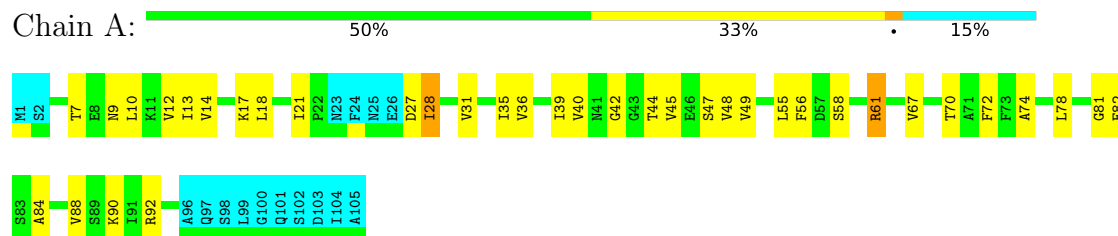


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

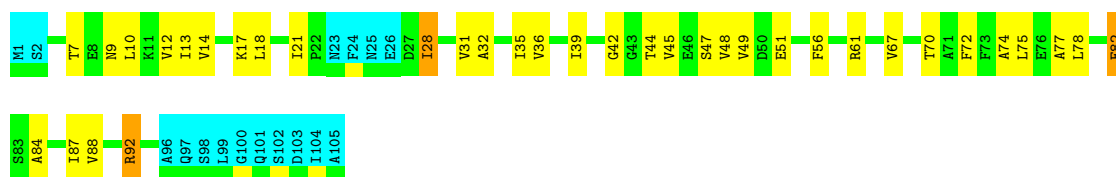
- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



4.2.2 Score per residue for model 2

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2

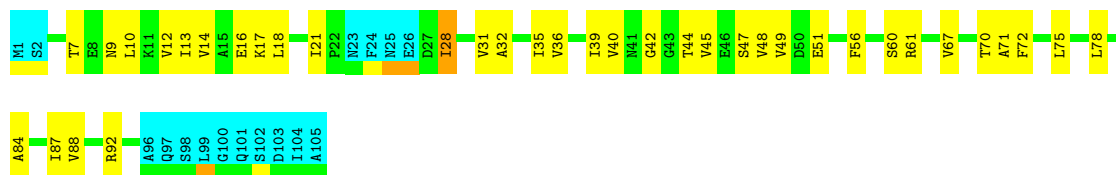




4.2.3 Score per residue for model 3

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2

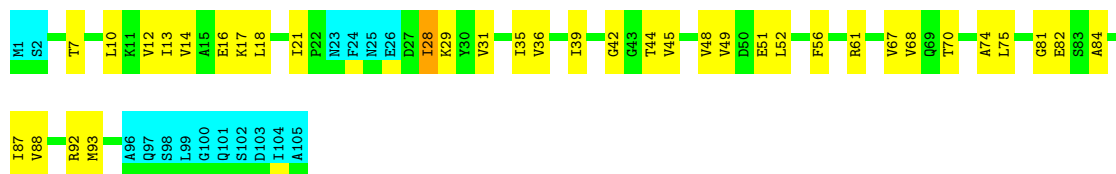
Chain A: 50% 34% 15%



4.2.4 Score per residue for model 4 (medoid)

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2

Chain A: 50% 33% 15%



4.2.5 Score per residue for model 5

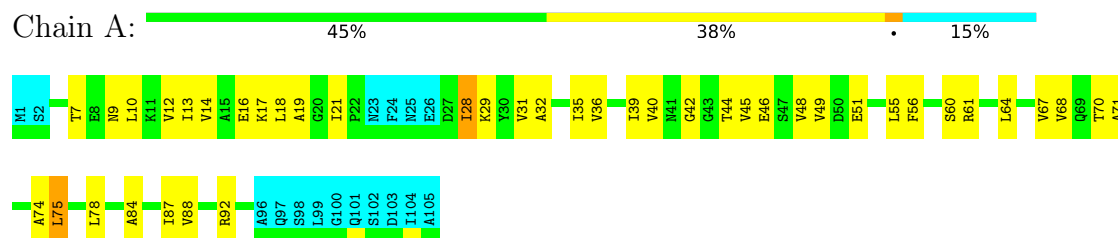
- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2

Chain A: 48% 35% 15%



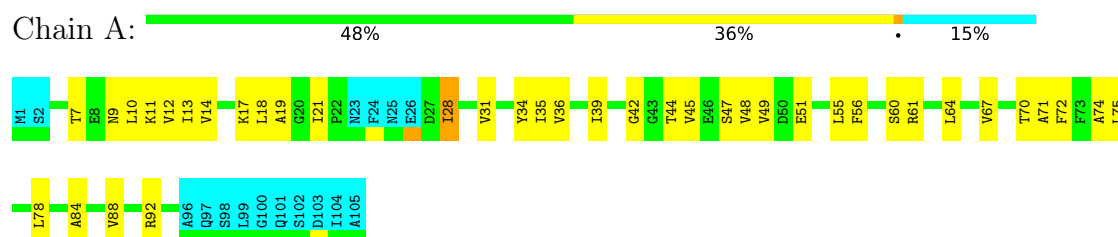
4.2.6 Score per residue for model 6

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



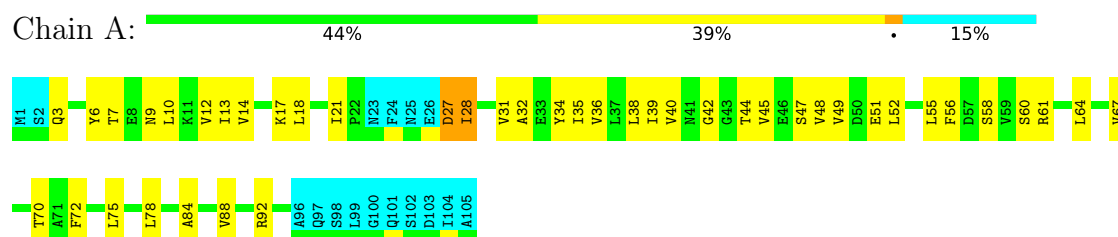
4.2.7 Score per residue for model 7

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



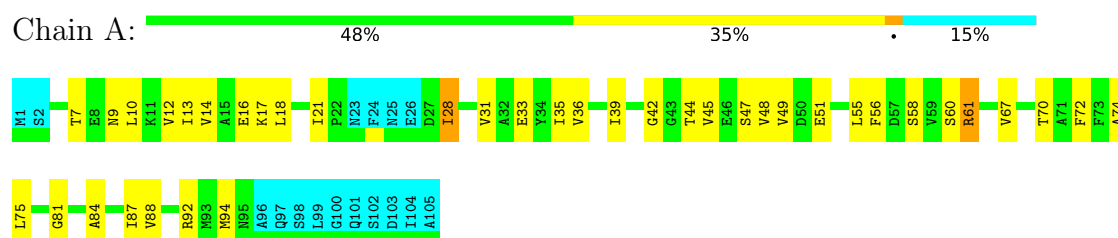
4.2.8 Score per residue for model 8

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



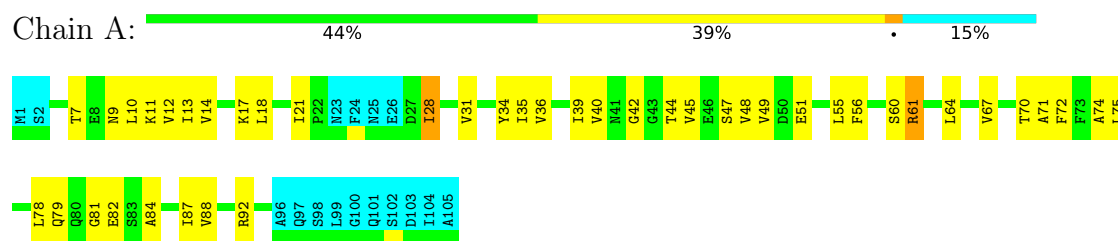
4.2.9 Score per residue for model 9

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



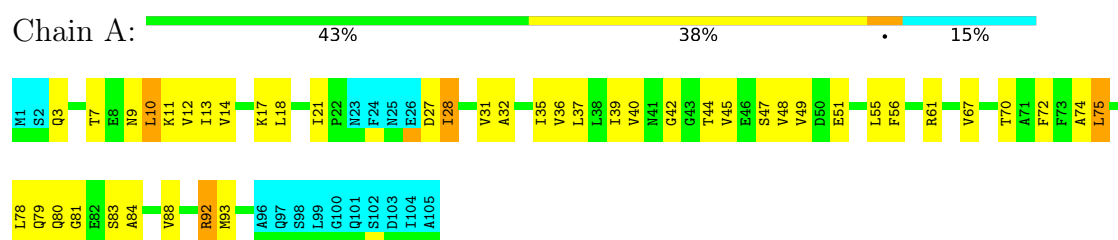
4.2.10 Score per residue for model 10

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



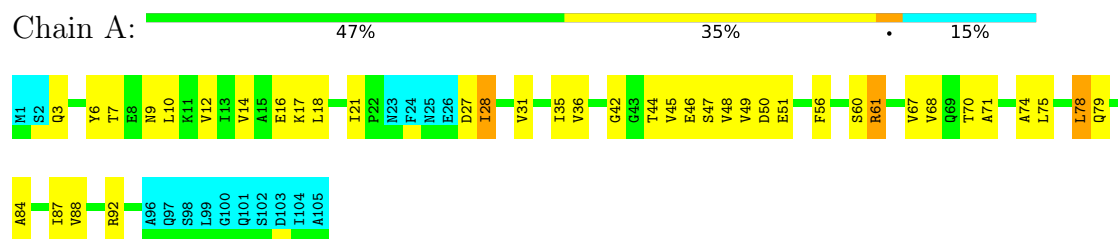
4.2.11 Score per residue for model 11

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



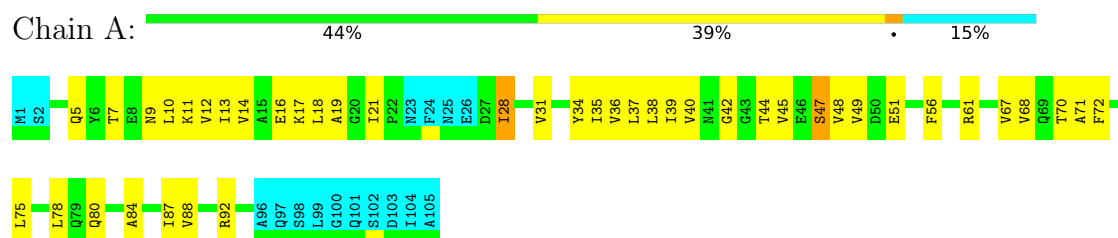
4.2.12 Score per residue for model 12

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



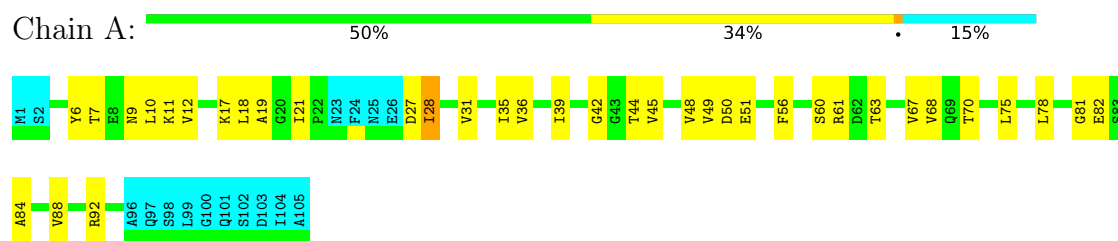
4.2.13 Score per residue for model 13

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



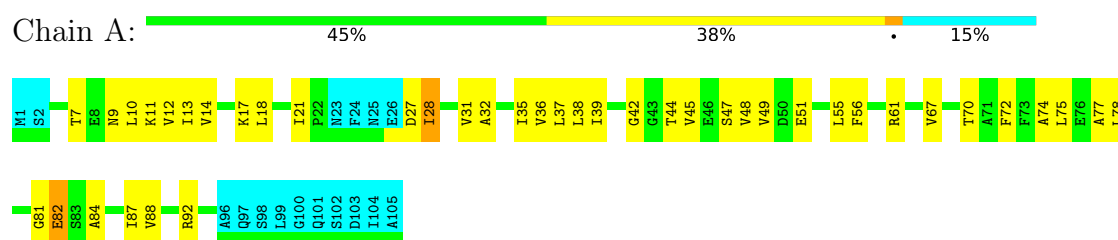
4.2.14 Score per residue for model 14

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



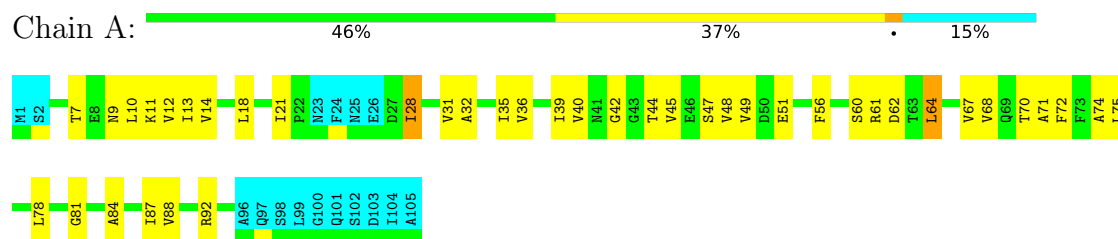
4.2.15 Score per residue for model 15

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



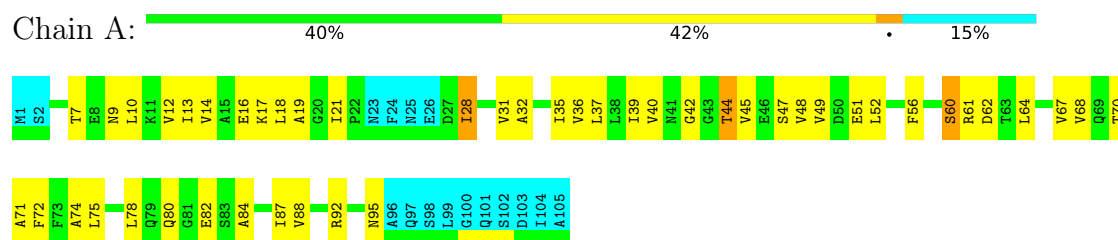
4.2.16 Score per residue for model 16

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



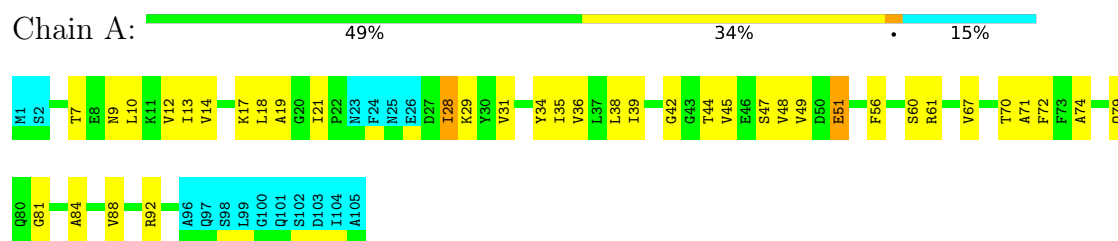
4.2.17 Score per residue for model 17

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



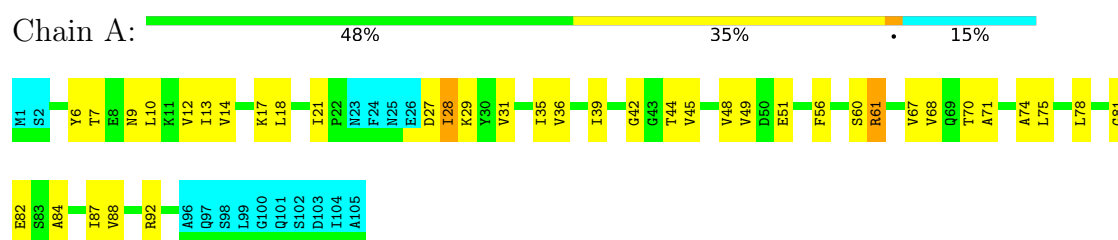
4.2.18 Score per residue for model 18

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



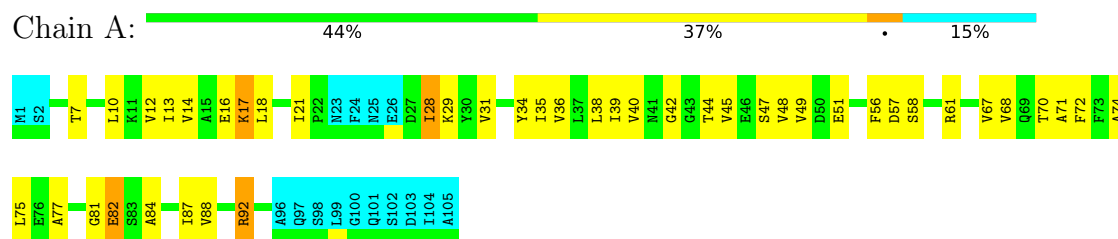
4.2.19 Score per residue for model 19

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



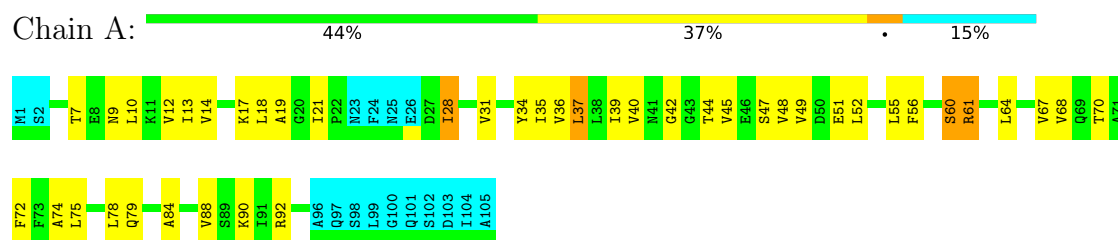
4.2.20 Score per residue for model 20

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



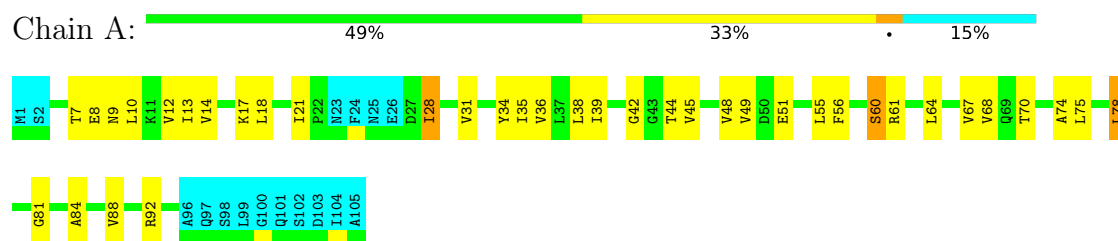
4.2.21 Score per residue for model 21

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



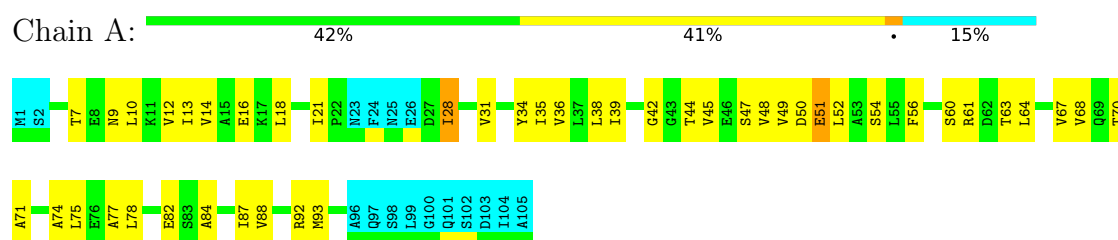
4.2.22 Score per residue for model 22

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



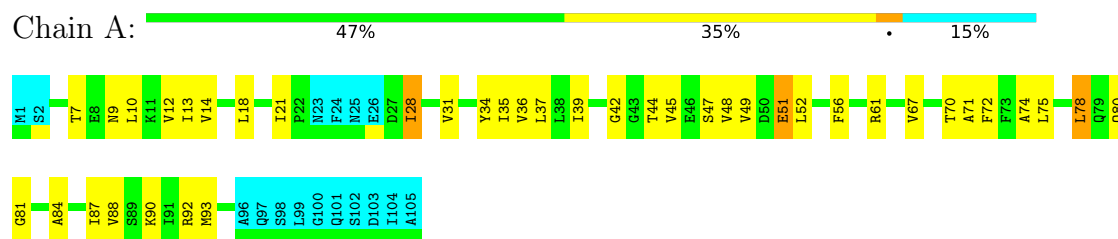
4.2.23 Score per residue for model 23

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



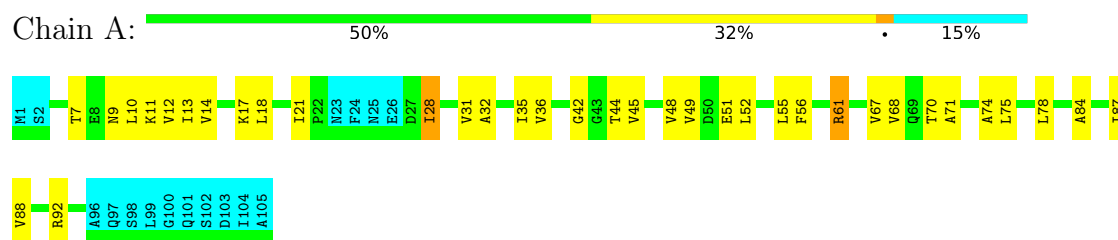
4.2.24 Score per residue for model 24

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



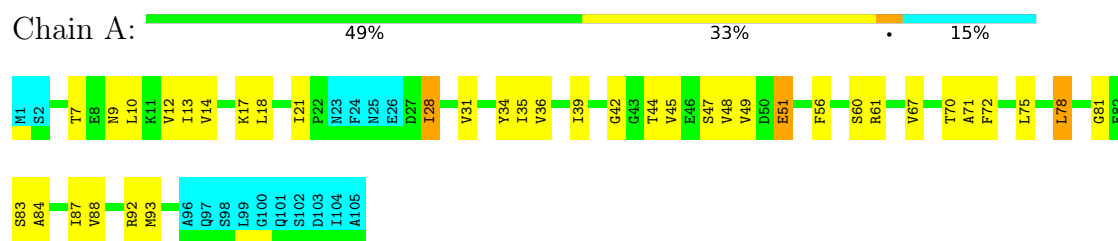
4.2.25 Score per residue for model 25

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



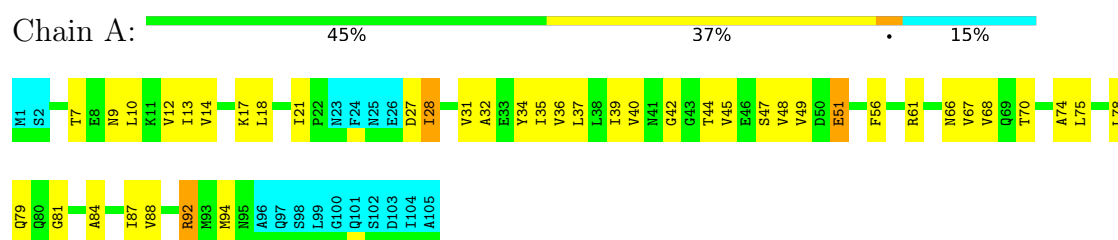
4.2.26 Score per residue for model 26

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



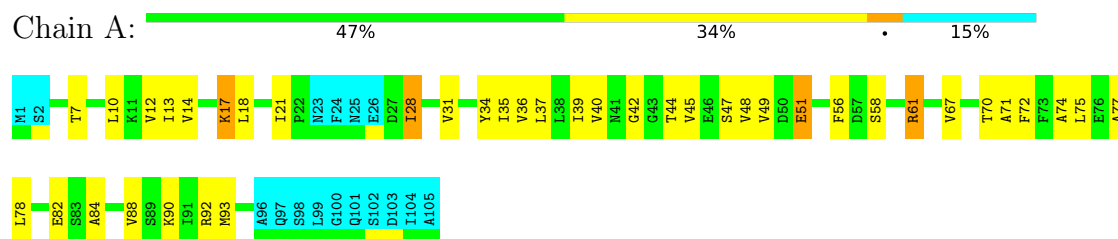
4.2.27 Score per residue for model 27

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



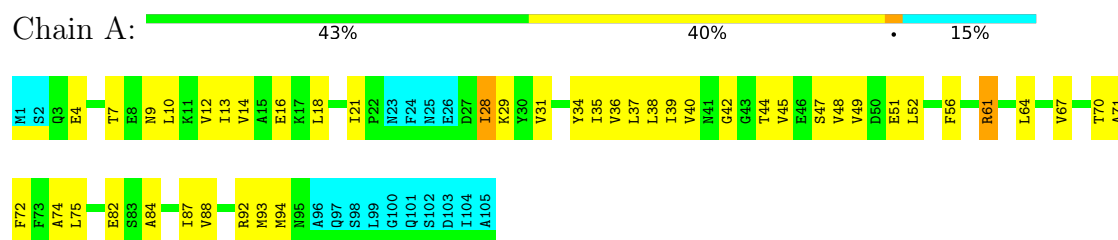
4.2.28 Score per residue for model 28

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



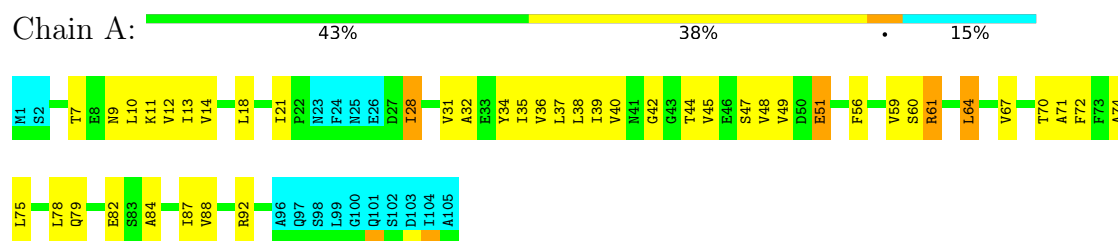
4.2.29 Score per residue for model 29

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



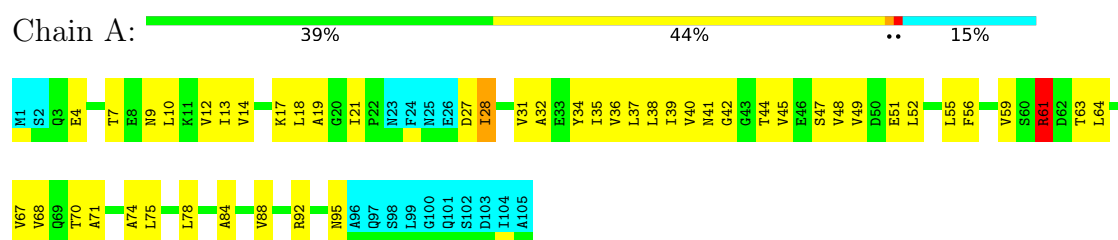
4.2.30 Score per residue for model 30

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



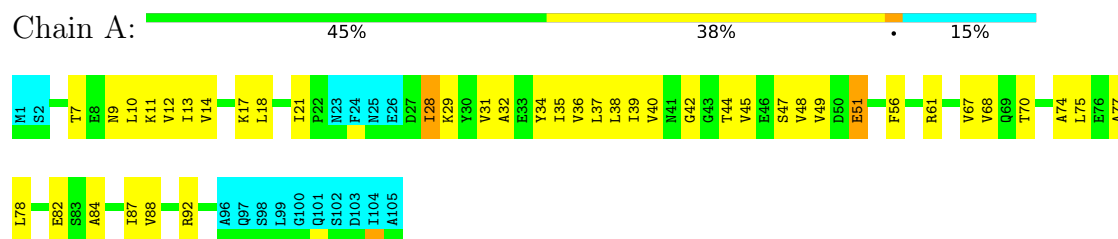
4.2.31 Score per residue for model 31

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



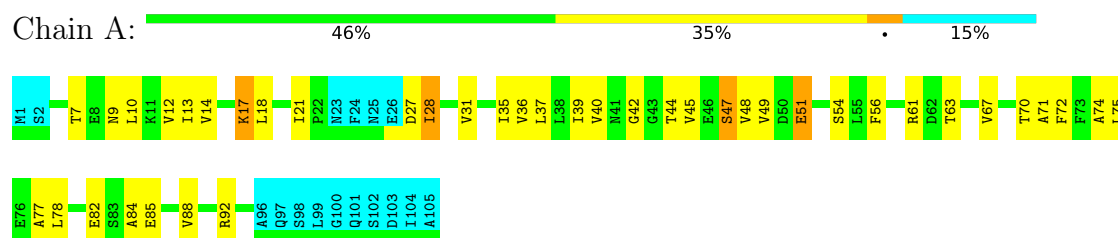
4.2.32 Score per residue for model 32

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



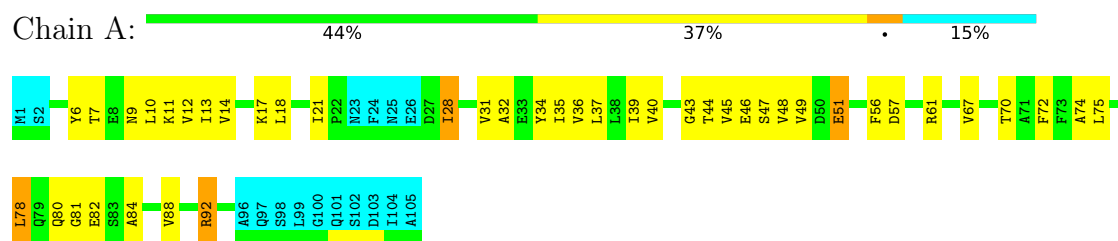
4.2.33 Score per residue for model 33

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



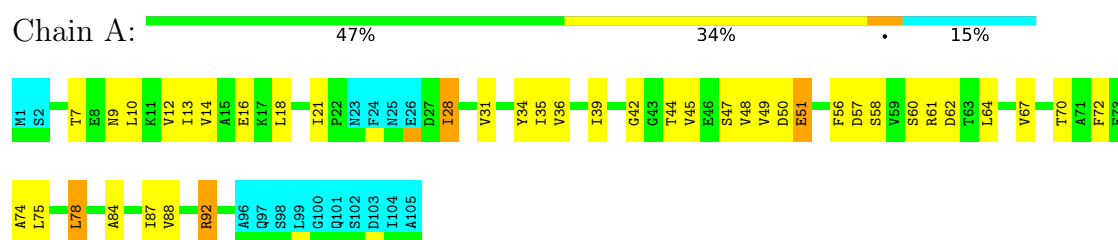
4.2.34 Score per residue for model 34

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



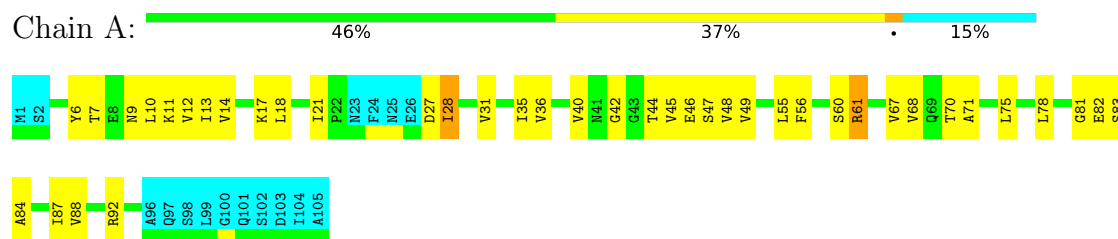
4.2.35 Score per residue for model 35

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



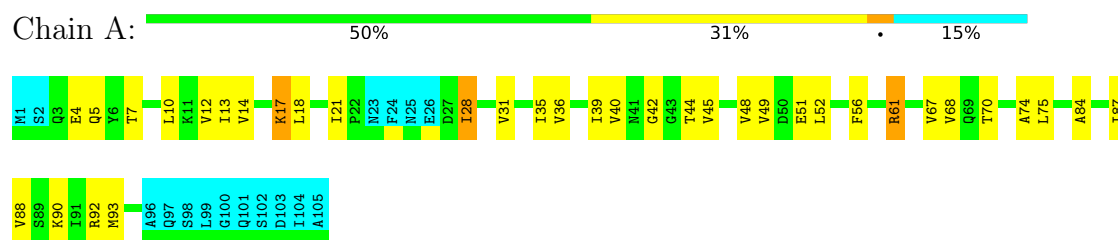
4.2.36 Score per residue for model 36

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



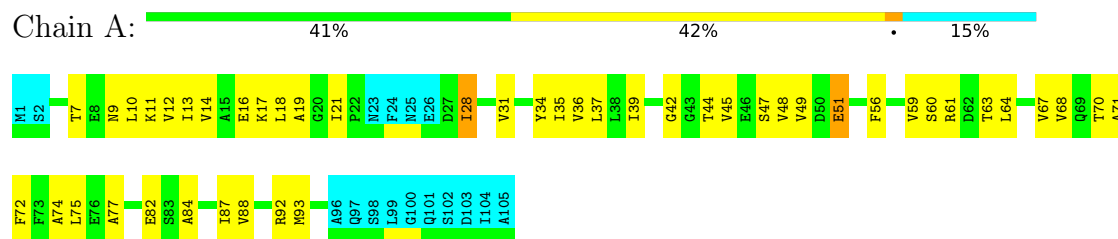
4.2.37 Score per residue for model 37

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



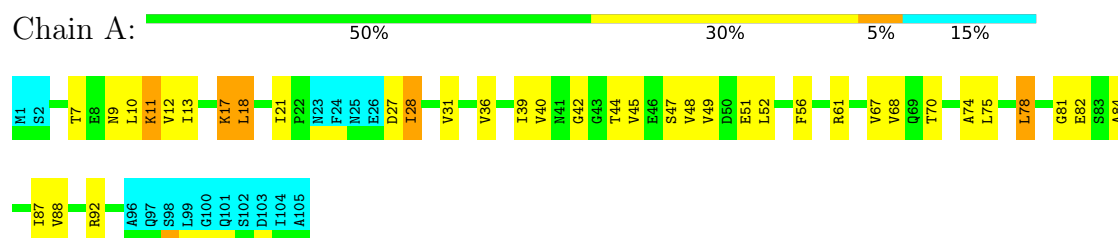
4.2.38 Score per residue for model 38

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



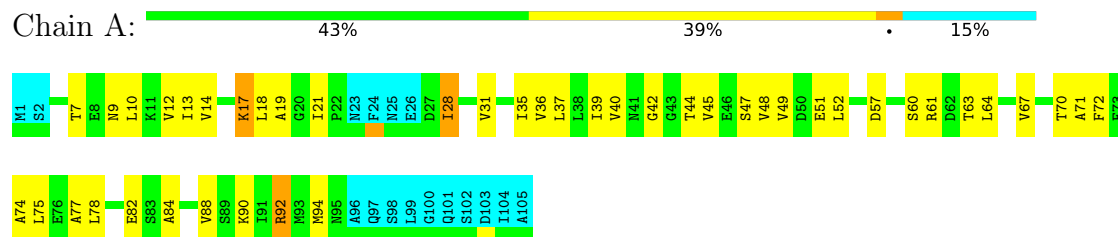
4.2.39 Score per residue for model 39

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



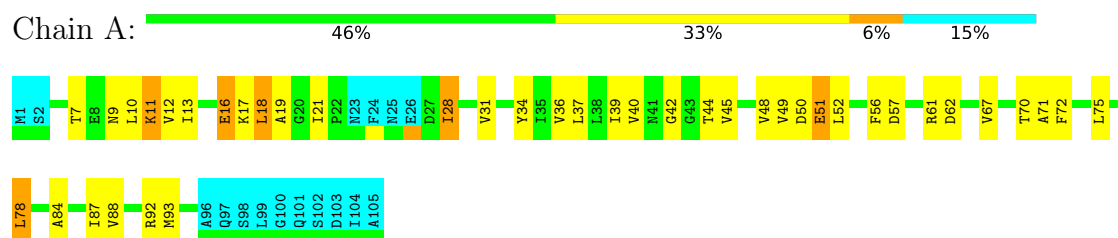
4.2.40 Score per residue for model 40

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



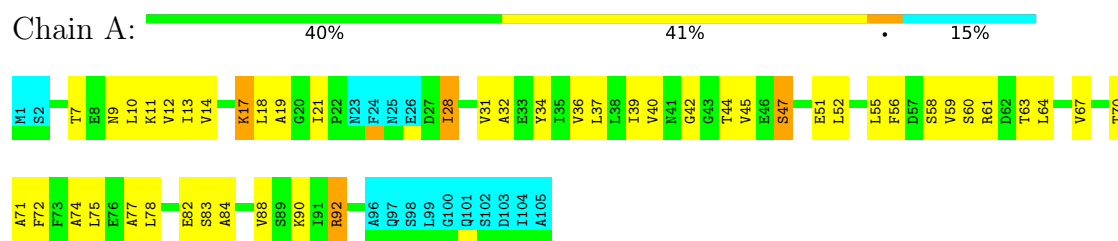
4.2.41 Score per residue for model 41

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



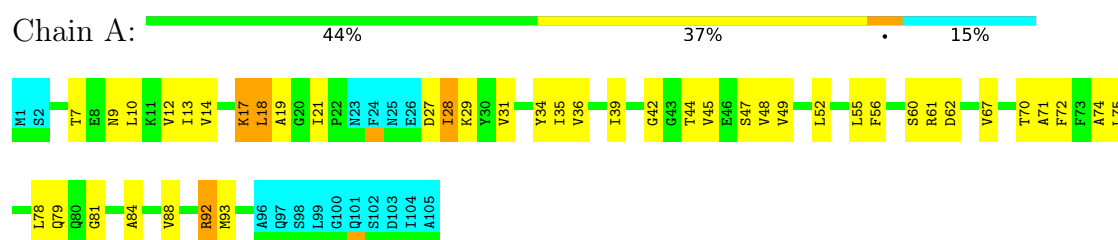
4.2.42 Score per residue for model 42

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



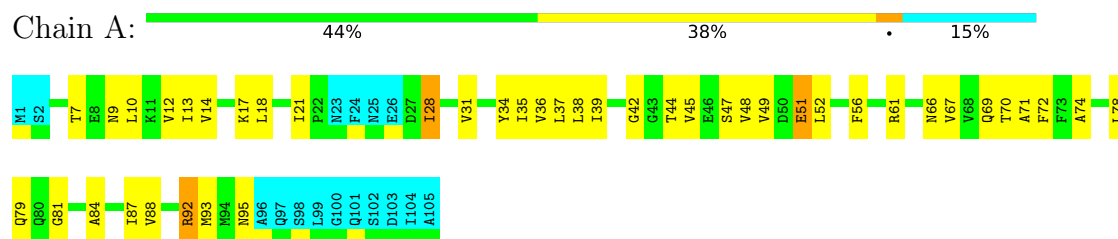
4.2.43 Score per residue for model 43

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



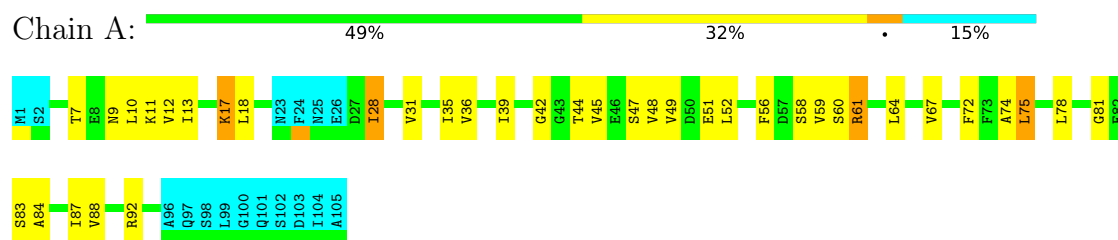
4.2.44 Score per residue for model 44

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



4.2.45 Score per residue for model 45

- Molecule 1: Nuclear polyadenylated RNA-binding protein NAB2



5 Refinement protocol and experimental data overview

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

Of the 50 calculated structures, 45 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
X-PLOR	structure solution	
X-PLOR	refinement	

No chemical shift data was provided.

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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

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	2.0±0.0
All	All	0	90

There are no bond-length outliers.

There are no bond-angle outliers.

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	61	ARG	Sidechain	45
1	A	92	ARG	Sidechain	45

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	685	696	696	37±4
All	All	30825	31320	31320	1681

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 27.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:13:ILE:HG21	1:A:74:ALA:HB2	0.94	1.36	27	32
1:A:31:VAL:HG23	1:A:56:PHE:CE2	0.89	2.03	12	34
1:A:13:ILE:HD13	1:A:74:ALA:HB1	0.89	1.43	23	24
1:A:31:VAL:HG23	1:A:56:PHE:CZ	0.87	2.04	31	18
1:A:18:LEU:HD21	1:A:31:VAL:HG12	0.81	1.51	45	6
1:A:7:THR:HG23	1:A:36:VAL:HG11	0.78	1.56	10	42
1:A:9:ASN:CB	1:A:78:LEU:HD21	0.77	2.09	40	19
1:A:10:LEU:HD23	1:A:36:VAL:HG13	0.77	1.55	5	17
1:A:28:ILE:O	1:A:28:ILE:HD13	0.75	1.81	17	44
1:A:13:ILE:HG21	1:A:74:ALA:CB	0.74	2.13	45	8
1:A:10:LEU:O	1:A:14:VAL:HG23	0.73	1.83	24	41
1:A:18:LEU:CD1	1:A:67:VAL:HG21	0.73	2.14	39	5
1:A:18:LEU:HD13	1:A:31:VAL:HG13	0.72	1.60	1	18
1:A:17:LYS:HB3	1:A:67:VAL:HG22	0.72	1.62	40	2
1:A:10:LEU:CD1	1:A:39:ILE:HG21	0.71	2.14	11	2
1:A:31:VAL:HG22	1:A:56:PHE:CZ	0.71	2.20	8	6
1:A:18:LEU:HA	1:A:21:ILE:HD12	0.71	1.63	8	43
1:A:12:VAL:HB	1:A:84:ALA:HB1	0.70	1.61	43	45
1:A:39:ILE:CG2	1:A:75:LEU:HD12	0.70	2.17	21	4
1:A:13:ILE:HD13	1:A:74:ALA:CB	0.70	2.17	19	5
1:A:60:SER:O	1:A:64:LEU:HD12	0.70	1.87	22	11
1:A:45:VAL:HG23	1:A:72:PHE:CE2	0.69	2.22	7	27
1:A:18:LEU:CD2	1:A:67:VAL:HG21	0.69	2.16	1	21
1:A:36:VAL:O	1:A:40:VAL:HG23	0.69	1.88	30	21
1:A:10:LEU:HD11	1:A:75:LEU:HD13	0.69	1.64	27	1
1:A:7:THR:HG23	1:A:36:VAL:CG1	0.68	2.19	10	43
1:A:9:ASN:O	1:A:13:ILE:HD12	0.68	1.87	27	27
1:A:21:ILE:HD11	1:A:67:VAL:CG2	0.68	2.18	44	10
1:A:18:LEU:CD1	1:A:67:VAL:HG11	0.67	2.19	42	6
1:A:12:VAL:HG11	1:A:84:ALA:O	0.67	1.89	45	41
1:A:18:LEU:HD11	1:A:31:VAL:CG1	0.67	2.20	44	1
1:A:9:ASN:HB3	1:A:78:LEU:HD21	0.66	1.67	41	17
1:A:18:LEU:HD13	1:A:31:VAL:CG1	0.66	2.20	1	3
1:A:18:LEU:HD13	1:A:67:VAL:HG11	0.66	1.67	44	6
1:A:7:THR:HG23	1:A:36:VAL:HG12	0.66	1.68	45	16
1:A:18:LEU:HD21	1:A:35:ILE:CD1	0.66	2.20	43	1
1:A:27:ASP:O	1:A:31:VAL:HG23	0.65	1.90	39	4
1:A:10:LEU:CD2	1:A:39:ILE:HG21	0.65	2.21	45	18
1:A:18:LEU:HD21	1:A:35:ILE:HD12	0.64	1.68	43	2
1:A:84:ALA:HA	1:A:87:ILE:HD12	0.64	1.68	16	24
1:A:10:LEU:HD22	1:A:75:LEU:HD21	0.64	1.68	43	13
1:A:52:LEU:HB3	1:A:64:LEU:HD23	0.64	1.69	23	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:10:LEU:CD1	1:A:74:ALA:HB3	0.63	2.24	32	12
1:A:17:LYS:CG	1:A:67:VAL:HG22	0.63	2.23	39	2
1:A:35:ILE:HD13	1:A:67:VAL:CG1	0.63	2.23	24	36
1:A:10:LEU:HD11	1:A:75:LEU:HG	0.63	1.70	23	3
1:A:34:TYR:CE2	1:A:38:LEU:HD11	0.62	2.29	31	2
1:A:18:LEU:CD2	1:A:31:VAL:HG12	0.62	2.24	45	4
1:A:10:LEU:HD11	1:A:71:ALA:HA	0.62	1.69	33	15
1:A:44:THR:O	1:A:48:VAL:HG23	0.62	1.95	45	42
1:A:48:VAL:HG11	1:A:68:VAL:HG13	0.62	1.70	32	18
1:A:9:ASN:CB	1:A:78:LEU:HD11	0.61	2.25	24	6
1:A:18:LEU:HD23	1:A:67:VAL:HG21	0.61	1.71	1	3
1:A:61:ARG:HA	1:A:64:LEU:HD12	0.61	1.70	31	4
1:A:7:THR:OG1	1:A:40:VAL:HG21	0.61	1.95	29	3
1:A:9:ASN:HB2	1:A:78:LEU:HD11	0.60	1.72	24	6
1:A:39:ILE:CG2	1:A:75:LEU:HD22	0.60	2.25	22	2
1:A:18:LEU:HD21	1:A:31:VAL:CG1	0.60	2.25	44	2
1:A:9:ASN:HB2	1:A:78:LEU:HD21	0.60	1.73	1	10
1:A:10:LEU:HD23	1:A:14:VAL:HG23	0.60	1.72	19	3
1:A:77:ALA:HB1	1:A:82:GLU:HG3	0.60	1.74	28	5
1:A:45:VAL:O	1:A:49:VAL:HG23	0.59	1.97	40	44
1:A:16:GLU:OE2	1:A:87:ILE:HG23	0.59	1.97	20	10
1:A:17:LYS:HG2	1:A:67:VAL:HG22	0.59	1.73	45	2
1:A:18:LEU:HD12	1:A:67:VAL:HG21	0.59	1.75	45	2
1:A:18:LEU:HD11	1:A:67:VAL:HG11	0.59	1.74	42	2
1:A:18:LEU:HB2	1:A:28:ILE:HD11	0.59	1.75	5	13
1:A:39:ILE:HG21	1:A:75:LEU:HD21	0.59	1.74	17	13
1:A:45:VAL:HG22	1:A:72:PHE:CE2	0.59	2.33	34	3
1:A:10:LEU:HD11	1:A:39:ILE:HG21	0.58	1.74	11	1
1:A:38:LEU:HD22	1:A:51:GLU:OE1	0.58	1.98	15	2
1:A:32:ALA:HA	1:A:35:ILE:HD12	0.58	1.74	31	12
1:A:17:LYS:CB	1:A:67:VAL:HG22	0.58	2.29	40	2
1:A:10:LEU:HD11	1:A:75:LEU:CD2	0.58	2.28	2	4
1:A:39:ILE:HG23	1:A:75:LEU:HD12	0.58	1.76	21	3
1:A:71:ALA:O	1:A:75:LEU:HD23	0.58	1.99	25	16
1:A:35:ILE:HD13	1:A:67:VAL:HG11	0.57	1.75	24	18
1:A:34:TYR:CE2	1:A:55:LEU:HD12	0.57	2.34	10	2
1:A:10:LEU:HD13	1:A:75:LEU:HD22	0.57	1.75	25	4
1:A:18:LEU:HD22	1:A:31:VAL:HG11	0.57	1.76	36	8
1:A:12:VAL:HG13	1:A:88:VAL:CG2	0.57	2.30	44	43
1:A:18:LEU:HD11	1:A:35:ILE:HD12	0.57	1.76	9	17
1:A:18:LEU:HD11	1:A:31:VAL:HG11	0.57	1.77	44	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:7:THR:HA	1:A:36:VAL:HG11	0.57	1.75	5	2
1:A:9:ASN:CG	1:A:78:LEU:HD21	0.56	2.20	23	1
1:A:77:ALA:HB1	1:A:82:GLU:OE1	0.56	2.01	40	2
1:A:12:VAL:HG13	1:A:88:VAL:HG23	0.55	1.76	25	19
1:A:10:LEU:HD23	1:A:14:VAL:CG2	0.55	2.31	19	2
1:A:67:VAL:O	1:A:70:THR:HG22	0.55	2.01	28	41
1:A:34:TYR:CZ	1:A:38:LEU:HD11	0.55	2.36	31	4
1:A:31:VAL:HG13	1:A:56:PHE:CE2	0.55	2.36	43	1
1:A:12:VAL:CB	1:A:84:ALA:HB1	0.54	2.30	43	38
1:A:18:LEU:HD11	1:A:35:ILE:CD1	0.54	2.32	2	17
1:A:13:ILE:CG2	1:A:74:ALA:HB2	0.54	2.23	27	2
1:A:18:LEU:HD23	1:A:28:ILE:O	0.54	2.01	44	1
1:A:77:ALA:HB1	1:A:82:GLU:CD	0.54	2.22	40	2
1:A:31:VAL:HG22	1:A:56:PHE:CE2	0.54	2.38	22	7
1:A:11:LYS:HG2	1:A:36:VAL:HG21	0.54	1.80	11	1
1:A:18:LEU:HB3	1:A:28:ILE:HD11	0.54	1.79	44	1
1:A:52:LEU:HB3	1:A:64:LEU:HD22	0.54	1.79	31	2
1:A:11:LYS:HA	1:A:36:VAL:HG21	0.54	1.79	45	3
1:A:11:LYS:CG	1:A:36:VAL:HG21	0.54	2.33	14	2
1:A:39:ILE:CG2	1:A:75:LEU:HD11	0.53	2.33	33	14
1:A:48:VAL:CG1	1:A:68:VAL:HG13	0.53	2.34	32	13
1:A:17:LYS:CD	1:A:70:THR:HG21	0.53	2.34	42	1
1:A:31:VAL:HG12	1:A:35:ILE:CD1	0.52	2.34	36	2
1:A:18:LEU:CD1	1:A:32:ALA:HB2	0.52	2.34	31	3
1:A:78:LEU:O	1:A:78:LEU:HD23	0.52	2.04	36	1
1:A:10:LEU:HD21	1:A:71:ALA:HB1	0.52	1.81	19	2
1:A:59:VAL:HG22	1:A:63:THR:HB	0.52	1.81	31	1
1:A:78:LEU:O	1:A:78:LEU:HD13	0.52	2.04	22	1
1:A:21:ILE:HD13	1:A:63:THR:HG23	0.52	1.82	23	1
1:A:34:TYR:CZ	1:A:38:LEU:HD21	0.52	2.40	31	1
1:A:13:ILE:CG1	1:A:87:ILE:HD13	0.52	2.34	37	1
1:A:21:ILE:HG21	1:A:63:THR:CG2	0.51	2.35	14	4
1:A:9:ASN:HB3	1:A:78:LEU:HD11	0.51	1.82	5	5
1:A:28:ILE:HD13	1:A:28:ILE:C	0.51	2.25	26	44
1:A:77:ALA:HB1	1:A:82:GLU:OE2	0.51	2.05	15	2
1:A:17:LYS:HB2	1:A:70:THR:HG21	0.51	1.81	33	5
1:A:18:LEU:CD2	1:A:31:VAL:HG11	0.51	2.36	8	4
1:A:48:VAL:HG12	1:A:68:VAL:CG2	0.51	2.35	17	1
1:A:13:ILE:HG21	1:A:74:ALA:HB1	0.51	1.82	45	2
1:A:10:LEU:HD11	1:A:75:LEU:HD21	0.50	1.82	9	5
1:A:44:THR:OG1	1:A:47:SER:OG	0.50	2.28	32	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:18:LEU:HD22	1:A:31:VAL:CG1	0.50	2.36	31	5
1:A:13:ILE:HG22	1:A:70:THR:OG1	0.50	2.07	23	1
1:A:6:TYR:CD1	1:A:78:LEU:HD12	0.50	2.42	34	1
1:A:35:ILE:HD13	1:A:67:VAL:HG12	0.49	1.83	8	9
1:A:19:ALA:N	1:A:28:ILE:HD11	0.49	2.23	17	12
1:A:64:LEU:O	1:A:68:VAL:HG23	0.49	2.07	21	2
1:A:14:VAL:HG12	1:A:18:LEU:CD1	0.49	2.38	3	7
1:A:13:ILE:CD1	1:A:74:ALA:HB1	0.48	2.31	19	1
1:A:10:LEU:HD11	1:A:71:ALA:CA	0.48	2.38	33	5
1:A:39:ILE:CG2	1:A:75:LEU:HD21	0.48	2.37	28	9
1:A:18:LEU:HD13	1:A:67:VAL:CG1	0.48	2.38	41	2
1:A:17:LYS:HG3	1:A:70:THR:HG21	0.48	1.85	43	3
1:A:10:LEU:HD21	1:A:39:ILE:HG21	0.48	1.85	28	7
1:A:10:LEU:HD13	1:A:39:ILE:HG21	0.47	1.86	11	1
1:A:59:VAL:HG13	1:A:64:LEU:HD11	0.47	1.84	30	2
1:A:45:VAL:HG22	1:A:72:PHE:CD2	0.47	2.45	34	1
1:A:34:TYR:CE1	1:A:38:LEU:HD11	0.47	2.44	22	2
1:A:10:LEU:HD22	1:A:39:ILE:HG21	0.47	1.85	43	3
1:A:10:LEU:HG	1:A:36:VAL:HG22	0.47	1.87	36	1
1:A:18:LEU:CD1	1:A:31:VAL:HG13	0.47	2.36	1	3
1:A:28:ILE:O	1:A:31:VAL:HG12	0.47	2.10	26	4
1:A:44:THR:OG1	1:A:47:SER:CB	0.47	2.62	42	3
1:A:44:THR:HG1	1:A:47:SER:HG	0.47	1.52	38	2
1:A:39:ILE:CD1	1:A:72:PHE:CE1	0.47	2.98	1	24
1:A:10:LEU:HD13	1:A:75:LEU:CD2	0.47	2.40	43	1
1:A:7:THR:CG2	1:A:36:VAL:HG11	0.46	2.38	44	5
1:A:34:TYR:OH	1:A:51:GLU:CG	0.46	2.63	23	15
1:A:39:ILE:HD13	1:A:72:PHE:CZ	0.46	2.45	34	1
1:A:18:LEU:CB	1:A:28:ILE:HD11	0.46	2.40	5	7
1:A:45:VAL:CG2	1:A:72:PHE:CE2	0.45	2.99	38	3
1:A:39:ILE:HG13	1:A:71:ALA:HB1	0.45	1.88	31	3
1:A:59:VAL:HG12	1:A:63:THR:HB	0.45	1.88	42	2
1:A:34:TYR:CE1	1:A:38:LEU:HD21	0.45	2.46	29	3
1:A:31:VAL:CG2	1:A:56:PHE:CE2	0.45	2.98	20	9
1:A:12:VAL:CG1	1:A:88:VAL:HG23	0.45	2.42	25	35
1:A:10:LEU:HD21	1:A:71:ALA:O	0.45	2.11	23	1
1:A:14:VAL:HG12	1:A:18:LEU:HD12	0.45	1.88	3	2
1:A:34:TYR:CD2	1:A:52:LEU:HD23	0.45	2.47	21	3
1:A:52:LEU:N	1:A:52:LEU:HD22	0.45	2.27	44	4
1:A:37:LEU:HA	1:A:40:VAL:HG12	0.45	1.87	33	1
1:A:7:THR:HG22	1:A:11:LYS:NZ	0.45	2.27	25	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:14:VAL:HG13	1:A:35:ILE:HG21	0.44	1.89	40	1
1:A:11:LYS:CA	1:A:36:VAL:HG21	0.44	2.40	45	1
1:A:39:ILE:HG21	1:A:75:LEU:CD2	0.44	2.42	41	3
1:A:35:ILE:HA	1:A:38:LEU:HD12	0.44	1.90	30	2
1:A:52:LEU:HD12	1:A:68:VAL:CG2	0.44	2.42	37	1
1:A:12:VAL:HG11	1:A:84:ALA:C	0.43	2.32	25	3
1:A:48:VAL:O	1:A:52:LEU:HD12	0.43	2.13	39	2
1:A:10:LEU:HD21	1:A:71:ALA:CB	0.43	2.43	19	1
1:A:77:ALA:HB3	1:A:82:GLU:OE2	0.43	2.14	33	1
1:A:38:LEU:HD21	1:A:51:GLU:HG2	0.43	1.91	30	4
1:A:10:LEU:CD2	1:A:74:ALA:HB3	0.43	2.44	23	1
1:A:40:VAL:HG13	1:A:41:ASN:ND2	0.43	2.29	31	1
1:A:35:ILE:HG12	1:A:52:LEU:HD11	0.43	1.88	8	1
1:A:43:GLY:HA3	1:A:48:VAL:HG23	0.43	1.90	34	1
1:A:18:LEU:CG	1:A:67:VAL:HG11	0.43	2.44	36	1
1:A:10:LEU:HD21	1:A:75:LEU:HD22	0.43	1.91	38	1
1:A:66:ASN:O	1:A:70:THR:HG23	0.43	2.14	44	1
1:A:48:VAL:HG12	1:A:68:VAL:HG22	0.42	1.91	17	1
1:A:52:LEU:HD22	1:A:68:VAL:CG2	0.42	2.44	31	1
1:A:14:VAL:HG21	1:A:36:VAL:HG22	0.42	1.92	37	2
1:A:6:TYR:CD2	1:A:78:LEU:HD23	0.42	2.50	19	2
1:A:6:TYR:CD1	1:A:78:LEU:HD22	0.42	2.50	36	1
1:A:12:VAL:CG1	1:A:88:VAL:CG2	0.42	2.98	37	1
1:A:34:TYR:CE2	1:A:55:LEU:CD1	0.42	3.02	10	2
1:A:16:GLU:OE2	1:A:87:ILE:HD12	0.42	2.15	38	1
1:A:3:GLN:HB2	1:A:40:VAL:HG13	0.42	1.90	11	1
1:A:31:VAL:CG1	1:A:35:ILE:HD11	0.42	2.45	36	1
1:A:16:GLU:CB	1:A:87:ILE:CG2	0.41	2.98	41	1
1:A:39:ILE:CG2	1:A:75:LEU:CD1	0.41	2.99	4	8
1:A:13:ILE:HG12	1:A:87:ILE:HD13	0.41	1.90	37	1
1:A:32:ALA:O	1:A:36:VAL:HG23	0.41	2.15	8	1
1:A:18:LEU:CD2	1:A:31:VAL:CG1	0.41	2.98	39	3
1:A:45:VAL:HG23	1:A:72:PHE:CZ	0.41	2.50	29	1
1:A:10:LEU:HD12	1:A:75:LEU:HG	0.41	1.91	19	1
1:A:37:LEU:O	1:A:40:VAL:HG12	0.41	2.16	21	1
1:A:51:GLU:O	1:A:54:SER:OG	0.41	2.38	33	1
1:A:34:TYR:OH	1:A:51:GLU:HG2	0.41	2.16	27	4
1:A:10:LEU:HB3	1:A:36:VAL:HG22	0.41	1.92	38	1
1:A:17:LYS:CB	1:A:70:THR:HG21	0.41	2.46	33	1
1:A:52:LEU:HD22	1:A:52:LEU:N	0.41	2.30	40	1
1:A:19:ALA:N	1:A:28:ILE:HD13	0.41	2.31	43	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:44:THR:O	1:A:46:GLU:N	0.40	2.55	34	1
1:A:17:LYS:O	1:A:21:ILE:HD12	0.40	2.16	40	1
1:A:3:GLN:OE1	1:A:6:TYR:CD1	0.40	2.75	8	2
1:A:16:GLU:CG	1:A:87:ILE:CG2	0.40	3.00	17	2
1:A:44:THR:OG1	1:A:47:SER:HB3	0.40	2.16	13	1
1:A:43:GLY:O	1:A:44:THR:OG1	0.40	2.36	34	1
1:A:52:LEU:CD1	1:A:68:VAL:CG2	0.40	3.00	4	3
1:A:10:LEU:CD2	1:A:14:VAL:CG2	0.40	2.99	11	1
1:A:44:THR:OG1	1:A:47:SER:HB2	0.40	2.16	33	1
1:A:18:LEU:CD2	1:A:32:ALA:N	0.40	2.84	42	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	89/105 (85%)	84±1 (95±1%)	3±1 (4±1%)	1±1 (2±1%)	13	57
All	All	4005/4725 (85%)	3786 (95%)	153 (4%)	66 (2%)	13	57

All 3 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	42	GLY	44
1	A	81	GLY	21
1	A	27	ASP	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	76/89 (85%)	68±2 (89±3%)	8±2 (11±3%)	9	53
All	All	3420/4005 (85%)	3041 (89%)	379 (11%)	9	53

All 41 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	28	ILE	45
1	A	51	GLU	39
1	A	17	LYS	36
1	A	47	SER	34
1	A	37	LEU	19
1	A	60	SER	17
1	A	82	GLU	14
1	A	11	LYS	14
1	A	55	LEU	13
1	A	93	MET	12
1	A	27	ASP	11
1	A	61	ARG	11
1	A	92	ARG	10
1	A	79	GLN	10
1	A	78	LEU	10
1	A	58	SER	8
1	A	29	LYS	8
1	A	90	LYS	7
1	A	57	ASP	6
1	A	80	GLN	5
1	A	83	SER	5
1	A	50	ASP	5
1	A	62	ASP	5
1	A	75	LEU	4
1	A	94	MET	4
1	A	46	GLU	3
1	A	95	ASN	3
1	A	4	GLU	3
1	A	18	LEU	3
1	A	85	GLU	2
1	A	5	GLN	2
1	A	64	LEU	2
1	A	33	GLU	1
1	A	10	LEU	1
1	A	44	THR	1
1	A	8	GLU	1

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Mol	Chain	Res	Type	Models (Total)
1	A	54	SER	1
1	A	66	ASN	1
1	A	88	VAL	1
1	A	16	GLU	1
1	A	69	GLN	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

No chemical shift data were provided