Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	2KHI
Title	:	NMR structure of the domain 4 of the E. coli ribosomal protein S1
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Deposited on	:	2009-04-07

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:

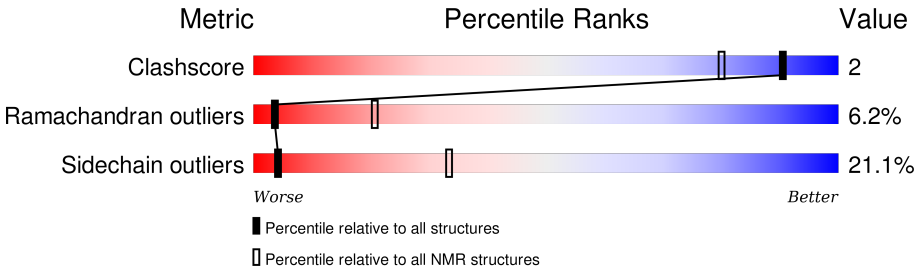
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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	115	43% 13% • 26% 17%

2 Ensemble composition and analysis

This entry contains 12 models. Model 6 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative.

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:274-A:306, A:322-A:353 (65)	0.65	6

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 2 clusters and 2 single-model clusters were found.

Cluster number	Models
1	1, 4, 8, 10, 11, 12
2	2, 6, 7, 9
Single-model clusters	3; 5

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1510 atoms, of which 749 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	95	1510	479	749	133	145	4	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	247	MET	-	EXPRESSION TAG	UNP P0AG67
A	248	GLY	-	EXPRESSION TAG	UNP P0AG67
A	249	SER	-	EXPRESSION TAG	UNP P0AG67
A	250	SER	-	EXPRESSION TAG	UNP P0AG67
A	251	HIS	-	EXPRESSION TAG	UNP P0AG67
A	252	HIS	-	EXPRESSION TAG	UNP P0AG67
A	253	HIS	-	EXPRESSION TAG	UNP P0AG67
A	254	HIS	-	EXPRESSION TAG	UNP P0AG67
A	255	HIS	-	EXPRESSION TAG	UNP P0AG67
A	256	HIS	-	EXPRESSION TAG	UNP P0AG67
A	257	SER	-	EXPRESSION TAG	UNP P0AG67
A	258	SER	-	EXPRESSION TAG	UNP P0AG67
A	259	GLY	-	EXPRESSION TAG	UNP P0AG67
A	260	LEU	-	EXPRESSION TAG	UNP P0AG67
A	261	VAL	-	EXPRESSION TAG	UNP P0AG67
A	262	PRO	-	EXPRESSION TAG	UNP P0AG67
A	263	ARG	-	EXPRESSION TAG	UNP P0AG67
A	264	GLY	-	EXPRESSION TAG	UNP P0AG67
A	265	SER	-	EXPRESSION TAG	UNP P0AG67
A	266	HIS	-	EXPRESSION TAG	UNP P0AG67

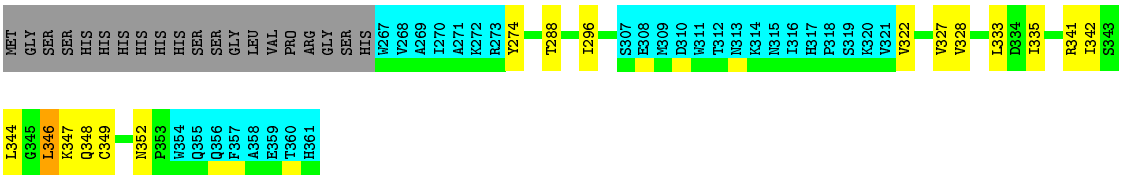
4 Residue-property plots

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: 30S ribosomal protein S1

Chain A:



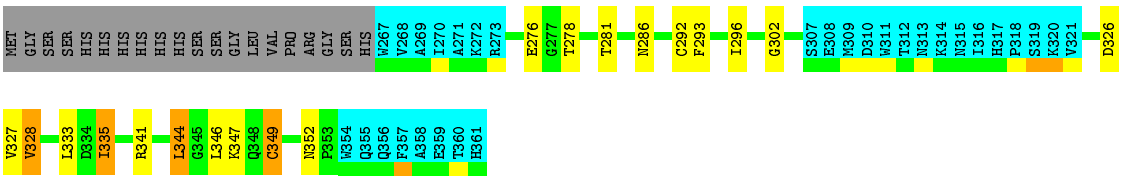
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: 30S ribosomal protein S1

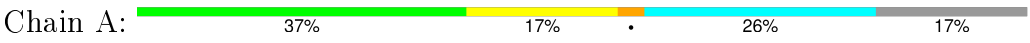
Chain A:

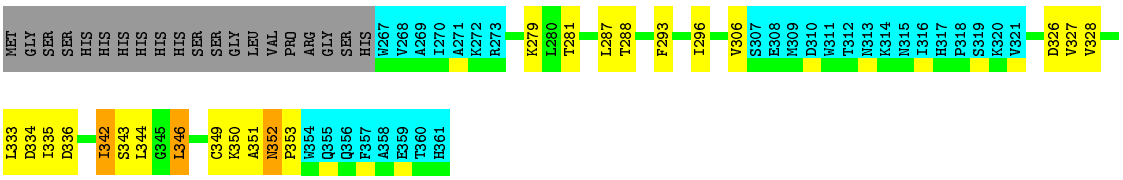


4.2.2 Score per residue for model 2

- Molecule 1: 30S ribosomal protein S1

Chain A:

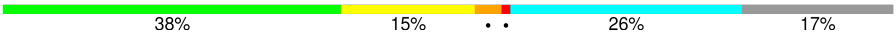


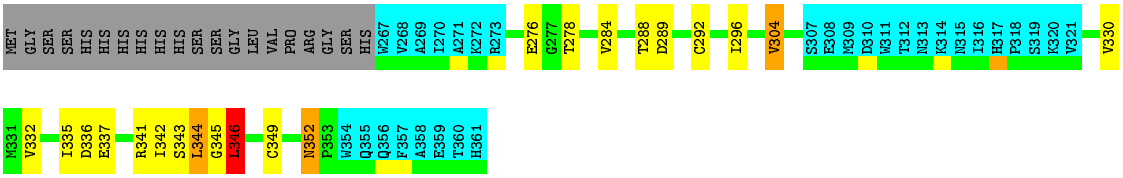


4.2.3 Score per residue for model 3

- Molecule 1: 30S ribosomal protein S1

Chain A:

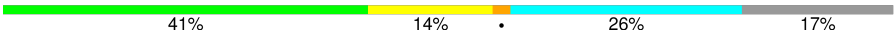


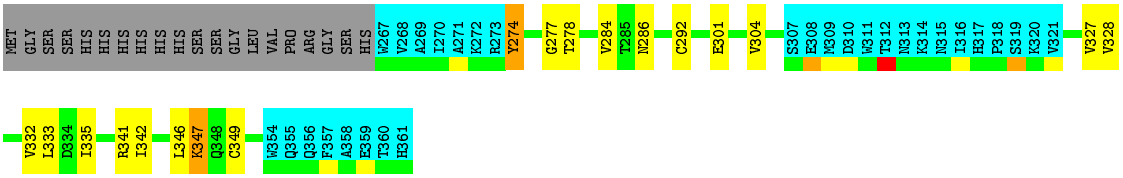


4.2.4 Score per residue for model 4

- Molecule 1: 30S ribosomal protein S1

Chain A:

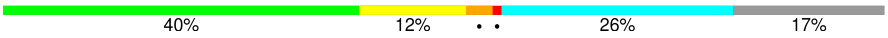


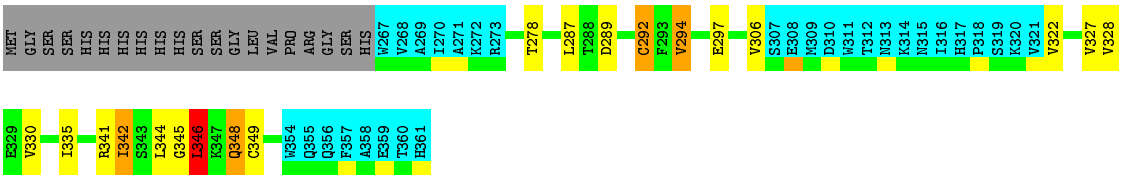


4.2.5 Score per residue for model 5

- Molecule 1: 30S ribosomal protein S1

Chain A:

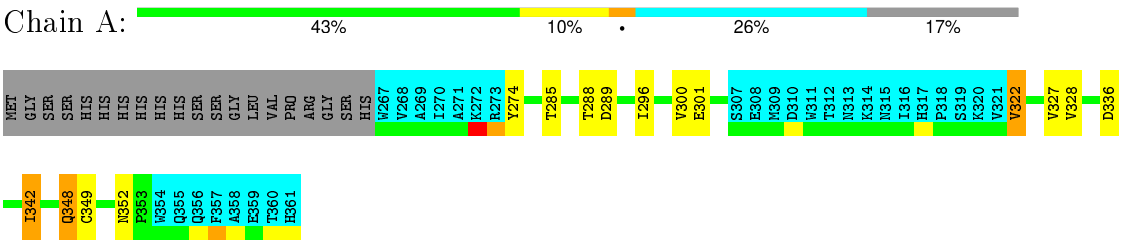




4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: 30S ribosomal protein S1

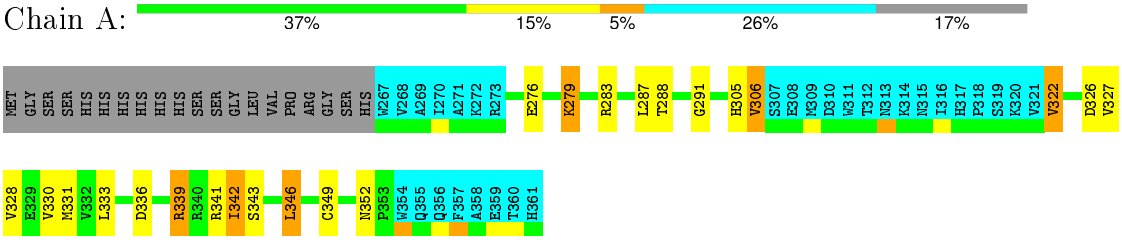
Chain A:



4.2.7 Score per residue for model 7

- Molecule 1: 30S ribosomal protein S1

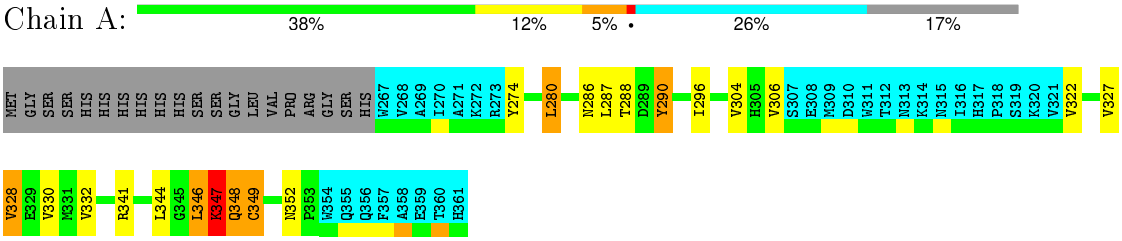
Chain A:



4.2.8 Score per residue for model 8

- Molecule 1: 30S ribosomal protein S1

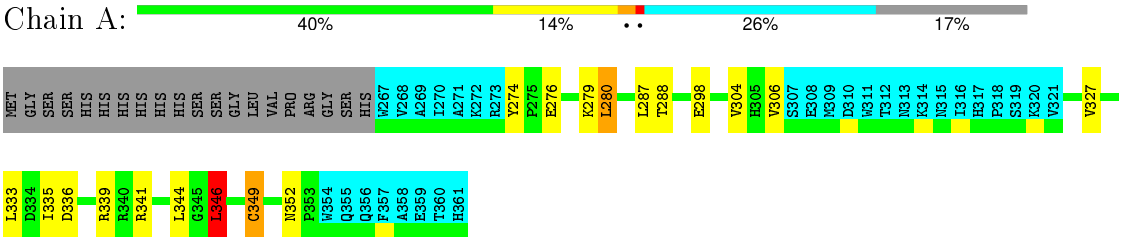
Chain A:



4.2.9 Score per residue for model 9

- Molecule 1: 30S ribosomal protein S1

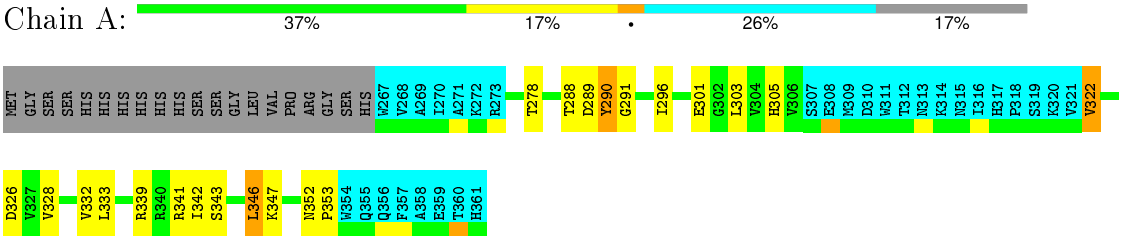
Chain A:



4.2.10 Score per residue for model 10

- Molecule 1: 30S ribosomal protein S1

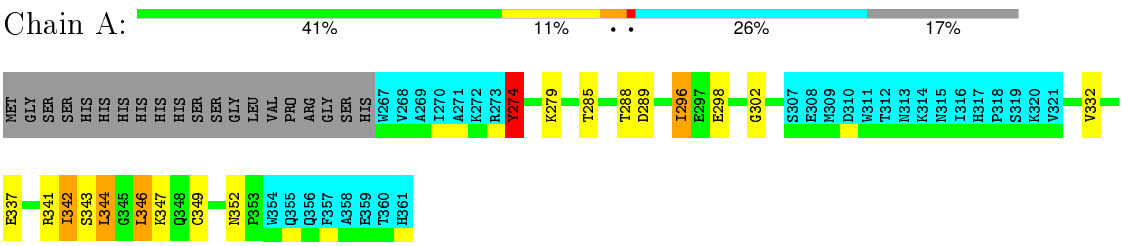
Chain A:



4.2.11 Score per residue for model 11

- Molecule 1: 30S ribosomal protein S1

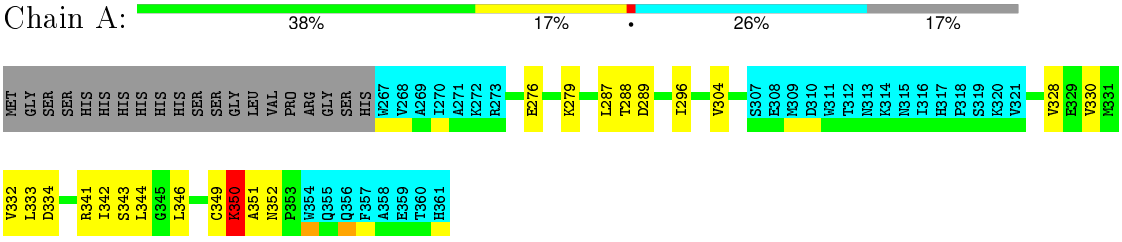
Chain A:



4.2.12 Score per residue for model 12

- Molecule 1: 30S ribosomal protein S1

Chain A:



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 12 were deposited, based on the following criterion: *12 structures for lowest energy.*

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

Software name	Classification	Version
INCA	structure solution	
INCA	refinement	

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.01±0.02	0±0/509 (0.0±0.0%)	1.51±0.05	4±1/690 (0.6±0.2%)
All	All	1.01	0/6108 (0.0%)	1.51	51/8280 (0.6%)

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

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.2±0.4
All	All	0	3

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	297	GLU	C-N-CA	8.55	143.07	121.70	5	1
1	A	290	TYR	CB-CG-CD1	8.36	126.01	121.00	8	1
1	A	290	TYR	CB-CG-CD2	-7.89	116.26	121.00	8	1
1	A	346	LEU	N-CA-CB	7.73	125.85	110.40	8	5
1	A	348	GLN	C-N-CA	7.17	139.63	121.70	6	2
1	A	274	TYR	CB-CG-CD1	7.12	125.27	121.00	6	2
1	A	294	VAL	CA-CB-CG1	6.72	120.98	110.90	5	1
1	A	274	TYR	CB-CG-CD2	-6.63	117.02	121.00	6	1
1	A	346	LEU	N-CA-C	6.58	128.78	111.00	3	5
1	A	339	ARG	N-CA-CB	-6.55	98.81	110.60	7	1
1	A	293	PHE	N-CA-CB	6.25	121.85	110.60	1	2
1	A	342	ILE	N-CA-C	-6.23	94.18	111.00	12	5
1	A	284	VAL	CA-CB-CG2	-6.12	101.72	110.90	4	2
1	A	349	CYS	N-CA-CB	6.11	121.59	110.60	9	1
1	A	349	CYS	CA-C-N	-5.88	104.26	117.20	3	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	351	ALA	C-N-CA	5.80	136.20	121.70	2	1
1	A	284	VAL	CA-CB-CG1	5.76	119.54	110.90	3	1
1	A	347	LYS	N-CA-CB	5.70	120.86	110.60	8	1
1	A	297	GLU	CA-C-N	-5.60	104.88	117.20	5	1
1	A	280	LEU	N-CA-CB	5.57	121.55	110.40	9	1
1	A	337	GLU	C-N-CA	5.47	135.38	121.70	3	1
1	A	345	GLY	C-N-CA	5.47	135.37	121.70	5	1
1	A	306	VAL	CA-CB-CG1	5.41	119.02	110.90	7	1
1	A	277	GLY	C-N-CA	5.37	135.14	121.70	4	1
1	A	350	LYS	CB-CG-CD	5.37	125.55	111.60	12	1
1	A	290	TYR	N-CA-CB	5.36	120.25	110.60	10	1
1	A	339	ARG	C-N-CA	5.26	134.86	121.70	9	1
1	A	278	THR	N-CA-CB	5.23	120.24	110.30	5	1
1	A	304	VAL	CA-CB-CG2	-5.21	103.09	110.90	12	1
1	A	352	ASN	N-CA-CB	5.14	119.86	110.60	2	1
1	A	349	CYS	C-N-CA	5.13	134.53	121.70	12	1
1	A	291	GLY	N-CA-C	-5.05	100.47	113.10	10	2
1	A	292	CYS	CB-CA-C	5.05	120.50	110.40	5	1
1	A	327	VAL	C-N-CA	5.04	134.30	121.70	1	1

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
1	A	274	TYR	Sidechain	1
1	A	305	HIS	Sidechain	1
1	A	290	TYR	Sidechain	1

6.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	503	505	505	2±1
All	All	6036	6060	6059	26

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 2.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:328:VAL:HG23	1:A:349:CYS:H	0.64	1.53	5	1
1:A:332:VAL:HG12	1:A:344:LEU:HD12	0.55	1.79	11	1
1:A:304:VAL:HG21	1:A:347:LYS:HG3	0.54	1.78	8	1
1:A:335:ILE:HD13	1:A:342:ILE:HG23	0.52	1.82	5	1
1:A:328:VAL:HG21	1:A:346:LEU:HG	0.51	1.82	5	1
1:A:304:VAL:CG2	1:A:346:LEU:H	0.51	2.18	3	1
1:A:328:VAL:HA	1:A:349:CYS:HA	0.50	1.81	8	2
1:A:332:VAL:HB	1:A:344:LEU:HD12	0.47	1.87	3	1
1:A:304:VAL:HG13	1:A:346:LEU:H	0.44	1.72	9	1
1:A:300:VAL:HG13	1:A:342:ILE:HG13	0.44	1.88	6	1
1:A:296:ILE:HG12	1:A:344:LEU:HD21	0.43	1.88	11	1
1:A:283:ARG:HG2	1:A:327:VAL:HG22	0.43	1.90	7	1
1:A:304:VAL:HG21	1:A:347:LYS:HB2	0.43	1.89	4	1
1:A:302:GLY:HA3	1:A:344:LEU:HD22	0.42	1.90	11	2
1:A:280:LEU:HD21	1:A:332:VAL:HG22	0.42	1.89	8	1
1:A:334:ASP:N	1:A:343:SER:HB2	0.42	2.29	12	1
1:A:304:VAL:HA	1:A:345:GLY:HA2	0.42	1.90	3	1
1:A:278:THR:O	1:A:332:VAL:HG12	0.42	2.14	10	2
1:A:296:ILE:HB	1:A:300:VAL:HG12	0.42	1.91	6	1
1:A:330:VAL:HA	1:A:346:LEU:HA	0.41	1.91	7	1
1:A:279:LYS:HA	1:A:331:MET:HA	0.41	1.91	7	1
1:A:336:ASP:HB3	1:A:339:ARG:HB2	0.40	1.91	7	1
1:A:328:VAL:HG13	1:A:349:CYS:HA	0.40	1.94	1	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	65/115 (57%)	52±2 (81±3%)	9±2 (13±2%)	4±1 (6±2%)	4	21
All	All	780/1380 (57%)	629 (81%)	103 (13%)	48 (6%)	4	21

All 13 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	352	ASN	10
1	A	296	ILE	6
1	A	349	CYS	6
1	A	347	LYS	5
1	A	322	VAL	5
1	A	276	GLU	5
1	A	306	VAL	4
1	A	353	PRO	2
1	A	351	ALA	1
1	A	346	LEU	1
1	A	350	LYS	1
1	A	274	TYR	1
1	A	348	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	57/101 (56%)	45±2 (79±4%)	12±2 (21±4%)	4	33
All	All	684/1212 (56%)	540 (79%)	144 (21%)	4	33

All 39 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	341	ARG	10
1	A	288	THR	9
1	A	346	LEU	8
1	A	344	LEU	8
1	A	342	ILE	7
1	A	333	LEU	7
1	A	328	VAL	7
1	A	289	ASP	6
1	A	287	LEU	6
1	A	327	VAL	6
1	A	279	LYS	5

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Mol	Chain	Res	Type	Models (Total)
1	A	335	ILE	5
1	A	343	SER	5
1	A	330	VAL	4
1	A	292	CYS	4
1	A	326	ASP	4
1	A	336	ASP	4
1	A	274	TYR	4
1	A	286	ASN	3
1	A	348	GLN	3
1	A	301	GLU	3
1	A	322	VAL	3
1	A	350	LYS	2
1	A	280	LEU	2
1	A	298	GLU	2
1	A	285	THR	2
1	A	278	THR	2
1	A	281	THR	2
1	A	296	ILE	1
1	A	306	VAL	1
1	A	337	GLU	1
1	A	334	ASP	1
1	A	339	ARG	1
1	A	304	VAL	1
1	A	294	VAL	1
1	A	290	TYR	1
1	A	332	VAL	1
1	A	352	ASN	1
1	A	349	CYS	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