

Full wwPDB NMR Structure Validation Report (i)

Feb 26, 2022 – 08:24 AM EST

PDB ID	:	2COB
Title	:	Solution structures of the HTH domain of human LCoR protein
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Deposited on	:	2005-05-17

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 (i)) were used in the production of this report:

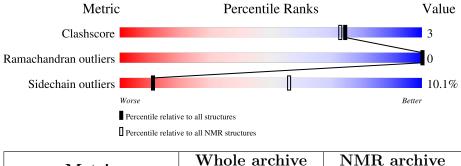
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.27
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

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 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)	(#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	Quali	ty of chain	L
1	А	70	51%	7%	41%



2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 18 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:14-A:54 (41)	0.16	18		

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 2 single-model clusters were found.

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



3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1119 atoms, of which 575 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called LCoR protein.

Mol	Chain	Residues	Atoms				Trace		
1	٨	70	Total	С	Η	Ν	0	S	0
	A	70	1119	339	575	100	101	4	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	1	GLY	-	cloning artifact	UNP Q5VW16
А	2	SER	-	cloning artifact	UNP Q5VW16
А	3	SER	-	cloning artifact	-
А	4	GLY	-	cloning artifact	UNP Q5VW16
А	5	SER	-	cloning artifact	UNP Q5VW16
А	6	SER	-	cloning artifact	UNP Q5VW16
А	7	GLY	-	cloning artifact	UNP Q5VW16



4 Residue-property plots (i)

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: LCoR protein

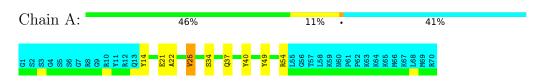


4.2 Scores per residue for each member of the ensemble

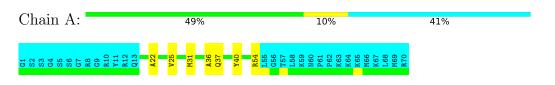
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: LCoR protein



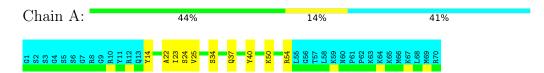
4.2.2 Score per residue for model 2





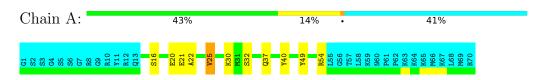
4.2.3 Score per residue for model 3

• Molecule 1: LCoR protein



4.2.4 Score per residue for model 4

• Molecule 1: LCoR protein



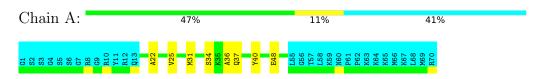
4.2.5 Score per residue for model 5

• Molecule 1: LCoR protein

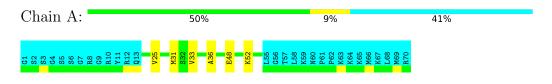
Chain A:	49%	9% •	41%
G1 S2 S3 G4 G4 S5 G4 G4 G4 C4 C9 C9 C9 R10 R12 Q13 Q13	A22 V25 S28 Q37 Y40 Y45 S45	R64 L55 L55 T57 T57 T57 K59 N60 P61 P61 K53 K64 K65 K65 K65 K65 M66 M66 M66 M66 M66	

4.2.6 Score per residue for model 6

• Molecule 1: LCoR protein



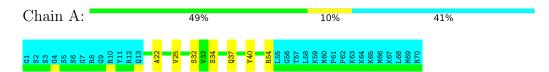
4.2.7 Score per residue for model 7





4.2.8 Score per residue for model 8

• Molecule 1: LCoR protein



4.2.9 Score per residue for model 9

• Molecule 1: LCoR protein

Chain A:	47%	10% •	41%
61 82 85 85 85 85 85 85 86 87 87 87 87 87 87 83 83 84 94 33	A22 123 224 V26 q37 q37 142 142	80 155 157 157 157 157 158 158 158 158 158 158 158 158 158 158	

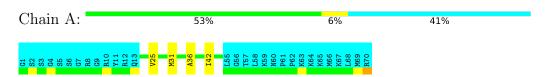
4.2.10 Score per residue for model 10

• Molecule 1: LCoR protein

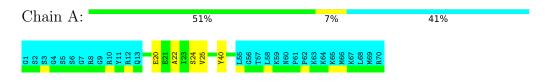
Chain A:	47%	10% •	41%	
G1 S2 S3 S5 S5 G7 R8 R8 C9 R10 R12 R12 R12 R12	E21 A22 A25 Q37 S38 S38 T39 T40 T40 S45	ະບັບບົບບົບບົບບົບ 7	M66 K67 M69 R70	

4.2.11 Score per residue for model 11

• Molecule 1: LCoR protein



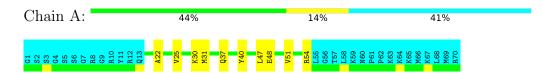
4.2.12 Score per residue for model 12





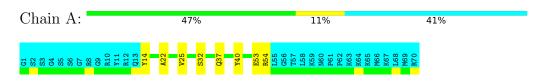
4.2.13 Score per residue for model 13

• Molecule 1: LCoR protein



4.2.14 Score per residue for model 14

• Molecule 1: LCoR protein



4.2.15 Score per residue for model 15

• Molecule 1: LCoR protein

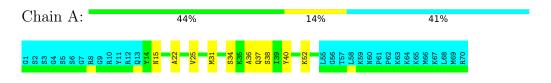
Chain A:	49%	10%	41%
G1 S2 S3 S5 G4 S5 S6 S5 S6 S6 S6 S6 S6 S6 S7 C1 1 2 13 2 13 2 13	A22 123 524 824 825 40 740 845 845 K50	L55 C56 C56 C56 C58 K59 K63 K64 K63 K64 K67 K67 K67 K67 K67 K67 K67 K67 K67 K67	

4.2.16 Score per residue for model 16

• Molecule 1: LCoR protein



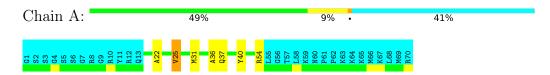
4.2.17 Score per residue for model 17





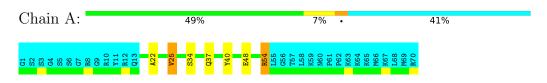
4.2.18 Score per residue for model 18 (medoid)

• Molecule 1: LCoR protein



4.2.19 Score per residue for model 19

• Molecule 1: LCoR protein



4.2.20 Score per residue for model 20

Chain A:	49%	9% •	41%
G1 S2 S3 G4 S5 G4 G5 G7 G1 R10 R12 R12 R12 R12 R12 R12	A22 V25 M31 834 A35 A35 A35 A35 A37 A37 A37	L55 G56 G56 L58 L58 N60 P61 P61 P62 K63 K64 K65 K64 K65 K66 K66 M66 M66 M66 M66 M67 R70	



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: torsion angle dynamics, restrained molecular dynamics.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: target function, structures with the lowest energy, 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	1.0.7
OPALp	refinement	1.2

No chemical shift data was provided.



6 Model quality (i)

6.1 Standard geometry (i)

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		B	ond lengths	Bond angles		
	Unam	RMSZ	$\#Z{>}5$	RMSZ	#Z > 5	
1	А	$0.58 {\pm} 0.01$	$0{\pm}0/326~(~0.0{\pm}~0.0\%)$	1.00 ± 0.04	$0{\pm}0/438~(~0.0{\pm}~0.1\%)$	
All	All	0.58	0/6520 ($0.0%$)	1.00	4/8760 ($0.0%$)	

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	А	$0.0{\pm}0.0$	$0.5 {\pm} 0.7$
All	All	0	10

There are no bond-length outliers.

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

Mal	Chain	Dec	Trune	AtomsZObserved($^{\circ}$)Ideal($^{\circ}$)		$\mathbf{Z} = \mathbf{Observed}(^{o})$	Models		
Mol	Chain	res	Type	Atoms		Observed()	Ideal(*)	Worst	Total
1	А	54	ARG	NE-CZ-NH2	-6.08	117.26	120.30	2	2
1	А	49	TYR	CB-CG-CD1	-5.26	117.84	121.00	1	1
1	А	54	ARG	NE-CZ-NH1	5.00	122.80	120.30	8	1

There are no chirality outliers.

All 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	А	54	ARG	Sidechain	6
1	А	14	TYR	Sidechain	3
1	А	49	TYR	Sidechain	1



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	321	328	328	2 ± 1
All	All	6420	6560	6560	41

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 3.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models		
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total	
1:A:22:ALA:HB2	1:A:40:TYR:CG	0.58	2.34	12	17	
1:A:31:MET:SD	1:A:36:ALA:HB2	0.49	2.48	2	8	
1:A:23:ILE:HD11	1:A:50:LYS:HB3	0.46	1.86	9	3	
1:A:33:VAL:HG11	1:A:48:GLU:CG	0.45	2.41	7	1	
1:A:25:VAL:HG21	1:A:40:TYR:CE1	0.45	2.47	9	6	
1:A:21:GLU:O	1:A:25:VAL:HG22	0.44	2.13	4	3	
1:A:47:LEU:O	1:A:51:VAL:HG23	0.44	2.13	13	1	
1:A:22:ALA:HB2	1:A:40:TYR:CD2	0.42	2.50	9	2	

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	41/70~(59%)	$37 \pm 1 (90 \pm 3\%)$	$4\pm1~(10\pm3\%)$	0±0 (0±0%)	100 100
All	All	820/1400 (59%)	735~(90%)	85 (10%)	0 (0%)	100 100

There are no Ramachandran outliers.



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	Pe	erce	ntiles
1	А	37/61~(61%)	$33 \pm 1 (90 \pm 3\%)$	$4\pm1~(10\pm3\%)$		11	56
All	All	740/1220~(61%)	665~(90%)	75 (10%)		11	56

All 18 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	А	25	VAL	20
1	А	37	GLN	17
1	А	34	SER	7
1	А	48	GLU	4
1	А	24	SER	3
1	А	20	GLU	3
1	А	32	SER	3
1	А	45	SER	3
1	А	30	LYS	2
1	А	54	ARG	2
1	А	52	LYS	2
1	А	42	ILE	2
1	А	38	SER	2
1	А	16	SER	1
1	А	28	SER	1
1	А	31	MET	1
1	А	53	GLU	1
1	А	15	ASN	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 monosaccharides 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 (i)

No chemical shift data were provided

