

Full wwPDB NMR Structure Validation Report (i)

May 28, 2020 – 11:43 pm BST

PDB ID	:	2MDG
Title	:	Solution NMR Structure of Zinc finger protein 423 from Homo sapiens, North-
		east Structural Genomics Consortium (NESG) Target HR7298F
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		Consortium (NESG)
Deposited on	:	2013-09-10

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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

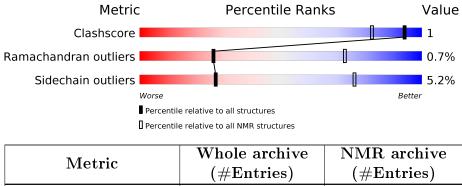
Cyrange	:	Kirchner and Güntert (2011)
$\operatorname{NmrClust}$:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
\mathbf{PANAV}	:	Wang et al. (2010)
${ m ShiftChecker}$:	2.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $SOLUTION\ NMR$

The overall completeness of chemical shifts assignment is 78%.

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	$(\# { m Entries})$	$(\# { m Entries})$
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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 <=5%

Mol	Chain	Length	Quality of chain		
1	А	55	78%	•	18%



2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 3 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:5-A:26 (22)	0.36	19			
2	A:33-A:55 (23)	0.34	3			

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 1 single-model cluster was found.

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



3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 871 atoms, of which 428 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called Zinc finger protein 423.

Mol	Chain	Residues	Atoms			Trace			
1	٨	55	Total	С	Η	Ν	Ο	S	0
	А	55	869	273	428	85	77	6	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	1	MET	-	INITIATING METHIONINE	UNP Q2M1K9

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

Mol	Chain	Residues	Atoms		
2	А	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 finger protein 423

Chain A:	78%	• 18%
M1 62 62 83 83 83 62 829 829 829 830 831 832		

4.2 Scores per residue for each member of the ensemble

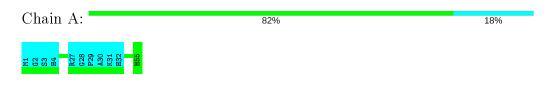
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: Zinc finger protein 423



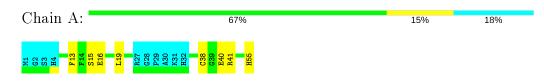
4.2.2 Score per residue for model 2





4.2.3 Score per residue for model 3 (medoid)

• Molecule 1: Zinc finger protein 423



4.2.4 Score per residue for model 4

• Molecule 1: Zinc finger protein 423

Chain A:			75%	7%	18%
M 62 83 84 84 82 827	G 28 P29 K31 H32	C38 639 R41 R41	2 2 2		

4.2.5 Score per residue for model 5

• Molecule 1: Zinc finger protein 423

Chain A:	67%	15%	18%
M1 G2 S3 H4 K5 K5 H26 H26	R27 R28 P29 F29 F240 F44 F44 F44 F44 F44		

4.2.6 Score per residue for model 6

• Molecule 1: Zinc finger protein 423

Chain A:		80%	·	18%
M1 62 62 73 72 729 729 729 731 731	H2 240			

4.2.7 Score per residue for model 7

Molecule 1: Zinc finger protein 423
Chain A: 75%



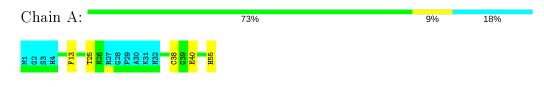


5% •

18%

4.2.8 Score per residue for model 8

• Molecule 1: Zinc finger protein 423



4.2.9 Score per residue for model 9

• Molecule 1: Zinc finger protein 423

Chain A:	71	1%	11%	18%
M 22 22 22 22 22 22 22 22 22 22 22 22 22	123 123 123 123 123 123 123 123 123 123			

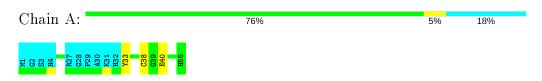
4.2.10 Score per residue for model 10

• Molecule 1: Zinc finger protein 423

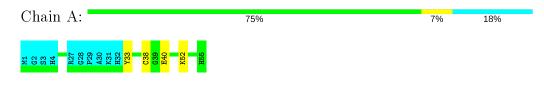
Chain A:		75%	7%	18%
83 20 81 81 81 81 81 81 81 81 81 81 81 81 81	R27 G28 P29 K31 H32 H32	Hee		

4.2.11 Score per residue for model 11

• Molecule 1: Zinc finger protein 423



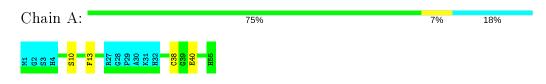
4.2.12 Score per residue for model 12





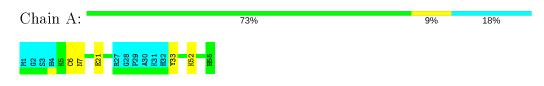
4.2.13 Score per residue for model 13

• Molecule 1: Zinc finger protein 423



4.2.14 Score per residue for model 14

• Molecule 1: Zinc finger protein 423



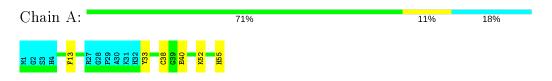
4.2.15 Score per residue for model 15

• Molecule 1: Zinc finger protein 423

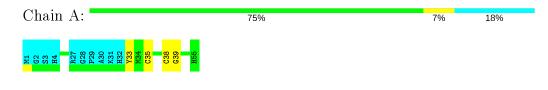
Chain	A:						76%	5%	18%
M1 62 H4	L23	R27 G28	P29 A30	K31 H32	E40	H55			

4.2.16 Score per residue for model 16

• Molecule 1: Zinc finger protein 423



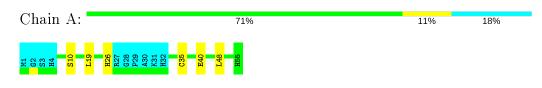
4.2.17 Score per residue for model 17





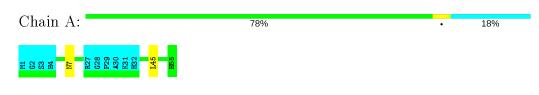
4.2.18 Score per residue for model 18

• Molecule 1: Zinc finger protein 423



4.2.19 Score per residue for model 19

• Molecule 1: Zinc finger protein 423



4.2.20 Score per residue for model 20

Chain 4	A: '			_		76%	5%	18%
M1 G2 H4	/M	K31 H32	E40	S44	H55			



5 Refinement protocol and experimental data overview (i)

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures* with the least restraint violations.

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

Software name	Classification	Version
CYANA	structure solution	3.0
CNS	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	$input_cs.cif$
Number of chemical shift lists	1
Total number of shifts	598
Number of shifts mapped to atoms	598
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	78%

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

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 (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	А	367	352	352	1±1
All	All	7380	7040	7040	18

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 1.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models		
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total	
1:A:38:CYS:SG	1:A:40:GLU:HG2	0.73	2.23	7	4	
1:A:38:CYS:SG	1:A:40:GLU:OE1	0.50	2.70	8	6	
1:A:6:CYS:O	1:A:6:CYS:SG	0.45	2.74	14	1	
1:A:35:CYS:HB3	1:A:39:GLY:N	0.45	2.26	9	2	
1:A:46:LEU:O	1:A:50:GLU:HG2	0.45	2.12	5	1	
1:A:35:CYS:HB3	1:A:39:GLY:H	0.44	1.73	17	1	
1:A:38:CYS:SG	1:A:40:GLU:HG3	0.44	2.52	16	1	
1:A:35:CYS:HA	1:A:48:LEU:HD21	0.44	1.89	18	1	
1:A:13:PHE:HD1	1:A:15:SER:H	0.42	1.58	3	1	

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



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	А	44/55~(80%)	$40\pm1~(91\pm3\%)$	$4\pm1~(8\pm3\%)$	0±0 (1±1%)	26 73
All	All	880/1100 (80%)	803~(91%)	71 (8%)	6 (1%)	26 73

All 3 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	\mathbf{Res}	Type	Models (Total)
1	А	10	SER	3
1	А	7	ASN	2
1	А	46	LEU	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	А	43/50~(86%)	$41 \pm 1 (95 \pm 3\%)$	$2\pm1~(5\pm3\%)$	27 76
All	All	860/1000 (86%)	815 (95%)	45~(5%)	27 76

All 17 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	\mathbf{Res}	Type	Models (Total)
1	А	33	TYR	5
1	А	41	ARG	5
1	А	13	PHE	5
1	А	55	HIS	5
1	А	52	LYS	4
1	А	40	GLU	4
1	А	16	GLU	3

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Mol	Chain	Res	Type	Models (Total)
1	А	7	ASN	2
1	А	38	CYS	2
1	А	45	LEU	2
1	А	26	HIS	2
1	А	23	LEU	1
1	А	21	GLU	1
1	А	50	GLU	1
1	А	5	LYS	1
1	А	25	THR	1
1	А	19	LEU	1

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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 (i)

The completeness of assignment taking into account all chemical shift lists is 78% for the well-defined parts and 78% for the entire structure.

7.1 Chemical shift list 1

File name: input_cs.cif

Chemical shift list name: assigned_chem_shift_list_1

7.1.1 Bookkeeping (i)

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	598
Number of shifts mapped to atoms	598
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	${\bf Correction}\pm{\bf precision},ppm$	Suggested action
$^{13}C_{\alpha}$	55	-0.49 ± 0.24	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	51	0.06 ± 0.20	None needed (< 0.5 ppm)
$^{13}C'$	51	1.19 ± 0.41	Should be applied
¹⁵ N	51	0.18 ± 0.52	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 78%, i.e. 448 atoms were assigned a chemical shift out of a possible 573. 6 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathrm{H}$	$^{13}\mathrm{C}$	$^{15}\mathbf{N}$
Backbone	218/221~(99%)	88/88~(100%)	87/90~(97%)	43/43~(100%)
Sidechain	230/289~(80%)	145/172~(84%)	85/103~(83%)	0/14~(0%)

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	Total	$^{1}\mathrm{H}$	$^{13}\mathrm{C}$	$^{15}\mathbf{N}$
Aromatic	0/63~(0%)	0/35~(0%)	0/24~(0%)	0/4~(0%)
Overall	448/573~(78%)	233/295~(79%)	172/217 (79%)	43/61~(70%)

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The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 78%, i.e. 540 atoms were assigned a chemical shift out of a possible 696. 6 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathrm{H}$	$^{13}\mathrm{C}$	15 N
Backbone	263/269~(98%)	106/107~(99%)	106/110~(96%)	51/52~(98%)
Sidechain	277/348~(80%)	176/209~(84%)	101/121~(83%)	0/18~(0%)
Aromatic	0/79~(0%)	0/43~(0%)	0/28~(0%)	0/8~(0%)
Overall	540/696~(78%)	282/359~(79%)	207/259~(80%)	51/78~(65%)

7.1.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots (1)

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:

