



Full wwPDB NMR Structure Validation Report ⓘ

Apr 27, 2016 – 05:17 AM BST

PDB ID : 2RQG
Title : Structure of GSPT1/ERF3A-PABC
Authors : Osawa, M.; Nakanishi, T.; Hosoda, N.; Uchida, S.; Hoshino, T.; Katada, I.; Shimada, I.
Deposited on : 2009-05-08

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
<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-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

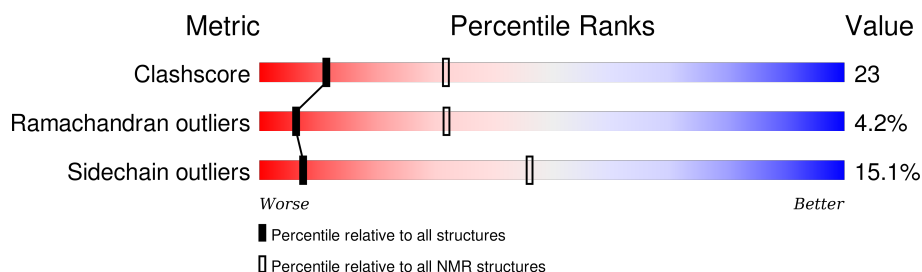
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 72%.

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	19	
2	B	83	

2 Ensemble composition and analysis

This entry contains 20 models. Model 1 is the overall representative, medoid model (most similar to other models).

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:68-A:78, B:550-B:615 (77)	0.20	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 5 clusters and 2 single-model clusters were found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1564 atoms, of which 789 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called G1 to S phase transition 1.

Mol	Chain	Residues	Atoms					Trace
1	A	19	Total	C	H	N	O	0
			298	96	149	29	24	

- Molecule 2 is a protein called Polyadenylate-binding protein 1.

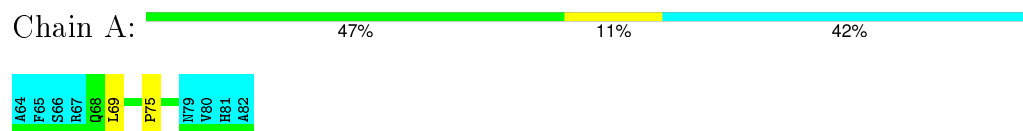
Mol	Chain	Residues	Atoms						Trace
2	B	83	Total	C	H	N	O	S	0
			1266	392	640	107	122	5	

4 Residue-property plots [i](#)

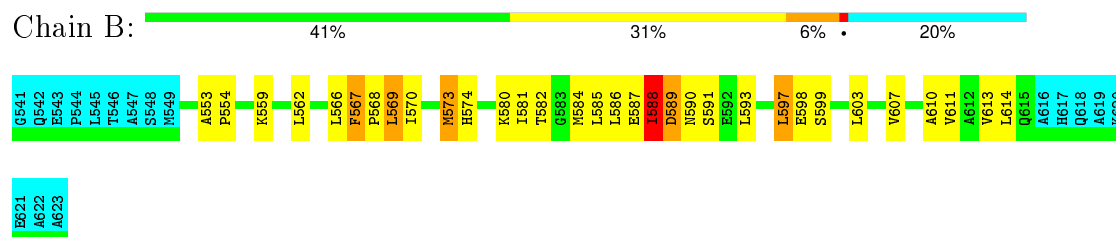
4.1 Average score per residue in the NMR ensemble

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: G1 to S phase transition 1



- Molecule 2: Polyadenylate-binding protein 1

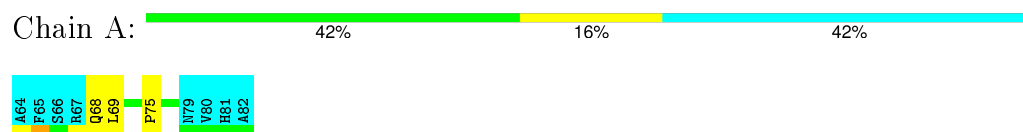


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

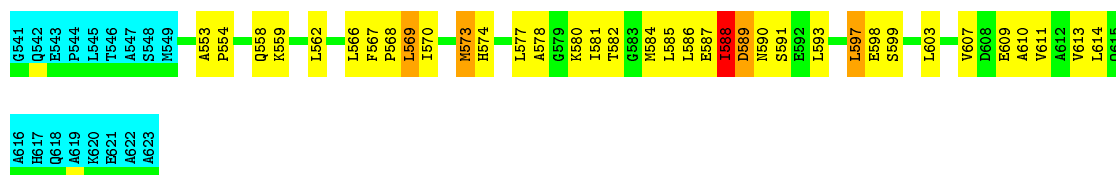
4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: G1 to S phase transition 1



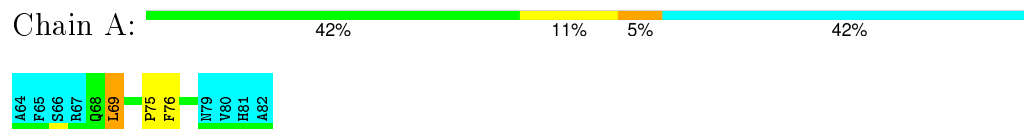
- Molecule 2: Polyadenylate-binding protein 1



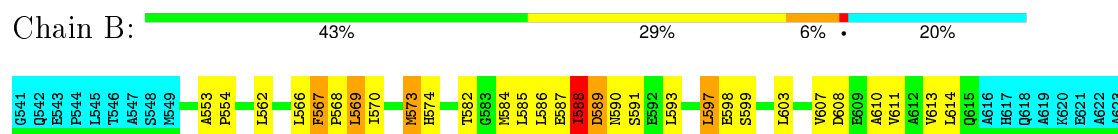


4.2.2 Score per residue for model 2

- Molecule 1: G1 to S phase transition 1

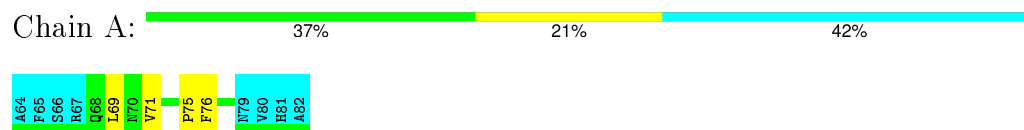


- Molecule 2: Polyadenylate-binding protein 1

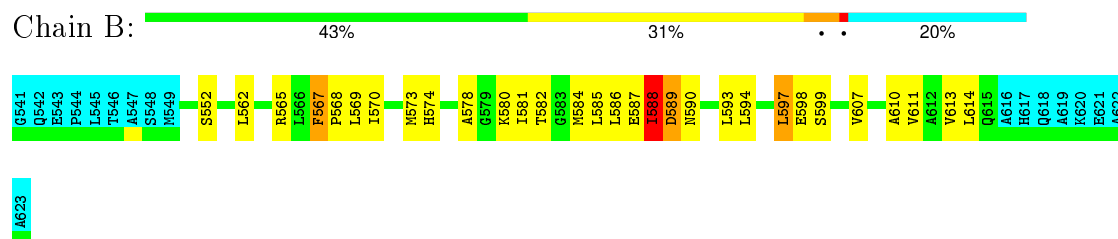


4.2.3 Score per residue for model 3

- Molecule 1: G1 to S phase transition 1



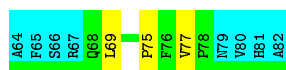
- Molecule 2: Polyadenylate-binding protein 1



4.2.4 Score per residue for model 4

- Molecule 1: G1 to S phase transition 1



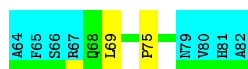


- Molecule 2: Polyadenylate-binding protein 1

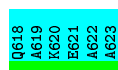


4.2.5 Score per residue for model 5

- Molecule 1: G1 to S phase transition 1

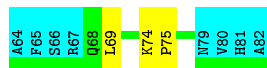


- Molecule 2: Polyadenylate-binding protein 1



4.2.6 Score per residue for model 6

- Molecule 1: G1 to S phase transition 1

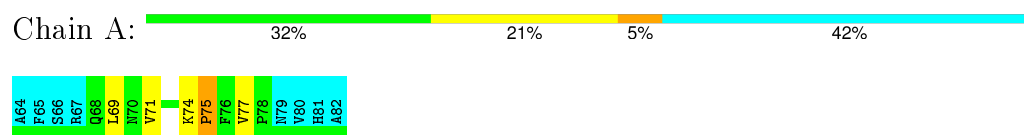


- Molecule 2: Polyadenylate-binding protein 1

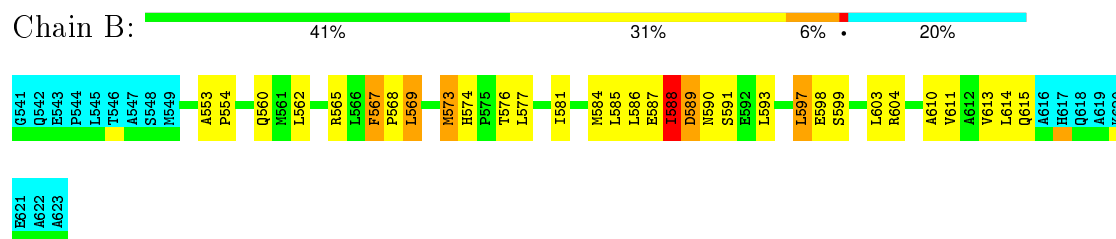


4.2.7 Score per residue for model 7

- Molecule 1: G1 to S phase transition 1

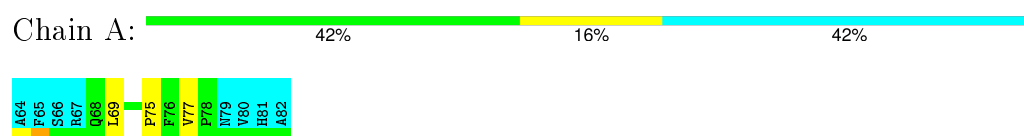


- Molecule 2: Polyadenylate-binding protein 1

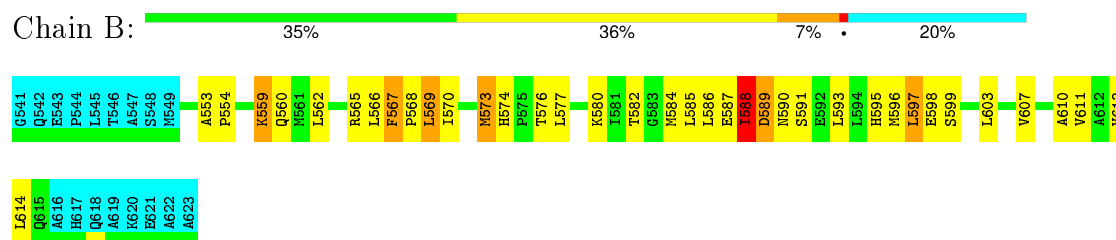


4.2.8 Score per residue for model 8

- Molecule 1: G1 to S phase transition 1

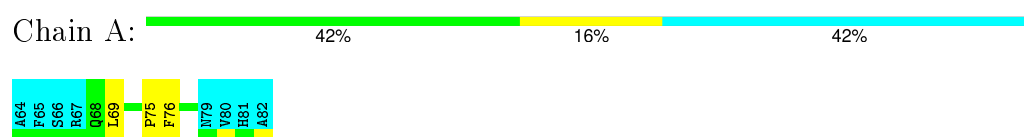


- Molecule 2: Polyadenylate-binding protein 1

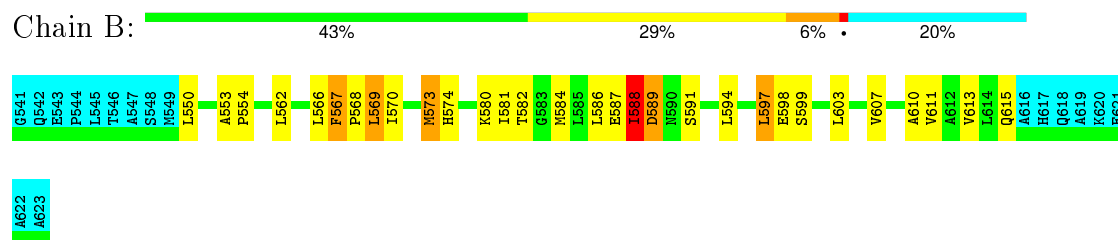


4.2.9 Score per residue for model 9

- Molecule 1: G1 to S phase transition 1

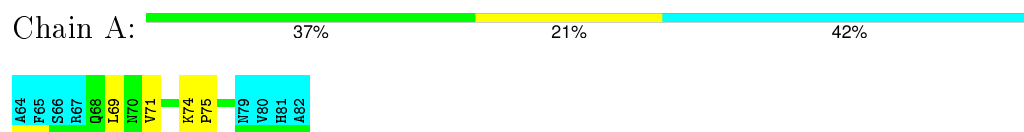


- Molecule 2: Polyadenylate-binding protein 1

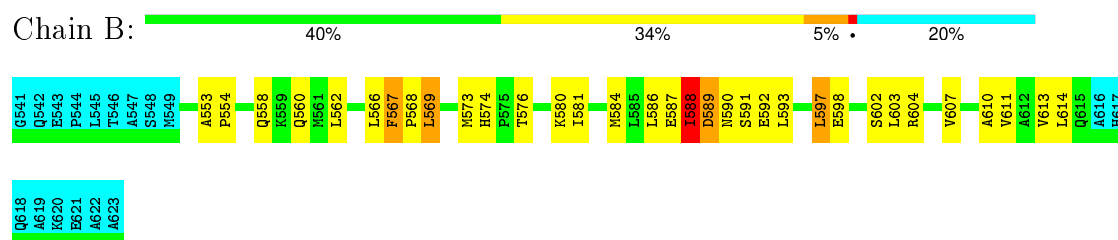


4.2.10 Score per residue for model 10

- Molecule 1: G1 to S phase transition 1

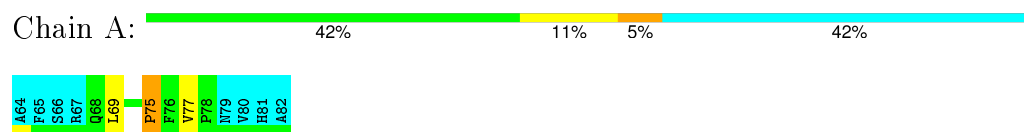


- Molecule 2: Polyadenylate-binding protein 1

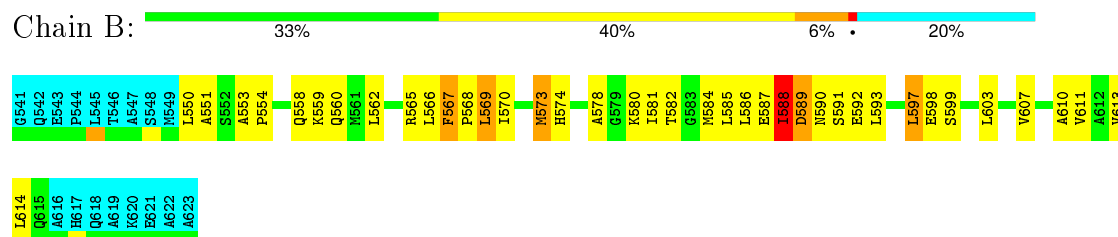


4.2.11 Score per residue for model 11

- Molecule 1: G1 to S phase transition 1

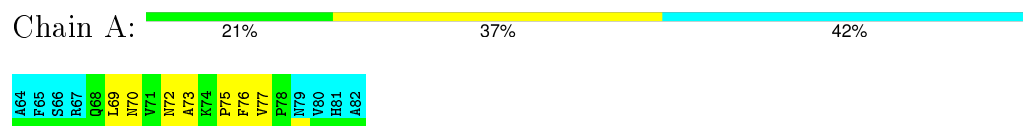


- Molecule 2: Polyadenylate-binding protein 1

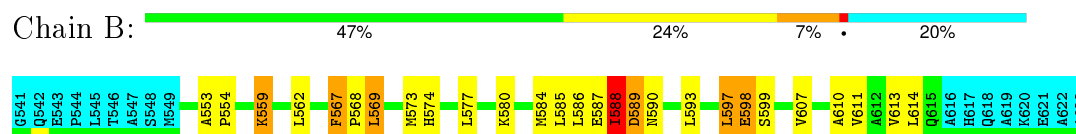


4.2.12 Score per residue for model 12

- Molecule 1: G1 to S phase transition 1

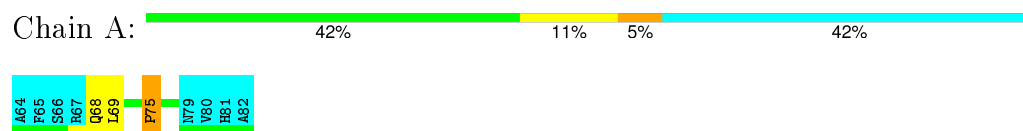


- Molecule 2: Polyadenylate-binding protein 1

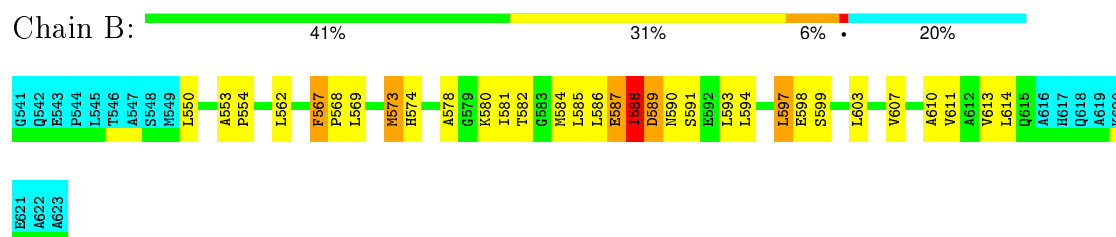


4.2.13 Score per residue for model 13

- Molecule 1: G1 to S phase transition 1

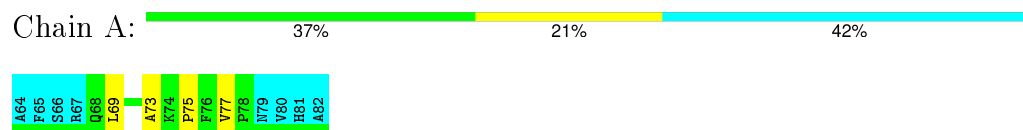


- Molecule 2: Polyadenylate-binding protein 1



4.2.14 Score per residue for model 14

- Molecule 1: G1 to S phase transition 1



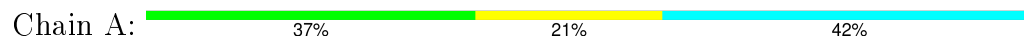
- Molecule 2: Polyadenylate-binding protein 1



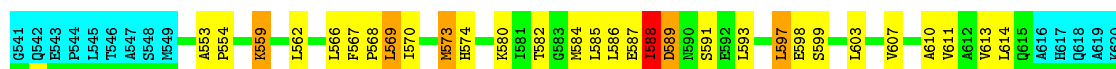


4.2.15 Score per residue for model 15

- Molecule 1: G1 to S phase transition 1

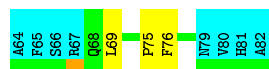


- Molecule 2: Polyadenylate-binding protein 1

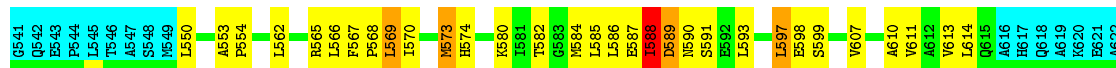


4.2.16 Score per residue for model 16

- Molecule 1: G1 to S phase transition 1

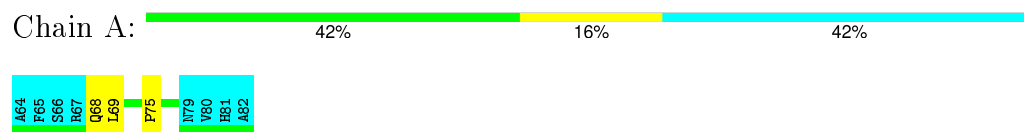


- Molecule 2: Polyadenylate-binding protein 1

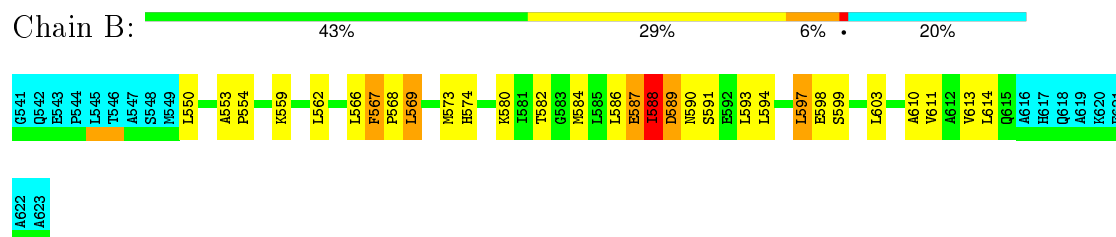


4.2.17 Score per residue for model 17

- Molecule 1: G1 to S phase transition 1

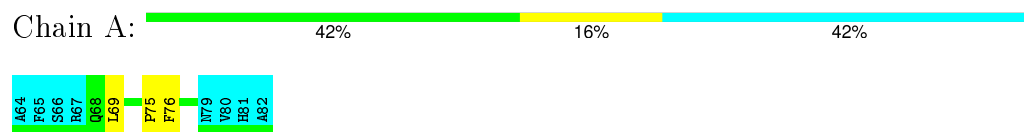


- Molecule 2: Polyadenylate-binding protein 1

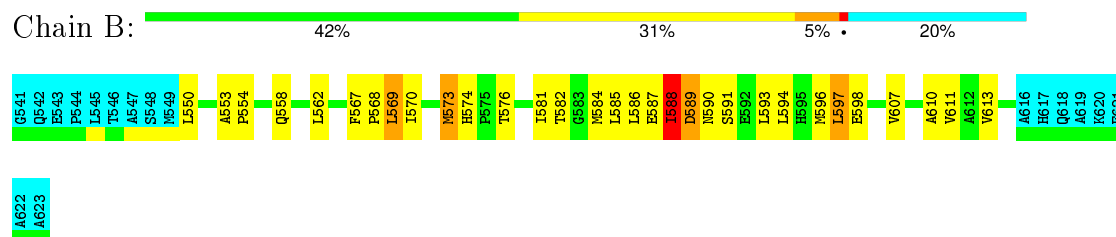


4.2.18 Score per residue for model 18

- Molecule 1: G1 to S phase transition 1

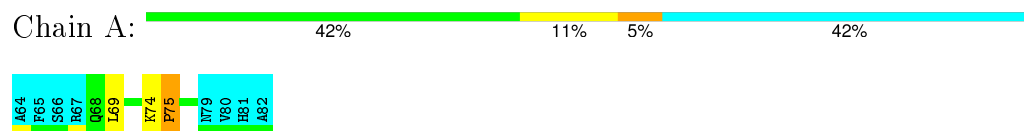


- Molecule 2: Polyadenylate-binding protein 1



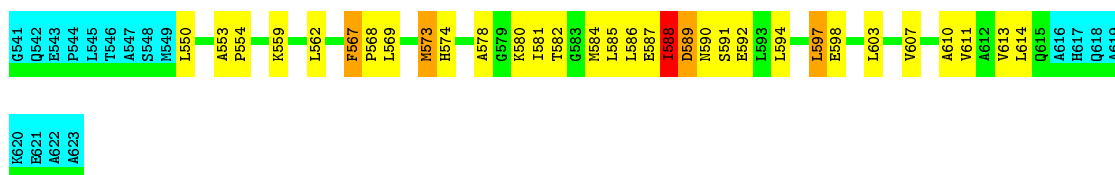
4.2.19 Score per residue for model 19

- Molecule 1: G1 to S phase transition 1



- Molecule 2: Polyadenylate-binding protein 1

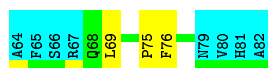




4.2.20 Score per residue for model 20

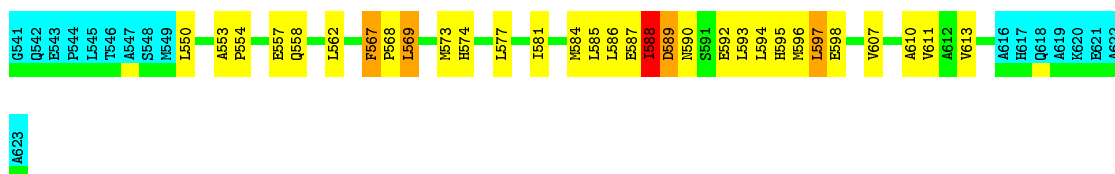
- Molecule 1: G1 to S phase transition 1

Chain A: 42% 16% 42%



- Molecule 2: Polyadenylate-binding protein 1

Chain B: 42% 31% 5% 20%



5 Refinement protocol and experimental data overview

The models were refined using the following method: *TORSION ANGLE DYNAMICS*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *TARGET FUNCTION*.

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

Software name	Classification	Version
CYANA	structure solution	2.1
CYANA	refinement	2.1

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)	BMRB entry 10019
Number of chemical shift lists	1
Total number of shifts	1008
Number of shifts mapped to atoms	1008
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	72%

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	86	90	90	5±2
2	B	506	525	525	28±3
All	All	11840	12300	12300	562

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 23.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:550:LEU:HD12	2:B:594:LEU:HD11	0.85	1.48	18	2
2:B:597:LEU:HD13	2:B:598:GLU:N	0.77	1.95	8	20
2:B:597:LEU:O	2:B:597:LEU:HD22	0.73	1.83	5	12
2:B:597:LEU:HD22	2:B:597:LEU:O	0.73	1.84	12	8
2:B:597:LEU:HD22	2:B:597:LEU:C	0.69	2.08	11	4
2:B:597:LEU:C	2:B:597:LEU:HD22	0.69	2.09	2	16
2:B:574:HIS:CE1	2:B:611:VAL:HG21	0.68	2.24	15	9
1:A:77:VAL:HG23	2:B:560:GLN:HG2	0.64	1.69	11	1
2:B:574:HIS:CE1	2:B:611:VAL:HG11	0.62	2.29	10	8
2:B:550:LEU:CD1	2:B:594:LEU:HD11	0.62	2.24	20	2
2:B:562:LEU:HD13	2:B:590:ASN:HB2	0.61	1.70	18	1
2:B:573:MET:HE3	2:B:607:VAL:HG21	0.60	1.71	5	3
2:B:574:HIS:CD2	2:B:611:VAL:HG21	0.60	2.32	7	9

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:573:MET:CE	2:B:607:VAL:HG21	0.60	2.27	5	4
2:B:573:MET:HG3	2:B:607:VAL:HG11	0.60	1.73	1	8
1:A:75:PRO:O	2:B:586:LEU:HD22	0.60	1.97	11	4
2:B:562:LEU:HD13	2:B:590:ASN:OD1	0.59	1.98	10	1
2:B:562:LEU:HD21	2:B:593:LEU:HD12	0.59	1.74	4	16
2:B:584:MET:CE	2:B:614:LEU:HD21	0.59	2.27	2	7
2:B:570:ILE:HD12	2:B:582:THR:HB	0.59	1.73	6	8
2:B:584:MET:CE	2:B:610:ALA:HB1	0.58	2.29	13	20
1:A:69:LEU:HG	2:B:613:VAL:HG21	0.58	1.76	2	20
2:B:584:MET:HE1	2:B:610:ALA:HB1	0.57	1.74	13	20
1:A:69:LEU:CD1	2:B:613:VAL:HG21	0.57	2.29	1	19
2:B:562:LEU:HD13	2:B:590:ASN:HB3	0.56	1.78	1	14
2:B:573:MET:HE3	2:B:603:LEU:HD11	0.56	1.76	19	2
2:B:607:VAL:O	2:B:611:VAL:HG23	0.55	2.01	11	16
2:B:562:LEU:HD22	2:B:590:ASN:OD1	0.55	2.01	20	8
2:B:573:MET:CE	2:B:603:LEU:HD11	0.54	2.32	19	6
2:B:580:LYS:HD3	2:B:614:LEU:HD22	0.54	1.79	17	4
1:A:76:PHE:HB3	2:B:586:LEU:HD22	0.54	1.79	9	6
2:B:569:LEU:O	2:B:569:LEU:HD13	0.53	2.03	8	10
2:B:559:LYS:HB2	2:B:586:LEU:HD11	0.53	1.81	1	3
2:B:569:LEU:HD13	2:B:569:LEU:O	0.52	2.04	18	8
1:A:70:ASN:OD1	1:A:73:ALA:HB2	0.52	2.05	12	1
2:B:581:ILE:HD11	2:B:611:VAL:HG22	0.52	1.80	9	8
2:B:562:LEU:HD23	2:B:566:LEU:HD13	0.51	1.82	9	2
1:A:77:VAL:HG23	2:B:560:GLN:HG3	0.51	1.83	8	1
1:A:69:LEU:HD12	2:B:613:VAL:HG11	0.51	1.83	1	14
1:A:77:VAL:HG23	2:B:559:LYS:CE	0.50	2.36	12	3
2:B:559:LYS:HB2	2:B:586:LEU:HD21	0.50	1.83	6	5
2:B:550:LEU:HD22	2:B:594:LEU:HD11	0.50	1.84	13	3
2:B:581:ILE:HG22	2:B:585:LEU:HD22	0.49	1.84	6	5
1:A:68:GLN:HG3	2:B:613:VAL:HG22	0.49	1.85	1	1
2:B:574:HIS:NE2	2:B:611:VAL:HG21	0.49	2.23	13	4
1:A:70:ASN:CG	1:A:73:ALA:HB2	0.48	2.28	12	1
1:A:73:ALA:HB1	2:B:587:GLU:OE1	0.48	2.08	14	1
2:B:550:LEU:HD22	2:B:558:GLN:HA	0.48	1.85	18	2
2:B:567:PHE:N	2:B:568:PRO:HD2	0.48	2.24	6	20
2:B:574:HIS:O	2:B:578:ALA:HB2	0.47	2.08	19	5
2:B:597:LEU:CD2	2:B:597:LEU:C	0.47	2.80	11	6
1:A:76:PHE:CB	2:B:586:LEU:HD22	0.47	2.39	16	2
1:A:71:VAL:HG23	2:B:614:LEU:HD23	0.47	1.86	7	1
2:B:550:LEU:HD21	2:B:562:LEU:HB2	0.47	1.86	16	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:597:LEU:C	2:B:597:LEU:CD2	0.47	2.82	13	12
2:B:587:GLU:O	2:B:588:ILE:C	0.47	2.54	9	20
2:B:580:LYS:HD3	2:B:614:LEU:HD13	0.47	1.86	16	3
1:A:71:VAL:HG23	2:B:614:LEU:CD2	0.47	2.40	10	2
2:B:585:LEU:O	2:B:593:LEU:HD11	0.46	2.10	18	13
2:B:585:LEU:O	2:B:593:LEU:HD21	0.46	2.09	2	10
1:A:77:VAL:HG23	2:B:560:GLN:CG	0.46	2.37	11	1
2:B:580:LYS:HE2	2:B:614:LEU:HD22	0.46	1.87	1	1
1:A:77:VAL:HG13	2:B:560:GLN:CG	0.46	2.40	7	1
2:B:580:LYS:HB3	2:B:614:LEU:HD11	0.46	1.88	10	1
2:B:576:THR:OG1	2:B:577:LEU:HD22	0.46	2.10	8	2
2:B:584:MET:HE2	2:B:614:LEU:HD21	0.45	1.87	13	2
2:B:597:LEU:C	2:B:597:LEU:HD13	0.45	2.32	5	5
2:B:559:LYS:CB	2:B:586:LEU:HD21	0.45	2.41	6	2
1:A:70:ASN:ND2	1:A:73:ALA:HB2	0.45	2.27	12	1
1:A:69:LEU:CG	2:B:613:VAL:HG21	0.44	2.41	9	16
2:B:570:ILE:HD13	2:B:581:ILE:HG22	0.44	1.89	1	8
2:B:553:ALA:HB1	2:B:554:PRO:HD2	0.44	1.89	20	19
2:B:581:ILE:HD11	2:B:611:VAL:CG2	0.44	2.41	10	3
1:A:76:PHE:HB3	2:B:586:LEU:HD13	0.44	1.89	12	1
2:B:603:LEU:HD13	2:B:604:ARG:N	0.44	2.28	5	1
2:B:580:LYS:HB2	2:B:614:LEU:HD11	0.43	1.90	15	1
2:B:567:PHE:CB	2:B:568:PRO:CD	0.43	2.97	12	20
2:B:597:LEU:HD13	2:B:597:LEU:C	0.43	2.34	6	4
2:B:562:LEU:HD13	2:B:590:ASN:CG	0.43	2.33	10	1
1:A:77:VAL:HG23	2:B:559:LYS:HE2	0.43	1.91	12	1
2:B:586:LEU:HA	2:B:593:LEU:HD11	0.43	1.89	17	4
2:B:559:LYS:CA	2:B:586:LEU:HD11	0.42	2.44	17	1
2:B:569:LEU:HD13	2:B:569:LEU:C	0.42	2.34	3	1
2:B:550:LEU:HD11	2:B:562:LEU:HD12	0.42	1.91	20	1
2:B:569:LEU:C	2:B:569:LEU:HD13	0.42	2.34	13	1
2:B:550:LEU:HB2	2:B:594:LEU:HD11	0.42	1.89	19	1
2:B:559:LYS:O	2:B:586:LEU:HD11	0.42	2.13	15	1
1:A:76:PHE:CB	2:B:586:LEU:HD13	0.42	2.45	12	2
2:B:584:MET:HE3	2:B:610:ALA:HB1	0.42	1.92	10	1
2:B:586:LEU:HD23	2:B:586:LEU:O	0.41	2.16	12	2
2:B:603:LEU:C	2:B:603:LEU:HD13	0.41	2.35	15	4
2:B:603:LEU:HD13	2:B:603:LEU:C	0.41	2.35	1	2
2:B:577:LEU:HD22	2:B:577:LEU:N	0.40	2.32	12	1
1:A:77:VAL:HG23	2:B:559:LYS:HD2	0.40	1.92	14	1
2:B:577:LEU:N	2:B:577:LEU:HD22	0.40	2.32	4	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:77:VAL:HG22	2:B:559:LYS:CE	0.40	2.47	8	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	11/19 (58%)	8±1 (69±8%)	2±1 (21±7%)	1±0 (10±2%)	2	11
2	B	66/83 (80%)	58±1 (88±2%)	5±1 (8±2%)	2±0 (3±1%)	8	39
All	All	1540/2040 (75%)	1320 (86%)	155 (10%)	65 (4%)	6	32

All 5 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	B	588	ILE	20
1	A	75	PRO	20
2	B	589	ASP	20
2	B	558	GLN	4
1	A	68	GLN	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	10/16 (62%)	10±0 (96±5%)	0±0 (4±5%)	47	88
2	B	57/68 (84%)	47±1 (83±2%)	10±1 (17±2%)	6	42
All	All	1340/1680 (80%)	1138 (85%)	202 (15%)	7	46

All 31 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)
2	B	588	ILE	20
2	B	597	LEU	20
2	B	589	ASP	20
2	B	573	MET	20
2	B	569	LEU	17
2	B	591	SER	17
2	B	599	SER	13
2	B	567	PHE	13
2	B	566	LEU	9
2	B	582	THR	7
2	B	559	LYS	4
1	A	74	LYS	4
2	B	565	ARG	4
2	B	596	MET	4
2	B	587	GLU	3
2	B	595	HIS	3
2	B	615	GLN	3
2	B	580	LYS	3
2	B	560	GLN	2
2	B	557	GLU	2
2	B	604	ARG	2
2	B	602	SER	2
2	B	576	THR	2
2	B	608	ASP	1
1	A	68	GLN	1
1	A	69	LEU	1
2	B	598	GLU	1
1	A	72	ASN	1
2	B	609	GLU	1
2	B	605	SER	1
2	B	552	SER	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [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 72% for the well-defined parts and 70% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 10019

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	1008
Number of shifts mapped to atoms	1008
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	83	1.79 ± 0.24	Should be applied
$^{13}\text{C}_\beta$	79	2.49 ± 0.14	Should be applied
$^{13}\text{C}'$	0	—	—
^{15}N	75	0.62 ± 0.28	Should be applied

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 72%, i.e. 686 atoms were assigned a chemical shift out of a possible 947. 15 out of 18 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	272/371 (73%)	146/147 (99%)	66/154 (43%)	60/70 (86%)
Sidechain	407/544 (75%)	262/320 (82%)	143/205 (70%)	2/19 (11%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	7/32 (22%)	7/18 (39%)	0/12 (0%)	0/2 (0%)
Overall	686/947 (72%)	415/485 (86%)	209/371 (56%)	62/91 (68%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 70%, i.e. 865 atoms were assigned a chemical shift out of a possible 1230. 16 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	352/494 (71%)	194/196 (99%)	83/204 (41%)	75/94 (80%)
Sidechain	500/681 (73%)	327/401 (82%)	171/254 (67%)	2/26 (8%)
Aromatic	13/55 (24%)	13/31 (42%)	0/20 (0%)	0/4 (0%)
Overall	865/1230 (70%)	534/628 (85%)	254/478 (53%)	77/124 (62%)

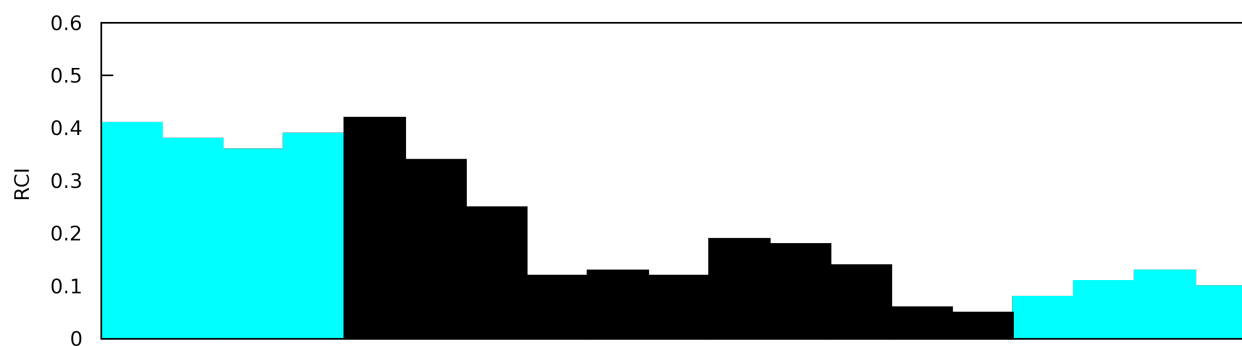
7.1.4 Statistically unusual chemical shifts ⓘ

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots ⓘ

The images below report *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:



Random coil index (RCI) for chain B:

