



# Full wwPDB NMR Structure Validation Report ⓘ

May 28, 2020 – 11:38 pm BST

PDB ID : 2M6B  
Title : Structure of full-length transmembrane domains of human glycine receptor alpha1 monomer subunit  
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Deposited on : 2013-03-28

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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

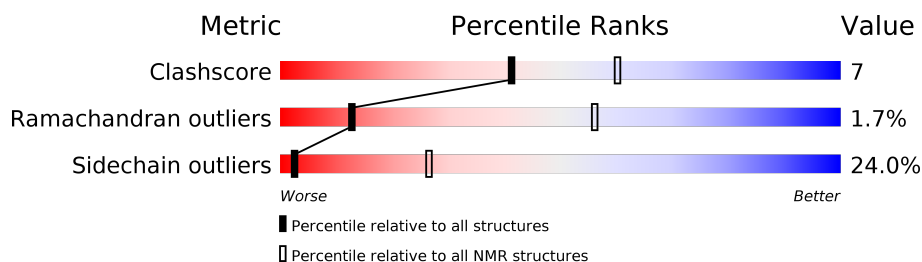
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 53%.

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  $\geq 3$ , 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	150	<div> <div style="width: 57%; background-color: green;"></div> <div style="width: 27%; background-color: yellow;"></div> <div style="width: 15%; background-color: cyan;"></div> <div style="width: 1%; background-color: grey;"></div> </div> <div>57% 27% • 15%</div>

## 2 Ensemble composition and analysis ⓘ

This entry contains 15 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:216-A:308, A:390-A:424 (128)	0.73	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. No single-model clusters were found.

Cluster number	Models
1	1, 3, 4, 5, 6, 9, 11, 13
2	7, 10, 12, 14
3	2, 8, 15

### 3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2489 atoms, of which 1260 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Full-Length Transmembrane Domains of Human Glycine Receptor alpha1 Subunit.

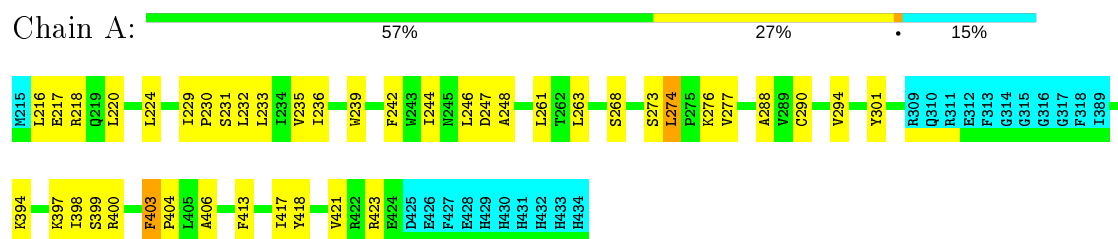
Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	150	2489	819	1260	207	201	2	0

## 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: Full-Length Transmembrane Domains of Human Glycine Receptor alpha1 Sub-unit

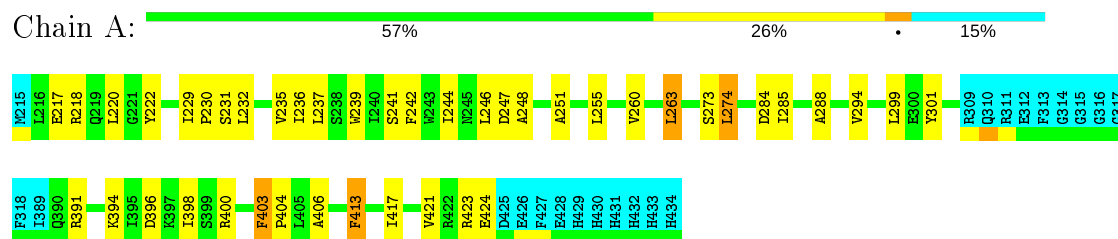


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

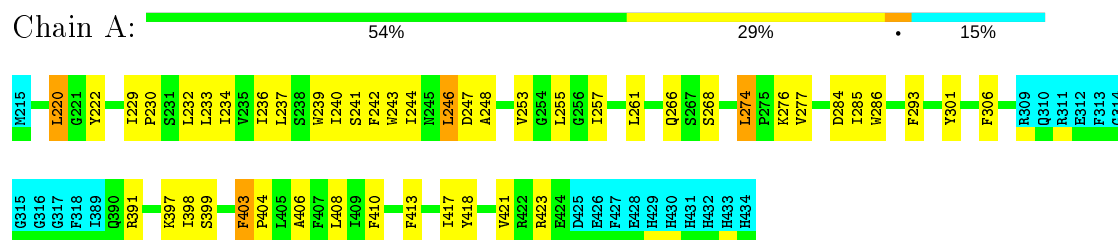
#### 4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: Full-Length Transmembrane Domains of Human Glycine Receptor alpha1 Sub-unit



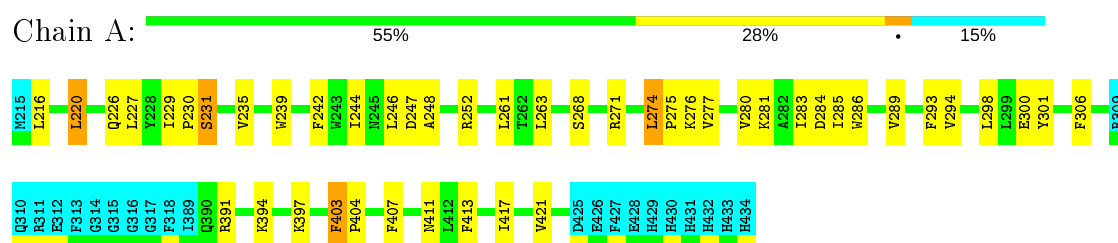
#### 4.2.2 Score per residue for model 2

- Molecule 1: Full-Length Transmembrane Domains of Human Glycine Receptor alpha1 Sub-unit



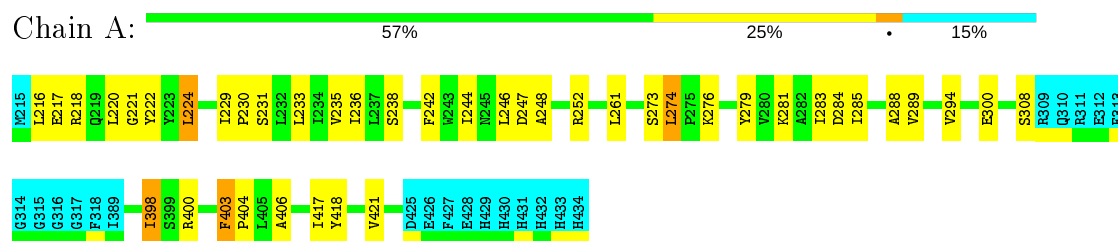
### 4.2.3 Score per residue for model 3

- Molecule 1: Full-Length Transmembrane Domains of Human Glycine Receptor alpha1 Sub-unit



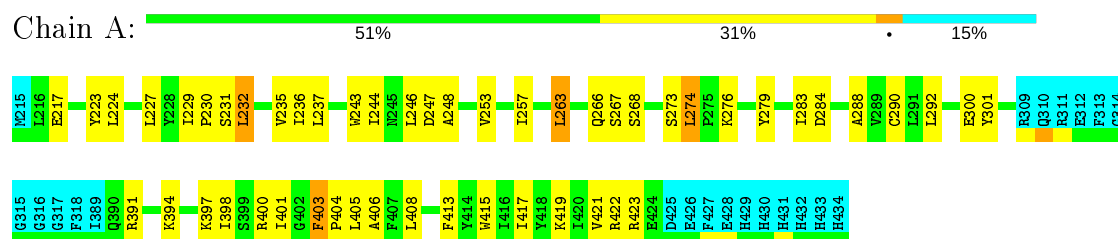
### 4.2.4 Score per residue for model 4

- Molecule 1: Full-Length Transmembrane Domains of Human Glycine Receptor alpha1 Sub-unit



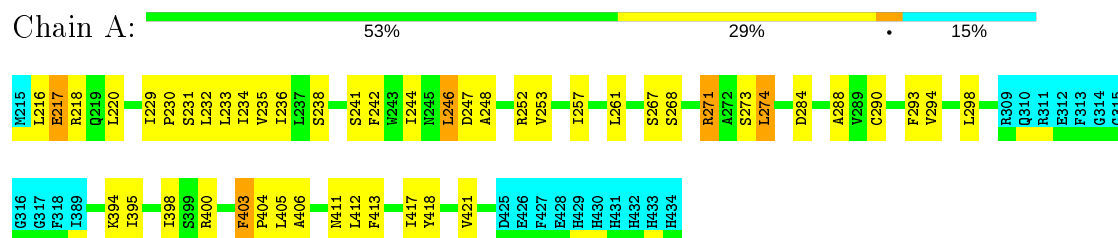
### 4.2.5 Score per residue for model 5

- Molecule 1: Full-Length Transmembrane Domains of Human Glycine Receptor alpha1 Sub-unit



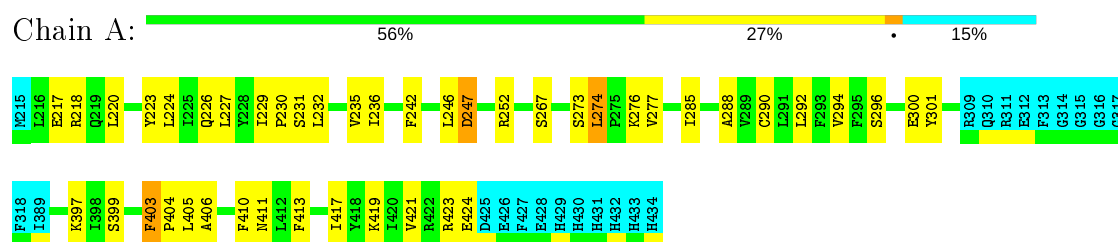
#### 4.2.6 Score per residue for model 6

- Molecule 1: Full-Length Transmembrane Domains of Human Glycine Receptor alpha1 Sub-unit



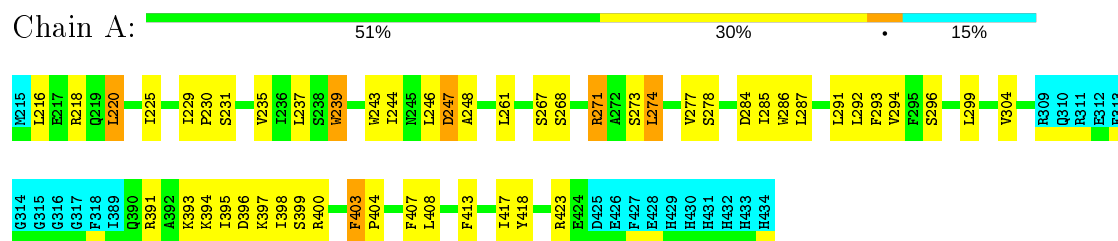
#### 4.2.7 Score per residue for model 7

- Molecule 1: Full-Length Transmembrane Domains of Human Glycine Receptor alpha1 Sub-unit



#### 4.2.8 Score per residue for model 8

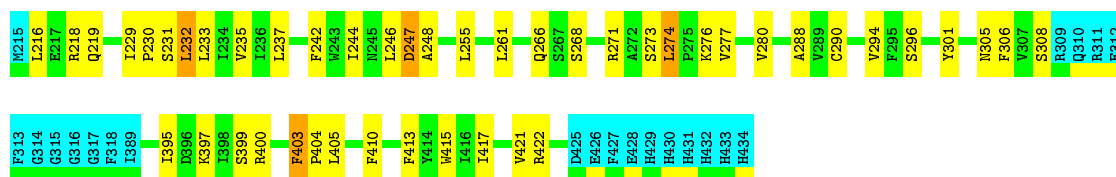
- Molecule 1: Full-Length Transmembrane Domains of Human Glycine Receptor alpha1 Sub-unit



#### 4.2.9 Score per residue for model 9

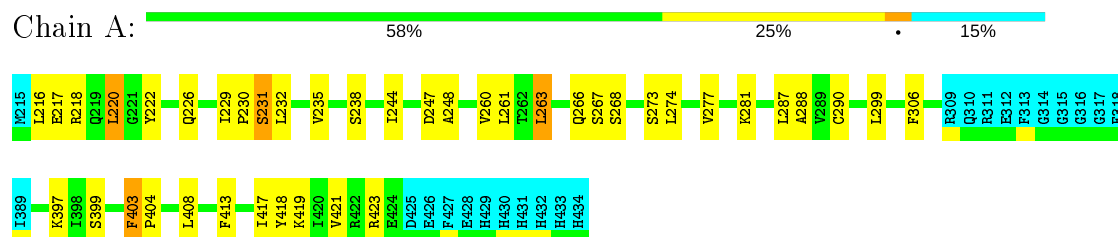
- Molecule 1: Full-Length Transmembrane Domains of Human Glycine Receptor alpha1 Sub-unit





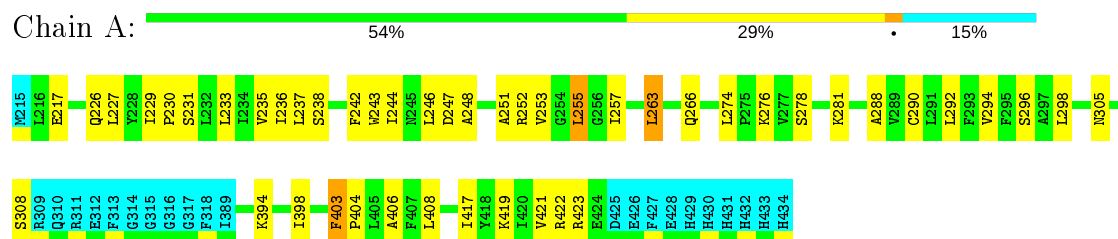
#### 4.2.10 Score per residue for model 10

- Molecule 1: Full-Length Transmembrane Domains of Human Glycine Receptor alpha1 Sub-unit



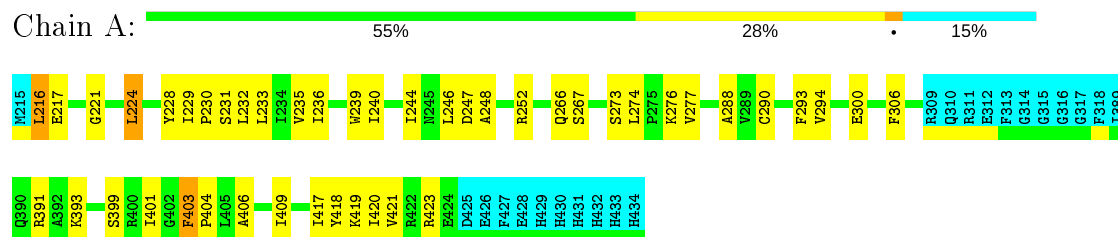
#### 4.2.11 Score per residue for model 11

- Molecule 1: Full-Length Transmembrane Domains of Human Glycine Receptor alpha1 Sub-unit



#### 4.2.12 Score per residue for model 12

- Molecule 1: Full-Length Transmembrane Domains of Human Glycine Receptor alpha1 Sub-unit







## 5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 15 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
CYANA	refinement	3.0

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	1145
Number of shifts mapped to atoms	1145
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	53%

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

## 6 Model quality ⓘ

### 6.1 Standard geometry ⓘ

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	1038	1103	1103	16±3
All	All	15570	16545	16545	237

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 7.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:220:LEU:HD22	1:A:274:LEU:HD11	0.93	1.39	8	1
1:A:236:ILE:HD11	1:A:406:ALA:HB1	0.80	1.52	6	2
1:A:220:LEU:HD13	1:A:274:LEU:HD11	0.80	1.54	2	1
1:A:220:LEU:HD22	1:A:274:LEU:HD13	0.78	1.54	3	1
1:A:227:LEU:HD21	1:A:263:LEU:HD22	0.77	1.55	3	1
1:A:227:LEU:HD11	1:A:263:LEU:HD12	0.73	1.61	5	1
1:A:220:LEU:HD11	1:A:272:ALA:HB3	0.70	1.64	13	2
1:A:279:TYR:CZ	1:A:283:ILE:HD11	0.68	2.23	5	2
1:A:236:ILE:HG23	1:A:406:ALA:HB1	0.67	1.65	2	4
1:A:220:LEU:HD23	1:A:271:ARG:HD3	0.64	1.69	8	1
1:A:242:PHE:CE2	1:A:246:LEU:HD12	0.62	2.29	9	3
1:A:236:ILE:HD12	1:A:406:ALA:HB1	0.62	1.72	15	2
1:A:242:PHE:CZ	1:A:246:LEU:HD12	0.61	2.30	13	7
1:A:221:GLY:HA2	1:A:224:LEU:HD23	0.61	1.71	12	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:280:VAL:HA	1:A:283:ILE:HD12	0.61	1.72	3	1
1:A:218:ARG:CD	1:A:277:VAL:HG11	0.60	2.25	7	1
1:A:227:LEU:HD11	1:A:263:LEU:CD1	0.60	2.26	5	1
1:A:242:PHE:CE1	1:A:246:LEU:HD12	0.59	2.32	11	2
1:A:231:SER:O	1:A:235:VAL:HG23	0.59	1.98	14	14
1:A:216:LEU:HD13	1:A:219:GLN:NE2	0.58	2.13	9	1
1:A:220:LEU:HD13	1:A:274:LEU:HD21	0.57	1.76	2	1
1:A:232:LEU:HD13	1:A:413:PHE:CD2	0.57	2.35	10	3
1:A:220:LEU:HD13	1:A:274:LEU:CD1	0.57	2.29	2	1
1:A:253:VAL:O	1:A:257:ILE:HG23	0.56	1.99	5	3
1:A:239:TRP:CZ3	1:A:398:ILE:HG22	0.56	2.34	8	1
1:A:417:ILE:O	1:A:421:VAL:HG23	0.55	2.02	10	14
1:A:243:TRP:HA	1:A:398:ILE:HG21	0.55	1.78	2	1
1:A:220:LEU:HD22	1:A:273:SER:OG	0.55	2.02	15	1
1:A:274:LEU:HD12	1:A:277:VAL:CG1	0.54	2.32	8	1
1:A:273:SER:O	1:A:277:VAL:HG22	0.54	2.03	13	1
1:A:243:TRP:HB3	1:A:398:ILE:HD11	0.54	1.79	8	2
1:A:232:LEU:HD13	1:A:413:PHE:CG	0.53	2.38	15	3
1:A:244:ILE:O	1:A:248:ALA:HB3	0.53	2.03	9	14
1:A:225:ILE:HG12	1:A:417:ILE:HD11	0.53	1.80	8	1
1:A:243:TRP:HB2	1:A:398:ILE:HG21	0.53	1.79	5	1
1:A:224:LEU:HD12	1:A:224:LEU:O	0.53	2.03	4	2
1:A:236:ILE:CD1	1:A:406:ALA:HB1	0.53	2.33	5	1
1:A:236:ILE:HG23	1:A:406:ALA:CB	0.52	2.35	2	3
1:A:220:LEU:HD13	1:A:273:SER:N	0.52	2.19	13	2
1:A:217:GLU:CG	1:A:274:LEU:HD22	0.52	2.35	7	1
1:A:285:ILE:O	1:A:289:VAL:HG13	0.51	2.05	4	2
1:A:220:LEU:HD22	1:A:273:SER:HB2	0.51	1.81	13	1
1:A:243:TRP:HA	1:A:398:ILE:HD13	0.51	1.80	5	1
1:A:246:LEU:HD23	1:A:247:ASP:HB2	0.51	1.83	8	2
1:A:236:ILE:CG2	1:A:406:ALA:HB1	0.51	2.36	7	3
1:A:288:ALA:O	1:A:292:LEU:HD12	0.51	2.06	13	1
1:A:279:TYR:CE1	1:A:283:ILE:HD11	0.50	2.42	4	2
1:A:232:LEU:HD11	1:A:409:ILE:CG2	0.49	2.36	12	1
1:A:232:LEU:HD11	1:A:410:PHE:HA	0.49	1.83	9	1
1:A:217:GLU:HG3	1:A:220:LEU:HD12	0.49	1.83	6	1
1:A:229:ILE:N	1:A:230:PRO:HD2	0.49	2.23	1	15
1:A:217:GLU:HG3	1:A:277:VAL:HG11	0.48	1.83	14	1
1:A:291:LEU:O	1:A:291:LEU:HD12	0.48	2.08	8	2
1:A:273:SER:CB	1:A:274:LEU:HD23	0.48	2.39	9	2
1:A:246:LEU:O	1:A:246:LEU:HD23	0.47	2.09	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:275:PRO:HB2	1:A:277:VAL:HG23	0.47	1.85	3	1
1:A:232:LEU:HD13	1:A:232:LEU:O	0.47	2.09	5	1
1:A:260:VAL:HA	1:A:263:LEU:HD23	0.47	1.85	10	2
1:A:273:SER:C	1:A:274:LEU:HD23	0.47	2.31	8	5
1:A:218:ARG:NE	1:A:277:VAL:HG11	0.47	2.25	9	3
1:A:236:ILE:HD13	1:A:406:ALA:HB1	0.47	1.86	4	1
1:A:220:LEU:HD21	1:A:273:SER:CB	0.47	2.40	7	1
1:A:220:LEU:HD23	1:A:273:SER:HB3	0.46	1.87	10	1
1:A:403:PHE:CB	1:A:404:PRO:CD	0.46	2.94	13	15
1:A:227:LEU:HD21	1:A:263:LEU:CD1	0.46	2.40	11	1
1:A:279:TYR:CE2	1:A:283:ILE:HD11	0.46	2.45	5	1
1:A:232:LEU:HD21	1:A:413:PHE:CE1	0.46	2.46	6	1
1:A:220:LEU:HD22	1:A:274:LEU:CD1	0.46	2.25	8	2
1:A:412:LEU:O	1:A:412:LEU:HD12	0.46	2.10	6	1
1:A:220:LEU:HD13	1:A:271:ARG:HH11	0.46	1.70	6	1
1:A:220:LEU:HD23	1:A:271:ARG:CD	0.46	2.39	8	1
1:A:232:LEU:HD23	1:A:413:PHE:CD2	0.46	2.46	5	1
1:A:274:LEU:HD12	1:A:277:VAL:HG12	0.45	1.88	2	2
1:A:253:VAL:O	1:A:257:ILE:HG22	0.45	2.11	11	1
1:A:220:LEU:CD2	1:A:274:LEU:HD13	0.45	2.36	3	1
1:A:216:LEU:HD12	1:A:273:SER:OG	0.45	2.12	12	1
1:A:251:ALA:O	1:A:255:LEU:HD12	0.45	2.11	11	2
1:A:273:SER:HB2	1:A:274:LEU:HD23	0.44	1.89	9	1
1:A:232:LEU:HD11	1:A:413:PHE:CD2	0.44	2.46	1	1
1:A:403:PHE:N	1:A:404:PRO:HD2	0.44	2.28	15	15
1:A:232:LEU:HD11	1:A:409:ILE:HG23	0.43	1.90	15	1
1:A:220:LEU:O	1:A:220:LEU:HD13	0.43	2.14	10	1
1:A:217:GLU:HG3	1:A:277:VAL:HG21	0.43	1.90	10	2
1:A:220:LEU:CD1	1:A:274:LEU:HD11	0.43	2.36	2	1
1:A:220:LEU:CD1	1:A:274:LEU:HD21	0.42	2.43	2	1
1:A:420:ILE:HD13	1:A:423:ARG:HD3	0.42	1.92	12	1
1:A:286:TRP:HB3	1:A:287:LEU:HD23	0.42	1.90	13	1
1:A:220:LEU:HD13	1:A:274:LEU:CD2	0.42	2.45	2	1
1:A:243:TRP:HB3	1:A:398:ILE:HG21	0.42	1.92	15	1
1:A:242:PHE:CD2	1:A:398:ILE:HD13	0.42	2.49	4	1
1:A:220:LEU:CD1	1:A:272:ALA:HB3	0.41	2.42	13	1
1:A:232:LEU:HD23	1:A:413:PHE:CE2	0.41	2.50	5	1
1:A:276:LYS:O	1:A:280:VAL:HG23	0.41	2.15	9	1
1:A:239:TRP:CZ3	1:A:398:ILE:HD11	0.41	2.51	2	1
1:A:229:ILE:HG22	1:A:230:PRO:N	0.41	2.31	13	7
1:A:216:LEU:HD22	1:A:219:GLN:NE2	0.41	2.31	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:220:LEU:HD13	1:A:273:SER:HB3	0.41	1.91	14	1
1:A:239:TRP:HZ3	1:A:398:ILE:HD11	0.41	1.74	2	1
1:A:408:LEU:O	1:A:412:LEU:HD23	0.41	2.15	14	1
1:A:220:LEU:CD2	1:A:274:LEU:HD11	0.41	2.29	8	1
1:A:239:TRP:CH2	1:A:401:ILE:HG23	0.41	2.51	12	1
1:A:395:ILE:HG22	1:A:398:ILE:CD1	0.40	2.46	6	1
1:A:229:ILE:CB	1:A:230:PRO:CD	0.40	3.00	10	2

## 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	128/150 (85%)	120±2 (94±1%)	6±1 (4±1%)	2±1 (2±1%)	13	56
All	All	1920/2250 (85%)	1803 (94%)	85 (4%)	32 (2%)	13	56

All 6 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	247	ASP	15
1	A	288	ALA	11
1	A	424	GLU	2
1	A	276	LYS	2
1	A	395	ILE	1
1	A	396	ASP	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	112/130 (86%)	85±4 (76±4%)	27±4 (24±4%)	2	26
All	All	1680/1950 (86%)	1277 (76%)	403 (24%)	2	26

All 78 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	274	LEU	15
1	A	403	PHE	14
1	A	294	VAL	12
1	A	268	SER	10
1	A	423	ARG	10
1	A	394	LYS	9
1	A	261	LEU	9
1	A	290	CYS	9
1	A	233	LEU	9
1	A	397	LYS	8
1	A	220	LEU	8
1	A	399	SER	8
1	A	400	ARG	8
1	A	418	TYR	8
1	A	301	TYR	8
1	A	266	GLN	7
1	A	306	PHE	7
1	A	267	SER	7
1	A	276	LYS	7
1	A	293	PHE	7
1	A	405	LEU	7
1	A	252	ARG	7
1	A	391	ARG	7
1	A	216	LEU	7
1	A	284	ASP	7
1	A	246	LEU	6
1	A	237	LEU	6
1	A	300	GLU	6
1	A	238	SER	6
1	A	292	LEU	6
1	A	224	LEU	6
1	A	286	TRP	5
1	A	296	SER	5
1	A	422	ARG	5
1	A	299	LEU	5
1	A	281	LYS	5

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Mol	Chain	Res	Type	Models (Total)
1	A	408	LEU	5
1	A	285	ILE	5
1	A	419	LYS	5
1	A	287	LEU	5
1	A	413	PHE	5
1	A	217	GLU	5
1	A	218	ARG	5
1	A	239	TRP	5
1	A	222	TYR	5
1	A	226	GLN	4
1	A	308	SER	4
1	A	298	LEU	4
1	A	263	LEU	4
1	A	393	LYS	4
1	A	232	LEU	4
1	A	271	ARG	4
1	A	231	SER	4
1	A	415	TRP	4
1	A	240	ILE	3
1	A	241	SER	3
1	A	407	PHE	3
1	A	255	LEU	3
1	A	411	ASN	3
1	A	396	ASP	3
1	A	410	PHE	2
1	A	257	ILE	2
1	A	234	ILE	2
1	A	305	ASN	2
1	A	273	SER	2
1	A	398	ILE	2
1	A	247	ASP	2
1	A	223	TYR	2
1	A	424	GLU	2
1	A	278	SER	2
1	A	264	THR	1
1	A	395	ILE	1
1	A	279	TYR	1
1	A	401	ILE	1
1	A	412	LEU	1
1	A	270	SER	1
1	A	228	TYR	1
1	A	227	LEU	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

The completeness of assignment taking into account all chemical shift lists is 53% for the well-defined parts and 51% 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

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	1145
Number of shifts mapped to atoms	1145
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
$^{13}\text{C}_\alpha$	133	$-0.27 \pm 0.17$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	112	$0.29 \pm 0.12$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	18	—	None (insufficient data)
$^{15}\text{N}$	146	$0.91 \pm 0.16$	Should be applied

#### 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 53%, i.e. 873 atoms were assigned a chemical shift out of a possible 1661. 0 out of 30 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	476/632 (75%)	225/252 (89%)	127/256 (50%)	124/124 (100%)
Sidechain	382/853 (45%)	256/496 (52%)	118/323 (37%)	8/34 (24%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	15/176 (9%)	15/92 (16%)	0/80 (0%)	0/4 (0%)
Overall	873/1661 (53%)	496/840 (59%)	245/659 (37%)	132/162 (81%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 51%, i.e. 996 atoms were assigned a chemical shift out of a possible 1955. 0 out of 30 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	558/742 (75%)	261/296 (88%)	151/300 (50%)	146/146 (100%)
Sidechain	421/968 (43%)	276/566 (49%)	136/361 (38%)	9/41 (22%)
Aromatic	17/245 (7%)	17/131 (13%)	0/104 (0%)	0/10 (0%)
Overall	996/1955 (51%)	554/993 (56%)	287/765 (38%)	155/197 (79%)

#### 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:

