



Full wwPDB NMR Structure Validation Report ⓘ

Dec 4, 2016 – 10:37 AM EST

PDB ID : 2MQI
Title : human Fyn SH2 free state
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Deposited on : 2014-06-20

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 ⓘ 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
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-20028442
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20028442

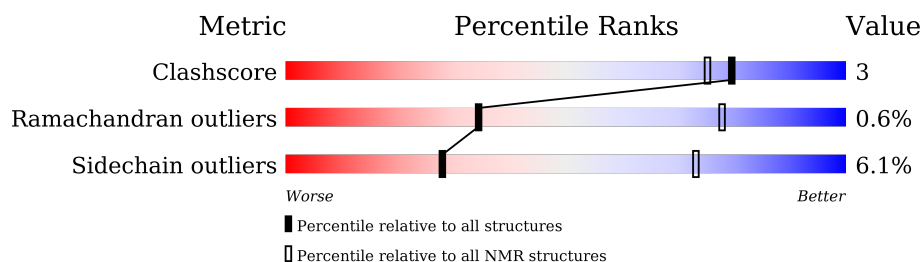
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 87%.

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	111	 84% 5% • 10%

2 Ensemble composition and analysis

This entry contains 20 models. Model 1 is the overall representative, medoid model (most similar to other models).

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:151-A:248 (98)	0.50	1

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 3 clusters and 1 single-model cluster was found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1635 atoms, of which 812 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Tyrosine-protein kinase Fyn.

Mol	Chain	Residues	Atoms						Trace
1	A	100	Total	C	H	N	O	S	0
			1635	520	812	152	147	4	

There are 10 discrepancies between the modelled and reference sequences:

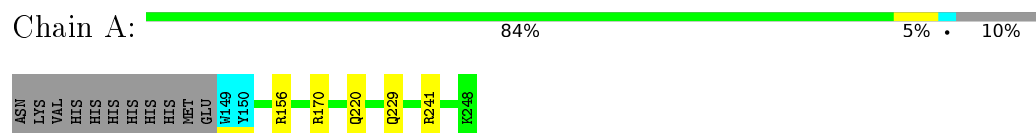
Chain	Residue	Modelled	Actual	Comment	Reference
A	138	ASN	-	EXPRESSION TAG	UNP P06241
A	139	LYS	-	EXPRESSION TAG	UNP P06241
A	140	VAL	-	EXPRESSION TAG	UNP P06241
A	141	HIS	-	EXPRESSION TAG	UNP P06241
A	142	HIS	-	EXPRESSION TAG	UNP P06241
A	143	HIS	-	EXPRESSION TAG	UNP P06241
A	144	HIS	-	EXPRESSION TAG	UNP P06241
A	145	HIS	-	EXPRESSION TAG	UNP P06241
A	146	HIS	-	EXPRESSION TAG	UNP P06241
A	147	MET	-	EXPRESSION TAG	UNP P06241

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: Tyrosine-protein kinase Fyn

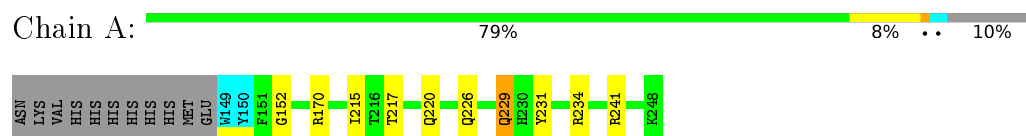


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

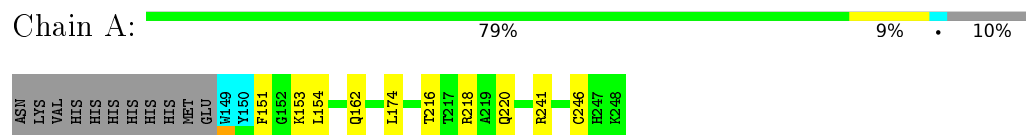
4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: Tyrosine-protein kinase Fyn



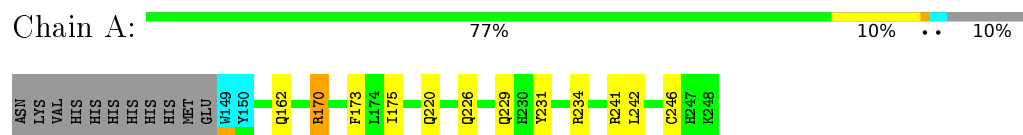
4.2.2 Score per residue for model 2

- Molecule 1: Tyrosine-protein kinase Fyn



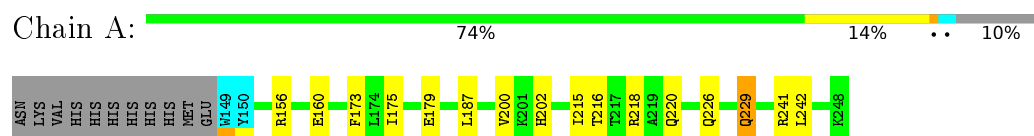
4.2.3 Score per residue for model 3

- Molecule 1: Tyrosine-protein kinase Fyn



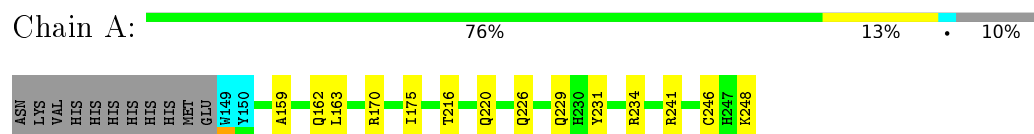
4.2.4 Score per residue for model 4

- Molecule 1: Tyrosine-protein kinase Fyn



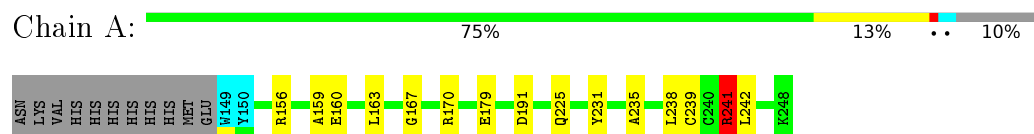
4.2.5 Score per residue for model 5

- Molecule 1: Tyrosine-protein kinase Fyn



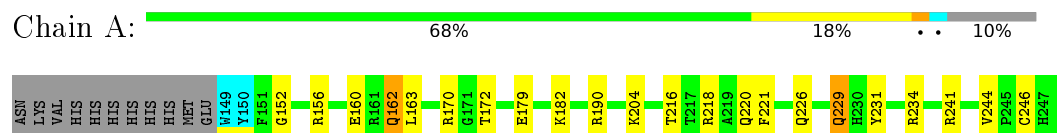
4.2.6 Score per residue for model 6

- Molecule 1: Tyrosine-protein kinase Fyn



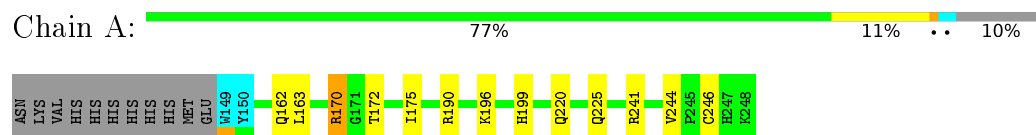
4.2.7 Score per residue for model 7

- Molecule 1: Tyrosine-protein kinase Fyn



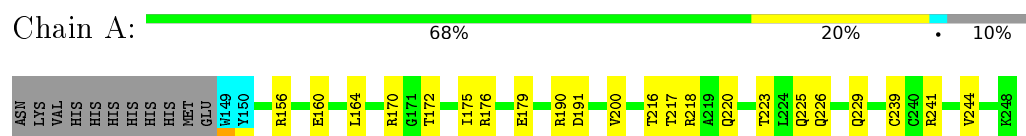
4.2.8 Score per residue for model 8

- Molecule 1: Tyrosine-protein kinase Fyn



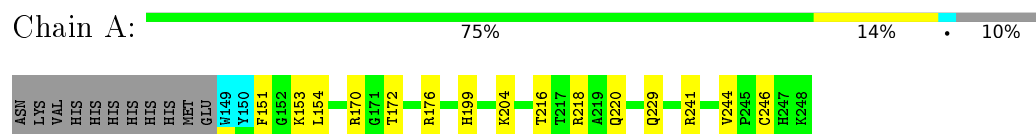
4.2.9 Score per residue for model 9

- Molecule 1: Tyrosine-protein kinase Fyn



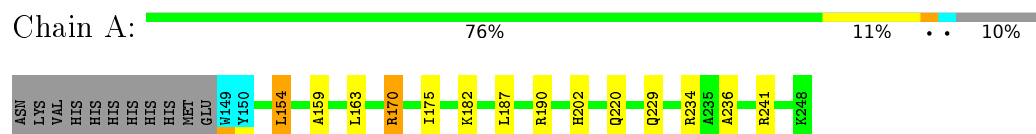
4.2.10 Score per residue for model 10

- Molecule 1: Tyrosine-protein kinase Fyn



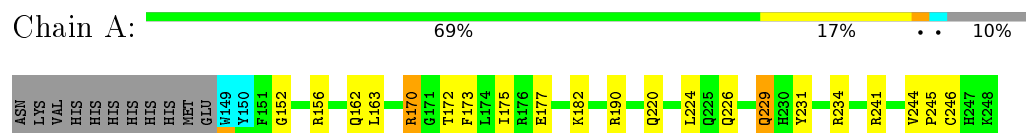
4.2.11 Score per residue for model 11

- Molecule 1: Tyrosine-protein kinase Fyn



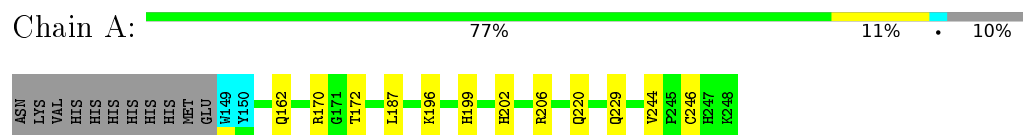
4.2.12 Score per residue for model 12

- Molecule 1: Tyrosine-protein kinase Fyn



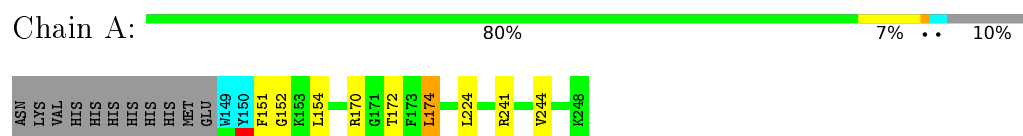
4.2.13 Score per residue for model 13

- Molecule 1: Tyrosine-protein kinase Fyn



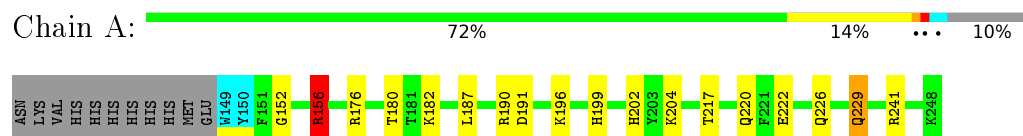
4.2.14 Score per residue for model 14

- Molecule 1: Tyrosine-protein kinase Fyn



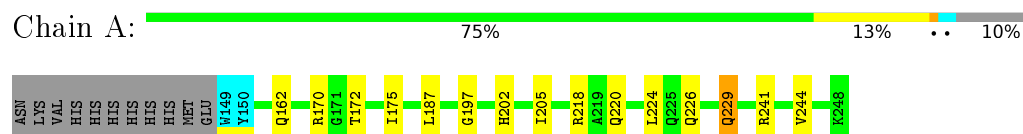
4.2.15 Score per residue for model 15

- Molecule 1: Tyrosine-protein kinase Fyn



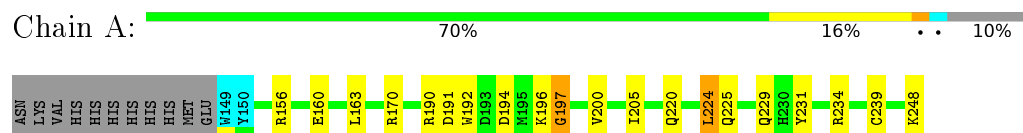
4.2.16 Score per residue for model 16

- Molecule 1: Tyrosine-protein kinase Fyn



4.2.17 Score per residue for model 17

- Molecule 1: Tyrosine-protein kinase Fyn



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 20 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
CYANA	structure solution	
CNS	refinement	
TALOS	geometry optimization	
TALOS	structure solution	
TALOS	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)	2mqi_cs.cif
Number of chemical shift lists	1
Total number of shifts	1332
Number of shifts mapped to atoms	1332
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	87%

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	0.82±0.03	0±0/813 (0.0±0.0%)	0.67±0.02	0±0/1088 (0.0±0.0%)
All	All	0.82	3/16260 (0.0%)	0.67	2/21760 (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	0.2±0.4
All	All	0	4

All 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	197	GLY	CA-C	-6.98	1.40	1.51	17	1
1	A	152	GLY	N-CA	-5.45	1.37	1.46	14	1
1	A	241	ARG	N-CA	-5.16	1.36	1.46	6	1

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(°)	Ideal(°)	Models	
								Worst	Total
1	A	197	GLY	N-CA-C	6.05	128.23	113.10	17	1
1	A	196	LYS	C-N-CA	-5.06	111.67	122.30	17	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	156	ARG	Sidechain	2
1	A	241	ARG	Sidechain	1
1	A	206	ARG	Sidechain	1

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	797	793	793	5±3
All	All	15940	15860	15860	107

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:241:ARG:NE	1:A:241:ARG:HA	0.80	1.91	6	1
1:A:192:TRP:CH2	1:A:194:ASP:HA	0.79	2.12	17	1
1:A:160:GLU:HG2	1:A:200:VAL:HG21	0.65	1.67	17	1
1:A:162:GLN:HB3	1:A:246:CYS:SG	0.64	2.31	12	7
1:A:226:GLN:O	1:A:229:GLN:HG2	0.60	1.96	3	8
1:A:170:ARG:HD2	1:A:170:ARG:O	0.53	2.03	12	2
1:A:231:TYR:HA	1:A:234:ARG:O	0.53	2.03	1	7
1:A:172:THR:HA	1:A:244:VAL:O	0.53	2.03	13	9
1:A:196:LYS:O	1:A:199:HIS:HB2	0.53	2.04	13	3
1:A:156:ARG:O	1:A:160:GLU:HG3	0.52	2.05	7	5
1:A:216:THR:HG23	1:A:218:ARG:HG2	0.52	1.81	9	3
1:A:238:LEU:HD12	1:A:241:ARG:HH22	0.52	1.65	6	1
1:A:152:GLY:O	1:A:177:GLU:HG3	0.51	2.04	12	1
1:A:170:ARG:NE	1:A:170:ARG:H	0.51	2.04	3	1
1:A:187:LEU:O	1:A:202:HIS:HA	0.51	2.06	15	6
1:A:191:ASP:OD1	1:A:239:CYS:HB2	0.50	2.05	9	2
1:A:235:ALA:N	1:A:241:ARG:HD2	0.49	2.22	6	1
1:A:160:GLU:HA	1:A:200:VAL:HG21	0.49	1.85	18	1
1:A:231:TYR:HB3	1:A:241:ARG:CZ	0.48	2.38	6	1
1:A:235:ALA:HA	1:A:241:ARG:HD2	0.48	1.86	6	1
1:A:163:LEU:O	1:A:190:ARG:HD2	0.47	2.09	11	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:223:THR:HG22	1:A:226:GLN:HG2	0.47	1.84	9	1
1:A:175:ILE:HG21	1:A:224:LEU:HD13	0.47	1.85	12	1
1:A:159:ALA:O	1:A:163:LEU:HD22	0.47	2.09	5	1
1:A:216:THR:CG2	1:A:218:ARG:HG2	0.46	2.41	7	3
1:A:241:ARG:CZ	1:A:241:ARG:HA	0.46	2.37	6	1
1:A:238:LEU:HD12	1:A:241:ARG:NH2	0.46	2.25	6	1
1:A:173:PHE:CD1	1:A:242:LEU:HB3	0.45	2.46	19	2
1:A:235:ALA:HA	1:A:241:ARG:NH1	0.45	2.26	6	1
1:A:173:PHE:O	1:A:245:PRO:HA	0.45	2.12	12	1
1:A:205:ILE:HD13	1:A:224:LEU:HD11	0.45	1.89	16	1
1:A:170:ARG:HG2	1:A:192:TRP:HB2	0.44	1.89	19	1
1:A:216:THR:CG2	1:A:218:ARG:HG3	0.44	2.43	10	1
1:A:154:LEU:HD21	1:A:159:ALA:HB2	0.43	1.89	11	1
1:A:151:PHE:CG	1:A:174:LEU:HB2	0.43	2.48	2	1
1:A:235:ALA:CA	1:A:241:ARG:HD2	0.42	2.44	6	1
1:A:151:PHE:O	1:A:176:ARG:HA	0.42	2.14	10	1
1:A:192:TRP:CD1	1:A:197:GLY:O	0.42	2.72	17	1
1:A:164:LEU:HA	1:A:190:ARG:CZ	0.42	2.45	9	1
1:A:169:PRO:HB2	1:A:170:ARG:NH2	0.42	2.30	18	1
1:A:173:PHE:HA	1:A:188:SER:O	0.42	2.14	19	1
1:A:191:ASP:OD2	1:A:239:CYS:HB2	0.41	2.14	17	1
1:A:156:ARG:HA	1:A:176:ARG:CZ	0.41	2.46	15	1
1:A:173:PHE:CE1	1:A:242:LEU:HB3	0.41	2.50	4	1
1:A:159:ALA:O	1:A:163:LEU:HG	0.41	2.14	6	1
1:A:170:ARG:HD3	1:A:170:ARG:N	0.41	2.30	11	1
1:A:160:GLU:HG2	1:A:200:VAL:CG2	0.41	2.45	9	1
1:A:169:PRO:HB2	1:A:170:ARG:CZ	0.41	2.45	18	1
1:A:160:GLU:HG2	1:A:200:VAL:HB	0.41	1.92	4	1
1:A:221:PHE:HB3	1:A:226:GLN:HB2	0.41	1.92	7	1
1:A:153:LYS:HB2	1:A:177:GLU:OE1	0.41	2.16	19	1
1:A:172:THR:CG2	1:A:246:CYS:HA	0.40	2.46	10	1
1:A:205:ILE:HD13	1:A:224:LEU:HD21	0.40	1.94	17	1
1:A:231:TYR:O	1:A:242:LEU:HG	0.40	2.17	6	1
1:A:216:THR:HG23	1:A:218:ARG:HG3	0.40	1.93	10	1
1:A:234:ARG:HG3	1:A:236:ALA:HB2	0.40	1.94	11	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	97/111 (87%)	93±1 (96±1%)	4±1 (4±1%)	1±1 (1±1%)	34	78
All	All	1940/2220 (87%)	1855 (96%)	74 (4%)	11 (1%)	34	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	182	LYS	6
1	A	153	LYS	2
1	A	197	GLY	2
1	A	167	GLY	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	84/97 (87%)	79±2 (94±2%)	5±2 (6±2%)	28	73
All	All	1680/1940 (87%)	1577 (94%)	103 (6%)	28	73

All 25 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	220	GLN	17
1	A	241	ARG	16
1	A	170	ARG	16
1	A	229	GLN	12
1	A	179	GLU	5
1	A	154	LEU	4

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Mol	Chain	Res	Type	Models (Total)
1	A	225	GLN	4
1	A	217	THR	3
1	A	162	GLN	3
1	A	204	LYS	3
1	A	174	LEU	2
1	A	248	LYS	2
1	A	224	LEU	2
1	A	156	ARG	2
1	A	215	ILE	2
1	A	190	ARG	1
1	A	206	ARG	1
1	A	191	ASP	1
1	A	222	GLU	1
1	A	218	ARG	1
1	A	180	THR	1
1	A	182	LYS	1
1	A	199	HIS	1
1	A	216	THR	1
1	A	151	PHE	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

The completeness of assignment taking into account all chemical shift lists is 87% for the well-defined parts and 88% for the entire structure.

7.1 Chemical shift list 1

File name: 2mqi_cs.cif

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	1332
Number of shifts mapped to atoms	1332
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

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	107	-0.35 ± 0.20	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	98	-0.10 ± 0.13	None needed (< 0.5 ppm)
$^{13}\text{C}'$	103	0.04 ± 0.19	None needed (< 0.5 ppm)
^{15}N	103	-0.45 ± 0.26	None needed (< 0.5 ppm)

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 87%, i.e. 1105 atoms were assigned a chemical shift out of a possible 1267. 1 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	483/486 (99%)	194/194 (100%)	193/196 (98%)	96/96 (100%)
Sidechain	534/665 (80%)	333/393 (85%)	194/230 (84%)	7/42 (17%)

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	Total	^1H	^{13}C	^{15}N
Aromatic	88/116 (76%)	46/62 (74%)	41/49 (84%)	1/5 (20%)
Overall	1105/1267 (87%)	573/649 (88%)	428/475 (90%)	104/143 (73%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 88%, i.e. 1141 atoms were assigned a chemical shift out of a possible 1303. 1 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	493/496 (99%)	198/198 (100%)	197/200 (98%)	98/98 (100%)
Sidechain	540/671 (80%)	337/397 (85%)	196/232 (84%)	7/42 (17%)
Aromatic	108/136 (79%)	56/72 (78%)	50/58 (86%)	2/6 (33%)
Overall	1141/1303 (88%)	591/667 (89%)	443/490 (90%)	107/146 (73%)

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:

