



Full wwPDB NMR Structure Validation Report ⓘ

Dec 18, 2017 – 12:15 PM EST

PDB ID : 5N5B
Title : Structure of Tau(292-319) bound to F-actin
Authors : Fontela, Y.C.; Kadavath, H.; Zweckstetter, M.
Deposited on : 2017-02-13

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
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20030736
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030736

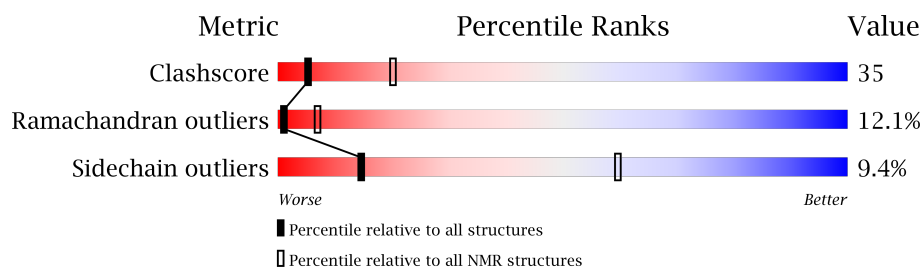
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR


The overall completeness of chemical shifts assignment is 10%.

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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	28	

2 Ensemble composition and analysis

This entry contains 20 models. Model 13 is the overall representative, medoid model (most similar to other models). The authors have identified model 12 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:293-A:319 (27)	1.06	13

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 423 atoms, of which 217 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Microtubule-associated protein tau.

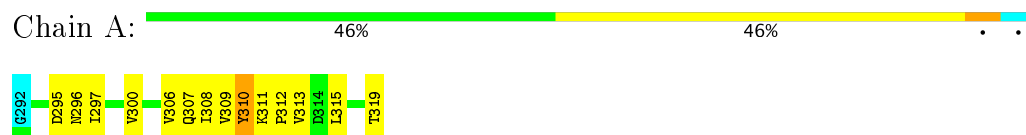
Mol	Chain	Residues	Atoms					Trace
1	A	28	Total	C	H	N	O	0
			423	130	217	36	40	

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: Microtubule-associated protein tau



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: Microtubule-associated protein tau



4.2.2 Score per residue for model 2

- Molecule 1: Microtubule-associated protein tau



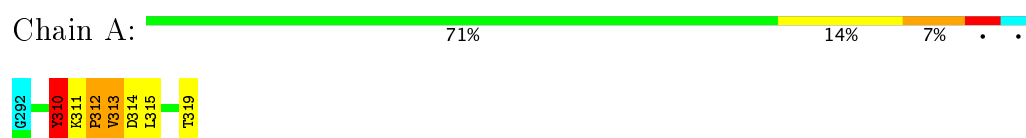
4.2.3 Score per residue for model 3

- Molecule 1: Microtubule-associated protein tau



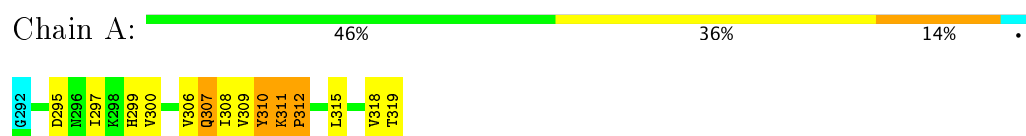
4.2.4 Score per residue for model 4

- Molecule 1: Microtubule-associated protein tau



4.2.5 Score per residue for model 5

- Molecule 1: Microtubule-associated protein tau



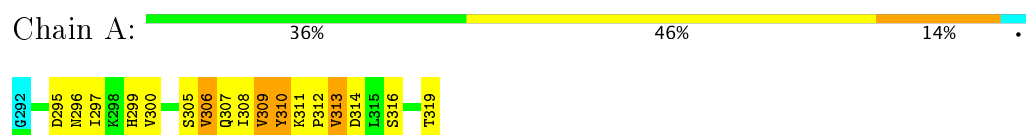
4.2.6 Score per residue for model 6

- Molecule 1: Microtubule-associated protein tau



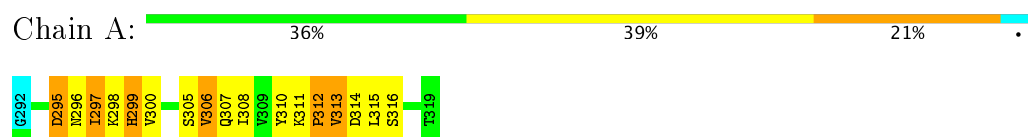
4.2.7 Score per residue for model 7

- Molecule 1: Microtubule-associated protein tau



4.2.8 Score per residue for model 8

- Molecule 1: Microtubule-associated protein tau



4.2.9 Score per residue for model 9

- Molecule 1: Microtubule-associated protein tau



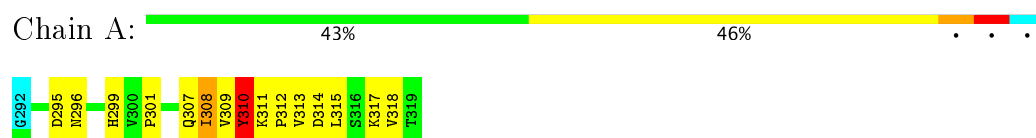
4.2.10 Score per residue for model 10

- Molecule 1: Microtubule-associated protein tau



4.2.11 Score per residue for model 11

- Molecule 1: Microtubule-associated protein tau



4.2.12 Score per residue for model 12

- Molecule 1: Microtubule-associated protein tau



4.2.13 Score per residue for model 13 (medoid)

- Molecule 1: Microtubule-associated protein tau



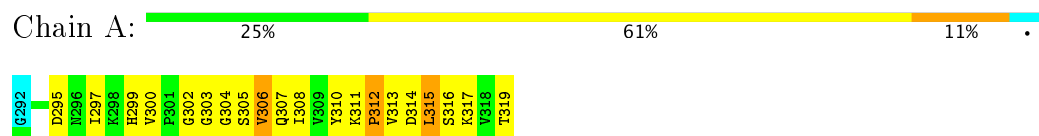
4.2.14 Score per residue for model 14

- Molecule 1: Microtubule-associated protein tau



4.2.15 Score per residue for model 15

- Molecule 1: Microtubule-associated protein tau



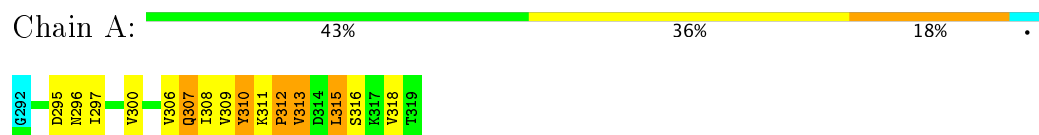
4.2.16 Score per residue for model 16

- Molecule 1: Microtubule-associated protein tau



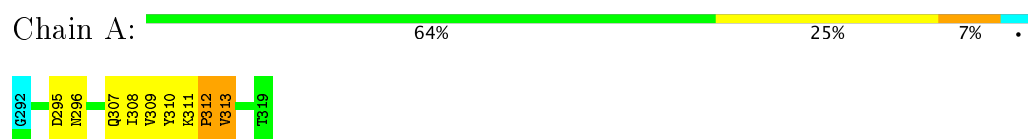
4.2.17 Score per residue for model 17

- Molecule 1: Microtubule-associated protein tau



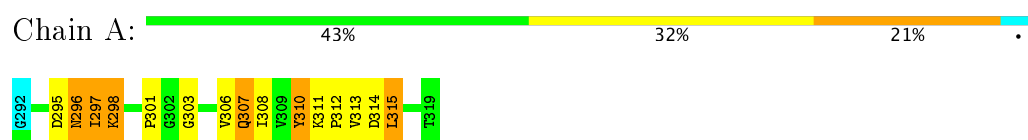
4.2.18 Score per residue for model 18

- Molecule 1: Microtubule-associated protein tau



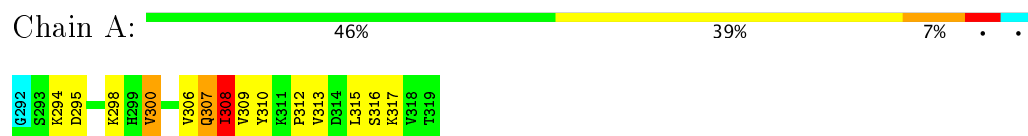
4.2.19 Score per residue for model 19

- Molecule 1: Microtubule-associated protein tau



4.2.20 Score per residue for model 20

- Molecule 1: Microtubule-associated protein tau



5 Refinement protocol and experimental data overview

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

Of the 200 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
X-PLOR NIH	refinement	
CYANA	structure calculation	

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)	5n5b_cs.cif
Number of chemical shift lists	1
Total number of shifts	32
Number of shifts mapped to atoms	32
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	10%

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	0.55±0.05	0±0/205 (0.0±0.0%)	0.90±0.06	0±0/275 (0.1±0.1%)
All	All	0.55	0/4100 (0.0%)	0.91	4/5500 (0.1%)

There are no bond-length outliers.

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	310	TYR	CB-CG-CD2	-6.81	116.91	121.00	9	4

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	202	214	213	15±4
All	All	4040	4280	4260	291

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 35.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:308:ILE:O	1:A:310:TYR:N	1.00	1.94	7	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:308:ILE:HD11	1:A:310:TYR:CZ	0.90	2.02	12	1
1:A:306:VAL:O	1:A:307:GLN:O	0.86	1.94	3	2
1:A:315:LEU:HD22	1:A:315:LEU:H	0.85	1.31	2	3
1:A:308:ILE:HG23	1:A:310:TYR:CD2	0.82	2.09	13	4
1:A:310:TYR:CD1	1:A:311:LYS:N	0.81	2.49	11	1
1:A:314:ASP:OD2	1:A:315:LEU:HD12	0.79	1.77	4	1
1:A:309:VAL:HG13	1:A:310:TYR:H	0.79	1.38	16	1
1:A:312:PRO:O	1:A:314:ASP:N	0.78	2.17	7	5
1:A:309:VAL:O	1:A:309:VAL:HG12	0.77	1.79	7	2
1:A:297:ILE:HG23	1:A:297:ILE:O	0.73	1.83	13	4
1:A:315:LEU:O	1:A:318:VAL:HG12	0.71	1.86	10	3
1:A:297:ILE:HG22	1:A:298:LYS:N	0.71	2.00	19	1
1:A:310:TYR:CG	1:A:311:LYS:N	0.71	2.58	11	1
1:A:310:TYR:CD1	1:A:310:TYR:O	0.69	2.45	1	1
1:A:315:LEU:HD22	1:A:315:LEU:N	0.69	2.02	2	4
1:A:295:ASP:OD1	1:A:296:ASN:N	0.68	2.26	19	2
1:A:313:VAL:HG22	1:A:316:SER:OG	0.67	1.90	17	2
1:A:309:VAL:HG13	1:A:310:TYR:N	0.67	2.04	16	3
1:A:303:GLY:O	1:A:305:SER:N	0.66	2.28	15	1
1:A:309:VAL:CG1	1:A:310:TYR:CD1	0.66	2.79	11	1
1:A:308:ILE:HG22	1:A:311:LYS:H	0.66	1.48	15	3
1:A:315:LEU:N	1:A:315:LEU:HD22	0.65	2.05	3	5
1:A:313:VAL:HG13	1:A:316:SER:OG	0.65	1.90	10	1
1:A:315:LEU:CD2	1:A:315:LEU:N	0.65	2.59	14	6
1:A:313:VAL:O	1:A:313:VAL:HG13	0.65	1.89	8	2
1:A:315:LEU:N	1:A:315:LEU:CD2	0.65	2.59	9	2
1:A:314:ASP:OD2	1:A:315:LEU:N	0.65	2.29	4	1
1:A:295:ASP:OD2	1:A:296:ASN:N	0.65	2.30	8	1
1:A:306:VAL:O	1:A:307:GLN:CB	0.64	2.45	1	6
1:A:315:LEU:HD12	1:A:315:LEU:H	0.64	1.53	8	2
1:A:307:GLN:HG3	1:A:308:ILE:H	0.63	1.50	16	1
1:A:296:ASN:O	1:A:297:ILE:O	0.63	2.17	8	1
1:A:307:GLN:O	1:A:308:ILE:O	0.63	2.16	11	2
1:A:309:VAL:HG13	1:A:310:TYR:CD1	0.63	2.29	11	1
1:A:315:LEU:O	1:A:318:VAL:HG22	0.63	1.93	17	1
1:A:297:ILE:HG22	1:A:298:LYS:H	0.63	1.52	19	1
1:A:296:ASN:N	1:A:296:ASN:HD22	0.62	1.90	13	1
1:A:311:LYS:O	1:A:313:VAL:N	0.61	2.31	8	2
1:A:307:GLN:O	1:A:309:VAL:N	0.61	2.33	20	1
1:A:315:LEU:CD2	1:A:315:LEU:H	0.61	2.05	2	5
1:A:310:TYR:O	1:A:310:TYR:CG	0.61	2.52	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:315:LEU:HD12	1:A:315:LEU:N	0.61	2.10	8	1
1:A:296:ASN:ND2	1:A:296:ASN:N	0.60	2.49	13	1
1:A:308:ILE:HG22	1:A:310:TYR:H	0.60	1.57	19	1
1:A:301:PRO:O	1:A:306:VAL:HG23	0.60	1.97	19	2
1:A:295:ASP:O	1:A:296:ASN:CB	0.60	2.49	2	1
1:A:308:ILE:O	1:A:308:ILE:HG13	0.59	1.97	8	1
1:A:308:ILE:HG23	1:A:308:ILE:O	0.59	1.95	1	3
1:A:307:GLN:HG2	1:A:308:ILE:H	0.59	1.56	6	1
1:A:315:LEU:H	1:A:315:LEU:HD12	0.59	1.58	12	1
1:A:298:LYS:O	1:A:299:HIS:C	0.58	2.42	8	1
1:A:311:LYS:O	1:A:312:PRO:C	0.58	2.40	9	13
1:A:310:TYR:CD1	1:A:312:PRO:CD	0.58	2.86	19	1
1:A:297:ILE:CD1	1:A:299:HIS:CD2	0.58	2.87	15	1
1:A:309:VAL:CG1	1:A:309:VAL:O	0.57	2.51	7	1
1:A:299:HIS:CE1	1:A:301:PRO:CD	0.57	2.86	11	1
1:A:308:ILE:C	1:A:310:TYR:H	0.57	2.02	9	2
1:A:310:TYR:CD1	1:A:310:TYR:N	0.57	2.68	6	2
1:A:312:PRO:O	1:A:313:VAL:C	0.57	2.43	16	6
1:A:311:LYS:O	1:A:312:PRO:O	0.56	2.24	9	4
1:A:313:VAL:HG13	1:A:313:VAL:O	0.56	2.01	2	2
1:A:308:ILE:HG23	1:A:310:TYR:CG	0.56	2.35	13	1
1:A:297:ILE:CG2	1:A:297:ILE:O	0.56	2.54	13	3
1:A:313:VAL:HG12	1:A:315:LEU:H	0.55	1.61	11	1
1:A:315:LEU:N	1:A:315:LEU:HD12	0.55	2.16	12	2
1:A:309:VAL:CG1	1:A:310:TYR:H	0.55	2.13	16	1
1:A:297:ILE:HD11	1:A:299:HIS:CD2	0.55	2.36	15	1
1:A:308:ILE:HG23	1:A:310:TYR:CE2	0.54	2.37	13	4
1:A:308:ILE:C	1:A:310:TYR:N	0.54	2.61	9	1
1:A:309:VAL:HG13	1:A:310:TYR:CG	0.54	2.37	11	1
1:A:308:ILE:O	1:A:310:TYR:CD2	0.53	2.61	3	1
1:A:296:ASN:CG	1:A:297:ILE:H	0.53	2.05	13	3
1:A:307:GLN:O	1:A:309:VAL:HG23	0.53	2.04	3	1
1:A:311:LYS:N	1:A:312:PRO:CD	0.53	2.71	19	1
1:A:305:SER:O	1:A:306:VAL:C	0.52	2.47	7	5
1:A:308:ILE:HD11	1:A:310:TYR:CE2	0.52	2.39	12	1
1:A:296:ASN:O	1:A:297:ILE:C	0.52	2.47	8	2
1:A:314:ASP:O	1:A:317:LYS:O	0.52	2.27	3	1
1:A:315:LEU:HD12	1:A:315:LEU:O	0.52	2.03	17	1
1:A:312:PRO:O	1:A:314:ASP:OD2	0.51	2.29	7	1
1:A:309:VAL:CG1	1:A:310:TYR:N	0.51	2.74	16	3
1:A:308:ILE:HG22	1:A:311:LYS:N	0.51	2.20	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:305:SER:O	1:A:306:VAL:O	0.50	2.29	12	3
1:A:308:ILE:HG21	1:A:312:PRO:CD	0.50	2.36	6	1
1:A:308:ILE:HG21	1:A:312:PRO:HD3	0.50	1.82	11	2
1:A:301:PRO:C	1:A:303:GLY:H	0.50	2.08	19	1
1:A:308:ILE:O	1:A:308:ILE:CG2	0.50	2.59	10	1
1:A:297:ILE:O	1:A:297:ILE:HG23	0.49	2.06	5	1
1:A:308:ILE:CG2	1:A:310:TYR:CG	0.49	2.95	13	4
1:A:310:TYR:CD1	1:A:312:PRO:HD3	0.49	2.42	19	3
1:A:313:VAL:O	1:A:313:VAL:CG1	0.49	2.61	8	1
1:A:310:TYR:O	1:A:311:LYS:C	0.49	2.50	14	2
1:A:306:VAL:HG23	1:A:307:GLN:H	0.49	1.66	15	3
1:A:306:VAL:O	1:A:307:GLN:HB3	0.49	2.08	9	3
1:A:318:VAL:HG13	1:A:319:THR:OG1	0.48	2.08	10	1
1:A:308:ILE:CD1	1:A:310:TYR:CZ	0.48	2.89	12	1
1:A:315:LEU:CD1	1:A:315:LEU:O	0.48	2.61	17	1
1:A:295:ASP:C	1:A:295:ASP:OD1	0.48	2.52	15	1
1:A:295:ASP:OD1	1:A:295:ASP:C	0.48	2.52	5	3
1:A:315:LEU:O	1:A:318:VAL:O	0.47	2.32	6	1
1:A:306:VAL:HG23	1:A:307:GLN:N	0.47	2.24	7	2
1:A:313:VAL:CG1	1:A:316:SER:OG	0.47	2.62	10	1
1:A:295:ASP:OD2	1:A:295:ASP:C	0.47	2.52	18	4
1:A:313:VAL:O	1:A:316:SER:OG	0.47	2.25	15	2
1:A:298:LYS:NZ	1:A:300:VAL:HG13	0.47	2.25	20	1
1:A:308:ILE:HG21	1:A:312:PRO:HD2	0.47	1.86	6	1
1:A:296:ASN:O	1:A:297:ILE:CB	0.47	2.62	13	1
1:A:293:SER:O	1:A:294:LYS:O	0.46	2.33	1	1
1:A:315:LEU:CD1	1:A:315:LEU:H	0.46	2.20	8	1
1:A:314:ASP:C	1:A:314:ASP:OD2	0.46	2.54	11	1
1:A:297:ILE:CG2	1:A:298:LYS:H	0.46	2.20	19	1
1:A:295:ASP:C	1:A:295:ASP:OD2	0.46	2.53	9	3
1:A:306:VAL:O	1:A:307:GLN:HB2	0.46	2.10	17	2
1:A:307:GLN:HG2	1:A:308:ILE:HG23	0.46	1.87	20	1
1:A:315:LEU:HD23	1:A:315:LEU:H	0.46	1.71	16	3
1:A:312:PRO:C	1:A:314:ASP:N	0.46	2.69	19	1
1:A:308:ILE:CG2	1:A:310:TYR:CD1	0.45	2.99	9	3
1:A:313:VAL:HG12	1:A:315:LEU:N	0.45	2.26	11	1
1:A:296:ASN:O	1:A:297:ILE:HB	0.45	2.10	13	1
1:A:308:ILE:HG12	1:A:310:TYR:CE1	0.45	2.46	12	1
1:A:315:LEU:H	1:A:315:LEU:HD23	0.45	1.71	9	2
1:A:315:LEU:C	1:A:315:LEU:CD1	0.45	2.85	17	1
1:A:312:PRO:C	1:A:314:ASP:H	0.45	2.16	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:318:VAL:O	1:A:319:THR:C	0.45	2.54	5	1
1:A:318:VAL:O	1:A:319:THR:OG1	0.45	2.32	14	1
1:A:307:GLN:O	1:A:308:ILE:C	0.44	2.54	1	1
1:A:306:VAL:O	1:A:307:GLN:CG	0.44	2.65	5	2
1:A:314:ASP:O	1:A:317:LYS:HG2	0.44	2.12	11	1
1:A:307:GLN:HG2	1:A:308:ILE:N	0.44	2.28	17	1
1:A:299:HIS:CE1	1:A:301:PRO:CG	0.44	3.01	6	1
1:A:301:PRO:O	1:A:306:VAL:CG2	0.44	2.66	19	2
1:A:310:TYR:CG	1:A:312:PRO:HD3	0.44	2.48	19	1
1:A:295:ASP:O	1:A:296:ASN:HB2	0.43	2.13	2	1
1:A:315:LEU:C	1:A:315:LEU:HD12	0.43	2.33	17	1
1:A:315:LEU:CD1	1:A:315:LEU:N	0.43	2.80	8	1
1:A:310:TYR:CE1	1:A:312:PRO:HD3	0.43	2.48	20	2
1:A:306:VAL:O	1:A:307:GLN:HG2	0.43	2.13	9	1
1:A:306:VAL:CG2	1:A:307:GLN:H	0.43	2.26	7	3
1:A:315:LEU:H	1:A:315:LEU:CD2	0.43	2.25	9	1
1:A:297:ILE:HD11	1:A:299:HIS:CE1	0.42	2.48	5	1
1:A:308:ILE:CG1	1:A:308:ILE:O	0.42	2.66	8	1
1:A:317:LYS:CG	1:A:318:VAL:N	0.42	2.82	11	1
1:A:308:ILE:CG2	1:A:311:LYS:H	0.42	2.27	18	2
1:A:308:ILE:HG21	1:A:310:TYR:CD1	0.42	2.50	18	1
1:A:297:ILE:CG2	1:A:298:LYS:N	0.42	2.70	19	1
1:A:307:GLN:HG3	1:A:308:ILE:N	0.42	2.27	16	1
1:A:303:GLY:C	1:A:305:SER:N	0.41	2.74	3	1
1:A:300:VAL:C	1:A:302:GLY:N	0.41	2.74	15	1
1:A:318:VAL:O	1:A:319:THR:OXT	0.41	2.38	1	1
1:A:310:TYR:O	1:A:311:LYS:CB	0.41	2.66	5	1
1:A:315:LEU:H	1:A:315:LEU:CD1	0.41	2.26	12	1
1:A:313:VAL:HG13	1:A:316:SER:HB2	0.41	1.92	20	1
1:A:308:ILE:HG13	1:A:310:TYR:CZ	0.41	2.50	3	1
1:A:308:ILE:CG1	1:A:310:TYR:CE1	0.40	3.04	12	1
1:A:298:LYS:HZ3	1:A:300:VAL:HG13	0.40	1.75	20	1
1:A:310:TYR:O	1:A:311:LYS:HB2	0.40	2.16	3	1
1:A:310:TYR:HD1	1:A:311:LYS:N	0.40	2.15	4	1
1:A:295:ASP:O	1:A:296:ASN:C	0.40	2.59	12	1
1:A:318:VAL:C	1:A:319:THR:OG1	0.40	2.59	14	1
1:A:299:HIS:O	1:A:299:HIS:ND1	0.40	2.54	14	1
1:A:310:TYR:CE1	1:A:312:PRO:CD	0.40	3.04	19	1
1:A:314:ASP:O	1:A:317:LYS:CB	0.40	2.70	15	1
1:A:309:VAL:HG13	1:A:310:TYR:CD2	0.40	2.52	16	1
1:A:313:VAL:HG12	1:A:317:LYS:HG3	0.40	1.93	20	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	26/28 (93%)	21±1 (79±5%)	2±1 (9±5%)	3±1 (12±4%)	1	7
All	All	520/560 (93%)	412 (79%)	45 (9%)	63 (12%)	1	7

All 15 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	312	PRO	12
1	A	307	GLN	10
1	A	313	VAL	8
1	A	306	VAL	6
1	A	296	ASN	6
1	A	309	VAL	5
1	A	297	ILE	4
1	A	308	ILE	4
1	A	299	HIS	2
1	A	293	SER	1
1	A	294	LYS	1
1	A	295	ASP	1
1	A	304	GLY	1
1	A	310	TYR	1
1	A	298	LYS	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	24/24 (100%)	22±1 (91±4%)	2±1 (9±4%)	14	60
All	All	480/480 (100%)	435 (91%)	45 (9%)	14	60

All 10 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	300	VAL	10
1	A	310	TYR	9
1	A	319	THR	7
1	A	315	LEU	7
1	A	311	LYS	3
1	A	309	VAL	3
1	A	294	LYS	2
1	A	296	ASN	2
1	A	306	VAL	1
1	A	308	ILE	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 10% for the well-defined parts and 10% for the entire structure.

7.1 Chemical shift list 1

File name: 5n5b_cs.cif

Chemical shift list name: *Tau292-319_Factin_shift.tab*

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	32
Number of shifts mapped to atoms	32
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

No chemical shift referencing corrections were calculated (not enough data).

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 10%, i.e. 31 atoms were assigned a chemical shift out of a possible 318. 0 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	27/131 (21%)	27/52 (52%)	0/54 (0%)	0/25 (0%)
Sidechain	4/171 (2%)	4/100 (4%)	0/65 (0%)	0/6 (0%)
Aromatic	0/16 (0%)	0/8 (0%)	0/6 (0%)	0/2 (0%)
Overall	31/318 (10%)	31/160 (19%)	0/125 (0%)	0/33 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 10%, i.e. 31 atoms were assigned a chemical shift out of a possible 323. 0 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	27/136 (20%)	27/54 (50%)	0/56 (0%)	0/26 (0%)
Sidechain	4/171 (2%)	4/100 (4%)	0/65 (0%)	0/6 (0%)
Aromatic	0/16 (0%)	0/8 (0%)	0/6 (0%)	0/2 (0%)
Overall	31/323 (10%)	31/162 (19%)	0/127 (0%)	0/34 (0%)

7.1.4 Statistically unusual chemical shifts ⓘ

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots ⓘ

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:

