



Full wwPDB NMR Structure Validation Report ⓘ

Mar 6, 2026 – 12:18 AM UTC

PDB ID : 2LD4 / pdb_00002ld4
BMRB ID : 17646
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

A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

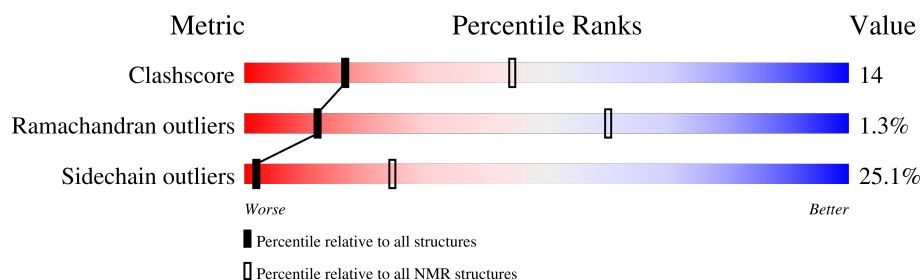
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 89%.

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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	176	

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)	0.22	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:

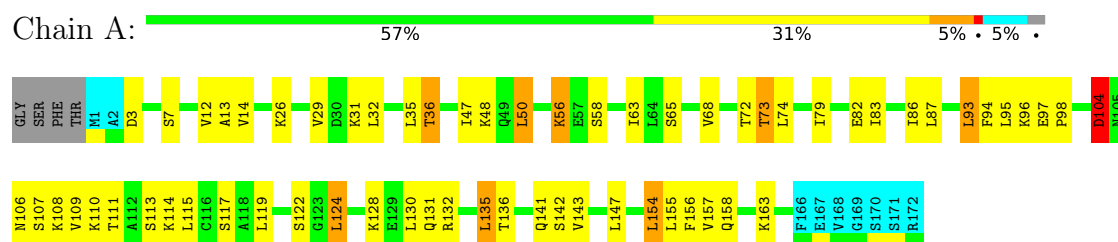
Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q6FI81
A	-2	SER	-	expression tag	UNP Q6FI81
A	-1	PHE	-	expression tag	UNP Q6FI81
A	0	THR	-	expression tag	UNP Q6FI81

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide 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

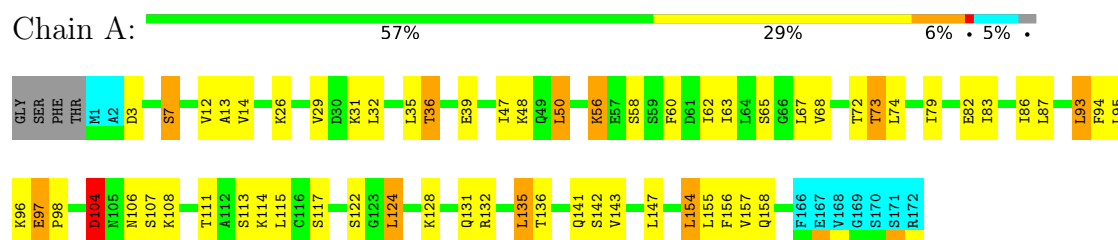


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

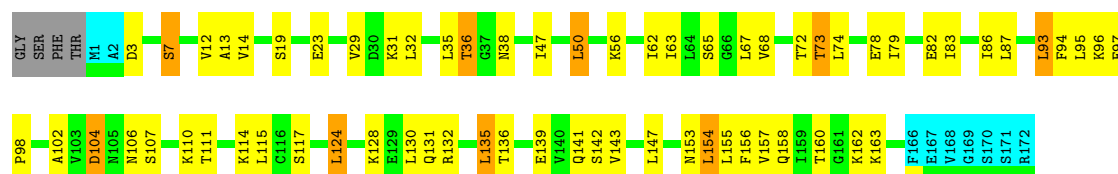
- Molecule 1: Anamorsin



4.2.2 Score per residue for model 2 (medoid)

- Molecule 1: Anamorsin

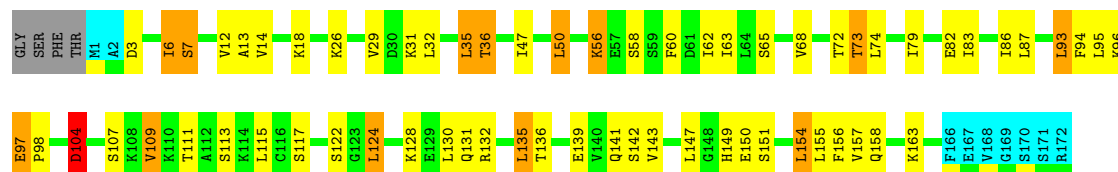




4.2.3 Score per residue for model 3

- Molecule 1: Anamorsin

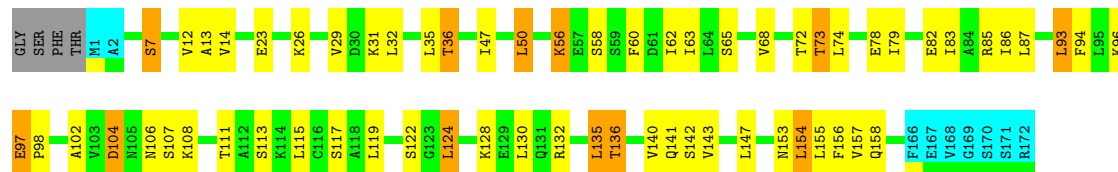
Chain A: 56% 29% 7% 5%



4.2.4 Score per residue for model 4

- Molecule 1: Anamorsin

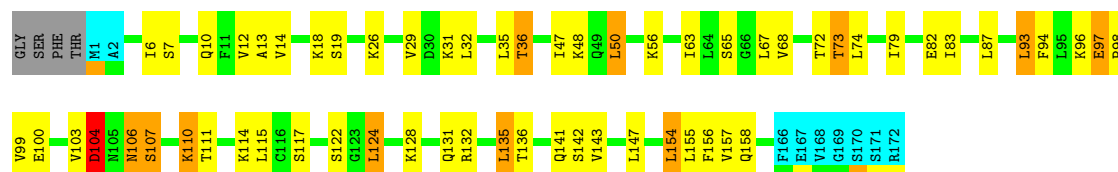
Chain A: 57% 29% 7% 5%



4.2.5 Score per residue for model 5

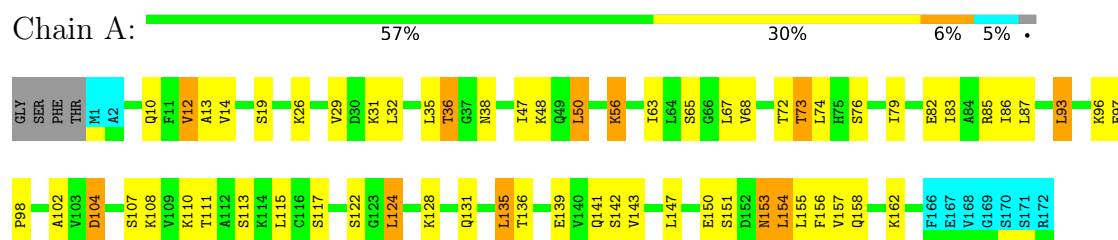
- Molecule 1: Anamorsin

Chain A: 58% 28% 6% 5%



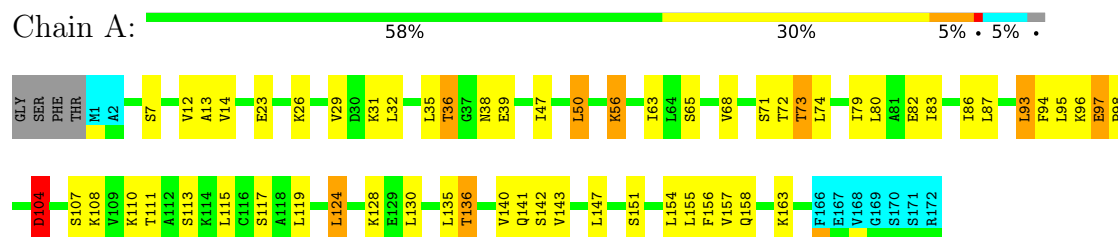
4.2.6 Score per residue for model 6

- Molecule 1: Anamorsin



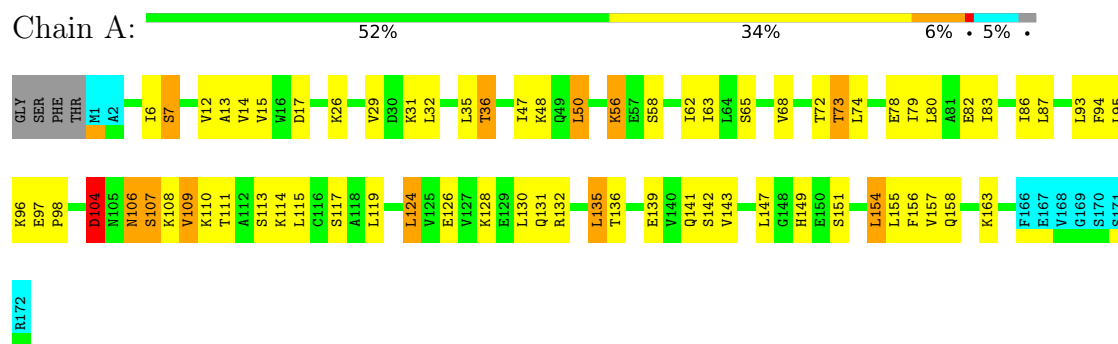
4.2.7 Score per residue for model 7

- Molecule 1: Anamorsin



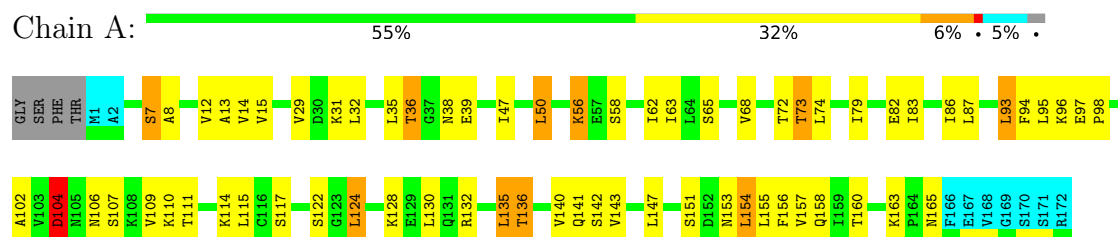
4.2.8 Score per residue for model 8

- Molecule 1: Anamorsin



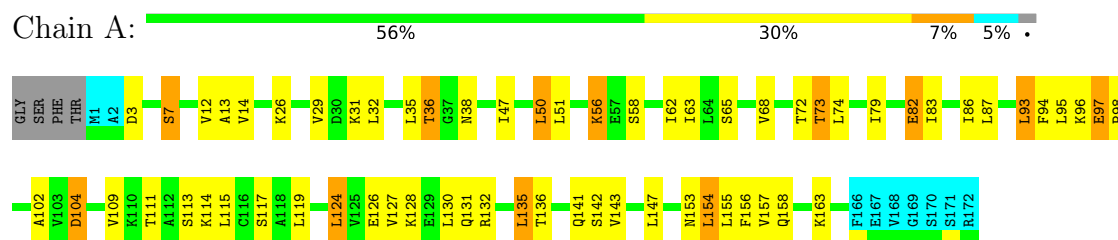
4.2.9 Score per residue for model 9

- Molecule 1: Anamorsin



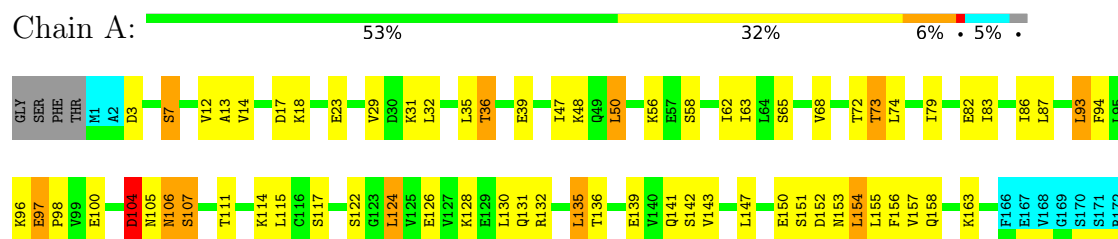
4.2.10 Score per residue for model 10

- Molecule 1: Anamorsin



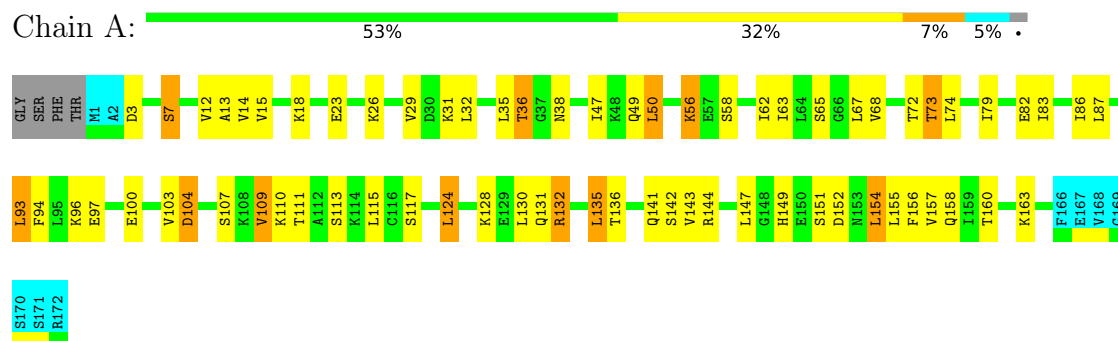
4.2.11 Score per residue for model 11

- Molecule 1: Anamorsin



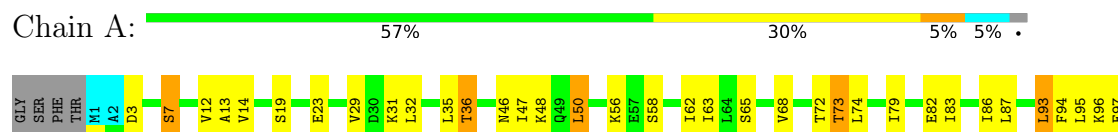
4.2.12 Score per residue for model 12

- Molecule 1: Anamorsin



4.2.13 Score per residue for model 13

- Molecule 1: Anamorsin

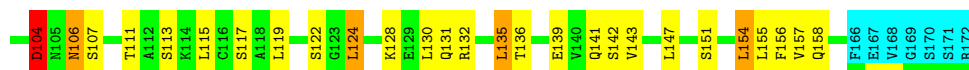
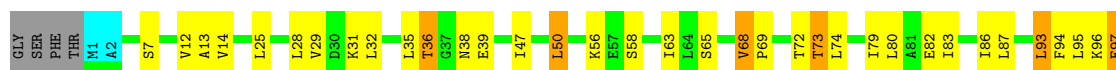




4.2.14 Score per residue for model 14

- Molecule 1: Anamorsin

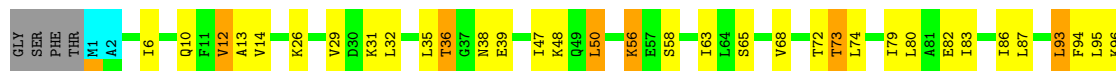
Chain A: 57% 29% 6% • 5% •



4.2.15 Score per residue for model 15

- Molecule 1: Anamorsin

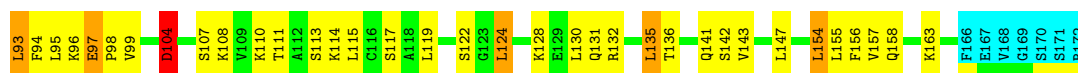
Chain A: 56% 31% 6% 5% •



4.2.16 Score per residue for model 16

- Molecule 1: Anamorsin

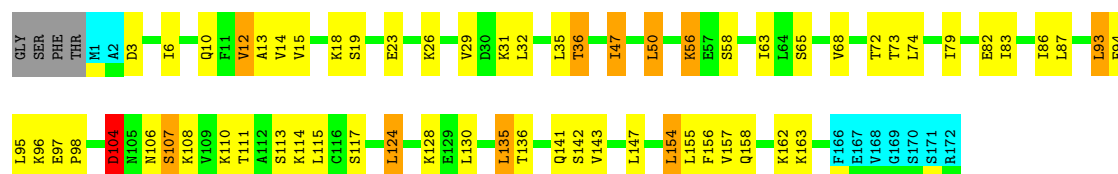
Chain A: 53% 31% 7% • 5% •



4.2.17 Score per residue for model 17

- Molecule 1: Anamorsin

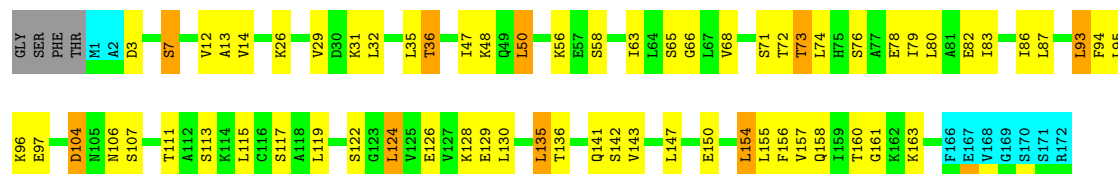
Chain A: 57% 30% 6% • 5% •



4.2.18 Score per residue for model 18

- Molecule 1: Anamorsin

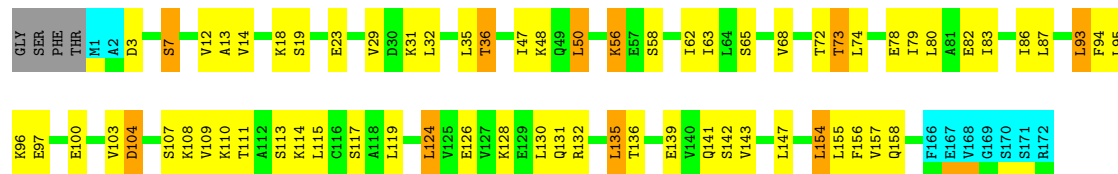
Chain A: 55% 32% 5% 5% .



4.2.19 Score per residue for model 19

- Molecule 1: Anamorsin

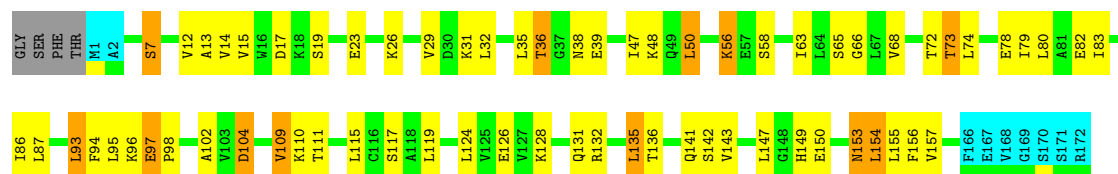
Chain A: 54% 33% 6% 5% .



4.2.20 Score per residue for model 20

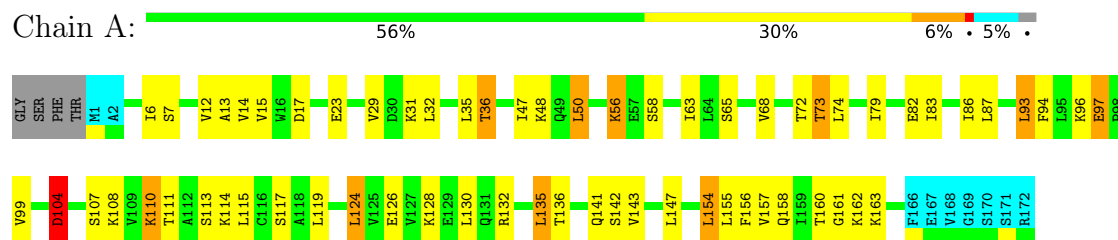
- Molecule 1: Anamorsin

Chain A: 55% 31% 7% 5% .



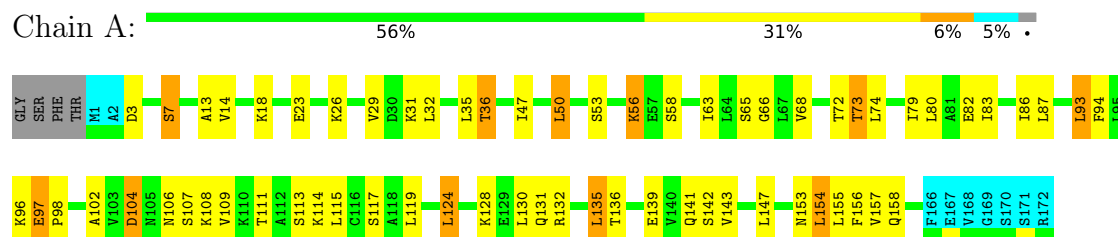
4.2.21 Score per residue for model 21

- Molecule 1: Anamorsin



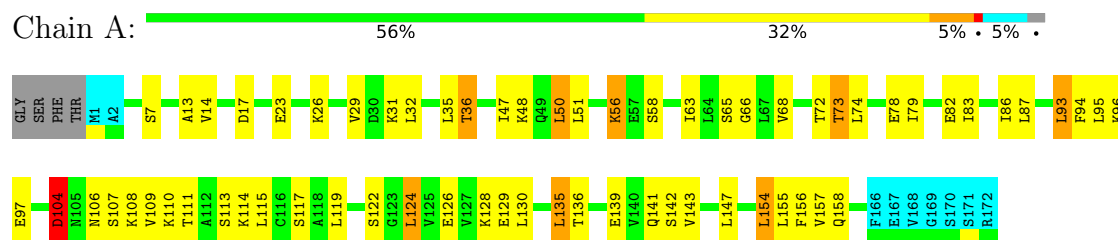
4.2.22 Score per residue for model 22

- Molecule 1: Anamorsin



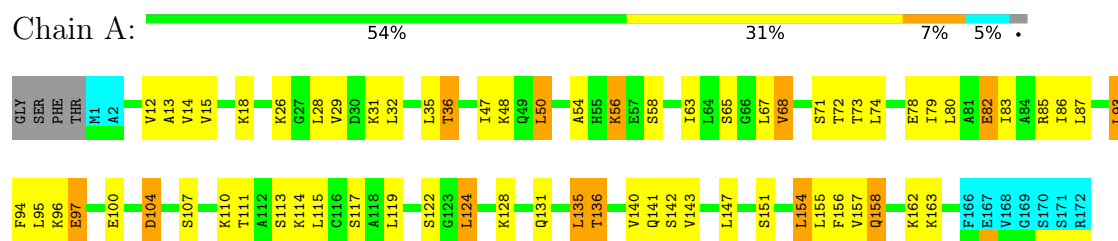
4.2.23 Score per residue for model 23

- Molecule 1: Anamorsin



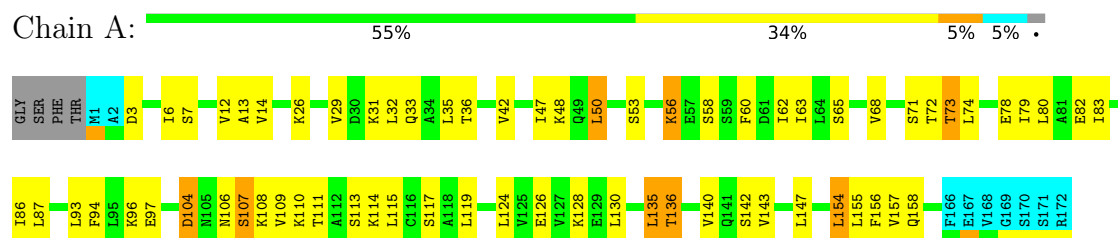
4.2.24 Score per residue for model 24

- Molecule 1: Anamorsin



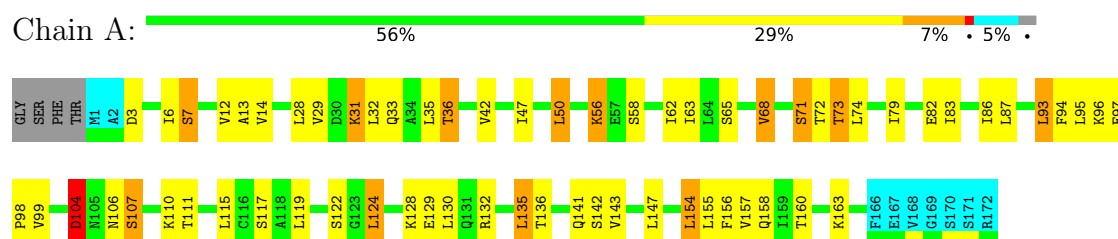
4.2.25 Score per residue for model 25

- Molecule 1: Anamorsin



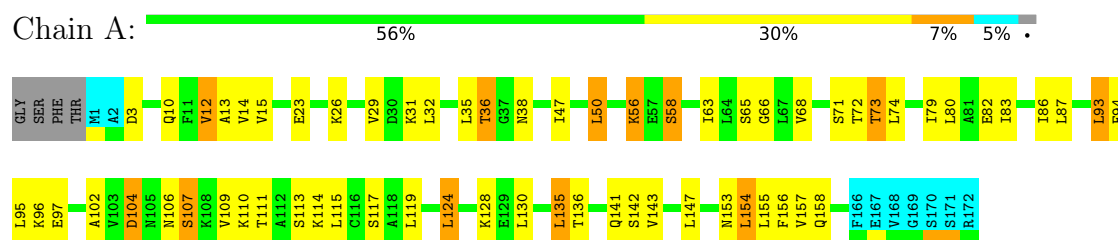
4.2.26 Score per residue for model 26

- Molecule 1: Anamorsin



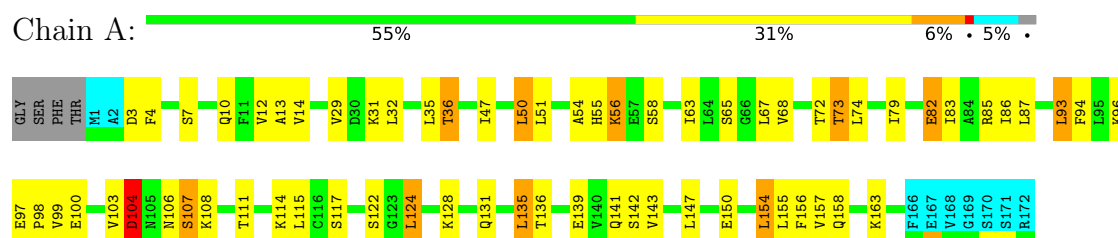
4.2.27 Score per residue for model 27

- Molecule 1: Anamorsin



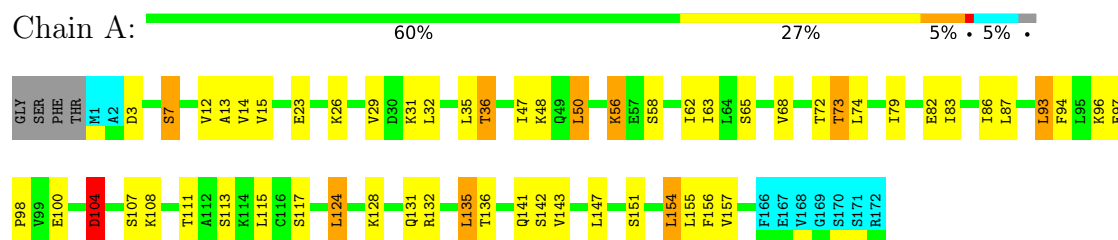
4.2.28 Score per residue for model 28

- Molecule 1: Anamorsin



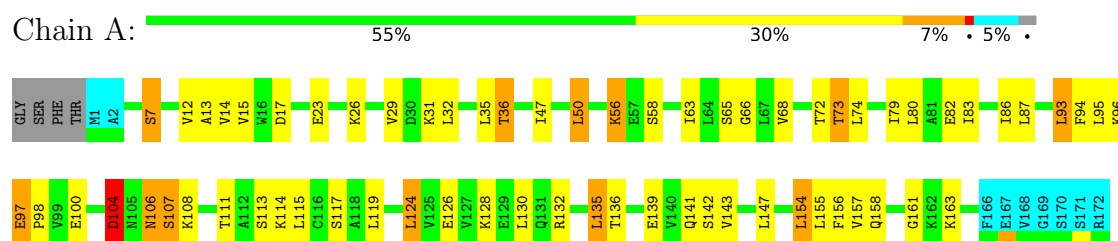
4.2.29 Score per residue for model 29

• 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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	2033
Number of shifts mapped to atoms	2032
Number of unparsed shifts	0
Number of shifts with mapping errors	1
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	89%

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	35±3
All	All	37020	38100	38100	1054

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 14.

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

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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:102:ALA:HB3	1:A:153:ASN:CG	0.62	2.19	9	8
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: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:132:ARG:HG2	1:A:155:LEU:HD11	0.56	1.77	19	21
1:A:130:LEU:HD13	1:A:158:GLN:HG2	0.56	1.76	19	20
1:A:97:GLU:OE1	1:A:115:LEU:HD23	0.56	2.01	16	11
1:A:93:LEU:HB3	1:A:124:LEU:HD21	0.55	1.79	29	25
1:A:104:ASP:O	1:A:111:THR:HG21	0.55	2.01	2	30
1:A:109:VAL:HG21	1:A:149:HIS:CE1	0.55	2.37	3	5
1:A:50:LEU:CD1	1:A:79:ILE:HG23	0.55	2.28	8	3
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:47:ILE:HA	1:A:50:LEU:HD12	0.54	1.79	5	4
1:A:80:LEU:HD13	1:A:119:LEU:HA	0.54	1.78	15	10
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:C	1:A:93:LEU:HD13	0.53	2.29	8	16
1:A:93:LEU:HD22	1:A:94:PHE:N	0.52	2.20	30	29
1:A:115:LEU:C	1:A:115:LEU:HD13	0.51	2.31	9	30
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	28
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

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:124:LEU:HD23	1:A:161:GLY:HA3	0.47	1.86	21	3
1:A:95:LEU:O	1:A:95:LEU:HD12	0.47	2.09	7	16
1:A:100:GLU:CD	1:A:103:VAL:HG21	0.47	2.34	19	5
1:A:25:LEU:HA	1:A:28:LEU:HD12	0.47	1.87	14	1
1:A:99:VAL:HG22	1:A:155:LEU:O	0.47	2.10	28	5
1:A:50:LEU:HD13	1:A:53:SER:HB3	0.47	1.87	25	2
1:A:17:ASP:HB3	1:A:47:ILE:HD12	0.47	1.87	23	6
1:A:93:LEU:HD13	1:A:93:LEU:C	0.46	2.34	20	14
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: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:HD13	1:A:50:LEU:O	0.45	2.11	12	3
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:35:LEU:C	1:A:35:LEU:HD12	0.44	2.38	25	29
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:15:VAL:HG12	1:A:47:ILE:CG1	0.44	2.43	27	3
1:A:93:LEU:HD22	1:A:93:LEU:C	0.43	2.38	30	6
1:A:82:GLU:OE2	1:A:86:ILE:HG23	0.43	2.13	10	1
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:67:LEU:HD13	1:A:158:GLN:CD	0.42	2.39	24	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:25:LEU:HD13	1:A:25:LEU:C	0.41	2.40	16	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

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	163/176 (93%)	147±1 (90±1%)	14±1 (8±1%)	2±1 (1±1%)	12	60
All	All	4890/5280 (93%)	4418 (90%)	410 (8%)	62 (1%)	12	60

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	106	ASN	6
1	A	66	GLY	6
1	A	55	HIS	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	140/150 (93%)	105±3 (75±2%)	35±3 (25±2%)	2	24
All	All	4200/4500 (93%)	3146 (75%)	1054 (25%)	2	24

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	31	LYS	30
1	A	36	THR	30
1	A	50	LEU	30
1	A	65	SER	30

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Mol	Chain	Res	Type	Models (Total)
1	A	68	VAL	30
1	A	82	GLU	30
1	A	87	LEU	30
1	A	96	LYS	30
1	A	97	GLU	30
1	A	104	ASP	30
1	A	117	SER	30
1	A	124	LEU	30
1	A	128	LYS	30
1	A	135	LEU	30
1	A	136	THR	30
1	A	142	SER	30
1	A	154	LEU	30
1	A	157	VAL	30
1	A	141	GLN	29
1	A	73	THR	28
1	A	93	LEU	28
1	A	56	LYS	25
1	A	113	SER	23
1	A	26	LYS	21
1	A	7	SER	19
1	A	114	LYS	18
1	A	131	GLN	18
1	A	106	ASN	17
1	A	107	SER	17
1	A	110	LYS	17
1	A	163	LYS	17
1	A	3	ASP	16
1	A	48	LYS	16
1	A	108	LYS	16
1	A	122	SER	16
1	A	23	GLU	15
1	A	58	SER	13
1	A	139	GLU	12
1	A	109	VAL	11
1	A	151	SER	11
1	A	38	ASN	10
1	A	126	GLU	10
1	A	78	GLU	9
1	A	18	LYS	9
1	A	19	SER	8
1	A	39	GLU	6

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Mol	Chain	Res	Type	Models (Total)
1	A	150	GLU	6
1	A	10	GLN	6
1	A	71	SER	6
1	A	162	LYS	5
1	A	85	ARG	4
1	A	12	VAL	4
1	A	100	GLU	4
1	A	153	ASN	3
1	A	51	LEU	3
1	A	129	GLU	3
1	A	6	ILE	2
1	A	76	SER	2
1	A	152	ASP	2
1	A	35	LEU	1
1	A	105	ASN	1
1	A	49	GLN	1
1	A	132	ARG	1
1	A	144	ARG	1
1	A	46	ASN	1
1	A	25	LEU	1
1	A	47	ILE	1
1	A	158	GLN	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 oligosaccharides 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 89% for the well-defined parts and 89% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	2033
Number of shifts mapped to atoms	2032
Number of unparsed shifts	0
Number of shifts with mapping errors	1
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	6

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- No matching atom found in the structure. All 1 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	1	MET	H	0.0	0.0	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
$^{13}\text{C}_\alpha$	172	0.36 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	159	0.48 ± 0.17	None needed (< 0.5 ppm)
$^{13}\text{C}'$	163	0.21 ± 0.11	None needed (< 0.5 ppm)
^{15}N	164	0.16 ± 0.36	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 89%, i.e. 1948 atoms were assigned a chemical shift out of a possible 2183. 0 out of 38 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	802/813 (99%)	330/331 (100%)	317/326 (97%)	155/156 (99%)
Sidechain	1108/1276 (87%)	737/834 (88%)	358/402 (89%)	13/40 (32%)
Aromatic	38/94 (40%)	30/47 (64%)	0/38 (0%)	8/9 (89%)
Overall	1948/2183 (89%)	1097/1212 (91%)	675/766 (88%)	176/205 (86%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 89%, i.e. 2033 atoms were assigned a chemical shift out of a possible 2297. 0 out of 39 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	847/859 (99%)	348/350 (99%)	335/344 (97%)	164/165 (99%)
Sidechain	1145/1334 (86%)	760/872 (87%)	372/419 (89%)	13/43 (30%)
Aromatic	41/104 (39%)	33/52 (63%)	0/43 (0%)	8/9 (89%)
Overall	2033/2297 (89%)	1141/1274 (90%)	707/806 (88%)	185/217 (85%)

7.1.4 Statistically unusual chemical shifts [i](#)

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.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	1	MET	C	0.00	166.12 – 186.43	-86.8
1	A	1	MET	N	0.00	102.99 – 137.21	-35.1
1	A	1	MET	CA	0.00	45.26 – 67.07	-25.8
1	A	1	MET	CG	0.00	25.46 – 38.60	-24.4
1	A	1	MET	CB	0.00	22.22 – 43.61	-15.4
1	A	1	MET	H	0.00	5.39 – 11.10	-14.4

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

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble

composition. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:

