



wwPDB NMR Structure Validation Summary Report ⓘ

Mar 10, 2026 – 03:33 AM UTC

PDB ID : 6O22 / pdb_00006o22
BMRB ID : 30576
Title : Structure of Asf1-H3:H4-Rtt109-Vps75 histone chaperone-lysine acetyltransferase complex with the histone substrate.
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Deposited on : 2019-02-22

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

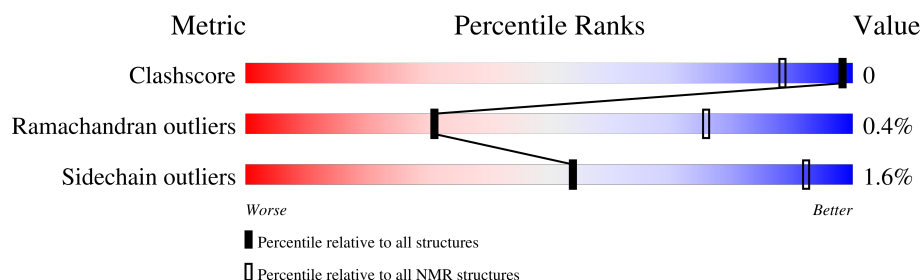
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR, SOLUTION SCATTERING

The overall completeness of chemical shifts assignment is 2%.

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	264	51% 34% . 13%
1	B	264	48% 30% . 18%
2	C	442	55% 39% . .
3	D	279	34% 24% . 41%
4	E	136	27% 25% . 45%
5	F	103	44% 34% . . 20%

2 Ensemble composition and analysis ⓘ

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.

3 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 19411 atoms, of which 9680 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Vacuolar protein sorting-associated protein 75.

Mol	Chain	Residues	Atoms						Trace
1	A	230	Total	C	H	N	O	S	0
			3733	1221	1825	309	372	6	
1	B	217	Total	C	H	N	O	S	0
			3562	1168	1752	294	343	5	

- Molecule 2 is a protein called Histone acetyltransferase RTT109.

Mol	Chain	Residues	Atoms						Trace
2	C	424	Total	C	H	N	O	S	0
			6917	2205	3480	585	637	10	

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	GLY	-	expression tag	UNP Q07794
C	-4	MET	-	expression tag	UNP Q07794
C	-3	ASP	-	expression tag	UNP Q07794
C	-2	PRO	-	expression tag	UNP Q07794
C	-1	ASN	-	expression tag	UNP Q07794
C	0	SER	-	expression tag	UNP Q07794

- Molecule 3 is a protein called Histone chaperone ASF1.

Mol	Chain	Residues	Atoms						Trace
3	D	164	Total	C	H	N	O	S	0
			2592	840	1280	212	258	2	

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	SER	-	expression tag	UNP P32447

- Molecule 4 is a protein called Histone H3.2.

Mol	Chain	Residues	Atoms						Trace
4	E	75	Total	C	H	N	O	S	0
			1243	384	636	114	106	3	

- Molecule 5 is a protein called Histone H4.

Mol	Chain	Residues	Atoms						Trace
5	F	82	Total	C	H	N	O	S	0
			1364	416	707	128	112	1	



5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 150 calculated structures, 1 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
HADDOCK	structure calculation	
Amber	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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	368
Number of shifts mapped to atoms	368
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	2%

6 Model quality

6.1 Standard geometry

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	1.94	39/1956 (2.0%)	2.32	99/2633 (3.8%)
1	B	1.96	37/1858 (2.0%)	2.35	101/2503 (4.0%)
2	C	1.97	74/3515 (2.1%)	2.35	184/4758 (3.9%)
3	D	2.01	27/1344 (2.0%)	2.32	67/1835 (3.7%)
4	E	2.10	15/614 (2.4%)	2.44	36/823 (4.4%)
5	F	2.06	16/664 (2.4%)	2.40	39/889 (4.4%)
All	All	1.99	208/9951 (2.1%)	2.35	526/13441 (3.9%)

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	4
1	B	0	8
2	C	0	9
3	D	0	4
4	E	0	3
5	F	0	4
All	All	0	32

5 of 208 bond outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	130	VAL	N-CA	9.93	1.58	1.46
1	B	103	PHE	CA-C	9.05	1.63	1.52
1	A	118	GLU	N-CA	8.83	1.57	1.46
1	B	196	HIS	CD2-NE2	-8.61	1.28	1.37
1	B	209	TYR	CA-C	8.53	1.63	1.52

5 of 526 angle outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	84	PHE	CA-CB-CG	12.83	126.63	113.80
1	B	222	ASP	CA-CB-CG	11.01	123.61	112.60
1	A	164	ARG	NE-CZ-NH2	10.24	128.42	119.20
1	B	72	ILE	CA-C-N	10.08	135.18	120.87
1	B	72	ILE	C-N-CA	10.08	135.18	120.87

There are no chirality outliers.

5 of 32 planar outliers are listed below.

Mol	Chain	Res	Type	Group
1	A	35	TYR	Sidechain
1	A	50	TYR	Sidechain
1	A	172	TYR	Sidechain
1	A	197	GLY	Mainchain
1	B	35	TYR	Sidechain

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	1908	1825	1824	2
2	C	3437	3480	3480	2
4	E	607	636	634	1
All	All	9731	9680	9675	5

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 0.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)
2:C:365:ILE:N	2:C:365:ILE:HD12	0.52	2.19
1:A:164:ARG:O	1:A:169:LYS:HE3	0.44	2.12
4:E:71:VAL:HG12	4:E:84:PHE:CZ	0.43	2.49
1:A:116:PHE:CE1	1:A:119:GLN:NE2	0.40	2.88
2:C:293:PHE:CD1	2:C:311:PHE:CE1	0.40	3.10

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	228/264 (86%)	209 (92%)	19 (8%)	0 (0%)	100	100
1	B	215/264 (81%)	203 (94%)	11 (5%)	1 (0%)	26	74
2	C	422/442 (95%)	389 (92%)	31 (7%)	2 (0%)	26	74
3	D	162/279 (58%)	155 (96%)	6 (4%)	1 (1%)	23	72
4	E	73/136 (54%)	67 (92%)	5 (7%)	1 (1%)	11	58
5	F	80/103 (78%)	78 (98%)	2 (2%)	0 (0%)	100	100
All	All	1180/1488 (79%)	1101 (93%)	74 (6%)	5 (0%)	31	76

All 5 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	B	132	ASP
2	C	14	SER
2	C	203	ASP
3	D	90	VAL
4	E	133	GLU

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	205/235 (87%)	203 (99%)	2 (1%)	65	95
1	B	194/235 (83%)	190 (98%)	4 (2%)	46	90
2	C	388/403 (96%)	383 (99%)	5 (1%)	59	94
3	D	151/252 (60%)	148 (98%)	3 (2%)	48	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	E	64/111 (58%)	64 (100%)	0 (0%)	100	100
5	F	68/79 (86%)	65 (96%)	3 (4%)	27	77
All	All	1070/1315 (81%)	1053 (98%)	17 (2%)	54	92

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

Mol	Chain	Res	Type
1	A	68	PHE
1	A	132	ASP
1	B	112	ILE
1	B	220	GLN
1	B	222	ASP

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 2% for the well-defined parts and 2% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list*

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	368
Number of shifts mapped to atoms	368
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	6

7.1.2 Chemical shift referencing

No chemical shift referencing corrections were calculated (not enough data).

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 2%, i.e. 368 atoms were assigned a chemical shift out of a possible 16842. 0 out of 181 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	0/5901 (0%)	0/2382 (0%)	0/2384 (0%)	0/1135 (0%)
Sidechain	368/9499 (4%)	276/6138 (4%)	92/2970 (3%)	0/391 (0%)
Aromatic	0/1442 (0%)	0/707 (0%)	0/697 (0%)	0/38 (0%)
Overall	368/16842 (2%)	276/9227 (3%)	92/6051 (2%)	0/1564 (0%)

7.1.4 Statistically unusual chemical shifts [i](#)

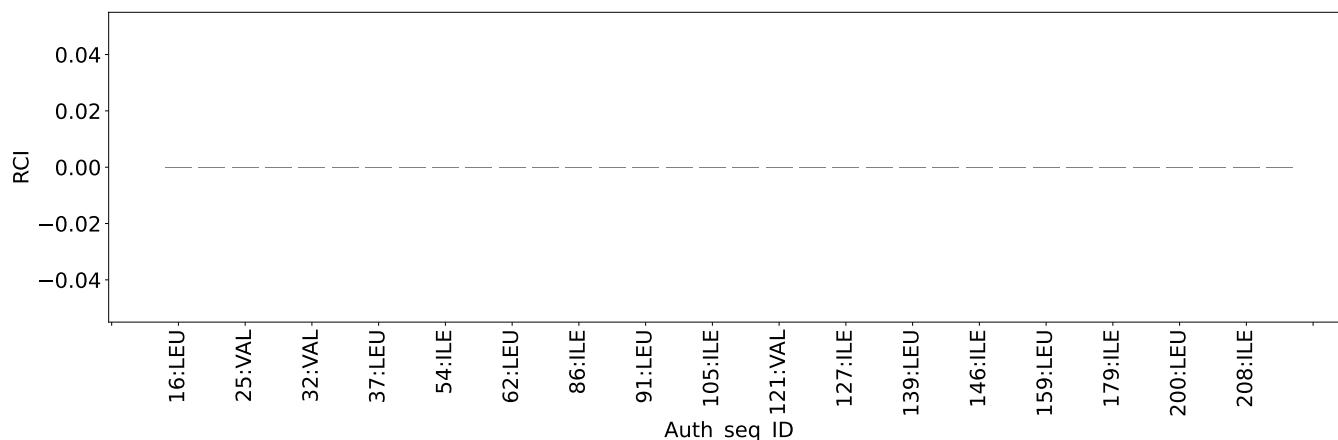
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	200	LEU	HD21	-0.69	-0.65 – 2.13	-5.1
1	A	200	LEU	HD22	-0.69	-0.65 – 2.13	-5.1
1	A	200	LEU	HD23	-0.69	-0.65 – 2.13	-5.1
1	B	200	LEU	HD21	-0.68	-0.65 – 2.13	-5.1
1	B	200	LEU	HD22	-0.68	-0.65 – 2.13	-5.1
1	B	200	LEU	HD23	-0.68	-0.65 – 2.13	-5.1

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:



Random coil index (RCI) for chain B:

