



Full wwPDB NMR Structure Validation Report ⓘ

May 29, 2020 – 12:03 am BST

PDB ID : 2MOW
Title : Structure of Nrd1p CID - Trf4p NIM complex
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Deposited on : 2014-05-06

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : 2.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

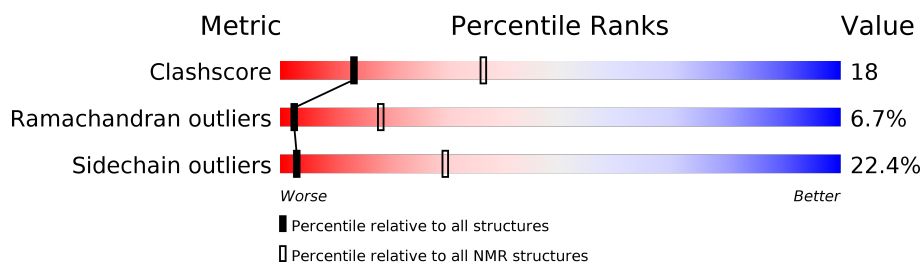
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 69%.

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	161	
2	B	12	

2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 8 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:6-A:20, A:24-A:85, A:91-A:134, A:144-A:152, B:1008-B:1010 (133)	0.32	8

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2722 atoms, of which 1339 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Protein NRD1.

Mol	Chain	Residues	Atoms						Trace
1	A	161	Total	C	H	N	O	S	0
			2549	801	1265	228	249	6	

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	154	LEU	-	EXPRESSION TAG	UNP P53617
A	155	GLU	-	EXPRESSION TAG	UNP P53617
A	156	HIS	-	EXPRESSION TAG	UNP P53617
A	157	HIS	-	EXPRESSION TAG	UNP P53617
A	158	HIS	-	EXPRESSION TAG	UNP P53617
A	159	HIS	-	EXPRESSION TAG	UNP P53617
A	160	HIS	-	EXPRESSION TAG	UNP P53617
A	161	HIS	-	EXPRESSION TAG	UNP P53617

- Molecule 2 is a protein called Poly(A) RNA polymerase protein 2.

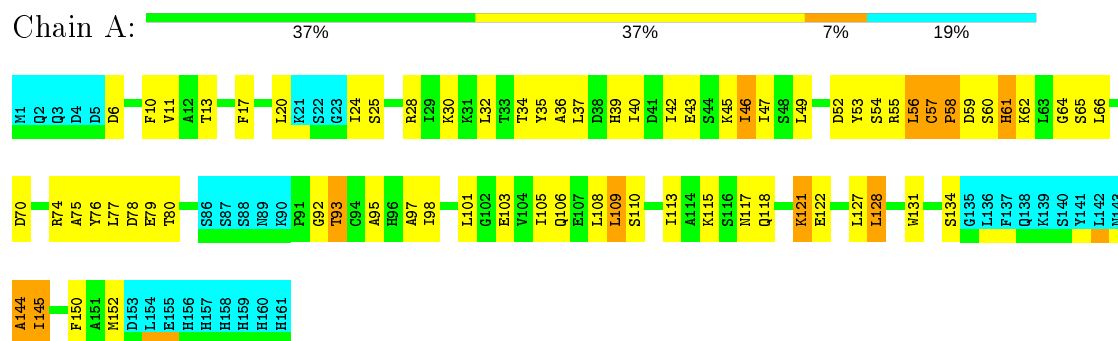
Mol	Chain	Residues	Atoms					Trace
2	B	12	Total	C	H	N	O	0
			173	60	74	13	26	

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 NRD1



• Molecule 2: Poly(A) RNA polymerase protein 2

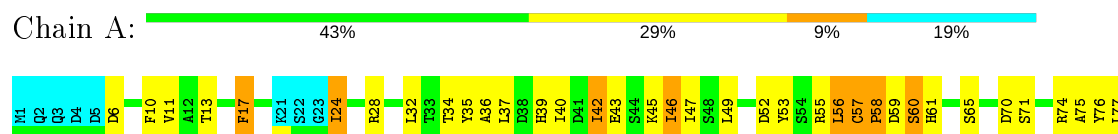


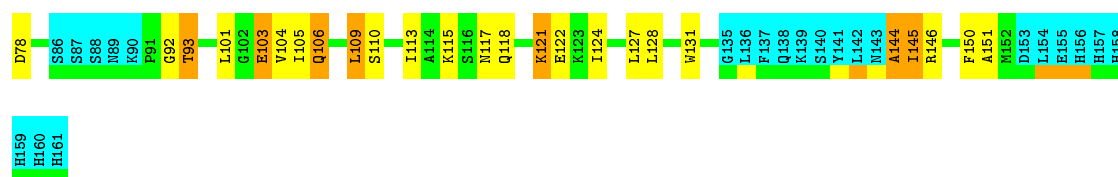
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

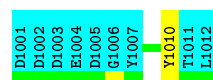
4.2.1 Score per residue for model 1

• Molecule 1: Protein NRD1



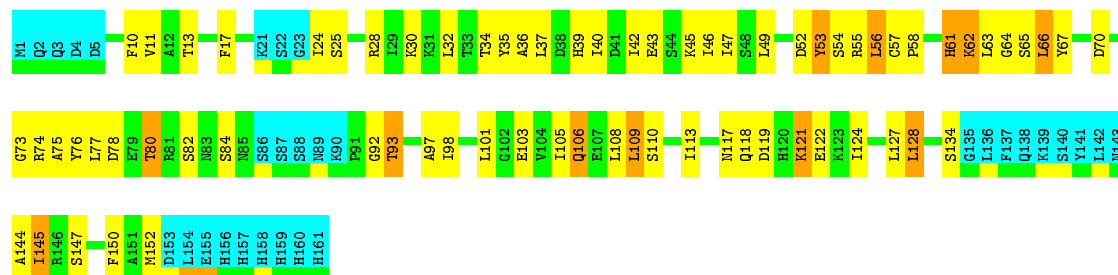
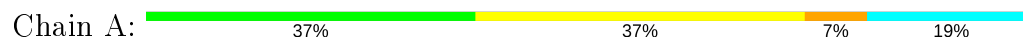


- Molecule 2: Poly(A) RNA polymerase protein 2



4.2.2 Score per residue for model 2

- Molecule 1: Protein NRD1

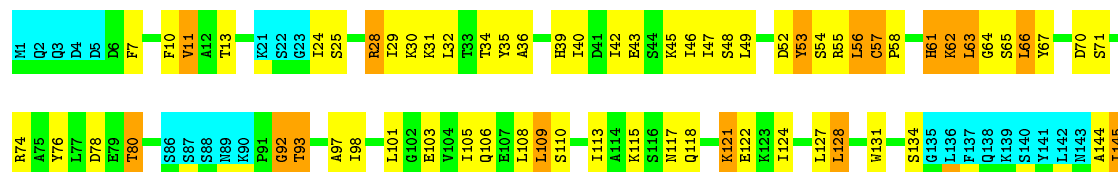


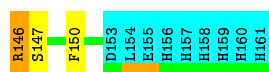
- Molecule 2: Poly(A) RNA polymerase protein 2



4.2.3 Score per residue for model 3

- Molecule 1: Protein NRD1



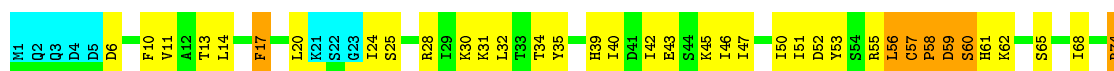


- Molecule 2: Poly(A) RNA polymerase protein 2

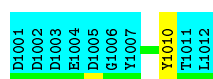


4.2.4 Score per residue for model 4

- Molecule 1: Protein NRD1

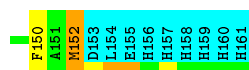
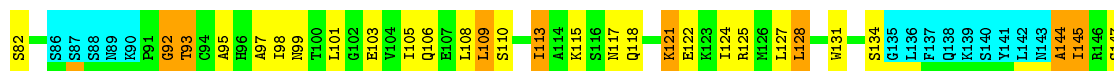


- Molecule 2: Poly(A) RNA polymerase protein 2



4.2.5 Score per residue for model 5

- Molecule 1: Protein NRD1

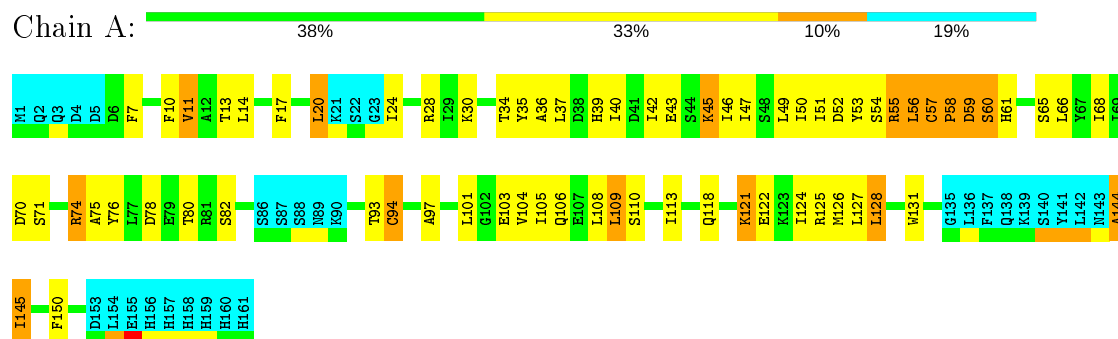


- Molecule 2: Poly(A) RNA polymerase protein 2



4.2.6 Score per residue for model 6

- Molecule 1: Protein NRD1

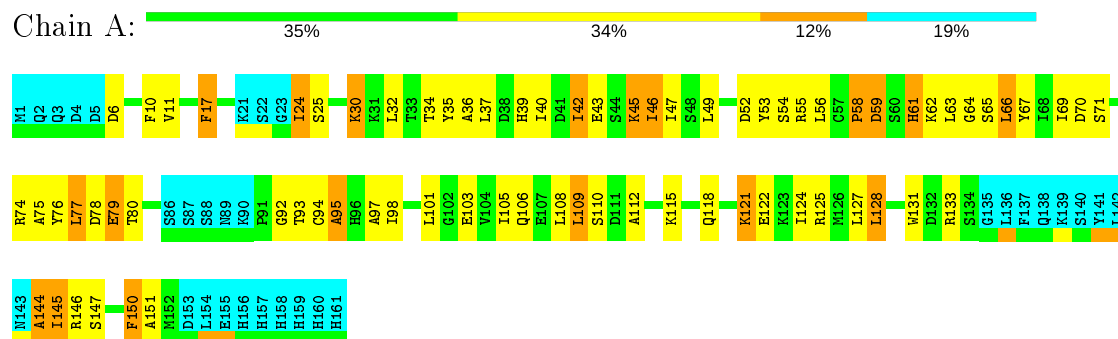


- Molecule 2: Poly(A) RNA polymerase protein 2



4.2.7 Score per residue for model 7

- Molecule 1: Protein NRD1

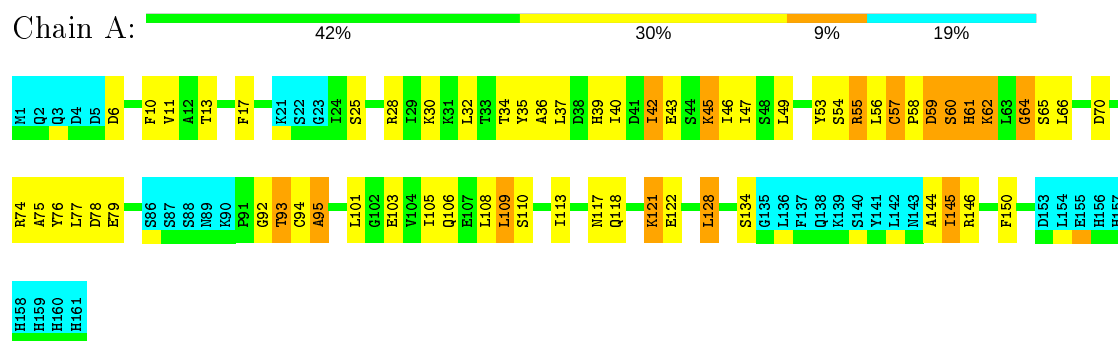


- Molecule 2: Poly(A) RNA polymerase protein 2



4.2.8 Score per residue for model 8 (medoid)

- Molecule 1: Protein NRD1

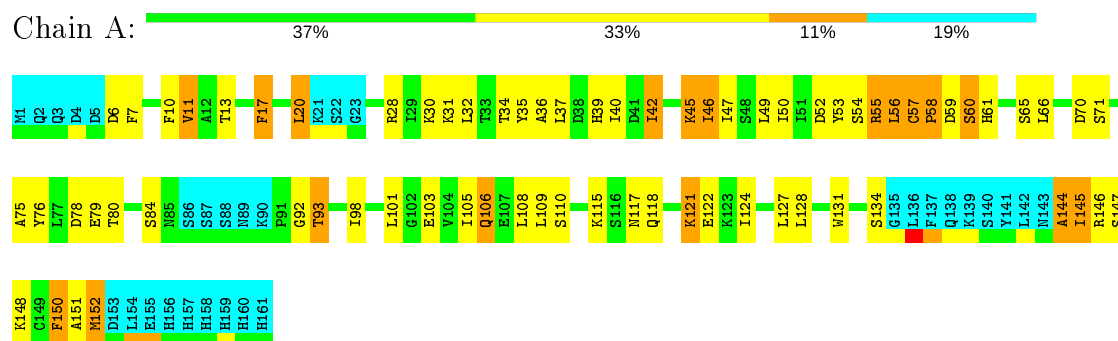


- Molecule 2: Poly(A) RNA polymerase protein 2



4.2.9 Score per residue for model 9

- Molecule 1: Protein NRD1

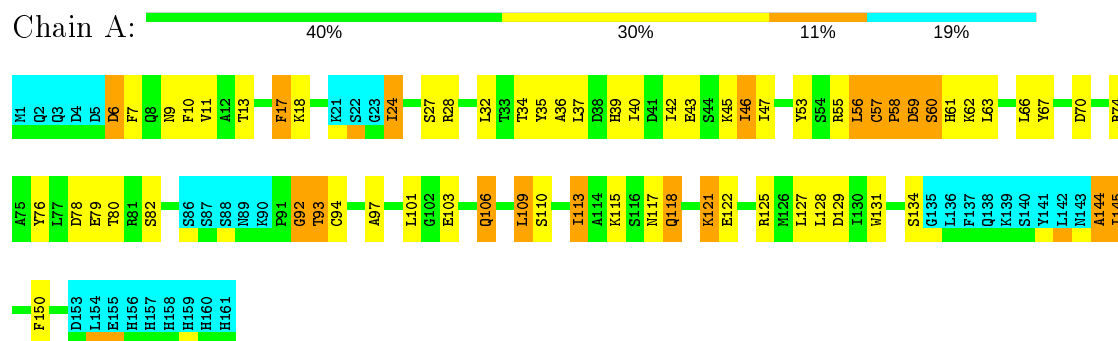


- Molecule 2: Poly(A) RNA polymerase protein 2



4.2.10 Score per residue for model 10

- Molecule 1: Protein NRD1

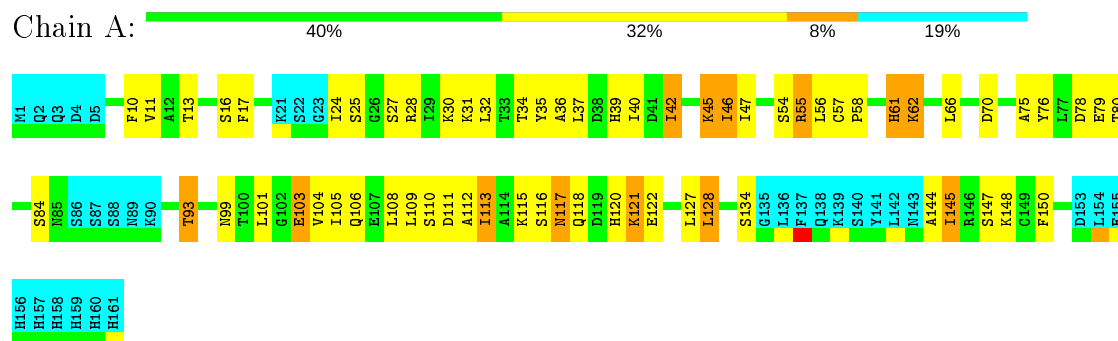


- Molecule 2: Poly(A) RNA polymerase protein 2



4.2.11 Score per residue for model 11

- Molecule 1: Protein NRD1

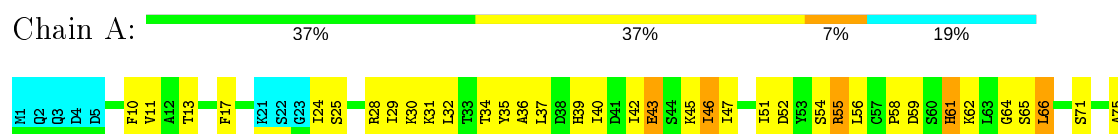


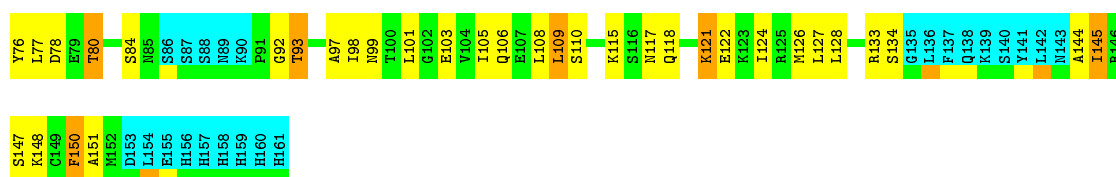
- Molecule 2: Poly(A) RNA polymerase protein 2



4.2.12 Score per residue for model 12

- Molecule 1: Protein NRD1



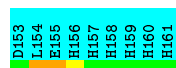
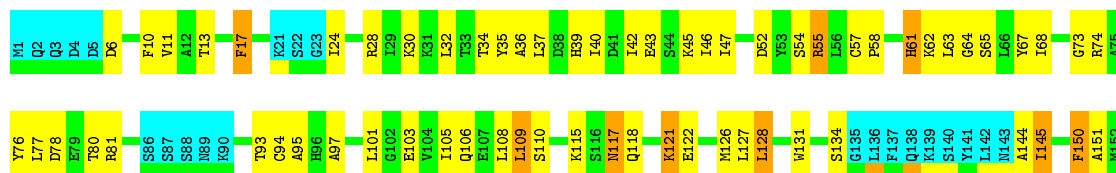


- Molecule 2: Poly(A) RNA polymerase protein 2



4.2.13 Score per residue for model 13

- Molecule 1: Protein NRD1

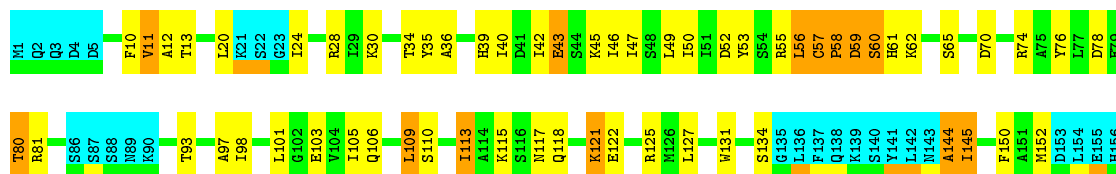


- Molecule 2: Poly(A) RNA polymerase protein 2



4.2.14 Score per residue for model 14

- Molecule 1: Protein NRD1



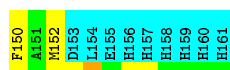
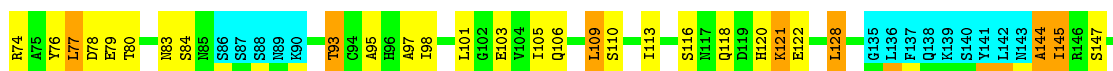


- Molecule 2: Poly(A) RNA polymerase protein 2



4.2.15 Score per residue for model 15

- Molecule 1: Protein NRD1

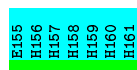


- Molecule 2: Poly(A) RNA polymerase protein 2



4.2.16 Score per residue for model 16

- Molecule 1: Protein NRD1

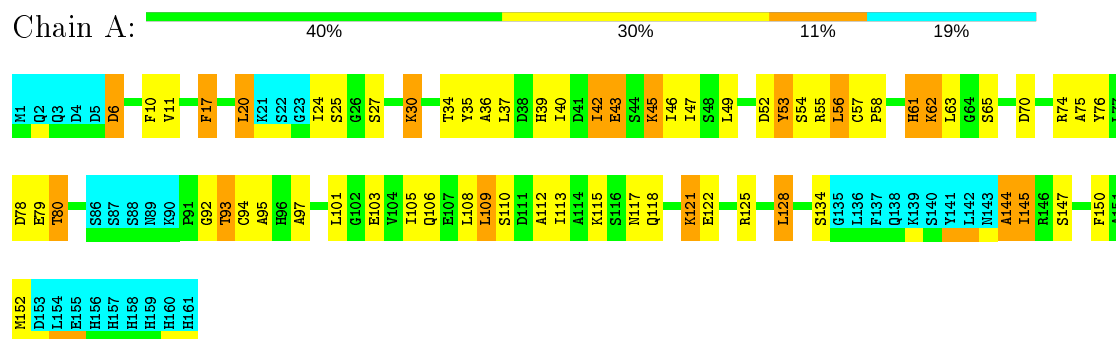


- Molecule 2: Poly(A) RNA polymerase protein 2



4.2.17 Score per residue for model 17

- Molecule 1: Protein NRD1

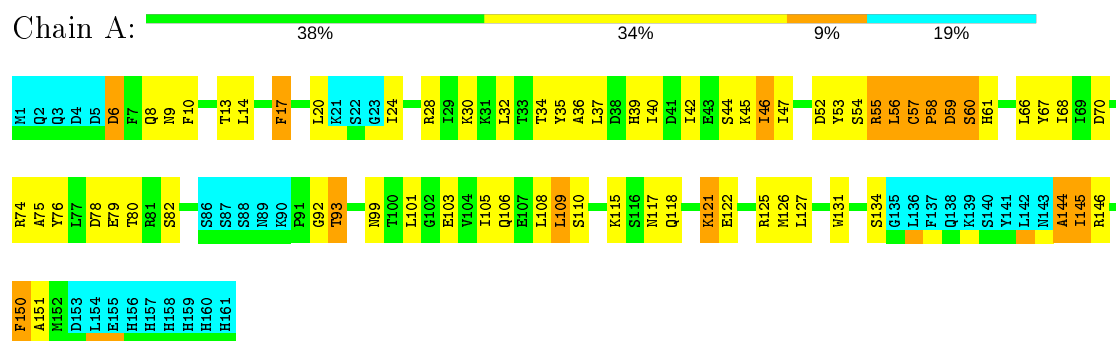


- Molecule 2: Poly(A) RNA polymerase protein 2



4.2.18 Score per residue for model 18

- Molecule 1: Protein NRD1

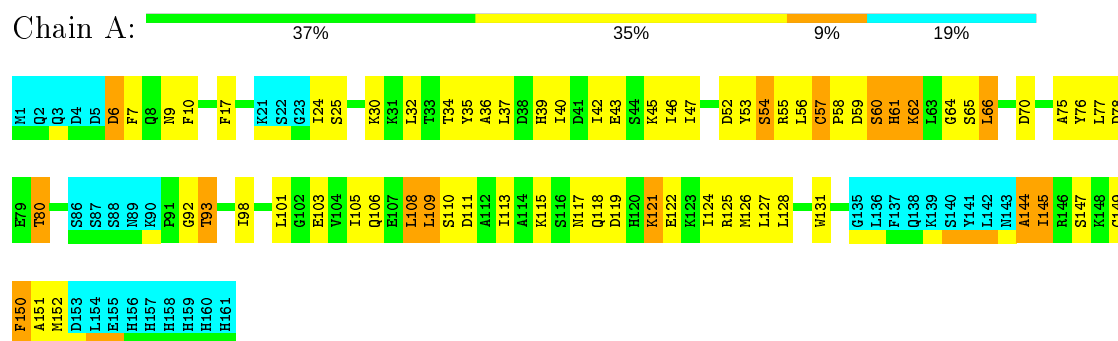


- Molecule 2: Poly(A) RNA polymerase protein 2



4.2.19 Score per residue for model 19

- Molecule 1: Protein NRD1

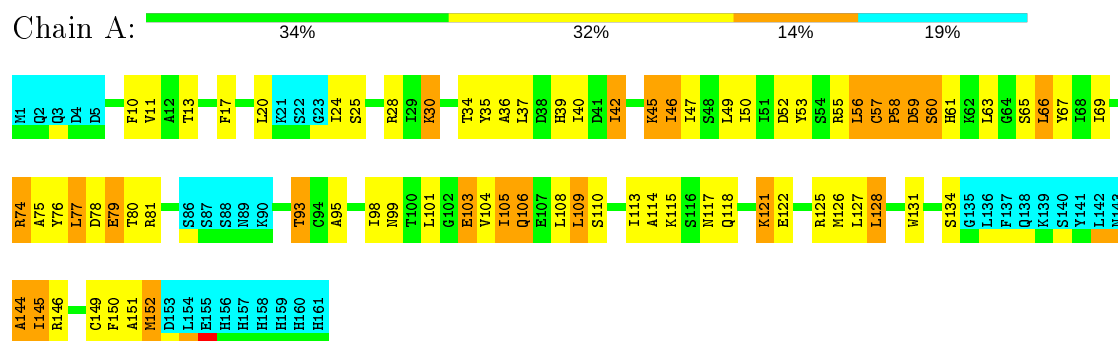


- Molecule 2: Poly(A) RNA polymerase protein 2



4.2.20 Score per residue for model 20

- Molecule 1: Protein NRD1



- Molecule 2: Poly(A) RNA polymerase protein 2



5 Refinement protocol and experimental data overview

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
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)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	1475
Number of shifts mapped to atoms	1475
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	69%

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

6 Model quality

6.1 Standard geometry

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

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	1028	1039	1039	39±5
2	B	27	22	22	0±0
All	All	21100	21220	21220	776

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 18.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:128:LEU:HD11	1:A:145:ILE:HG21	0.85	1.46	12	6
1:A:17:PHE:O	1:A:20:LEU:HD22	0.84	1.71	9	3
1:A:109:LEU:HD22	1:A:128:LEU:HD11	0.83	1.50	9	2
1:A:47:ILE:HD12	1:A:101:LEU:HD11	0.82	1.47	20	20
1:A:109:LEU:HD13	1:A:145:ILE:HD12	0.82	1.49	12	12
1:A:150:PHE:CG	1:A:151:ALA:N	0.71	2.58	16	3
1:A:106:GLN:HA	1:A:144:ALA:HB2	0.71	1.61	9	2
1:A:20:LEU:C	1:A:20:LEU:HD23	0.71	2.06	6	2
1:A:105:ILE:HG13	1:A:109:LEU:HD12	0.70	1.64	18	18
1:A:10:PHE:CZ	1:A:46:ILE:HG23	0.69	2.22	13	20
1:A:37:LEU:HD21	1:A:75:ALA:HB1	0.68	1.66	7	10
1:A:63:LEU:HD12	1:A:67:TYR:CE2	0.67	2.25	3	1
1:A:105:ILE:CG1	1:A:109:LEU:HD12	0.66	2.20	13	17

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:20:LEU:HD23	1:A:20:LEU:O	0.66	1.91	6	2
1:A:150:PHE:CD1	1:A:151:ALA:N	0.66	2.64	20	3
1:A:66:LEU:HD22	1:A:127:LEU:HD23	0.65	1.69	2	5
1:A:66:LEU:CD2	1:A:127:LEU:HD23	0.65	2.22	19	4
1:A:62:LYS:O	1:A:66:LEU:HD12	0.65	1.91	3	8
1:A:128:LEU:HD11	1:A:145:ILE:HG13	0.64	1.70	4	6
1:A:37:LEU:HD11	1:A:75:ALA:CB	0.64	2.23	11	13
1:A:17:PHE:CD2	1:A:68:ILE:HD11	0.63	2.27	4	3
1:A:128:LEU:HD11	1:A:145:ILE:CB	0.63	2.24	8	6
1:A:54:SER:OG	1:A:55:ARG:N	0.62	2.32	5	13
1:A:127:LEU:HD12	2:B:1009:PRO:HG3	0.62	1.71	20	4
1:A:20:LEU:O	1:A:20:LEU:HD23	0.62	1.95	9	1
1:A:150:PHE:CE1	1:A:151:ALA:HB2	0.62	2.30	16	2
1:A:36:ALA:HB1	1:A:76:TYR:OH	0.61	1.95	3	18
1:A:109:LEU:HD13	1:A:145:ILE:CD1	0.61	2.26	13	8
1:A:53:TYR:HA	1:A:56:LEU:HD12	0.60	1.73	17	12
1:A:20:LEU:HD23	1:A:20:LEU:C	0.60	2.17	9	1
1:A:54:SER:O	1:A:61:HIS:CG	0.60	2.54	11	11
1:A:76:TYR:O	1:A:80:THR:HG22	0.60	1.96	16	18
1:A:57:CYS:HB2	1:A:61:HIS:CG	0.59	2.31	16	9
1:A:20:LEU:HD11	1:A:24:ILE:N	0.58	2.13	6	1
1:A:39:HIS:CB	1:A:42:ILE:HD11	0.58	2.28	8	16
1:A:54:SER:OG	1:A:108:LEU:HD22	0.58	1.99	6	9
1:A:37:LEU:HD11	1:A:75:ALA:HB1	0.58	1.75	12	8
1:A:40:ILE:CG2	1:A:93:THR:HG22	0.58	2.28	18	4
1:A:80:THR:HG21	1:A:98:ILE:HD12	0.57	1.76	12	6
1:A:17:PHE:CZ	1:A:24:ILE:HG23	0.57	2.34	10	3
1:A:42:ILE:HG22	1:A:45:LYS:CE	0.57	2.29	8	7
1:A:66:LEU:HD23	1:A:127:LEU:HD23	0.57	1.75	19	2
1:A:61:HIS:CG	1:A:62:LYS:N	0.57	2.73	5	11
1:A:77:LEU:HD22	1:A:98:ILE:HD13	0.57	1.77	7	2
1:A:40:ILE:O	1:A:40:ILE:HG22	0.57	1.99	8	8
1:A:30:LYS:O	1:A:34:THR:HG22	0.57	2.00	5	18
1:A:47:ILE:CD1	1:A:101:LEU:HD11	0.56	2.29	20	13
1:A:128:LEU:HD11	1:A:145:ILE:CG1	0.56	2.30	20	8
1:A:105:ILE:HA	1:A:108:LEU:HD12	0.56	1.76	11	4
1:A:109:LEU:CD1	1:A:128:LEU:HD21	0.56	2.30	9	2
1:A:128:LEU:HD11	1:A:145:ILE:HB	0.56	1.76	8	2
1:A:66:LEU:HD22	1:A:127:LEU:CD2	0.56	2.30	6	3
1:A:128:LEU:HD11	1:A:145:ILE:HD12	0.55	1.79	3	2
1:A:39:HIS:HB2	1:A:42:ILE:HD11	0.55	1.77	15	11

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:118:GLN:O	1:A:121:LYS:HG3	0.54	2.03	6	20
1:A:40:ILE:HG22	1:A:93:THR:HG22	0.54	1.79	18	12
1:A:128:LEU:HD13	1:A:145:ILE:HG21	0.54	1.77	9	2
1:A:127:LEU:HD21	1:A:131:TRP:CZ2	0.54	2.37	10	11
1:A:53:TYR:C	1:A:53:TYR:CD1	0.53	2.81	16	8
1:A:47:ILE:HD12	1:A:101:LEU:CD1	0.53	2.34	8	18
1:A:43:GLU:HB2	1:A:97:ALA:HB2	0.53	1.81	14	12
1:A:6:ASP:O	1:A:9:ASN:ND2	0.53	2.42	10	3
1:A:13:THR:HG23	1:A:28:ARG:HD3	0.52	1.82	18	1
1:A:58:PRO:O	1:A:59:ASP:C	0.52	2.47	18	10
1:A:40:ILE:HG22	1:A:40:ILE:O	0.52	2.05	12	9
1:A:24:ILE:HD11	1:A:63:LEU:HB3	0.52	1.80	3	1
1:A:39:HIS:HB3	1:A:42:ILE:HD11	0.52	1.82	7	4
1:A:109:LEU:HD13	1:A:128:LEU:HD21	0.52	1.82	10	2
1:A:24:ILE:HD11	1:A:63:LEU:HG	0.51	1.82	5	3
1:A:145:ILE:HD13	1:A:145:ILE:H	0.51	1.66	12	1
1:A:62:LYS:HB3	1:A:62:LYS:HZ2	0.51	1.66	14	1
1:A:105:ILE:HG12	1:A:109:LEU:HD12	0.51	1.82	13	1
1:A:104:VAL:HG23	1:A:108:LEU:HD11	0.51	1.83	11	1
1:A:37:LEU:HD23	1:A:79:GLU:CD	0.51	2.26	17	1
1:A:57:CYS:O	1:A:61:HIS:HB3	0.50	2.06	2	6
1:A:37:LEU:HD23	1:A:79:GLU:HG3	0.50	1.84	18	7
1:A:13:THR:HG21	1:A:28:ARG:O	0.50	2.07	12	17
1:A:150:PHE:O	1:A:151:ALA:C	0.50	2.49	19	2
1:A:66:LEU:HD13	1:A:124:ILE:HG12	0.49	1.83	5	6
1:A:37:LEU:HD23	1:A:79:GLU:CG	0.49	2.37	11	7
1:A:53:TYR:CD1	1:A:53:TYR:C	0.49	2.85	14	4
1:A:24:ILE:HD12	1:A:67:TYR:CD2	0.49	2.42	5	3
1:A:51:ILE:HD13	1:A:104:VAL:HG21	0.49	1.85	4	2
1:A:128:LEU:HD11	1:A:145:ILE:CG2	0.49	2.38	16	3
1:A:128:LEU:HD13	1:A:145:ILE:HD12	0.49	1.84	9	1
1:A:10:PHE:CD1	1:A:32:LEU:HD23	0.48	2.43	18	16
1:A:63:LEU:HD11	1:A:67:TYR:CZ	0.48	2.43	15	5
1:A:92:GLY:O	1:A:93:THR:HG23	0.48	2.09	2	7
1:A:59:ASP:O	1:A:60:SER:C	0.48	2.50	10	11
1:A:77:LEU:HD12	1:A:81:ARG:CD	0.48	2.39	20	1
1:A:113:ILE:HG12	1:A:124:ILE:HG21	0.48	1.84	16	3
1:A:14:LEU:CD1	1:A:68:ILE:HD13	0.48	2.39	18	3
1:A:109:LEU:HD22	1:A:145:ILE:HG21	0.47	1.86	2	1
1:A:61:HIS:O	1:A:62:LYS:C	0.47	2.52	14	6
1:A:66:LEU:CD1	1:A:124:ILE:HG23	0.47	2.40	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:7:PHE:CE2	1:A:11:VAL:HG23	0.46	2.45	10	4
1:A:10:PHE:CE2	1:A:49:LEU:HD23	0.46	2.45	7	12
1:A:128:LEU:HD21	1:A:145:ILE:HB	0.46	1.87	19	1
1:A:80:THR:HG21	1:A:98:ILE:CD1	0.46	2.40	15	2
1:A:66:LEU:HD12	1:A:124:ILE:HG12	0.46	1.86	9	1
1:A:94:CYS:O	1:A:97:ALA:HB3	0.46	2.11	17	4
1:A:53:TYR:O	1:A:56:LEU:HB2	0.46	2.11	18	1
1:A:69:ILE:HG23	1:A:101:LEU:HD22	0.45	1.88	20	1
1:A:40:ILE:O	1:A:40:ILE:CG2	0.45	2.65	8	1
1:A:57:CYS:CB	1:A:58:PRO:HD2	0.45	2.41	14	9
1:A:145:ILE:O	1:A:146:ARG:C	0.45	2.55	9	3
1:A:62:LYS:CB	1:A:62:LYS:HZ2	0.45	2.23	14	1
1:A:93:THR:O	1:A:94:CYS:C	0.45	2.55	8	1
1:A:17:PHE:CE2	1:A:68:ILE:HD11	0.45	2.46	4	1
1:A:116:SER:HB2	1:A:120:HIS:CB	0.45	2.42	15	2
1:A:128:LEU:HD21	1:A:145:ILE:HG13	0.45	1.88	8	5
1:A:117:ASN:O	1:A:118:GLN:C	0.45	2.55	13	2
1:A:61:HIS:CD2	1:A:61:HIS:C	0.45	2.90	8	2
1:A:109:LEU:O	1:A:110:SER:C	0.44	2.55	1	20
1:A:61:HIS:C	1:A:61:HIS:CD2	0.44	2.90	15	1
1:A:94:CYS:O	1:A:95:ALA:C	0.44	2.56	8	2
1:A:17:PHE:CE1	1:A:24:ILE:HD13	0.43	2.48	7	1
1:A:103:GLU:HG2	1:A:104:VAL:HG13	0.43	1.89	4	5
1:A:34:THR:HG23	1:A:35:TYR:N	0.43	2.29	20	20
1:A:117:ASN:O	1:A:121:LYS:N	0.43	2.48	13	4
1:A:109:LEU:O	1:A:112:ALA:HB3	0.43	2.14	11	1
1:A:64:GLY:O	1:A:65:SER:C	0.43	2.58	2	9
1:A:65:SER:O	1:A:69:ILE:HD12	0.43	2.14	7	1
1:A:20:LEU:CD2	1:A:20:LEU:C	0.42	2.78	6	1
1:A:17:PHE:O	1:A:20:LEU:CD2	0.42	2.58	9	1
1:A:61:HIS:O	1:A:65:SER:N	0.42	2.52	19	3
1:A:128:LEU:HD22	1:A:145:ILE:CD1	0.42	2.45	9	1
1:A:47:ILE:HA	1:A:50:ILE:HD11	0.42	1.92	9	5
1:A:37:LEU:HD11	1:A:75:ALA:HB3	0.42	1.91	11	2
1:A:29:ILE:HA	1:A:32:LEU:HD12	0.41	1.92	12	2
1:A:62:LYS:CD	1:A:112:ALA:HA	0.41	2.45	7	3
1:A:18:LYS:CB	1:A:61:HIS:CE1	0.41	3.04	10	1
1:A:37:LEU:HA	1:A:40:ILE:HD11	0.41	1.92	13	1
1:A:11:VAL:HG12	1:A:12:ALA:N	0.41	2.32	14	1
1:A:47:ILE:HG22	1:A:51:ILE:CD1	0.40	2.46	12	1
1:A:113:ILE:CD1	1:A:150:PHE:CE1	0.40	3.05	20	1

6.3 Torsion angles

6.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	130/161 (81%)	94±4 (72±3%)	27±4 (21±3%)	9±2 (7±1%)	2	17
2	B	3/12 (25%)	3±0 (100±0%)	0±0 (0±0%)	0±0 (0±0%)	100	100
All	All	2660/3460 (77%)	1936 (73%)	545 (20%)	179 (7%)	2	18

All 23 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	58	PRO	20
1	A	144	ALA	20
1	A	56	LEU	18
1	A	150	PHE	17
1	A	134	SER	14
1	A	46	ILE	10
1	A	92	GLY	9
1	A	60	SER	9
1	A	24	ILE	9
1	A	95	ALA	8
1	A	147	SER	8
1	A	42	ILE	7
1	A	62	LYS	6
1	A	20	LEU	5
1	A	108	LEU	4
1	A	79	GLU	3
1	A	106	GLN	3
1	A	6	ASP	3
1	A	84	SER	2
1	A	85	ASN	1
1	A	109	LEU	1
1	A	133	ARG	1
1	A	64	GLY	1

6.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	116/145 (80%)	90±2 (78±2%)	26±2 (22±2%)	3	30
2	B	3/11 (27%)	2±0 (70±10%)	1±0 (30±10%)	1	16
All	All	2380/3120 (76%)	1848 (78%)	532 (22%)	3	29

All 65 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	121	LYS	20
1	A	103	GLU	20
1	A	122	GLU	20
1	A	145	ILE	20
1	A	93	THR	20
1	A	106	GLN	20
1	A	78	ASP	20
1	A	45	LYS	20
2	B	1010	TYR	18
1	A	17	PHE	17
1	A	109	LEU	17
1	A	52	ASP	17
1	A	11	VAL	17
1	A	115	LYS	16
1	A	55	ARG	15
1	A	57	CYS	15
1	A	128	LEU	14
1	A	117	ASN	14
1	A	70	ASP	13
1	A	25	SER	12
1	A	61	HIS	11
1	A	74	ARG	11
1	A	59	ASP	10
1	A	125	ARG	10
1	A	6	ASP	10
1	A	66	LEU	9
1	A	80	THR	8
1	A	53	TYR	8

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Mol	Chain	Res	Type	Models (Total)
1	A	43	GLU	8
1	A	65	SER	7
1	A	126	MET	7
1	A	99	ASN	6
1	A	82	SER	6
1	A	71	SER	5
1	A	30	LYS	5
1	A	27	SER	5
1	A	31	LYS	5
1	A	146	ARG	4
1	A	113	ILE	4
1	A	77	LEU	4
1	A	152	MET	4
1	A	84	SER	3
1	A	20	LEU	3
1	A	119	ASP	3
1	A	62	LYS	3
1	A	148	LYS	3
1	A	83	ASN	2
1	A	81	ARG	2
1	A	147	SER	2
1	A	94	CYS	2
1	A	111	ASP	2
1	A	60	SER	2
1	A	54	SER	1
1	A	28	ARG	1
1	A	16	SER	1
1	A	24	ILE	1
1	A	105	ILE	1
1	A	44	SER	1
1	A	133	ARG	1
1	A	129	ASP	1
1	A	48	SER	1
1	A	63	LEU	1
1	A	8	GLN	1
1	A	7	PHE	1
1	A	118	GLN	1

6.3.3 RNA ⓘ

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

The completeness of assignment taking into account all chemical shift lists is 69% for the well-defined parts and 61% for the entire structure.

7.1 Chemical shift list 1

File name: input_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping

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

Total number of shifts	1475
Number of shifts mapped to atoms	1475
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	5

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	147	1.79 ± 0.13	Should be applied
$^{13}\text{C}_\beta$	111	2.53 ± 0.14	Should be applied
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	146	0.33 ± 0.21	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 69%, i.e. 1141 atoms were assigned a chemical shift out of a possible 1652. 10 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	507/659 (77%)	257/263 (98%)	126/266 (47%)	124/130 (95%)
Sidechain	619/877 (71%)	405/513 (79%)	209/325 (64%)	5/39 (13%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	15/116 (13%)	15/62 (24%)	0/49 (0%)	0/5 (0%)
Overall	1141/1652 (69%)	677/838 (81%)	335/640 (52%)	129/174 (74%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 61%, i.e. 1297 atoms were assigned a chemical shift out of a possible 2134. 11 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	592/859 (69%)	299/343 (87%)	147/346 (42%)	146/170 (86%)
Sidechain	690/1092 (63%)	463/640 (72%)	221/405 (55%)	6/47 (13%)
Aromatic	15/183 (8%)	15/99 (15%)	0/73 (0%)	0/11 (0%)
Overall	1297/2134 (61%)	777/1082 (72%)	368/824 (45%)	152/228 (67%)

7.1.4 Statistically unusual chemical shifts ⓘ

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

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	55	ARG	NE	110.24	92.63 – 76.73	16.1
1	A	81	ARG	NE	107.90	92.63 – 76.73	14.6
1	A	21	LYS	CE	47.66	46.00 – 37.80	7.0
1	A	139	LYS	CE	47.65	46.00 – 37.80	7.0
1	A	128	LEU	CD1	14.95	32.77 – 16.57	-6.0

7.1.5 Random Coil Index (RCI) plots ⓘ

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

Random coil index (RCI) for chain A:

