



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 11:39 AM GMT

PDB ID : 3PGW  
Title : Crystal structure of human U1 snRNP  
Authors : Weber, G.; Trowitzsch, S.; Kastner, B.; Luehrmann, R.; Wahl, M.C.  
Deposited on : 2010-11-02  
Resolution : 4.40 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) 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

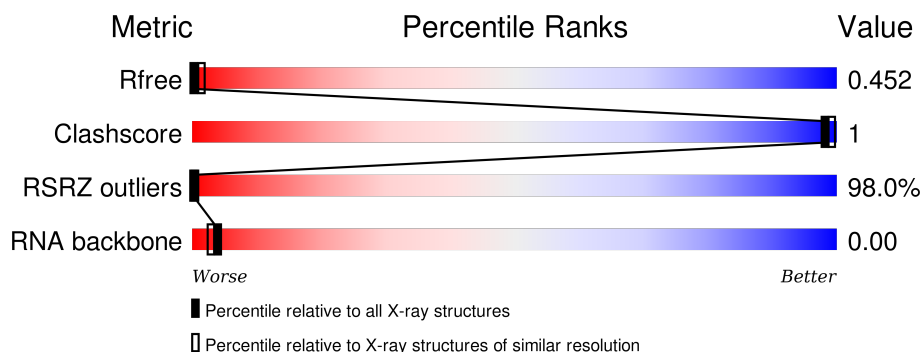
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 4.40 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<br>(#Entries) | Similar resolution<br>(#Entries, resolution range(Å)) |
|---------------|-----------------------------|---|
| $R_{free}$    | 91344                       | 1067 (5.20-3.60)                                      |
| Clashscore    | 102246                      | 1175 (5.20-3.60)                                      |
| RSRZ outliers | 91569                       | 1071 (5.20-3.60)                                      |
| RNA backbone  | 2183                        | 1090 (6.00-2.80)                                      |

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  $\geq 3$ , 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  $\leq 5\%$ . 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     | 282    | <div> <div>37%</div> <div>38%</div> <div>62%</div> </div> |
| 1   | P     | 282    | <div> <div>38%</div> <div>40%</div> <div>60%</div> </div> |
| 2   | L     | 437    | <div> <div>33%</div> <div>34%</div> <div>66%</div> </div> |
| 2   | S     | 437    | <div> <div>33%</div> <div>34%</div> <div>66%</div> </div> |
| 3   | W     | 126    | <div> <div>72%</div> <div>73%</div> <div>27%</div> </div> |
| 3   | Z     | 126    | <div> <div>62%</div> <div>63%</div> <div>37%</div> </div> |

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| Mol | Chain | Length | Quality of chain                             |
|-----|-------|--------|--|
| 4   | B     | 231    | <div> <div>35%</div> <div>65%</div> </div>   |
| 4   | Q     | 231    | <div> <div>33%</div> <div>67%</div> </div>   |
| 5   | U     | 119    | <div> <div>71%</div> <div>29%</div> </div>   |
| 5   | X     | 119    | <div> <div>69%</div> <div>29%</div> </div>   |
| 6   | V     | 118    | <div> <div>86%</div> <div>13%</div> </div>   |
| 6   | Y     | 118    | <div> <div>87%</div> <div>6%</div> </div>    |
| 7   | F     | 86     | <div> <div>95%</div> <div>99%</div> </div>   |
| 7   | I     | 86     | <div> <div>86%</div> <div>14%</div> </div>   |
| 8   | E     | 92     | <div> <div>85%</div> <div>9%</div> </div>    |
| 8   | H     | 92     | <div> <div>92%</div> <div>97%</div> </div>   |
| 9   | G     | 76     | <div> <div>100%</div> <div>100%</div> </div> |
| 9   | J     | 76     | <div> <div>100%</div> <div>100%</div> </div> |
| 10  | N     | 164    | <div> <div>99%</div> <div>99%</div> </div>   |
| 10  | R     | 164    | <div> <div>99%</div> <div>99%</div> </div>   |
| 11  | D     | 9      | <div> <div>89%</div> <div>11%</div> </div>   |
| 11  | M     | 9      | <div> <div>89%</div> <div>11%</div> </div>   |

## 2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 2058 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 U1-A.

| Mol | Chain | Residues | Atoms |     | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|---------|---------|-------|
| 1   | A     | 108      | Total | C   | 0       | 0       | 108   |
|     |       |          | 108   | 108 |         |         |       |
| 1   | P     | 113      | Total | C   | 0       | 0       | 113   |
|     |       |          | 113   | 113 |         |         |       |

- Molecule 2 is a protein called U1-70K.

| Mol | Chain | Residues | Atoms |     | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|---------|---------|-------|
| 2   | S     | 150      | Total | C   | 0       | 0       | 150   |
|     |       |          | 150   | 150 |         |         |       |
| 2   | L     | 148      | Total | C   | 0       | 0       | 148   |
|     |       |          | 148   | 148 |         |         |       |

- Molecule 3 is a protein called Sm-D3.

| Mol | Chain | Residues | Atoms |    | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|----|---------|---------|-------|
| 3   | Z     | 80       | Total | C  | 0       | 0       | 80    |
|     |       |          | 80    | 80 |         |         |       |
| 3   | W     | 92       | Total | C  | 0       | 0       | 92    |
|     |       |          | 92    | 92 |         |         |       |

- Molecule 4 is a protein called Sm B.

| Mol | Chain | Residues | Atoms |    | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|----|---------|---------|-------|
| 4   | B     | 81       | Total | C  | 0       | 0       | 81    |
|     |       |          | 81    | 81 |         |         |       |
| 4   | Q     | 76       | Total | C  | 0       | 0       | 76    |
|     |       |          | 76    | 76 |         |         |       |

- Molecule 5 is a protein called Sm-D1.

| Mol | Chain | Residues | Atoms            | ZeroOcc | AltConf | Trace |
|-----|-------|----------|------------------|---------|---------|-------|
| 5   | X     | 85       | Total C<br>85 85 | 0       | 0       | 85    |
| 5   | U     | 85       | Total C<br>85 85 | 0       | 0       | 85    |

- Molecule 6 is a protein called Sm-D2.

| Mol | Chain | Residues | Atoms              | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------------|---------|---------|-------|
| 6   | Y     | 111      | Total C<br>111 111 | 7       | 0       | 111   |
| 6   | V     | 103      | Total C<br>103 103 | 0       | 0       | 103   |

- Molecule 7 is a protein called Sm-F.

| Mol | Chain | Residues | Atoms            | ZeroOcc | AltConf | Trace |
|-----|-------|----------|------------------|---------|---------|-------|
| 7   | F     | 85       | Total C<br>85 85 | 0       | 0       | 85    |
| 7   | I     | 74       | Total C<br>74 74 | 0       | 0       | 74    |

- Molecule 8 is a protein called Sm-E.

| Mol | Chain | Residues | Atoms            | ZeroOcc | AltConf | Trace |
|-----|-------|----------|------------------|---------|---------|-------|
| 8   | E     | 84       | Total C<br>84 84 | 0       | 0       | 84    |
| 8   | H     | 89       | Total C<br>89 89 | 0       | 0       | 89    |

- Molecule 9 is a protein called Sm G.

| Mol | Chain | Residues | Atoms            | ZeroOcc | AltConf | Trace |
|-----|-------|----------|------------------|---------|---------|-------|
| 9   | G     | 76       | Total C<br>76 76 | 0       | 0       | 76    |
| 9   | J     | 76       | Total C<br>76 76 | 0       | 0       | 76    |

- Molecule 10 is a RNA chain called U1 snRNA.

| Mol | Chain | Residues | Atoms              | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------------|---------|---------|-------|
| 10  | R     | 163      | Total P<br>163 163 | 0       | 0       | 163   |

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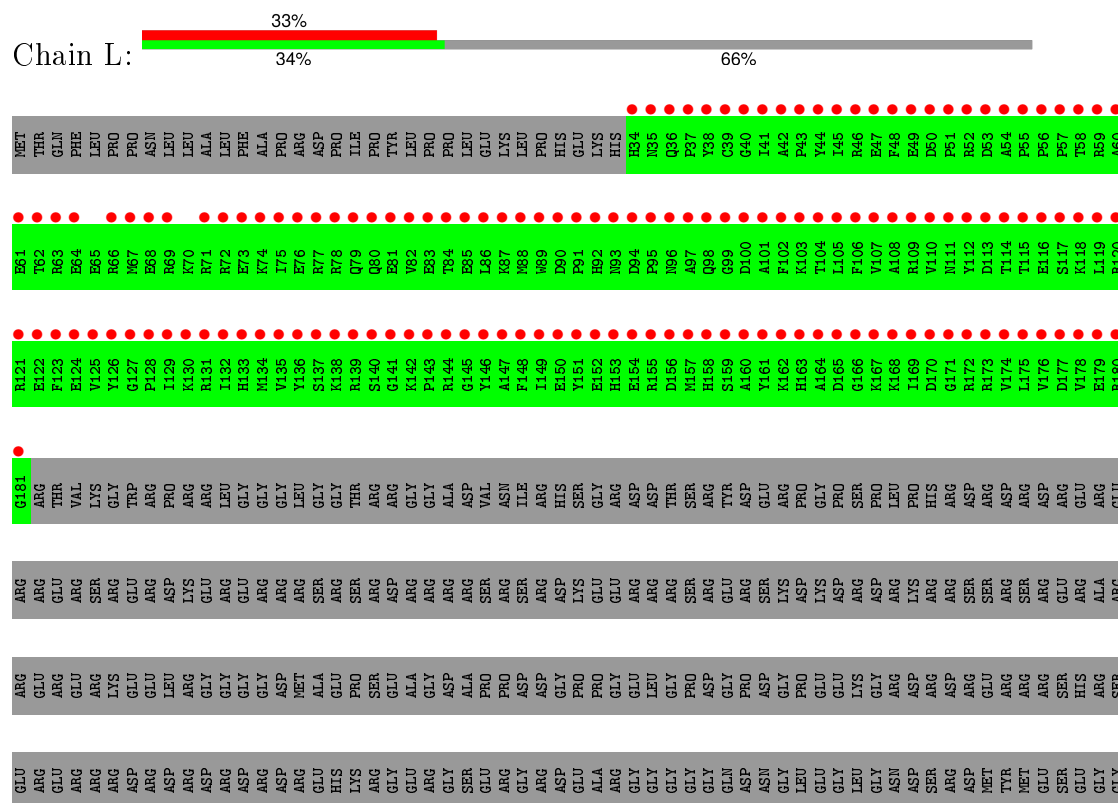
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| Mol | Chain | Residues | Atoms        |          | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------|----------|---------|---------|-------|
| 10  | N     | 163      | Total<br>163 | P<br>163 | 0       | 0       | 163   |

- Molecule 11 is a DNA chain called DNA 5'-D(\*AP\*GP\*GP\*TP\*AP\*AP\*GP\*TP\*A)-3'.

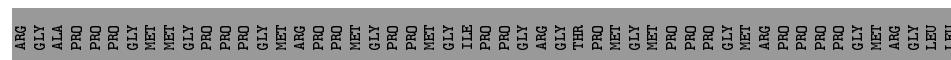
| Mol | Chain | Residues | Atoms      |        | ZeroOcc | AltConf | Trace |
|-----|-------|----------|------------|--------|---------|---------|-------|
| 11  | D     | 8        | Total<br>8 | P<br>8 | 0       | 0       | 8     |
| 11  | M     | 8        | Total<br>8 | P<br>8 | 0       | 0       | 8     |



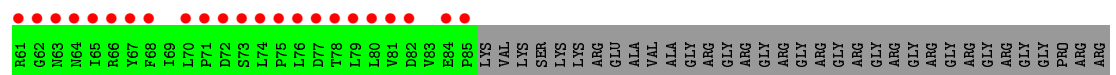




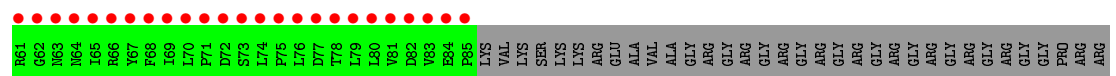
[illegible]

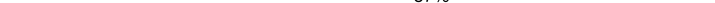


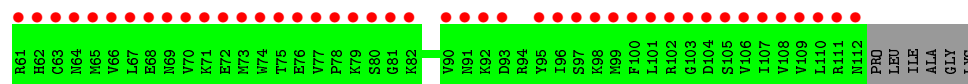
Chain X:  69% 71% 29%

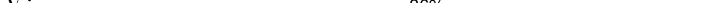


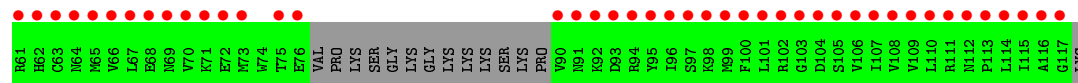
Chain U:  71% 29%



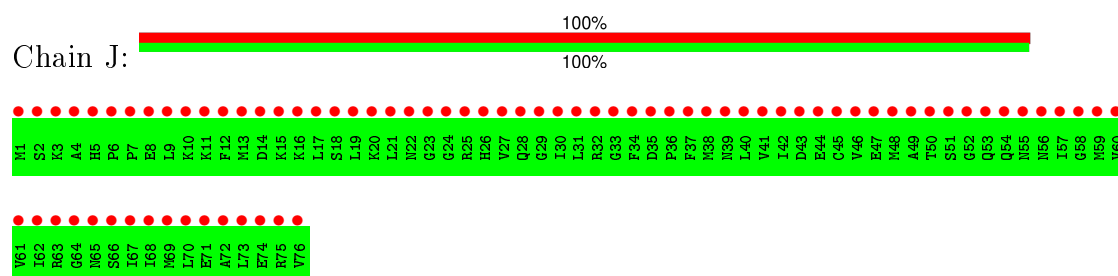
Chain Y:  87% 92% 6%



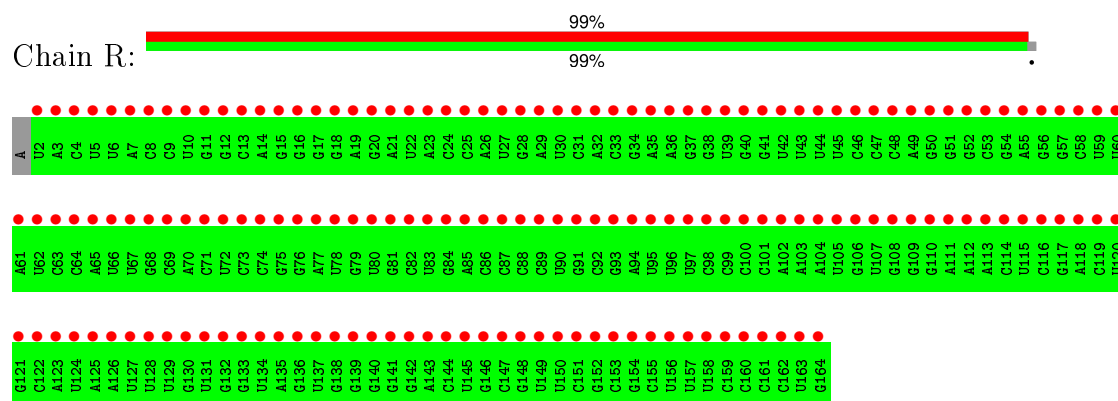
Chain V:  86% 86% • 13%



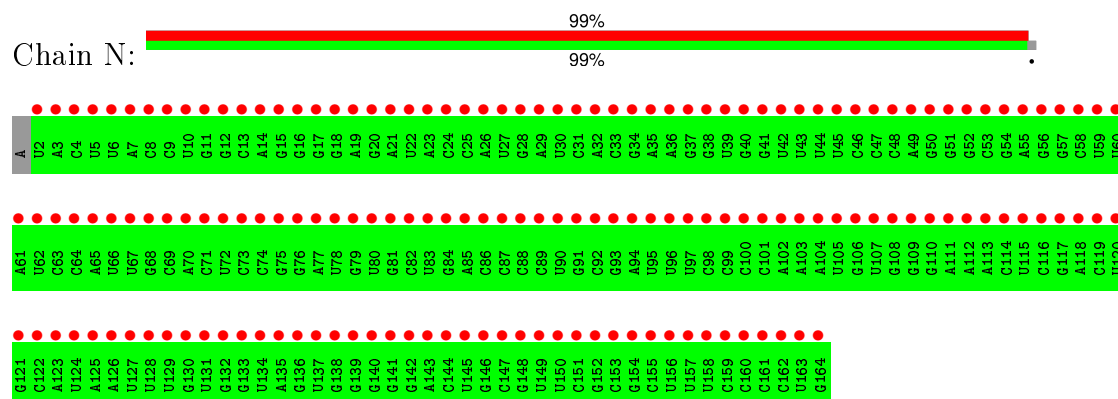




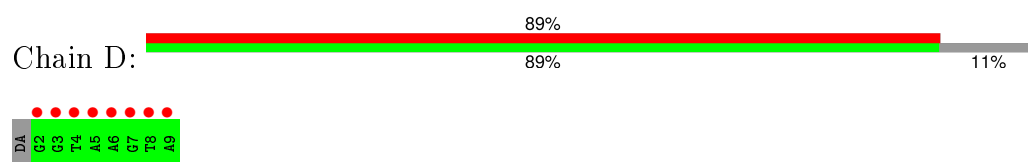
- Molecule 10: U1 snRNA



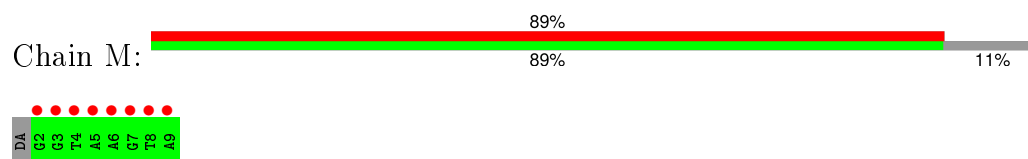
- Molecule 10: U1 snRNA



- Molecule 11: DNA 5'-D(\*AP\*GP\*GP\*TP\*AP\*AP\*GP\*TP\*A)-3'



- Molecule 11: DNA 5'-D(\*AP\*GP\*GP\*TP\*AP\*AP\*GP\*TP\*A)-3'



## 4 Data and refinement statistics

| Property  | Value   | Source           |
|---|---|------------------|
| Space group   | C 1 2 1   | Depositor        |
| Cell constants<br>a, b, c, $\alpha$ , $\beta$ , $\gamma$                | 358.42Å 88.22Å 150.90Å<br>90.00° 111.88° 90.00°             | Depositor        |
| Resolution (Å)  | 100.00 – 4.40<br>140.03 – 4.40                              | Depositor<br>EDS |
| % Data completeness<br>(in resolution range)                            | (Not available) (100.00-4.40)<br>99.5 (140.03-4.40)         | Depositor<br>EDS |
| $R_{merge}$   | (Not available)   | Depositor        |
| $R_{sym}$   | (Not available)   | Depositor        |
| $\langle I/\sigma(I) \rangle$ <sup>1</sup>                              | 2.43 (at 4.47Å)   | Xtriage          |
| Refinement program  | PHENIX.REFINE, CNS 1.3                                      | Depositor        |
| R, $R_{free}$   | 0.299 , 0.348<br>0.434 , 0.452                              | Depositor<br>DCC |
| $R_{free}$ test set   | 1403 reflections (5.00%)                                    | DCC              |
| Wilson B-factor (Å <sup>2</sup> )                                       | 222.6   | Xtriage          |
| Anisotropy  | 0.203   | Xtriage          |
| Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> ) | 0.54 , 0.8  | EDS              |
| Estimated twinning fraction   | 0.037 for -h-2*k,l  | Xtriage          |
| L-test for twinning <sup>2</sup>  | $\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$ | Xtriage          |
| Outliers  | 0 of 28079 reflections                                      | Xtriage          |
| $F_o, F_c$ correlation  | 0.70  | EDS              |
| Total number of atoms   | 2058  | wwPDB-VP         |
| Average B, all atoms (Å <sup>2</sup> )                                  | 255.0   | wwPDB-VP         |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.03% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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     | 108   | 0        | 0        | 0       | 0            |
| 1   | P     | 113   | 0        | 0        | 0       | 0            |
| 2   | L     | 148   | 0        | 0        | 0       | 0            |
| 2   | S     | 150   | 0        | 0        | 0       | 0            |
| 3   | W     | 92    | 0        | 0        | 0       | 0            |
| 3   | Z     | 80    | 0        | 0        | 0       | 0            |
| 4   | B     | 81    | 0        | 0        | 0       | 0            |
| 4   | Q     | 76    | 0        | 0        | 0       | 0            |
| 5   | U     | 85    | 0        | 0        | 0       | 0            |
| 5   | X     | 85    | 0        | 0        | 0       | 0            |
| 6   | V     | 103   | 0        | 0        | 1       | 0            |
| 6   | Y     | 111   | 0        | 0        | 1       | 0            |
| 7   | F     | 85    | 0        | 0        | 0       | 0            |
| 7   | I     | 74    | 0        | 0        | 0       | 0            |
| 8   | E     | 84    | 0        | 0        | 0       | 0            |
| 8   | H     | 89    | 0        | 0        | 0       | 0            |
| 9   | G     | 76    | 0        | 0        | 0       | 0            |
| 9   | J     | 76    | 0        | 0        | 0       | 0            |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 10  | N     | 163   | 0        | 0        | 0       | 0            |
| 10  | R     | 163   | 0        | 0        | 0       | 0            |
| 11  | D     | 8     | 0        | 0        | 0       | 0            |
| 11  | M     | 8     | 0        | 0        | 0       | 0            |
| All | All   | 2058  | 0        | 0        | 2       | 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 1.

All (2) 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) |
|--------------|--------------|--------------------------|-------------------|
| 6:V:6:LYS:CA | 6:V:7:PRO:CA | 2.81                     | 0.58              |
| 6:Y:6:LYS:CA | 6:Y:7:PRO:CA | 2.83                     | 0.56              |

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

### 5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

### 5.3.3 RNA [i](#)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|----------|-------------------|-----------------|
| 10  | N     | 0/164    | -                 | -               |
| 10  | R     | 0/164    | -                 | -               |
| All | All   | 0/328    | -                 | -               |

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

## 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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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<sup>th</sup> 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 <sup>2</sup> ) | Q<0.9              |   |
|-----|-------|-----------------|--------|------------|-----------------------|--------------------|---|
| 1   | A     | 108/282 (38%)   | 10.63  | 104 (96%)  | 00                    | 135, 201, 306, 344 | 0 |
| 1   | P     | 113/282 (40%)   | 10.39  | 108 (95%)  | 00                    | 135, 202, 310, 344 | 0 |
| 2   | L     | 148/437 (33%)   | 12.20  | 146 (98%)  | 00                    | 189, 268, 352, 389 | 0 |
| 2   | S     | 150/437 (34%)   | 8.88   | 143 (95%)  | 00                    | 185, 269, 352, 390 | 0 |
| 3   | W     | 92/126 (73%)    | 11.00  | 91 (98%)   | 00                    | 153, 228, 354, 392 | 0 |
| 3   | Z     | 80/126 (63%)    | 11.04  | 78 (97%)   | 00                    | 152, 225, 260, 292 | 0 |
| 4   | B     | 81/231 (35%)    | 9.37   | 80 (98%)   | 00                    | 160, 250, 322, 350 | 0 |
| 4   | Q     | 76/231 (32%)    | 11.08  | 76 (100%)  | 00                    | 159, 232, 298, 350 | 0 |
| 5   | U     | 85/119 (71%)    | 9.82   | 85 (100%)  | 00                    | 151, 223, 260, 359 | 0 |
| 5   | X     | 85/119 (71%)    | 10.15  | 82 (96%)   | 00                    | 153, 222, 259, 363 | 0 |
| 6   | V     | 103/118 (87%)   | 10.71  | 102 (99%)  | 00                    | 149, 234, 295, 321 | 0 |
| 6   | Y     | 104/118 (88%)   | 10.12  | 103 (99%)  | 00                    | 150, 233, 300, 490 | 0 |
| 7   | F     | 85/86 (98%)     | 8.87   | 82 (96%)   | 00                    | 150, 224, 303, 373 | 0 |
| 7   | I     | 74/86 (86%)     | 9.88   | 74 (100%)  | 00                    | 151, 217, 265, 283 | 0 |
| 8   | E     | 84/92 (91%)     | 10.87  | 78 (92%)   | 00                    | 184, 243, 359, 423 | 0 |
| 8   | H     | 89/92 (96%)     | 9.97   | 85 (95%)   | 00                    | 181, 246, 362, 385 | 0 |
| 9   | G     | 76/76 (100%)    | 10.04  | 76 (100%)  | 00                    | 179, 237, 302, 315 | 0 |
| 9   | J     | 76/76 (100%)    | 9.19   | 76 (100%)  | 00                    | 180, 241, 307, 363 | 0 |
| 10  | N     | 163/164 (99%)   | 24.25  | 163 (100%) | 00                    | 182, 295, 494, 557 | 0 |
| 10  | R     | 163/164 (99%)   | 24.32  | 163 (100%) | 00                    | 183, 289, 494, 557 | 0 |
| 11  | D     | 8/9 (88%)       | 13.93  | 8 (100%)   | 00                    | 431, 501, 523, 526 | 0 |
| 11  | M     | 8/9 (88%)       | 13.11  | 8 (100%)   | 00                    | 431, 500, 522, 525 | 0 |
| All | All   | 2051/3480 (58%) | 12.52  | 2011 (98%) | 00                    | 135, 242, 379, 557 | 0 |

The worst 5 of 2011 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 10  | R     | 41  | G    | 65.1 |
| 10  | R     | 34  | G    | 61.3 |
| 10  | N     | 52  | G    | 57.5 |
| 10  | N     | 70  | A    | 55.5 |
| 10  | R     | 84  | G    | 53.4 |

## 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.