Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	1WKI
Title	:	solution structure of ribosomal protein L16 from thermus thermophilus HB8
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Deposited on	:	2004-05-31

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 (i) symbol.

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

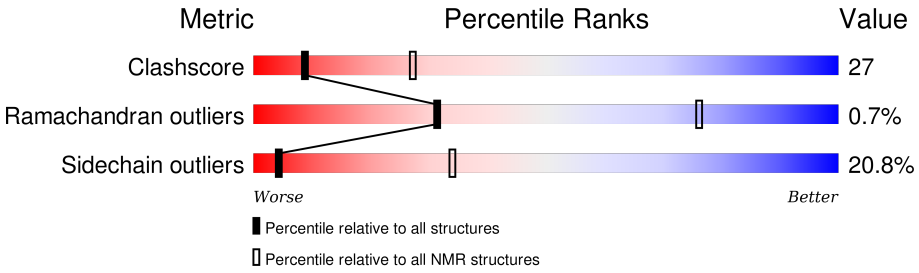
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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 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	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 <=5%

Mol	Chain	Length	Quality of chain
1	A	141	26% 28% · 43%

2 Ensemble composition and analysis

This entry contains 30 models. Model 16 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:31-A:70, A:94-A:133 (80)	0.12	16

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. No single-model clusters were found.

Cluster number	Models
1	1, 2, 4, 8, 9, 10, 12, 18, 23, 27, 28
2	3, 5, 6, 13, 16, 17, 19, 21, 25, 26
3	20, 24, 30
4	14, 15, 22
5	7, 11, 29

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2303 atoms, of which 1181 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called LSU ribosomal protein L16P.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	141	2303	715	1181	212	188	7	0

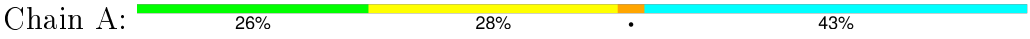
4 Residue-property plots

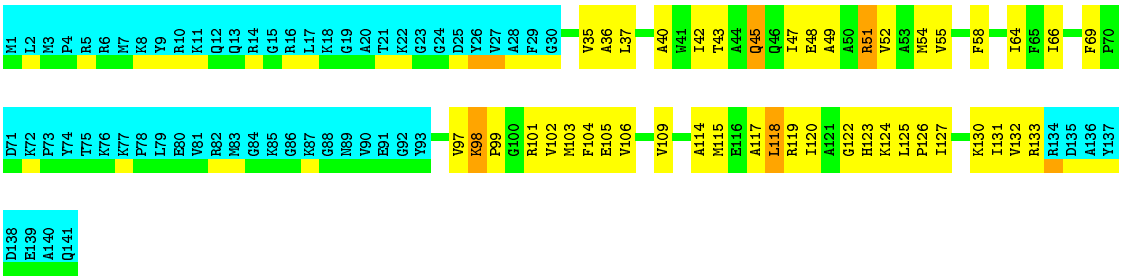
4.1 Average score per residue in the NMR ensemble

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: LSU ribosomal protein L16P

Chain A:





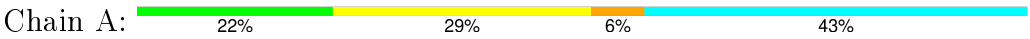
4.2 Scores per residue for each member of the ensemble

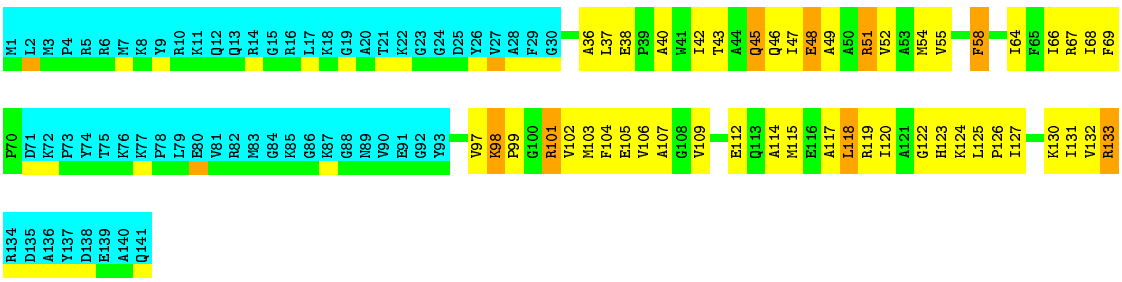
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: LSU ribosomal protein L16P

Chain A:

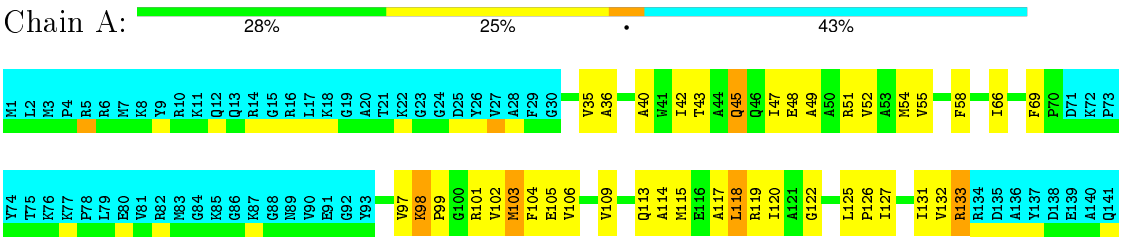




4.2.2 Score per residue for model 2

• Molecule 1: LSU ribosomal protein L16P

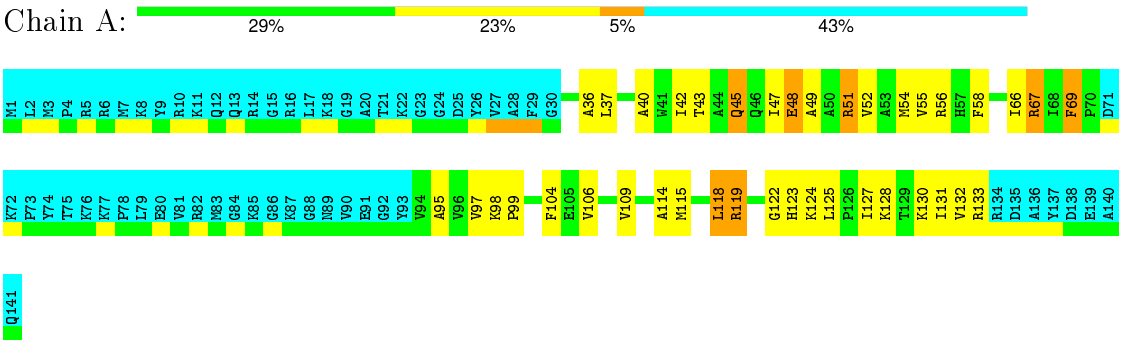
Chain A:



4.2.3 Score per residue for model 3

• Molecule 1: LSU ribosomal protein L16P

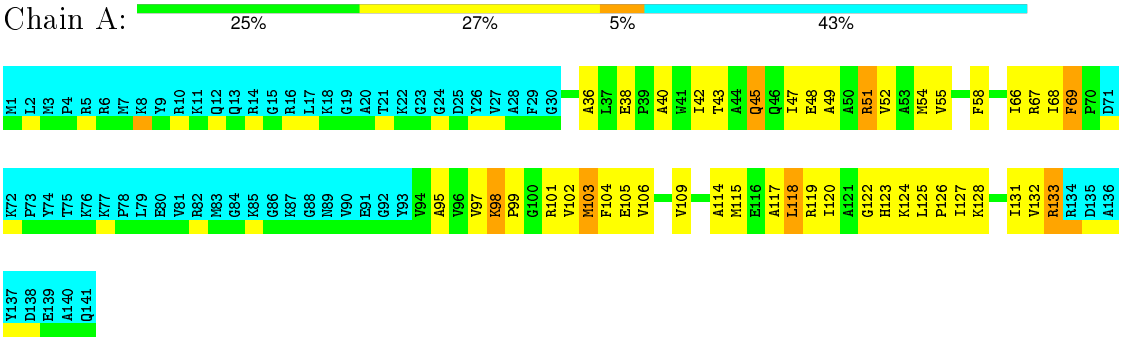
Chain A:



4.2.4 Score per residue for model 4

• Molecule 1: LSU ribosomal protein L16P

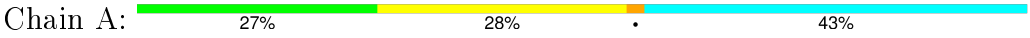
Chain A:

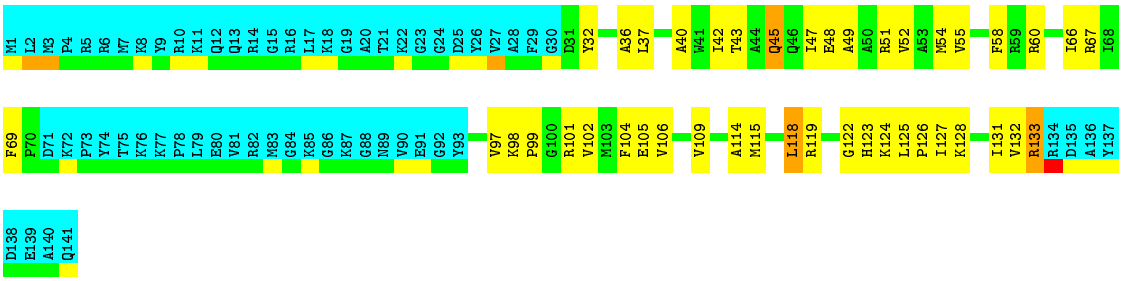


4.2.5 Score per residue for model 5

• Molecule 1: LSU ribosomal protein L16P

Chain A:

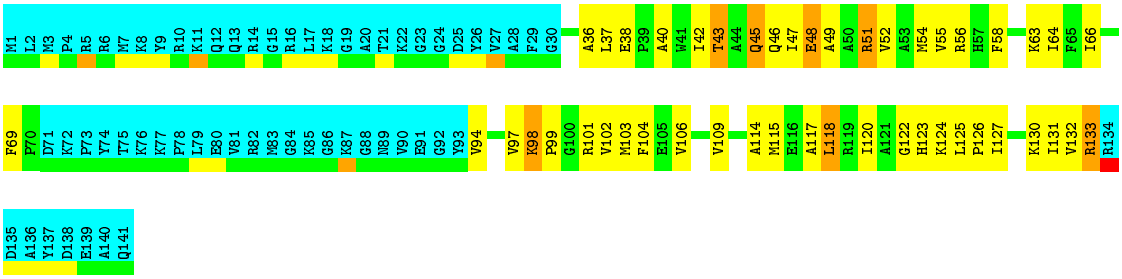




4.2.6 Score per residue for model 6

- Molecule 1: LSU ribosomal protein L16P

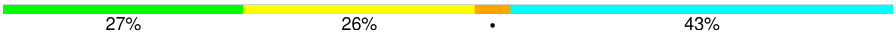
Chain A:

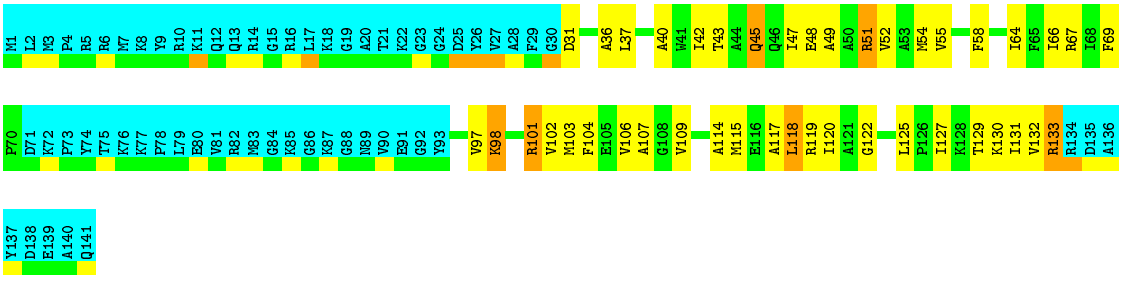


4.2.7 Score per residue for model 7

- Molecule 1: LSU ribosomal protein L16P

Chain A:

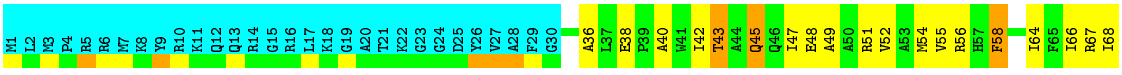


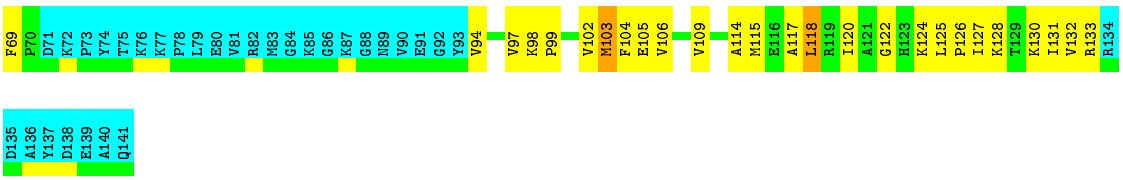


4.2.8 Score per residue for model 8

- Molecule 1: LSU ribosomal protein L16P

Chain A:

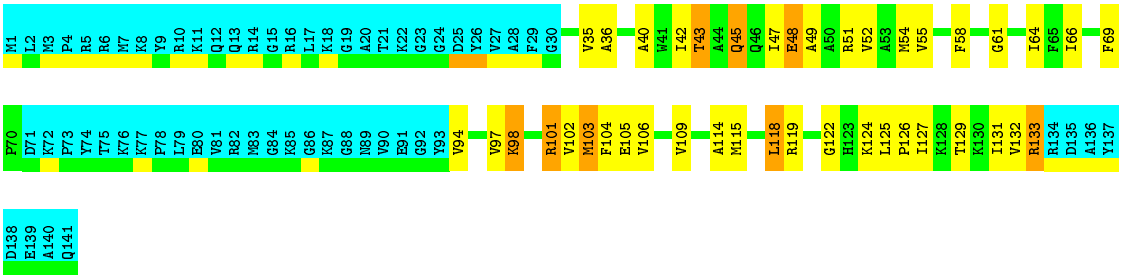




4.2.9 Score per residue for model 9

- Molecule 1: LSU ribosomal protein L16P

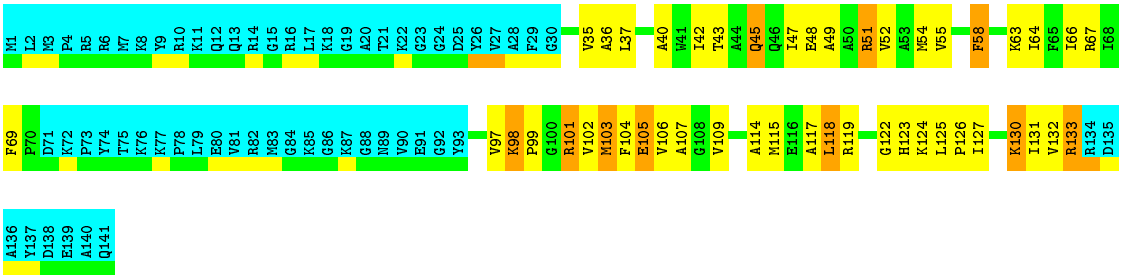
Chain A: 28% 23% 6% 43%



4.2.10 Score per residue for model 10

- Molecule 1: LSU ribosomal protein L16P

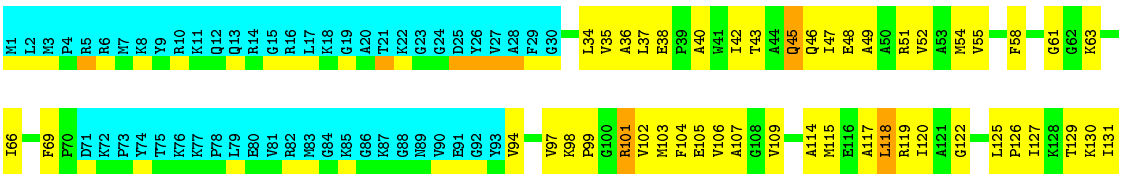
Chain A: 24% 26% 7% 43%

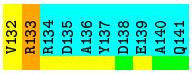


4.2.11 Score per residue for model 11

- Molecule 1: LSU ribosomal protein L16P

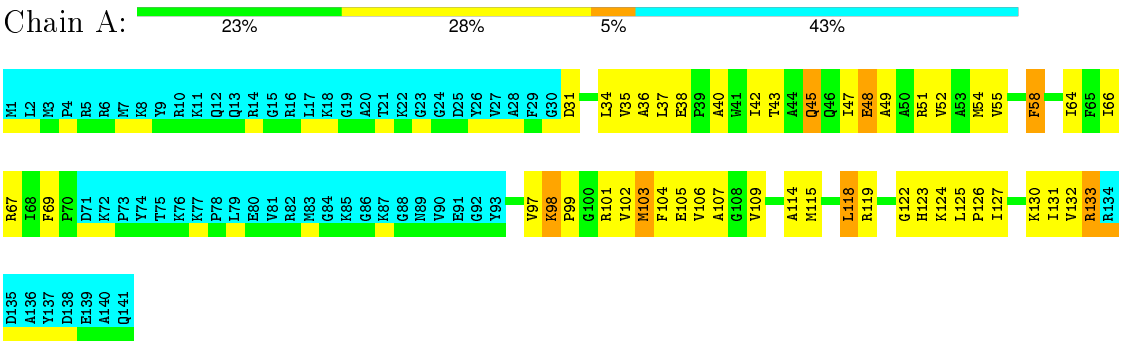
Chain A: 22% 32% • 43%





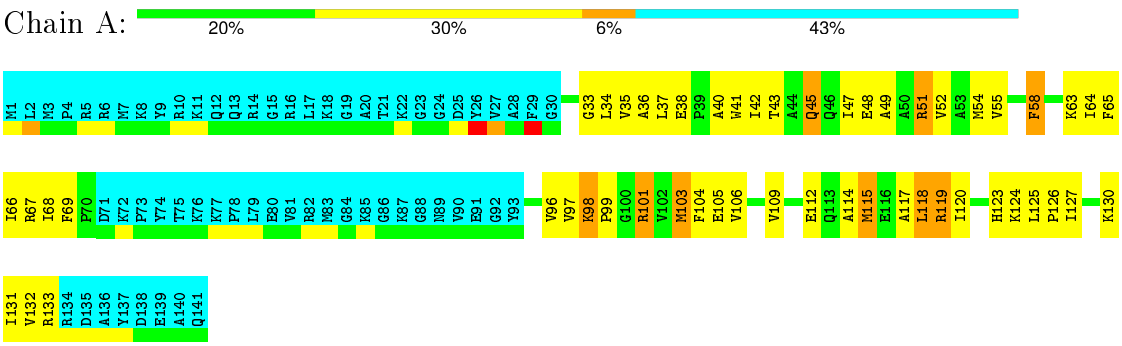
4.2.12 Score per residue for model 12

- Molecule 1: LSU ribosomal protein L16P



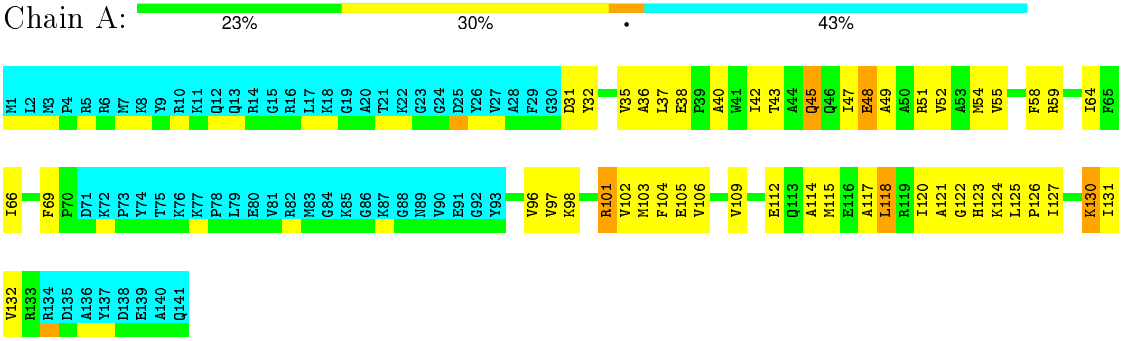
4.2.13 Score per residue for model 13

- Molecule 1: LSU ribosomal protein L16P



4.2.14 Score per residue for model 14

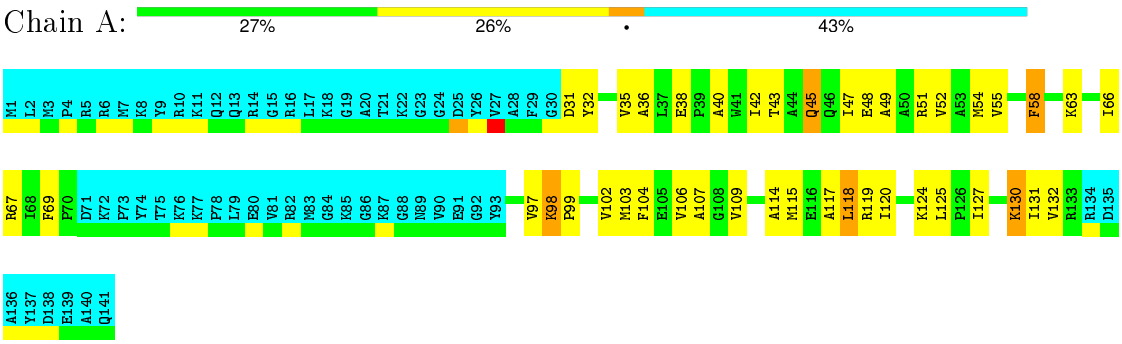
- Molecule 1: LSU ribosomal protein L16P



4.2.15 Score per residue for model 15

• Molecule 1: LSU ribosomal protein L16P

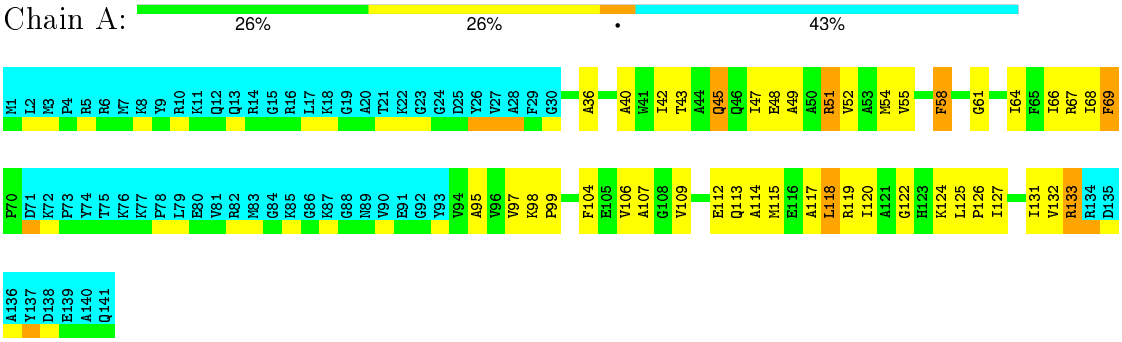
Chain A:



4.2.16 Score per residue for model 16 (medoid)

• Molecule 1: LSU ribosomal protein L16P

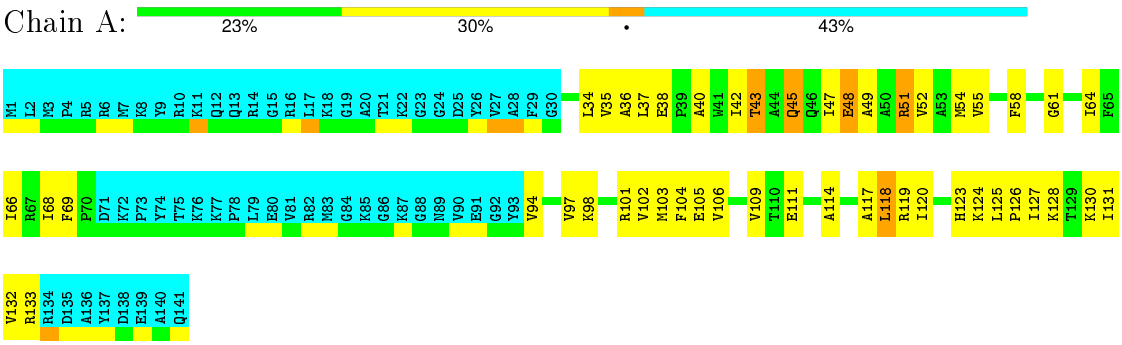
Chain A:



4.2.17 Score per residue for model 17

• Molecule 1: LSU ribosomal protein L16P

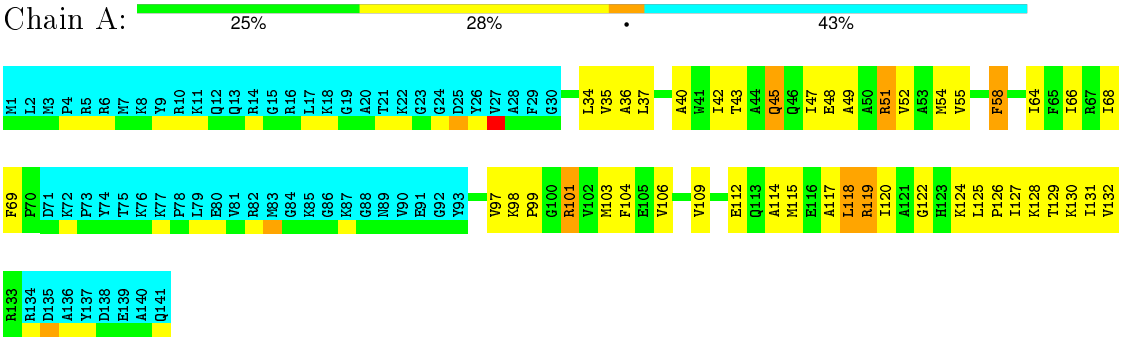
Chain A:



4.2.18 Score per residue for model 18

• Molecule 1: LSU ribosomal protein L16P

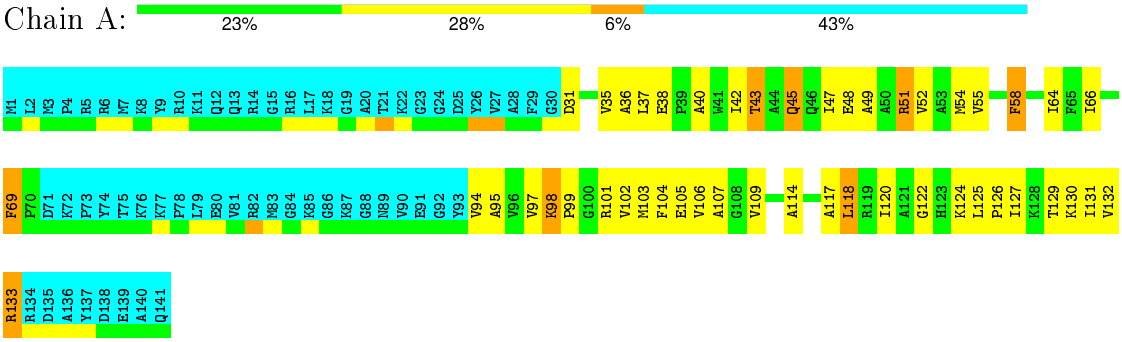
Chain A:



4.2.19 Score per residue for model 19

• Molecule 1: LSU ribosomal protein L16P

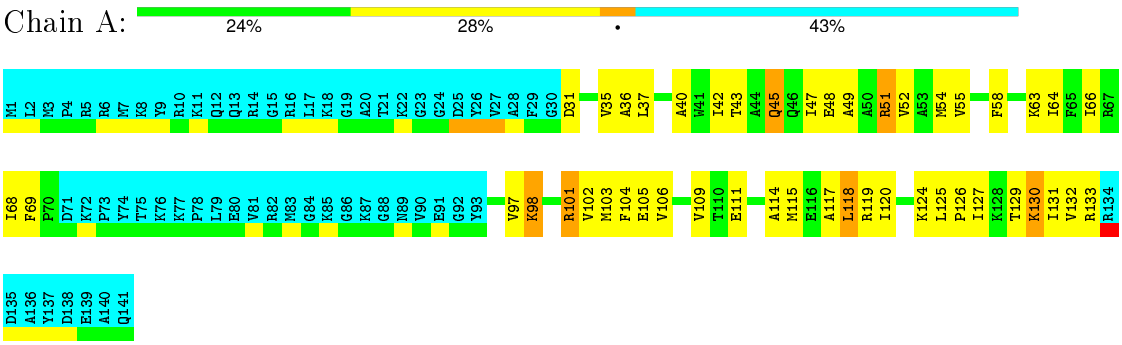
Chain A:



4.2.20 Score per residue for model 20

• Molecule 1: LSU ribosomal protein L16P

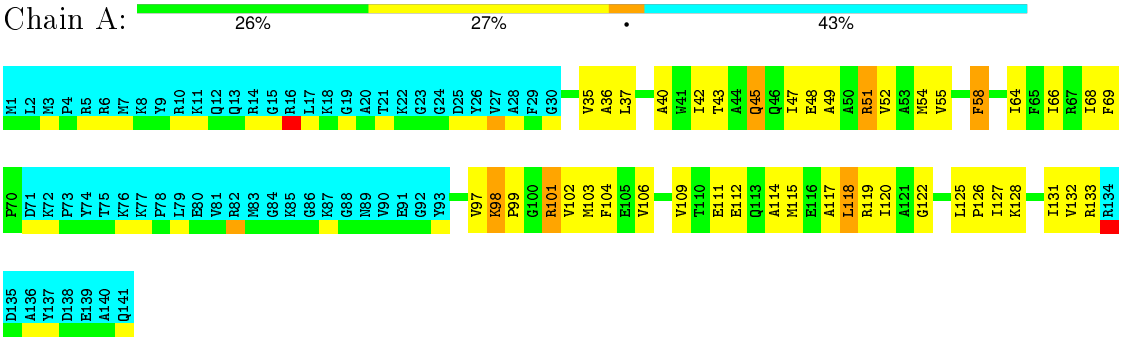
Chain A:



4.2.21 Score per residue for model 21

• Molecule 1: LSU ribosomal protein L16P

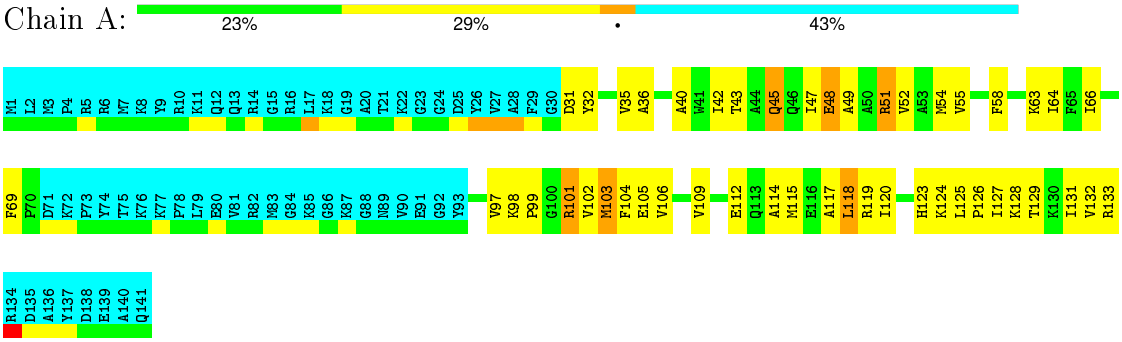
Chain A:



4.2.22 Score per residue for model 22

• Molecule 1: LSU ribosomal protein L16P

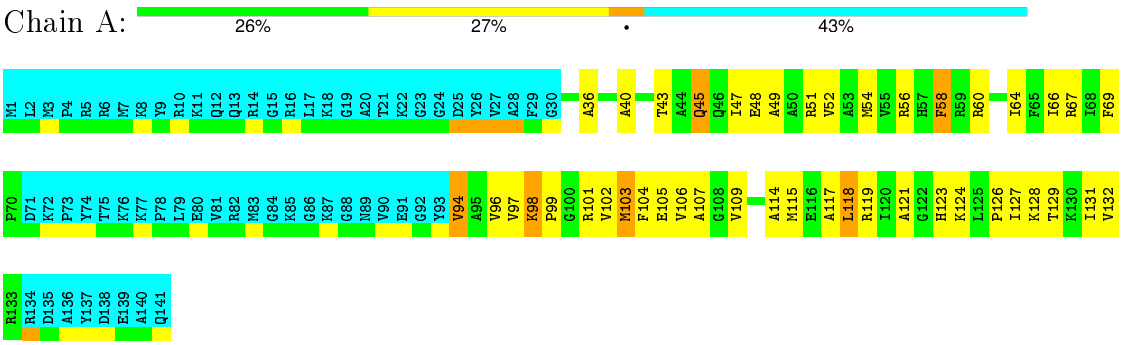
Chain A:



4.2.23 Score per residue for model 23

• Molecule 1: LSU ribosomal protein L16P

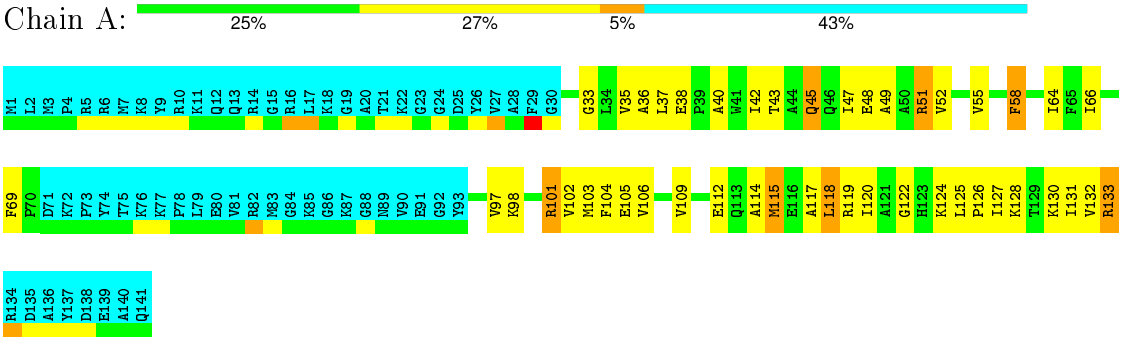
Chain A:



4.2.24 Score per residue for model 24

• Molecule 1: LSU ribosomal protein L16P

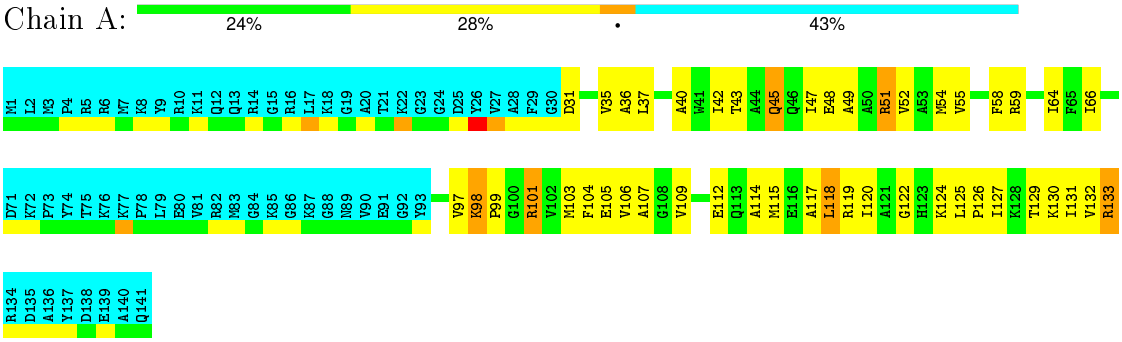
Chain A:



4.2.25 Score per residue for model 25

• Molecule 1: LSU ribosomal protein L16P

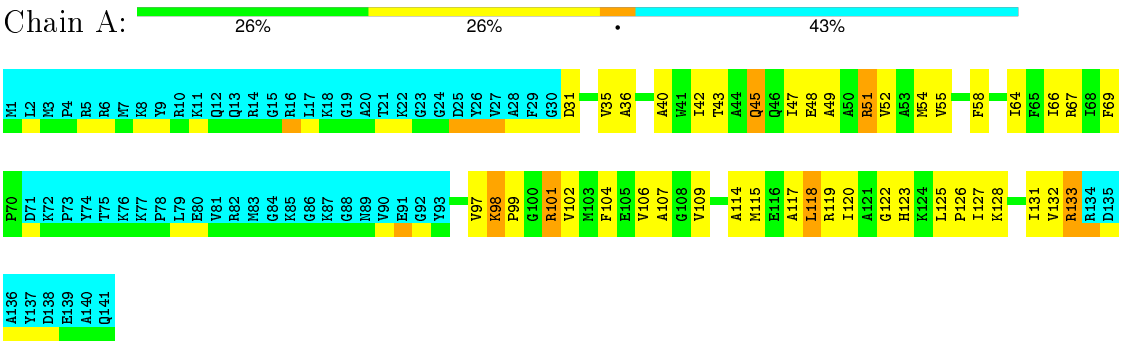
Chain A:



4.2.26 Score per residue for model 26

• Molecule 1: LSU ribosomal protein L16P

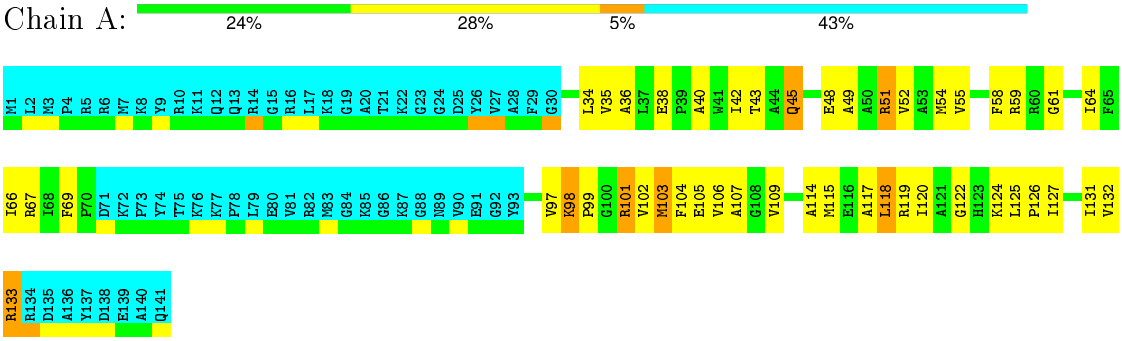
Chain A:



4.2.27 Score per residue for model 27

• Molecule 1: LSU ribosomal protein L16P

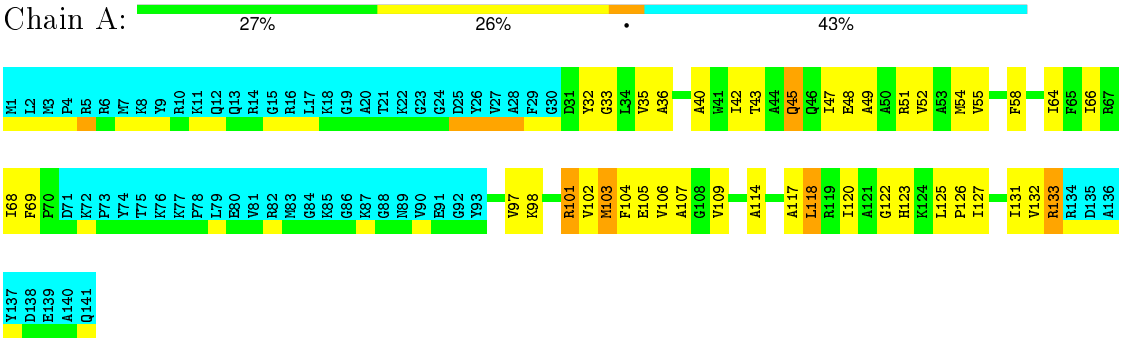
Chain A:



4.2.28 Score per residue for model 28

• Molecule 1: LSU ribosomal protein L16P

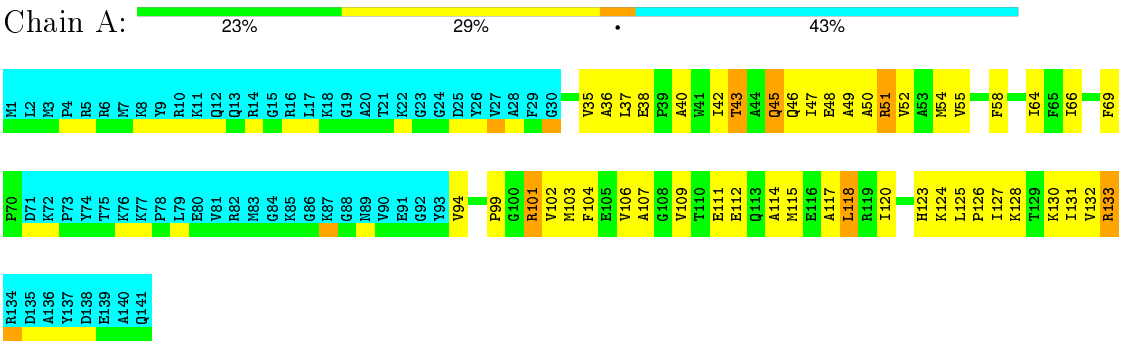
Chain A:



4.2.29 Score per residue for model 29

• Molecule 1: LSU ribosomal protein L16P

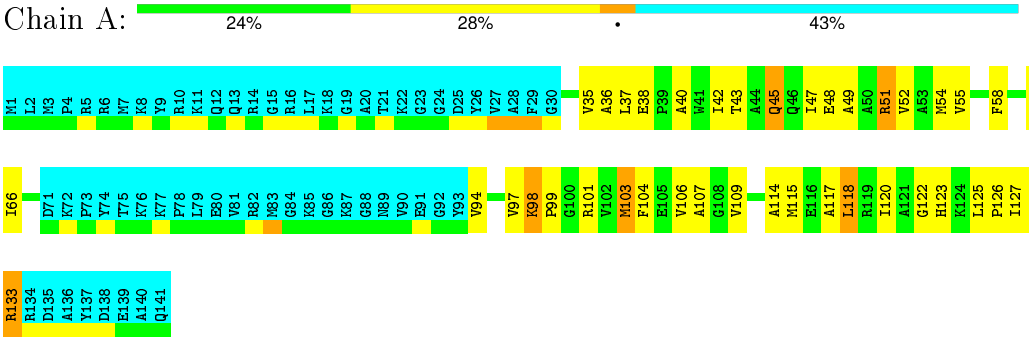
Chain A:



4.2.30 Score per residue for model 30

- Molecule 1: LSU ribosomal protein L16P

Chain A:



5 Refinement protocol and experimental data overview

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

Of the 700 calculated structures, 30 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
CNS	refinement	1.1
CNS	structure solution	1.1

No chemical shift data was provided. 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	630	675	673	36±4
All	All	18900	20250	20190	1072

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:109:VAL:HG23	1:A:114:ALA:HB2	0.94	1.36	28	30
1:A:47:ILE:HG23	1:A:66:ILE:HG21	0.87	1.43	14	29
1:A:58:PHE:CD1	1:A:109:VAL:HG11	0.83	2.09	7	30
1:A:42:ILE:HD12	1:A:125:LEU:HD22	0.82	1.49	30	29
1:A:48:GLU:O	1:A:52:VAL:HG23	0.79	1.78	23	30
1:A:51:ARG:O	1:A:55:VAL:HG23	0.77	1.79	1	29
1:A:102:VAL:HG12	1:A:105:GLU:OE2	0.76	1.81	2	12
1:A:40:ALA:HB2	1:A:127:ILE:HG23	0.72	1.60	15	30
1:A:51:ARG:HG2	1:A:64:ILE:HD12	0.72	1.61	23	14
1:A:118:LEU:HD23	1:A:131:ILE:HG23	0.72	1.62	29	30
1:A:42:ILE:HD12	1:A:125:LEU:CD2	0.71	2.16	2	29
1:A:40:ALA:HB2	1:A:127:ILE:CG2	0.70	2.16	22	30
1:A:106:VAL:HG13	1:A:118:LEU:HD11	0.69	1.65	19	30
1:A:42:ILE:CD1	1:A:125:LEU:HD22	0.69	2.18	6	29

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:36:ALA:HB2	1:A:103:MET:CE	0.68	2.18	25	25
1:A:46:GLN:OE1	1:A:125:LEU:HD23	0.68	1.89	6	1
1:A:118:LEU:CB	1:A:131:ILE:HD12	0.67	2.19	11	30
1:A:35:VAL:HG11	1:A:130:LYS:HE3	0.67	1.64	15	2
1:A:66:ILE:HD12	1:A:104:PHE:CE2	0.67	2.25	8	24
1:A:40:ALA:HB1	1:A:126:PRO:HG2	0.66	1.67	22	27
1:A:117:ALA:HA	1:A:120:ILE:HD12	0.66	1.67	28	24
1:A:119:ARG:HG3	1:A:131:ILE:HD11	0.65	1.67	20	7
1:A:54:MET:CE	1:A:64:ILE:HD13	0.64	2.22	9	1
1:A:66:ILE:HD12	1:A:104:PHE:CD2	0.63	2.28	27	23
1:A:109:VAL:CG2	1:A:114:ALA:HB2	0.62	2.23	24	11
1:A:42:ILE:HG21	1:A:68:ILE:HD12	0.62	1.71	16	4
1:A:37:LEU:HD21	1:A:130:LYS:HG2	0.61	1.72	6	14
1:A:118:LEU:HB3	1:A:131:ILE:HD12	0.61	1.70	22	30
1:A:47:ILE:CG2	1:A:66:ILE:HG21	0.59	2.24	9	18
1:A:36:ALA:HB2	1:A:103:MET:SD	0.58	2.37	15	16
1:A:122:GLY:HA2	1:A:125:LEU:HD12	0.57	1.76	5	23
1:A:36:ALA:HB2	1:A:103:MET:HE1	0.57	1.75	25	1
1:A:102:VAL:HG12	1:A:105:GLU:OE1	0.56	2.00	1	1
1:A:45:GLN:O	1:A:49:ALA:CB	0.56	2.52	27	30
1:A:45:GLN:O	1:A:49:ALA:HB3	0.56	2.01	29	30
1:A:45:GLN:O	1:A:49:ALA:N	0.55	2.38	21	30
1:A:51:ARG:CG	1:A:64:ILE:HD12	0.55	2.32	28	3
1:A:69:PHE:O	1:A:95:ALA:HB2	0.55	2.02	4	4
1:A:35:VAL:HG23	1:A:101:ARG:N	0.52	2.19	10	20
1:A:68:ILE:HD13	1:A:103:MET:HB3	0.52	1.81	1	4
1:A:54:MET:HE1	1:A:104:PHE:CD2	0.51	2.39	15	15
1:A:54:MET:HE3	1:A:64:ILE:HD13	0.51	1.81	9	1
1:A:37:LEU:HD11	1:A:130:LYS:HG2	0.51	1.82	12	1
1:A:54:MET:SD	1:A:121:ALA:HB2	0.50	2.46	14	2
1:A:66:ILE:HG22	1:A:68:ILE:HG12	0.50	1.82	13	3
1:A:118:LEU:HB2	1:A:131:ILE:HD12	0.50	1.84	11	13
1:A:51:ARG:HD3	1:A:64:ILE:HD12	0.48	1.85	18	2
1:A:54:MET:CE	1:A:104:PHE:CD2	0.47	2.97	4	28
1:A:115:MET:HA	1:A:131:ILE:HG21	0.47	1.86	13	2
1:A:54:MET:HE3	1:A:64:ILE:CD1	0.47	2.40	9	1
1:A:37:LEU:HD12	1:A:128:LYS:HG2	0.47	1.85	5	1
1:A:54:MET:HE3	1:A:104:PHE:CD2	0.47	2.45	27	2
1:A:97:VAL:HG12	1:A:98:LYS:N	0.47	2.24	2	29
1:A:58:PHE:CG	1:A:109:VAL:HG11	0.47	2.45	14	3
1:A:40:ALA:HB2	1:A:127:ILE:HG21	0.47	1.84	7	10

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:58:PHE:CE1	1:A:117:ALA:CB	0.46	2.98	10	10
1:A:36:ALA:O	1:A:99:PRO:HA	0.46	2.09	30	23
1:A:106:VAL:CG1	1:A:118:LEU:HD11	0.46	2.39	19	1
1:A:51:ARG:HD3	1:A:66:ILE:HD11	0.46	1.87	5	1
1:A:34:LEU:HD23	1:A:118:LEU:HB3	0.46	1.88	13	4
1:A:58:PHE:CZ	1:A:117:ALA:CB	0.46	2.98	19	5
1:A:97:VAL:CG1	1:A:101:ARG:CB	0.46	2.94	26	4
1:A:35:VAL:HG11	1:A:130:LYS:CE	0.46	2.38	15	1
1:A:43:THR:HG23	1:A:94:VAL:CG1	0.46	2.40	19	6
1:A:54:MET:HE1	1:A:64:ILE:HG21	0.45	1.88	9	1
1:A:97:VAL:CG1	1:A:101:ARG:HB3	0.45	2.42	12	5
1:A:66:ILE:CD1	1:A:104:PHE:CD2	0.45	3.00	16	9
1:A:32:TYR:CD2	1:A:114:ALA:CB	0.45	3.00	14	3
1:A:127:ILE:HD12	1:A:127:ILE:O	0.45	2.10	16	4
1:A:37:LEU:HD21	1:A:130:LYS:CD	0.45	2.41	17	1
1:A:42:ILE:HG23	1:A:46:GLN:OE1	0.44	2.13	1	1
1:A:64:ILE:HG23	1:A:106:VAL:CG1	0.44	2.43	29	2
1:A:34:LEU:HD23	1:A:131:ILE:HD13	0.44	1.90	17	1
1:A:127:ILE:HD12	1:A:127:ILE:C	0.44	2.33	14	10
1:A:33:GLY:O	1:A:132:VAL:HG22	0.44	2.13	13	2
1:A:37:LEU:HD12	1:A:128:LYS:HG3	0.43	1.89	18	1
1:A:66:ILE:N	1:A:66:ILE:HD13	0.43	2.28	13	1
1:A:127:ILE:C	1:A:127:ILE:HD12	0.43	2.33	22	9
1:A:32:TYR:CE1	1:A:133:ARG:HG3	0.43	2.49	5	2
1:A:118:LEU:HD23	1:A:131:ILE:CG2	0.43	2.41	15	9
1:A:132:VAL:O	1:A:132:VAL:HG23	0.43	2.12	17	2
1:A:54:MET:CB	1:A:64:ILE:HD11	0.43	2.44	16	5
1:A:51:ARG:HG3	1:A:64:ILE:HD12	0.43	1.90	8	1
1:A:34:LEU:HD13	1:A:34:LEU:C	0.43	2.35	17	1
1:A:106:VAL:HG13	1:A:118:LEU:CD1	0.42	2.44	13	4
1:A:119:ARG:HD3	1:A:131:ILE:HD11	0.42	1.89	18	1
1:A:42:ILE:HG21	1:A:68:ILE:CD1	0.42	2.42	16	1
1:A:127:ILE:CD1	1:A:129:THR:CG2	0.42	2.98	18	8
1:A:61:GLY:O	1:A:109:VAL:HG12	0.42	2.13	17	2
1:A:54:MET:O	1:A:58:PHE:CD2	0.42	2.73	10	14
1:A:132:VAL:HG23	1:A:132:VAL:O	0.42	2.15	29	2
1:A:51:ARG:HG3	1:A:66:ILE:HD11	0.42	1.92	13	1
1:A:34:LEU:HD11	1:A:129:THR:CB	0.41	2.46	11	1
1:A:127:ILE:O	1:A:127:ILE:HD12	0.41	2.14	13	8
1:A:54:MET:O	1:A:58:PHE:CE2	0.41	2.74	8	2
1:A:119:ARG:NH2	1:A:131:ILE:CG1	0.41	2.84	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:41:TRP:CD1	1:A:96:VAL:HG22	0.41	2.49	13	1
1:A:46:GLN:O	1:A:50:ALA:HB3	0.41	2.15	29	1
1:A:118:LEU:CD2	1:A:131:ILE:HG23	0.41	2.42	11	1
1:A:46:GLN:NE2	1:A:125:LEU:HD23	0.40	2.30	11	1
1:A:33:GLY:N	1:A:132:VAL:O	0.40	2.54	24	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	80/141 (57%)	75±2 (94±2%)	4±2 (5±2%)	1±1 (1±1%)	31	76
All	All	2400/4230 (57%)	2259 (94%)	125 (5%)	16 (1%)	31	76

All 2 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	PHE	12
1	A	61	GLY	4

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	63/111 (57%)	50±2 (79±4%)	13±2 (21±4%)	4	34
All	All	1890/3330 (57%)	1497 (79%)	393 (21%)	4	34

All 28 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	43	THR	30
1	A	118	LEU	30
1	A	45	GLN	30
1	A	69	PHE	28
1	A	115	MET	27
1	A	124	LYS	23
1	A	101	ARG	21
1	A	133	ARG	21
1	A	51	ARG	20
1	A	98	LYS	18
1	A	119	ARG	17
1	A	123	HIS	16
1	A	38	GLU	15
1	A	67	ARG	14
1	A	103	MET	12
1	A	128	LYS	11
1	A	112	GLU	10
1	A	48	GLU	8
1	A	63	LYS	8
1	A	31	ASP	7
1	A	130	LYS	6
1	A	105	GLU	5
1	A	111	GLU	4
1	A	56	ARG	4
1	A	59	ARG	3
1	A	113	GLN	2
1	A	60	ARG	2
1	A	94	VAL	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

There are no carbohydrates in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided