



# Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 11:57 pm GMT

PDB ID : 2LD4  
Title : Solution structure of the N-terminal domain of human anamorsin  
Authors : Banci, L.; Bertini, I.; Ciofi-Baffoni, S.; Boscaro, F.; Chatzi, A.; Mikolajczyk, M.; Tokatlidis, K.; Winkelmann, J.  
Deposited on : 2011-05-13

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.

---

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

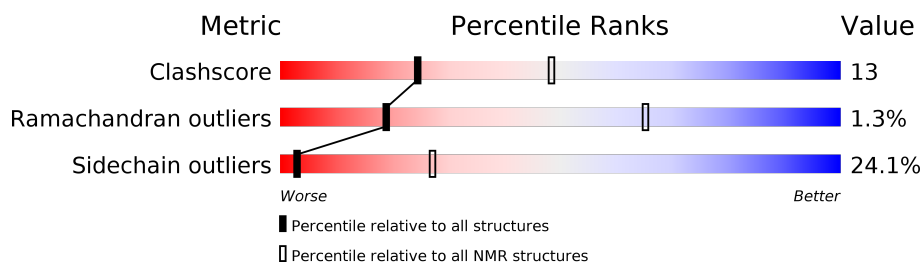
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 88%.

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	176	 59% 30% . . 5% .

## 2 Ensemble composition and analysis

This entry contains 30 models. Model 2 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations*.

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:3-A:165 (163)	0.12	2

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 5 clusters and 8 single-model clusters were found.

Cluster number	Models
1	2, 4, 6, 8, 10, 12, 13, 19
2	9, 18, 20, 22, 23, 27
3	1, 5, 11, 14
4	21, 30
5	7, 17
Single-model clusters	3; 15; 16; 24; 25; 26; 28; 29

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2634 atoms, of which 1333 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Anamorsin.

Mol	Chain	Residues	Atoms						Trace
1	A	172	Total	C	H	N	O	S	0
			2634	819	1333	224	255	3	

There are 4 discrepancies between the modelled and reference sequences:

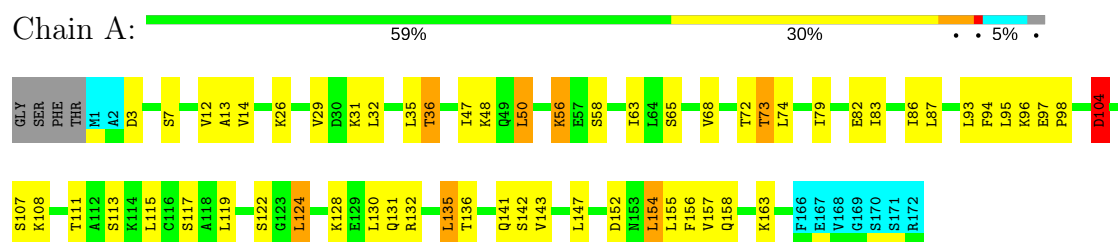
Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	EXPRESSION TAG	UNP Q6FI81
A	-2	SER	-	EXPRESSION TAG	UNP Q6FI81
A	-1	PHE	-	EXPRESSION TAG	UNP Q6FI81
A	0	THR	-	EXPRESSION TAG	UNP Q6FI81

## 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: Anamorsin

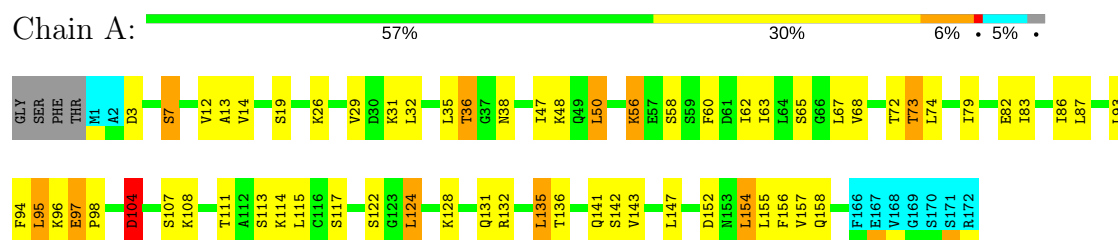


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1

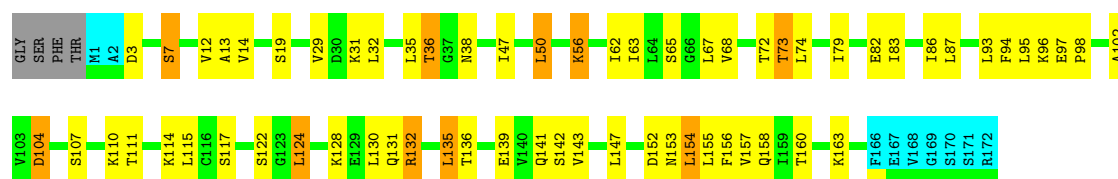
- Molecule 1: Anamorsin



#### 4.2.2 Score per residue for model 2 (medoid)

- Molecule 1: Anamorsin

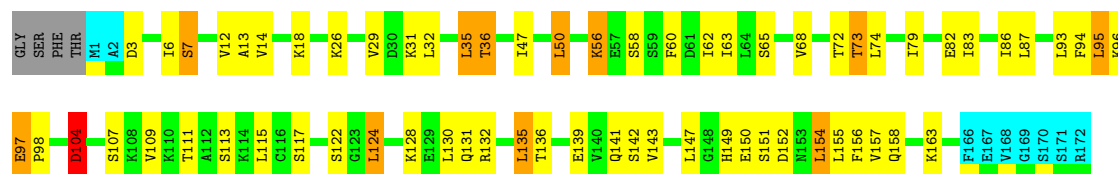




### 4.2.3 Score per residue for model 3

- Molecule 1: Anamorsin

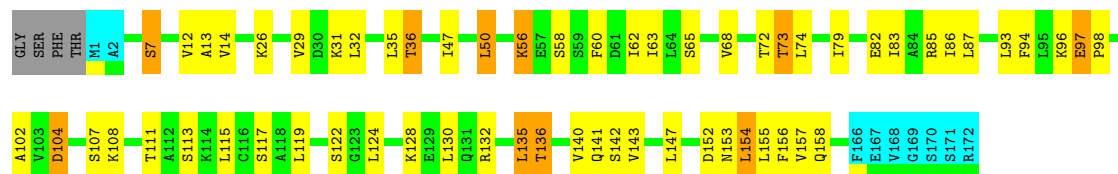
Chain A: 55% 31% 6% 5%



### 4.2.4 Score per residue for model 4

- Molecule 1: Anamorsin

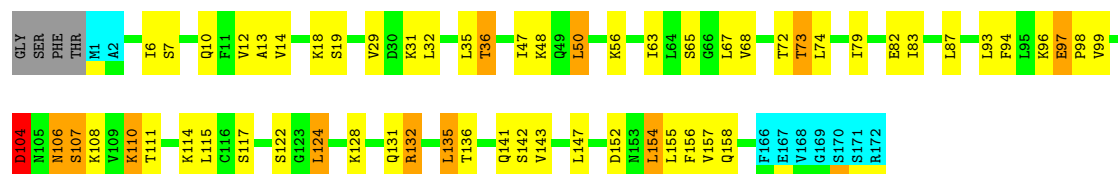
Chain A: 58% 29% 6% 5%



### 4.2.5 Score per residue for model 5

- Molecule 1: Anamorsin

Chain A: 59% 27% 6% 5%

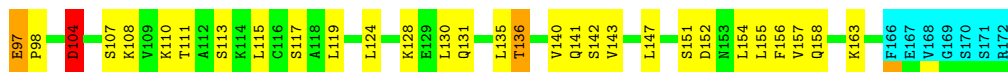


### 4.2.6 Score per residue for model 6

- Molecule 1: Anamorsin



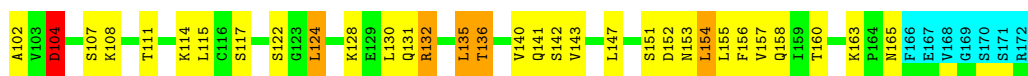
- Molecule 1: Anamorsin



- Molecule 1: Anamorsin

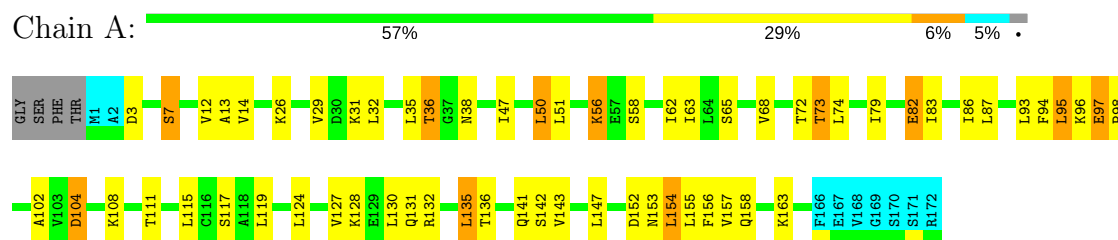


- Molecule 1: Anamorsin



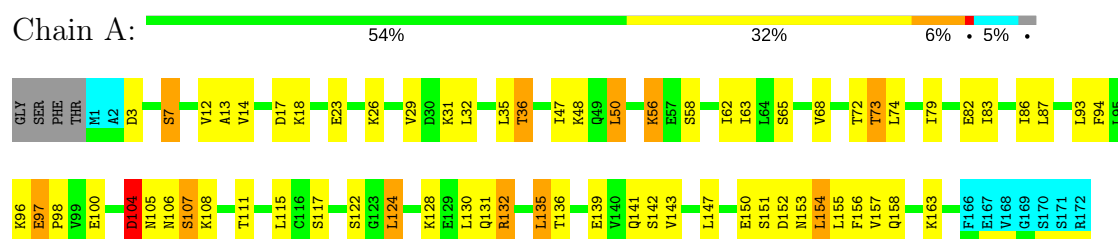
## 4.2.10 Score per residue for model 10

- Molecule 1: Anamorsin



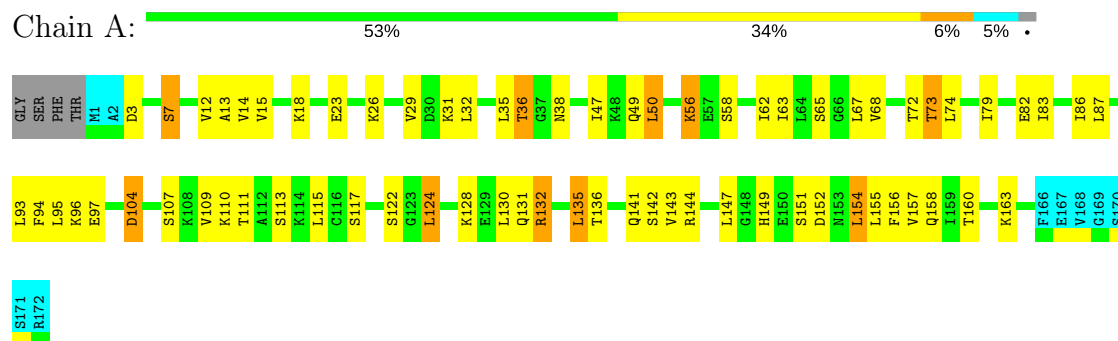
## 4.2.11 Score per residue for model 11

- Molecule 1: Anamorsin



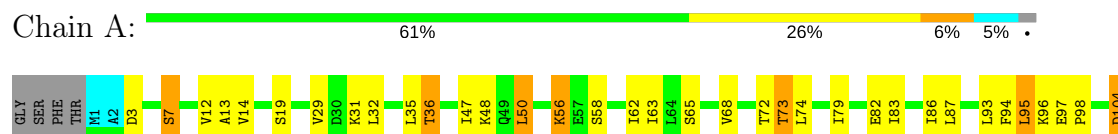
## 4.2.12 Score per residue for model 12

- Molecule 1: Anamorsin



## 4.2.13 Score per residue for model 13

- Molecule 1: Anamorsin







#### 4.2.14 Score per residue for model 14

- Molecule 1: Anamorsin

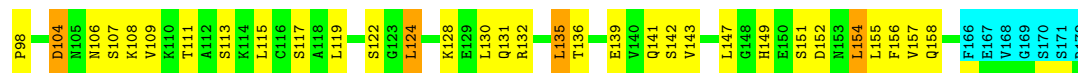
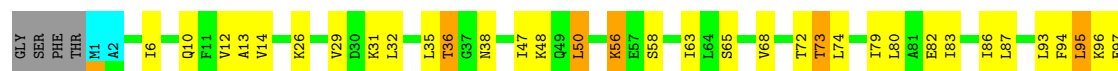
Chain A: 57% 30% 5% 5%



#### 4.2.15 Score per residue for model 15

- Molecule 1: Anamorsin

Chain A: 55% 32% 5% 5%



#### 4.2.16 Score per residue for model 16

- Molecule 1: Anamorsin

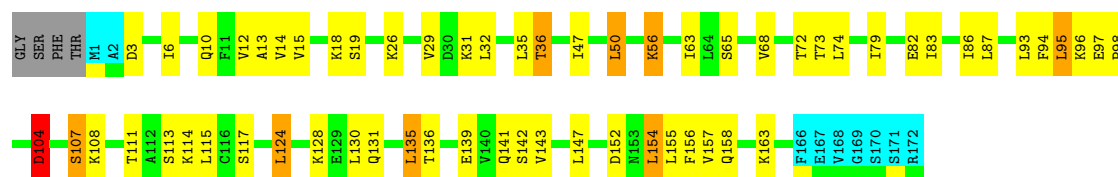
Chain A: 53% 32% 6% 5%



#### 4.2.17 Score per residue for model 17

- Molecule 1: Anamorsin

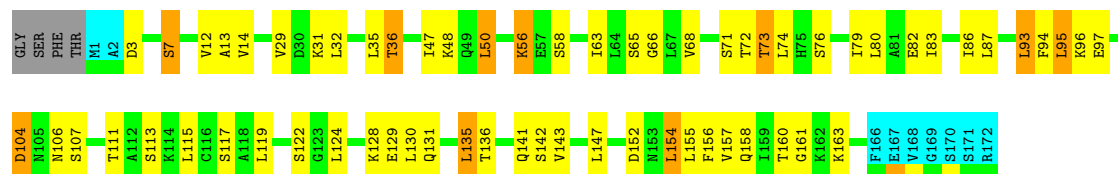
Chain A: 58% 30% 5% 5%



#### 4.2.18 Score per residue for model 18

- Molecule 1: Anamorsin

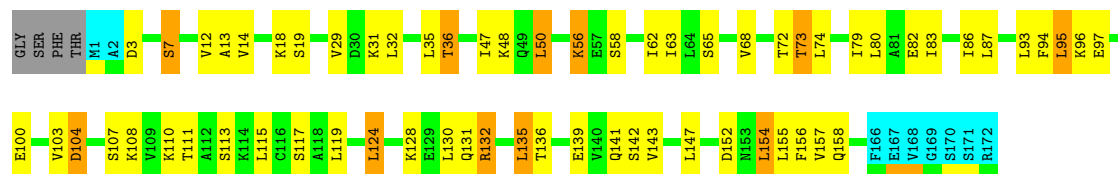
Chain A: 56% 31% 6% 5% •



#### 4.2.19 Score per residue for model 19

- Molecule 1: Anamorsin

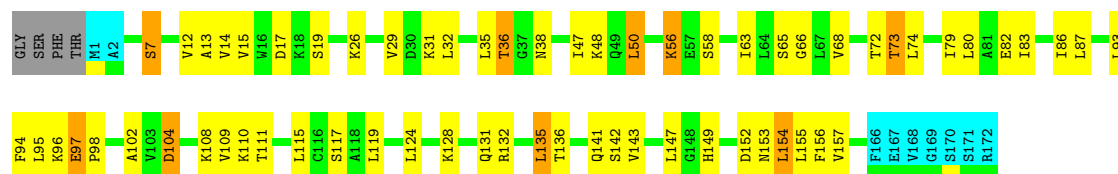
Chain A: 56% 30% 6% 5% •



#### 4.2.20 Score per residue for model 20

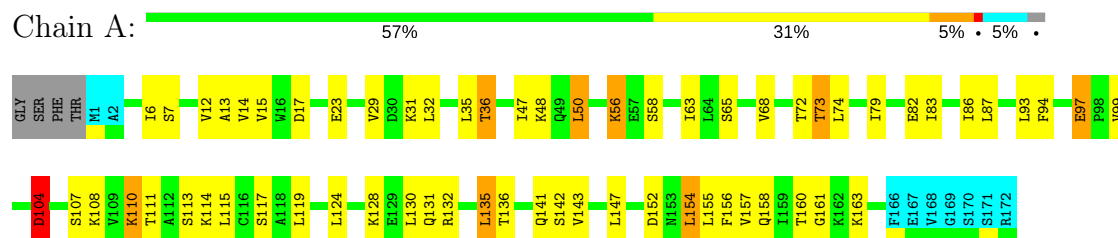
- Molecule 1: Anamorsin

Chain A: 56% 31% 5% 5% •



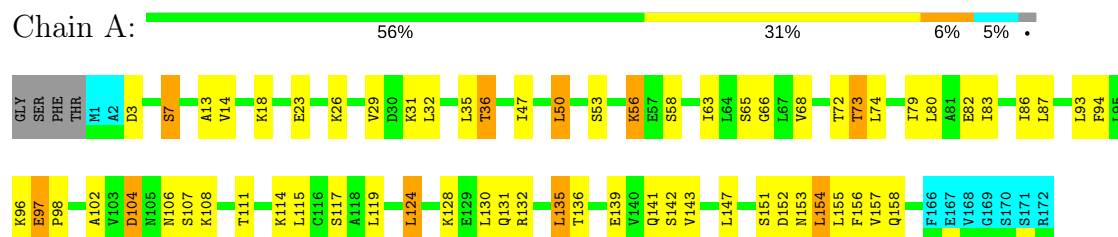
#### 4.2.21 Score per residue for model 21

- Molecule 1: Anamorsin



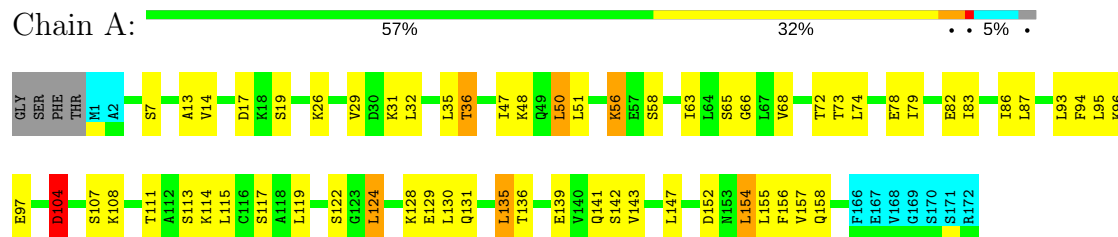
#### 4.2.22 Score per residue for model 22

- Molecule 1: Anamorsin



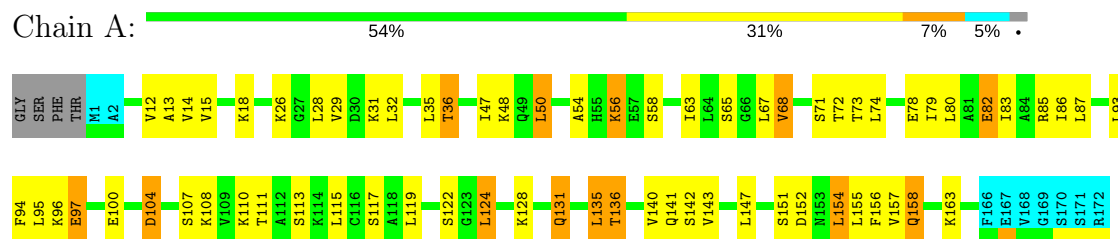
#### 4.2.23 Score per residue for model 23

- Molecule 1: Anamorsin



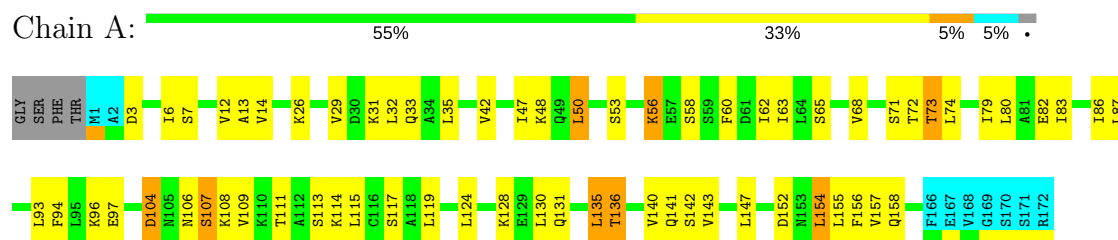
#### 4.2.24 Score per residue for model 24

- Molecule 1: Anamorsin



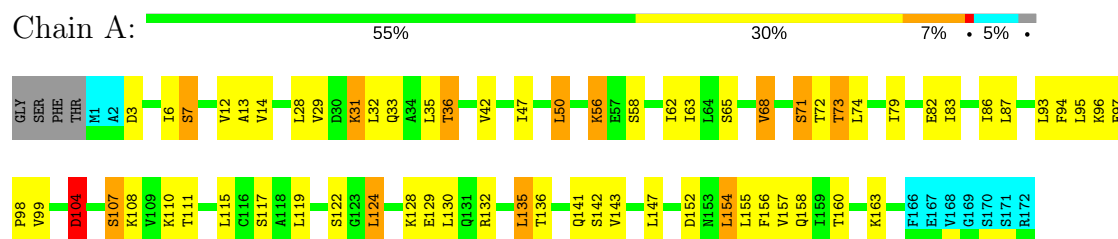
## 4.2.25 Score per residue for model 25

- Molecule 1: Anamorsin



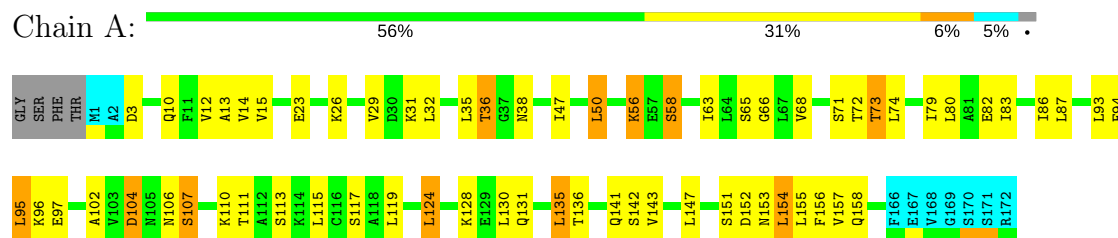
## 4.2.26 Score per residue for model 26

- Molecule 1: Anamorsin



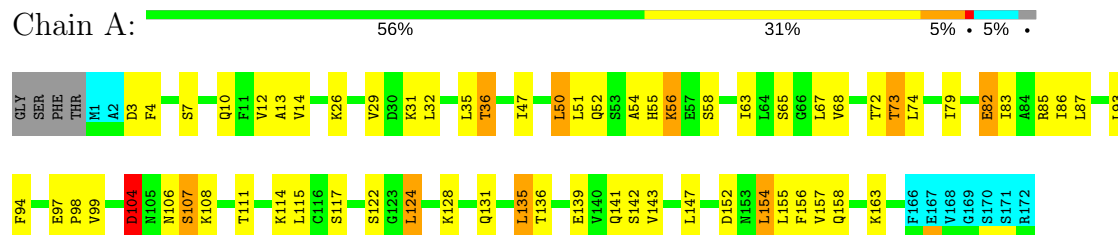
## 4.2.27 Score per residue for model 27

- Molecule 1: Anamorsin



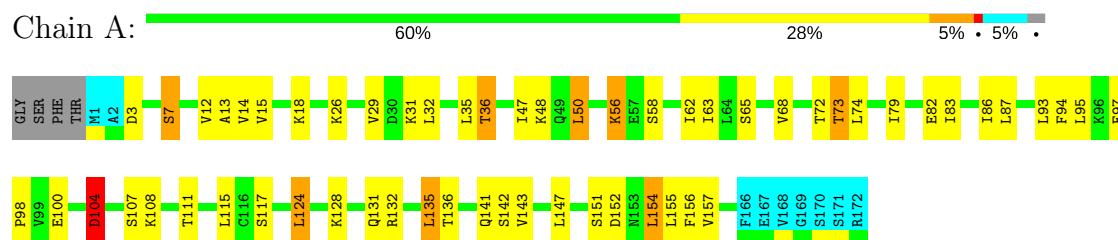
## 4.2.28 Score per residue for model 28

- Molecule 1: Anamorsin



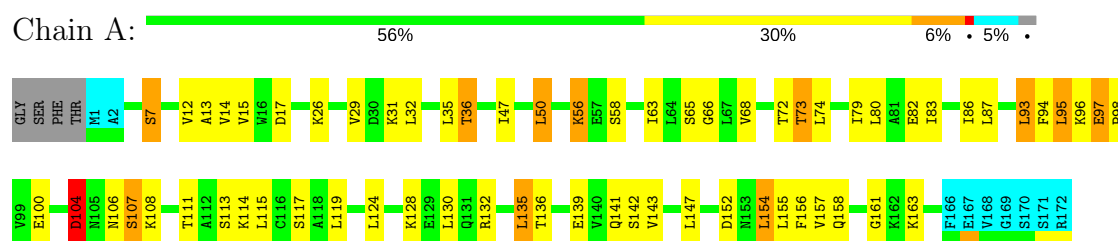
### 4.2.29 Score per residue for model 29

#### • Molecule 1: Anamorsin



### 4.2.30 Score per residue for model 30

#### • Molecule 1: Anamorsin



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *molecular dynamics*.

Of the 300 calculated structures, 30 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	structure solution	1.3
AMBER	refinement	10.0

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)	2ld4_cs.str
Number of chemical shift lists	1
Total number of shifts	2033
Number of shifts mapped to atoms	2033
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	88%

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	1234	1270	1270	34±3
All	All	37020	38100	38100	1010

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 13.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:74:LEU:HD12	1:A:147:LEU:HD22	0.99	1.33	24	30
1:A:28:LEU:HD11	1:A:68:VAL:HG13	0.92	1.39	14	2
1:A:47:ILE:HD13	1:A:73:THR:HG21	0.85	1.45	24	30
1:A:50:LEU:HD13	1:A:79:ILE:HG23	0.82	1.49	6	4
1:A:63:ILE:HG21	1:A:83:ILE:HG23	0.81	1.51	27	30
1:A:14:VAL:HG11	1:A:29:VAL:HG12	0.75	1.58	30	29
1:A:32:LEU:HD23	1:A:35:LEU:HD21	0.71	1.61	25	30
1:A:6:ILE:HD13	1:A:32:LEU:HD21	0.68	1.66	25	3
1:A:13:ALA:HB3	1:A:63:ILE:CD1	0.67	2.19	23	30
1:A:13:ALA:HB3	1:A:63:ILE:HD13	0.67	1.66	22	30
1:A:143:VAL:HG23	1:A:147:LEU:HD13	0.67	1.67	14	30
1:A:72:THR:HG22	1:A:156:PHE:CZ	0.65	2.25	2	30
1:A:12:VAL:HG12	1:A:36:THR:HG21	0.65	1.68	24	9
1:A:47:ILE:CD1	1:A:73:THR:HG21	0.64	2.21	11	30

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:6:ILE:HG23	1:A:12:VAL:HG21	0.63	1.68	3	1
1:A:7:SER:O	1:A:36:THR:HG23	0.63	1.93	16	24
1:A:50:LEU:HG	1:A:79:ILE:HG23	0.62	1.70	24	26
1:A:74:LEU:CD1	1:A:147:LEU:HD22	0.62	2.24	28	27
1:A:56:LYS:O	1:A:86:ILE:HG22	0.62	1.94	29	29
1:A:63:ILE:HG21	1:A:83:ILE:HD12	0.62	1.72	20	18
1:A:67:LEU:HD13	1:A:158:GLN:OE1	0.59	1.98	24	7
1:A:155:LEU:HD13	1:A:156:PHE:O	0.57	1.98	18	30
1:A:102:ALA:HB3	1:A:153:ASN:CG	0.57	2.19	9	8
1:A:15:VAL:HG12	1:A:47:ILE:HG13	0.57	1.76	12	7
1:A:74:LEU:HD23	1:A:97:GLU:OE1	0.56	2.00	22	3
1:A:68:VAL:HG23	1:A:71:SER:HB2	0.56	1.78	26	1
1:A:14:VAL:HG11	1:A:29:VAL:CG1	0.56	2.30	27	28
1:A:130:LEU:HD13	1:A:158:GLN:HG2	0.56	1.76	19	20
1:A:132:ARG:HG2	1:A:155:LEU:HD11	0.56	1.77	19	21
1:A:97:GLU:OE1	1:A:115:LEU:HD23	0.56	2.01	16	11
1:A:104:ASP:O	1:A:111:THR:HG21	0.55	2.01	2	30
1:A:93:LEU:HB3	1:A:124:LEU:HD21	0.55	1.79	29	25
1:A:50:LEU:CD1	1:A:79:ILE:HG23	0.55	2.28	8	3
1:A:109:VAL:HG21	1:A:149:HIS:CE1	0.55	2.37	3	5
1:A:135:LEU:HG	1:A:154:LEU:HD13	0.55	1.77	28	29
1:A:135:LEU:HD23	1:A:155:LEU:HA	0.55	1.78	29	23
1:A:80:LEU:HD13	1:A:119:LEU:HA	0.54	1.78	15	10
1:A:47:ILE:HA	1:A:50:LEU:HD12	0.54	1.79	5	4
1:A:28:LEU:HD12	1:A:68:VAL:HG13	0.54	1.80	24	2
1:A:80:LEU:HD22	1:A:119:LEU:CD1	0.54	2.33	30	5
1:A:54:ALA:HB2	1:A:82:GLU:HG3	0.53	1.78	28	2
1:A:50:LEU:HD13	1:A:79:ILE:CG2	0.53	2.31	5	2
1:A:135:LEU:HD22	1:A:156:PHE:CD2	0.53	2.38	15	27
1:A:93:LEU:HD22	1:A:94:PHE:N	0.52	2.20	30	29
1:A:136:THR:O	1:A:140:VAL:HG12	0.50	2.05	25	5
1:A:12:VAL:CG1	1:A:36:THR:HG21	0.50	2.35	21	11
1:A:12:VAL:HG22	1:A:62:ILE:HB	0.50	1.84	3	15
1:A:119:LEU:HD23	1:A:127:VAL:HG13	0.50	1.83	10	1
1:A:93:LEU:HD13	1:A:93:LEU:O	0.50	2.06	30	18
1:A:63:ILE:HG21	1:A:83:ILE:CG2	0.50	2.34	12	7
1:A:68:VAL:HG12	1:A:69:PRO:HD2	0.49	1.84	14	1
1:A:6:ILE:CG2	1:A:12:VAL:HG21	0.49	2.38	3	1
1:A:119:LEU:HD23	1:A:127:VAL:CG1	0.48	2.39	10	1
1:A:93:LEU:HD13	1:A:93:LEU:C	0.48	2.29	8	12
1:A:124:LEU:HD23	1:A:161:GLY:HA3	0.47	1.86	21	3

*Continued on next page...*



Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:93:LEU:O	1:A:93:LEU:HD13	0.47	2.08	22	10
1:A:95:LEU:O	1:A:95:LEU:HD12	0.47	2.09	7	8
1:A:25:LEU:HA	1:A:28:LEU:HD12	0.47	1.87	14	1
1:A:50:LEU:HD13	1:A:53:SER:HB3	0.47	1.87	25	2
1:A:99:VAL:HG22	1:A:155:LEU:O	0.47	2.10	28	5
1:A:17:ASP:HB3	1:A:47:ILE:HD12	0.47	1.87	23	6
1:A:95:LEU:HD12	1:A:95:LEU:O	0.47	2.10	17	8
1:A:93:LEU:HD11	1:A:95:LEU:HD23	0.46	1.86	23	4
1:A:131:GLN:NE2	1:A:158:GLN:HE21	0.46	2.09	24	1
1:A:74:LEU:HD21	1:A:98:PRO:HG2	0.46	1.87	6	21
1:A:115:LEU:C	1:A:115:LEU:HD13	0.46	2.31	9	17
1:A:25:LEU:HD13	1:A:26:LYS:N	0.46	2.25	16	1
1:A:108:LYS:HG3	1:A:109:VAL:HG13	0.46	1.86	25	1
1:A:14:VAL:HG21	1:A:29:VAL:CB	0.46	2.41	16	1
1:A:12:VAL:HG13	1:A:36:THR:HG21	0.46	1.87	20	3
1:A:93:LEU:HD12	1:A:119:LEU:HD11	0.45	1.87	21	6
1:A:6:ILE:HD13	1:A:32:LEU:CD2	0.45	2.41	3	2
1:A:8:ALA:HB1	1:A:39:GLU:HB2	0.45	1.88	9	1
1:A:50:LEU:O	1:A:50:LEU:HD13	0.45	2.11	12	2
1:A:54:ALA:HB2	1:A:82:GLU:CG	0.45	2.42	24	1
1:A:74:LEU:HD22	1:A:110:LYS:H	0.45	1.71	5	3
1:A:50:LEU:HD11	1:A:83:ILE:CD1	0.44	2.42	28	1
1:A:4:PHE:CE1	1:A:67:LEU:HD12	0.44	2.48	28	1
1:A:93:LEU:C	1:A:93:LEU:HD13	0.44	2.33	6	15
1:A:15:VAL:HG12	1:A:47:ILE:CG1	0.44	2.43	27	3
1:A:82:GLU:OE2	1:A:86:ILE:HG23	0.43	2.13	10	1
1:A:115:LEU:HD13	1:A:115:LEU:C	0.43	2.34	25	13
1:A:13:ALA:HB2	1:A:60:PHE:CE1	0.43	2.49	4	4
1:A:33:GLN:HA	1:A:42:VAL:HG21	0.43	1.91	25	3
1:A:50:LEU:HD13	1:A:50:LEU:O	0.42	2.14	7	1
1:A:100:GLU:CD	1:A:103:VAL:HG21	0.42	2.34	19	1
1:A:130:LEU:HD11	1:A:160:THR:N	0.42	2.30	26	5
1:A:80:LEU:HD22	1:A:119:LEU:HD13	0.42	1.92	7	1
1:A:109:VAL:HG21	1:A:149:HIS:NE2	0.41	2.30	3	1
1:A:31:LYS:O	1:A:35:LEU:HD23	0.41	2.16	26	1
1:A:12:VAL:O	1:A:42:VAL:HG13	0.41	2.16	16	1
1:A:130:LEU:HD21	1:A:160:THR:CG2	0.40	2.46	18	1
1:A:130:LEU:HD21	1:A:160:THR:HG21	0.40	1.93	18	1
1:A:13:ALA:HB2	1:A:60:PHE:CD1	0.40	2.52	25	2
1:A:83:ILE:HG21	1:A:93:LEU:HG	0.40	1.94	18	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	163/176 (93%)	147±1 (90±1%)	14±1 (8±1%)	2±1 (1±1%)	19	65
All	All	4890/5280 (93%)	4418 (90%)	410 (8%)	62 (1%)	19	65

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	107	SER	19
1	A	104	ASP	16
1	A	58	SER	14
1	A	66	GLY	6
1	A	106	ASN	6
1	A	55	HIS	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	140/150 (93%)	106±3 (76±2%)	34±3 (24±2%)	3	27
All	All	4200/4500 (93%)	3187 (76%)	1013 (24%)	3	27

All 63 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	50	LEU	30
1	A	128	LYS	30
1	A	104	ASP	30
1	A	135	LEU	30

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Models (Total)
1	A	136	THR	30
1	A	154	LEU	30
1	A	87	LEU	30
1	A	152	ASP	30
1	A	31	LYS	30
1	A	65	SER	30
1	A	68	VAL	30
1	A	157	VAL	30
1	A	82	GLU	30
1	A	97	GLU	30
1	A	117	SER	30
1	A	141	GLN	30
1	A	142	SER	30
1	A	56	LYS	30
1	A	36	THR	27
1	A	131	GLN	27
1	A	96	LYS	27
1	A	73	THR	26
1	A	124	LEU	24
1	A	108	LYS	24
1	A	26	LYS	21
1	A	7	SER	19
1	A	113	SER	19
1	A	122	SER	18
1	A	3	ASP	17
1	A	107	SER	17
1	A	163	LYS	17
1	A	48	LYS	16
1	A	95	LEU	15
1	A	151	SER	13
1	A	139	GLU	13
1	A	114	LYS	12
1	A	58	SER	12
1	A	110	LYS	11
1	A	19	SER	11
1	A	18	LYS	10
1	A	38	ASN	10
1	A	132	ARG	9
1	A	106	ASN	7
1	A	71	SER	6
1	A	10	GLN	6
1	A	23	GLU	6

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Models (Total)
1	A	100	GLU	4
1	A	85	ARG	4
1	A	129	GLU	3
1	A	51	LEU	3
1	A	150	GLU	3
1	A	78	GLU	2
1	A	76	SER	2
1	A	153	ASN	2
1	A	93	LEU	2
1	A	6	ILE	1
1	A	35	LEU	1
1	A	162	LYS	1
1	A	52	GLN	1
1	A	49	GLN	1
1	A	144	ARG	1
1	A	105	ASN	1
1	A	158	GLN	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 88% for the well-defined parts and 87% for the entire structure.

### 7.1 Chemical shift list 1

File name: 2ld4\_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	2033
Number of shifts mapped to atoms	2033
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	6

#### 7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	172	$0.36 \pm 0.13$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	159	$0.47 \pm 0.08$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	163	$0.21 \pm 0.09$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	164	$0.15 \pm 0.36$	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 88%, i.e. 1708 atoms were assigned a chemical shift out of a possible 1944. 37 out of 38 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	790/801 (99%)	318/319 (100%)	317/326 (97%)	155/156 (99%)
Sidechain	880/1054 (83%)	517/612 (84%)	350/402 (87%)	13/40 (32%)

*Continued on next page...*

Continued from previous page...

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	38/89 (43%)	30/47 (64%)	0/33 (0%)	8/9 (89%)
Overall	1708/1944 (88%)	865/978 (88%)	667/761 (88%)	176/205 (86%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 87%, i.e. 1786 atoms were assigned a chemical shift out of a possible 2048. 38 out of 39 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	834/846 (99%)	335/337 (99%)	335/344 (97%)	164/165 (99%)
Sidechain	911/1104 (83%)	534/642 (83%)	364/419 (87%)	13/43 (30%)
Aromatic	41/98 (42%)	33/52 (63%)	0/37 (0%)	8/9 (89%)
Overall	1786/2048 (87%)	902/1031 (87%)	699/800 (87%)	185/217 (85%)

#### 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	1	MET	C	0.00	186.66 – 165.76	-84.3
1	A	1	MET	N	0.00	137.94 – 102.24	-33.6
1	A	1	MET	CG	0.00	38.33 – 25.73	-25.4
1	A	1	MET	CA	0.00	67.38 – 44.88	-24.9
1	A	1	MET	CB	0.00	44.20 – 21.80	-14.7
1	A	1	MET	H	0.00	11.26 – 5.26	-13.8

#### 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:

