



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 2GA7 / pdb_00002ga7
Title : Solution structure of the copper(I) form of the third metal-binding domain of ATP7A protein (menkes disease protein)
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This is a wwPDB NMR Structure Validation Summary 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

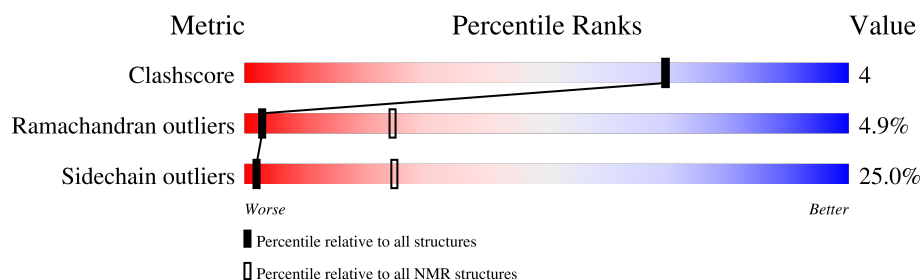
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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	90	

2 Ensemble composition and analysis ⓘ

This entry contains 30 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:2-A:49, A:54-A:74 (69)	0.70	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 2 clusters. No single-model clusters were found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1151 atoms, of which 577 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Copper-transporting ATPase 1.

Mol	Chain	Residues	Atoms						Trace
1	A	77	Total	C	H	N	O	S	0
			1150	356	577	95	119	3	

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	46	VAL	LYS	engineered mutation	UNP Q04656
A	79	ILE	-	cloning artifact	UNP Q04656
A	80	GLU	-	cloning artifact	UNP Q04656
A	81	GLY	-	cloning artifact	UNP Q04656
A	82	ARG	-	cloning artifact	UNP Q04656
A	83	LEU	-	cloning artifact	UNP Q04656
A	84	GLU	-	cloning artifact	UNP Q04656
A	85	HIS	-	expression tag	UNP Q04656
A	86	HIS	-	expression tag	UNP Q04656
A	87	HIS	-	expression tag	UNP Q04656
A	88	HIS	-	expression tag	UNP Q04656
A	89	HIS	-	expression tag	UNP Q04656
A	90	HIS	-	expression tag	UNP Q04656

- Molecule 2 is COPPER (I) ION (CCD ID: CU1) (formula: Cu).

Mol	Chain	Residues	Atoms	
2	A	1	Total	Cu
			1	1

5 Refinement protocol and experimental data overview

The models were refined using the following method: *Torsion angle dynamics coupled with simulated annealing followed by restrained energy minimization.*

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	2.1
Amber	refinement	8.0

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CU1

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	0.82±0.02	0±0/524 (0.0± 0.0%)	1.65±0.05	7±3/713 (0.9± 0.4%)
All	All	0.82	0/15720 (0.0%)	1.65	200/21390 (0.9%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	1.3±0.8
All	All	0	38

There are no bond-length outliers.

5 of 57 unique angle 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(°)	Ideal(°)	Models	
								Worst	Total
1	A	20	ASN	CA-CB-CG	9.57	122.17	112.60	27	6
1	A	17	CYS	N-CA-CB	-8.36	96.37	110.49	25	26
1	A	35	VAL	CA-CB-CG1	8.26	124.44	110.40	9	2
1	A	18	VAL	CA-CB-CG1	8.12	124.20	110.40	11	11
1	A	18	VAL	CB-CA-C	-7.68	101.77	112.14	28	6

There are no chirality outliers.

5 of 6 unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	47	TYR	Sidechain	14

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	7	PHE	Sidechain	9
1	A	41	ARG	Sidechain	6
1	A	58	ARG	Sidechain	5
1	A	69	TYR	Sidechain	2

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	517	525	525	4±2
All	All	15540	15750	15749	114

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 4.

5 of 36 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:7:PHE:CD2	1:A:73:ILE:HD12	0.71	2.21	27	14
1:A:20:ASN:HD21	1:A:64:VAL:HG11	0.65	1.51	12	1
1:A:21:ILE:HG22	1:A:25:LEU:HD23	0.63	1.68	15	1
1:A:18:VAL:HG11	1:A:38:LEU:HA	0.59	1.73	26	3
1:A:15:LYS:O	1:A:18:VAL:HG13	0.57	1.99	9	6

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	69/90 (77%)	56±2 (82±3%)	9±2 (13±3%)	3±1 (5±2%)	3	24
All	All	2070/2700 (77%)	1694 (82%)	274 (13%)	102 (5%)	3	24

5 of 16 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	35	VAL	30
1	A	70	ARG	11
1	A	17	CYS	9
1	A	40	ASN	8
1	A	41	ARG	8

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	61/81 (75%)	46±3 (75±5%)	15±3 (25±5%)	2	25
All	All	1830/2430 (75%)	1372 (75%)	458 (25%)	2	25

5 of 47 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	34	ILE	30
1	A	35	VAL	29
1	A	38	LEU	29
1	A	20	ASN	28
1	A	31	VAL	26

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](#)

Of 1 ligands modelled in this entry, 1 is 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

No chemical shift data were provided