



# Full wwPDB NMR Structure Validation Report ⓘ

Feb 13, 2017 – 02:28 am GMT

PDB ID : 2Z4F  
Title : Solution structure of the Discoidin Domain of DDR2  
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Deposited on : 2007-06-16

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

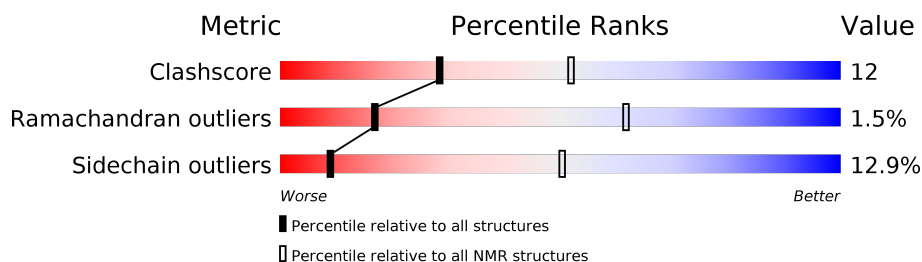
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 85%.

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	173	 61% 23% • 9% 7%

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 10 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:29-A:105, A:113-A:144, A:150-A:186 (146)	0.37	10

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 6 single-model clusters were found.

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

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2493 atoms, of which 1216 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Discoidin domain-containing receptor 2.

Mol	Chain	Residues	Atoms						Trace
1	A	161	Total	C	H	N	O	S	0
			2493	807	1216	223	239	8	

There are 12 discrepancies between the modelled and reference sequences:

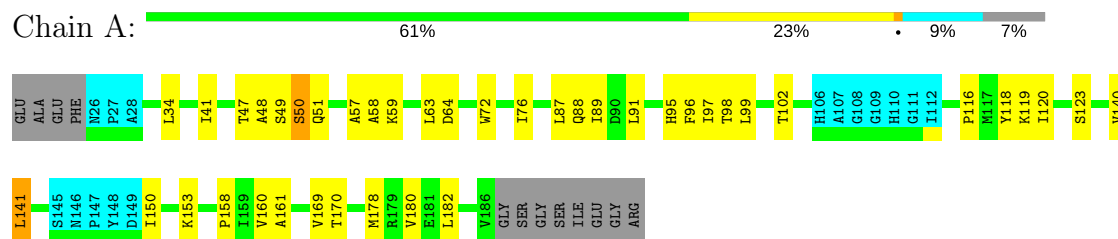
Chain	Residue	Modelled	Actual	Comment	Reference
A	22	GLU	-	EXPRESSION TAG	UNP Q16832
A	23	ALA	-	EXPRESSION TAG	UNP Q16832
A	24	GLU	-	EXPRESSION TAG	UNP Q16832
A	25	PHE	-	EXPRESSION TAG	UNP Q16832
A	187	GLY	-	EXPRESSION TAG	UNP Q16832
A	188	SER	-	EXPRESSION TAG	UNP Q16832
A	189	GLY	-	EXPRESSION TAG	UNP Q16832
A	190	SER	-	EXPRESSION TAG	UNP Q16832
A	191	ILE	-	EXPRESSION TAG	UNP Q16832
A	192	GLU	-	EXPRESSION TAG	UNP Q16832
A	193	GLY	-	EXPRESSION TAG	UNP Q16832
A	194	ARG	-	EXPRESSION TAG	UNP Q16832

## 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: Discoidin domain-containing receptor 2

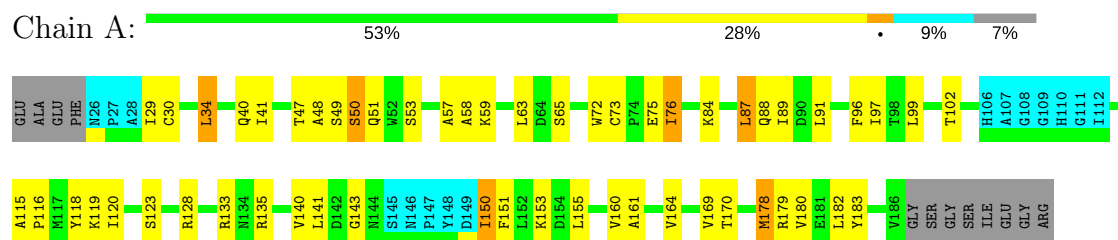


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1

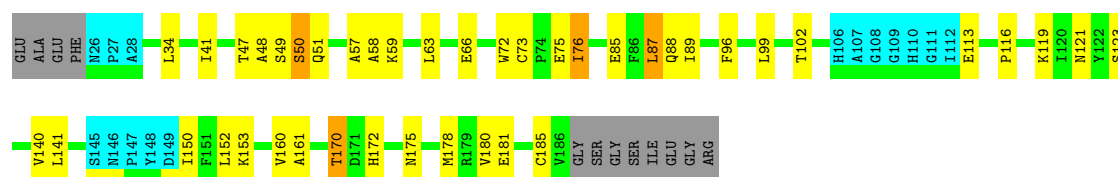
- Molecule 1: Discoidin domain-containing receptor 2



#### 4.2.2 Score per residue for model 2

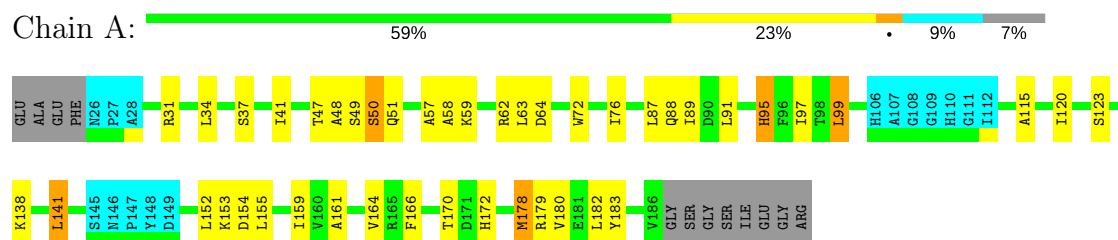
- Molecule 1: Discoidin domain-containing receptor 2





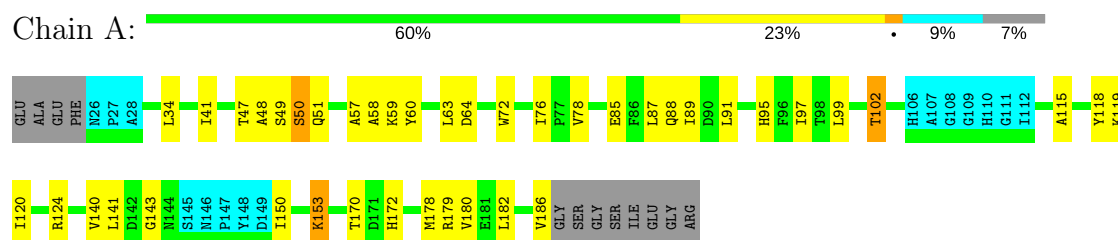
### 4.2.3 Score per residue for model 3

- Molecule 1: Discoidin domain-containing receptor 2



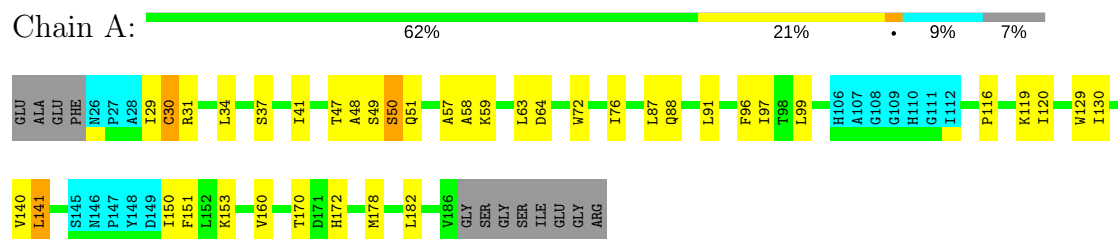
### 4.2.4 Score per residue for model 4

- Molecule 1: Discoidin domain-containing receptor 2



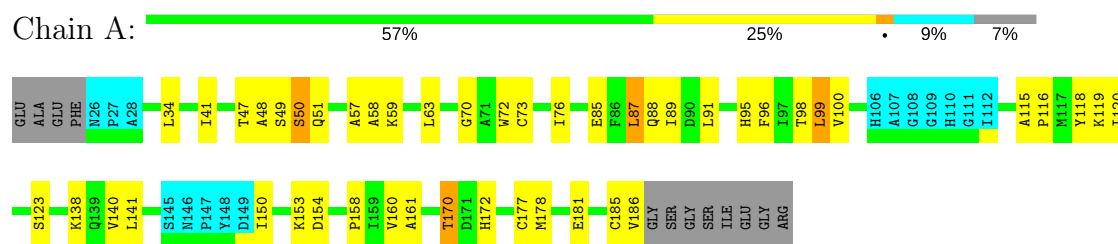
### 4.2.5 Score per residue for model 5

- Molecule 1: Discoidin domain-containing receptor 2



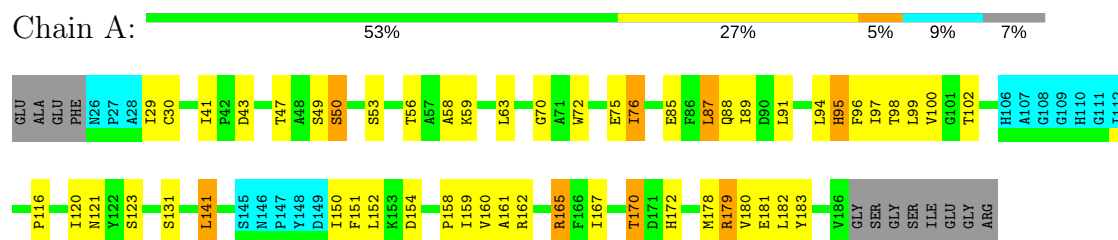
### 4.2.6 Score per residue for model 6

- Molecule 1: Discoidin domain-containing receptor 2



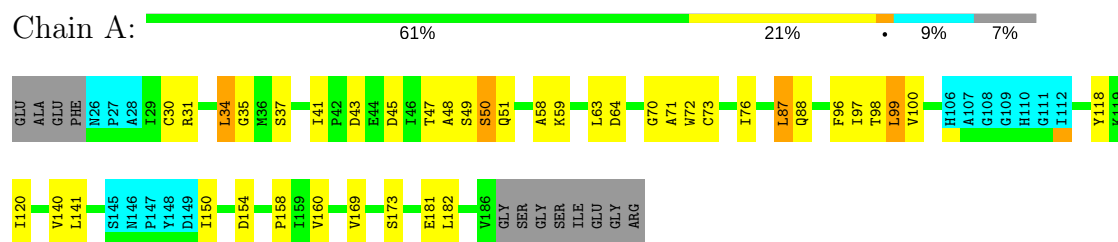
#### 4.2.7 Score per residue for model 7

- Molecule 1: Discoidin domain-containing receptor 2



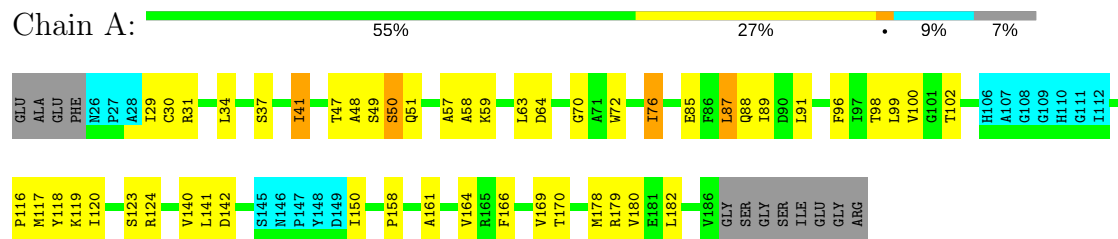
#### 4.2.8 Score per residue for model 8

- Molecule 1: Discoidin domain-containing receptor 2



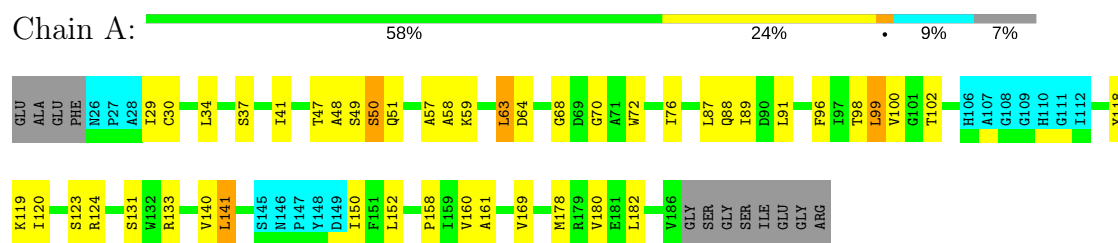
#### 4.2.9 Score per residue for model 9

- Molecule 1: Discoidin domain-containing receptor 2



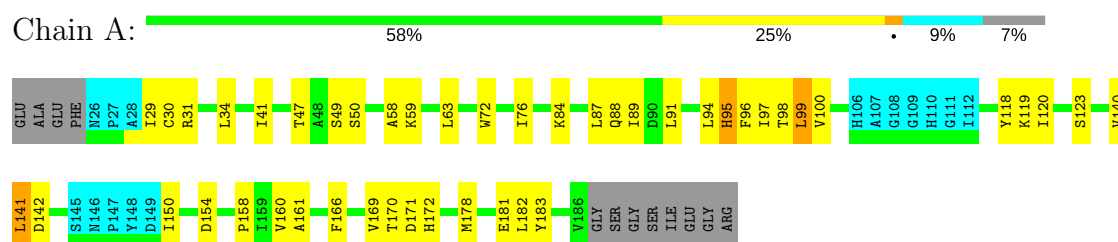
#### 4.2.10 Score per residue for model 10 (medoid)

- Molecule 1: Discoidin domain-containing receptor 2



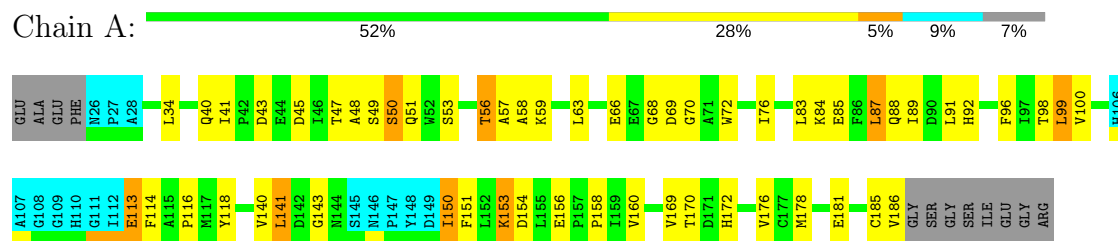
#### 4.2.11 Score per residue for model 11

- Molecule 1: Discoidin domain-containing receptor 2



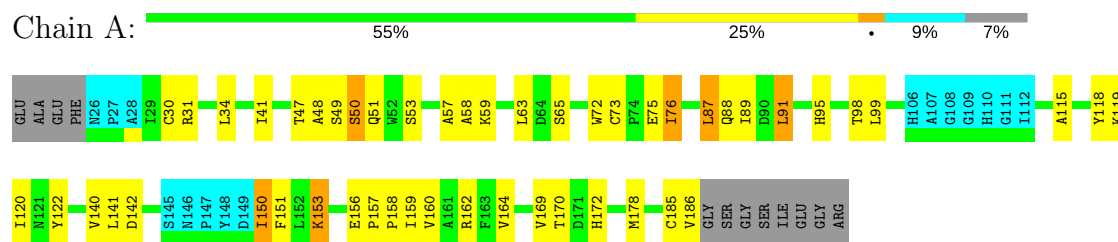
#### 4.2.12 Score per residue for model 12

- Molecule 1: Discoidin domain-containing receptor 2



#### 4.2.13 Score per residue for model 13

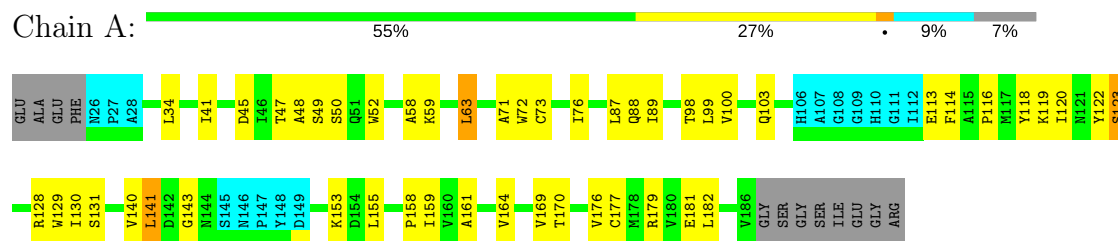
- Molecule 1: Discoidin domain-containing receptor 2





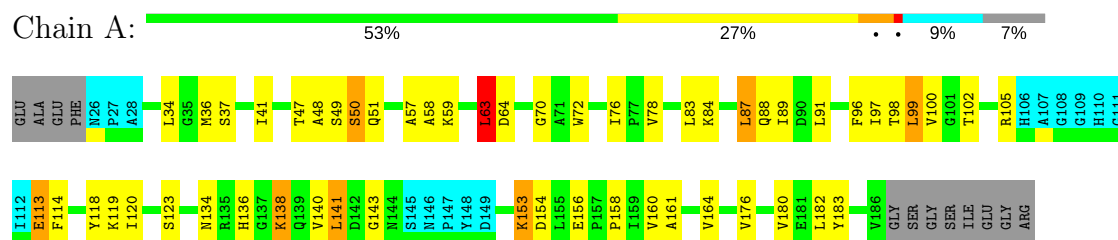
## 4.2.14 Score per residue for model 14

- Molecule 1: Discoidin domain-containing receptor 2



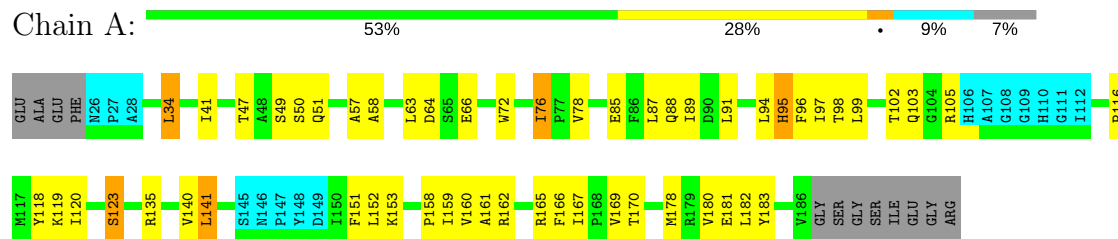
## 4.2.15 Score per residue for model 15

- Molecule 1: Discoidin domain-containing receptor 2



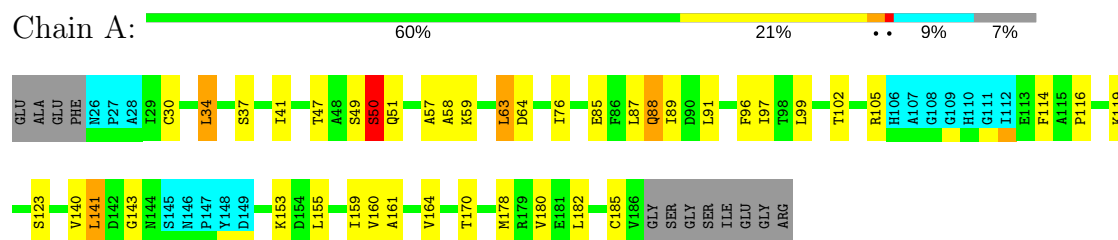
## 4.2.16 Score per residue for model 16

- Molecule 1: Discoidin domain-containing receptor 2



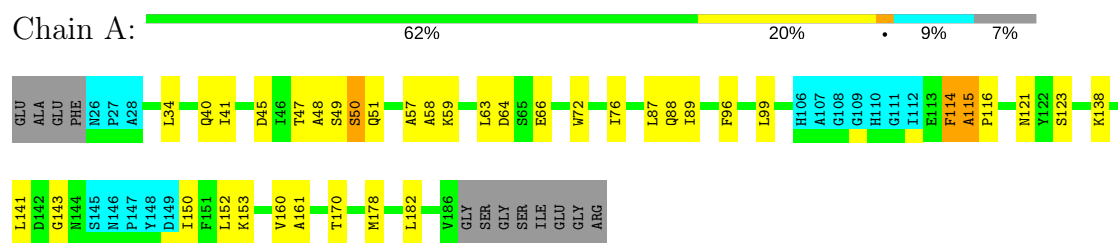
## 4.2.17 Score per residue for model 17

- Molecule 1: Discoidin domain-containing receptor 2



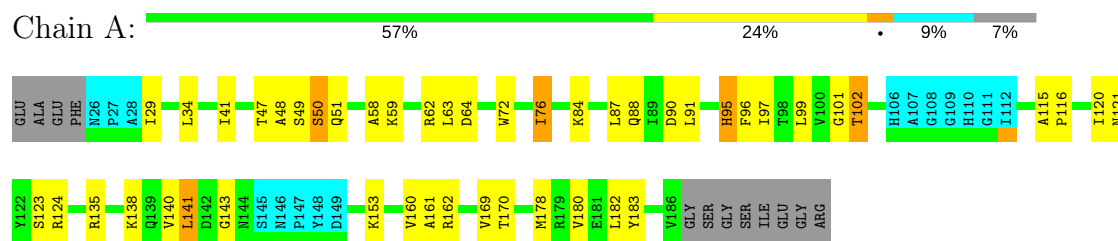
### 4.2.18 Score per residue for model 18

- Molecule 1: Discoidin domain-containing receptor 2



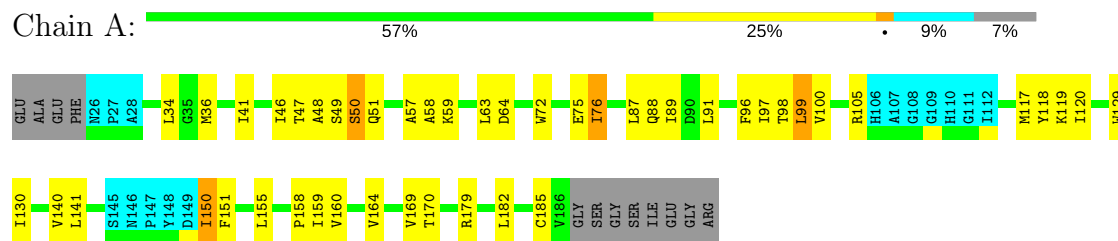
### 4.2.19 Score per residue for model 19

- Molecule 1: Discoidin domain-containing receptor 2



### 4.2.20 Score per residue for model 20

- Molecule 1: Discoidin domain-containing receptor 2



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *TORSION ANGLE DYNAMICS*.

Of the 200 calculated structures, 20 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	2.1
CYANA	structure solution	2.1

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)	BMRB entry 15315
Number of chemical shift lists	1
Total number of shifts	1868
Number of shifts mapped to atoms	1868
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	85%

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	1171	1128	1128	27±5
All	All	23420	22560	22560	548

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 12.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:34:LEU:HD11	1:A:182:LEU:HD12	0.85	1.46	20	5
1:A:58:ALA:HB2	1:A:87:LEU:HD21	0.85	1.49	8	19
1:A:120:ILE:HD11	1:A:141:LEU:HD22	0.80	1.53	8	11
1:A:63:LEU:HD11	1:A:150:ILE:HD12	0.80	1.53	5	3
1:A:91:LEU:HD21	1:A:182:LEU:HD13	0.77	1.54	3	3
1:A:63:LEU:HD21	1:A:150:ILE:HD11	0.76	1.57	6	7
1:A:34:LEU:HD13	1:A:91:LEU:HD22	0.75	1.59	10	3
1:A:97:ILE:HG21	1:A:182:LEU:HD12	0.73	1.56	15	3
1:A:155:LEU:HD13	1:A:159:ILE:HD12	0.72	1.61	20	2
1:A:91:LEU:HD11	1:A:164:VAL:HG23	0.70	1.63	1	6
1:A:72:TRP:CZ2	1:A:87:LEU:HD23	0.69	2.23	3	19
1:A:95:HIS:CE1	1:A:186:VAL:HG13	0.68	2.24	13	2
1:A:34:LEU:HD22	1:A:91:LEU:HD22	0.67	1.65	4	2
1:A:96:PHE:CD1	1:A:160:VAL:HG13	0.67	2.24	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:91:LEU:HD21	1:A:164:VAL:HG23	0.66	1.66	9	1
1:A:91:LEU:HD13	1:A:95:HIS:CD2	0.66	2.26	19	4
1:A:120:ILE:HD12	1:A:141:LEU:HD13	0.65	1.66	9	3
1:A:102:THR:HG22	1:A:180:VAL:HG12	0.65	1.66	10	10
1:A:99:LEU:HD13	1:A:100:VAL:N	0.64	2.07	9	8
1:A:63:LEU:HD11	1:A:150:ILE:CD1	0.64	2.23	18	4
1:A:120:ILE:HG23	1:A:166:PHE:CE1	0.64	2.27	9	3
1:A:122:TYR:CG	1:A:159:ILE:HG21	0.64	2.28	13	2
1:A:72:TRP:CE2	1:A:87:LEU:HD23	0.63	2.29	19	10
1:A:99:LEU:HD12	1:A:153:LYS:O	0.62	1.94	5	10
1:A:122:TYR:CZ	1:A:159:ILE:HD13	0.62	2.29	13	2
1:A:34:LEU:HD21	1:A:91:LEU:HD22	0.62	1.70	11	1
1:A:119:LYS:CG	1:A:140:VAL:HG22	0.62	2.23	4	6
1:A:122:TYR:OH	1:A:159:ILE:HD13	0.62	1.94	13	2
1:A:34:LEU:CD2	1:A:91:LEU:HD22	0.61	2.25	11	3
1:A:98:THR:HG22	1:A:158:PRO:HB3	0.61	1.73	13	12
1:A:34:LEU:HD11	1:A:182:LEU:CD1	0.61	2.25	10	3
1:A:155:LEU:HD13	1:A:159:ILE:CD1	0.61	2.26	20	2
1:A:96:PHE:CD1	1:A:160:VAL:HG23	0.61	2.29	5	11
1:A:63:LEU:HD13	1:A:64:ASP:N	0.60	2.11	3	11
1:A:116:PRO:CG	1:A:170:THR:HG22	0.60	2.25	18	12
1:A:120:ILE:CD1	1:A:141:LEU:HD13	0.60	2.26	13	5
1:A:63:LEU:HD22	1:A:181:GLU:CB	0.60	2.27	12	4
1:A:123:SER:O	1:A:161:ALA:HB1	0.60	1.96	11	14
1:A:48:ALA:HB2	1:A:58:ALA:CB	0.60	2.26	3	2
1:A:99:LEU:HD22	1:A:154:ASP:HA	0.60	1.73	11	6
1:A:119:LYS:HG2	1:A:140:VAL:HG22	0.59	1.73	1	11
1:A:96:PHE:CE1	1:A:160:VAL:HG23	0.59	2.32	5	12
1:A:87:LEU:HD13	1:A:88:GLN:N	0.59	2.12	14	20
1:A:122:TYR:CD2	1:A:159:ILE:HG21	0.59	2.33	14	2
1:A:91:LEU:HD13	1:A:95:HIS:NE2	0.58	2.12	11	4
1:A:120:ILE:HG22	1:A:122:TYR:CE1	0.58	2.34	13	2
1:A:76:ILE:HD11	1:A:85:GLU:OE1	0.58	1.99	12	2
1:A:48:ALA:HB3	1:A:51:GLN:OE1	0.58	1.98	10	14
1:A:87:LEU:HD12	1:A:89:ILE:HD11	0.58	1.74	3	17
1:A:75:GLU:HG3	1:A:76:ILE:HG23	0.58	1.75	20	3
1:A:97:ILE:HG21	1:A:182:LEU:CD1	0.57	2.29	1	1
1:A:95:HIS:ND1	1:A:186:VAL:HG23	0.57	2.15	6	1
1:A:129:TRP:O	1:A:130:ILE:HD13	0.57	1.99	20	3
1:A:122:TYR:CD2	1:A:164:VAL:HG22	0.56	2.35	13	2
1:A:96:PHE:CD2	1:A:160:VAL:HG13	0.56	2.35	2	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:141:LEU:HD11	1:A:153:LYS:CE	0.56	2.30	13	2
1:A:97:ILE:HG21	1:A:182:LEU:HD22	0.55	1.79	20	1
1:A:34:LEU:HD13	1:A:91:LEU:HG	0.55	1.77	20	1
1:A:29:ILE:HD12	1:A:30:CYS:HB2	0.55	1.78	5	6
1:A:34:LEU:HD21	1:A:182:LEU:HD13	0.55	1.79	16	1
1:A:34:LEU:HD21	1:A:182:LEU:HD12	0.54	1.77	9	1
1:A:165:ARG:NH2	1:A:167:ILE:HD11	0.54	2.16	16	1
1:A:58:ALA:CB	1:A:87:LEU:HD21	0.54	2.30	8	7
1:A:76:ILE:O	1:A:76:ILE:HD12	0.54	2.03	14	3
1:A:34:LEU:HD21	1:A:182:LEU:CD1	0.54	2.32	16	1
1:A:97:ILE:HG12	1:A:182:LEU:HD22	0.54	1.79	8	4
1:A:34:LEU:HD21	1:A:91:LEU:HD23	0.54	1.80	13	1
1:A:91:LEU:CD1	1:A:164:VAL:HG23	0.54	2.33	1	3
1:A:164:VAL:HG11	1:A:182:LEU:HD21	0.53	1.80	3	2
1:A:89:ILE:HG21	1:A:182:LEU:HD12	0.53	1.79	9	1
1:A:87:LEU:HD12	1:A:89:ILE:CD1	0.53	2.33	10	16
1:A:91:LEU:HD12	1:A:162:ARG:CA	0.53	2.34	7	2
1:A:63:LEU:HD12	1:A:181:GLU:HB2	0.53	1.80	14	1
1:A:97:ILE:HG23	1:A:183:TYR:O	0.52	2.04	11	7
1:A:140:VAL:HG23	1:A:169:VAL:HG21	0.52	1.81	8	2
1:A:155:LEU:HD23	1:A:159:ILE:HD12	0.52	1.81	3	1
1:A:34:LEU:HD22	1:A:91:LEU:CD2	0.52	2.34	20	1
1:A:51:GLN:NE2	1:A:57:ALA:HB2	0.52	2.20	1	14
1:A:114:PHE:O	1:A:176:VAL:HG12	0.51	2.04	14	3
1:A:78:VAL:HG12	1:A:85:GLU:HG3	0.51	1.83	4	1
1:A:36:MET:CG	1:A:46:ILE:HD11	0.51	2.35	20	1
1:A:95:HIS:CE1	1:A:186:VAL:HG23	0.51	2.41	6	1
1:A:34:LEU:HD22	1:A:91:LEU:HD23	0.51	1.83	20	2
1:A:97:ILE:O	1:A:155:LEU:HD12	0.50	2.06	17	1
1:A:118:TYR:OH	1:A:141:LEU:HD22	0.50	2.07	6	3
1:A:63:LEU:HD11	1:A:150:ILE:HD11	0.50	1.81	1	1
1:A:34:LEU:CD1	1:A:91:LEU:HD22	0.49	2.37	6	2
1:A:141:LEU:HD21	1:A:153:LYS:HG2	0.49	1.85	1	2
1:A:102:THR:CG2	1:A:180:VAL:HG12	0.49	2.38	4	1
1:A:141:LEU:HD23	1:A:142:ASP:O	0.49	2.08	9	2
1:A:151:PHE:O	1:A:152:LEU:HD13	0.49	2.07	16	1
1:A:91:LEU:HD12	1:A:162:ARG:HA	0.48	1.85	16	2
1:A:99:LEU:HD23	1:A:154:ASP:OD2	0.48	2.09	7	1
1:A:63:LEU:HD12	1:A:179:ARG:HG3	0.48	1.85	7	1
1:A:118:TYR:HA	1:A:169:VAL:HG23	0.48	1.86	16	9
1:A:48:ALA:HB2	1:A:58:ALA:HB3	0.48	1.85	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:120:ILE:HD11	1:A:141:LEU:HD13	0.48	1.84	4	3
1:A:91:LEU:HD12	1:A:162:ARG:C	0.48	2.29	19	2
1:A:34:LEU:C	1:A:41:ILE:HD12	0.48	2.28	9	1
1:A:115:ALA:HB3	1:A:178:MET:SD	0.47	2.49	19	6
1:A:34:LEU:HD21	1:A:91:LEU:CD2	0.47	2.38	13	1
1:A:96:PHE:CE1	1:A:160:VAL:HG13	0.47	2.43	15	1
1:A:91:LEU:HD21	1:A:182:LEU:CD1	0.47	2.40	19	1
1:A:118:TYR:CZ	1:A:141:LEU:HD22	0.47	2.45	6	4
1:A:76:ILE:HD11	1:A:85:GLU:CD	0.47	2.29	16	1
1:A:119:LYS:HG3	1:A:140:VAL:HG22	0.46	1.87	4	3
1:A:150:ILE:HG23	1:A:152:LEU:HD21	0.46	1.87	7	1
1:A:119:LYS:CD	1:A:140:VAL:HG22	0.46	2.40	15	1
1:A:63:LEU:HD11	1:A:150:ILE:HG13	0.46	1.88	20	1
1:A:122:TYR:CE2	1:A:164:VAL:HG13	0.46	2.46	14	1
1:A:91:LEU:HD11	1:A:164:VAL:CG2	0.46	2.40	15	3
1:A:91:LEU:HD12	1:A:162:ARG:O	0.46	2.11	13	1
1:A:155:LEU:HD23	1:A:159:ILE:CD1	0.46	2.40	3	1
1:A:97:ILE:HD12	1:A:159:ILE:O	0.46	2.11	16	2
1:A:48:ALA:HA	1:A:87:LEU:HD22	0.46	1.87	12	4
1:A:78:VAL:CG2	1:A:83:LEU:HD23	0.45	2.41	15	1
1:A:71:ALA:HB3	1:A:177:CYS:SG	0.45	2.51	14	1
1:A:56:THR:HG23	1:A:69:ASP:HB2	0.45	1.88	12	1
1:A:34:LEU:HD12	1:A:35:GLY:N	0.44	2.27	8	1
1:A:99:LEU:HD13	1:A:100:VAL:H	0.44	1.72	15	4
1:A:120:ILE:CD1	1:A:141:LEU:HD22	0.44	2.32	8	1
1:A:34:LEU:HD21	1:A:182:LEU:HB2	0.44	1.88	1	1
1:A:34:LEU:HD12	1:A:35:GLY:H	0.44	1.72	8	1
1:A:99:LEU:HD22	1:A:154:ASP:CA	0.44	2.43	11	1
1:A:150:ILE:HD13	1:A:151:PHE:N	0.43	2.27	20	4
1:A:101:GLY:O	1:A:102:THR:HG23	0.43	2.13	19	1
1:A:119:LYS:HG3	1:A:169:VAL:HG21	0.43	1.90	9	1
1:A:150:ILE:HD13	1:A:151:PHE:H	0.43	1.74	1	4
1:A:99:LEU:HD11	1:A:152:LEU:HB3	0.43	1.91	10	1
1:A:99:LEU:HD12	1:A:153:LYS:C	0.43	2.34	14	6
1:A:76:ILE:HD13	1:A:76:ILE:H	0.42	1.74	19	4
1:A:34:LEU:HD11	1:A:182:LEU:HB2	0.42	1.90	1	2
1:A:57:ALA:HB3	1:A:60:TYR:CD2	0.42	2.48	4	1
1:A:63:LEU:HD22	1:A:181:GLU:HB2	0.42	1.89	11	1
1:A:76:ILE:H	1:A:76:ILE:HD13	0.42	1.74	2	2
1:A:63:LEU:CD2	1:A:150:ILE:HD11	0.42	2.45	11	1
1:A:63:LEU:HD21	1:A:103:GLN:HB2	0.42	1.90	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:34:LEU:CD2	1:A:91:LEU:HD23	0.42	2.44	13	1
1:A:165:ARG:NH1	1:A:167:ILE:HD11	0.42	2.28	7	1
1:A:140:VAL:HG21	1:A:169:VAL:HG11	0.42	1.91	19	1
1:A:52:TRP:C	1:A:52:TRP:CD1	0.42	2.93	14	1
1:A:166:PHE:CE2	1:A:180:VAL:HG11	0.41	2.50	3	1
1:A:50:SER:O	1:A:50:SER:OG	0.41	2.37	17	1
1:A:100:VAL:HB	1:A:155:LEU:HD21	0.41	1.92	14	1
1:A:141:LEU:HD11	1:A:153:LYS:HE3	0.41	1.91	15	1
1:A:63:LEU:HD13	1:A:64:ASP:H	0.41	1.75	17	2
1:A:152:LEU:N	1:A:152:LEU:HD22	0.41	2.31	3	2
1:A:141:LEU:HD11	1:A:153:LYS:HG2	0.41	1.91	4	1
1:A:63:LEU:HD13	1:A:64:ASP:HB2	0.41	1.92	5	1
1:A:156:GLU:HA	1:A:157:PRO:C	0.41	2.34	13	1
1:A:152:LEU:HD22	1:A:152:LEU:N	0.40	2.31	18	1
1:A:164:VAL:HG21	1:A:182:LEU:CD1	0.40	2.46	17	1
1:A:114:PHE:O	1:A:115:ALA:HB2	0.40	2.16	18	1
1:A:155:LEU:N	1:A:155:LEU:HD22	0.40	2.32	1	1
1:A:34:LEU:HA	1:A:186:VAL:HG22	0.40	1.94	12	1
1:A:160:VAL:O	1:A:160:VAL:HG13	0.40	2.16	13	1
1:A:34:LEU:HD21	1:A:182:LEU:CB	0.40	2.46	14	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	145/173 (84%)	123±3 (85±2%)	20±2 (14±2%)	2±1 (2±1%)	17	62
All	All	2900/3460 (84%)	2460 (85%)	396 (14%)	44 (2%)	17	62

All 11 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	50	SER	19
1	A	143	GLY	8

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Mol	Chain	Res	Type	Models (Total)
1	A	70	GLY	7
1	A	94	LEU	2
1	A	68	GLY	2
1	A	92	HIS	1
1	A	113	GLU	1
1	A	115	ALA	1
1	A	63	LEU	1
1	A	138	LYS	1
1	A	134	ASN	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	128/146 (88%)	112±3 (87±2%)	17±3 (13±2%)	9	50
All	All	2560/2920 (88%)	2230 (87%)	330 (13%)	9	50

All 68 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	47	THR	20
1	A	41	ILE	20
1	A	49	SER	20
1	A	59	LYS	19
1	A	50	SER	18
1	A	76	ILE	17
1	A	141	LEU	13
1	A	178	MET	12
1	A	87	LEU	9
1	A	172	HIS	9
1	A	170	THR	8
1	A	99	LEU	8
1	A	34	LEU	7
1	A	179	ARG	7
1	A	37	SER	7
1	A	73	CYS	6

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Mol	Chain	Res	Type	Models (Total)
1	A	153	LYS	6
1	A	185	CYS	6
1	A	150	ILE	5
1	A	85	GLU	5
1	A	95	HIS	5
1	A	84	LYS	5
1	A	138	LYS	5
1	A	113	GLU	4
1	A	53	SER	4
1	A	124	ARG	4
1	A	30	CYS	4
1	A	121	ASN	4
1	A	45	ASP	4
1	A	63	LEU	4
1	A	66	GLU	4
1	A	105	ARG	3
1	A	131	SER	3
1	A	43	ASP	3
1	A	40	GLN	3
1	A	135	ARG	3
1	A	31	ARG	2
1	A	102	THR	2
1	A	56	THR	2
1	A	156	GLU	2
1	A	65	SER	2
1	A	151	PHE	2
1	A	133	ARG	2
1	A	62	ARG	2
1	A	128	ARG	2
1	A	181	GLU	2
1	A	75	GLU	2
1	A	114	PHE	2
1	A	123	SER	2
1	A	117	MET	2
1	A	78	VAL	1
1	A	83	LEU	1
1	A	142	ASP	1
1	A	175	ASN	1
1	A	29	ILE	1
1	A	165	ARG	1
1	A	96	PHE	1
1	A	64	ASP	1

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Mol	Chain	Res	Type	Models (Total)
1	A	136	HIS	1
1	A	173	SER	1
1	A	91	LEU	1
1	A	88	GLN	1
1	A	90	ASP	1
1	A	36	MET	1
1	A	94	LEU	1
1	A	103	GLN	1
1	A	171	ASP	1
1	A	177	CYS	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 85% for the well-defined parts and 85% for the entire structure.

### 7.1 Chemical shift list 1

File name: BMRB entry 15315

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	1868
Number of shifts mapped to atoms	1868
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

#### 7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	161	$2.81 \pm 0.13$	Should be applied
$^{13}\text{C}_\beta$	145	$2.55 \pm 0.12$	Should be applied
$^{13}\text{C}'$	154	$3.17 \pm 0.10$	Should be applied
$^{15}\text{N}$	149	$1.41 \pm 0.44$	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 85%, i.e. 1547 atoms were assigned a chemical shift out of a possible 1820. 20 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	704/712 (99%)	282/283 (100%)	286/292 (98%)	136/137 (99%)
Sidechain	777/938 (83%)	483/553 (87%)	282/341 (83%)	12/44 (27%)

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	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Aromatic	66/170 (39%)	52/90 (58%)	10/72 (14%)	4/8 (50%)
Overall	1547/1820 (85%)	817/926 (88%)	578/705 (82%)	152/189 (80%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 85%, i.e. 1673 atoms were assigned a chemical shift out of a possible 1974. 20 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Backbone	774/783 (99%)	310/311 (100%)	315/322 (98%)	149/150 (99%)
Sidechain	830/999 (83%)	516/590 (87%)	301/363 (83%)	13/46 (28%)
Aromatic	69/192 (36%)	55/102 (54%)	10/80 (12%)	4/10 (40%)
Overall	1673/1974 (85%)	881/1003 (88%)	626/765 (82%)	166/206 (81%)

#### 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
1	A	59	LYS	HG2	-0.33	2.67 – 0.07	-6.5
1	A	126	GLY	HA2	1.90	5.87 – 2.07	-5.4

#### 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:

