



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 24, 2024 – 04:56 PM EDT

PDB ID : 5WNR
Title : Crystal Structure of 30S ribosomal subunit from *Thermus thermophilus*
Authors : DeMirici, H.
Deposited on : 2017-08-01
Resolution : 3.50 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

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 | : | 4.02b-467 |
| Mogul | : | 1.8.5 (274361), CSD as541be (2020) |
| Xtriage (Phenix) | : | 1.13 |
| EDS | : | 2.37.1 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| Refmac | : | 5.8.0158 |
| CCP4 | : | 7.0.044 (Gargrove) |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.37.1 |

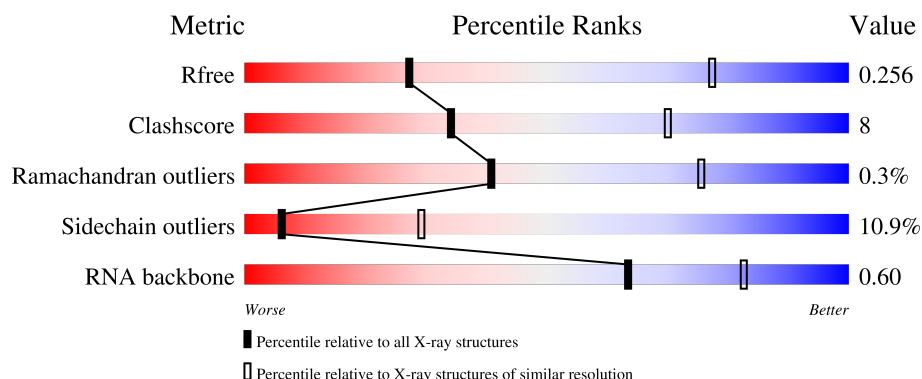
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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} | 130704 | 1659 (3.60-3.40) |
| Clashscore | 141614 | 1036 (3.58-3.42) |
| Ramachandran outliers | 138981 | 1005 (3.58-3.42) |
| Sidechain outliers | 138945 | 1006 (3.58-3.42) |
| RNA backbone | 3102 | 1002 (4.00-3.00) |

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 | 1522 | |
| 2 | B | 234 | |
| 3 | C | 206 | |
| 4 | D | 208 | |
| 5 | E | 150 | |
| 6 | F | 101 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|---|
| 7 | G | 155 |  80% 17% . |
| 8 | H | 138 |  73% 24% . |
| 9 | I | 127 |  61% 33% 6% |
| 10 | J | 98 |  62% 31% 6% . |
| 11 | K | 116 |  66% 30% . |
| 12 | L | 124 |  68% 28% . |
| 13 | M | 118 |  59% 35% 6% |
| 14 | N | 60 |  60% 35% 5% |
| 15 | O | 87 |  72% 22% 6% |
| 16 | P | 83 |  78% 18% . |
| 17 | Q | 99 |  79% 21% |
| 18 | R | 70 |  81% 16% . |
| 19 | S | 80 |  70% 30% |
| 20 | T | 99 |  68% 25% 5% . |
| 21 | U | 24 |  63% 38% |

2 Entry composition

There are 24 unique types of molecules in this entry. The entry contains 52227 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 RNA chain called 16S Ribosomal RNA rRNA.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|---------|-------|
| 1 | A | 1512 | Total | C | N | O | P | 0 | 6 | 0 |
| | | | 32644 | 14540 | 6039 | 10547 | 1518 | | | |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|-------------|
| A | 1534 | C | A | conflict | GB 55771382 |
| A | 1535 | A | C | conflict | GB 55771382 |

- Molecule 2 is a protein called 30S ribosomal protein S2.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 2 | B | 234 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1900 | 1213 | 341 | 341 | 5 | | | |

- Molecule 3 is a protein called 30S ribosomal protein S3.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 3 | C | 206 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1612 | 1016 | 314 | 281 | 1 | | | |

- Molecule 4 is a protein called 30S ribosomal protein S4.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 4 | D | 208 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1703 | 1066 | 339 | 291 | 7 | | | |

- Molecule 5 is a protein called 30S ribosomal protein S5.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 5 | E | 150 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1146 | 724 | 217 | 201 | 4 | | | |

- Molecule 6 is a protein called 30S ribosomal protein S6.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 6 | F | 101 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 843 | 531 | 155 | 154 | 3 | | | |

- Molecule 7 is a protein called 30S ribosomal protein S7.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 7 | G | 155 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1257 | 781 | 252 | 218 | 6 | | | |

- Molecule 8 is a protein called 30S ribosomal protein S8.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 8 | H | 138 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1116 | 705 | 215 | 193 | 3 | | | |

- Molecule 9 is a protein called 30S ribosomal protein S9.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|---------|-------|
| 9 | I | 127 | Total | C | N | O | 0 | 0 | 0 |
| | | | 1010 | 639 | 197 | 174 | | | |

- Molecule 10 is a protein called 30S ribosomal protein S10.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 10 | J | 98 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 792 | 498 | 156 | 137 | 1 | | | |

- Molecule 11 is a protein called 30S ribosomal protein S11.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 11 | K | 116 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 864 | 537 | 164 | 160 | 3 | | | |

- Molecule 12 is a protein called 30S ribosomal protein S12.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 12 | L | 124 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 972 | 612 | 195 | 163 | 2 | | | |

- Molecule 13 is a protein called 30S ribosomal protein S13.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 13 | M | 118 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 937 | 579 | 193 | 163 | 2 | | | |

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|---------|-------|
| 14 | N | 60 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 492 | 312 | 104 | 72 | 4 | | | |

- Molecule 15 is a protein called 30S ribosomal protein S15.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 15 | O | 87 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 729 | 457 | 146 | 124 | 2 | | | |

- Molecule 16 is a protein called 30S ribosomal protein S16.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 16 | P | 83 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 700 | 443 | 139 | 117 | 1 | | | |

- Molecule 17 is a protein called 30S ribosomal protein S17.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 17 | Q | 99 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 823 | 528 | 152 | 141 | 2 | | | |

- Molecule 18 is a protein called 30S ribosomal protein S18.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---------|---------|-------|
| 18 | R | 70 | Total | C | N | O | 0 | 0 | 0 |
| | | | 574 | 367 | 112 | 95 | | | |

- Molecule 19 is a protein called 30S ribosomal protein S19.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 19 | S | 80 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 647 | 414 | 119 | 112 | 2 | | | |

- Molecule 20 is a protein called 30S ribosomal protein S20.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 20 | T | 99 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 763 | 470 | 162 | 129 | 2 | | | |

- Molecule 21 is a protein called 30S ribosomal protein Thx.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|---------|-------|
| 21 | U | 24 | Total | C | N | O | 0 | 0 | 0 |
| | | | 208 | 128 | 50 | 30 | | | |

- Molecule 22 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|-----|---------|---------|
| 22 | A | 234 | Total | Mg | 0 | 0 |
| | | | 234 | 234 | | |
| 22 | B | 3 | Total | Mg | 0 | 0 |
| | | | 3 | 3 | | |
| 22 | C | 3 | Total | Mg | 0 | 0 |
| | | | 3 | 3 | | |
| 22 | D | 4 | Total | Mg | 0 | 0 |
| | | | 4 | 4 | | |
| 22 | E | 1 | Total | Mg | 0 | 0 |
| | | | 1 | 1 | | |
| 22 | F | 1 | Total | Mg | 0 | 0 |
| | | | 1 | 1 | | |
| 22 | I | 1 | Total | Mg | 0 | 0 |
| | | | 1 | 1 | | |
| 22 | P | 2 | Total | Mg | 0 | 0 |
| | | | 2 | 2 | | |
| 22 | Q | 2 | Total | Mg | 0 | 0 |
| | | | 2 | 2 | | |
| 22 | S | 2 | Total | Mg | 0 | 0 |
| | | | 2 | 2 | | |
| 22 | U | 1 | Total | Mg | 0 | 0 |
| | | | 1 | 1 | | |

- Molecule 23 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|---------|---------|
| 23 | D | 1 | Total | Zn | 0 | 0 |
| | | | 1 | 1 | | |
| 23 | N | 1 | Total | Zn | 0 | 0 |
| | | | 1 | 1 | | |

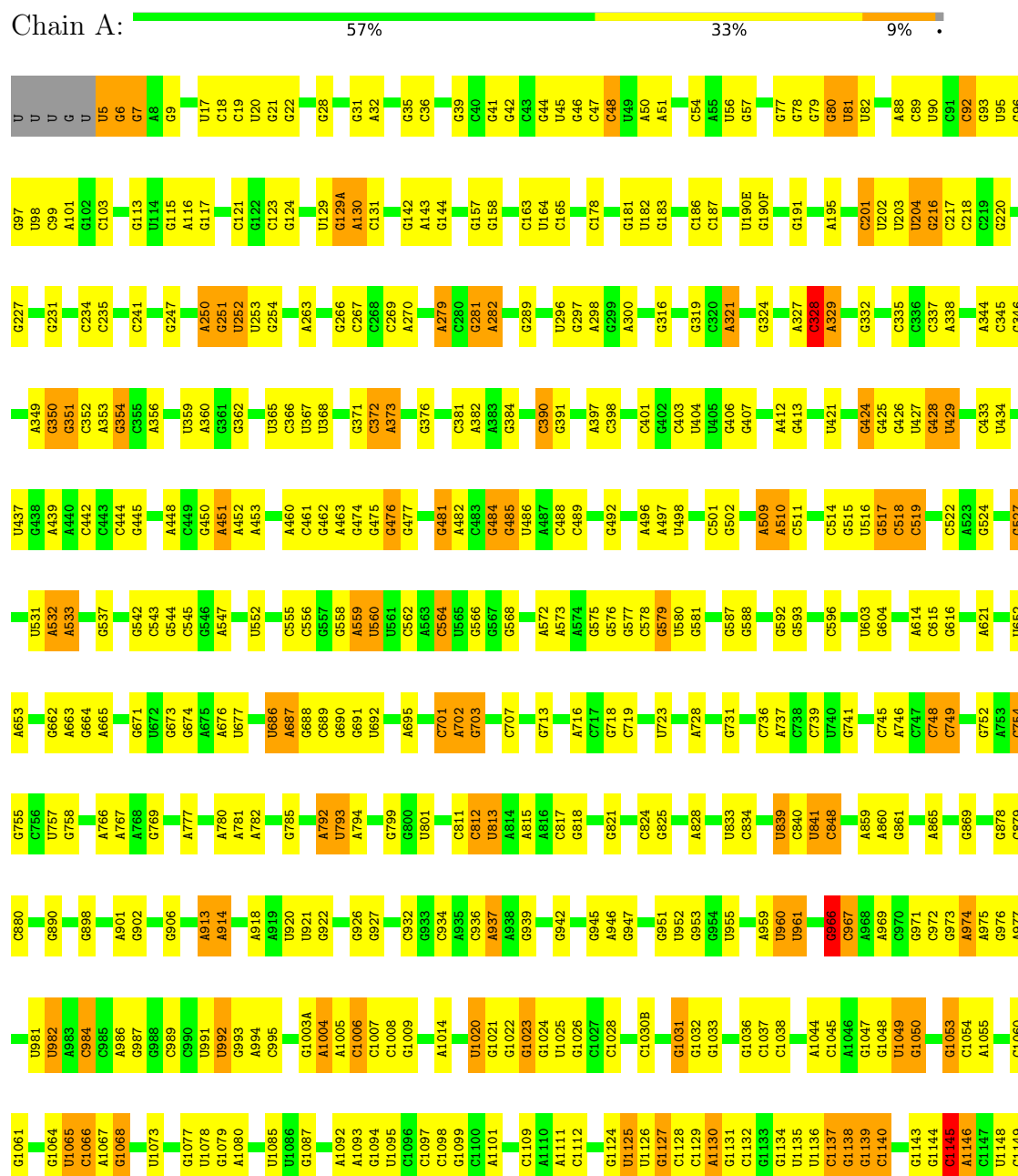
- Molecule 24 is water.

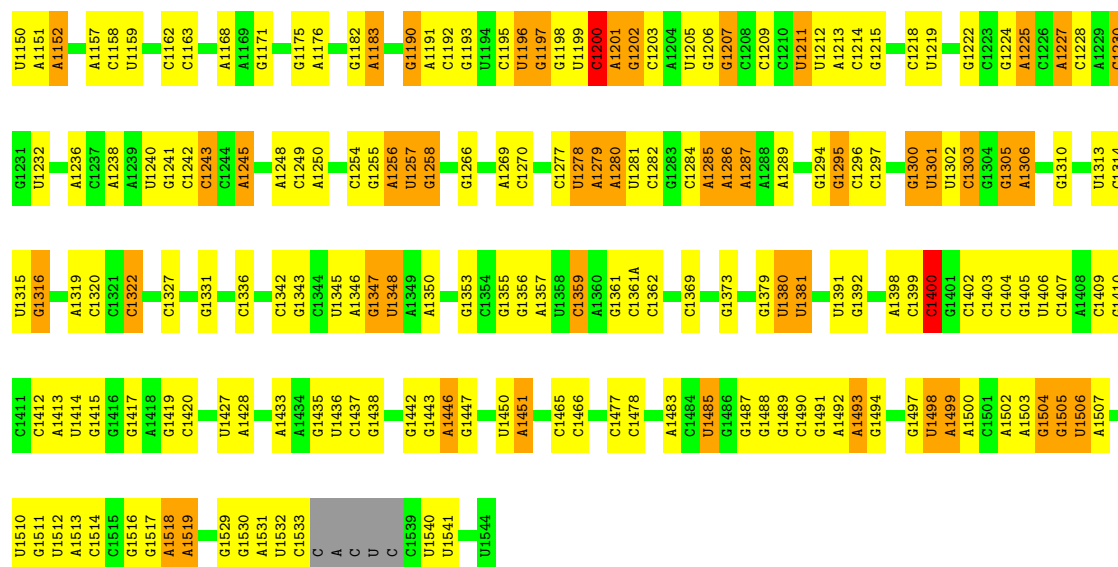
| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|--------------|----------|---------|---------|
| 24 | A | 225 | Total 225 | O 225 | 0 | 0 |
| 24 | D | 2 | Total 2 | O 2 | 0 | 0 |
| 24 | E | 5 | Total 5 | O 5 | 0 | 0 |
| 24 | L | 2 | Total 2 | O 2 | 0 | 0 |
| 24 | N | 1 | Total 1 | O 1 | 0 | 0 |
| 24 | Q | 2 | Total 2 | O 2 | 0 | 0 |
| 24 | T | 2 | Total 2 | O 2 | 0 | 0 |

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

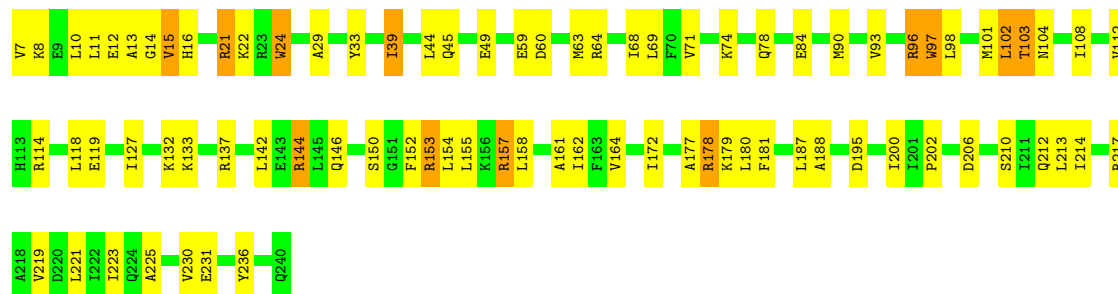
• Molecule 1: 16S Ribosomal RNA rRNA





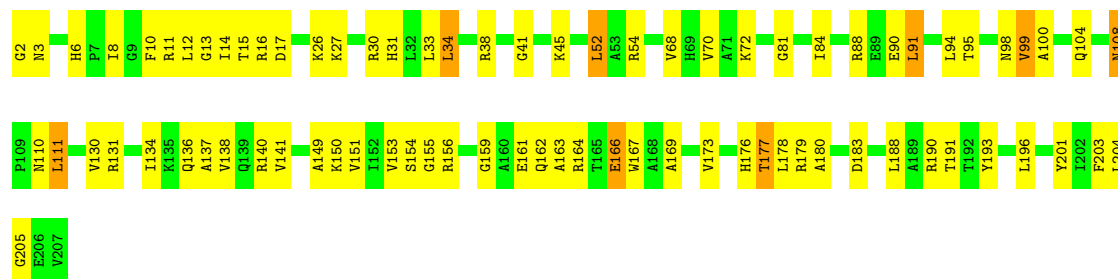
• Molecule 2: 30S ribosomal protein S2

Chain B: 65% 30% 5%



• Molecule 3: 30S ribosomal protein S3

Chain C: 62% 34% 4%



• Molecule 4: 30S ribosomal protein S4

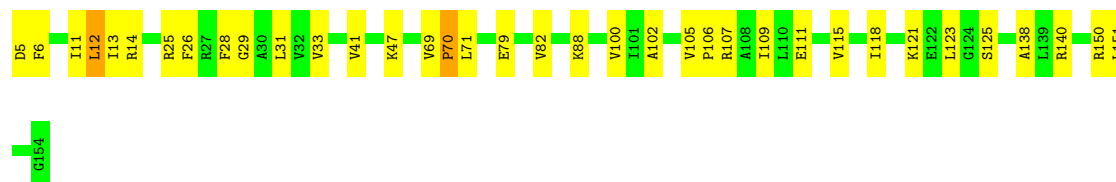
Chain D: 68% 29% 3%





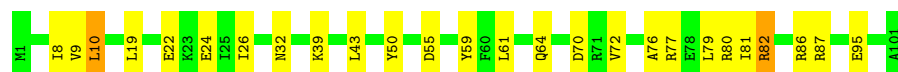
- Molecule 5: 30S ribosomal protein S5

Chain E: 76% 23%



- Molecule 6: 30S ribosomal protein S6

Chain F: 74% 24%



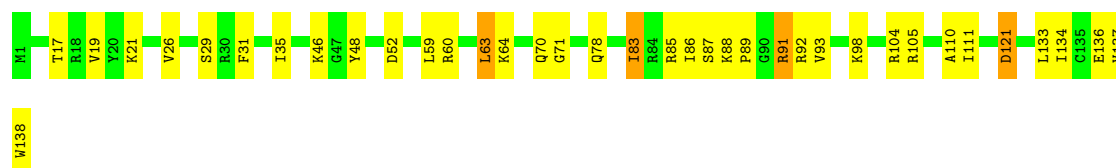
- Molecule 7: 30S ribosomal protein S7

Chain G: 80% 17%



- Molecule 8: 30S ribosomal protein S8

Chain H: 73% 24%

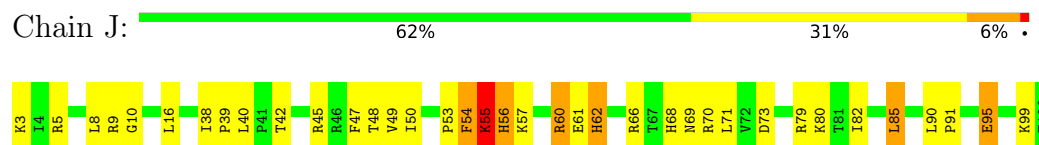


- Molecule 9: 30S ribosomal protein S9

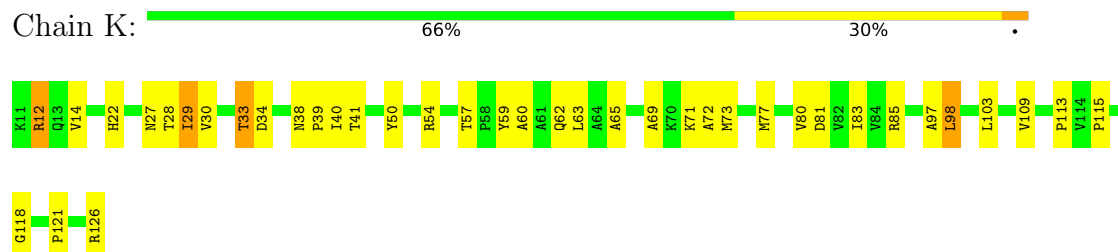
Chain I: 61% 33% 6%



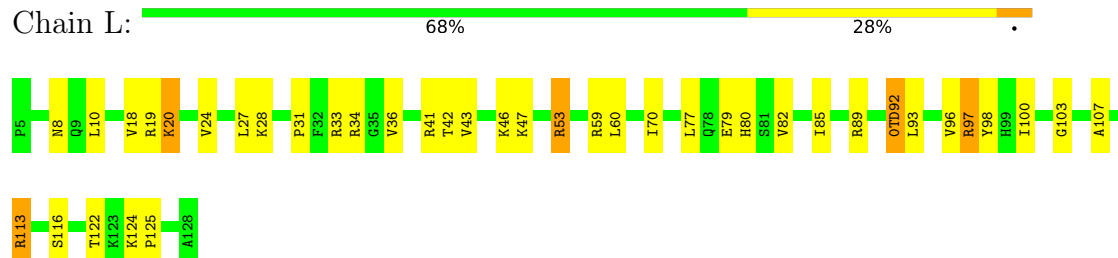
- Molecule 10: 30S ribosomal protein S10



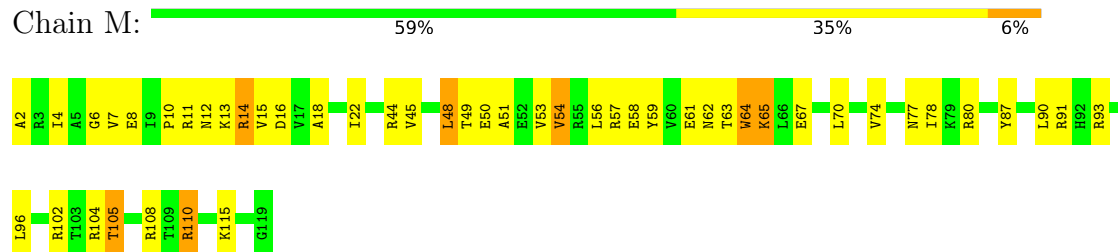
- Molecule 11: 30S ribosomal protein S11



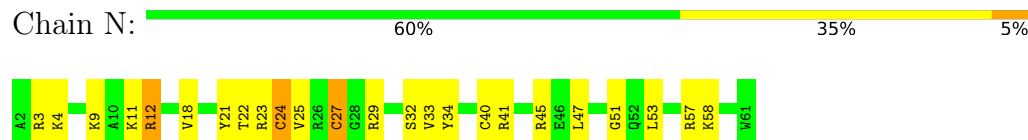
- Molecule 12: 30S ribosomal protein S12



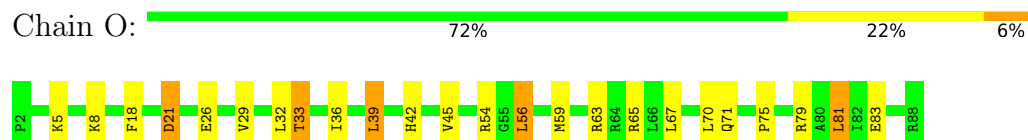
- Molecule 13: 30S ribosomal protein S13




- Molecule 14: 30S ribosomal protein S14 type Z



- Molecule 15: 30S ribosomal protein S15




- Molecule 16: 30S ribosomal protein S16

Chain P:  78% 18% .




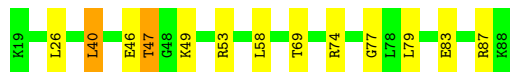
- Molecule 17: 30S ribosomal protein S17

Chain Q:  79% 21%



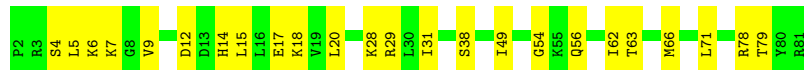
- Molecule 18: 30S ribosomal protein S18

Chain R:  81% 16% .



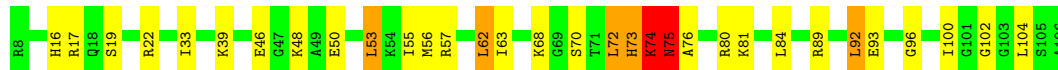
- Molecule 19: 30S ribosomal protein S19

Chain S:  70% 30%



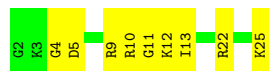
- Molecule 20: 30S ribosomal protein S20

Chain T:  68% 25% 5% .



- Molecule 21: 30S ribosomal protein Thx

Chain U:  63% 38%



4 Data and refinement statistics

| Property | Value | Source |
|---|---|------------------|
| Space group | P 41 21 2 | Depositor |
| Cell constants a, b, c, α , β , γ | 400.00Å 400.00Å 173.00Å 90.00° 90.00° 90.00° | Depositor |
| Resolution (Å) | 29.98 – 3.50 39.78 – 2.92 | Depositor EDS |
| % Data completeness (in resolution range) | 91.5 (29.98-3.50) 71.0 (39.78-2.92) | Depositor EDS |
| R_{merge} | 1.18 | Depositor |
| R_{sym} | (Not available) | Depositor |
| $\langle I/\sigma(I) \rangle$ ¹ | 0.46 (at 2.90Å) | Xtriage |
| Refinement program | PHENIX | Depositor |
| R, R_{free} | 0.214 , 0.256 0.217 , 0.256 | Depositor DCC |
| R_{free} test set | 2000 reflections (0.67%) | wwPDB-VP |
| Wilson B-factor (Å ²) | 58.0 | Xtriage |
| Anisotropy | 0.303 | Xtriage |
| Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²) | 0.07 , -10.0 | EDS |
| L-test for twinning ² | $\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$ | Xtriage |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| F_o, F_c correlation | 0.90 | EDS |
| Total number of atoms | 52227 | wwPDB-VP |
| Average B, all atoms (Å ²) | 232.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.56% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: M2G, 0TD, ZN, MG, PSU, 5MC, UR3, 2MG, 4OC, MA6, 7MG

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 | 0.19 | 0/36139 | 0.80 | 22/56396 (0.0%) |
| 2 | B | 0.25 | 0/1935 | 0.43 | 0/2609 |
| 3 | C | 0.25 | 0/1636 | 0.47 | 0/2205 |
| 4 | D | 0.24 | 0/1733 | 0.40 | 0/2318 |
| 5 | E | 0.25 | 0/1162 | 0.45 | 0/1564 |
| 6 | F | 0.23 | 0/856 | 0.43 | 0/1154 |
| 7 | G | 0.24 | 0/1276 | 0.40 | 0/1709 |
| 8 | H | 0.24 | 0/1136 | 0.46 | 0/1527 |
| 9 | I | 0.26 | 0/1029 | 0.45 | 0/1379 |
| 10 | J | 0.25 | 0/805 | 0.52 | 0/1082 |
| 11 | K | 0.26 | 0/879 | 0.47 | 0/1187 |
| 12 | L | 0.25 | 0/977 | 0.51 | 0/1306 |
| 13 | M | 0.23 | 0/947 | 0.45 | 0/1270 |
| 14 | N | 0.25 | 0/501 | 0.46 | 0/664 |
| 15 | O | 0.24 | 0/740 | 0.39 | 0/987 |
| 16 | P | 0.24 | 0/716 | 0.44 | 0/963 |
| 17 | Q | 0.24 | 0/836 | 0.46 | 0/1117 |
| 18 | R | 0.24 | 0/579 | 0.44 | 0/768 |
| 19 | S | 0.24 | 0/661 | 0.51 | 0/890 |
| 20 | T | 0.25 | 0/765 | 0.43 | 0/1007 |
| 21 | U | 0.22 | 0/212 | 0.42 | 0/277 |
| All | All | 0.21 | 0/55520 | 0.71 | 22/82379 (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 outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 2 | B | 0 | 1 |
| 3 | C | 0 | 1 |

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| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 10 | J | 0 | 2 |
| 13 | M | 0 | 1 |
| 14 | N | 0 | 1 |
| 20 | T | 0 | 1 |
| All | All | 0 | 7 |

There are no bond length outliers.

The worst 5 of 22 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|-----------|-------|-------------|----------|
| 1 | A | 328 | C | C2-N1-C1' | 7.91 | 127.50 | 118.80 |
| 1 | A | 1139 | G | P-O3'-C3' | 7.69 | 128.93 | 119.70 |
| 1 | A | 1127 | G | N1-C6-O6 | -7.66 | 115.30 | 119.90 |
| 1 | A | 328 | C | N1-C2-O2 | 7.39 | 123.33 | 118.90 |
| 1 | A | 1127 | G | C5-C6-O6 | 7.22 | 132.93 | 128.60 |

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 2 | B | 15 | VAL | Peptide |
| 3 | C | 166 | GLU | Peptide |
| 10 | J | 54 | PHE | Peptide |
| 10 | J | 55 | LYS | Peptide |
| 13 | M | 6 | GLY | 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 | 32644 | 0 | 16507 | 384 | 2 |
| 2 | B | 1900 | 0 | 1951 | 43 | 0 |
| 3 | C | 1612 | 0 | 1677 | 49 | 0 |
| 4 | D | 1703 | 0 | 1763 | 43 | 0 |
| 5 | E | 1146 | 0 | 1207 | 19 | 0 |
| 6 | F | 843 | 0 | 857 | 13 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 7 | G | 1257 | 0 | 1296 | 18 | 0 |
| 8 | H | 1116 | 0 | 1177 | 21 | 0 |
| 9 | I | 1010 | 0 | 1037 | 32 | 0 |
| 10 | J | 792 | 0 | 835 | 24 | 0 |
| 11 | K | 864 | 0 | 881 | 25 | 0 |
| 12 | L | 972 | 0 | 1058 | 23 | 0 |
| 13 | M | 937 | 0 | 995 | 31 | 0 |
| 14 | N | 492 | 0 | 529 | 23 | 0 |
| 15 | O | 729 | 0 | 768 | 10 | 0 |
| 16 | P | 700 | 0 | 720 | 12 | 0 |
| 17 | Q | 823 | 0 | 893 | 11 | 0 |
| 18 | R | 574 | 0 | 644 | 9 | 0 |
| 19 | S | 647 | 0 | 673 | 14 | 0 |
| 20 | T | 763 | 0 | 861 | 19 | 0 |
| 21 | U | 208 | 0 | 221 | 10 | 0 |
| 22 | A | 234 | 0 | 0 | 0 | 0 |
| 22 | B | 3 | 0 | 0 | 0 | 0 |
| 22 | C | 3 | 0 | 0 | 0 | 0 |
| 22 | D | 4 | 0 | 0 | 0 | 0 |
| 22 | E | 1 | 0 | 0 | 0 | 0 |
| 22 | F | 1 | 0 | 0 | 0 | 0 |
| 22 | I | 1 | 0 | 0 | 0 | 0 |
| 22 | P | 2 | 0 | 0 | 0 | 0 |
| 22 | Q | 2 | 0 | 0 | 0 | 0 |
| 22 | S | 2 | 0 | 0 | 0 | 0 |
| 22 | U | 1 | 0 | 0 | 0 | 0 |
| 23 | D | 1 | 0 | 0 | 0 | 0 |
| 23 | N | 1 | 0 | 0 | 0 | 0 |
| 24 | A | 225 | 0 | 0 | 1 | 0 |
| 24 | D | 2 | 0 | 0 | 0 | 0 |
| 24 | E | 5 | 0 | 0 | 0 | 0 |
| 24 | L | 2 | 0 | 0 | 1 | 0 |
| 24 | N | 1 | 0 | 0 | 0 | 0 |
| 24 | Q | 2 | 0 | 0 | 0 | 0 |
| 24 | T | 2 | 0 | 0 | 0 | 0 |
| All | All | 52227 | 0 | 36550 | 722 | 2 |

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 8.

The worst 5 of 722 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) |
|-------------------|----------------|--------------------------|-------------------|
| 1:A:664:G:H22 | 1:A:741:G:H1 | 1.23 | 0.86 |
| 20:T:100:ILE:HG22 | 20:T:102:GLY:H | 1.41 | 0.86 |
| 1:A:1443:G:H5'' | 1:A:1446:A:H5' | 1.57 | 0.85 |
| 1:A:1125:U:OP2 | 1:A:1145:C:N4 | 2.11 | 0.81 |
| 1:A:1347:G:O6 | 9:I:10:ARG:NH2 | 2.12 | 0.81 |

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|-------------|------------------------|--------------------------|-------------------|
| 1:A:82:U:O2 | 1:A:1400:5MC:C2[3_545] | 1.99 | 0.21 |
| 1:A:82:U:O2 | 1:A:1400:5MC:C4[3_545] | 2.11 | 0.09 |

5.3 Torsion angles ⓘ

5.3.1 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 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 | |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 2 | B | 232/234 (99%) | 213 (92%) | 18 (8%) | 1 (0%) | 34 | 72 |
| 3 | C | 204/206 (99%) | 188 (92%) | 16 (8%) | 0 | 100 | 100 |
| 4 | D | 206/208 (99%) | 202 (98%) | 4 (2%) | 0 | 100 | 100 |
| 5 | E | 148/150 (99%) | 143 (97%) | 5 (3%) | 0 | 100 | 100 |
| 6 | F | 99/101 (98%) | 98 (99%) | 1 (1%) | 0 | 100 | 100 |
| 7 | G | 153/155 (99%) | 149 (97%) | 4 (3%) | 0 | 100 | 100 |
| 8 | H | 136/138 (99%) | 134 (98%) | 2 (2%) | 0 | 100 | 100 |
| 9 | I | 125/127 (98%) | 115 (92%) | 10 (8%) | 0 | 100 | 100 |
| 10 | J | 96/98 (98%) | 80 (83%) | 13 (14%) | 3 (3%) | 4 | 30 |
| 11 | K | 114/116 (98%) | 108 (95%) | 6 (5%) | 0 | 100 | 100 |
| 12 | L | 121/124 (98%) | 109 (90%) | 12 (10%) | 0 | 100 | 100 |
| 13 | M | 116/118 (98%) | 105 (90%) | 11 (10%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-----------------|------------|----------|----------|-------------|-----|
| 14 | N | 58/60 (97%) | 49 (84%) | 9 (16%) | 0 | 100 | 100 |
| 15 | O | 85/87 (98%) | 83 (98%) | 2 (2%) | 0 | 100 | 100 |
| 16 | P | 81/83 (98%) | 79 (98%) | 2 (2%) | 0 | 100 | 100 |
| 17 | Q | 97/99 (98%) | 94 (97%) | 3 (3%) | 0 | 100 | 100 |
| 18 | R | 68/70 (97%) | 68 (100%) | 0 | 0 | 100 | 100 |
| 19 | S | 78/80 (98%) | 72 (92%) | 6 (8%) | 0 | 100 | 100 |
| 20 | T | 97/99 (98%) | 84 (87%) | 10 (10%) | 3 (3%) | 4 | 30 |
| 21 | U | 22/24 (92%) | 21 (96%) | 1 (4%) | 0 | 100 | 100 |
| All | All | 2336/2377 (98%) | 2194 (94%) | 135 (6%) | 7 (0%) | 41 | 75 |

5 of 7 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 10 | J | 55 | LYS |
| 20 | T | 74 | LYS |
| 20 | T | 75 | ASN |
| 10 | J | 56 | HIS |
| 20 | T | 73 | HIS |

5.3.2 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 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 | |
|-----|-------|----------------|-----------|----------|-------------|----|
| 2 | B | 202/202 (100%) | 175 (87%) | 27 (13%) | 4 | 21 |
| 3 | C | 160/160 (100%) | 136 (85%) | 24 (15%) | 3 | 17 |
| 4 | D | 180/180 (100%) | 169 (94%) | 11 (6%) | 18 | 51 |
| 5 | E | 115/115 (100%) | 104 (90%) | 11 (10%) | 8 | 34 |
| 6 | F | 90/90 (100%) | 82 (91%) | 8 (9%) | 9 | 37 |
| 7 | G | 126/126 (100%) | 116 (92%) | 10 (8%) | 12 | 41 |
| 8 | H | 119/119 (100%) | 109 (92%) | 10 (8%) | 11 | 40 |
| 9 | I | 98/98 (100%) | 82 (84%) | 16 (16%) | 2 | 13 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles |
|-----|-------|------------------|------------|-----------|-------------|
| 10 | J | 87/88 (99%) | 77 (88%) | 10 (12%) | 5 26 |
| 11 | K | 88/88 (100%) | 83 (94%) | 5 (6%) | 20 53 |
| 12 | L | 103/103 (100%) | 88 (85%) | 15 (15%) | 3 18 |
| 13 | M | 94/94 (100%) | 77 (82%) | 17 (18%) | 1 9 |
| 14 | N | 49/49 (100%) | 43 (88%) | 6 (12%) | 5 23 |
| 15 | O | 79/79 (100%) | 66 (84%) | 13 (16%) | 2 13 |
| 16 | P | 72/72 (100%) | 65 (90%) | 7 (10%) | 8 33 |
| 17 | Q | 94/94 (100%) | 89 (95%) | 5 (5%) | 22 55 |
| 18 | R | 61/61 (100%) | 57 (93%) | 4 (7%) | 16 49 |
| 19 | S | 71/71 (100%) | 65 (92%) | 6 (8%) | 10 39 |
| 20 | T | 76/76 (100%) | 65 (86%) | 11 (14%) | 3 18 |
| 21 | U | 19/19 (100%) | 18 (95%) | 1 (5%) | 22 55 |
| All | All | 1983/1984 (100%) | 1766 (89%) | 217 (11%) | 6 29 |

5 of 217 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 9 | I | 113 | LYS |
| 12 | L | 96 | VAL |
| 19 | S | 15 | LEU |
| 10 | J | 45 | ARG |
| 11 | K | 81 | ASP |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2 | B | 204 | ASN |
| 2 | B | 212 | GLN |
| 9 | I | 3 | GLN |
| 16 | P | 82 | GLN |

5.3.3 RNA ⓘ

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 1 | A | 1504/1522 (98%) | 255 (16%) | 46 (3%) |

5 of 255 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 6 | G |
| 1 | A | 7 | G |
| 1 | A | 9 | G |
| 1 | A | 32 | A |
| 1 | A | 39 | G |

5 of 46 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 1 | A | 1067 | A |
| 1 | A | 1201 | A |
| 1 | A | 1126 | U |
| 1 | A | 1145 | C |
| 1 | A | 1257 | U |

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

17 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|---------|------|--------------|------|-------------|-------------|------|-------------|
| | | | | | Counts | RMSZ | # $ Z > 2$ | Counts | RMSZ | # $ Z > 2$ |
| 12 | 0TD | L | 92 | 12 | 7,9,10 | 1.06 | 0 | 6,11,13 | 2.24 | 2 (33%) |
| 1 | 5MC | A | 967 | 1 | 18,22,23 | 1.06 | 2 (11%) | 26,32,35 | 0.95 | 1 (3%) |
| 1 | 2MG | A | 1207 | 1 | 18,26,27 | 1.30 | 4 (22%) | 16,38,41 | 1.41 | 2 (12%) |
| 1 | 5MC | A | 1407 | 1 | 18,22,23 | 1.04 | 2 (11%) | 26,32,35 | 0.95 | 2 (7%) |
| 1 | MA6 | A | 1518[B] | 1 | 18,26,27 | 0.65 | 0 | 19,38,41 | 0.91 | 1 (5%) |
| 1 | MA6 | A | 1519[B] | 1 | 18,26,27 | 0.66 | 0 | 19,38,41 | 0.91 | 1 (5%) |
| 1 | PSU | A | 1541 | 1 | 18,21,22 | 2.01 | 7 (38%) | 22,30,33 | 1.42 | 4 (18%) |
| 1 | 7MG | A | 527 | 1 | 22,26,27 | 5.09 | 4 (18%) | 29,39,42 | 2.10 | 9 (31%) |
| 1 | 4OC | A | 1402 | 1 | 20,23,24 | 1.00 | 2 (10%) | 26,32,35 | 0.72 | 1 (3%) |
| 1 | UR3 | A | 1498 | 1 | 19,22,23 | 0.72 | 1 (5%) | 26,32,35 | 1.03 | 1 (3%) |
| 1 | PSU | A | 516 | 1 | 18,21,22 | 2.00 | 7 (38%) | 22,30,33 | 1.42 | 4 (18%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|---------|------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 1 | M2G | A | 966 | 1 | 20,27,28 | 1.42 | 4 (20%) | 22,40,43 | 1.33 | 3 (13%) |
| 1 | MA6 | A | 1518[A] | 1 | 18,26,27 | 0.63 | 0 | 19,38,41 | 0.87 | 1 (5%) |
| 1 | MA6 | A | 1519[A] | 1 | 18,26,27 | 0.66 | 0 | 19,38,41 | 0.95 | 1 (5%) |
| 1 | PSU | A | 1540 | 1 | 18,21,22 | 1.99 | 6 (33%) | 22,30,33 | 1.47 | 4 (18%) |
| 1 | 5MC | A | 1404 | 1 | 18,22,23 | 1.04 | 2 (11%) | 26,32,35 | 0.98 | 2 (7%) |
| 1 | 5MC | A | 1400 | 1 | 18,22,23 | 1.07 | 2 (11%) | 26,32,35 | 0.95 | 2 (7%) |

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|---------|------|---------|-----------|---------|
| 12 | 0TD | L | 92 | 12 | - | 2/7/12/14 | - |
| 1 | 5MC | A | 967 | 1 | - | 2/7/25/26 | 0/2/2/2 |
| 1 | 2MG | A | 1207 | 1 | - | 2/5/27/28 | 0/3/3/3 |
| 1 | 5MC | A | 1407 | 1 | - | 0/7/25/26 | 0/2/2/2 |
| 1 | MA6 | A | 1518[B] | 1 | - | 0/7/29/30 | 0/3/3/3 |
| 1 | MA6 | A | 1519[B] | 1 | - | 0/7/29/30 | 0/3/3/3 |
| 1 | PSU | A | 1541 | 1 | - | 1/7/25/26 | 0/2/2/2 |
| 1 | 7MG | A | 527 | 1 | - | 2/7/37/38 | 0/3/3/3 |
| 1 | 4OC | A | 1402 | 1 | - | 2/9/29/30 | 0/2/2/2 |
| 1 | UR3 | A | 1498 | 1 | - | 0/7/25/26 | 0/2/2/2 |
| 1 | PSU | A | 516 | 1 | - | 0/7/25/26 | 0/2/2/2 |
| 1 | M2G | A | 966 | 1 | - | 3/7/29/30 | 0/3/3/3 |
| 1 | MA6 | A | 1518[A] | 1 | - | 1/7/29/30 | 0/3/3/3 |
| 1 | MA6 | A | 1519[A] | 1 | - | 1/7/29/30 | 0/3/3/3 |
| 1 | PSU | A | 1540 | 1 | - | 0/7/25/26 | 0/2/2/2 |
| 1 | 5MC | A | 1404 | 1 | - | 0/7/25/26 | 0/2/2/2 |
| 1 | 5MC | A | 1400 | 1 | - | 2/7/25/26 | 0/2/2/2 |

The worst 5 of 43 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|-------|--------|-------------|----------|
| 1 | A | 527 | 7MG | C8-N9 | -23.12 | 1.33 | 1.46 |
| 1 | A | 527 | 7MG | C2-N2 | 3.79 | 1.43 | 1.34 |
| 1 | A | 1540 | PSU | C2-N1 | -3.60 | 1.31 | 1.36 |
| 1 | A | 1541 | PSU | C2-N1 | -3.58 | 1.31 | 1.36 |
| 1 | A | 1541 | PSU | C6-C5 | 3.57 | 1.39 | 1.35 |

The worst 5 of 41 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|-----------|-------|-------------|----------|
| 1 | A | 527 | 7MG | C5-C6-N1 | 4.93 | 119.67 | 110.99 |
| 1 | A | 527 | 7MG | C2-N3-C4 | 4.56 | 120.42 | 112.30 |
| 1 | A | 527 | 7MG | N9-C4-N3 | 4.28 | 131.88 | 125.47 |
| 12 | L | 92 | 0TD | CSB-SB-CB | -4.06 | 95.10 | 102.44 |
| 1 | A | 1207 | 2MG | O6-C6-N1 | -4.04 | 115.88 | 120.65 |

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|-----|-------|---------|------|-----------------|
| 1 | A | 527 | 7MG | C3'-C4'-C5'-O5' |
| 1 | A | 1207 | 2MG | O4'-C4'-C5'-O5' |
| 1 | A | 1400 | 5MC | O4'-C4'-C5'-O5' |
| 1 | A | 1518[A] | MA6 | C5-C6-N6-C10 |
| 1 | A | 1207 | 2MG | C3'-C4'-C5'-O5' |

There are no ring outliers.

9 monomers are involved in 16 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|---------|------|---------|--------------|
| 12 | L | 92 | 0TD | 2 | 0 |
| 1 | A | 967 | 5MC | 2 | 0 |
| 1 | A | 1518[B] | MA6 | 1 | 0 |
| 1 | A | 1519[B] | MA6 | 2 | 0 |
| 1 | A | 1498 | UR3 | 4 | 0 |
| 1 | A | 966 | M2G | 1 | 0 |
| 1 | A | 1518[A] | MA6 | 3 | 0 |
| 1 | A | 1519[A] | MA6 | 1 | 0 |
| 1 | A | 1400 | 5MC | 1 | 2 |

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 256 ligands modelled in this entry, 256 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.