# wwPDB NMR Structure Validation Summary Report

May 31, 2020 – 11:34 am BST

| | | |
|---|---|---|
| PDB ID | : | 6O22 |
| Title | : | Structure of Asf1-H3:H4-Rtt109-Vps75 histone chaperone-lysine acetyltransferase complex with the histone substrate. |
| Authors | : | Danilenko, N.; Carlomagno, T.; Kirkpatrick, J.P. |
| 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 (i) symbol.

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

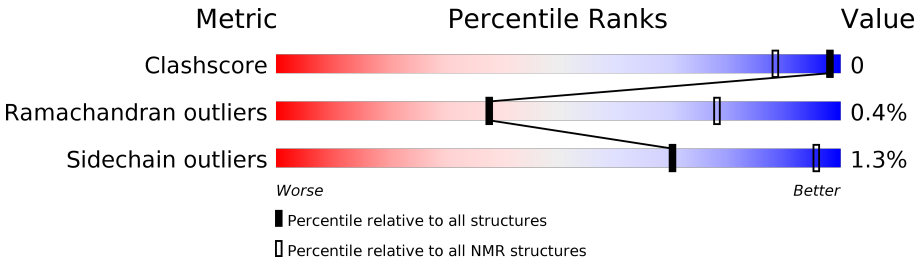
| | | |
|---|---|---|
| Cyrange | : | Kirchner and Güntert (2011) |
| NmrClust | : | Kelley et al. (1996) |
| MolProbity | : | 4.02b-467 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| RCI | : | v_1n_11_5_13_A (Berjanski et al., 2005) |
| PANAV | : | Wang et al. (2010) |
| 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

The following experimental techniques were used to determine the structure:
*SOLUTION NMR, SOLUTION SCATTERING*

The overall completeness of chemical shifts assignment is 1%.

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 | 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 | A | 264 | 68% 17% • 13% |
| 1 | B | 264 | 63% 17% • 18% |
| 2 | C | 442 | 74% 20% • • |
| 3 | D | 279 | 46% 11% • 41% |
| 4 | E | 136 | 44% 9% • 45% |
| 5 | F | 103 | 58% 17% • • 20% |

## 2 Ensemble composition and analysis (i)

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

# 3 Entry composition

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.

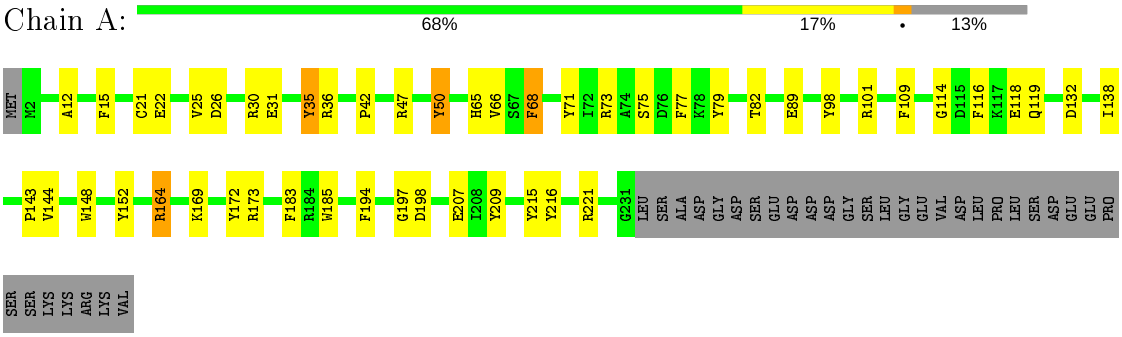
| Mol | Chain | Residues | Atoms | | | | | | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 5 | F | 82 | Total | C | H | N | O | S | 0 |
| | | | 1364 | 416 | 707 | 128 | 112 | 1 | |

# 4 Residue-property plots (i)

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.

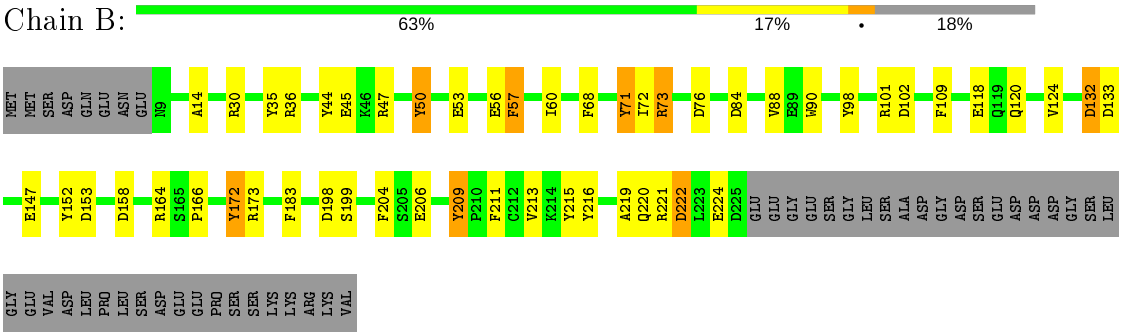
- Molecule 1: Vacuolar protein sorting-associated protein 75

Chain A:



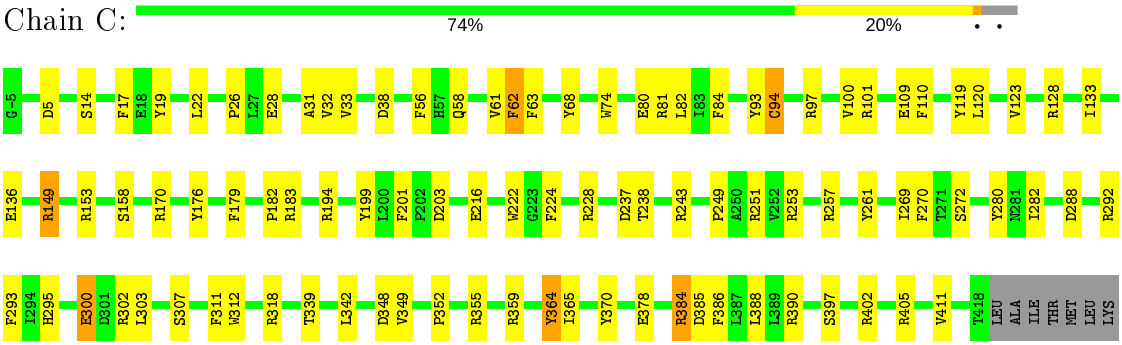

- Molecule 1: Vacuolar protein sorting-associated protein 75

Chain B:



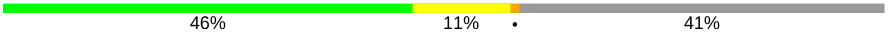

- Molecule 2: Histone acetyltransferase RTT109

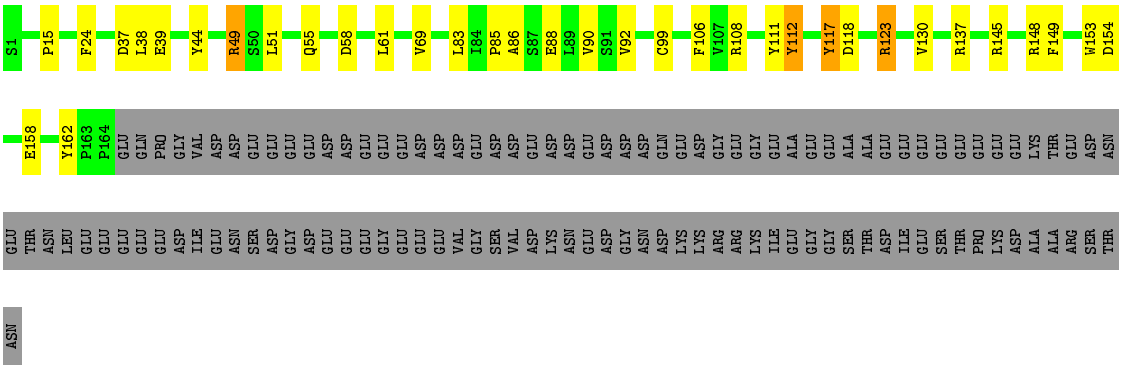
Chain C:




- Molecule 3: Histone chaperone ASF1

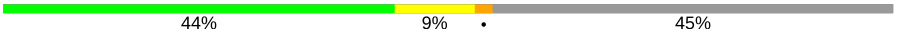
Chain D:

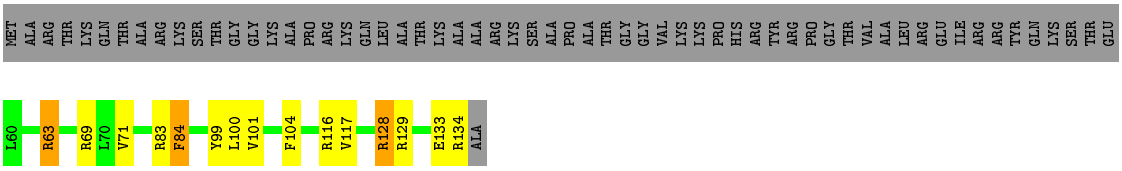



- Molecule 4: Histone H3.2

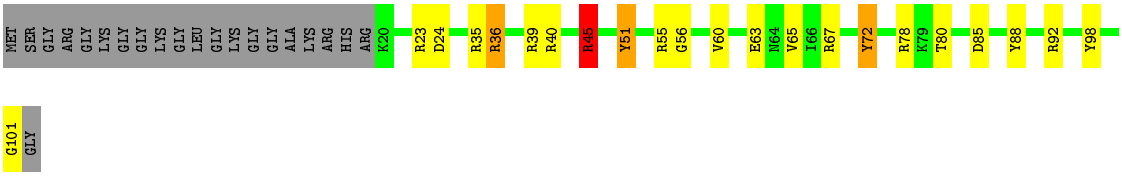
Chain E:




- Molecule 5: Histone H4

Chain F:

# 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 6 of this report.

| Chemical shift file(s) | input_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) | 1% |

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

COVALENT-GEOMETRY INFOmissingINFO

## 5.1 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 |

## 5.2 Torsion angles (i)

### 5.2.1 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 | 228/264 (86%) | 209 (92%) | 19 (8%) | 0 (0%) | 100 | 100 |
| 1 | B | 215/264 (81%) | 203 (94%) | 11 (5%) | 1 (0%) | 32 | 76 |
| 2 | C | 422/442 (95%) | 389 (92%) | 31 (7%) | 2 (0%) | 32 | 76 |
| 3 | D | 162/279 (58%) | 155 (96%) | 6 (4%) | 1 (1%) | 29 | 74 |
| 4 | E | 73/136 (54%) | 67 (92%) | 5 (7%) | 1 (1%) | 15 | 61 |
| 5 | F | 80/103 (78%) | 78 (98%) | 2 (2%) | 0 (0%) | 100 | 100 |
| All | All | 1180/1488 (79%) | 1101 (93%) | 74 (6%) | 5 (0%) | 38 | 78 |

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

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

### 5.2.2 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 | 205/235 (87%) | 204 (100%) | 1 (0%) | 89 97 |
| 1 | B | 194/235 (83%) | 191 (98%) | 3 (2%) | 66 95 |
| 2 | C | 388/403 (96%) | 383 (99%) | 5 (1%) | 70 96 |
| 3 | D | 151/252 (60%) | 148 (98%) | 3 (2%) | 57 93 |
| 4 | E | 64/111 (58%) | 64 (100%) | 0 (0%) | 100 100 |
| 5 | F | 68/79 (86%) | 66 (97%) | 2 (3%) | 45 89 |
| All | All | 1070/1315 (81%) | 1056 (99%) | 14 (1%) | 70 96 |

5 of 14 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 | B | 222 | ASP |
| 2 | C | 300 | GLU |
| 1 | B | 220 | GLN |
| 2 | C | 62 | PHE |
| 2 | C | 237 | ASP |

#### 5.2.3 RNA

There are no RNA molecules in this entry.

### 5.3 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.4 Carbohydrates

There are no carbohydrates in this entry.

### 5.5 Ligand geometry

There are no ligands in this entry.

## 5.6 Other polymers

There are no such molecules in this entry.

## 5.7 Polymer linkage issues

There are no chain breaks in this entry.

# 6 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 1% for the well-defined parts and 1% for the entire structure.

## 6.1 Chemical shift list 1

File name: input_cs.cif

Chemical shift list name: *assigned_chem_shift_list*

### 6.1.1 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 |

### 6.1.2 Chemical shift referencing

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

### 6.1.3 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 1%, i.e. 184 atoms were assigned a chemical shift out of a possible 15339. 20 out of 181 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

| | Total | $^{1}$H | $^{13}$C | $^{15}$N |
|---|---|---|---|---|
| Backbone | 0/5846 (0%) | 0/2327 (0%) | 0/2384 (0%) | 0/1135 (0%) |
| Sidechain | 184/8165 (2%) | 92/4804 (2%) | 92/2970 (3%) | 0/391 (0%) |
| Aromatic | 0/1328 (0%) | 0/707 (0%) | 0/583 (0%) | 0/38 (0%) |
| Overall | 184/15339 (1%) | 92/7838 (1%) | 92/5937 (2%) | 0/1564 (0%) |

### 6.1.4 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.

| Mol | Chain | Res | Type | Atom | Shift, *ppm* | Expected range, *ppm* | Z-score |
|---|---|---|---|---|---|---|---|
| 1 | A | 200 | LEU | HD23 | -0.69 | 2.14 – -0.66 | -5.1 |
| 1 | A | 200 | LEU | HD22 | -0.69 | 2.14 – -0.66 | -5.1 |
| 1 | A | 200 | LEU | HD21 | -0.69 | 2.14 – -0.66 | -5.1 |
| 1 | B | 200 | LEU | HD23 | -0.68 | 2.14 – -0.66 | -5.1 |
| 1 | B | 200 | LEU | HD21 | -0.68 | 2.14 – -0.66 | -5.1 |
| 1 | B | 200 | LEU | HD22 | -0.68 | 2.14 – -0.66 | -5.1 |

### 6.1.5 Random Coil Index (RCI) plots (i)

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned_chem_shift_list). RCI is only applicable to proteins.