



## Full wwPDB NMR Structure Validation Report ⓘ

Feb 13, 2017 – 01:24 am GMT

PDB ID : 2MWN  
Title : Talin-F3 / RIAM N-terminal Peptide complex  
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Deposited on : 2014-11-13

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

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

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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 : 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 : trunk28760  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

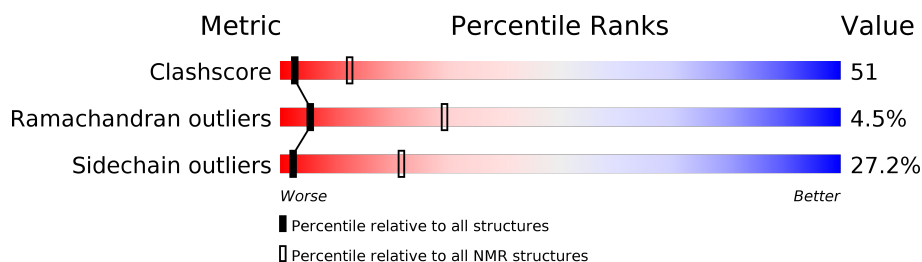
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*



The overall completeness of chemical shifts assignment is 48%.

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  $\geq 3$ , 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	24	
2	B	93	

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 15 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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:15-A:18, B:310-B:317, B:326-B:400 (87)	0.10	15

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

### 3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1885 atoms, of which 949 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Amyloid beta A4 precursor protein-binding family B member 1-interacting protein.

Mol	Chain	Residues	Atoms						Trace
1	A	24	Total	C	H	N	O	S	0
			362	113	179	26	42	2	

- Molecule 2 is a protein called Talin-1.

Mol	Chain	Residues	Atoms						Trace
2	B	93	Total	C	H	N	O	S	0
			1523	488	770	121	141	3	

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	352	SER	ASN	CONFLICT	UNP Q9Y490

## 4 Residue-property plots

### 4.1 Average score per residue in the NMR ensemble

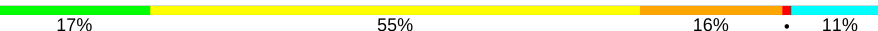
These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain 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.

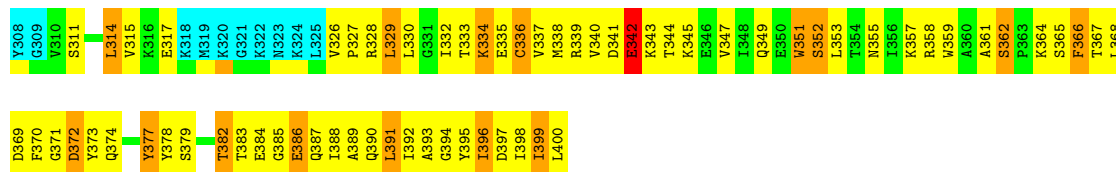
- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein

Chain A: 



- Molecule 2: Talin-1

Chain B: 



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

Colouring as in section 4.1 above.

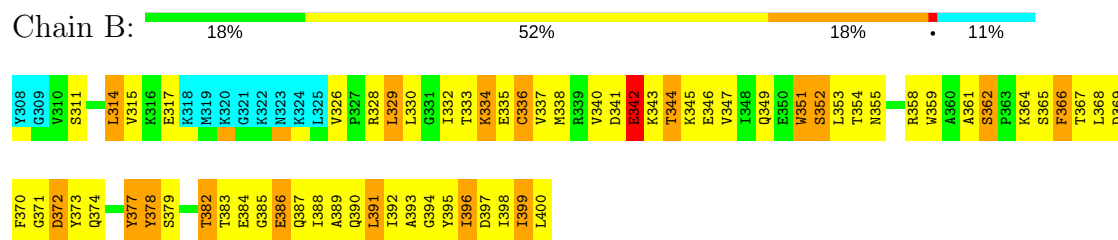
#### 4.2.1 Score per residue for model 1

- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein

Chain A: 



- Molecule 2: Talin-1

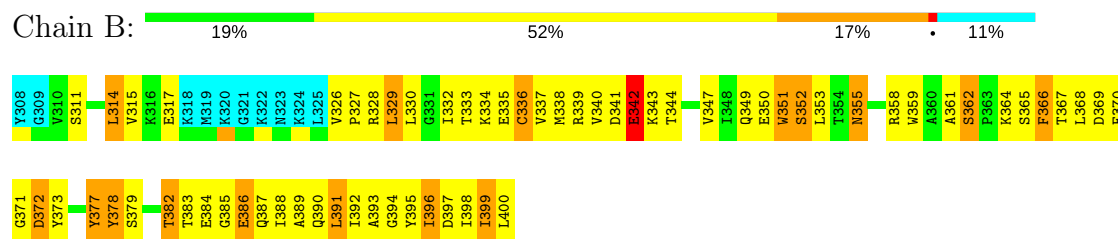


## 4.2.2 Score per residue for model 2

- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein



- Molecule 2: Talin-1

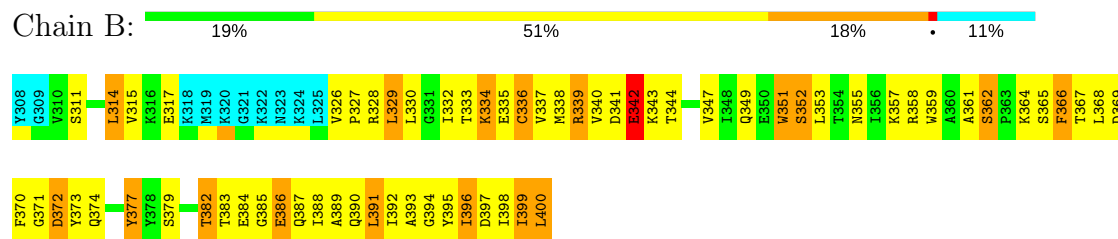


## 4.2.3 Score per residue for model 3

- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein



- Molecule 2: Talin-1



#### 4.2.4 Score per residue for model 4

- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein

Chain A: 



- Molecule 2: Talin-1

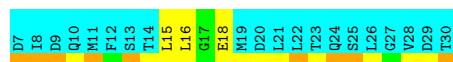
Chain B: 



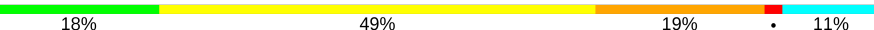
#### 4.2.5 Score per residue for model 5

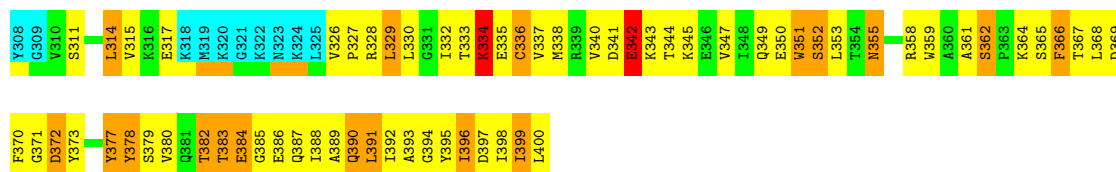
- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein

Chain A: 



- Molecule 2: Talin-1

Chain B: 



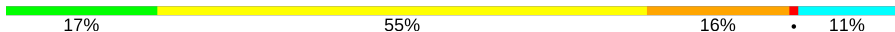
#### 4.2.6 Score per residue for model 6

- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein

Chain A: 



- Molecule 2: Talin-1

Chain B: 



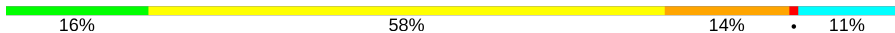
#### 4.2.7 Score per residue for model 7

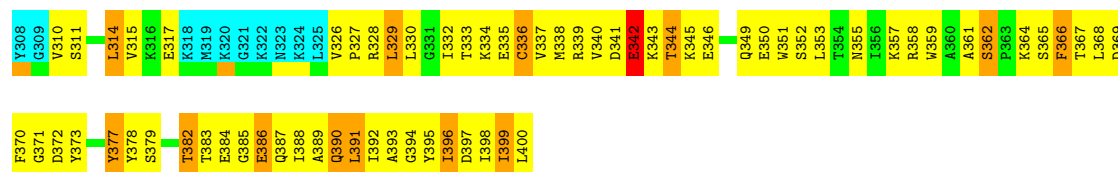
- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein

Chain A: 



- Molecule 2: Talin-1

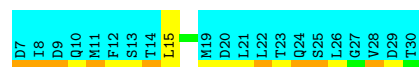
Chain B: 



#### 4.2.8 Score per residue for model 8

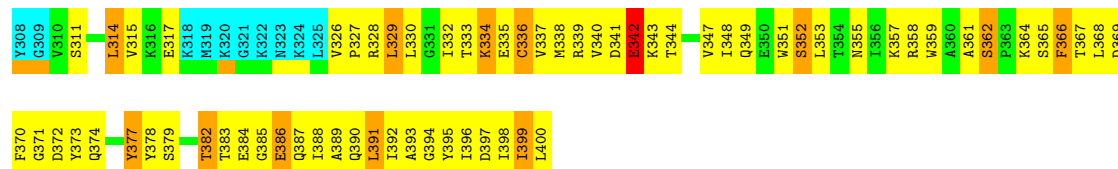
- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein

Chain A: 



- Molecule 2: Talin-1

Chain B: 





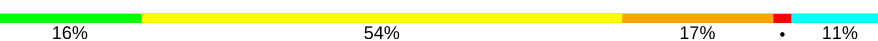
### 4.2.9 Score per residue for model 9

- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein

Chain A: 



- Molecule 2: Talin-1

Chain B: 




### 4.2.10 Score per residue for model 10

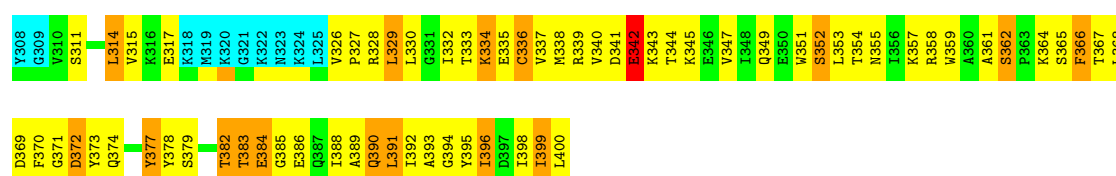
- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein

Chain A: 



- Molecule 2: Talin-1

Chain B: 



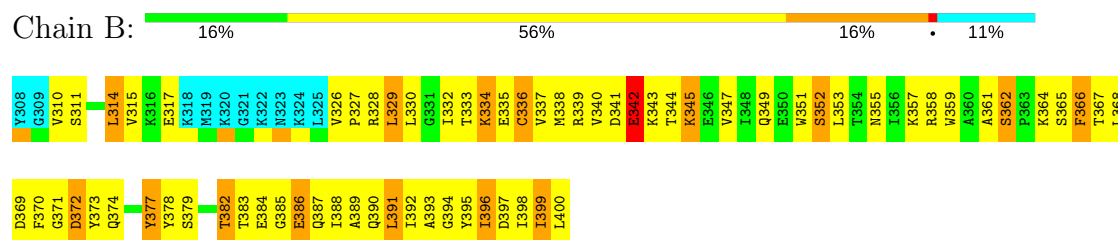
### 4.2.11 Score per residue for model 11

- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein

Chain A: 



- Molecule 2: Talin-1

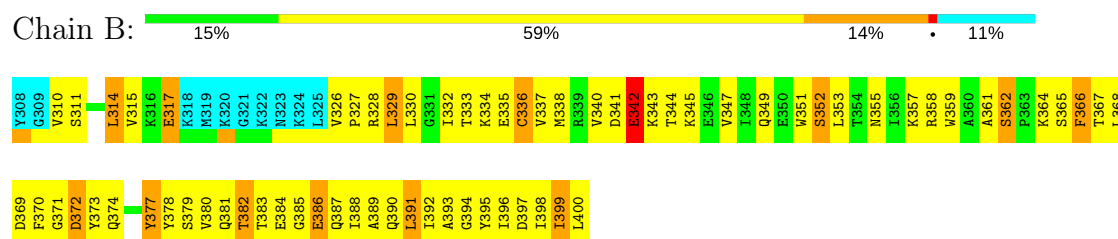


#### 4.2.12 Score per residue for model 12

- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein



- Molecule 2: Talin-1

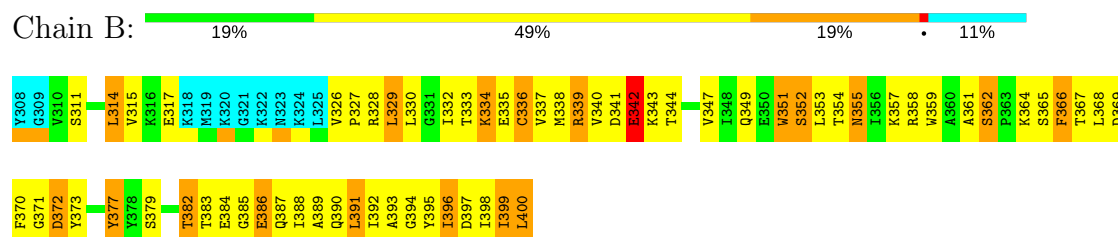


#### 4.2.13 Score per residue for model 13

- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein



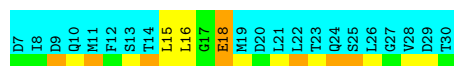
- Molecule 2: Talin-1



#### 4.2.14 Score per residue for model 14

- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein

Chain A: 8% 83%



- Molecule 2: Talin-1

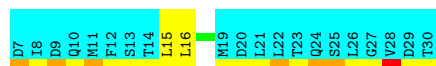
Chain B: 16% 54% 18% 11%



#### 4.2.15 Score per residue for model 15 (medoid)

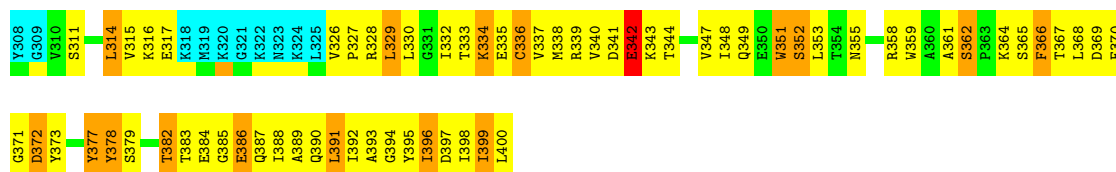
- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein

Chain A: 8% 8% 83%



- Molecule 2: Talin-1

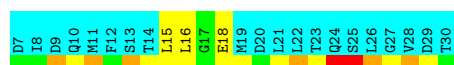
Chain B: 18% 53% 17% 11%



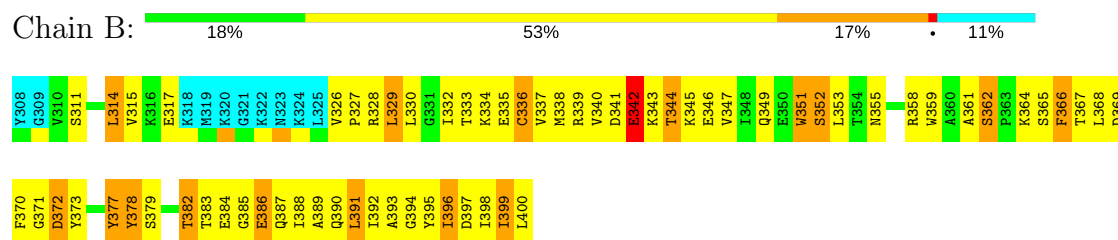
#### 4.2.16 Score per residue for model 16

- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein

Chain A: 13% 83%



- Molecule 2: Talin-1

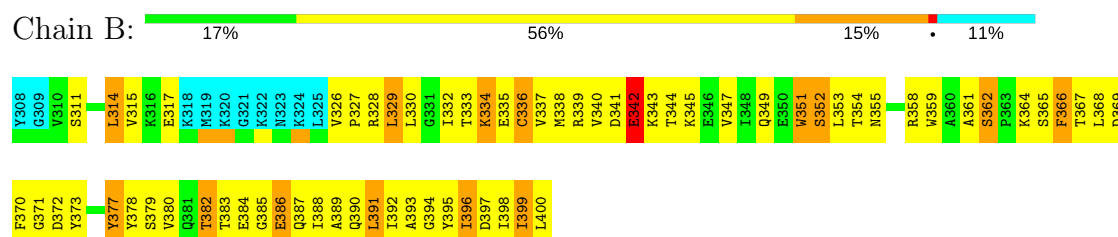


#### 4.2.17 Score per residue for model 17

- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein

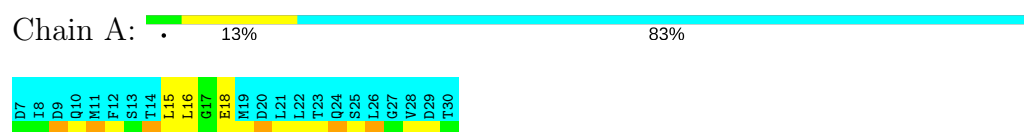


- Molecule 2: Talin-1

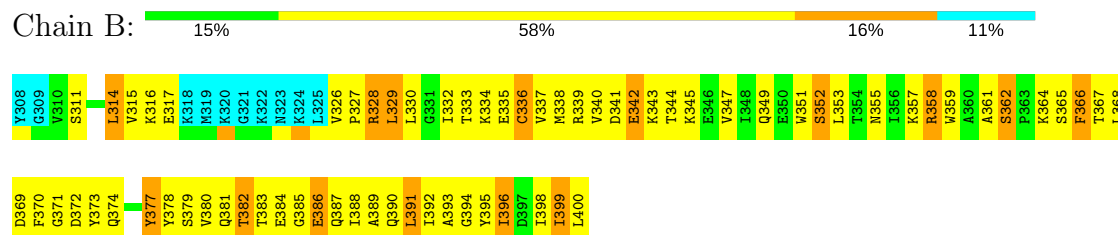


#### 4.2.18 Score per residue for model 18

- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein



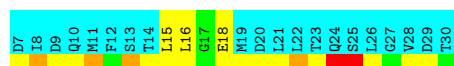
- Molecule 2: Talin-1



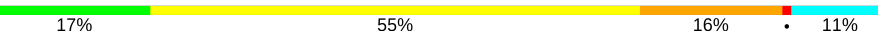
### 4.2.19 Score per residue for model 19

- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein

Chain A:  13% 83%



- Molecule 2: Talin-1

Chain B:  17% 55% 16% 11%



### 4.2.20 Score per residue for model 20

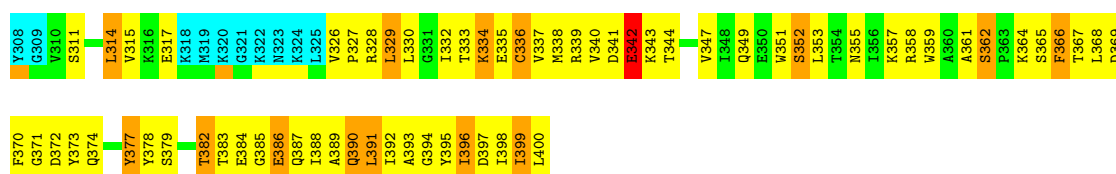
- Molecule 1: Amyloid beta A4 precursor protein-binding family B member 1-interacting protein

Chain A:  13% 83%



- Molecule 2: Talin-1

Chain B:  18% 55% 15% 11%



## 5 Refinement protocol and experimental data overview

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

Of the 99 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	structure solution	
X-PLOR NIH	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)	2mwn_cs.str
Number of chemical shift lists	1
Total number of shifts	841
Number of shifts mapped to atoms	841
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	48%

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	29	31	31	3±1
2	B	673	675	675	72±4
All	All	14040	14120	14120	1450

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 51.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:314:LEU:O	2:B:314:LEU:HD13	0.84	1.73	13	10
2:B:314:LEU:HD13	2:B:314:LEU:O	0.83	1.74	16	10
2:B:330:LEU:HD12	2:B:338:MET:O	0.74	1.81	5	20
2:B:377:TYR:CD1	2:B:377:TYR:N	0.70	2.58	9	10
2:B:377:TYR:N	2:B:377:TYR:CD1	0.69	2.58	10	10
2:B:314:LEU:O	2:B:314:LEU:HD22	0.68	1.88	4	9
2:B:314:LEU:HD22	2:B:314:LEU:O	0.68	1.89	15	11
2:B:315:VAL:O	2:B:328:ARG:N	0.67	2.28	11	20
2:B:329:LEU:O	2:B:340:VAL:N	0.66	2.29	3	20
2:B:339:ARG:NH2	2:B:378:TYR:CG	0.65	2.64	9	1
2:B:354:THR:O	2:B:354:THR:HG22	0.65	1.92	19	4
2:B:361:ALA:HB2	2:B:389:ALA:HB2	0.64	1.69	17	20
2:B:336:CYS:SG	2:B:337:VAL:N	0.62	2.72	19	20

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:334:LYS:NZ	2:B:395:TYR:CE1	0.62	2.68	1	2
2:B:333:THR:C	2:B:335:GLU:H	0.61	1.98	17	20
2:B:314:LEU:C	2:B:314:LEU:HD22	0.61	2.16	14	5
2:B:314:LEU:HD22	2:B:314:LEU:C	0.60	2.17	6	15
2:B:333:THR:OG1	2:B:336:CYS:N	0.60	2.34	11	20
2:B:330:LEU:HD13	2:B:339:ARG:HH12	0.59	1.58	6	2
2:B:355:ASN:O	2:B:370:PHE:CD1	0.59	2.56	14	11
2:B:333:THR:O	2:B:335:GLU:N	0.58	2.36	10	20
2:B:337:VAL:N	2:B:351:TRP:O	0.58	2.37	9	20
2:B:391:LEU:HG	2:B:392:ILE:N	0.57	2.13	4	20
2:B:328:ARG:NH2	2:B:348:ILE:HD12	0.57	2.15	8	1
2:B:330:LEU:HD21	2:B:332:ILE:HD11	0.56	1.75	12	20
2:B:371:GLY:O	2:B:373:TYR:N	0.56	2.38	20	20
2:B:382:THR:HG1	2:B:384:GLU:CD	0.56	2.03	10	2
2:B:341:ASP:O	2:B:344:THR:N	0.56	2.38	14	20
2:B:314:LEU:CD1	2:B:314:LEU:O	0.56	2.52	8	10
2:B:333:THR:O	2:B:353:LEU:HD12	0.56	2.01	10	20
2:B:361:ALA:HB2	2:B:389:ALA:CB	0.55	2.31	7	20
2:B:339:ARG:NH1	2:B:349:GLN:NE2	0.55	2.54	17	1
2:B:341:ASP:O	2:B:343:LYS:N	0.55	2.39	13	20
2:B:338:MET:SD	2:B:347:VAL:HG21	0.55	2.41	19	19
2:B:385:GLY:O	2:B:388:ILE:N	0.55	2.39	2	20
2:B:314:LEU:O	2:B:314:LEU:CD1	0.55	2.53	19	10
2:B:362:SER:N	2:B:365:SER:O	0.55	2.39	18	20
1:A:18:GLU:OE1	1:A:18:GLU:N	0.55	2.40	14	1
2:B:339:ARG:HH21	2:B:349:GLN:NE2	0.54	1.99	9	1
2:B:327:PRO:O	2:B:328:ARG:NE	0.54	2.41	18	1
2:B:327:PRO:O	2:B:328:ARG:NH2	0.54	2.41	18	1
2:B:317:GLU:O	2:B:326:VAL:N	0.54	2.40	18	20
2:B:370:PHE:CD2	2:B:370:PHE:O	0.53	2.62	9	4
2:B:391:LEU:O	2:B:395:TYR:N	0.53	2.41	10	20
2:B:386:GLU:O	2:B:390:GLN:NE2	0.53	2.41	11	1
2:B:328:ARG:CG	2:B:329:LEU:H	0.53	2.17	17	15
2:B:317:GLU:OE1	2:B:339:ARG:NE	0.53	2.42	18	3
2:B:317:GLU:OE2	2:B:339:ARG:NH2	0.53	2.42	10	1
1:A:18:GLU:OE2	2:B:377:TYR:CE2	0.53	2.62	9	8
2:B:370:PHE:O	2:B:370:PHE:CD2	0.52	2.62	10	5
2:B:352:SER:OG	2:B:355:ASN:ND2	0.52	2.43	3	14
2:B:333:THR:C	2:B:335:GLU:N	0.52	2.63	20	20
1:A:18:GLU:OE2	2:B:377:TYR:CD2	0.52	2.62	18	3
2:B:357:LYS:NZ	2:B:373:TYR:OH	0.51	2.42	3	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:18:GLU:OE1	2:B:377:TYR:CG	0.51	2.63	6	7
2:B:339:ARG:NH2	2:B:349:GLN:NE2	0.51	2.58	2	2
2:B:317:GLU:OE2	2:B:339:ARG:NH1	0.51	2.44	7	3
2:B:386:GLU:O	2:B:390:GLN:CG	0.51	2.59	20	20
2:B:358:ARG:O	2:B:369:ASP:CB	0.51	2.59	14	20
2:B:317:GLU:OE1	2:B:339:ARG:NH1	0.51	2.44	15	1
2:B:330:LEU:HD13	2:B:339:ARG:NH1	0.50	2.20	6	2
2:B:315:VAL:HG12	2:B:382:THR:HB	0.50	1.83	17	20
2:B:400:LEU:C	2:B:400:LEU:HD12	0.50	2.26	14	10
2:B:400:LEU:HD12	2:B:400:LEU:C	0.50	2.26	7	8
2:B:399:ILE:O	2:B:400:LEU:C	0.49	2.49	13	1
2:B:384:GLU:CD	2:B:384:GLU:N	0.49	2.65	10	2
2:B:354:THR:HG22	2:B:354:THR:O	0.49	2.08	9	2
2:B:338:MET:CB	2:B:349:GLN:O	0.49	2.61	16	20
2:B:367:THR:HG22	2:B:368:LEU:N	0.49	2.23	18	10
2:B:359:TRP:N	2:B:359:TRP:CE3	0.48	2.81	7	10
2:B:371:GLY:C	2:B:373:TYR:N	0.48	2.66	19	20
2:B:370:PHE:N	2:B:370:PHE:CD1	0.48	2.81	12	6
2:B:326:VAL:O	2:B:327:PRO:C	0.48	2.52	18	19
2:B:359:TRP:CH2	2:B:396:ILE:HD12	0.48	2.44	14	17
1:A:15:LEU:HD22	1:A:15:LEU:N	0.48	2.24	12	1
2:B:328:ARG:HH21	2:B:348:ILE:CD1	0.48	2.22	15	1
2:B:370:PHE:CG	2:B:370:PHE:O	0.48	2.65	9	1
1:A:18:GLU:CD	2:B:377:TYR:CD2	0.48	2.87	20	6
2:B:396:ILE:O	2:B:400:LEU:HD12	0.48	2.09	19	1
2:B:359:TRP:CE3	2:B:359:TRP:N	0.48	2.82	16	10
1:A:15:LEU:HD12	2:B:367:THR:CG2	0.48	2.39	8	20
2:B:344:THR:O	2:B:345:LYS:CB	0.48	2.62	7	5
2:B:370:PHE:O	2:B:370:PHE:CG	0.47	2.65	10	8
2:B:358:ARG:NH2	2:B:369:ASP:OD2	0.47	2.47	15	6
2:B:354:THR:O	2:B:354:THR:CG2	0.47	2.61	19	1
2:B:366:PHE:O	2:B:379:SER:OG	0.47	2.33	20	20
2:B:384:GLU:N	2:B:384:GLU:OE2	0.47	2.47	5	1
2:B:358:ARG:CZ	2:B:369:ASP:OD2	0.47	2.63	17	7
2:B:395:TYR:HA	2:B:398:ILE:HD12	0.47	1.87	13	20
2:B:341:ASP:C	2:B:343:LYS:N	0.46	2.66	17	20
2:B:358:ARG:NH1	2:B:369:ASP:CG	0.46	2.69	5	6
2:B:328:ARG:CG	2:B:329:LEU:N	0.46	2.79	14	15
2:B:314:LEU:O	2:B:314:LEU:CD2	0.46	2.61	4	9
2:B:367:THR:CG2	2:B:368:LEU:N	0.46	2.78	18	20
2:B:384:GLU:CD	2:B:384:GLU:H	0.46	2.14	10	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:390:GLN:OE1	2:B:391:LEU:CA	0.46	2.64	20	3
2:B:314:LEU:CD2	2:B:314:LEU:O	0.45	2.61	15	7
2:B:391:LEU:HD12	2:B:391:LEU:C	0.45	2.31	6	11
2:B:341:ASP:O	2:B:345:LYS:N	0.45	2.40	10	7
2:B:315:VAL:HG21	2:B:339:ARG:NH2	0.45	2.26	8	2
2:B:370:PHE:CD1	2:B:370:PHE:N	0.45	2.84	4	3
2:B:391:LEU:C	2:B:391:LEU:HD12	0.45	2.31	11	9
2:B:339:ARG:NH1	2:B:339:ARG:CG	0.45	2.79	13	2
2:B:332:ILE:CD1	2:B:337:VAL:HG13	0.45	2.42	17	15
2:B:339:ARG:HH21	2:B:349:GLN:HE22	0.45	1.54	9	1
2:B:399:ILE:O	2:B:400:LEU:OXT	0.45	2.34	8	10
2:B:399:ILE:O	2:B:400:LEU:O	0.45	2.34	10	9
2:B:391:LEU:O	2:B:394:GLY:N	0.44	2.50	1	20
2:B:400:LEU:O	2:B:400:LEU:HD12	0.44	2.12	6	5
2:B:339:ARG:HE	2:B:349:GLN:CB	0.44	2.25	19	3
2:B:385:GLY:C	2:B:387:GLN:N	0.44	2.70	19	19
2:B:400:LEU:HD12	2:B:400:LEU:OXT	0.44	2.12	2	8
2:B:400:LEU:HD12	2:B:400:LEU:O	0.44	2.12	15	3
2:B:339:ARG:HH11	2:B:339:ARG:CG	0.44	2.25	13	1
2:B:357:LYS:CB	2:B:369:ASP:O	0.44	2.65	11	9
2:B:383:THR:N	2:B:384:GLU:OE2	0.44	2.51	5	2
2:B:327:PRO:O	2:B:328:ARG:CZ	0.44	2.65	18	1
2:B:334:LYS:HZ3	2:B:398:ILE:CD1	0.44	2.25	5	1
2:B:390:GLN:NE2	2:B:391:LEU:CB	0.43	2.81	4	3
2:B:391:LEU:CG	2:B:392:ILE:N	0.43	2.81	2	20
2:B:329:LEU:CD2	2:B:329:LEU:C	0.43	2.86	3	10
2:B:384:GLU:OE2	2:B:384:GLU:N	0.43	2.51	10	1
2:B:317:GLU:CD	2:B:380:VAL:CG1	0.43	2.87	12	1
2:B:400:LEU:OXT	2:B:400:LEU:HD12	0.43	2.13	18	2
2:B:385:GLY:O	2:B:387:GLN:N	0.43	2.51	19	16
2:B:365:SER:HA	2:B:382:THR:H	0.43	1.74	18	20
2:B:392:ILE:HG22	2:B:393:ALA:N	0.43	2.27	19	20
1:A:15:LEU:HD12	2:B:367:THR:HG21	0.43	1.90	18	6
2:B:329:LEU:C	2:B:329:LEU:CD2	0.43	2.87	7	10
2:B:364:LYS:C	2:B:382:THR:O	0.43	2.57	5	20
2:B:390:GLN:OE1	2:B:391:LEU:CB	0.43	2.67	20	3
2:B:337:VAL:O	2:B:351:TRP:N	0.43	2.52	19	7
2:B:339:ARG:NH1	2:B:349:GLN:HE22	0.43	2.12	17	1
2:B:351:TRP:CZ3	2:B:378:TYR:CE2	0.43	3.07	19	7
2:B:366:PHE:CE2	2:B:388:ILE:HG21	0.42	2.49	18	9
2:B:339:ARG:CZ	2:B:349:GLN:NE2	0.42	2.82	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:340:VAL:CG1	2:B:345:LYS:O	0.42	2.66	7	3
2:B:367:THR:OG1	2:B:379:SER:OG	0.42	2.36	7	1
2:B:341:ASP:O	2:B:342:GLU:C	0.42	2.58	8	20
2:B:339:ARG:CZ	2:B:349:GLN:CD	0.42	2.88	19	3
2:B:372:ASP:O	2:B:372:ASP:OD1	0.42	2.37	3	8
2:B:361:ALA:HB1	2:B:385:GLY:C	0.42	2.35	3	6
2:B:357:LYS:NZ	2:B:373:TYR:CE1	0.42	2.84	9	1
2:B:357:LYS:HZ2	2:B:372:ASP:HB3	0.42	1.75	9	1
2:B:329:LEU:HD23	2:B:330:LEU:N	0.42	2.29	12	13
2:B:398:ILE:O	2:B:400:LEU:CD1	0.42	2.67	13	1
2:B:315:VAL:O	2:B:328:ARG:CB	0.42	2.68	4	2
2:B:386:GLU:O	2:B:390:GLN:OE1	0.42	2.37	3	6
2:B:344:THR:OG1	2:B:346:GLU:CG	0.42	2.67	16	3
2:B:372:ASP:OD1	2:B:372:ASP:O	0.42	2.38	13	5
2:B:390:GLN:CG	2:B:391:LEU:N	0.41	2.83	18	13
2:B:317:GLU:CD	2:B:339:ARG:HE	0.41	2.18	3	2
2:B:340:VAL:HG13	2:B:346:GLU:O	0.41	2.15	6	3
2:B:352:SER:OG	2:B:355:ASN:CG	0.41	2.59	3	6
2:B:334:LYS:NZ	2:B:395:TYR:CZ	0.41	2.85	9	1
2:B:349:GLN:CG	2:B:350:GLU:N	0.41	2.83	7	4
2:B:400:LEU:C	2:B:400:LEU:CD1	0.41	2.89	7	5
2:B:390:GLN:OE1	2:B:391:LEU:N	0.41	2.54	20	2
2:B:339:ARG:CG	2:B:339:ARG:HH11	0.41	2.28	3	1
2:B:314:LEU:CD2	2:B:314:LEU:C	0.41	2.89	6	2
2:B:332:ILE:HG21	2:B:391:LEU:HD11	0.41	1.93	10	5
2:B:400:LEU:CD1	2:B:400:LEU:C	0.41	2.89	14	13
2:B:314:LEU:C	2:B:314:LEU:CD2	0.41	2.89	2	2
2:B:391:LEU:CD1	2:B:395:TYR:CE2	0.41	3.04	6	1
2:B:336:CYS:HA	2:B:353:LEU:N	0.40	2.31	14	1
2:B:354:THR:OG1	2:B:400:LEU:O	0.40	2.38	13	1
2:B:372:ASP:CG	2:B:377:TYR:OH	0.40	2.60	4	1
2:B:316:LYS:O	2:B:380:VAL:CB	0.40	2.70	18	1
2:B:332:ILE:CG2	2:B:391:LEU:HD11	0.40	2.47	10	1
2:B:339:ARG:HE	2:B:349:GLN:CD	0.40	2.19	9	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	4/24 (17%)	4±0 (100±0%)	0±0 (0±0%)	0±0 (0±0%)	100	100
2	B	82/93 (88%)	66±1 (81±1%)	12±1 (14±1%)	4±0 (5±0%)	5	28
All	All	1720/2340 (74%)	1406 (82%)	237 (14%)	77 (4%)	5	29

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)
2	B	334	LYS	20
2	B	342	GLU	20
2	B	372	ASP	20
2	B	386	GLU	17

### 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	3/22 (14%)	2±0 (68±13%)	1±0 (32±13%)	1	14
2	B	74/82 (90%)	54±1 (73±2%)	20±1 (27±2%)	2	22
All	All	1540/2080 (74%)	1121 (73%)	419 (27%)	2	21

All 35 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)
2	B	336	CYS	20
2	B	352	SER	20
2	B	391	LEU	20
2	B	396	ILE	20
2	B	382	THR	20
2	B	383	THR	20
2	B	362	SER	20
2	B	366	PHE	20
2	B	311	SER	20

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Mol	Chain	Res	Type	Models (Total)
2	B	314	LEU	20
2	B	399	ILE	20
2	B	329	LEU	20
2	B	384	GLU	20
2	B	377	TYR	20
2	B	342	GLU	19
2	B	397	ASP	18
1	A	16	LEU	18
2	B	378	TYR	18
2	B	374	GLN	11
2	B	351	TRP	11
2	B	334	LYS	11
2	B	355	ASN	6
2	B	390	GLN	4
2	B	380	VAL	4
2	B	344	THR	3
2	B	339	ARG	3
2	B	338	MET	2
2	B	400	LEU	2
2	B	358	ARG	2
2	B	328	ARG	2
1	A	18	GLU	1
2	B	381	GLN	1
2	B	341	ASP	1
2	B	345	LYS	1
2	B	317	GLU	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 48% for the well-defined parts and 47% for the entire structure.

### 7.1 Chemical shift list 1

File name: 2mwn\_cs.str

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	841
Number of shifts mapped to atoms	841
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

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	0	—	None (insufficient data)
$^{13}\text{C}_\beta$	0	—	None (insufficient data)
$^{13}\text{C}'$	0	—	None (insufficient data)
$^{15}\text{N}$	88	$-0.10 \pm 0.48$	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 48%, i.e. 522 atoms were assigned a chemical shift out of a possible 1089. 0 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	241/431 (56%)	160/172 (93%)	0/174 (0%)	81/85 (95%)
Sidechain	241/566 (43%)	241/328 (73%)	0/217 (0%)	0/21 (0%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	40/92 (43%)	38/48 (79%)	0/42 (0%)	2/2 (100%)
Overall	522/1089 (48%)	439/548 (80%)	0/433 (0%)	83/108 (77%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 47%, i.e. 679 atoms were assigned a chemical shift out of a possible 1450. 0 out of 21 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	299/581 (51%)	211/232 (91%)	0/234 (0%)	88/115 (77%)
Sidechain	336/760 (44%)	336/441 (76%)	0/291 (0%)	0/28 (0%)
Aromatic	44/109 (40%)	42/57 (74%)	0/50 (0%)	2/2 (100%)
Overall	679/1450 (47%)	589/730 (81%)	0/575 (0%)	90/145 (62%)

#### 7.1.4 Statistically unusual chemical shifts ⓘ

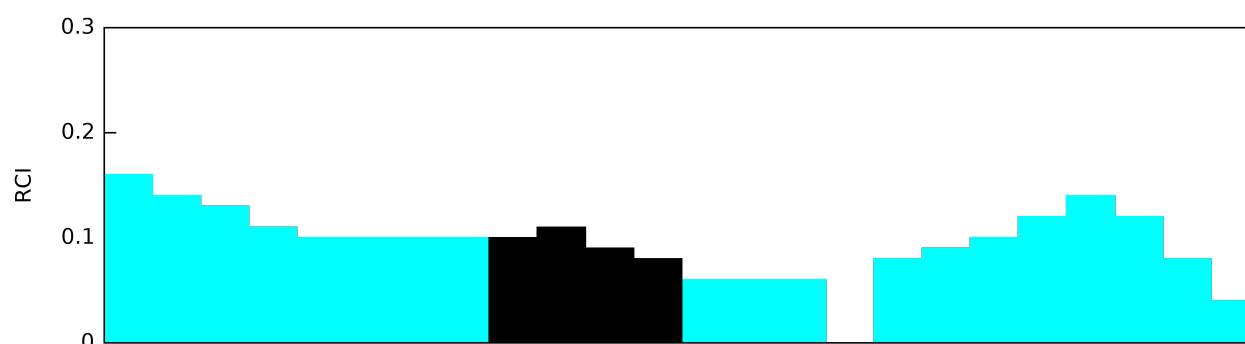
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
2	B	349	GLN	HB2	0.68	3.30 – 0.80	-5.5

#### 7.1.5 Random Coil Index (RCI) plots ⓘ

The images below report *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:





Random coil index (RCI) for chain B:

