# wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 04:42 AM GMT

| | | |
|---|---|---|
| PDB ID | : | 2NXN |
| Title | : | T. thermophilus ribosomal protein L11 methyltransferase (PrmA) in complex with ribosomal protein L11 |
| Authors | : | Demirci, H.; Gregory, S.T.; Dahlberg, A.E.; Jogl, G. |
| Deposited on | : | 2006-11-17 |
| Resolution | : | 2.40 Å(reported) |

This is a wwPDB X-ray 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
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:

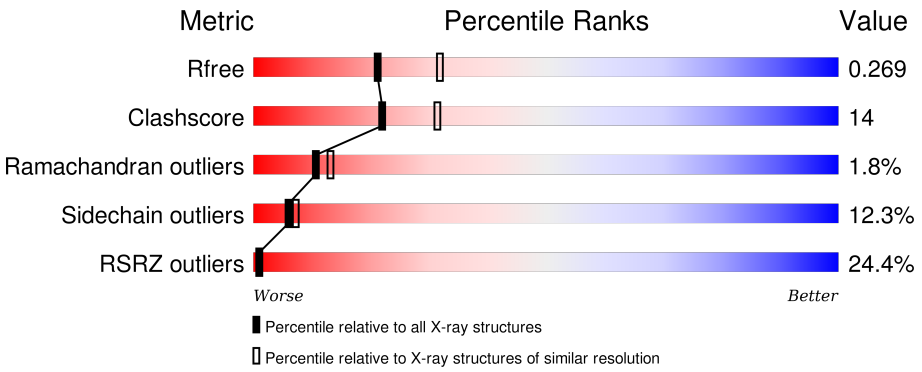
| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Mogul | : | 1.7 (RC4), CSD as536be (2015) |
| Xtriage (Phenix) | : | 1.9-1692 |
| EDS | : | rb-20026688 |
| Percentile statistics | : | 20151230.v01 (using entries in the PDB archive December 30th 2015) |
| Refmac | : | 5.8.0135 |
| CCP4 | : | 6.5.0 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | trunk26865 |

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 Å.

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) | Similar resolution (#Entries, resolution range(Å)) |
|---|---|---|
| $R_{free}$ | 91344 | 2919 (2.40-2.40) |
| Clashscore | 102246 | 3407 (2.40-2.40) |
| Ramachandran outliers | 100387 | 3351 (2.40-2.40) |
| Sidechain outliers | 100360 | 3352 (2.40-2.40) |
| RSRZ outliers | 91569 | 2928 (2.40-2.40) |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | A | 254 | 18%; 72%; 21%; 6%; • |
| 2 | B | 147 | 34%; 54%; 33%; 7%; 5% |

# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3054 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Ribosomal protein L11 methyltransferase.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 1 | A | 250 | 1926 | 1250 | 335 | 337 | 4 | 0 | 0 | 0 |

- Molecule 2 is a protein called 50S ribosomal protein L11.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 2 | B | 139 | 1033 | 659 | 182 | 186 | 6 | 0 | 0 | 0 |

- Molecule 3 is water.

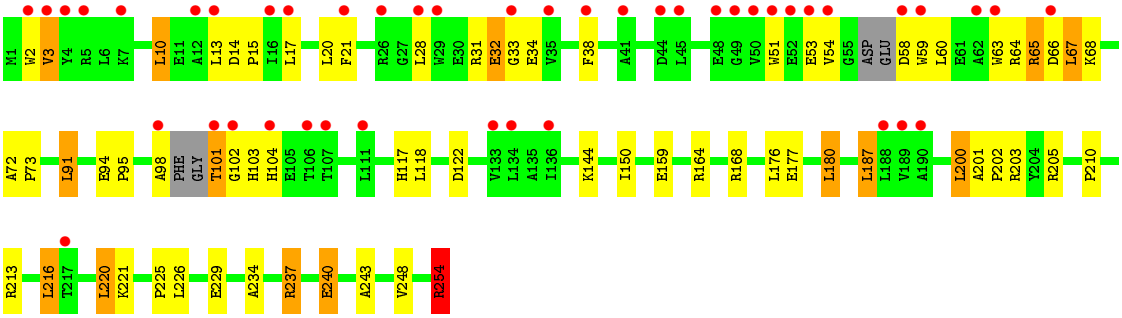
| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|
| | | | Total | O | | |
| 3 | A | 68 | 68 | 68 | 0 | 0 |
| | | | Total | O | | |
| 3 | B | 27 | 27 | 27 | 0 | 0 |

# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-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. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

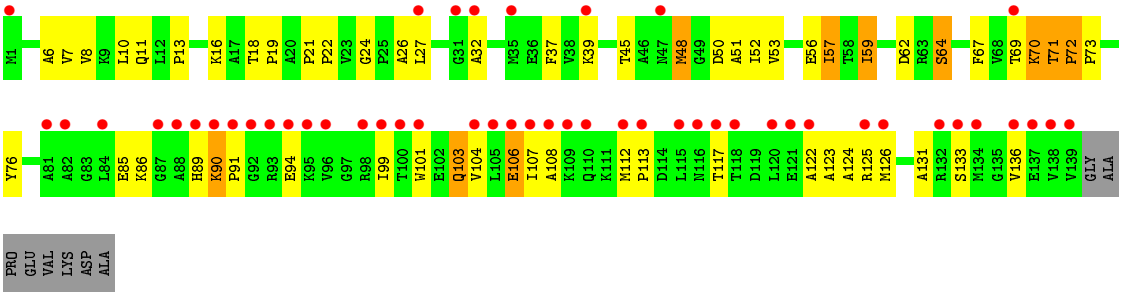
- Molecule 1: Ribosomal protein L11 methyltransferase

Chain A:




- Molecule 2: 50S ribosomal protein L11

Chain B:



# 4 Data and refinement statistics (i)

| Property | Value | Source |
|---|---|---|
| Space group | P 65 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 132.84Å 132.84Å 46.01Å<br>90.00° 90.00° 120.00° | Depositor |
| Resolution (Å) | 30.00 – 2.40<br>28.76 – 2.40 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 99.0 (30.00-2.40)<br>98.9 (28.76-2.40) | Depositor<br>EDS |
| $R_{merge}$ | 0.08 | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 3.11 (at 2.39Å) | Xtriage |
| Refinement program | REFMAC 5.2.0019 | Depositor |
| R, $R_{free}$ | 0.220 , 0.273<br>0.215 , 0.269 | Depositor<br>DCC |
| $R_{free}$ test set | 940 reflections (5.43%) | DCC |
| Wilson B-factor (Å$^2$) | 46.5 | Xtriage |
| Anisotropy | 0.037 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.28 , 60.4 | EDS |
| Estimated twinning fraction | 0.052 for h,-h-k,-l | Xtriage |
| L-test for twinning[2] | $< \|L\| > = 0.47$, $< L^2 > = 0.30$ | Xtriage |
| Outliers | 0 of 18330 reflections | Xtriage |
| $F_o$,$F_c$ correlation | 0.93 | EDS |
| Total number of atoms | 3054 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 62.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.21% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

# 5 Model quality (i)

## 5.1 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 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 | 0.83 | 1/1980 (0.1%) | 0.89 | 8/2697 (0.3%) |
| 2 | B | 0.53 | 0/1052 | 0.73 | 2/1425 (0.1%) |
| All | All | 0.74 | 1/3032 (0.0%) | 0.84 | 10/4122 (0.2%) |

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 outliers | #Planarity outliers |
|---|---|---|---|
| 2 | B | 0 | 1 |

All (1) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 1 | A | 10 | LEU | C-N | 6.11 | 1.48 | 1.34 |

The worst 5 of 10 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 1 | A | 168 | ARG | NE-CZ-NH2 | -6.83 | 116.89 | 120.30 |
| 1 | A | 122 | ASP | CB-CG-OD1 | 6.14 | 123.82 | 118.30 |
| 1 | A | 220 | LEU | CA-CB-CG | 5.99 | 129.06 | 115.30 |
| 1 | A | 254 | ARG | NE-CZ-NH2 | -5.82 | 117.39 | 120.30 |
| 2 | B | 71 | THR | N-CA-C | 5.18 | 124.98 | 111.00 |

There are no chirality outliers.

All (1) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 2 | B | 70 | LYS | Peptide |

## 5.2 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 the 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 within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 1 | A | 1926 | 0 | 1931 | 48 | 0 |
| 2 | B | 1033 | 0 | 1086 | 42 | 0 |
| 3 | A | 68 | 0 | 0 | 10 | 0 |
| 3 | B | 27 | 0 | 0 | 1 | 0 |
| All | All | 3054 | 0 | 3017 | 83 | 0 |

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 14.

The worst 5 of 83 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 2:B:72:PRO:HB2 | 2:B:73:PRO:CD | 1.82 | 1.08 |
| 1:A:31:ARG:HG2 | 1:A:32:GLU:H | 1.31 | 0.93 |
| 2:B:72:PRO:HB2 | 2:B:73:PRO:HD2 | 1.57 | 0.86 |
| 2:B:72:PRO:HB2 | 2:B:73:PRO:HD3 | 1.64 | 0.79 |
| 1:A:101:THR:HG23 | 3:A:257:HOH:O | 1.82 | 0.78 |

There are no symmetry-related clashes.

## 5.3 Torsion angles (i)

### 5.3.1 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 X-ray entries followed by that with respect to entries of similar resolution.

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 | 244/254 (96%) | 227 (93%) | 14 (6%) | 3 (1%) | 16 23 |
| 2 | B | 137/147 (93%) | 107 (78%) | 26 (19%) | 4 (3%) | 6 5 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles |
|---|---|---|---|---|---|---|
| All | All | 381/401 (95%) | 334 (88%) | 40 (10%) | 7 (2%) | 11 13 |

5 of 7 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 32 | GLU |
| 1 | A | 33 | GLY |
| 2 | B | 72 | PRO |
| 2 | B | 101 | TRP |
| 2 | B | 106 | GLU |

### 5.3.2 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 X-ray entries followed by that with respect to entries of similar resolution.

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 | 186/189 (98%) | 167 (90%) | 19 (10%) | 9 13 |
| 2 | B | 106/111 (96%) | 89 (84%) | 17 (16%) | 3 3 |
| All | All | 292/300 (97%) | 256 (88%) | 36 (12%) | 6 7 |

5 of 36 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 237 | ARG |
| 2 | B | 50 | ASP |
| 2 | B | 125 | ARG |
| 1 | A | 254 | ARG |
| 2 | B | 53 | VAL |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains (i)

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

## 5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry (i)

There are no ligands in this entry.

## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

# 6 Fit of model and data (i)

## 6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, $95^{th}$ percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | | | OWAB(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|
| 1 | A | 250/254 (98%) | 0.79 | 45 (18%) | 2 | 2 | 28, 39, 100, 100 | 0 |
| 2 | B | 139/147 (94%) | 2.20 | 50 (35%) | 0 | 0 | 51, 71, 100, 100 | 0 |
| All | All | 389/401 (97%) | 1.29 | 95 (24%) | 1 | 1 | 28, 56, 100, 100 | 0 |

The worst 5 of 95 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 2 | B | 105 | LEU | 19.6 |
| 2 | B | 92 | GLY | 13.8 |
| 2 | B | 88 | ALA | 12.4 |
| 2 | B | 96 | VAL | 12.0 |
| 2 | B | 89 | HIS | 11.2 |

## 6.2 Non-standard residues in protein, DNA, RNA chains (i)

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

## 6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

## 6.4 Ligands (i)

There are no ligands in this entry.

## 6.5 Other polymers (i)

There are no such residues in this entry.