Full wwPDB NMR Structure Validation Report (i)

Apr 26, 2016 – 04:41 PM BST

PDB ID	:	1RFH
Title	:	Solution structure of the C1 domain of Nore1, a novel Ras effector
Authors	:	Guiberman, E.; Wohlgemuth, S.; Herrmann, C.; Harjes, S.; Mueller, K.H.; Bayer, P.
Deposited on	:	2003-11-09

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:

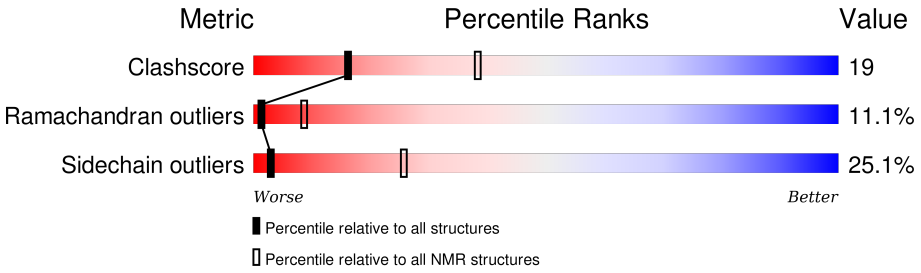
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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 is 58%.

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	59	37% 32% 5% 25%

2 Ensemble composition and analysis

This entry contains 21 models. The atoms present in the NMR models are not consistent. Some calculations may have failed as a result. All residues are included in the validation scores. Model 21 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *minimized average structure*.

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:118-A:123, A:129-A:166 (44)	0.25	21

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

NmrClust was unable to cluster the ensemble.

Error message: Inconsistent models in file

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 924 atoms, of which 458 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Ras association (RalGDS/AF-6) domain family 5.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	59	922	282	458	95	80	7	0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
			Total	Zn
2	A	2	2	2

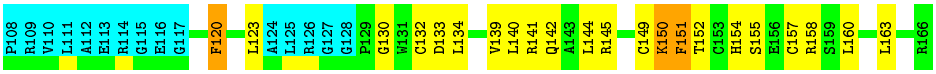
4 Residue-property plots (i)

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: Ras association (RalGDS/AF-6) domain family 5

Chain A:



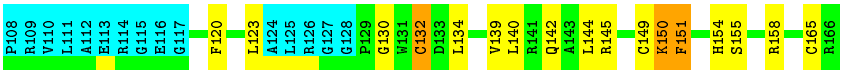
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

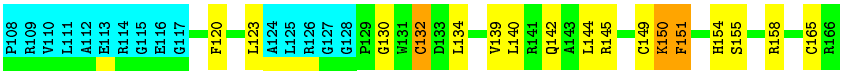
Chain A:



4.2.2 Score per residue for model 2

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

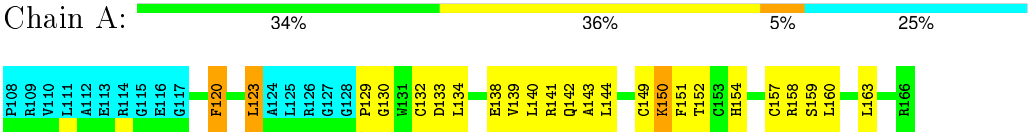
Chain A:



4.2.3 Score per residue for model 3

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

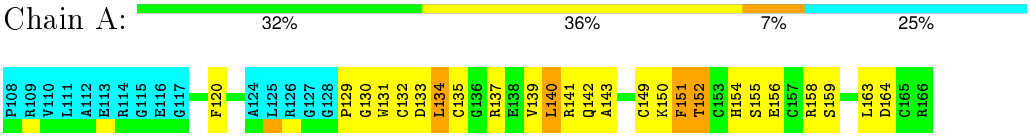
Chain A:



4.2.4 Score per residue for model 4

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

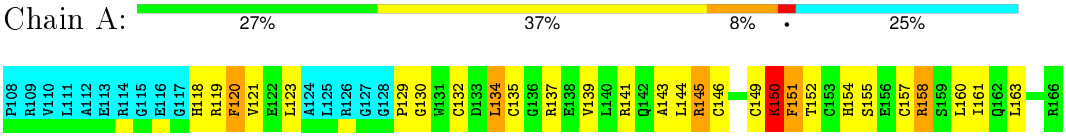
Chain A:



4.2.5 Score per residue for model 5

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

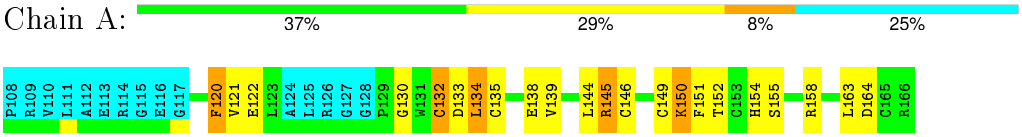
Chain A:



4.2.6 Score per residue for model 6

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

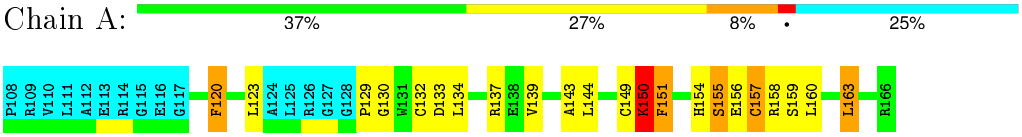
Chain A:



4.2.7 Score per residue for model 7

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

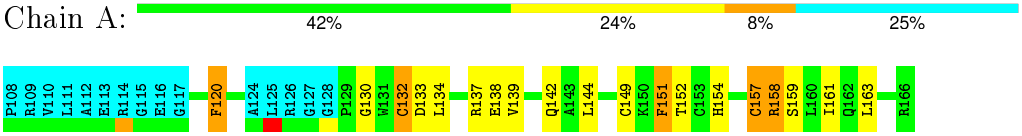
Chain A:



4.2.8 Score per residue for model 8

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

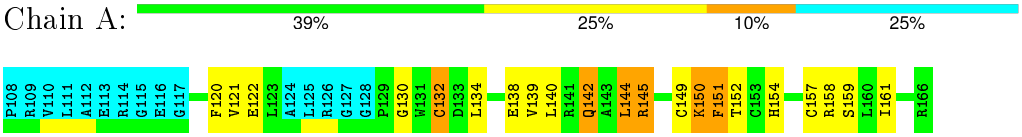
Chain A:



4.2.9 Score per residue for model 9

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

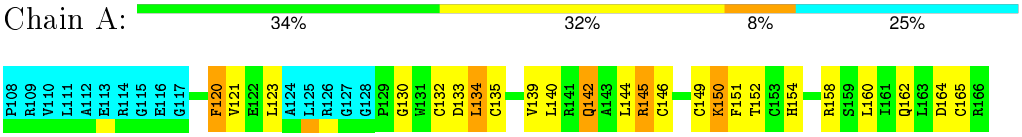
Chain A:



4.2.10 Score per residue for model 10

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

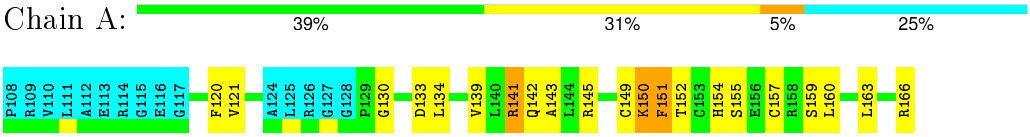
Chain A:



4.2.11 Score per residue for model 11

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

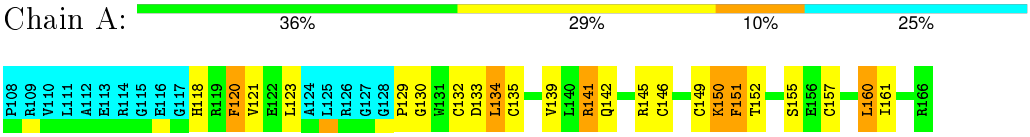
Chain A:



4.2.12 Score per residue for model 12

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

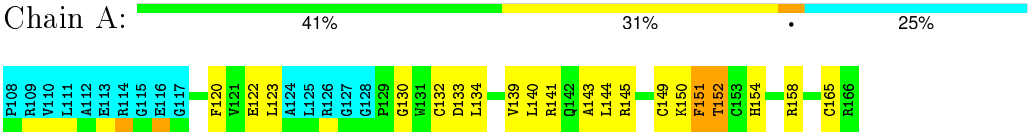
Chain A:



4.2.13 Score per residue for model 13

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

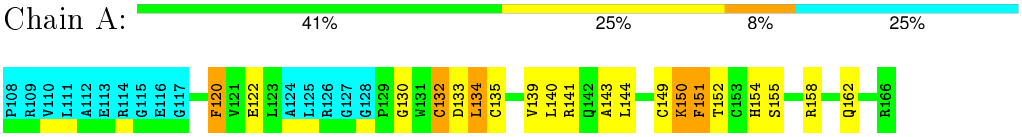
Chain A:



4.2.14 Score per residue for model 14

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

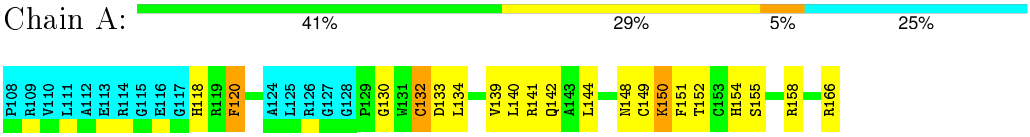
Chain A:



4.2.15 Score per residue for model 15

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

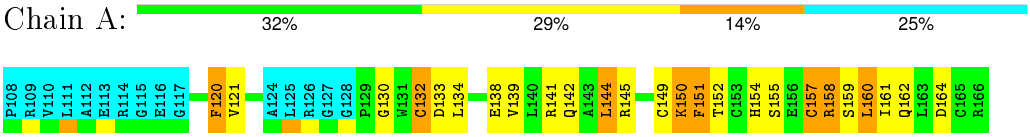
Chain A:



4.2.16 Score per residue for model 16

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

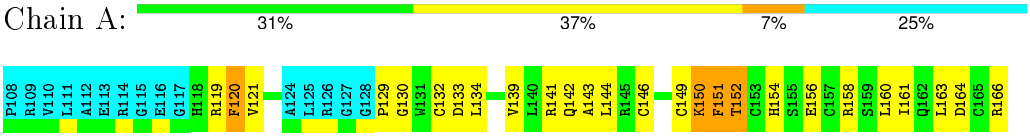
Chain A:



4.2.17 Score per residue for model 17

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

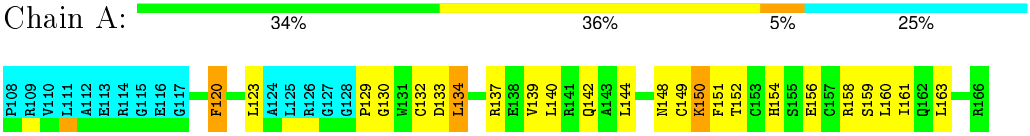
Chain A:



4.2.18 Score per residue for model 18

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

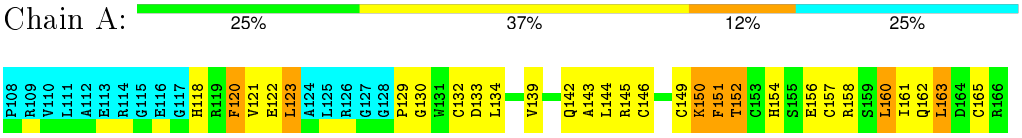
Chain A:



4.2.19 Score per residue for model 19

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

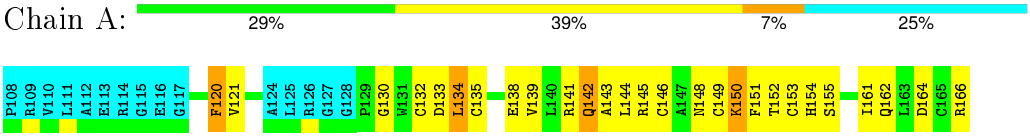
Chain A:



4.2.20 Score per residue for model 20

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

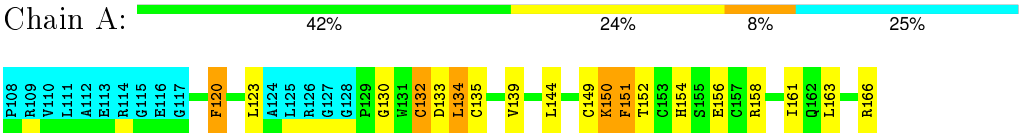
Chain A:



4.2.21 Score per residue for model 21 (medoid)

• Molecule 1: Ras association (RalGDS/AF-6) domain family 5

Chain A:



5 Refinement protocol and experimental data overview

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

Of the 50 calculated structures, 21 were deposited, based on the following criterion: *structures with the least restraint violations,structures with the lowest energy*.

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

Software name	Classification	Version
CNS	structure solution	1.1
CNS	refinement	1.1

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 6059
Number of chemical shift lists	1
Total number of shifts	494
Number of shifts mapped to atoms	494
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	58%

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

6 Model quality

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	356	345	345	13±4
All	All	7519	7245	7245	276

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 19.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:139:VAL:HG12	1:A:154:HIS:CD2	0.84	2.07	18	20
1:A:139:VAL:HG21	1:A:143:ALA:HB2	0.83	1.50	4	7
1:A:160:LEU:O	1:A:160:LEU:HD22	0.76	1.81	12	1
1:A:121:VAL:HG22	1:A:145:ARG:O	0.74	1.82	19	9
1:A:160:LEU:HD13	1:A:161:ILE:N	0.73	1.98	12	1
1:A:123:LEU:HD22	1:A:152:THR:HG21	0.73	1.61	13	1
1:A:133:ASP:OD2	1:A:152:THR:HG22	0.72	1.85	14	10
1:A:150:LYS:NZ	1:A:161:ILE:HG21	0.71	2.00	19	1
1:A:130:GLY:O	1:A:139:VAL:HG22	0.71	1.85	4	19
1:A:157:CYS:O	1:A:160:LEU:HD12	0.70	1.86	12	1
1:A:120:PHE:HB3	1:A:144:LEU:HD12	0.70	1.62	7	1
1:A:158:ARG:HA	1:A:161:ILE:HD12	0.70	1.62	8	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:120:PHE:HB3	1:A:144:LEU:HD22	0.68	1.65	8	12
1:A:130:GLY:C	1:A:139:VAL:HG22	0.67	2.08	6	20
1:A:143:ALA:HB1	1:A:152:THR:HG22	0.66	1.66	19	4
1:A:144:LEU:HD13	1:A:158:ARG:HD2	0.65	1.68	5	2
1:A:157:CYS:HA	1:A:160:LEU:HD12	0.64	1.69	16	2
1:A:150:LYS:HZ1	1:A:161:ILE:HG21	0.64	1.51	19	1
1:A:150:LYS:HE3	1:A:161:ILE:HD11	0.61	1.73	17	1
1:A:139:VAL:HG12	1:A:154:HIS:NE2	0.60	2.10	1	17
1:A:150:LYS:HE2	1:A:161:ILE:HG21	0.60	1.73	5	1
1:A:139:VAL:HG23	1:A:139:VAL:O	0.59	1.98	17	5
1:A:144:LEU:HD13	1:A:158:ARG:HG3	0.58	1.75	13	1
1:A:130:GLY:O	1:A:139:VAL:HG13	0.58	1.98	4	1
1:A:161:ILE:HG23	1:A:161:ILE:O	0.57	1.99	18	3
1:A:123:LEU:HD23	1:A:143:ALA:HB3	0.56	1.78	3	1
1:A:160:LEU:O	1:A:160:LEU:HD12	0.55	2.01	7	1
1:A:139:VAL:O	1:A:139:VAL:HG23	0.54	2.02	18	7
1:A:144:LEU:HD13	1:A:158:ARG:CD	0.54	2.32	5	1
1:A:123:LEU:CD2	1:A:143:ALA:HB3	0.53	2.33	3	2
1:A:123:LEU:HD12	1:A:123:LEU:O	0.53	2.03	5	1
1:A:156:GLU:O	1:A:160:LEU:HD23	0.53	2.03	17	1
1:A:160:LEU:C	1:A:160:LEU:HD13	0.52	2.24	12	1
1:A:121:VAL:O	1:A:121:VAL:HG23	0.52	2.05	19	2
1:A:123:LEU:HD22	1:A:145:ARG:HD3	0.52	1.81	12	1
1:A:139:VAL:HG21	1:A:143:ALA:CB	0.52	2.29	4	1
1:A:157:CYS:O	1:A:161:ILE:HD12	0.52	2.04	9	1
1:A:157:CYS:HA	1:A:160:LEU:HD23	0.51	1.82	19	1
1:A:152:THR:O	1:A:152:THR:HG23	0.51	2.06	16	4
1:A:160:LEU:C	1:A:160:LEU:HD22	0.51	2.24	12	1
1:A:143:ALA:CB	1:A:152:THR:HG22	0.51	2.35	19	3
1:A:121:VAL:HG23	1:A:121:VAL:O	0.51	2.06	5	3
1:A:123:LEU:HD21	1:A:152:THR:HG21	0.50	1.84	5	1
1:A:130:GLY:CA	1:A:139:VAL:HG22	0.50	2.37	14	19
1:A:123:LEU:CD2	1:A:152:THR:HG21	0.49	2.36	19	1
1:A:134:LEU:HD13	1:A:161:ILE:HD12	0.49	1.85	18	1
1:A:160:LEU:HD12	1:A:160:LEU:O	0.48	2.09	19	1
1:A:150:LYS:NZ	1:A:163:LEU:HD13	0.48	2.24	7	1
1:A:123:LEU:HD22	1:A:143:ALA:HB3	0.46	1.87	7	1
1:A:156:GLU:O	1:A:160:LEU:HD12	0.46	2.09	18	1
1:A:146:CYS:HB3	1:A:150:LYS:CG	0.46	2.41	19	1
1:A:152:THR:HG23	1:A:152:THR:O	0.46	2.11	11	2
1:A:134:LEU:HD23	1:A:135:CYS:SG	0.46	2.51	4	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:118:HIS:CB	1:A:120:PHE:CE2	0.46	2.99	19	4
1:A:151:PHE:N	1:A:151:PHE:CD1	0.46	2.84	13	6
1:A:132:CYS:HB2	1:A:154:HIS:CE1	0.45	2.47	9	9
1:A:151:PHE:CD1	1:A:151:PHE:N	0.45	2.85	7	7
1:A:154:HIS:HB2	1:A:157:CYS:HB2	0.44	1.89	8	5
1:A:120:PHE:CD1	1:A:146:CYS:HB2	0.44	2.48	17	6
1:A:132:CYS:CB	1:A:154:HIS:CE1	0.44	3.00	21	2
1:A:123:LEU:HD22	1:A:152:THR:CG2	0.44	2.39	13	1
1:A:120:PHE:HB3	1:A:144:LEU:HB3	0.44	1.89	16	1
1:A:122:GLU:HB3	1:A:144:LEU:HD23	0.43	1.90	9	1
1:A:131:TRP:O	1:A:133:ASP:N	0.43	2.52	4	1
1:A:133:ASP:HB2	1:A:151:PHE:CG	0.43	2.49	7	7
1:A:123:LEU:HD23	1:A:143:ALA:O	0.42	2.15	7	1
1:A:133:ASP:CB	1:A:151:PHE:CG	0.42	3.03	19	3
1:A:145:ARG:HG2	1:A:152:THR:HG23	0.42	1.91	12	1
1:A:145:ARG:HA	1:A:152:THR:HA	0.41	1.91	19	1
1:A:160:LEU:HD13	1:A:161:ILE:HG13	0.41	1.92	12	1
1:A:153:CYS:SG	1:A:161:ILE:HD11	0.41	2.56	20	1
1:A:139:VAL:CG2	1:A:139:VAL:O	0.41	2.67	17	1
1:A:123:LEU:H	1:A:123:LEU:HD23	0.41	1.76	7	1
1:A:150:LYS:NZ	1:A:163:LEU:CD1	0.41	2.84	7	1
1:A:130:GLY:HA3	1:A:139:VAL:HG22	0.41	1.93	14	1
1:A:118:HIS:HB2	1:A:120:PHE:CE2	0.40	2.52	12	1
1:A:118:HIS:CE1	1:A:163:LEU:O	0.40	2.75	19	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	43/59 (73%)	33±2 (77±4%)	5±2 (12±5%)	5±1 (11±2%)	1 9
All	All	903/1239 (73%)	694 (77%)	109 (12%)	100 (11%)	1 9

All 9 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	149	CYS	21
1	A	120	PHE	21
1	A	132	CYS	20
1	A	150	LYS	16
1	A	142	GLN	9
1	A	129	PRO	8
1	A	141	ARG	3
1	A	155	SER	1
1	A	163	LEU	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	40/49 (82%)	30±2 (75±4%)	10±2 (25±4%)	3	26
All	All	840/1029 (82%)	629 (75%)	211 (25%)	3	26

All 26 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	151	PHE	21
1	A	134	LEU	21
1	A	150	LYS	20
1	A	158	ARG	16
1	A	155	SER	12
1	A	140	LEU	10
1	A	141	ARG	10
1	A	163	LEU	10
1	A	142	GLN	8
1	A	159	SER	8
1	A	145	ARG	7
1	A	152	THR	6
1	A	164	ASP	6
1	A	160	LEU	6
1	A	138	GLU	6
1	A	165	CYS	5
1	A	162	GLN	5

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Mol	Chain	Res	Type	Models (Total)
1	A	166	ARG	5
1	A	137	ARG	5
1	A	122	GLU	4
1	A	156	GLU	4
1	A	123	LEU	4
1	A	144	LEU	4
1	A	157	CYS	3
1	A	148	ASN	3
1	A	119	ARG	2

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

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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

The completeness of assignment taking into account all chemical shift lists is 58% for the well-defined parts and 58% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 6059

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	494
Number of shifts mapped to atoms	494
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 ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	58	-0.25 ± 0.15	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	52	0.19 ± 0.15	None needed (< 0.5 ppm)
$^{13}C'$	0	—	—
^{15}N	55	-1.39 ± 0.84	None needed (imprecise)

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 58%, i.e. 335 atoms were assigned a chemical shift out of a possible 573. 0 out of 8 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	169/218 (78%)	83/87 (95%)	44/88 (50%)	42/43 (98%)
Sidechain	166/311 (53%)	124/185 (67%)	42/104 (40%)	0/22 (0%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	0/44 (0%)	0/24 (0%)	0/17 (0%)	0/3 (0%)
Overall	335/573 (58%)	207/296 (70%)	86/209 (41%)	42/68 (62%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 58%, i.e. 432 atoms were assigned a chemical shift out of a possible 751. 0 out of 11 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	221/291 (76%)	108/116 (93%)	58/118 (49%)	55/57 (96%)
Sidechain	211/416 (51%)	159/247 (64%)	52/138 (38%)	0/31 (0%)
Aromatic	0/44 (0%)	0/24 (0%)	0/17 (0%)	0/3 (0%)
Overall	432/751 (58%)	267/387 (69%)	110/273 (40%)	55/91 (60%)

7.1.4 Statistically unusual chemical shifts (i)

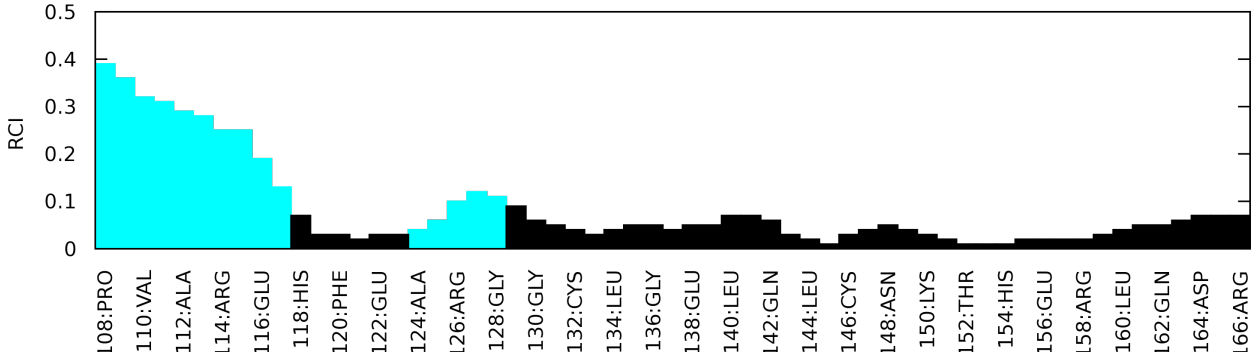
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	166	ARG	HG2	3.86	2.92 – 0.22	8.5
1	A	166	ARG	HD2	1.55	4.27 – 1.97	-6.8
1	A	166	ARG	HD3	1.55	4.36 – 1.86	-6.2
1	A	133	ASP	HB2	1.21	4.07 – 1.37	-5.6
1	A	166	ARG	HG3	3.16	3.00 – 0.10	5.6

7.1.5 Random Coil Index (RCI) plots (i)

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:


RCI
0.5
0.4
0.3
0.2
0.1
0
108:PRO
110:VAL
112:ALA
114:ARG
116:GLU
118:HIS
120:PHE
122:GLU
124:ALA
126:ARG
128:GLY
130:GLY
132:CYS
134:LEU
136:GLY
138:GLU
140:LEU
142:GLN
144:LEU
146:CYS
148:ASN
150:LYS
152:THR
154:HIS
156:GLU
158:ARG
160:LEU
162:GLN
164:ASP
166:ARG