



Full wwPDB NMR Structure Validation Report ⓘ

May 28, 2020 – 11:35 pm BST

PDB ID : 2M8T
Title : Solution NMR structure of the V209M variant of the human prion protein (residues 90-231)
Authors : Mills, J.L.; Surewicz, K.; Surewicz, W.; Soennichsen, F.D.
Deposited on : 2013-05-28

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

<https://www.wwpdb.org/validation/2017/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
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : 2.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

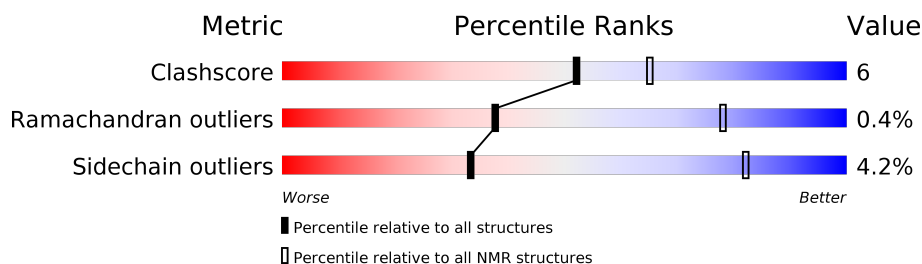
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 76%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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	146	

2 Ensemble composition and analysis

This entry contains 20 models. Model 17 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations*.

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:128-A:164, A:172-A:225 (91)	0.56	17

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 3 single-model clusters were found.

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

3 Entry composition

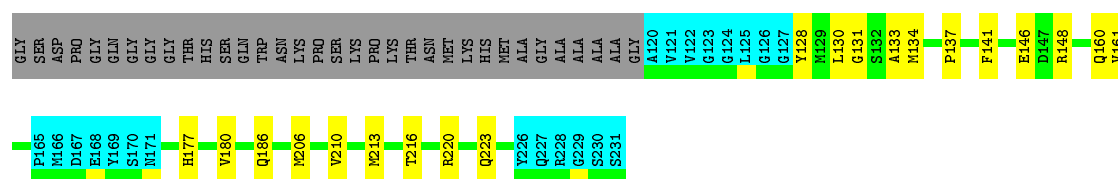
There is only 1 type of molecule in this entry. The entry contains 1777 atoms, of which 856 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Major prion protein.

Mol	Chain	Residues	Atoms						Trace
1	A	112	Total	C	H	N	O	S	0
			1777	569	856	161	181	10	

There are 5 discrepancies between the modelled and reference sequences:

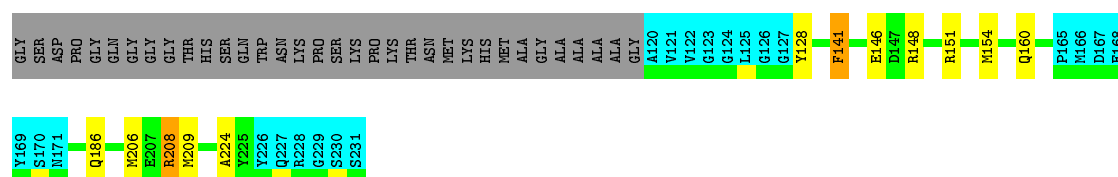
Chain	Residue	Modelled	Actual	Comment	Reference
A	86	GLY	-	EXPRESSION TAG	UNP P04156
A	87	SER	-	EXPRESSION TAG	UNP P04156
A	88	ASP	-	EXPRESSION TAG	UNP P04156
A	89	PRO	-	EXPRESSION TAG	UNP P04156
A	209	MET	VAL	ENGINEERED MUTATION	UNP P04156



4.2.3 Score per residue for model 3

- Molecule 1: Major prion protein

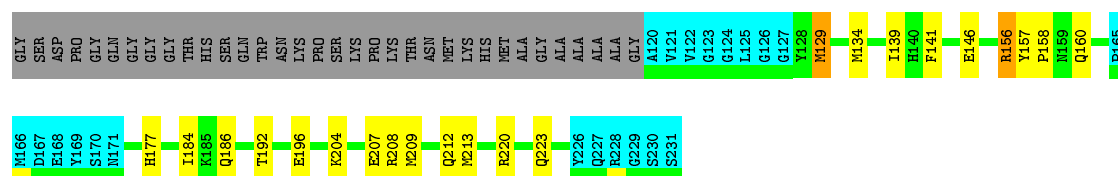
Chain A: 54% 7% 14% 23%



4.2.4 Score per residue for model 4

- Molecule 1: Major prion protein

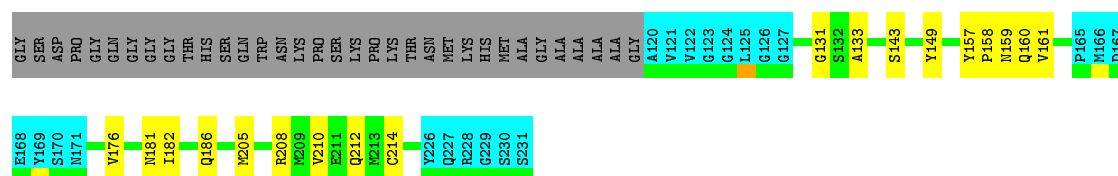
Chain A: 47% 14% 14% 23%



4.2.5 Score per residue for model 5

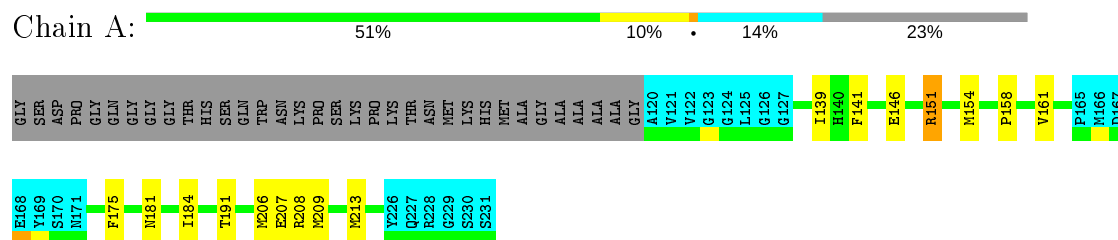
- Molecule 1: Major prion protein

Chain A: 50% 12% 14% 23%



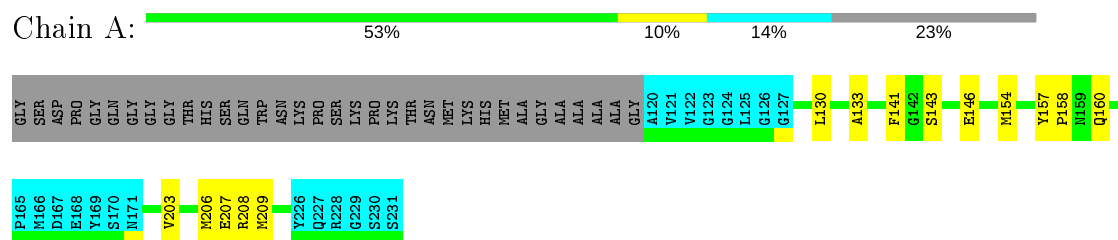
4.2.6 Score per residue for model 6

- Molecule 1: Major prion protein



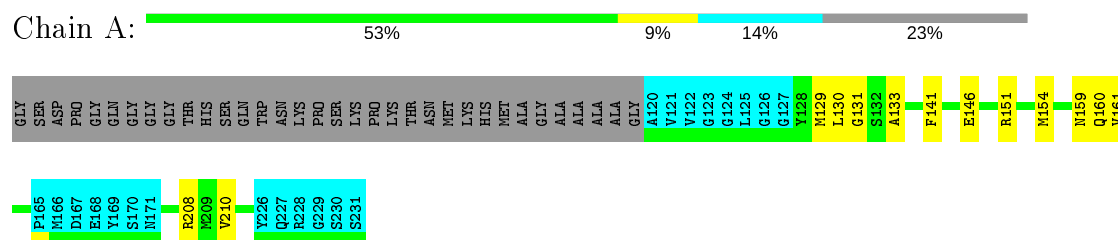
4.2.7 Score per residue for model 7

- Molecule 1: Major prion protein



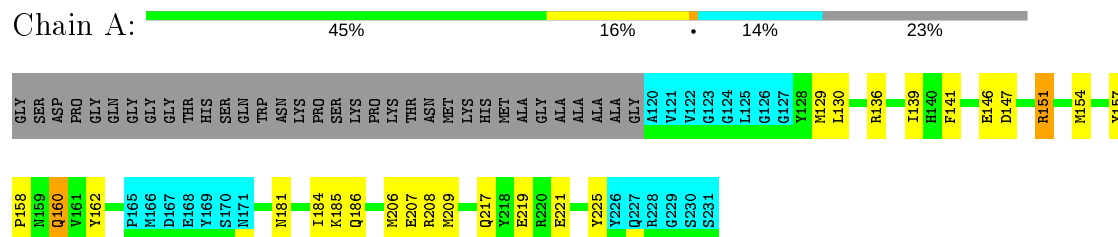
4.2.8 Score per residue for model 8

- Molecule 1: Major prion protein



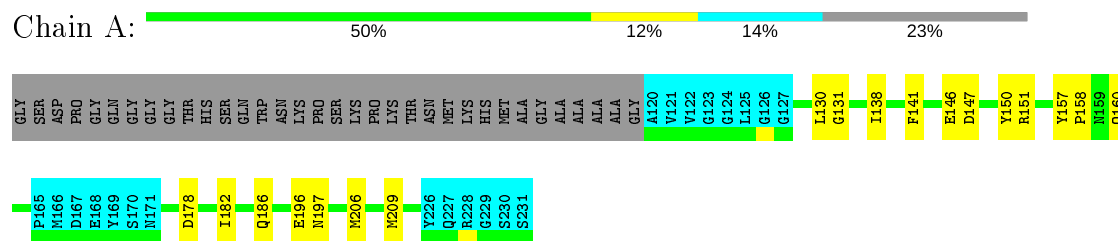
4.2.9 Score per residue for model 9

- Molecule 1: Major prion protein



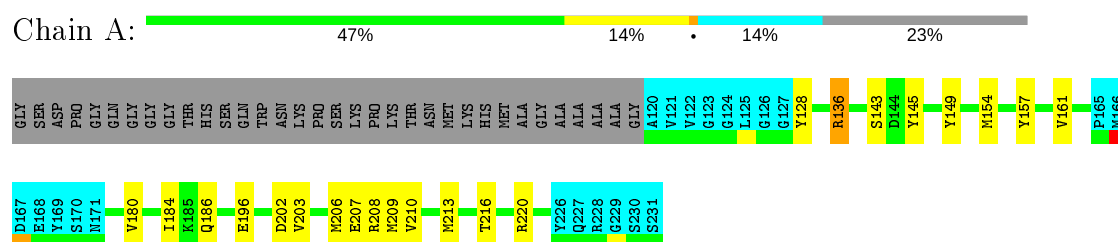
4.2.10 Score per residue for model 10

- Molecule 1: Major prion protein



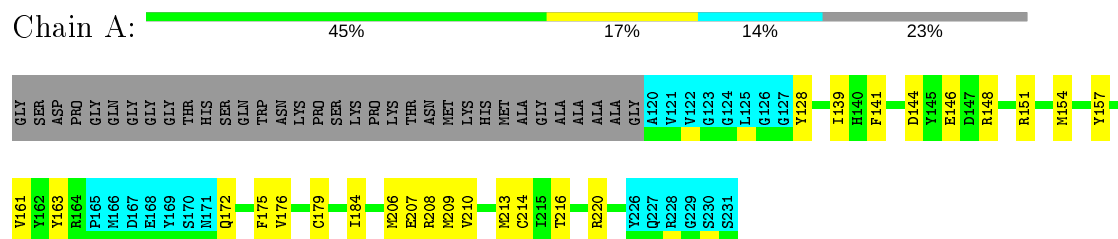
4.2.11 Score per residue for model 11

- Molecule 1: Major prion protein



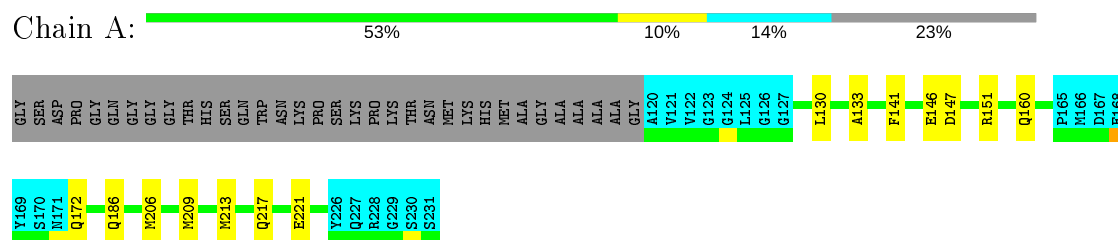
4.2.12 Score per residue for model 12

- Molecule 1: Major prion protein



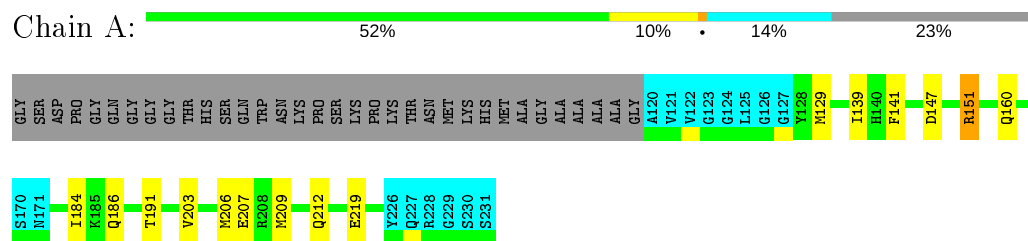
4.2.13 Score per residue for model 13

- Molecule 1: Major prion protein



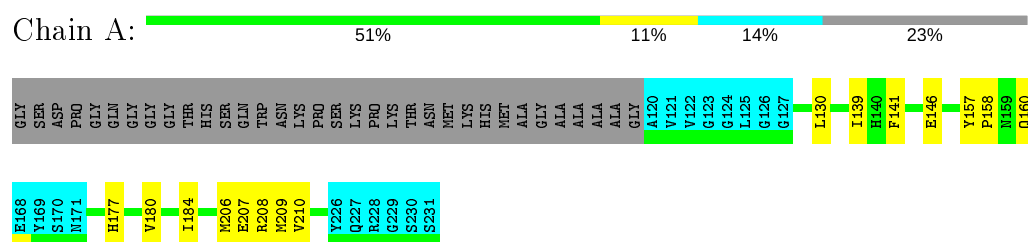
4.2.14 Score per residue for model 14

- Molecule 1: Major prion protein



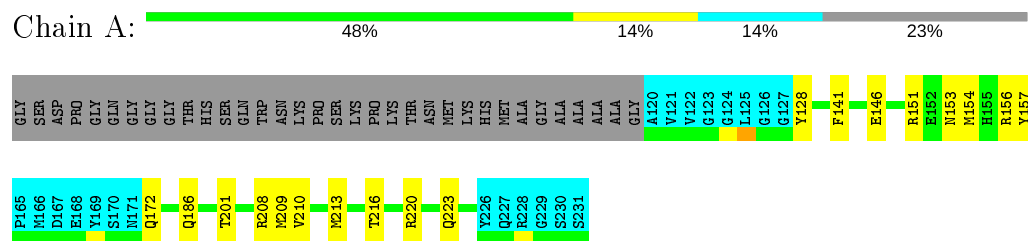
4.2.15 Score per residue for model 15

- Molecule 1: Major prion protein



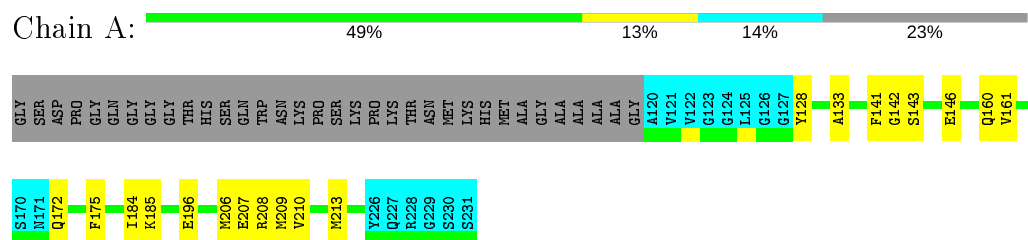
4.2.16 Score per residue for model 16

- Molecule 1: Major prion protein



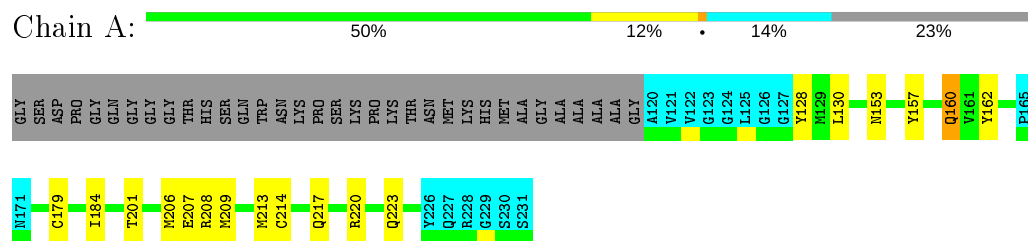
4.2.17 Score per residue for model 17 (medoid)

- Molecule 1: Major prion protein



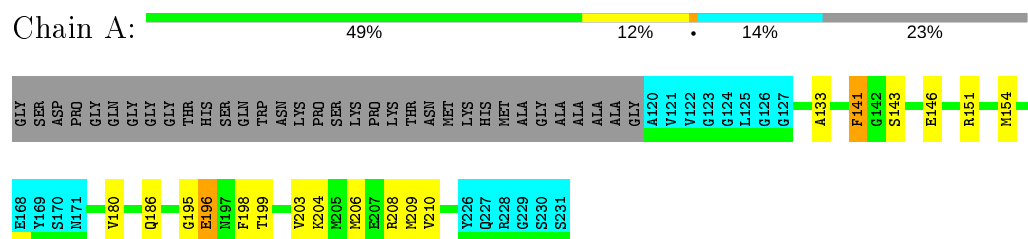
4.2.18 Score per residue for model 18

- Molecule 1: Major prion protein



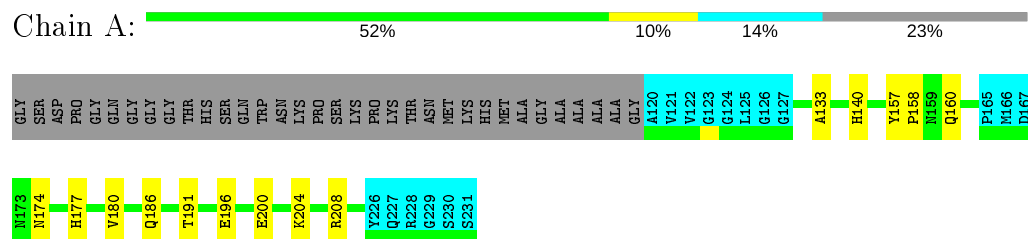
4.2.19 Score per residue for model 19

- Molecule 1: Major prion protein



4.2.20 Score per residue for model 20

- Molecule 1: Major prion protein



5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing, molecular dynamics, MOLECULAR DYNAMICS*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

Software name	Classification	Version
TALOS	geometry optimization	
CYANA	structure solution	
CNS	geometry optimization	
CYANA	refinement	
CNS	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)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	1503
Number of shifts mapped to atoms	1503
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	76%

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](#)

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 [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	772	721	723	9±3
All	All	15440	14420	14460	171

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 6.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:191:THR:HB	1:A:196:GLU:HB3	0.78	1.53	20	1
1:A:204:LYS:HE2	1:A:204:LYS:HA	0.76	1.57	4	1
1:A:130:LEU:HD11	1:A:160:GLN:HG3	0.67	1.65	13	9
1:A:153:ASN:O	1:A:156:ARG:HG2	0.63	1.93	16	1
1:A:163:TYR:HB3	1:A:179:CYS:HB3	0.62	1.71	12	1
1:A:161:VAL:HG13	1:A:213:MET:SD	0.60	2.37	16	4
1:A:220:ARG:HA	1:A:223:GLN:HG2	0.59	1.74	2	4
1:A:154:MET:HA	1:A:157:TYR:CD2	0.58	2.34	11	2
1:A:180:VAL:HA	1:A:210:VAL:HG11	0.58	1.74	11	4
1:A:147:ASP:O	1:A:151:ARG:HG2	0.57	1.98	13	2
1:A:156:ARG:HE	1:A:156:ARG:HA	0.56	1.60	4	1
1:A:139:ILE:HD12	1:A:208:ARG:HG3	0.56	1.77	15	5
1:A:133:ALA:HB2	1:A:160:GLN:HB3	0.56	1.77	5	5
1:A:206:MET:O	1:A:210:VAL:HG23	0.55	2.02	15	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:195:GLY:O	1:A:196:GLU:HG2	0.54	2.03	19	1
1:A:143:SER:HB2	1:A:146:GLU:OE2	0.53	2.03	7	2
1:A:206:MET:HA	1:A:209:MET:HG2	0.53	1.81	15	13
1:A:157:TYR:HB3	1:A:158:PRO:HD2	0.53	1.79	9	8
1:A:192:THR:HA	1:A:196:GLU:O	0.52	2.05	4	1
1:A:203:VAL:O	1:A:206:MET:HG2	0.52	2.05	11	1
1:A:163:TYR:HB3	1:A:179:CYS:SG	0.51	2.45	1	1
1:A:161:VAL:HG11	1:A:210:VAL:HG13	0.51	1.82	17	6
1:A:145:TYR:O	1:A:149:TYR:HB2	0.51	2.05	11	1
1:A:134:MET:SD	1:A:137:PRO:HA	0.51	2.46	2	1
1:A:141:PHE:HB2	1:A:146:GLU:OE1	0.50	2.06	8	13
1:A:213:MET:O	1:A:217:GLN:HG2	0.50	2.07	13	1
1:A:151:ARG:O	1:A:154:MET:HG2	0.49	2.07	12	7
1:A:141:PHE:CD1	1:A:146:GLU:HG2	0.48	2.42	7	2
1:A:133:ALA:HB1	1:A:159:ASN:OD1	0.48	2.08	19	1
1:A:184:ILE:HD11	1:A:207:GLU:CA	0.48	2.39	6	3
1:A:147:ASP:O	1:A:151:ARG:HB2	0.48	2.09	9	2
1:A:147:ASP:HB3	1:A:151:ARG:NH2	0.47	2.23	10	1
1:A:200:GLU:HB3	1:A:204:LYS:NZ	0.47	2.24	20	1
1:A:184:ILE:CD1	1:A:206:MET:HG3	0.47	2.39	14	5
1:A:216:THR:O	1:A:220:ARG:HG3	0.47	2.09	2	4
1:A:172:GLN:HG3	1:A:175:PHE:H	0.47	1.69	17	2
1:A:209:MET:O	1:A:213:MET:HG3	0.47	2.09	4	3
1:A:178:ASP:O	1:A:182:ILE:HG12	0.47	2.09	10	1
1:A:149:TYR:CD2	1:A:205:MET:HG3	0.47	2.45	5	1
1:A:177:HIS:O	1:A:180:VAL:HB	0.47	2.10	20	1
1:A:153:ASN:HB3	1:A:157:TYR:CZ	0.46	2.44	18	1
1:A:134:MET:HB2	1:A:213:MET:SD	0.46	2.50	2	1
1:A:141:PHE:CD2	1:A:146:GLU:HG2	0.46	2.44	2	2
1:A:156:ARG:NE	1:A:156:ARG:HA	0.46	2.26	4	1
1:A:139:ILE:HD11	1:A:209:MET:HA	0.46	1.88	12	1
1:A:133:ALA:CB	1:A:160:GLN:HB3	0.46	2.40	7	1
1:A:181:ASN:O	1:A:185:LYS:HG2	0.45	2.12	9	1
1:A:184:ILE:HD11	1:A:207:GLU:HA	0.45	1.88	6	7
1:A:176:VAL:HA	1:A:214:CYS:SG	0.45	2.52	5	2
1:A:141:PHE:CZ	1:A:208:ARG:HG3	0.45	2.47	3	1
1:A:136:ARG:O	1:A:136:ARG:HG2	0.44	2.12	11	1
1:A:149:TYR:HD2	1:A:205:MET:HG3	0.44	1.71	5	1
1:A:202:ASP:O	1:A:206:MET:HE2	0.44	2.12	11	1
1:A:144:ASP:OD2	1:A:148:ARG:HD3	0.44	2.12	12	1
1:A:139:ILE:HG21	1:A:141:PHE:CE2	0.44	2.48	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:217:GLN:O	1:A:221:GLU:HG2	0.43	2.13	9	1
1:A:204:LYS:CE	1:A:204:LYS:HA	0.43	2.38	4	1
1:A:134:MET:HE3	1:A:213:MET:HG2	0.43	1.90	4	1
1:A:182:ILE:O	1:A:186:GLN:HG2	0.43	2.14	5	1
1:A:185:LYS:HB2	1:A:185:LYS:NZ	0.42	2.29	17	1
1:A:157:TYR:CE2	1:A:206:MET:HB3	0.42	2.50	12	1
1:A:199:THR:O	1:A:203:VAL:HG23	0.41	2.16	19	1
1:A:185:LYS:HB2	1:A:185:LYS:HZ2	0.41	1.75	17	1
1:A:129:MET:HA	1:A:129:MET:CE	0.41	2.46	4	1
1:A:138:ILE:HA	1:A:150:TYR:CE2	0.41	2.51	10	1
1:A:209:MET:SD	1:A:210:VAL:HG13	0.41	2.56	16	1
1:A:203:VAL:O	1:A:207:GLU:HB2	0.41	2.16	7	1
1:A:179:CYS:HB2	1:A:214:CYS:SG	0.41	2.56	18	1
1:A:162:TYR:N	1:A:162:TYR:CD1	0.40	2.89	9	1
1:A:203:VAL:O	1:A:207:GLU:HG3	0.40	2.16	14	1
1:A:133:ALA:HA	1:A:160:GLN:HB3	0.40	1.94	20	1
1:A:184:ILE:HG13	1:A:207:GLU:HG2	0.40	1.93	15	1
1:A:157:TYR:HD2	1:A:209:MET:SD	0.40	2.40	12	1
1:A:209:MET:HG3	1:A:210:VAL:N	0.40	2.31	12	1
1:A:146:GLU:CD	1:A:146:GLU:H	0.40	2.19	15	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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	91/146 (62%)	87±1 (95±2%)	4±1 (4±1%)	0±1 (0±1%)	38	78
All	All	1820/2920 (62%)	1736 (95%)	76 (4%)	8 (0%)	38	78

All 4 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	GLY	4
1	A	141	PHE	2

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Mol	Chain	Res	Type	Models (Total)
1	A	142	GLY	1
1	A	196	GLU	1

6.3.2 Protein sidechains ⓘ

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	86/123 (70%)	82±2 (96±2%)	4±2 (4±2%)	33	82
All	All	1720/2460 (70%)	1648 (96%)	72 (4%)	33	82

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	208	ARG	11
1	A	186	GLN	11
1	A	160	GLN	7
1	A	129	MET	3
1	A	143	SER	3
1	A	212	GLN	3
1	A	196	GLU	3
1	A	177	HIS	3
1	A	151	ARG	3
1	A	159	ASN	2
1	A	172	GLN	2
1	A	201	THR	2
1	A	181	ASN	2
1	A	148	ARG	2
1	A	191	THR	2
1	A	136	ARG	2
1	A	219	GLU	2
1	A	221	GLU	1
1	A	158	PRO	1
1	A	162	TYR	1
1	A	197	ASN	1
1	A	156	ARG	1
1	A	204	LYS	1

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Mol	Chain	Res	Type	Models (Total)
1	A	198	PHE	1
1	A	217	GLN	1
1	A	140	HIS	1

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 76% for the well-defined parts and 74% for the entire structure.

7.1 Chemical shift list 1

File name: input_cs.cif

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	1503
Number of shifts mapped to atoms	1503
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 [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	142	-0.25 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	125	0.09 ± 0.09	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	133	0.06 ± 0.17	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 76%, i.e. 906 atoms were assigned a chemical shift out of a possible 1187. 7 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	352/451 (78%)	173/180 (96%)	91/182 (50%)	88/89 (99%)
Sidechain	482/609 (79%)	297/360 (82%)	166/213 (78%)	19/36 (53%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	72/127 (57%)	51/67 (76%)	21/56 (38%)	0/4 (0%)
Overall	906/1187 (76%)	521/607 (86%)	278/451 (62%)	107/129 (83%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 74%, i.e. 1048 atoms were assigned a chemical shift out of a possible 1407. 10 out of 10 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	416/554 (75%)	205/221 (93%)	108/224 (48%)	103/109 (94%)
Sidechain	548/710 (77%)	337/420 (80%)	189/249 (76%)	22/41 (54%)
Aromatic	84/143 (59%)	59/75 (79%)	25/64 (39%)	0/4 (0%)
Overall	1048/1407 (74%)	601/716 (84%)	322/537 (60%)	125/154 (81%)

7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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:

