wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2JOH
Title	:	NMR structure of rabbit prion protein mutation S173N
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This is a wwPDB NMR Structure Validation Summary 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:

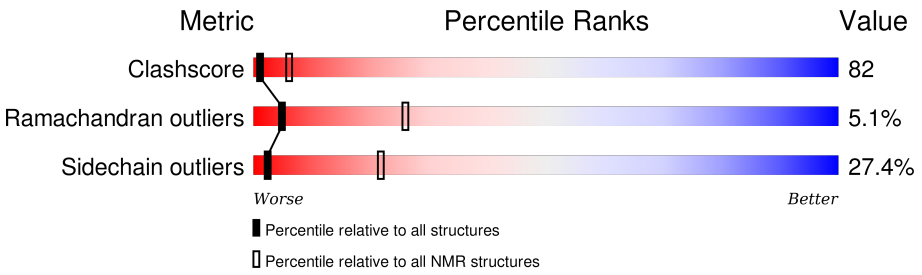
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal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

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	148	13% 36% 14% • 7% 29%

2 Ensemble composition and analysis (i)

This entry contains 15 models. Model 11 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:127-A:166, A:170-A:190, A:194-A:226 (94)	0.31	11

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, 2, 3, 4, 5, 8, 11, 12, 13
2	7, 10, 14, 15
Single-model clusters	6; 9

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1698 atoms, of which 822 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Major prion protein.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	105	1698	545	822	153	171	7	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	89	MET	-	INITIATING METHIONINE	UNP Q95211
A	90	HIS	-	EXPRESSION TAG	UNP Q95211
A	173	ASN	SER	ENGINEERED	UNP Q95211
A	229	LEU	-	EXPRESSION TAG	UNP Q95211
A	230	GLU	-	EXPRESSION TAG	UNP Q95211
A	231	HIS	-	EXPRESSION TAG	UNP Q95211
A	232	HIS	-	EXPRESSION TAG	UNP Q95211
A	233	HIS	-	EXPRESSION TAG	UNP Q95211
A	234	HIS	-	EXPRESSION TAG	UNP Q95211
A	235	HIS	-	EXPRESSION TAG	UNP Q95211
A	236	HIS	-	EXPRESSION TAG	UNP Q95211

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: Major prion protein

Chain A: 13% 36% 14% • 7% 29%

MET HIS GLN GLY GLY THR HIS ASN GLN TRP GLY LYS PRO SER LYS PRO LYS THR SER MET LYS HIS VAL ALA GLY ALA ALA ALA ALA ALA GLY ALA VAL VAL GLY GLY L124 G125 G126 Y127 M128 L129 G130 S131 A132 M133 S134 R135 P136 L137 I138 H139 F140 D143 Y144 E145 D146 R147 Y148 Y149

R150 E151 N152 M153 Y154 R155 Y156 P157 N158 Q159 V160 Y161 Y162 R163 P164 V165 D166 Q167 Y168 S169 N170 Q171 N172 N173 F174 V175 C178 V179 N180 I181 T182 V183 K184 Q185 H186 T187 V188 T189 T190 T191 T192 K193 G194 E195 N196 F197 T198 E199 T200 D201 I202 K203 I204 M205 E206 R207 V208 V209 E210

Q211 M212 C213 I214 T215 Q216 Y217 Q218 Q219 E220 S221 Q222 A223 A224 Y225 Q226 R227 A228 LEU GLU HIS HIS HIS HIS HIS HIS

4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 11. Colouring as in section 4.1 above.

- Molecule 1: Major prion protein

Chain A: 9% 37% 16% • 7% 29%

MET HIS GLN GLY GLY THR HIS ASN GLN TRP GLY LYS PRO SER LYS PRO LYS THR SER MET LYS HIS VAL ALA GLY ALA ALA ALA ALA ALA GLY ALA VAL VAL GLY GLY L124 G125 G126 Y127 M128 L129 G130 S131 A132 M133 S134 R135 P136 L137 I138 H139 F140 G141 N142 D143 Y144 E145 D146 R147 Y148

Y149 R150 E151 N152 M153 Y154 R155 Y156 P157 N158 Q159 V160 Y161 Y162 R163 P164 V165 D166 Q167 Y168 S169 N170 Q171 N172 N173 F174 V175 C178 V179 N180 I181 T182 V183 K184 Q185 H186 T187 V188 T189 T190 T191 T192 K193 G194 E195 N196 F197 T198 E199 T200 D201 I202 K203 I204 M205 E206 R207 V208 V209

E210 Q211 M212 C213 I214 T215 Q216 Y217 Q218 Q219 E220 S221 Q222 A223 A224 Y225 Q226 R227 A228 LEU GLU HIS HIS HIS HIS HIS HIS

5 Refinement protocol and experimental data overview (i)

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

Of the 200 calculated structures, 15 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
ARIA	structure solution	
ARIA	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	BMRB entry 15394
Number of chemical shift lists	1
Total number of shifts	1157
Number of shifts mapped to atoms	1157
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 (i)

6.1 Standard geometry (i)

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	0.74±0.06	1±1/813 (0.1±0.2%)	0.75±0.02	0±0/1103 (0.0±0.0%)
All	All	0.75	14/12195 (0.1%)	0.75	6/16545 (0.0%)

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	1.3±0.6
All	All	0	19

5 of 10 unique bond 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(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	156	TYR	CE1-CZ	10.99	1.52	1.38	2	1
1	A	156	TYR	CE2-CZ	-10.84	1.24	1.38	2	2
1	A	161	TYR	CE1-CZ	-7.96	1.28	1.38	2	2
1	A	161	TYR	CE2-CZ	7.59	1.48	1.38	2	2
1	A	127	TYR	CE2-CZ	-7.29	1.29	1.38	4	1

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	157	PRO	N-CA-CB	-5.78	96.25	102.60	6	6

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	156	TYR	Peptide,Sidechain	15
1	A	127	TYR	Sidechain	1
1	A	154	TYR	Sidechain	1
1	A	189	THR	Peptide	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	794	738	735	125±7
All	All	11910	11070	11025	1879

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 82.

5 of 532 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:165:VAL:HG13	1:A:220:GLU:HG3	1.08	1.13	7	4
1:A:165:VAL:HG13	1:A:220:GLU:HG2	0.98	1.31	10	5
1:A:179:VAL:HG13	1:A:209:VAL:HG22	0.96	1.34	5	2
1:A:216:GLN:HA	1:A:219:GLN:HG2	0.96	1.32	14	11
1:A:161:TYR:HB3	1:A:181:ILE:HD13	0.94	1.35	13	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	94/148 (64%)	72±3 (76±3%)	17±2 (19±2%)	5±1 (5±1%)	5	26
All	All	1410/2220 (64%)	1077 (76%)	261 (19%)	72 (5%)	5	26

5 of 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	131	SER	15
1	A	157	PRO	14
1	A	139	HIS	11
1	A	130	GLY	9
1	A	188	VAL	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	88/126 (70%)	64±3 (73±4%)	24±3 (27±4%)	2 22
All	All	1320/1890 (70%)	958 (73%)	362 (27%)	2 22

5 of 58 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	202	ILE	15
1	A	212	MET	15
1	A	179	VAL	15
1	A	157	PRO	15
1	A	184	LYS	15

6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates (i)

There are no carbohydrates in this entry.

6.6 Ligand geometry (i)

There are no ligands in this entry.

6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

7 Chemical shift validation (i)

The completeness of assignment taking into account all chemical shift lists is 72% for the well-defined parts and 72% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 15394

Chemical shift list name: *assigned_ chem_ shift_ list_ 1*

7.1.1 Bookkeeping (i)

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	1157
Number of shifts mapped to atoms	1157
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	114	-0.19 ± 0.13	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	102	0.14 ± 0.07	None needed (< 0.5 ppm)
$^{13}C'$	0	—	—
^{15}N	125	0.23 ± 0.15	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments (i)

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. 877 atoms were assigned a chemical shift out of a possible 1219. 10 out of 10 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	365/464 (79%)	183/185 (99%)	93/188 (49%)	89/91 (98%)
Sidechain	465/624 (75%)	296/367 (81%)	169/220 (77%)	0/37 (0%)

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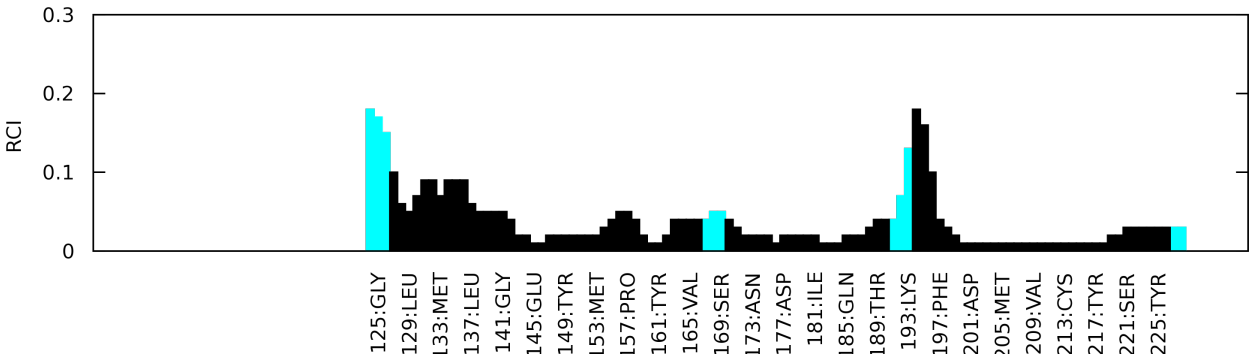
	Total	^{1}H	^{13}C	^{15}N
Aromatic	47/131 (36%)	47/67 (70%)	0/58 (0%)	0/6 (0%)
Overall	877/1219 (72%)	526/619 (85%)	262/466 (56%)	89/134 (66%)

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	217	TYR	HE2	8.29	7.86 – 5.56	6.8

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: