



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 08:31 PM BST

PDB ID : 2GHF
Title : Solution structure of the complete zinc-finger region of human zinc-fingers and homeoboxes 1 (ZHX1)
Authors : Wienk, H.; Structural Proteomics in Europe (SPINE)
Deposited on : 2006-03-27

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/NMRValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

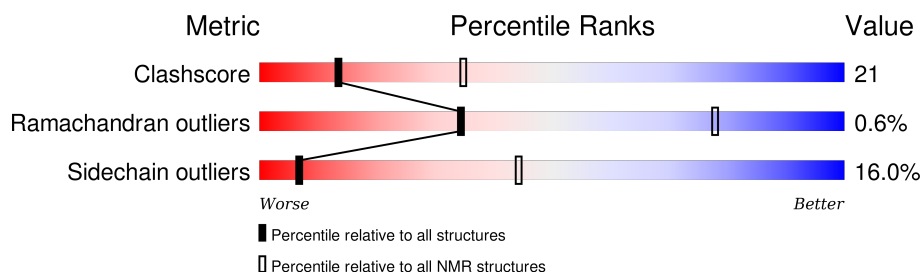
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 76%.

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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	102	 48% 29% • 20%

2 Ensemble composition and analysis

This entry contains 20 models. Model 5 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:66-A:93, A:100-A:153 (82)	0.27	5

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 2 clusters and 1 single-model cluster was found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1638 atoms, of which 785 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Zinc fingers and homeoboxes protein 1.

Mol	Chain	Residues	Atoms						Trace
1	A	102	Total	C	H	N	O	S	0
			1636	534	785	151	159	7	

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MET	-	CLONING ARTIFACT	UNP Q9UKY1
A	-7	ALA	-	CLONING ARTIFACT	UNP Q9UKY1
A	-6	HIS	-	EXPRESSION TAG	UNP Q9UKY1
A	-5	HIS	-	EXPRESSION TAG	UNP Q9UKY1
A	-4	HIS	-	EXPRESSION TAG	UNP Q9UKY1
A	-3	HIS	-	EXPRESSION TAG	UNP Q9UKY1
A	-2	HIS	-	EXPRESSION TAG	UNP Q9UKY1
A	-1	HIS	-	EXPRESSION TAG	UNP Q9UKY1

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
2	A	2	Total	Zn
			2	2

4 Residue-property plots [i](#)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Zinc fingers and homeoboxes protein 1

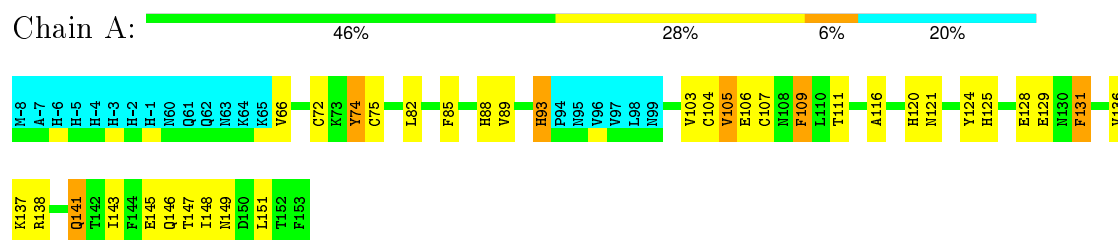


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

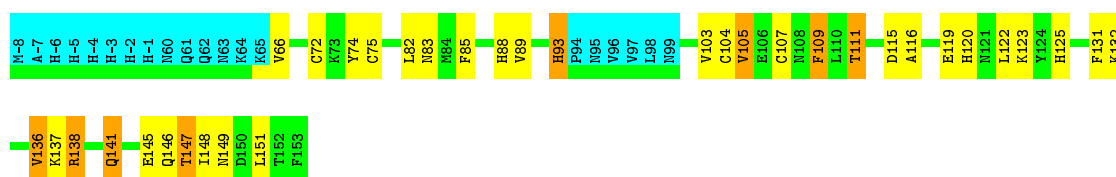
- Molecule 1: Zinc fingers and homeoboxes protein 1



4.2.2 Score per residue for model 2

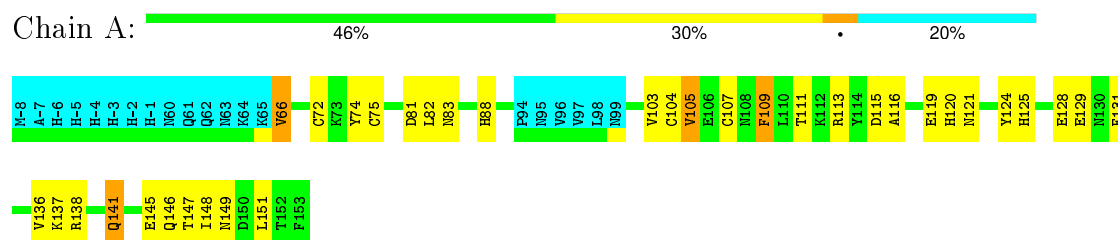
- Molecule 1: Zinc fingers and homeoboxes protein 1





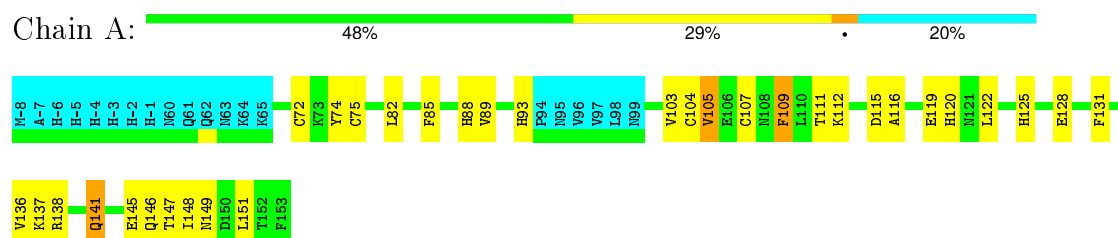
4.2.3 Score per residue for model 3

- Molecule 1: Zinc fingers and homeoboxes protein 1



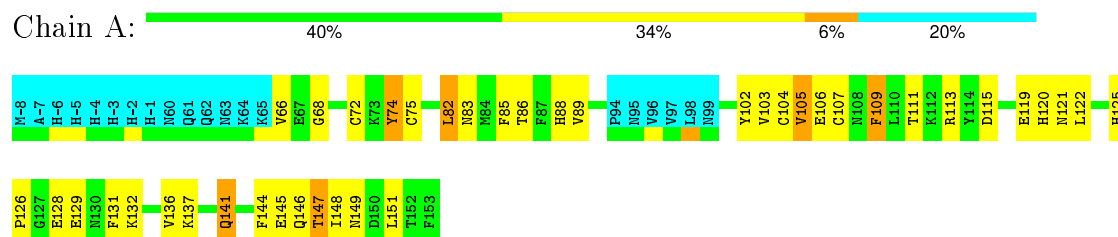
4.2.4 Score per residue for model 4

- Molecule 1: Zinc fingers and homeoboxes protein 1



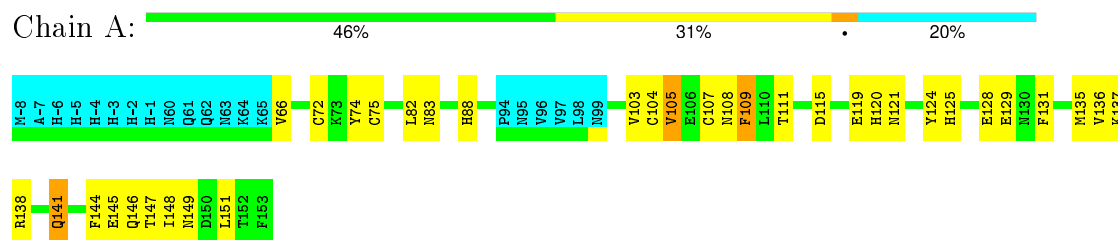
4.2.5 Score per residue for model 5 (medoid)

- Molecule 1: Zinc fingers and homeoboxes protein 1



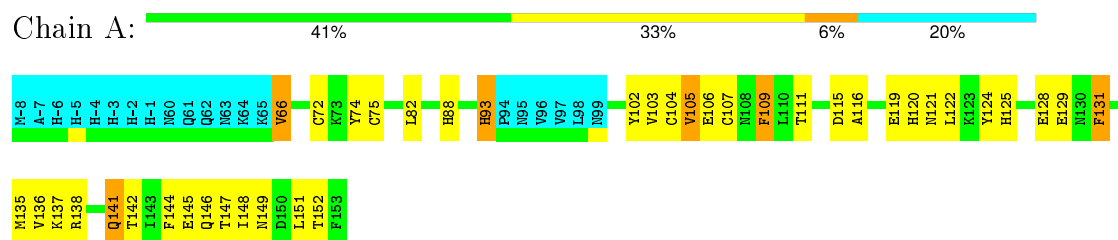
4.2.6 Score per residue for model 6

- Molecule 1: Zinc fingers and homeoboxes protein 1



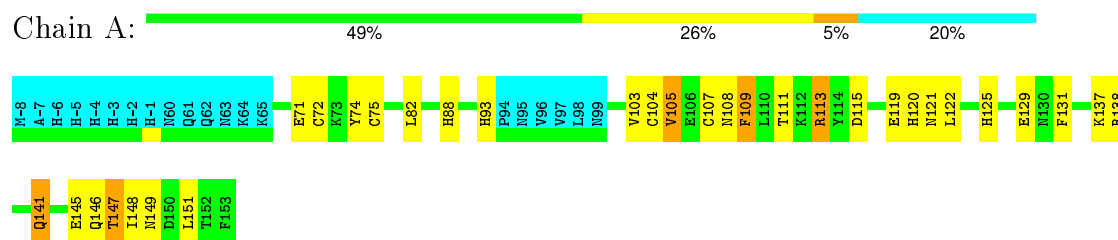
4.2.7 Score per residue for model 7

- Molecule 1: Zinc fingers and homeoboxes protein 1



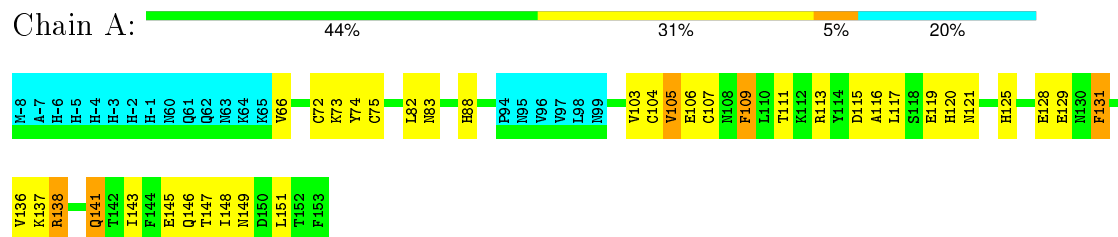
4.2.8 Score per residue for model 8

- Molecule 1: Zinc fingers and homeoboxes protein 1



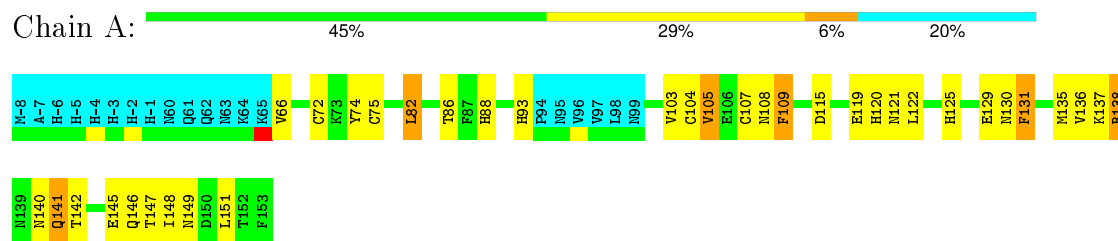
4.2.9 Score per residue for model 9

- Molecule 1: Zinc fingers and homeoboxes protein 1



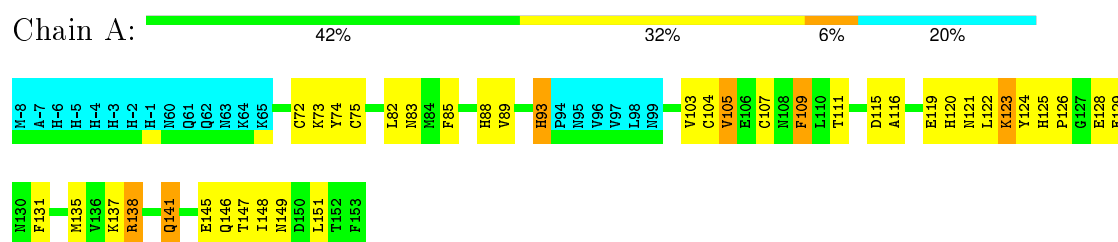
4.2.10 Score per residue for model 10

- Molecule 1: Zinc fingers and homeoboxes protein 1



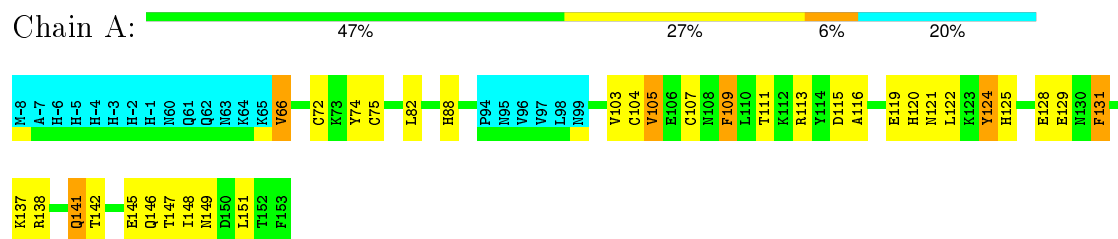
4.2.11 Score per residue for model 11

- Molecule 1: Zinc fingers and homeoboxes protein 1



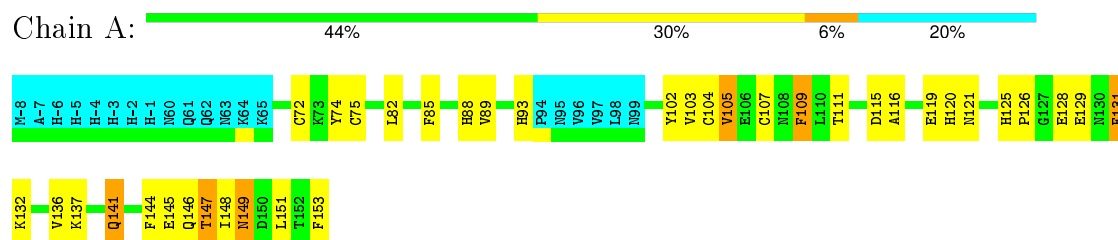
4.2.12 Score per residue for model 12

- Molecule 1: Zinc fingers and homeoboxes protein 1



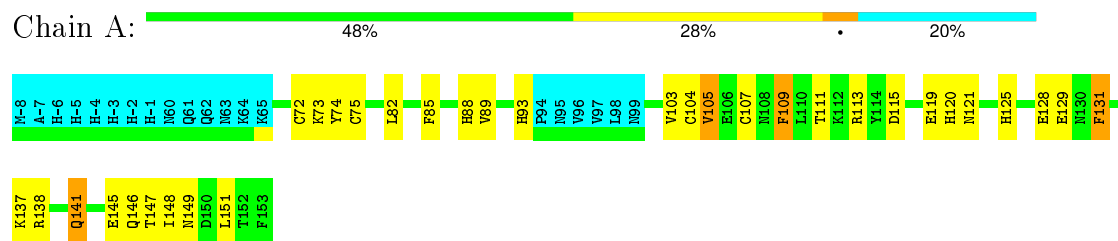
4.2.13 Score per residue for model 13

- Molecule 1: Zinc fingers and homeoboxes protein 1



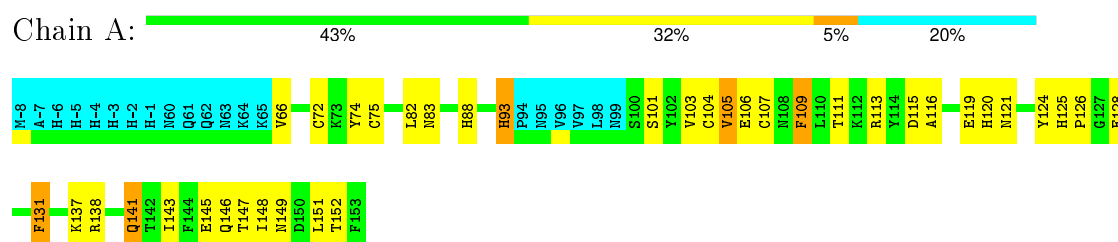
4.2.14 Score per residue for model 14

- Molecule 1: Zinc fingers and homeoboxes protein 1



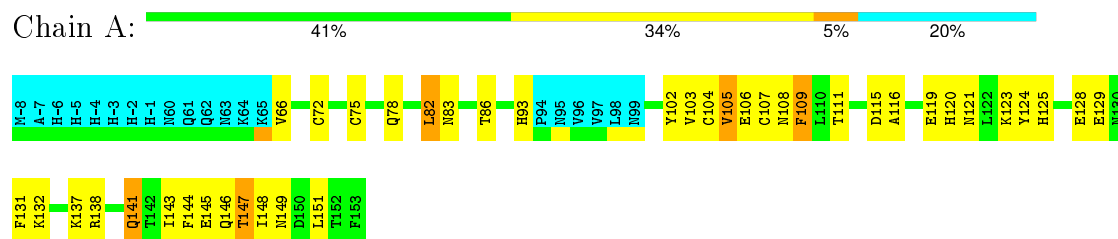
4.2.15 Score per residue for model 15

- Molecule 1: Zinc fingers and homeoboxes protein 1



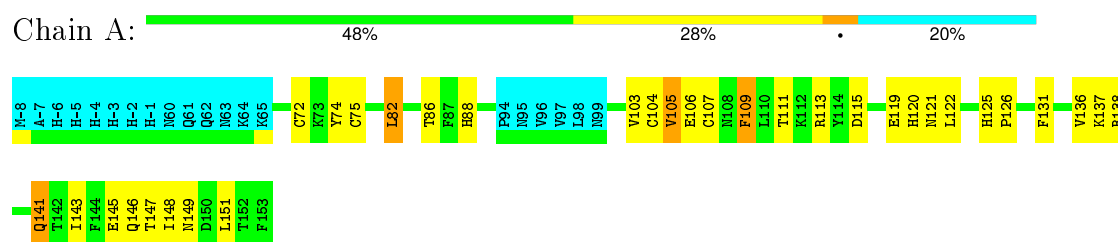
4.2.16 Score per residue for model 16

- Molecule 1: Zinc fingers and homeoboxes protein 1



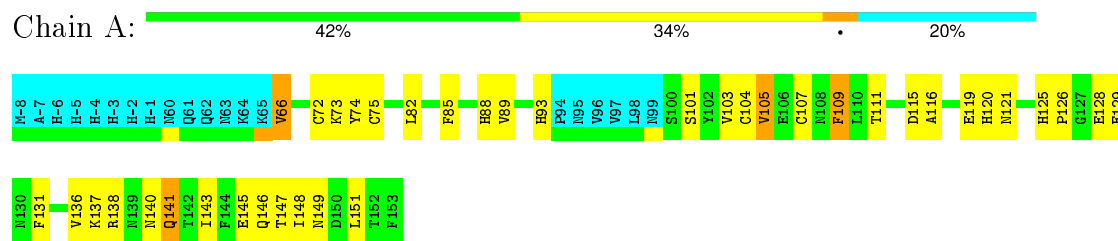
4.2.17 Score per residue for model 17

- Molecule 1: Zinc fingers and homeoboxes protein 1



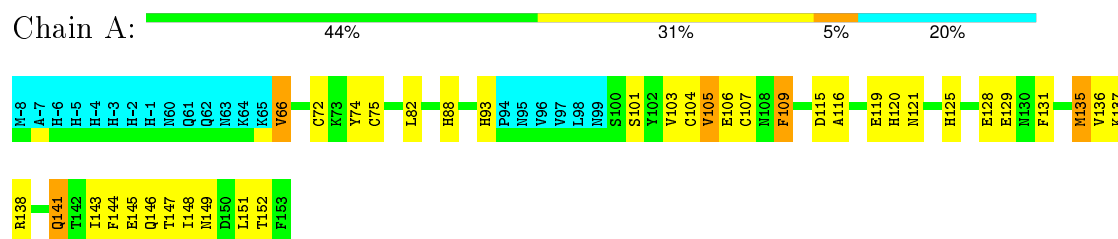
4.2.18 Score per residue for model 18

- Molecule 1: Zinc fingers and homeoboxes protein 1



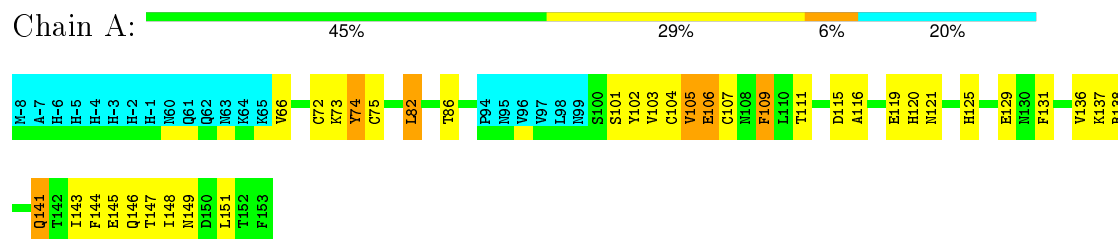
4.2.19 Score per residue for model 19

- Molecule 1: Zinc fingers and homeoboxes protein 1



4.2.20 Score per residue for model 20

- Molecule 1: Zinc fingers and homeoboxes protein 1



5 Refinement protocol and experimental data overview

The models were refined using the following method: *Sparky ASSIGNMENT - CYANA structure calculations; run1: use 70% most intense peaks for initial fold, run2: refine initial fold using all peaks - water refinement with CNS.*

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with acceptable covalent geometry, structures with the lowest energy, target function.*

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
CYANA	structure solution	2.1
CNS	refinement	1.1

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 7034
Number of chemical shift lists	1
Total number of shifts	927
Number of shifts mapped to atoms	927
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	76%

No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality [i](#)

6.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.96±0.02	0±0/698 (0.0±0.1%)	0.74±0.02	0±0/944 (0.0±0.0%)
All	All	0.96	2/13960 (0.0%)	0.74	0/18880 (0.0%)

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	106	GLU	CD-OE2	-6.80	1.18	1.25	20	1
1	A	106	GLU	CG-CD	-5.29	1.44	1.51	20	1

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	681	628	631	28±3
2	A	2	0	0	7±1
All	All	13660	12560	12639	553

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 21.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:72:CYS:HG	2:A:205:ZN:ZN	0.92	0.65	12	20
1:A:104:CYS:HG	2:A:305:ZN:ZN	0.87	0.79	14	14
1:A:107:CYS:HG	2:A:305:ZN:ZN	0.76	0.90	1	17
1:A:107:CYS:SG	2:A:305:ZN:ZN	0.73	1.77	1	19
1:A:75:CYS:SG	2:A:205:ZN:ZN	0.72	1.78	9	20
1:A:104:CYS:SG	1:A:107:CYS:SG	0.71	2.87	20	19
1:A:137:LYS:HB3	1:A:141:GLN:O	0.70	1.87	13	20
1:A:72:CYS:SG	2:A:205:ZN:ZN	0.69	1.78	15	19
1:A:109:PHE:CE1	1:A:111:THR:HB	0.68	2.24	17	4
1:A:105:VAL:HG22	1:A:145:GLU:HB3	0.67	1.66	1	20
1:A:104:CYS:SG	2:A:305:ZN:ZN	0.66	1.82	14	19
1:A:104:CYS:HG	1:A:107:CYS:HG	0.63	1.35	3	10
1:A:115:ASP:O	1:A:119:GLU:HG3	0.63	1.93	20	19
1:A:148:ILE:HD13	1:A:151:LEU:HB2	0.61	1.73	17	20
1:A:72:CYS:SG	1:A:75:CYS:SG	0.59	3.00	6	20
1:A:121:ASN:ND2	1:A:129:GLU:HA	0.59	2.12	5	16
1:A:148:ILE:HG21	1:A:151:LEU:HD12	0.58	1.73	11	20
1:A:104:CYS:SG	1:A:106:GLU:OE1	0.58	2.61	20	1
1:A:131:PHE:CD1	1:A:146:GLN:HG2	0.58	2.33	12	20
1:A:75:CYS:HG	2:A:205:ZN:ZN	0.57	1.13	6	3
1:A:104:CYS:SG	1:A:106:GLU:HB2	0.56	2.41	17	7
1:A:135:MET:HG2	1:A:144:PHE:CD2	0.55	2.36	6	1
1:A:103:VAL:HG23	1:A:109:PHE:C	0.53	2.25	12	20
1:A:72:CYS:HB2	1:A:75:CYS:SG	0.52	2.44	10	11
1:A:120:HIS:CD2	1:A:125:HIS:CD2	0.51	2.99	19	20
1:A:72:CYS:SG	1:A:88:HIS:NE2	0.51	2.83	6	15
1:A:141:GLN:H	1:A:141:GLN:NE2	0.50	2.05	15	3
1:A:101:SER:N	1:A:143:ILE:HG22	0.50	2.22	18	2
1:A:85:PHE:O	1:A:89:VAL:HG23	0.50	2.07	18	8
1:A:111:THR:HG21	1:A:116:ALA:HB3	0.49	1.82	9	7
1:A:151:LEU:HA	1:A:153:PHE:CE2	0.49	2.42	13	1
1:A:135:MET:HG3	1:A:144:PHE:CD2	0.49	2.42	19	1
1:A:121:ASN:O	1:A:126:PRO:HA	0.49	2.08	15	6
1:A:103:VAL:CG1	1:A:145:GLU:HG2	0.49	2.38	20	10
1:A:116:ALA:O	1:A:120:HIS:HB2	0.49	2.08	16	9
1:A:66:VAL:HG22	1:A:124:TYR:OH	0.48	2.09	6	6
1:A:136:VAL:HB	1:A:138:ARG:NH1	0.48	2.24	2	1
1:A:104:CYS:SG	1:A:120:HIS:NE2	0.48	2.87	4	17
1:A:89:VAL:HA	1:A:93:HIS:CE1	0.48	2.43	18	1
1:A:135:MET:SD	1:A:142:THR:HB	0.48	2.49	7	1
1:A:141:GLN:HG2	1:A:143:ILE:HG23	0.48	1.86	18	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:120:HIS:CD2	1:A:125:HIS:HD2	0.47	2.27	9	2
1:A:132:LYS:HE2	1:A:147:THR:OG1	0.47	2.10	13	4
1:A:102:TYR:HA	1:A:144:PHE:O	0.46	2.10	16	5
1:A:101:SER:H	1:A:143:ILE:HG22	0.46	1.70	19	4
1:A:107:CYS:SG	1:A:120:HIS:NE2	0.46	2.89	5	9
1:A:75:CYS:HG	1:A:93:HIS:CE1	0.46	2.29	14	2
1:A:130:ASN:O	1:A:148:ILE:HG23	0.45	2.11	10	1
1:A:113:ARG:HB2	1:A:115:ASP:OD1	0.45	2.10	12	1
1:A:141:GLN:NE2	1:A:141:GLN:H	0.45	2.10	1	2
1:A:105:VAL:HG13	1:A:145:GLU:CD	0.44	2.32	13	4
1:A:107:CYS:SG	1:A:125:HIS:NE2	0.44	2.91	11	6
1:A:81:ASP:OD2	1:A:83:ASN:HB3	0.44	2.12	3	1
1:A:119:GLU:O	1:A:122:LEU:HB3	0.44	2.13	12	9
1:A:75:CYS:SG	1:A:93:HIS:CE1	0.43	3.11	15	4
1:A:140:ASN:HB3	1:A:141:GLN:NE2	0.43	2.29	18	1
1:A:75:CYS:HG	1:A:93:HIS:HE2	0.43	1.56	18	1
1:A:89:VAL:HA	1:A:93:HIS:ND1	0.43	2.29	18	1
1:A:137:LYS:CD	1:A:143:ILE:HD11	0.43	2.42	18	1
1:A:71:GLU:CD	1:A:113:ARG:HH12	0.43	2.17	8	1
1:A:89:VAL:HA	1:A:93:HIS:CD2	0.42	2.49	14	2
1:A:75:CYS:SG	1:A:88:HIS:NE2	0.42	2.92	10	1
1:A:138:ARG:HD3	1:A:138:ARG:N	0.42	2.30	10	2
1:A:149:ASN:H	1:A:149:ASN:HD22	0.42	1.56	13	1
1:A:82:LEU:O	1:A:86:THR:HG22	0.42	2.15	10	5
1:A:105:VAL:CG2	1:A:147:THR:HG23	0.41	2.45	8	1
1:A:72:CYS:SG	1:A:88:HIS:CD2	0.41	3.14	9	2
1:A:123:LYS:HE3	1:A:124:TYR:CE1	0.41	2.51	11	1
1:A:104:CYS:O	1:A:108:ASN:N	0.41	2.54	10	1
1:A:106:GLU:OE1	1:A:152:THR:HG23	0.41	2.16	19	2
1:A:106:GLU:OE2	1:A:152:THR:HA	0.41	2.16	15	1
1:A:109:PHE:CE2	1:A:111:THR:HB	0.41	2.50	12	1
1:A:138:ARG:N	1:A:138:ARG:HD3	0.40	2.31	11	1
1:A:117:LEU:N	1:A:117:LEU:HD22	0.40	2.31	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	81/102 (79%)	72±1 (89±2%)	9±1 (11±2%)	0±1 (1±1%)	34 78
All	All	1620/2040 (79%)	1439 (89%)	172 (11%)	9 (1%)	34 78

All 3 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	66	VAL	7
1	A	140	ASN	1
1	A	68	GLY	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	78/97 (80%)	66±1 (84±2%)	13±1 (16±2%)	7 44
All	All	1560/1940 (80%)	1310 (84%)	250 (16%)	7 44

All 24 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	109	PHE	20
1	A	147	THR	20
1	A	141	GLN	20
1	A	105	VAL	20
1	A	149	ASN	20
1	A	82	LEU	20
1	A	74	TYR	19
1	A	138	ARG	18
1	A	128	GLU	15
1	A	136	VAL	14
1	A	93	HIS	11
1	A	131	PHE	8
1	A	83	ASN	7
1	A	113	ARG	7

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Mol	Chain	Res	Type	Models (Total)
1	A	111	THR	7
1	A	73	LYS	5
1	A	66	VAL	4
1	A	123	LYS	3
1	A	135	MET	3
1	A	108	ASN	3
1	A	142	THR	2
1	A	124	TYR	2
1	A	78	GLN	1
1	A	112	LYS	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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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 76% for the well-defined parts and 65% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 7034

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	927
Number of shifts mapped to atoms	927
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
$^{13}\text{C}_\alpha$	82	2.35 ± 0.11	Should be applied
$^{13}\text{C}_\beta$	79	3.09 ± 0.12	Should be applied
$^{13}\text{C}'$	72	-0.00 ± 0.18	None needed (< 0.5 ppm)
^{15}N	76	-0.48 ± 0.67	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 76%, i.e. 786 atoms were assigned a chemical shift out of a possible 1031. 9 out of 11 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	364/406 (90%)	147/162 (91%)	146/164 (89%)	71/80 (89%)
Sidechain	391/494 (79%)	247/290 (85%)	135/183 (74%)	9/21 (43%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	31/131 (24%)	31/71 (44%)	0/56 (0%)	0/4 (0%)
Overall	786/1031 (76%)	425/523 (81%)	281/403 (70%)	80/105 (76%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 65%, i.e. 846 atoms were assigned a chemical shift out of a possible 1303. 10 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	388/504 (77%)	158/201 (79%)	154/204 (75%)	76/99 (77%)
Sidechain	427/626 (68%)	269/369 (73%)	148/228 (65%)	10/29 (34%)
Aromatic	31/173 (18%)	31/95 (33%)	0/68 (0%)	0/10 (0%)
Overall	846/1303 (65%)	458/665 (69%)	302/500 (60%)	86/138 (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
1	A	128	GLU	HG3	1.14	3.31 – 1.21	-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:

