



wwPDB EM Validation Summary Report ⓘ

Dec 4, 2023 – 12:00 PM EST

PDB ID : 7MPJ
EMDB ID : EMD-23935
Title : Stm1 bound vacant 80S structure isolated from wild-type
Authors : Rai, J.; Zhao, Y.; Li, H.
Deposited on : 2021-05-04
Resolution : 2.70 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp>

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:

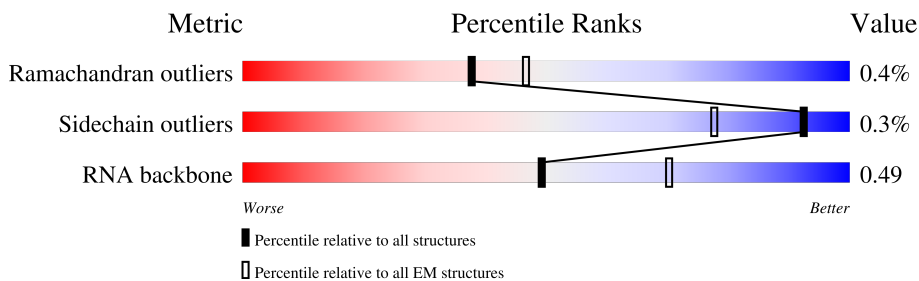
EMDB validation analysis : 0.0.1.dev70
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 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) | EM structures (#Entries) |
|-----------------------|-----------------------------|-----------------------------|
| Ramachandran outliers | 154571 | 4023 |
| Sidechain outliers | 154315 | 3826 |
| RNA backbone | 4643 | 859 |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | BA | 206 | |
| 2 | BB | 214 | |
| 3 | BC | 217 | |
| 4 | BD | 223 | |
| 5 | BE | 260 | |
| 6 | BF | 206 | |
| 7 | BG | 226 | |
| 8 | BH | 184 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 9 | BI | 188 | 11% 99% |
| 10 | BJ | 185 | 8% 97% |
| 11 | BK | 96 | 14% 96% |
| 12 | BL | 155 | 19% 99% |
| 13 | BM | 121 | 97% 99% |
| 14 | BN | 150 | 10% 98% |
| 15 | BO | 127 | 6% 98% |
| 16 | BP | 124 | 18% 98% |
| 17 | BQ | 141 | 97% 97% |
| 18 | BR | 121 | 31% 98% |
| 19 | BS | 145 | 9% 93% 7% |
| 20 | BT | 141 | 99% 99% |
| 21 | BU | 107 | 25% 99% |
| 22 | BV | 87 | 6% 100% |
| 23 | BW | 129 | 99% 99% |
| 24 | BX | 144 | 97% 97% |
| 25 | BY | 134 | 10% 97% |
| 26 | BZ | 69 | 12% 99% |
| 27 | Ba | 97 | 6% 94% 5% |
| 28 | Bb | 81 | 16% 100% |
| 29 | Bc | 63 | 14% 97% |
| 30 | Bd | 53 | 6% 96% |
| 31 | Be | 60 | 27% 97% |
| 32 | Bf | 57 | 100% 100% |
| 33 | Bg | 312 | 9% 98% |

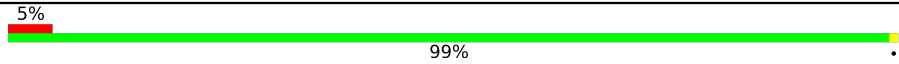

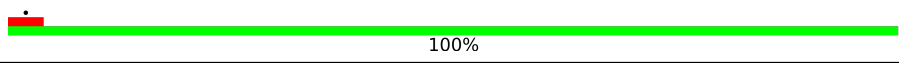
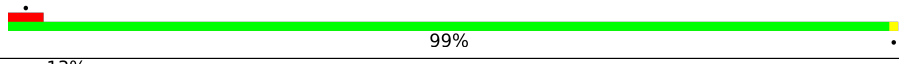
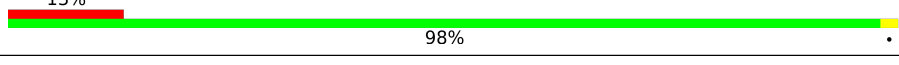
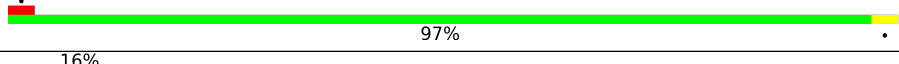
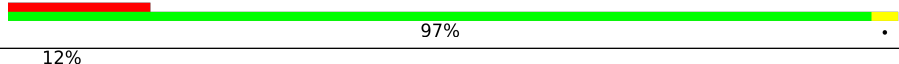
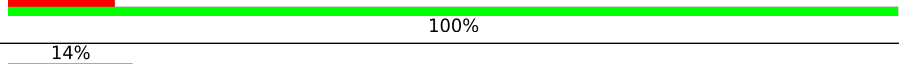
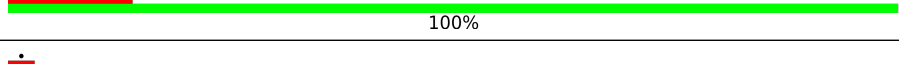
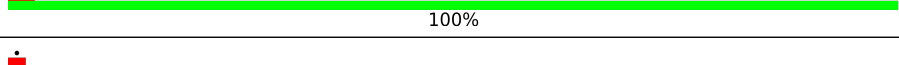
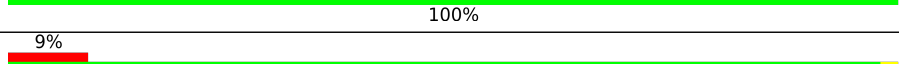
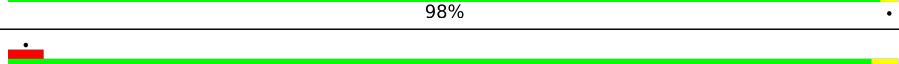
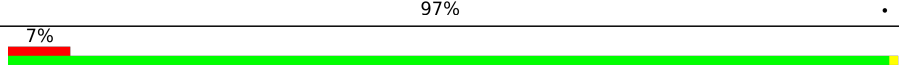
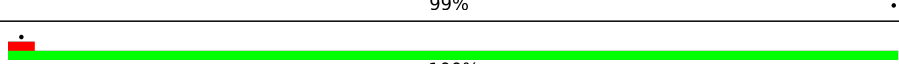
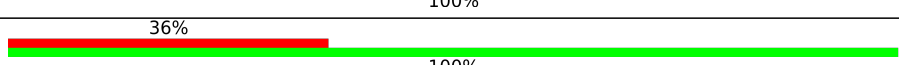
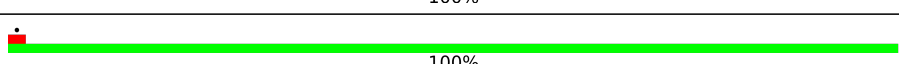
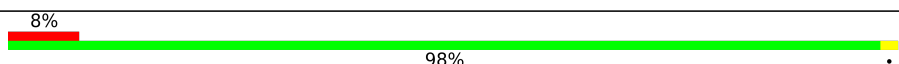
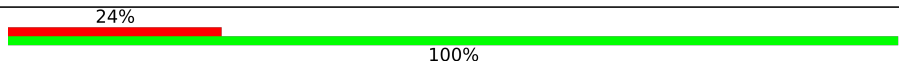
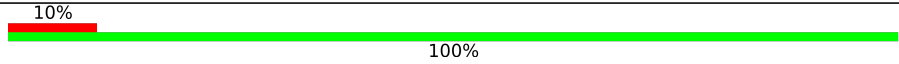
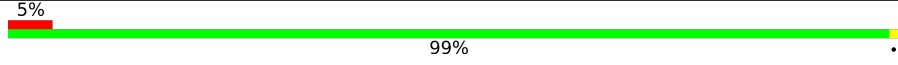

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|-------------------|
| 34 | Bh | 89 | 66% 97% |
| 35 | B5 | 1781 | 14% 67% 30% |
| 36 | A1 | 3137 | 9% 71% 26% |
| 37 | A3 | 121 | 84% 15% |
| 38 | A4 | 158 | 71% 28% |
| 39 | AA | 247 | 100% |
| 40 | AB | 386 | 98% |
| 41 | AC | 361 | 98% |
| 42 | AD | 292 | 16% 98% |
| 43 | AE | 156 | 12% 98% |
| 44 | AF | 222 | 98% |
| 45 | AG | 230 | 10% 97% |
| 46 | AH | 190 | 6% 99% |
| 47 | AI | 205 | 11% 99% |
| 48 | AJ | 169 | 36% 98% |
| 49 | AL | 193 | 11% 97% |
| 50 | AM | 136 | 6% 100% |
| 51 | AN | 203 | 99% |
| 52 | AO | 197 | 98% |
| 53 | AP | 175 | 9% 99% |
| 54 | AQ | 185 | 99% |
| 55 | AR | 188 | 22% 99% |
| 56 | AS | 172 | 99% |
| 57 | AT | 159 | 9% 99% |
| 58 | AU | 100 | 21% 98% |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|---|
| 59 | AV | 136 |  5% 99% |
| 60 | AW | 63 |  5% 100% |
| 61 | AX | 121 |  100% |
| 62 | AY | 126 |  99% |
| 63 | AZ | 135 |  13% 98% |
| 64 | Aa | 148 |  97% |
| 65 | Ab | 58 |  16% 97% |
| 66 | Ac | 97 |  12% 100% |
| 67 | Ad | 109 |  14% 100% |
| 68 | Ae | 127 |  100% |
| 69 | Af | 106 |  100% |
| 70 | Ag | 112 |  9% 98% |
| 71 | Ah | 119 |  97% |
| 72 | Ai | 99 |  7% 99% |
| 73 | Aj | 87 |  100% |
| 74 | Ak | 77 |  36% 100% |
| 75 | Al | 50 |  100% |
| 76 | Am | 52 |  8% 98% |
| 77 | An | 25 |  24% 100% |
| 78 | Ao | 105 |  10% 100% |
| 79 | Ap | 91 |  5% 99% |

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

| Mol | Type | Chain | Res | Chirality | Geometry | Clashes | Electron density |
|-----|------|-------|------|-----------|----------|---------|------------------|
| 35 | G7M | B5 | 1575 | X | - | - | - |

2 Entry composition [i](#)

There are 81 unique types of molecules in this entry. The entry contains 199813 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 40S ribosomal protein S0-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 1 | BA | 206 | 1612 | 1034 | 285 | 291 | 2 | 0 | 0 |

- Molecule 2 is a protein called 40S ribosomal protein S1-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 2 | BB | 214 | 1709 | 1084 | 310 | 311 | 4 | 0 | 0 |

- Molecule 3 is a protein called 40S ribosomal protein S2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 3 | BC | 217 | 1635 | 1047 | 289 | 297 | 2 | 0 | 0 |

- Molecule 4 is a protein called 40S ribosomal protein S3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 4 | BD | 223 | 1734 | 1101 | 313 | 314 | 6 | 0 | 0 |

- Molecule 5 is a protein called 40S ribosomal protein S4-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 5 | BE | 260 | 2068 | 1316 | 389 | 360 | 3 | 0 | 0 |

- Molecule 6 is a protein called 40S ribosomal protein S5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 6 | BF | 206 | 1609 | 1007 | 300 | 299 | 3 | 0 | 0 |

- Molecule 7 is a protein called 40S ribosomal protein S6-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 7 | BG | 226 | 1820 | 1142 | 350 | 325 | 3 | 0 | 0 |

- Molecule 8 is a protein called 40S ribosomal protein S7-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| | | | Total | C | N | O | | |
| 8 | BH | 184 | 1481 | 951 | 265 | 265 | 0 | 0 |

- Molecule 9 is a protein called 40S ribosomal protein S8-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 9 | BI | 188 | 1489 | 925 | 298 | 264 | 2 | 0 | 0 |

There are 11 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| BI | ? | - | LYS | deletion | UNP P0CX39 |
| BI | ? | - | LYS | deletion | UNP P0CX39 |
| BI | ? | - | ASN | deletion | UNP P0CX39 |
| BI | ? | - | VAL | deletion | UNP P0CX39 |
| BI | ? | - | LYS | deletion | UNP P0CX39 |
| BI | ? | - | GLU | deletion | UNP P0CX39 |
| BI | ? | - | GLU | deletion | UNP P0CX39 |
| BI | ? | - | GLU | deletion | UNP P0CX39 |
| BI | ? | - | THR | deletion | UNP P0CX39 |
| BI | ? | - | VAL | deletion | UNP P0CX39 |
| BI | ? | - | ALA | deletion | UNP P0CX39 |

- Molecule 10 is a protein called 40S ribosomal protein S9-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 10 | BJ | 185 | 1494 | 943 | 289 | 261 | 1 | 0 | 0 |

- Molecule 11 is a protein called 40S ribosomal protein S10-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 11 | BK | 96 | 817 | 529 | 133 | 153 | 2 | 0 | 0 |

- Molecule 12 is a protein called 40S ribosomal protein S11-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 12 | BL | 155 | 1244 | 798 | 235 | 208 | 3 | 0 | 0 |

- Molecule 13 is a protein called 40S ribosomal protein S12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 13 | BM | 121 | 913 | 574 | 162 | 175 | 2 | 0 | 0 |

- Molecule 14 is a protein called 40S ribosomal protein S13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 14 | BN | 150 | 1192 | 759 | 224 | 207 | 2 | 0 | 0 |

- Molecule 15 is a protein called 40S ribosomal protein S14-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 15 | BO | 127 | 941 | 578 | 186 | 174 | 3 | 0 | 0 |

- Molecule 16 is a protein called 40S ribosomal protein S15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 16 | BP | 124 | 991 | 631 | 187 | 166 | 7 | 0 | 0 |

- Molecule 17 is a protein called 40S ribosomal protein S16-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| | | | Total | C | N | O | | |
| 17 | BQ | 141 | 1105 | 708 | 203 | 194 | 0 | 0 |

- Molecule 18 is a protein called 40S ribosomal protein S17-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 18 | BR | 121 | 975 | 611 | 183 | 179 | 2 | 0 | 0 |

There are 4 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| BR | ? | - | SER | deletion | UNP P02407 |
| BR | ? | - | ASN | deletion | UNP P02407 |
| BR | ? | - | GLY | deletion | UNP P02407 |
| BR | ? | - | VAL | deletion | UNP P02407 |

- Molecule 19 is a protein called 40S ribosomal protein S18-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 19 | BS | 145 | 1192 | 743 | 237 | 210 | 2 | 0 | 0 |

- Molecule 20 is a protein called 40S ribosomal protein S19-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 20 | BT | 141 | 1095 | 685 | 206 | 202 | 2 | 0 | 0 |

- Molecule 21 is a protein called 40S ribosomal protein S20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 21 | BU | 107 | 855 | 539 | 156 | 159 | 1 | 0 | 0 |

- Molecule 22 is a protein called 40S ribosomal protein S21-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 22 | BV | 87 | 684 | 420 | 125 | 137 | 2 | 0 | 0 |

- Molecule 23 is a protein called 40S ribosomal protein S22-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 23 | BW | 129 | 1021 | 650 | 188 | 180 | 3 | 0 | 0 |

- Molecule 24 is a protein called 40S ribosomal protein S23-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 24 | BX | 144 | 1121 | 708 | 220 | 191 | 2 | 0 | 0 |

- Molecule 25 is a protein called 40S ribosomal protein S24-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 25 | BY | 134 | Total | C | N | O | 0 | 0 |
| | | | 1073 | 676 | 208 | 189 | | |

- Molecule 26 is a protein called 40S ribosomal protein S25-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---------|-------|
| 26 | BZ | 69 | Total | C | N | O | 0 | 0 |
| | | | 558 | 357 | 103 | 98 | | |

- Molecule 27 is a protein called 40S ribosomal protein S26-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 27 | Ba | 97 | Total | C | N | O | S | 0 | 0 |
| | | | 769 | 475 | 160 | 129 | 5 | | |

- Molecule 28 is a protein called 40S ribosomal protein S27-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 28 | Bb | 81 | Total | C | N | O | S | 0 | 0 |
| | | | 610 | 382 | 110 | 113 | 5 | | |

- Molecule 29 is a protein called 40S ribosomal protein S28-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 29 | Bc | 63 | Total | C | N | O | S | 0 | 0 |
| | | | 497 | 306 | 99 | 91 | 1 | | |

- Molecule 30 is a protein called 40S ribosomal protein S29-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 30 | Bd | 53 | Total | C | N | O | S | 0 | 0 |
| | | | 442 | 274 | 92 | 72 | 4 | | |

- Molecule 31 is a protein called 40S ribosomal protein S30-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 31 | Be | 60 | Total | C | N | O | S | 0 | 0 |
| | | | 475 | 299 | 98 | 77 | 1 | | |

- Molecule 32 is a protein called 40S ribosomal protein S31.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 32 | Bf | 57 | Total | C | N | O | S | 0 | 0 |
| | | | 454 | 288 | 86 | 77 | 3 | | |

There are 4 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| Bf | 97 | ALA | LYS | conflict | UNP P05759 |
| Bf | ? | - | CYS | deletion | UNP P05759 |
| Bf | ? | - | GLY | deletion | UNP P05759 |
| Bf | ? | - | ALA | deletion | UNP P05759 |

- Molecule 33 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 33 | Bg | 312 | Total | C | N | O | S | 0 | 0 |
| | | | 2401 | 1522 | 410 | 461 | 8 | | |

- Molecule 34 is a protein called Suppressor protein STM1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 34 | Bh | 89 | Total | C | N | O | 0 | 0 |
| | | | 675 | 391 | 137 | 147 | | |

- Molecule 35 is a RNA chain called 18S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|-------|
| 35 | B5 | 1781 | Total | C | N | O | P | 1 | 0 |
| | | | 37850 | 16932 | 6657 | 12480 | 1781 | | |

- Molecule 36 is a RNA chain called 25S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|-------|------|---------|-------|
| 36 | A1 | 3137 | Total | C | N | O | P | 0 | 0 |
| | | | 67139 | 30012 | 12094 | 21896 | 3137 | | |

- Molecule 37 is a RNA chain called 5S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 37 | A3 | 121 | Total | C | N | O | P | 0 | 0 |
| | | | 2579 | 1152 | 461 | 845 | 121 | | |

- Molecule 38 is a RNA chain called 5.8S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|------|-----|---------|-------|
| | | | Total | C | N | O | P | | |
| 38 | A4 | 158 | 3353 | 1500 | 586 | 1109 | 158 | 0 | 0 |

- Molecule 39 is a protein called 60S ribosomal protein L2-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 39 | AA | 247 | 1878 | 1170 | 381 | 326 | 1 | 0 | 0 |

- Molecule 40 is a protein called 60S ribosomal protein L3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 40 | AB | 386 | 3078 | 1953 | 584 | 533 | 8 | 0 | 0 |

- Molecule 41 is a protein called 60S ribosomal protein L4-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 41 | AC | 361 | 2748 | 1729 | 522 | 494 | 3 | 0 | 0 |

- Molecule 42 is a protein called 60S ribosomal protein L5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 42 | AD | 292 | 2341 | 1478 | 408 | 453 | 2 | 0 | 0 |

- Molecule 43 is a protein called 60S ribosomal protein L6-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 43 | AE | 156 | 1239 | 800 | 222 | 216 | 1 | 0 | 0 |

- Molecule 44 is a protein called 60S ribosomal protein L7-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 44 | AF | 222 | 1784 | 1151 | 324 | 308 | 1 | 0 | 0 |

- Molecule 45 is a protein called 60S ribosomal protein L8-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 45 | AG | 230 | 1798 | 1149 | 323 | 323 | 3 | 0 | 0 |

- Molecule 46 is a protein called 60S ribosomal protein L9-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 46 | AH | 190 | 1510 | 957 | 273 | 276 | 4 | 0 | 0 |

- Molecule 47 is a protein called 60S ribosomal protein L10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 47 | AI | 205 | 1672 | 1063 | 316 | 288 | 5 | 0 | 0 |

There are 12 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| AI | ? | - | MET | deletion | UNP P41805 |
| AI | ? | - | LEU | deletion | UNP P41805 |
| AI | ? | - | SER | deletion | UNP P41805 |
| AI | ? | - | CYS | deletion | UNP P41805 |
| AI | ? | - | ALA | deletion | UNP P41805 |
| AI | ? | - | GLY | deletion | UNP P41805 |
| AI | ? | - | ALA | deletion | UNP P41805 |
| AI | ? | - | ASP | deletion | UNP P41805 |
| AI | ? | - | ARG | deletion | UNP P41805 |
| AI | ? | - | LEU | deletion | UNP P41805 |
| AI | ? | - | GLN | deletion | UNP P41805 |
| AI | ? | - | GLN | deletion | UNP P41805 |

- Molecule 48 is a protein called 60S ribosomal protein L11-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 48 | AJ | 169 | 1353 | 847 | 253 | 249 | 4 | 0 | 0 |

- Molecule 49 is a protein called 60S ribosomal protein L13-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| | | | Total | C | N | O | | |
| 49 | AL | 193 | 1543 | 962 | 315 | 266 | 0 | 0 |

- Molecule 50 is a protein called 60S ribosomal protein L14-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 50 | AM | 136 | 1053 | 675 | 199 | 177 | 2 | 0 | 0 |

- Molecule 51 is a protein called 60S ribosomal protein L15-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 51 | AN | 203 | 1720 | 1077 | 361 | 281 | 1 | 0 | 0 |

- Molecule 52 is a protein called 60S ribosomal protein L16-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 52 | AO | 197 | 1555 | 1003 | 289 | 262 | 1 | 197 | 0 |

- Molecule 53 is a protein called 60S ribosomal protein L17-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| | | | Total | C | N | O | | |
| 53 | AP | 175 | 1388 | 862 | 277 | 249 | 0 | 0 |

There are 8 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| AP | ? | - | ALA | deletion | UNP P05740 |
| AP | ? | - | VAL | deletion | UNP P05740 |
| AP | ? | - | ALA | deletion | UNP P05740 |
| AP | ? | - | LYS | deletion | UNP P05740 |
| AP | ? | - | ALA | deletion | UNP P05740 |
| AP | ? | - | ALA | deletion | UNP P05740 |
| AP | ? | - | GLU | deletion | UNP P05740 |
| AP | ? | - | LYS | deletion | UNP P05740 |

- Molecule 54 is a protein called 60S ribosomal protein L18-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 54 | AQ | 185 | 1441 | 908 | 290 | 241 | 2 | 0 | 0 |

- Molecule 55 is a protein called 60S ribosomal protein L19-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| | | | Total | C | N | O | | |
| 55 | AR | 188 | 1521 | 935 | 326 | 260 | 0 | 0 |

- Molecule 56 is a protein called 60S ribosomal protein L20-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 56 | AS | 172 | 1445 | 930 | 267 | 244 | 4 | 0 | 0 |

- Molecule 57 is a protein called 60S ribosomal protein L21-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 57 | AT | 159 | 1276 | 805 | 246 | 221 | 4 | 0 | 0 |

- Molecule 58 is a protein called 60S ribosomal protein L22-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| | | | Total | C | N | O | | |
| 58 | AU | 100 | 796 | 516 | 131 | 149 | 0 | 0 |

- Molecule 59 is a protein called 60S ribosomal protein L23-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 59 | AV | 136 | 1003 | 628 | 189 | 179 | 7 | 0 | 0 |

- Molecule 60 is a protein called 60S ribosomal protein L24-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 60 | AW | 63 | 521 | 336 | 102 | 82 | 1 | 0 | 0 |

- Molecule 61 is a protein called 60S ribosomal protein L25.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 61 | AX | 121 | 968 | 623 | 170 | 173 | 2 | 0 | 0 |

- Molecule 62 is a protein called 60S ribosomal protein L26-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| | | | Total | C | N | O | | |
| 62 | AY | 126 | 993 | 625 | 192 | 176 | 0 | 0 |

- Molecule 63 is a protein called 60S ribosomal protein L27-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| | | | Total | C | N | O | | |
| 63 | AZ | 135 | 1092 | 710 | 202 | 180 | 0 | 0 |

- Molecule 64 is a protein called 60S ribosomal protein L28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 64 | Aa | 148 | 1173 | 749 | 231 | 190 | 3 | 0 | 0 |

- Molecule 65 is a protein called 60S ribosomal protein L29.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---------|-------|
| | | | Total | C | N | O | | |
| 65 | Ab | 58 | 462 | 289 | 100 | 73 | 0 | 0 |

- Molecule 66 is a protein called 60S ribosomal protein L30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 66 | Ac | 97 | 743 | 479 | 124 | 139 | 1 | 0 | 0 |

- Molecule 67 is a protein called 60S ribosomal protein L31-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 67 | Ad | 109 | 890 | 565 | 168 | 156 | 1 | 0 | 0 |

- Molecule 68 is a protein called 60S ribosomal protein L32.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 68 | Ae | 127 | 1020 | 647 | 205 | 167 | 1 | 0 | 0 |

- Molecule 69 is a protein called 60S ribosomal protein L33-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 69 | Af | 106 | 850 | 540 | 165 | 144 | 1 | 0 | 0 |

- Molecule 70 is a protein called 60S ribosomal protein L34-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 70 | Ag | 112 | 880 | 545 | 179 | 152 | 4 | 0 | 0 |

- Molecule 71 is a protein called 60S ribosomal protein L35-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 71 | Ah | 119 | 969 | 615 | 186 | 167 | 1 | 0 | 0 |

- Molecule 72 is a protein called 60S ribosomal protein L36-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 72 | Ai | 99 | 771 | 481 | 156 | 132 | 2 | 0 | 0 |

- Molecule 73 is a protein called 60S ribosomal protein L37-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 73 | Aj | 87 | 681 | 414 | 148 | 114 | 5 | 0 | 0 |

- Molecule 74 is a protein called 60S ribosomal protein L38.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| | | | Total | C | N | O | | |
| 74 | Ak | 77 | 612 | 391 | 115 | 106 | 0 | 0 |

- Molecule 75 is a protein called 60S ribosomal protein L39.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 75 | Al | 50 | 436 | 272 | 97 | 65 | 2 | 0 | 0 |

- Molecule 76 is a protein called 60S ribosomal protein L40-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 76 | Am | 52 | Total | C | N | O | S | 0 | 0 |
| | | | 417 | 259 | 86 | 67 | 5 | | |

- Molecule 77 is a protein called 60S ribosomal protein L41-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 77 | An | 25 | Total | C | N | O | S | 0 | 0 |
| | | | 233 | 142 | 63 | 27 | 1 | | |

- Molecule 78 is a protein called 60S ribosomal protein L42-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 78 | Ao | 105 | Total | C | N | O | S | 0 | 0 |
| | | | 847 | 534 | 170 | 138 | 5 | | |

- Molecule 79 is a protein called 60S ribosomal protein L43-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 79 | Ap | 91 | Total | C | N | O | S | 0 | 0 |
| | | | 694 | 429 | 138 | 121 | 6 | | |

- Molecule 80 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|-----|---------|
| 80 | BJ | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 80 | BT | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 80 | Be | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 80 | B5 | 122 | Total | Mg | 0 |
| | | | 122 | 122 | |
| 80 | A1 | 541 | Total | Mg | 0 |
| | | | 541 | 541 | |
| 80 | A3 | 3 | Total | Mg | 0 |
| | | | 3 | 3 | |
| 80 | A4 | 18 | Total | Mg | 0 |
| | | | 18 | 18 | |
| 80 | AA | 2 | Total | Mg | 0 |
| | | | 2 | 2 | |
| 80 | AB | 5 | Total | Mg | 0 |
| | | | 5 | 5 | |

Continued on next page...

Continued from previous page...

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| | | | Total | Mg | |
| 80 | AC | 6 | 6 | 6 | 0 |
| 80 | AF | 1 | 1 | 1 | 0 |
| 80 | AG | 1 | 1 | 1 | 0 |
| 80 | AI | 2 | 2 | 2 | 0 |
| 80 | AL | 2 | 2 | 2 | 0 |
| 80 | AM | 1 | 1 | 1 | 0 |
| 80 | AN | 5 | 5 | 5 | 0 |
| 80 | AO | 2 | 2 | 2 | 0 |
| 80 | AP | 2 | 2 | 2 | 0 |
| 80 | AQ | 3 | 3 | 3 | 0 |
| 80 | AR | 3 | 3 | 3 | 0 |
| 80 | AS | 3 | 3 | 3 | 0 |
| 80 | AY | 1 | 1 | 1 | 0 |
| 80 | Aa | 3 | 3 | 3 | 0 |
| 80 | Ad | 2 | 2 | 2 | 0 |
| 80 | Ae | 3 | 3 | 3 | 0 |
| 80 | Af | 2 | 2 | 2 | 0 |
| 80 | Ai | 1 | 1 | 1 | 0 |
| 80 | Aj | 5 | 5 | 5 | 0 |
| 80 | Am | 1 | 1 | 1 | 0 |
| 80 | Ao | 2 | 2 | 2 | 0 |

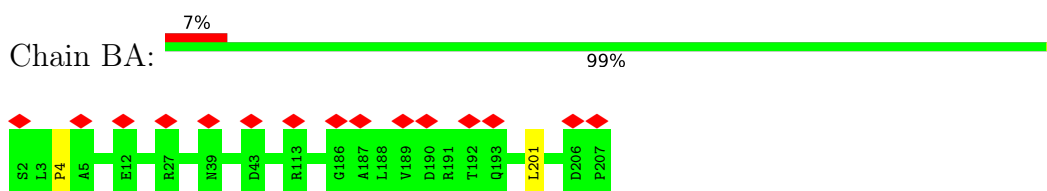
- Molecule 81 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|------------|---------|---------|
| 81 | Bb | 1 | Total 1 | Zn 1 | 0 |
| 81 | Ao | 1 | Total 1 | Zn 1 | 0 |

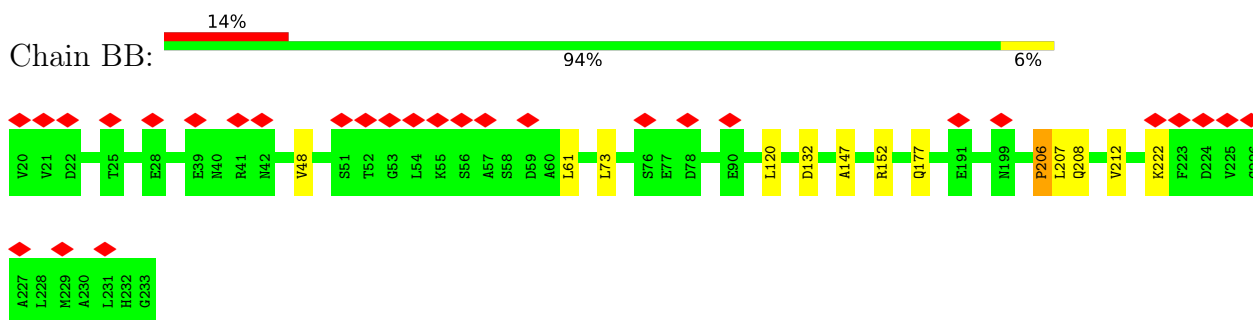
3 Residue-property plots

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 and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

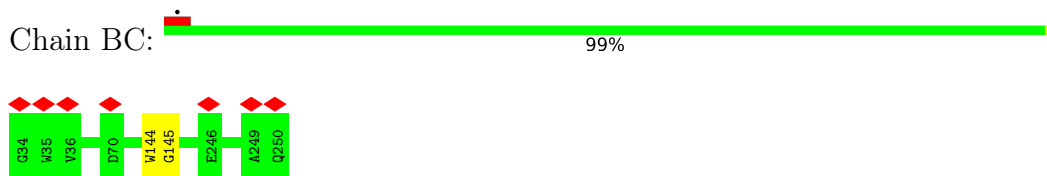
- Molecule 1: 40S ribosomal protein S0-A



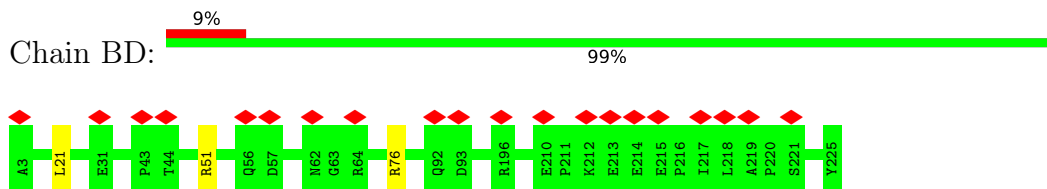
- Molecule 2: 40S ribosomal protein S1-A



- Molecule 3: 40S ribosomal protein S2

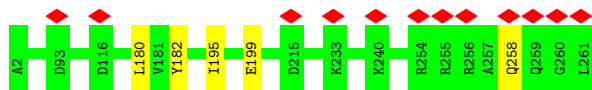


- Molecule 4: 40S ribosomal protein S3

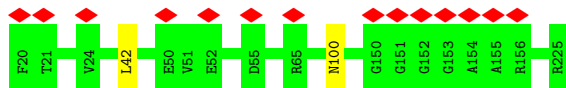


- Molecule 5: 40S ribosomal protein S4-A

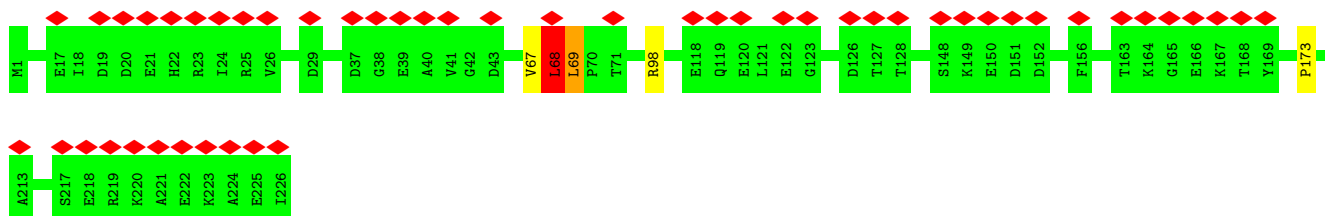




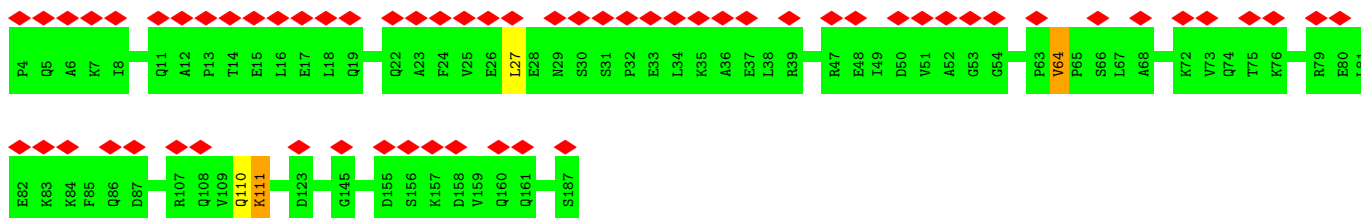
- Molecule 6: 40S ribosomal protein S5



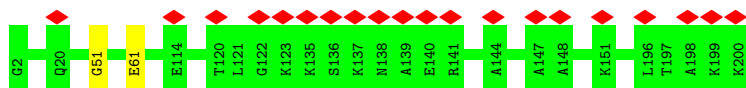
- Molecule 7: 40S ribosomal protein S6-A



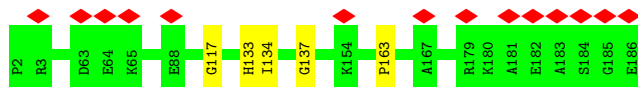
- Molecule 8: 40S ribosomal protein S7-A



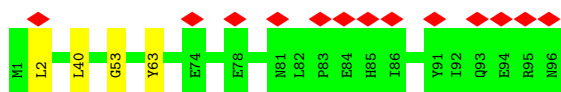
- Molecule 9: 40S ribosomal protein S8-A



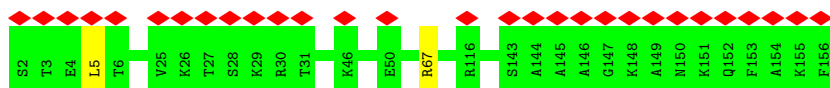
- Molecule 10: 40S ribosomal protein S9-A



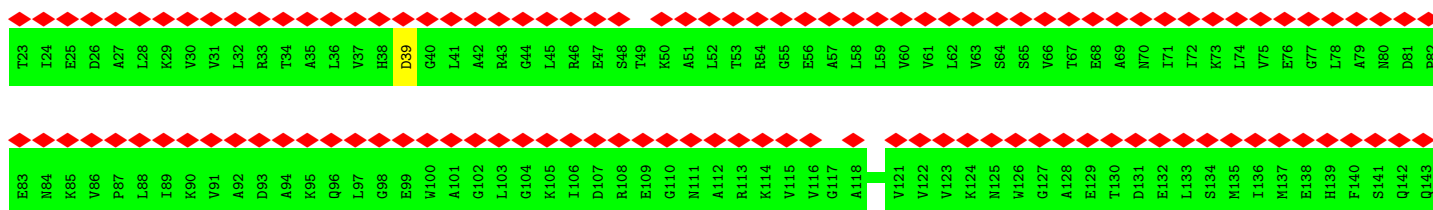
- Molecule 11: 40S ribosomal protein S10-A



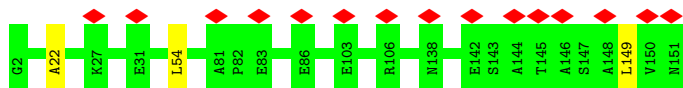
- Molecule 12: 40S ribosomal protein S11-A



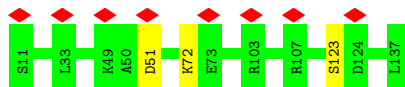
- Molecule 13: 40S ribosomal protein S12



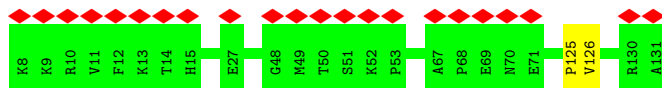
- Molecule 14: 40S ribosomal protein S13



- Molecule 15: 40S ribosomal protein S14-A

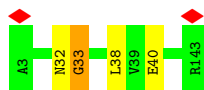


- Molecule 16: 40S ribosomal protein S15

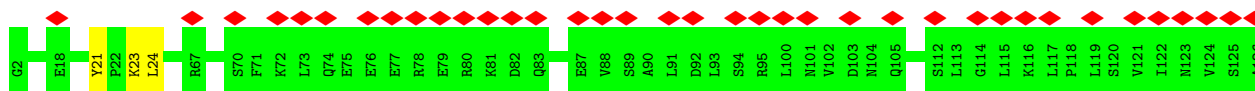


- Molecule 17: 40S ribosomal protein S16-A

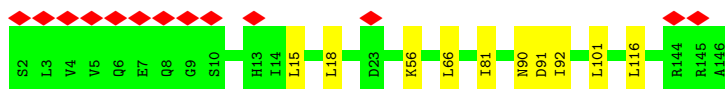
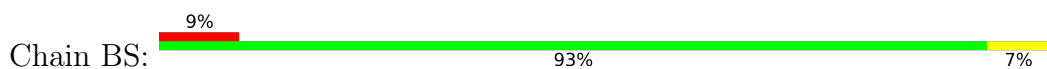




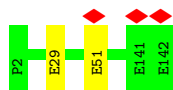
- Molecule 18: 40S ribosomal protein S17-A



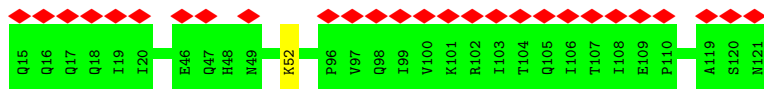
- Molecule 19: 40S ribosomal protein S18-A



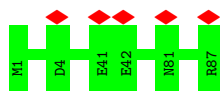
- Molecule 20: 40S ribosomal protein S19-A



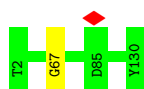
- Molecule 21: 40S ribosomal protein S20



- Molecule 22: 40S ribosomal protein S21-A

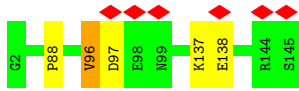


- Molecule 23: 40S ribosomal protein S22-A



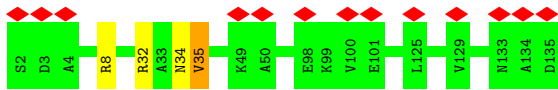
- Molecule 24: 40S ribosomal protein S23-A

Chain BX:  97%



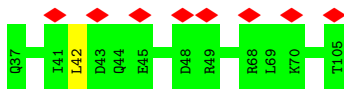
- Molecule 25: 40S ribosomal protein S24-A

Chain BY:  97%



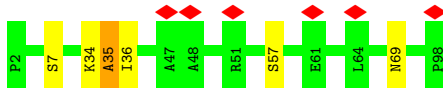
- Molecule 26: 40S ribosomal protein S25-A

Chain BZ:  99%



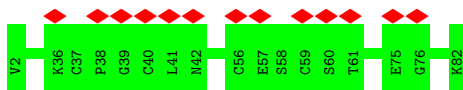
- Molecule 27: 40S ribosomal protein S26-A

Chain Ba:  94%



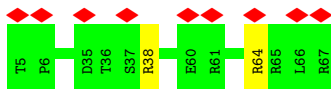
- Molecule 28: 40S ribosomal protein S27-A

Chain Bb:  100%



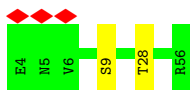
- Molecule 29: 40S ribosomal protein S28-A

Chain Bc:  97%

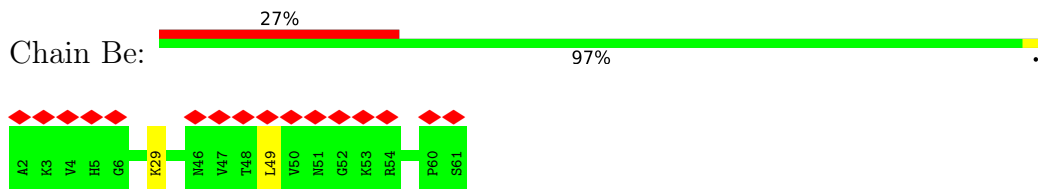


- Molecule 30: 40S ribosomal protein S29-A

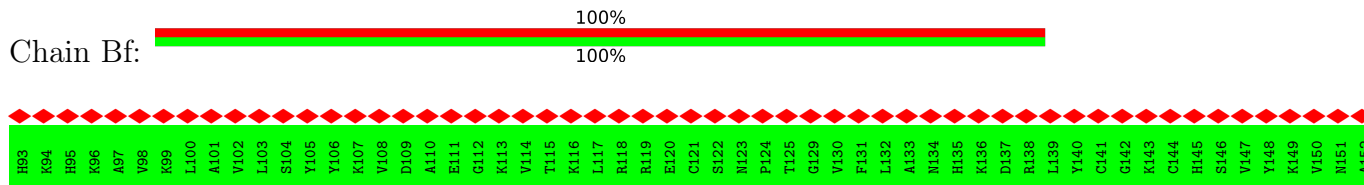
Chain Bd:  96%



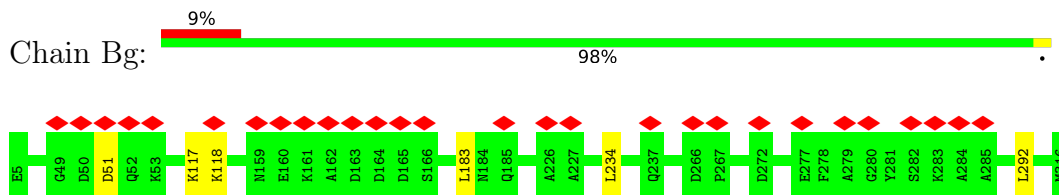
• Molecule 31: 40S ribosomal protein S30-A



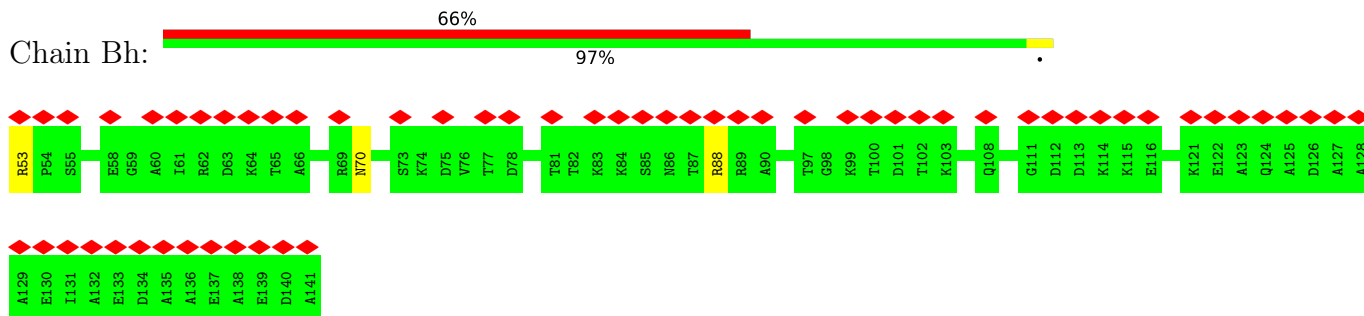
• Molecule 32: 40S ribosomal protein S31



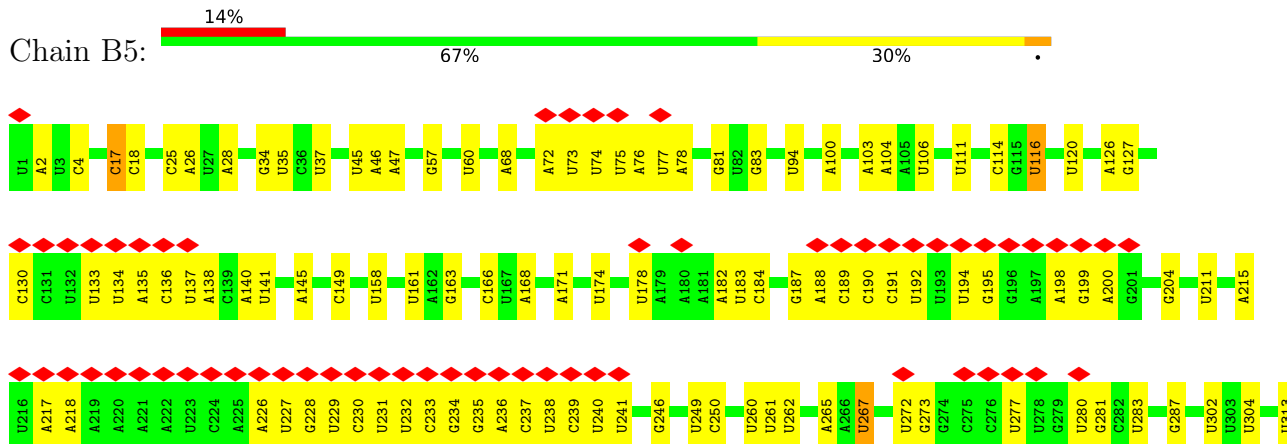
• Molecule 33: Guanine nucleotide-binding protein subunit beta-like protein

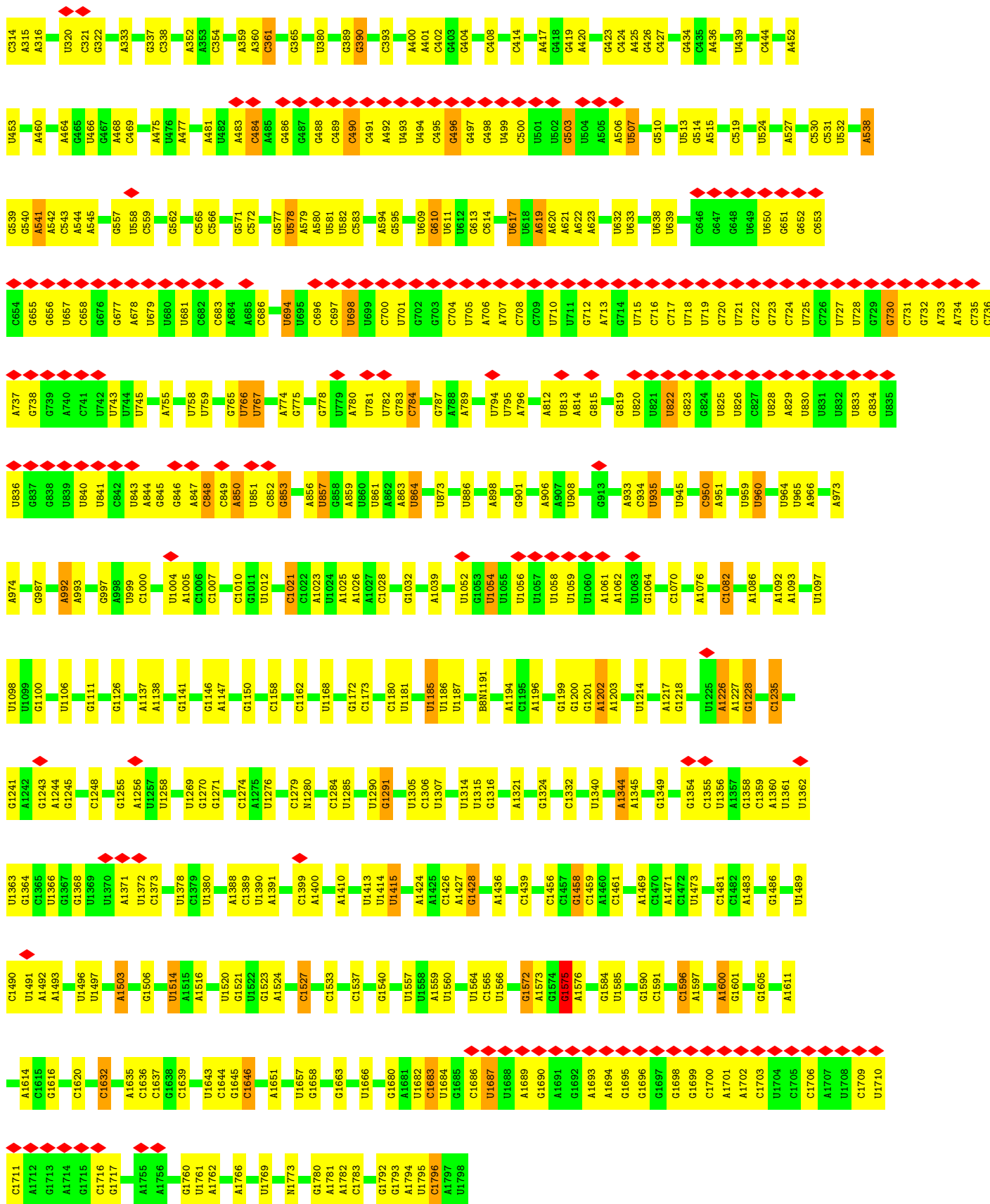


• Molecule 34: Suppressor protein STM1

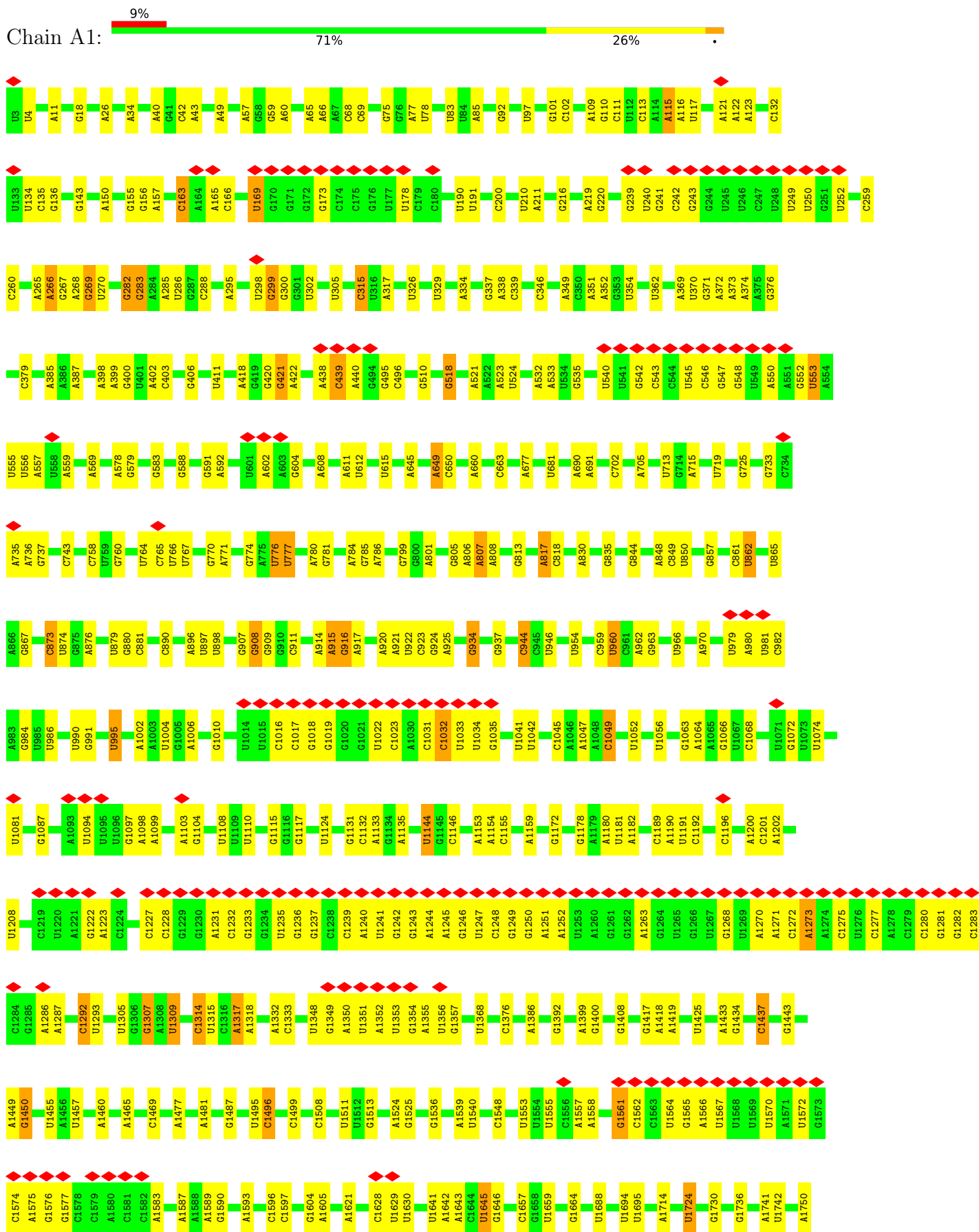


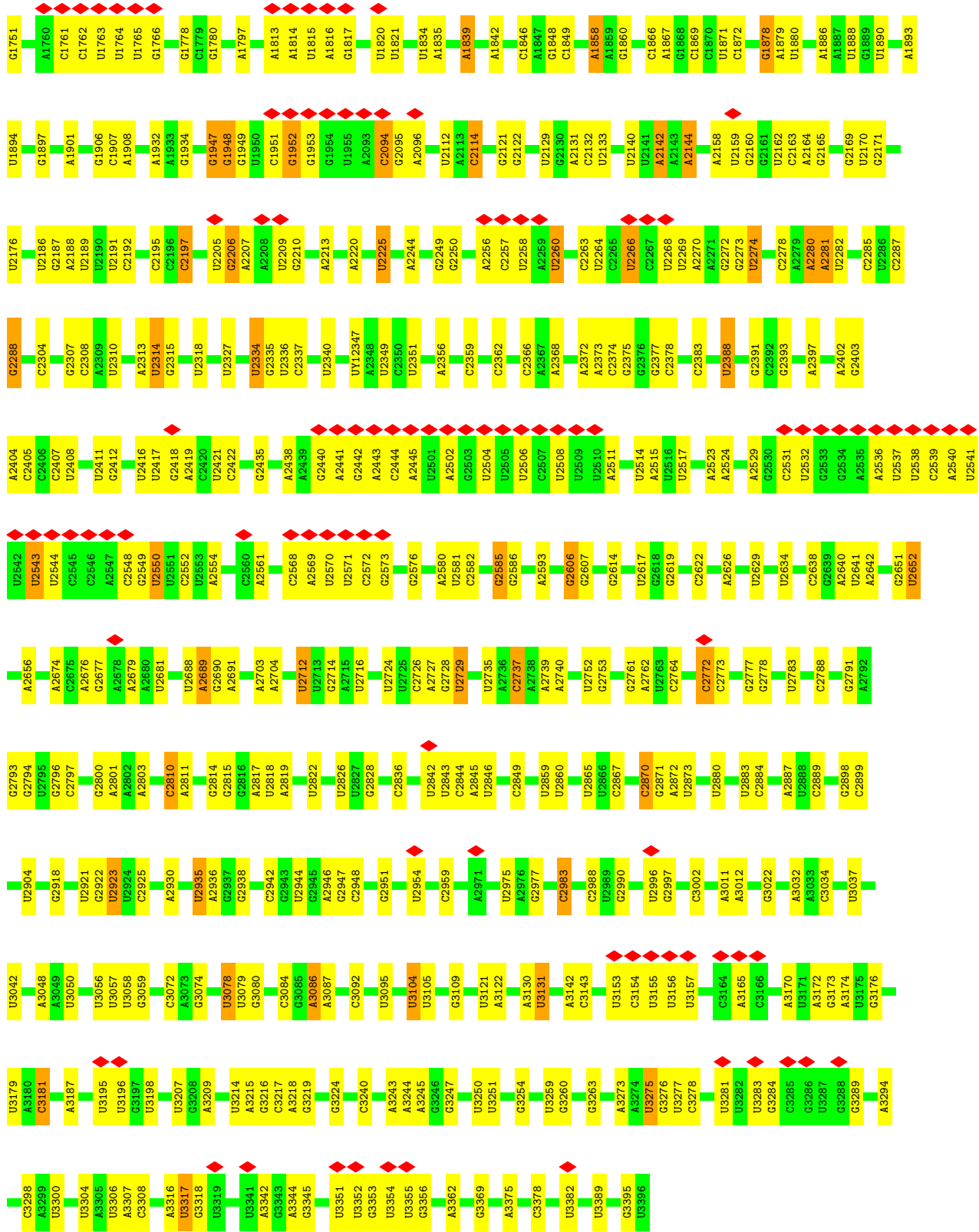
• Molecule 35: 18S rRNA



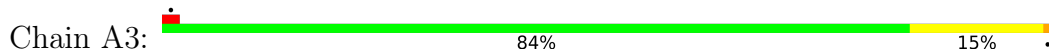


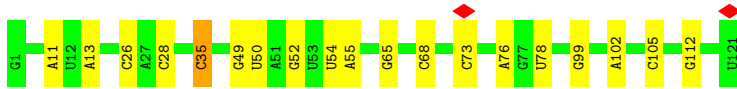
• Molecule 36: 25S rRNA



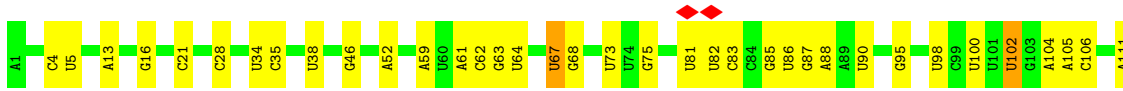


• Molecule 37: 5S rRNA

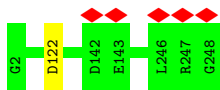




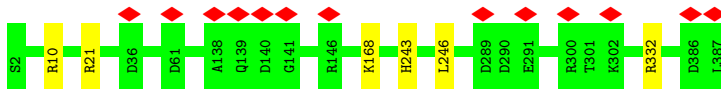
- Molecule 38: 5.8S rRNA



- Molecule 39: 60S ribosomal protein L2-A



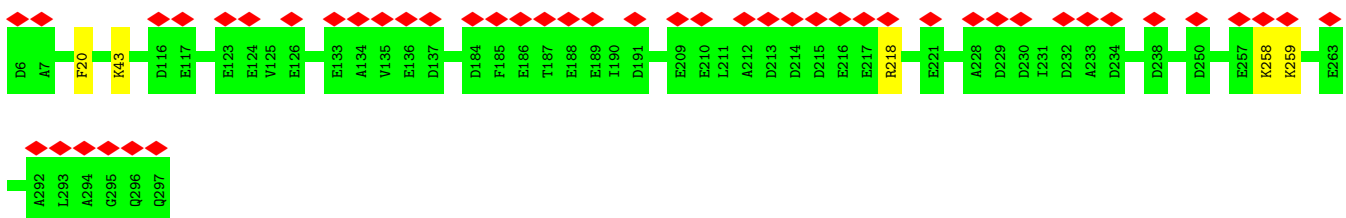
- Molecule 40: 60S ribosomal protein L3



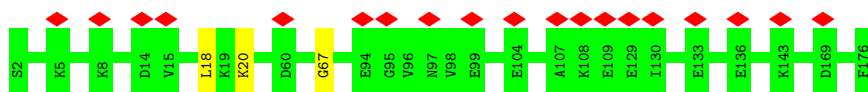
- Molecule 41: 60S ribosomal protein L4-A



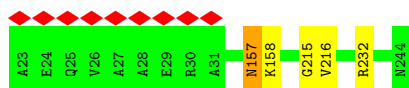
- Molecule 42: 60S ribosomal protein L5



- Molecule 43: 60S ribosomal protein L6-A



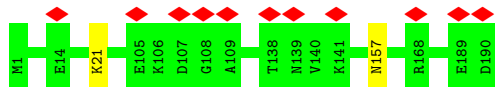
- Molecule 44: 60S ribosomal protein L7-A



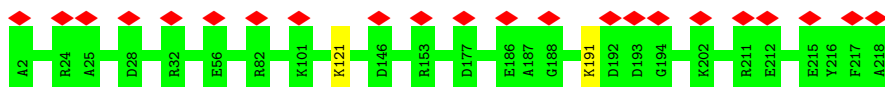
- Molecule 45: 60S ribosomal protein L8-A



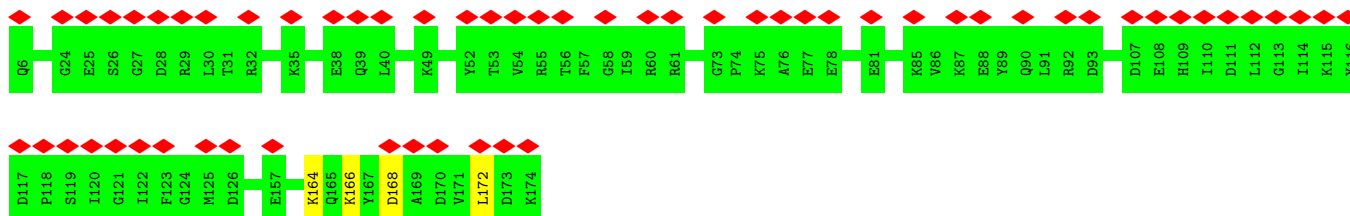
- Molecule 46: 60S ribosomal protein L9-A



- Molecule 47: 60S ribosomal protein L10

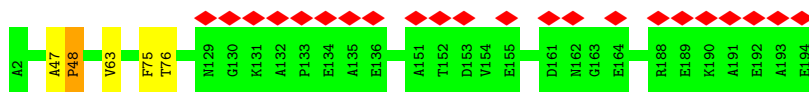


- Molecule 48: 60S ribosomal protein L11-A

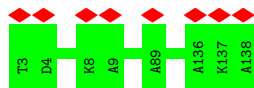


- Molecule 49: 60S ribosomal protein L13-A

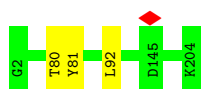




- Molecule 50: 60S ribosomal protein L14-A



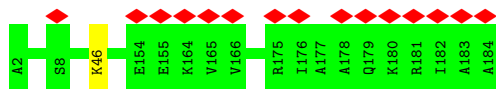
- Molecule 51: 60S ribosomal protein L15-A



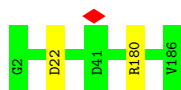
- Molecule 52: 60S ribosomal protein L16-A



- Molecule 53: 60S ribosomal protein L17-A



- Molecule 54: 60S ribosomal protein L18-A

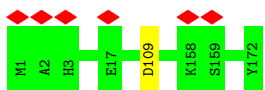


- Molecule 55: 60S ribosomal protein L19-A



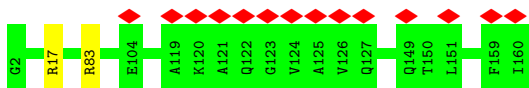
- Molecule 56: 60S ribosomal protein L20-A

Chain AS:  99%



- Molecule 57: 60S ribosomal protein L21-A

Chain AT:  99%



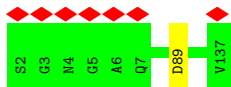
- Molecule 58: 60S ribosomal protein L22-A

Chain AU:  98%



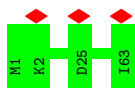
- Molecule 59: 60S ribosomal protein L23-A

Chain AV:  99%



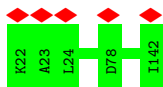
- Molecule 60: 60S ribosomal protein L24-A

Chain AW:  100%



- Molecule 61: 60S ribosomal protein L25

Chain AX:  100%

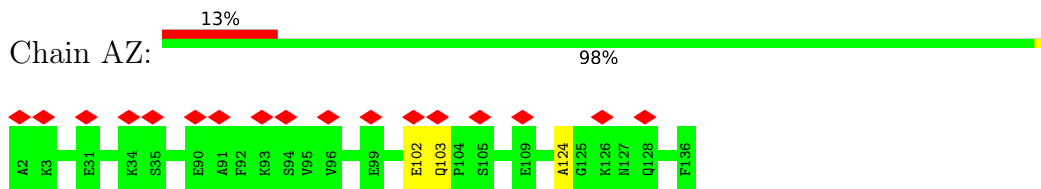


- Molecule 62: 60S ribosomal protein L26-A

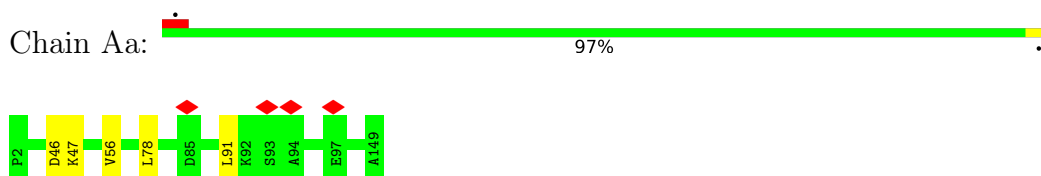
Chain AY:  99%



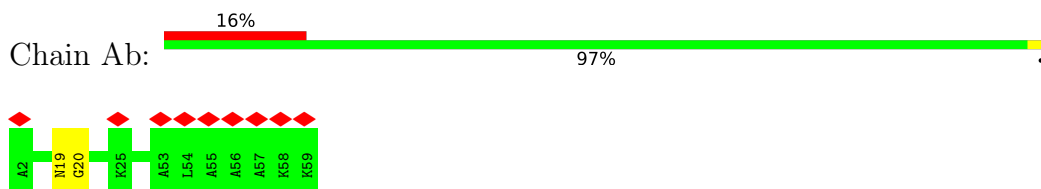
- Molecule 63: 60S ribosomal protein L27-A



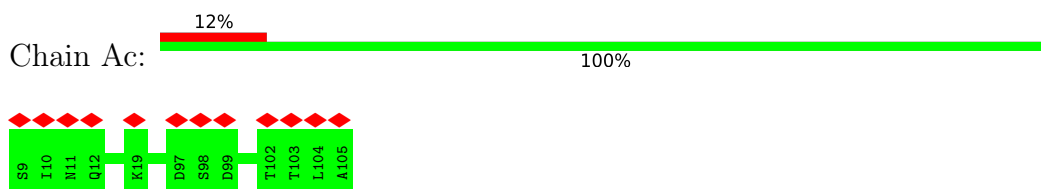
- Molecule 64: 60S ribosomal protein L28



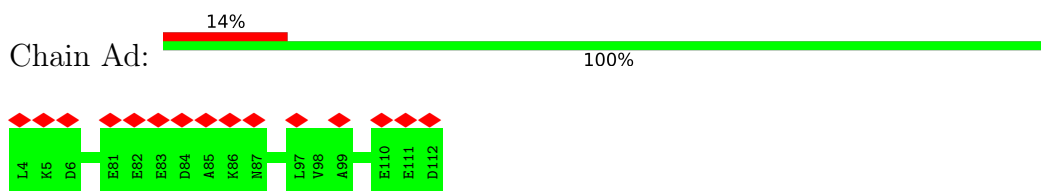
- Molecule 65: 60S ribosomal protein L29



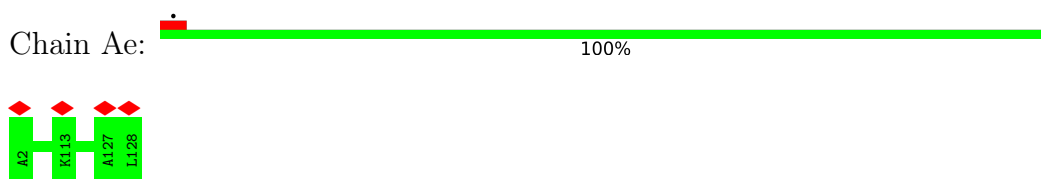
- Molecule 66: 60S ribosomal protein L30



- Molecule 67: 60S ribosomal protein L31-A

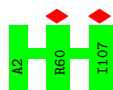


- Molecule 68: 60S ribosomal protein L32

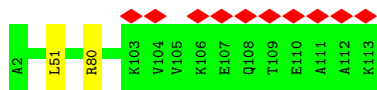


- Molecule 69: 60S ribosomal protein L33-A

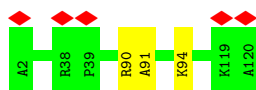




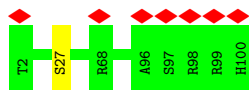
• Molecule 70: 60S ribosomal protein L34-A



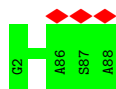
• Molecule 71: 60S ribosomal protein L35-A



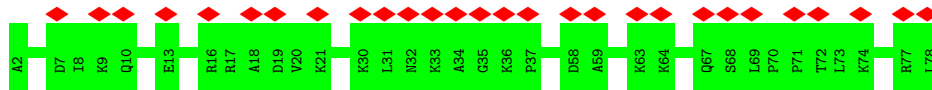
• Molecule 72: 60S ribosomal protein L36-A



• Molecule 73: 60S ribosomal protein L37-A



• Molecule 74: 60S ribosomal protein L38



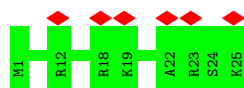
• Molecule 75: 60S ribosomal protein L39



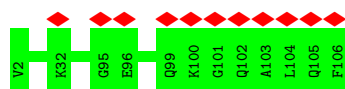
• Molecule 76: 60S ribosomal protein L40-A



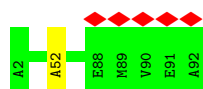
- Molecule 77: 60S ribosomal protein L41-A



- Molecule 78: 60S ribosomal protein L42-A



- Molecule 79: 60S ribosomal protein L43-A



4 Experimental information

| Property | Value | Source |
|--------------------------------------|---|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 289345 | Depositor |
| Resolution determination method | OTHER | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 61 | Depositor |
| Minimum defocus (nm) | Not provided | |
| Maximum defocus (nm) | Not provided | |
| Magnification | Not provided | |
| Image detector | GATAN K3 BIOQUANTUM (6k x 4k) | Depositor |
| Maximum map value | 0.428 | Depositor |
| Minimum map value | -0.074 | Depositor |
| Average map value | 0.004 | Depositor |
| Map value standard deviation | 0.012 | Depositor |
| Recommended contour level | 0.04 | Depositor |
| Map size (Å) | 463.968, 463.968, 463.968 | wwPDB |
| Map dimensions | 432, 432, 432 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.074, 1.074, 1.074 | Depositor |

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: OMC, A2M, 5MC, MA6, PSU, 1MA, UY1, OMG, G7M, OMU, ZN, MG, 4AC, B8N, HIC, UR3

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 | BA | 0.38 | 0/1653 | 0.61 | 1/2261 (0.0%) |
| 2 | BB | 0.35 | 0/1735 | 0.76 | 6/2335 (0.3%) |
| 3 | BC | 0.40 | 0/1665 | 0.66 | 0/2263 |
| 4 | BD | 0.39 | 0/1759 | 0.68 | 1/2368 (0.0%) |
| 5 | BE | 0.43 | 0/2109 | 0.68 | 2/2839 (0.1%) |
| 6 | BF | 0.40 | 0/1629 | 0.68 | 0/2202 |
| 7 | BG | 0.34 | 0/1844 | 0.67 | 2/2464 (0.1%) |
| 8 | BH | 0.37 | 0/1506 | 0.73 | 2/2028 (0.1%) |
| 9 | BI | 0.42 | 0/1514 | 0.73 | 1/2021 (0.0%) |
| 10 | BJ | 0.35 | 0/1519 | 0.65 | 0/2035 |
| 11 | BK | 0.45 | 0/837 | 0.77 | 1/1131 (0.1%) |
| 12 | BL | 0.42 | 0/1272 | 0.58 | 0/1712 |
| 13 | BM | 0.30 | 0/921 | 0.70 | 1/1245 (0.1%) |
| 14 | BN | 0.38 | 0/1215 | 0.66 | 3/1638 (0.2%) |
| 15 | BO | 0.40 | 0/952 | 0.75 | 2/1279 (0.2%) |
| 16 | BP | 0.42 | 0/1012 | 0.67 | 0/1356 |
| 17 | BQ | 0.42 | 0/1125 | 0.69 | 1/1510 (0.1%) |
| 18 | BR | 0.45 | 1/984 (0.1%) | 0.66 | 0/1318 |
| 19 | BS | 0.41 | 0/1211 | 0.78 | 4/1628 (0.2%) |
| 20 | BT | 0.47 | 0/1113 | 0.71 | 1/1494 (0.1%) |
| 21 | BU | 0.41 | 0/865 | 0.64 | 0/1169 |
| 22 | BV | 0.38 | 0/692 | 0.64 | 0/932 |
| 23 | BW | 0.44 | 0/1038 | 0.65 | 0/1395 |
| 24 | BX | 0.40 | 0/1139 | 0.72 | 0/1518 |
| 25 | BY | 0.42 | 0/1087 | 0.68 | 1/1449 (0.1%) |
| 26 | BZ | 0.38 | 0/566 | 0.70 | 1/761 (0.1%) |
| 27 | Ba | 0.41 | 0/782 | 0.70 | 0/1047 |
| 28 | Bb | 0.35 | 0/620 | 0.65 | 0/838 |
| 29 | Bc | 0.41 | 0/499 | 0.67 | 0/670 |
| 30 | Bd | 0.50 | 0/452 | 0.64 | 1/600 (0.2%) |
| 31 | Be | 0.38 | 0/483 | 0.62 | 1/643 (0.2%) |
| 32 | Bf | 0.31 | 0/462 | 0.62 | 0/617 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|----------------|-------------|-------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 33 | Bg | 0.38 | 0/2454 | 0.71 | 4/3340 (0.1%) |
| 34 | Bh | 0.31 | 0/678 | 0.56 | 0/905 |
| 35 | B5 | 0.80 | 4/41414 (0.0%) | 1.15 | 286/64521 (0.4%) |
| 36 | A1 | 0.89 | 0/73484 | 1.17 | 371/114569 (0.3%) |
| 37 | A3 | 0.74 | 0/2861 | 1.04 | 11/4457 (0.2%) |
| 38 | A4 | 0.87 | 0/3723 | 1.15 | 15/5794 (0.3%) |
| 39 | AA | 0.45 | 0/1912 | 0.65 | 1/2569 (0.0%) |
| 40 | AB | 0.46 | 0/3136 | 0.69 | 4/4213 (0.1%) |
| 41 | AC | 0.43 | 1/2800 (0.0%) | 0.66 | 1/3790 (0.0%) |
| 42 | AD | 0.38 | 0/2390 | 0.63 | 1/3225 (0.0%) |
| 43 | AE | 0.41 | 0/1260 | 0.60 | 1/1694 (0.1%) |
| 44 | AF | 0.48 | 0/1821 | 0.66 | 0/2451 |
| 45 | AG | 0.39 | 0/1830 | 0.59 | 1/2469 (0.0%) |
| 46 | AH | 0.40 | 0/1531 | 0.61 | 0/2062 |
| 47 | AI | 0.38 | 0/1708 | 0.61 | 0/2290 |
| 48 | AJ | 0.34 | 0/1374 | 0.71 | 2/1842 (0.1%) |
| 49 | AL | 0.40 | 0/1568 | 0.66 | 1/2106 (0.0%) |
| 50 | AM | 0.38 | 0/1068 | 0.56 | 0/1438 |
| 51 | AN | 0.49 | 0/1757 | 0.69 | 0/2354 |
| 52 | AO | 0.48 | 0/1585 | 0.65 | 1/2128 (0.0%) |
| 53 | AP | 0.42 | 0/1410 | 0.60 | 0/1893 |
| 54 | AQ | 0.41 | 0/1465 | 0.64 | 2/1965 (0.1%) |
| 55 | AR | 0.38 | 0/1538 | 0.56 | 0/2050 |
| 56 | AS | 0.47 | 0/1481 | 0.65 | 1/1990 (0.1%) |
| 57 | AT | 0.44 | 0/1300 | 0.65 | 0/1743 |
| 58 | AU | 0.37 | 0/812 | 0.68 | 2/1099 (0.2%) |
| 59 | AV | 0.45 | 0/1018 | 0.66 | 1/1369 (0.1%) |
| 60 | AW | 0.41 | 0/533 | 0.63 | 0/707 |
| 61 | AX | 0.44 | 0/983 | 0.65 | 0/1325 |
| 62 | AY | 0.40 | 0/1004 | 0.64 | 1/1341 (0.1%) |
| 63 | AZ | 0.37 | 0/1118 | 0.62 | 1/1497 (0.1%) |
| 64 | Aa | 0.48 | 0/1204 | 0.73 | 3/1612 (0.2%) |
| 65 | Ab | 0.34 | 0/473 | 0.59 | 0/629 |
| 66 | Ac | 0.39 | 0/751 | 0.67 | 0/1008 |
| 67 | Ad | 0.37 | 0/904 | 0.61 | 0/1213 |
| 68 | Ae | 0.45 | 0/1041 | 0.61 | 0/1394 |
| 69 | Af | 0.52 | 0/868 | 0.65 | 0/1168 |
| 70 | Ag | 0.44 | 0/890 | 0.68 | 1/1189 (0.1%) |
| 71 | Ah | 0.41 | 0/978 | 0.63 | 0/1301 |
| 72 | Ai | 0.41 | 0/778 | 0.74 | 0/1034 |
| 73 | Aj | 0.48 | 0/696 | 0.64 | 0/923 |
| 74 | Ak | 0.36 | 0/618 | 0.59 | 0/826 |
| 75 | Al | 0.38 | 0/443 | 0.64 | 0/588 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|-----------------|-------------|-------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 76 | Am | 0.41 | 0/423 | 0.61 | 1/562 (0.2%) |
| 77 | An | 0.38 | 0/234 | 0.65 | 0/300 |
| 78 | Ao | 0.40 | 0/860 | 0.61 | 0/1136 |
| 79 | Ap | 0.41 | 0/701 | 0.68 | 0/934 |
| All | All | 0.70 | 6/211138 (0.0%) | 1.00 | 745/309779 (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 | BB | 0 | 5 |
| 3 | BC | 0 | 2 |
| 5 | BE | 0 | 2 |
| 6 | BF | 0 | 2 |
| 7 | BG | 0 | 1 |
| 8 | BH | 0 | 3 |
| 9 | BI | 0 | 1 |
| 10 | BJ | 0 | 3 |
| 11 | BK | 0 | 3 |
| 12 | BL | 0 | 1 |
| 15 | BO | 0 | 1 |
| 17 | BQ | 0 | 3 |
| 19 | BS | 0 | 4 |
| 20 | BT | 0 | 1 |
| 24 | BX | 0 | 3 |
| 25 | BY | 0 | 1 |
| 27 | Ba | 0 | 4 |
| 35 | B5 | 3 | 0 |
| 41 | AC | 0 | 2 |
| 42 | AD | 0 | 2 |
| 43 | AE | 0 | 1 |
| 44 | AF | 0 | 3 |
| 45 | AG | 0 | 5 |
| 46 | AH | 0 | 1 |
| 48 | AJ | 0 | 2 |
| 49 | AL | 0 | 2 |
| 51 | AN | 0 | 2 |
| 52 | AO | 0 | 1 |
| 55 | AR | 0 | 1 |
| 57 | AT | 0 | 1 |

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| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 63 | AZ | 0 | 1 |
| 64 | Aa | 0 | 1 |
| 65 | Ab | 0 | 2 |
| 70 | Ag | 0 | 1 |
| 71 | Ah | 0 | 1 |
| 72 | Ai | 0 | 1 |
| All | All | 3 | 70 |

The worst 5 of 6 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|--------|-------|-------------|----------|
| 18 | BR | 21 | TYR | C-N | 7.06 | 1.47 | 1.34 |
| 35 | B5 | 1291 | G | C2-N3 | -6.61 | 1.27 | 1.32 |
| 35 | B5 | 992 | A | C2-N3 | -5.98 | 1.28 | 1.33 |
| 35 | B5 | 538 | A | C2-N3 | -5.74 | 1.28 | 1.33 |
| 41 | AC | 230 | VAL | CB-CG1 | -5.70 | 1.40 | 1.52 |

The worst 5 of 745 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|-----------|--------|-------------|----------|
| 36 | A1 | 1948 | G | O5'-P-OP1 | -31.38 | 73.04 | 110.70 |
| 36 | A1 | 266 | A | O5'-P-OP1 | -30.18 | 74.49 | 110.70 |
| 36 | A1 | 266 | A | OP1-P-OP2 | -27.41 | 78.48 | 119.60 |
| 36 | A1 | 1948 | G | O5'-P-OP2 | -23.68 | 82.28 | 110.70 |
| 36 | A1 | 266 | A | O5'-P-OP2 | 19.85 | 134.52 | 110.70 |

All (3) chirality outliers are listed below:

| Mol | Chain | Res | Type | Atom |
|-----|-------|------|------|-------------|
| 35 | B5 | 1575 | G7M | C2',C3',C4' |

5 of 70 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 2 | BB | 177 | GLN | Peptide |
| 2 | BB | 206 | PRO | Peptide |
| 2 | BB | 208 | GLN | Peptide |
| 2 | BB | 212 | VAL | Peptide |
| 2 | BB | 222 | LYS | Peptide |

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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 PDB entries followed by that with respect to all EM 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 | BA | 204/206 (99%) | 184 (90%) | 19 (9%) | 1 (0%) | 29 | 54 |
| 2 | BB | 212/214 (99%) | 178 (84%) | 32 (15%) | 2 (1%) | 17 | 40 |
| 3 | BC | 215/217 (99%) | 196 (91%) | 19 (9%) | 0 | 100 | 100 |
| 4 | BD | 221/223 (99%) | 208 (94%) | 13 (6%) | 0 | 100 | 100 |
| 5 | BE | 258/260 (99%) | 236 (92%) | 22 (8%) | 0 | 100 | 100 |
| 6 | BF | 204/206 (99%) | 190 (93%) | 14 (7%) | 0 | 100 | 100 |
| 7 | BG | 224/226 (99%) | 207 (92%) | 13 (6%) | 4 (2%) | 8 | 21 |
| 8 | BH | 182/184 (99%) | 165 (91%) | 16 (9%) | 1 (0%) | 29 | 54 |
| 9 | BI | 184/188 (98%) | 160 (87%) | 24 (13%) | 0 | 100 | 100 |
| 10 | BJ | 183/185 (99%) | 166 (91%) | 15 (8%) | 2 (1%) | 14 | 34 |
| 11 | BK | 94/96 (98%) | 84 (89%) | 10 (11%) | 0 | 100 | 100 |
| 12 | BL | 153/155 (99%) | 141 (92%) | 12 (8%) | 0 | 100 | 100 |
| 13 | BM | 119/121 (98%) | 89 (75%) | 30 (25%) | 0 | 100 | 100 |
| 14 | BN | 148/150 (99%) | 141 (95%) | 7 (5%) | 0 | 100 | 100 |
| 15 | BO | 125/127 (98%) | 112 (90%) | 13 (10%) | 0 | 100 | 100 |
| 16 | BP | 122/124 (98%) | 109 (89%) | 11 (9%) | 2 (2%) | 9 | 24 |
| 17 | BQ | 139/141 (99%) | 130 (94%) | 8 (6%) | 1 (1%) | 22 | 46 |
| 18 | BR | 117/121 (97%) | 107 (92%) | 8 (7%) | 2 (2%) | 9 | 23 |
| 19 | BS | 143/145 (99%) | 128 (90%) | 13 (9%) | 2 (1%) | 11 | 28 |
| 20 | BT | 139/141 (99%) | 127 (91%) | 12 (9%) | 0 | 100 | 100 |
| 21 | BU | 105/107 (98%) | 97 (92%) | 8 (8%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 22 | BV | 83/87 (95%) | 75 (90%) | 8 (10%) | 0 | 100 | 100 |
| 23 | BW | 127/129 (98%) | 118 (93%) | 8 (6%) | 1 (1%) | 19 | 43 |
| 24 | BX | 142/144 (99%) | 120 (84%) | 19 (13%) | 3 (2%) | 7 | 18 |
| 25 | BY | 132/134 (98%) | 124 (94%) | 7 (5%) | 1 (1%) | 19 | 43 |
| 26 | BZ | 67/69 (97%) | 62 (92%) | 5 (8%) | 0 | 100 | 100 |
| 27 | Ba | 95/97 (98%) | 78 (82%) | 15 (16%) | 2 (2%) | 7 | 18 |
| 28 | Bb | 79/81 (98%) | 66 (84%) | 13 (16%) | 0 | 100 | 100 |
| 29 | Bc | 61/63 (97%) | 58 (95%) | 3 (5%) | 0 | 100 | 100 |
| 30 | Bd | 51/53 (96%) | 51 (100%) | 0 | 0 | 100 | 100 |
| 31 | Be | 58/60 (97%) | 52 (90%) | 6 (10%) | 0 | 100 | 100 |
| 32 | Bf | 53/57 (93%) | 39 (74%) | 14 (26%) | 0 | 100 | 100 |
| 33 | Bg | 310/312 (99%) | 273 (88%) | 36 (12%) | 1 (0%) | 41 | 66 |
| 34 | Bh | 87/89 (98%) | 81 (93%) | 6 (7%) | 0 | 100 | 100 |
| 39 | AA | 245/247 (99%) | 233 (95%) | 12 (5%) | 0 | 100 | 100 |
| 40 | AB | 383/386 (99%) | 364 (95%) | 19 (5%) | 0 | 100 | 100 |
| 41 | AC | 359/361 (99%) | 329 (92%) | 27 (8%) | 3 (1%) | 19 | 43 |
| 42 | AD | 290/292 (99%) | 268 (92%) | 20 (7%) | 2 (1%) | 22 | 46 |
| 43 | AE | 152/156 (97%) | 144 (95%) | 8 (5%) | 0 | 100 | 100 |
| 44 | AF | 220/222 (99%) | 205 (93%) | 13 (6%) | 2 (1%) | 17 | 40 |
| 45 | AG | 228/230 (99%) | 214 (94%) | 14 (6%) | 0 | 100 | 100 |
| 46 | AH | 188/190 (99%) | 177 (94%) | 11 (6%) | 0 | 100 | 100 |
| 47 | AI | 201/205 (98%) | 193 (96%) | 8 (4%) | 0 | 100 | 100 |
| 48 | AJ | 167/169 (99%) | 147 (88%) | 20 (12%) | 0 | 100 | 100 |
| 49 | AL | 191/193 (99%) | 169 (88%) | 19 (10%) | 3 (2%) | 9 | 24 |
| 50 | AM | 134/136 (98%) | 127 (95%) | 7 (5%) | 0 | 100 | 100 |
| 51 | AN | 201/203 (99%) | 183 (91%) | 17 (8%) | 1 (0%) | 29 | 54 |
| 52 | AO | 195/197 (99%) | 191 (98%) | 3 (2%) | 1 (0%) | 29 | 54 |
| 53 | AP | 171/175 (98%) | 167 (98%) | 4 (2%) | 0 | 100 | 100 |
| 54 | AQ | 183/185 (99%) | 175 (96%) | 8 (4%) | 0 | 100 | 100 |
| 55 | AR | 186/188 (99%) | 179 (96%) | 7 (4%) | 0 | 100 | 100 |
| 56 | AS | 170/172 (99%) | 162 (95%) | 8 (5%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-------------------|-------------|----------|----------|-------------|-----|
| 57 | AT | 157/159 (99%) | 145 (92%) | 12 (8%) | 0 | 100 | 100 |
| 58 | AU | 98/100 (98%) | 91 (93%) | 7 (7%) | 0 | 100 | 100 |
| 59 | AV | 134/136 (98%) | 131 (98%) | 3 (2%) | 0 | 100 | 100 |
| 60 | AW | 61/63 (97%) | 61 (100%) | 0 | 0 | 100 | 100 |
| 61 | AX | 119/121 (98%) | 115 (97%) | 4 (3%) | 0 | 100 | 100 |
| 62 | AY | 124/126 (98%) | 121 (98%) | 3 (2%) | 0 | 100 | 100 |
| 63 | AZ | 133/135 (98%) | 120 (90%) | 12 (9%) | 1 (1%) | 19 | 43 |
| 64 | Aa | 146/148 (99%) | 123 (84%) | 22 (15%) | 1 (1%) | 22 | 46 |
| 65 | Ab | 56/58 (97%) | 48 (86%) | 8 (14%) | 0 | 100 | 100 |
| 66 | Ac | 95/97 (98%) | 93 (98%) | 2 (2%) | 0 | 100 | 100 |
| 67 | Ad | 107/109 (98%) | 102 (95%) | 5 (5%) | 0 | 100 | 100 |
| 68 | Ae | 125/127 (98%) | 119 (95%) | 6 (5%) | 0 | 100 | 100 |
| 69 | Af | 104/106 (98%) | 102 (98%) | 2 (2%) | 0 | 100 | 100 |
| 70 | Ag | 110/112 (98%) | 107 (97%) | 3 (3%) | 0 | 100 | 100 |
| 71 | Ah | 117/119 (98%) | 110 (94%) | 6 (5%) | 1 (1%) | 17 | 40 |
| 72 | Ai | 97/99 (98%) | 87 (90%) | 10 (10%) | 0 | 100 | 100 |
| 73 | Aj | 85/87 (98%) | 81 (95%) | 4 (5%) | 0 | 100 | 100 |
| 74 | Ak | 75/77 (97%) | 72 (96%) | 3 (4%) | 0 | 100 | 100 |
| 75 | Al | 48/50 (96%) | 46 (96%) | 2 (4%) | 0 | 100 | 100 |
| 76 | Am | 50/52 (96%) | 48 (96%) | 2 (4%) | 0 | 100 | 100 |
| 77 | An | 23/25 (92%) | 23 (100%) | 0 | 0 | 100 | 100 |
| 78 | Ao | 103/105 (98%) | 90 (87%) | 13 (13%) | 0 | 100 | 100 |
| 79 | Ap | 89/91 (98%) | 83 (93%) | 5 (6%) | 1 (1%) | 14 | 34 |
| All | All | 10956/11121 (98%) | 10097 (92%) | 818 (8%) | 41 (0%) | 38 | 60 |

5 of 41 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|--------|------|
| 41 | AC | 339 | LEU |
| 49 | AL | 48 | PRO |
| 49 | AL | 76 | THR |
| 51 | AN | 81 | TYR |
| 52 | AO | 111[A] | PRO |

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 PDB entries followed by that with respect to all EM 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 | BA | 173/173 (100%) | 173 (100%) | 0 | 100 | 100 |
| 2 | BB | 191/191 (100%) | 190 (100%) | 1 (0%) | 88 | 96 |
| 3 | BC | 176/176 (100%) | 176 (100%) | 0 | 100 | 100 |
| 4 | BD | 182/182 (100%) | 180 (99%) | 2 (1%) | 73 | 90 |
| 5 | BE | 221/221 (100%) | 220 (100%) | 1 (0%) | 88 | 96 |
| 6 | BF | 173/173 (100%) | 173 (100%) | 0 | 100 | 100 |
| 7 | BG | 193/193 (100%) | 192 (100%) | 1 (0%) | 88 | 96 |
| 8 | BH | 165/165 (100%) | 165 (100%) | 0 | 100 | 100 |
| 9 | BI | 150/150 (100%) | 150 (100%) | 0 | 100 | 100 |
| 10 | BJ | 158/158 (100%) | 158 (100%) | 0 | 100 | 100 |
| 11 | BK | 89/89 (100%) | 89 (100%) | 0 | 100 | 100 |
| 12 | BL | 136/136 (100%) | 135 (99%) | 1 (1%) | 84 | 94 |
| 13 | BM | 98/98 (100%) | 98 (100%) | 0 | 100 | 100 |
| 14 | BN | 127/127 (100%) | 127 (100%) | 0 | 100 | 100 |
| 15 | BO | 96/96 (100%) | 96 (100%) | 0 | 100 | 100 |
| 16 | BP | 104/104 (100%) | 104 (100%) | 0 | 100 | 100 |
| 17 | BQ | 117/117 (100%) | 117 (100%) | 0 | 100 | 100 |
| 18 | BR | 110/110 (100%) | 110 (100%) | 0 | 100 | 100 |
| 19 | BS | 128/128 (100%) | 128 (100%) | 0 | 100 | 100 |
| 20 | BT | 113/113 (100%) | 113 (100%) | 0 | 100 | 100 |
| 21 | BU | 100/100 (100%) | 99 (99%) | 1 (1%) | 76 | 91 |
| 22 | BV | 74/74 (100%) | 74 (100%) | 0 | 100 | 100 |
| 23 | BW | 110/110 (100%) | 110 (100%) | 0 | 100 | 100 |
| 24 | BX | 119/119 (100%) | 119 (100%) | 0 | 100 | 100 |
| 25 | BY | 112/112 (100%) | 110 (98%) | 2 (2%) | 59 | 83 |
| 26 | BZ | 61/61 (100%) | 61 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|------------|----------|-------------|-----|
| 27 | Ba | 83/83 (100%) | 82 (99%) | 1 (1%) | 71 | 88 |
| 28 | Bb | 70/70 (100%) | 70 (100%) | 0 | 100 | 100 |
| 29 | Bc | 56/56 (100%) | 54 (96%) | 2 (4%) | 35 | 64 |
| 30 | Bd | 47/47 (100%) | 46 (98%) | 1 (2%) | 53 | 80 |
| 31 | Be | 51/51 (100%) | 50 (98%) | 1 (2%) | 55 | 81 |
| 32 | Bf | 49/49 (100%) | 49 (100%) | 0 | 100 | 100 |
| 33 | Bg | 256/257 (100%) | 255 (100%) | 1 (0%) | 91 | 97 |
| 34 | Bh | 68/68 (100%) | 65 (96%) | 3 (4%) | 28 | 56 |
| 39 | AA | 189/189 (100%) | 189 (100%) | 0 | 100 | 100 |
| 40 | AB | 319/321 (99%) | 318 (100%) | 1 (0%) | 92 | 98 |
| 41 | AC | 288/288 (100%) | 287 (100%) | 1 (0%) | 92 | 98 |
| 42 | AD | 241/241 (100%) | 241 (100%) | 0 | 100 | 100 |
| 43 | AE | 134/134 (100%) | 133 (99%) | 1 (1%) | 84 | 94 |
| 44 | AF | 186/186 (100%) | 185 (100%) | 1 (0%) | 88 | 96 |
| 45 | AG | 189/189 (100%) | 189 (100%) | 0 | 100 | 100 |
| 46 | AH | 170/170 (100%) | 169 (99%) | 1 (1%) | 86 | 95 |
| 47 | AI | 176/176 (100%) | 174 (99%) | 2 (1%) | 73 | 90 |
| 48 | AJ | 147/147 (100%) | 147 (100%) | 0 | 100 | 100 |
| 49 | AL | 154/154 (100%) | 154 (100%) | 0 | 100 | 100 |
| 50 | AM | 107/107 (100%) | 107 (100%) | 0 | 100 | 100 |
| 51 | AN | 175/175 (100%) | 175 (100%) | 0 | 100 | 100 |
| 52 | AO | 160/160 (100%) | 160 (100%) | 0 | 100 | 100 |
| 53 | AP | 141/141 (100%) | 140 (99%) | 1 (1%) | 84 | 94 |
| 54 | AQ | 150/150 (100%) | 150 (100%) | 0 | 100 | 100 |
| 55 | AR | 153/153 (100%) | 153 (100%) | 0 | 100 | 100 |
| 56 | AS | 156/156 (100%) | 156 (100%) | 0 | 100 | 100 |
| 57 | AT | 136/136 (100%) | 135 (99%) | 1 (1%) | 84 | 94 |
| 58 | AU | 87/87 (100%) | 87 (100%) | 0 | 100 | 100 |
| 59 | AV | 104/104 (100%) | 104 (100%) | 0 | 100 | 100 |
| 60 | AW | 55/55 (100%) | 55 (100%) | 0 | 100 | 100 |
| 61 | AX | 105/105 (100%) | 105 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|------------------|-------------|----------|-------------|-----|
| 62 | AY | 109/109 (100%) | 109 (100%) | 0 | 100 | 100 |
| 63 | AZ | 115/115 (100%) | 115 (100%) | 0 | 100 | 100 |
| 64 | Aa | 118/118 (100%) | 118 (100%) | 0 | 100 | 100 |
| 65 | Ab | 46/46 (100%) | 46 (100%) | 0 | 100 | 100 |
| 66 | Ac | 81/81 (100%) | 81 (100%) | 0 | 100 | 100 |
| 67 | Ad | 96/96 (100%) | 96 (100%) | 0 | 100 | 100 |
| 68 | Ae | 109/109 (100%) | 109 (100%) | 0 | 100 | 100 |
| 69 | Af | 90/90 (100%) | 90 (100%) | 0 | 100 | 100 |
| 70 | Ag | 95/95 (100%) | 95 (100%) | 0 | 100 | 100 |
| 71 | Ah | 104/104 (100%) | 103 (99%) | 1 (1%) | 76 | 91 |
| 72 | Ai | 81/81 (100%) | 81 (100%) | 0 | 100 | 100 |
| 73 | Aj | 70/70 (100%) | 70 (100%) | 0 | 100 | 100 |
| 74 | Ak | 68/68 (100%) | 68 (100%) | 0 | 100 | 100 |
| 75 | Al | 45/45 (100%) | 45 (100%) | 0 | 100 | 100 |
| 76 | Am | 47/47 (100%) | 47 (100%) | 0 | 100 | 100 |
| 77 | An | 23/23 (100%) | 23 (100%) | 0 | 100 | 100 |
| 78 | Ao | 90/90 (100%) | 90 (100%) | 0 | 100 | 100 |
| 79 | Ap | 71/71 (100%) | 71 (100%) | 0 | 100 | 100 |
| All | All | 9336/9339 (100%) | 9308 (100%) | 28 (0%) | 92 | 98 |

5 of 28 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 33 | Bg | 118 | LYS |
| 71 | Ah | 94 | LYS |
| 34 | Bh | 88 | ARG |
| 47 | AI | 191 | LYS |
| 34 | Bh | 70 | ASN |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 64 | Aa | 49 | HIS |
| 67 | Ad | 57 | GLN |
| 41 | AC | 110 | ASN |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 42 | AD | 151 | GLN |
| 48 | AJ | 95 | ASN |

5.3.3 RNA [i](#)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 35 | B5 | 1774/1781 (99%) | 472 (26%) | 12 (0%) |
| 36 | A1 | 3130/3137 (99%) | 706 (22%) | 17 (0%) |
| 37 | A3 | 120/121 (99%) | 13 (10%) | 0 |
| 38 | A4 | 156/158 (98%) | 37 (23%) | 1 (0%) |
| All | All | 5180/5197 (99%) | 1228 (23%) | 30 (0%) |

5 of 1228 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 35 | B5 | 2 | A |
| 35 | B5 | 4 | C |
| 35 | B5 | 17 | C |
| 35 | B5 | 25 | C |
| 35 | B5 | 26 | A |

5 of 30 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 36 | A1 | 282 | G |
| 36 | A1 | 2870 | 5MC |
| 36 | A1 | 873 | C |
| 38 | A4 | 67 | U |
| 36 | A1 | 2372 | A |

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

110 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 |
| 36 | UY1 | A1 | 2347 | 36 | 19,22,23 | 2.59 | 3 (15%) | 22,31,34 | 2.48 | 4 (18%) |
| 36 | OMU | A1 | 2417 | 36 | 19,22,23 | 1.37 | 3 (15%) | 26,31,34 | 1.75 | 4 (15%) |
| 36 | OMG | A1 | 908 | 36 | 18,26,27 | 1.00 | 1 (5%) | 19,38,41 | 1.46 | 4 (21%) |
| 35 | PSU | B5 | 106 | 35 | 18,21,22 | 1.50 | 4 (22%) | 22,30,33 | 1.92 | 3 (13%) |
| 36 | PSU | A1 | 1042 | 36 | 18,21,22 | 1.45 | 3 (16%) | 22,30,33 | 1.84 | 4 (18%) |
| 35 | PSU | B5 | 1290 | 35 | 18,21,22 | 1.60 | 5 (27%) | 22,30,33 | 2.09 | 3 (13%) |
| 35 | A2M | B5 | 619 | 80,35 | 18,25,26 | 0.94 | 0 | 18,36,39 | 1.44 | 2 (11%) |
| 36 | OMU | A1 | 1888 | 36,80 | 19,22,23 | 1.27 | 3 (15%) | 26,31,34 | 1.82 | 4 (15%) |
| 36 | PSU | A1 | 2260 | 36 | 18,21,22 | 1.49 | 3 (16%) | 22,30,33 | 1.84 | 4 (18%) |
| 35 | MA6 | B5 | 1781 | 35 | 19,26,27 | 0.90 | 1 (5%) | 18,38,41 | 1.42 | 2 (11%) |
| 36 | PSU | A1 | 2880 | 36 | 18,21,22 | 1.53 | 5 (27%) | 22,30,33 | 1.93 | 5 (22%) |
| 35 | A2M | B5 | 796 | 35 | 18,25,26 | 0.99 | 1 (5%) | 18,36,39 | 1.34 | 3 (16%) |
| 35 | OMG | B5 | 562 | 35 | 18,26,27 | 0.98 | 1 (5%) | 19,38,41 | 1.14 | 2 (10%) |
| 36 | PSU | A1 | 2865 | 36 | 18,21,22 | 1.45 | 5 (27%) | 22,30,33 | 1.91 | 3 (13%) |
| 36 | A2M | A1 | 817 | 36,80 | 18,25,26 | 0.91 | 0 | 18,36,39 | 1.42 | 2 (11%) |
| 35 | PSU | B5 | 999 | 35 | 18,21,22 | 1.39 | 3 (16%) | 22,30,33 | 1.88 | 3 (13%) |
| 35 | PSU | B5 | 759 | 35 | 18,21,22 | 1.49 | 4 (22%) | 22,30,33 | 1.91 | 4 (18%) |
| 35 | MA6 | B5 | 1782 | 80,35 | 19,26,27 | 0.82 | 1 (5%) | 18,38,41 | 1.47 | 2 (11%) |
| 36 | OMC | A1 | 663 | 36 | 19,22,23 | 0.85 | 1 (5%) | 26,31,34 | 0.95 | 1 (3%) |
| 36 | A2M | A1 | 2220 | 36 | 18,25,26 | 0.94 | 1 (5%) | 18,36,39 | 1.66 | 2 (11%) |
| 35 | PSU | B5 | 766 | 35 | 18,21,22 | 1.49 | 5 (27%) | 22,30,33 | 1.99 | 4 (18%) |
| 36 | A2M | A1 | 2280 | 36,80 | 18,25,26 | 0.93 | 1 (5%) | 18,36,39 | 1.29 | 3 (16%) |
| 36 | PSU | A1 | 2129 | 36 | 18,21,22 | 1.54 | 4 (22%) | 22,30,33 | 2.01 | 4 (18%) |
| 36 | OMG | A1 | 2815 | 36 | 18,26,27 | 1.04 | 1 (5%) | 19,38,41 | 1.09 | 2 (10%) |
| 35 | 4AC | B5 | 1280 | 35 | 21,24,25 | 1.03 | 1 (4%) | 29,34,37 | 2.45 | 8 (27%) |
| 35 | PSU | B5 | 120 | 35 | 18,21,22 | 1.45 | 4 (22%) | 22,30,33 | 1.86 | 4 (18%) |
| 36 | PSU | A1 | 1004 | 36 | 18,21,22 | 1.44 | 4 (22%) | 22,30,33 | 1.91 | 3 (13%) |
| 36 | OMU | A1 | 2921 | 36,80 | 19,22,23 | 1.25 | 3 (15%) | 26,31,34 | 1.77 | 5 (19%) |
| 36 | PSU | A1 | 2349 | 36,80 | 18,21,22 | 1.53 | 4 (22%) | 22,30,33 | 1.85 | 4 (18%) |
| 35 | OMG | B5 | 1126 | 35 | 18,26,27 | 0.94 | 1 (5%) | 19,38,41 | 1.13 | 2 (10%) |
| 36 | PSU | A1 | 2266 | 36 | 18,21,22 | 1.41 | 4 (22%) | 22,30,33 | 1.98 | 5 (22%) |
| 36 | PSU | A1 | 2133 | 36 | 18,21,22 | 1.67 | 4 (22%) | 22,30,33 | 2.14 | 4 (18%) |
| 35 | OMC | B5 | 1007 | 35 | 19,22,23 | 0.93 | 1 (5%) | 26,31,34 | 1.35 | 3 (11%) |
| 36 | A2M | A1 | 807 | 36 | 18,25,26 | 1.05 | 1 (5%) | 18,36,39 | 1.60 | 3 (16%) |
| 35 | PSU | B5 | 302 | 35 | 18,21,22 | 1.48 | 4 (22%) | 22,30,33 | 2.00 | 4 (18%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|------|-------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 36 | 5MC | A1 | 2870 | 36,80 | 18,22,23 | 1.10 | 2 (11%) | 26,32,35 | 1.52 | 5 (19%) |
| 36 | OMG | A1 | 2922 | 36 | 18,26,27 | 0.92 | 1 (5%) | 19,38,41 | 1.05 | 2 (10%) |
| 35 | PSU | B5 | 1187 | 35 | 18,21,22 | 1.50 | 4 (22%) | 22,30,33 | 1.91 | 3 (13%) |
| 35 | OMC | B5 | 1639 | 35 | 19,22,23 | 0.84 | 0 | 26,31,34 | 0.78 | 1 (3%) |
| 35 | OMC | B5 | 414 | 35 | 19,22,23 | 0.82 | 0 | 26,31,34 | 0.80 | 1 (3%) |
| 35 | B8N | B5 | 1191 | 35 | 24,29,30 | 0.96 | 1 (4%) | 29,42,45 | 1.60 | 4 (13%) |
| 35 | PSU | B5 | 466 | 35 | 18,21,22 | 1.51 | 4 (22%) | 22,30,33 | 1.88 | 5 (22%) |
| 35 | A2M | B5 | 541 | 35 | 18,25,26 | 0.97 | 1 (5%) | 18,36,39 | 1.25 | 2 (11%) |
| 36 | PSU | A1 | 776 | 36 | 18,21,22 | 1.54 | 4 (22%) | 22,30,33 | 2.21 | 6 (27%) |
| 36 | A2M | A1 | 2946 | 36,80 | 18,25,26 | 0.98 | 1 (5%) | 18,36,39 | 1.37 | 3 (16%) |
| 36 | PSU | A1 | 990 | 36 | 18,21,22 | 1.46 | 3 (16%) | 22,30,33 | 1.97 | 3 (13%) |
| 36 | OMC | A1 | 650 | 36,80 | 19,22,23 | 0.80 | 1 (5%) | 26,31,34 | 0.88 | 1 (3%) |
| 35 | G7M | B5 | 1575 | 35 | 20,26,27 | 2.56 | 4 (20%) | 17,39,42 | 1.15 | 1 (5%) |
| 36 | PSU | A1 | 960 | 36 | 18,21,22 | 1.48 | 3 (16%) | 22,30,33 | 1.92 | 3 (13%) |
| 36 | 1MA | A1 | 645 | 36,80 | 16,25,26 | 1.24 | 2 (12%) | 18,37,40 | 1.10 | 2 (11%) |
| 36 | OMG | A1 | 2791 | 36 | 18,26,27 | 0.99 | 1 (5%) | 19,38,41 | 1.10 | 2 (10%) |
| 35 | PSU | B5 | 1415 | 35 | 18,21,22 | 1.60 | 4 (22%) | 22,30,33 | 1.97 | 4 (18%) |
| 36 | PSU | A1 | 1056 | 36 | 18,21,22 | 1.57 | 4 (22%) | 22,30,33 | 1.97 | 4 (18%) |
| 36 | OMG | A1 | 2288 | 36 | 18,26,27 | 1.06 | 1 (5%) | 19,38,41 | 1.02 | 2 (10%) |
| 36 | OMU | A1 | 898 | 36 | 19,22,23 | 1.34 | 4 (21%) | 26,31,34 | 1.77 | 5 (19%) |
| 36 | PSU | A1 | 2191 | 36 | 18,21,22 | 1.55 | 4 (22%) | 22,30,33 | 2.14 | 4 (18%) |
| 36 | PSU | A1 | 2340 | 36,80 | 18,21,22 | 1.62 | 4 (22%) | 22,30,33 | 1.92 | 4 (18%) |
| 36 | PSU | A1 | 2923 | 36 | 18,21,22 | 1.44 | 4 (22%) | 22,30,33 | 1.92 | 3 (13%) |
| 36 | A2M | A1 | 876 | 36 | 18,25,26 | 0.91 | 0 | 18,36,39 | 1.30 | 2 (11%) |
| 36 | OMU | A1 | 2729 | 36 | 19,22,23 | 1.38 | 4 (21%) | 26,31,34 | 1.62 | 7 (26%) |
| 35 | PSU | B5 | 211 | 35 | 18,21,22 | 1.49 | 4 (22%) | 22,30,33 | 1.95 | 3 (13%) |
| 35 | A2M | B5 | 974 | 35 | 18,25,26 | 0.91 | 1 (5%) | 18,36,39 | 1.20 | 2 (11%) |
| 36 | PSU | A1 | 2944 | 36,80 | 18,21,22 | 1.53 | 5 (27%) | 22,30,33 | 1.96 | 5 (22%) |
| 36 | PSU | A1 | 2975 | 36 | 18,21,22 | 1.49 | 4 (22%) | 22,30,33 | 2.01 | 4 (18%) |
| 35 | A2M | B5 | 420 | 35 | 18,25,26 | 0.93 | 1 (5%) | 18,36,39 | 1.32 | 3 (16%) |
| 36 | OMC | A1 | 2337 | 36 | 19,22,23 | 0.77 | 1 (5%) | 26,31,34 | 0.94 | 1 (3%) |
| 36 | PSU | A1 | 2826 | 36,80 | 18,21,22 | 1.53 | 5 (27%) | 22,30,33 | 2.17 | 5 (22%) |
| 36 | PSU | A1 | 2416 | 36,80 | 18,21,22 | 1.55 | 5 (27%) | 22,30,33 | 1.99 | 4 (18%) |
| 36 | PSU | A1 | 986 | 36 | 18,21,22 | 1.55 | 4 (22%) | 22,30,33 | 1.82 | 4 (18%) |
| 36 | PSU | A1 | 2264 | 36 | 18,21,22 | 1.37 | 3 (16%) | 22,30,33 | 1.95 | 4 (18%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|------|-------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 36 | A2M | A1 | 2640 | 36 | 18,25,26 | 0.95 | 0 | 18,36,39 | 1.16 | 2 (11%) |
| 36 | PSU | A1 | 2351 | 36 | 18,21,22 | 1.53 | 4 (22%) | 22,30,33 | 1.89 | 4 (18%) |
| 35 | OMG | B5 | 1428 | 80,35 | 18,26,27 | 1.00 | 1 (5%) | 19,38,41 | 1.18 | 2 (10%) |
| 36 | A2M | A1 | 2281 | 36,80 | 18,25,26 | 0.83 | 0 | 18,36,39 | 1.43 | 2 (11%) |
| 35 | OMU | B5 | 1269 | 80,35 | 19,22,23 | 1.31 | 4 (21%) | 26,31,34 | 1.87 | 7 (26%) |
| 36 | OMU | A1 | 2421 | 36 | 19,22,23 | 1.31 | 3 (15%) | 26,31,34 | 1.80 | 4 (15%) |
| 36 | PSU | A1 | 966 | 36,80 | 18,21,22 | 1.44 | 5 (27%) | 22,30,33 | 1.93 | 4 (18%) |
| 40 | HIC | AB | 243 | 40 | 8,11,12 | 1.42 | 1 (12%) | 6,14,16 | 0.73 | 0 |
| 36 | OMG | A1 | 1450 | 36 | 18,26,27 | 1.08 | 1 (5%) | 19,38,41 | 1.03 | 3 (15%) |
| 36 | OMC | A1 | 2959 | 36 | 19,22,23 | 0.82 | 0 | 26,31,34 | 0.96 | 1 (3%) |
| 36 | PSU | A1 | 1110 | 36 | 18,21,22 | 1.51 | 4 (22%) | 22,30,33 | 2.08 | 3 (13%) |
| 36 | PSU | A1 | 1052 | 36,80 | 18,21,22 | 1.46 | 4 (22%) | 22,30,33 | 1.97 | 3 (13%) |
| 35 | 4AC | B5 | 1773 | 35 | 21,24,25 | 1.11 | 3 (14%) | 29,34,37 | 2.62 | 7 (24%) |
| 36 | OMG | A1 | 2619 | 36,80 | 18,26,27 | 0.93 | 1 (5%) | 19,38,41 | 1.08 | 2 (10%) |
| 36 | A2M | A1 | 649 | 36 | 18,25,26 | 0.90 | 1 (5%) | 18,36,39 | 1.25 | 1 (5%) |
| 36 | 5MC | A1 | 2278 | 36,80 | 18,22,23 | 0.97 | 2 (11%) | 26,32,35 | 1.36 | 3 (11%) |
| 36 | OMG | A1 | 2793 | 36 | 18,26,27 | 1.00 | 1 (5%) | 19,38,41 | 1.10 | 3 (15%) |
| 36 | OMC | A1 | 2948 | 36,80 | 19,22,23 | 0.87 | 1 (5%) | 26,31,34 | 1.26 | 3 (11%) |
| 36 | PSU | A1 | 2735 | 36 | 18,21,22 | 1.48 | 5 (27%) | 22,30,33 | 1.92 | 4 (18%) |
| 35 | PSU | B5 | 632 | 35 | 18,21,22 | 1.60 | 5 (27%) | 22,30,33 | 1.94 | 4 (18%) |
| 35 | A2M | B5 | 28 | 80,35 | 18,25,26 | 0.95 | 1 (5%) | 18,36,39 | 1.26 | 3 (16%) |
| 36 | OMC | A1 | 1437 | 36,80 | 19,22,23 | 0.86 | 1 (5%) | 26,31,34 | 1.48 | 4 (15%) |
| 36 | OMG | A1 | 867 | 36 | 18,26,27 | 0.89 | 1 (5%) | 19,38,41 | 1.15 | 2 (10%) |
| 35 | A2M | B5 | 436 | 35 | 18,25,26 | 0.91 | 1 (5%) | 18,36,39 | 1.30 | 2 (11%) |
| 35 | OMU | B5 | 578 | 35 | 19,22,23 | 1.20 | 2 (10%) | 26,31,34 | 1.76 | 5 (19%) |
| 35 | OMG | B5 | 1572 | 35 | 18,26,27 | 0.98 | 1 (5%) | 19,38,41 | 1.11 | 1 (5%) |
| 36 | PSU | A1 | 2314 | 36 | 18,21,22 | 1.47 | 3 (16%) | 22,30,33 | 1.85 | 3 (13%) |
| 36 | A2M | A1 | 1449 | 36,80 | 18,25,26 | 0.94 | 1 (5%) | 18,36,39 | 1.31 | 2 (11%) |
| 37 | PSU | A3 | 50 | 37 | 18,21,22 | 1.44 | 3 (16%) | 22,30,33 | 1.93 | 3 (13%) |
| 36 | PSU | A1 | 1124 | 36 | 18,21,22 | 1.54 | 4 (22%) | 22,30,33 | 1.95 | 3 (13%) |
| 35 | PSU | B5 | 1181 | 35 | 18,21,22 | 1.54 | 4 (22%) | 22,30,33 | 1.90 | 3 (13%) |
| 35 | OMG | B5 | 1271 | 35 | 18,26,27 | 0.95 | 1 (5%) | 19,38,41 | 1.11 | 3 (15%) |
| 36 | OMU | A1 | 2724 | 36 | 19,22,23 | 1.26 | 3 (15%) | 26,31,34 | 1.65 | 5 (19%) |
| 36 | OMG | A1 | 805 | 36 | 18,26,27 | 0.95 | 1 (5%) | 19,38,41 | 1.28 | 3 (15%) |
| 36 | UR3 | A1 | 2634 | 36,80 | 19,22,23 | 0.93 | 1 (5%) | 26,32,35 | 1.45 | 2 (7%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|------|-------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 36 | OMC | A1 | 2197 | 36,80 | 19,22,23 | 0.80 | 0 | 26,31,34 | 0.87 | 1 (3%) |
| 38 | PSU | A4 | 73 | 38 | 18,21,22 | 1.48 | 4 (22%) | 22,30,33 | 1.97 | 4 (18%) |
| 36 | A2M | A1 | 1133 | 36,80 | 18,25,26 | 0.96 | 1 (5%) | 18,36,39 | 1.44 | 3 (16%) |
| 35 | A2M | B5 | 100 | 80,35 | 18,25,26 | 0.95 | 1 (5%) | 18,36,39 | 1.18 | 2 (11%) |
| 36 | 1MA | A1 | 2142 | 36,80 | 16,25,26 | 1.38 | 2 (12%) | 18,37,40 | 1.28 | 3 (16%) |

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 |
|-----|------|-------|------|-------|---------|------------|---------|
| 36 | UY1 | A1 | 2347 | 36 | - | 2/9/27/28 | 0/2/2/2 |
| 36 | OMU | A1 | 2417 | 36 | - | 1/9/27/28 | 0/2/2/2 |
| 36 | OMG | A1 | 908 | 36 | - | 3/5/27/28 | 0/3/3/3 |
| 35 | PSU | B5 | 106 | 35 | - | 0/7/25/26 | 0/2/2/2 |
| 36 | PSU | A1 | 1042 | 36 | - | 0/7/25/26 | 0/2/2/2 |
| 35 | PSU | B5 | 1290 | 35 | - | 0/7/25/26 | 0/2/2/2 |
| 35 | A2M | B5 | 619 | 80,35 | - | 2/5/27/28 | 0/3/3/3 |
| 36 | OMU | A1 | 1888 | 36,80 | - | 0/9/27/28 | 0/2/2/2 |
| 36 | PSU | A1 | 2260 | 36 | - | 2/7/25/26 | 0/2/2/2 |
| 35 | MA6 | B5 | 1781 | 35 | - | 0/7/29/30 | 0/3/3/3 |
| 36 | PSU | A1 | 2880 | 36 | - | 0/7/25/26 | 0/2/2/2 |
| 35 | A2M | B5 | 796 | 35 | - | 0/5/27/28 | 0/3/3/3 |
| 35 | OMG | B5 | 562 | 35 | - | 0/5/27/28 | 0/3/3/3 |
| 36 | PSU | A1 | 2865 | 36 | - | 0/7/25/26 | 0/2/2/2 |
| 36 | A2M | A1 | 817 | 36,80 | - | 2/5/27/28 | 0/3/3/3 |
| 35 | PSU | B5 | 999 | 35 | - | 0/7/25/26 | 0/2/2/2 |
| 35 | PSU | B5 | 759 | 35 | - | 0/7/25/26 | 0/2/2/2 |
| 35 | MA6 | B5 | 1782 | 80,35 | - | 3/7/29/30 | 0/3/3/3 |
| 36 | OMC | A1 | 663 | 36 | - | 0/9/27/28 | 0/2/2/2 |
| 36 | A2M | A1 | 2220 | 36 | - | 0/5/27/28 | 0/3/3/3 |
| 35 | PSU | B5 | 766 | 35 | - | 1/7/25/26 | 0/2/2/2 |
| 36 | A2M | A1 | 2280 | 36,80 | - | 2/5/27/28 | 0/3/3/3 |
| 36 | PSU | A1 | 2129 | 36 | - | 0/7/25/26 | 0/2/2/2 |
| 36 | OMG | A1 | 2815 | 36 | - | 0/5/27/28 | 0/3/3/3 |
| 35 | 4AC | B5 | 1280 | 35 | - | 3/11/29/30 | 0/2/2/2 |
| 35 | PSU | B5 | 120 | 35 | - | 0/7/25/26 | 0/2/2/2 |
| 36 | PSU | A1 | 1004 | 36 | - | 0/7/25/26 | 0/2/2/2 |
| 36 | OMU | A1 | 2921 | 36,80 | - | 0/9/27/28 | 0/2/2/2 |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|------|-------|---------|------------|---------|
| 36 | PSU | A1 | 2349 | 36,80 | - | 0/7/25/26 | 0/2/2/2 |
| 35 | OMG | B5 | 1126 | 35 | - | 0/5/27/28 | 0/3/3/3 |
| 36 | PSU | A1 | 2266 | 36 | - | 3/7/25/26 | 0/2/2/2 |
| 36 | PSU | A1 | 2133 | 36 | - | 0/7/25/26 | 0/2/2/2 |
| 35 | OMC | B5 | 1007 | 35 | - | 1/9/27/28 | 0/2/2/2 |
| 36 | A2M | A1 | 807 | 36 | - | 3/5/27/28 | 0/3/3/3 |
| 35 | PSU | B5 | 302 | 35 | - | 1/7/25/26 | 0/2/2/2 |
| 36 | 5MC | A1 | 2870 | 36,80 | - | 4/7/25/26 | 0/2/2/2 |
| 36 | OMG | A1 | 2922 | 36 | - | 1/5/27/28 | 0/3/3/3 |
| 35 | PSU | B5 | 1187 | 35 | - | 0/7/25/26 | 0/2/2/2 |
| 35 | OMC | B5 | 1639 | 35 | - | 1/9/27/28 | 0/2/2/2 |
| 35 | OMC | B5 | 414 | 35 | - | 0/9/27/28 | 0/2/2/2 |
| 35 | B8N | B5 | 1191 | 35 | - | 0/16/34/35 | 0/2/2/2 |
| 35 | PSU | B5 | 466 | 35 | - | 0/7/25/26 | 0/2/2/2 |
| 35 | A2M | B5 | 541 | 35 | - | 3/5/27/28 | 0/3/3/3 |
| 36 | PSU | A1 | 776 | 36 | - | 4/7/25/26 | 0/2/2/2 |
| 36 | A2M | A1 | 2946 | 36,80 | - | 1/5/27/28 | 0/3/3/3 |
| 36 | PSU | A1 | 990 | 36 | - | 0/7/25/26 | 0/2/2/2 |
| 36 | OMC | A1 | 650 | 36,80 | - | 0/9/27/28 | 0/2/2/2 |
| 35 | G7M | B5 | 1575 | 35 | 3/3/5/5 | 2/3/25/26 | 0/3/3/3 |
| 36 | PSU | A1 | 960 | 36 | - | 1/7/25/26 | 0/2/2/2 |
| 36 | 1MA | A1 | 645 | 36,80 | - | 0/3/25/26 | 0/3/3/3 |
| 36 | OMG | A1 | 2791 | 36 | - | 0/5/27/28 | 0/3/3/3 |
| 35 | PSU | B5 | 1415 | 35 | - | 1/7/25/26 | 0/2/2/2 |
| 36 | PSU | A1 | 1056 | 36 | - | 0/7/25/26 | 0/2/2/2 |
| 36 | OMG | A1 | 2288 | 36 | - | 2/5/27/28 | 0/3/3/3 |
| 36 | OMU | A1 | 898 | 36 | - | 0/9/27/28 | 0/2/2/2 |
| 36 | PSU | A1 | 2191 | 36 | - | 0/7/25/26 | 0/2/2/2 |
| 36 | PSU | A1 | 2340 | 36,80 | - | 1/7/25/26 | 0/2/2/2 |
| 36 | PSU | A1 | 2923 | 36 | - | 5/7/25/26 | 0/2/2/2 |
| 36 | A2M | A1 | 876 | 36 | - | 0/5/27/28 | 0/3/3/3 |
| 36 | OMU | A1 | 2729 | 36 | - | 3/9/27/28 | 0/2/2/2 |
| 35 | PSU | B5 | 211 | 35 | - | 0/7/25/26 | 0/2/2/2 |
| 35 | A2M | B5 | 974 | 35 | - | 0/5/27/28 | 0/3/3/3 |
| 36 | PSU | A1 | 2944 | 36,80 | - | 0/7/25/26 | 0/2/2/2 |
| 36 | PSU | A1 | 2975 | 36 | - | 0/7/25/26 | 0/2/2/2 |
| 35 | A2M | B5 | 420 | 35 | - | 0/5/27/28 | 0/3/3/3 |
| 36 | OMC | A1 | 2337 | 36 | - | 0/9/27/28 | 0/2/2/2 |
| 36 | PSU | A1 | 2826 | 36,80 | - | 0/7/25/26 | 0/2/2/2 |
| 36 | PSU | A1 | 2416 | 36,80 | - | 0/7/25/26 | 0/2/2/2 |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|------|-------|---------|------------|---------|
| 36 | PSU | A1 | 986 | 36 | - | 0/7/25/26 | 0/2/2/2 |
| 36 | PSU | A1 | 2264 | 36 | - | 0/7/25/26 | 0/2/2/2 |
| 36 | A2M | A1 | 2640 | 36 | - | 1/5/27/28 | 0/3/3/3 |
| 36 | PSU | A1 | 2351 | 36 | - | 0/7/25/26 | 0/2/2/2 |
| 35 | OMG | B5 | 1428 | 80,35 | - | 3/5/27/28 | 0/3/3/3 |
| 36 | A2M | A1 | 2281 | 36,80 | - | 2/5/27/28 | 0/3/3/3 |
| 35 | OMU | B5 | 1269 | 80,35 | - | 2/9/27/28 | 0/2/2/2 |
| 36 | OMU | A1 | 2421 | 36 | - | 0/9/27/28 | 0/2/2/2 |
| 36 | PSU | A1 | 966 | 36,80 | - | 0/7/25/26 | 0/2/2/2 |
| 40 | HIC | AB | 243 | 40 | - | 1/5/6/8 | 0/1/1/1 |
| 36 | OMG | A1 | 1450 | 36 | - | 2/5/27/28 | 0/3/3/3 |
| 36 | OMC | A1 | 2959 | 36 | - | 0/9/27/28 | 0/2/2/2 |
| 36 | PSU | A1 | 1110 | 36 | - | 0/7/25/26 | 0/2/2/2 |
| 36 | PSU | A1 | 1052 | 36,80 | - | 2/7/25/26 | 0/2/2/2 |
| 35 | 4AC | B5 | 1773 | 35 | - | 4/11/29/30 | 0/2/2/2 |
| 36 | OMG | A1 | 2619 | 36,80 | - | 1/5/27/28 | 0/3/3/3 |
| 36 | A2M | A1 | 649 | 36 | - | 0/5/27/28 | 0/3/3/3 |
| 36 | 5MC | A1 | 2278 | 36,80 | - | 0/7/25/26 | 0/2/2/2 |
| 36 | OMG | A1 | 2793 | 36 | - | 0/5/27/28 | 0/3/3/3 |
| 36 | OMC | A1 | 2948 | 36,80 | - | 0/9/27/28 | 0/2/2/2 |
| 36 | PSU | A1 | 2735 | 36 | - | 0/7/25/26 | 0/2/2/2 |
| 35 | PSU | B5 | 632 | 35 | - | 0/7/25/26 | 0/2/2/2 |
| 35 | A2M | B5 | 28 | 80,35 | - | 0/5/27/28 | 0/3/3/3 |
| 36 | OMC | A1 | 1437 | 36,80 | - | 4/9/27/28 | 0/2/2/2 |
| 36 | OMG | A1 | 867 | 36 | - | 0/5/27/28 | 0/3/3/3 |
| 35 | A2M | B5 | 436 | 35 | - | 0/5/27/28 | 0/3/3/3 |
| 35 | OMU | B5 | 578 | 35 | - | 0/9/27/28 | 0/2/2/2 |
| 35 | OMG | B5 | 1572 | 35 | - | 0/5/27/28 | 0/3/3/3 |
| 36 | PSU | A1 | 2314 | 36 | - | 3/7/25/26 | 0/2/2/2 |
| 36 | A2M | A1 | 1449 | 36,80 | - | 0/5/27/28 | 0/3/3/3 |
| 37 | PSU | A3 | 50 | 37 | - | 1/7/25/26 | 0/2/2/2 |
| 36 | PSU | A1 | 1124 | 36 | - | 2/7/25/26 | 0/2/2/2 |
| 35 | PSU | B5 | 1181 | 35 | - | 0/7/25/26 | 0/2/2/2 |
| 35 | OMG | B5 | 1271 | 35 | - | 0/5/27/28 | 0/3/3/3 |
| 36 | OMU | A1 | 2724 | 36 | - | 0/9/27/28 | 0/2/2/2 |
| 36 | OMG | A1 | 805 | 36 | - | 0/5/27/28 | 0/3/3/3 |
| 36 | UR3 | A1 | 2634 | 36,80 | - | 0/7/25/26 | 0/2/2/2 |
| 36 | OMC | A1 | 2197 | 36,80 | - | 6/9/27/28 | 0/2/2/2 |
| 38 | PSU | A4 | 73 | 38 | - | 0/7/25/26 | 0/2/2/2 |
| 36 | A2M | A1 | 1133 | 36,80 | - | 0/5/27/28 | 0/3/3/3 |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|------|-------|---------|-----------|---------|
| 35 | A2M | B5 | 100 | 80,35 | - | 1/5/27/28 | 0/3/3/3 |
| 36 | 1MA | A1 | 2142 | 36,80 | - | 2/3/25/26 | 0/3/3/3 |

The worst 5 of 266 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|-------|------|-------------|----------|
| 36 | A1 | 2347 | UY1 | C6-C5 | 9.58 | 1.46 | 1.35 |
| 35 | B5 | 1575 | G7M | C8-N9 | 7.98 | 1.47 | 1.33 |
| 35 | B5 | 1575 | G7M | C8-N7 | 5.66 | 1.43 | 1.33 |
| 35 | B5 | 1575 | G7M | C5-C4 | 4.27 | 1.47 | 1.39 |
| 36 | A1 | 2142 | 1MA | C2-N3 | 4.25 | 1.34 | 1.29 |

The worst 5 of 352 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|----------|-------|-------------|----------|
| 35 | B5 | 1773 | 4AC | N4-C4-N3 | 9.89 | 130.45 | 113.85 |
| 35 | B5 | 1280 | 4AC | N4-C4-N3 | 8.81 | 128.63 | 113.85 |
| 36 | A1 | 2133 | PSU | N1-C2-N3 | 7.45 | 123.57 | 115.13 |
| 36 | A1 | 2347 | UY1 | C6-C5-C4 | -7.11 | 113.23 | 118.20 |
| 36 | A1 | 2826 | PSU | N1-C2-N3 | 6.98 | 123.04 | 115.13 |

All (3) chirality outliers are listed below:

| Mol | Chain | Res | Type | Atom |
|-----|-------|------|------|------|
| 35 | B5 | 1575 | G7M | C2' |
| 35 | B5 | 1575 | G7M | C3' |
| 35 | B5 | 1575 | G7M | C4' |

5 of 95 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|-----|-------|------|------|-----------------|
| 40 | AB | 243 | HIC | CA-CB-CG-ND1 |
| 35 | B5 | 619 | A2M | O4'-C4'-C5'-O5' |
| 35 | B5 | 619 | A2M | C3'-C4'-C5'-O5' |
| 35 | B5 | 1280 | 4AC | O7-C7-N4-C4 |
| 35 | B5 | 1280 | 4AC | CM7-C7-N4-C4 |

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 747 ligands modelled in this entry, 747 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](#)

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 36 | A1 | 5 |
| 53 | AP | 1 |
| 9 | BI | 1 |
| 35 | B5 | 1 |
| 43 | AE | 1 |
| 47 | AI | 1 |
| 32 | Bf | 1 |
| 18 | BR | 1 |
| 22 | BV | 1 |
| 38 | A4 | 1 |

The worst 5 of 14 chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1 | A1 | 1955:U | O3' | 2093:A | P | 25.26 |
| 1 | A1 | 1253:U | O3' | 1260:A | P | 24.88 |
| 1 | AP | 155:GLU | C | 164:LYS | N | 23.99 |

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| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1 | BI | 123:LYS | C | 135:LYS | N | 20.70 |
| 1 | B5 | 658:C | O3' | 676:G | P | 18.22 |

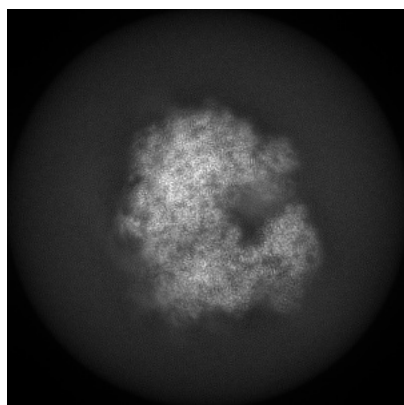
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23935. These allow visual inspection of the internal detail of the map and identification of artifacts.

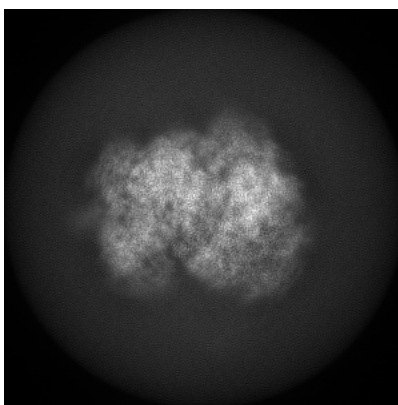
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

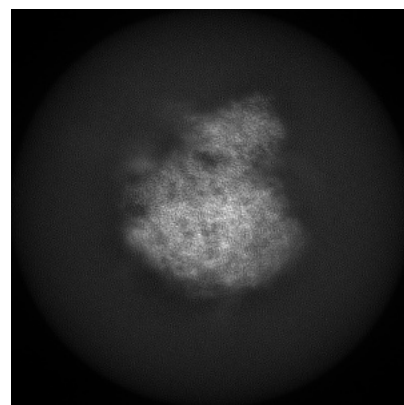
6.1.1 Primary map



X



Y

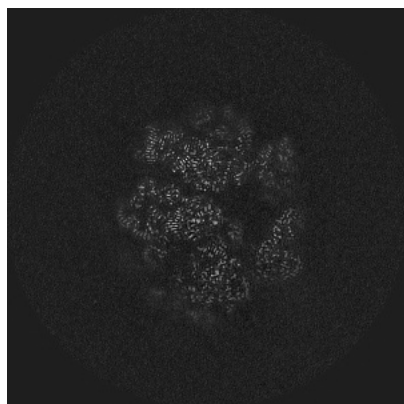


Z

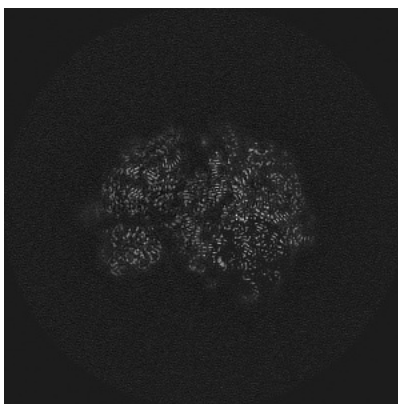
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

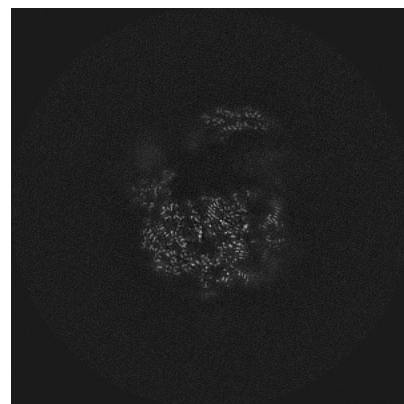
6.2.1 Primary map



X Index: 216



Y Index: 216

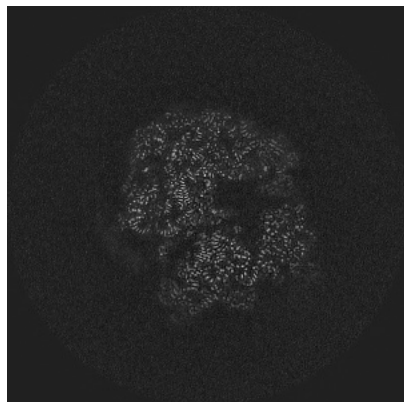


Z Index: 216

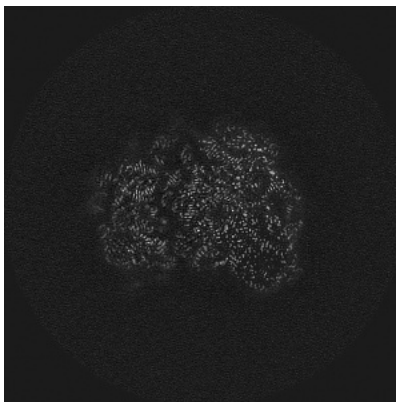
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

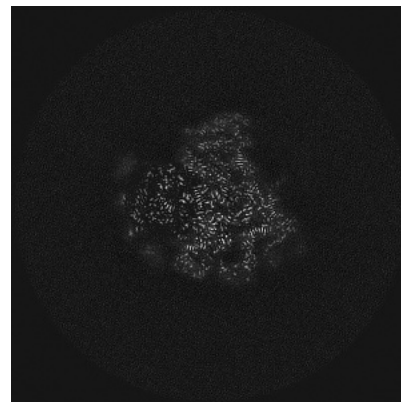
6.3.1 Primary map



X Index: 236



Y Index: 206

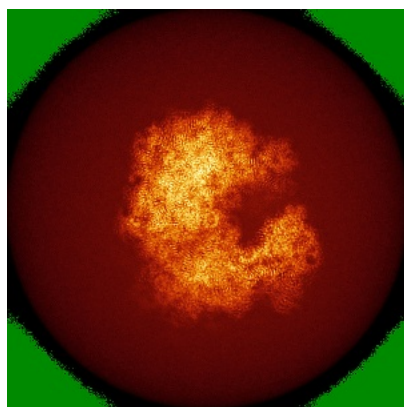


Z Index: 266

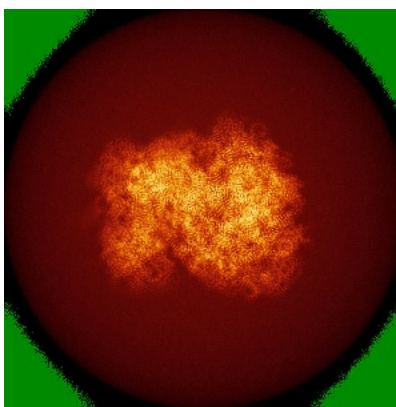
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

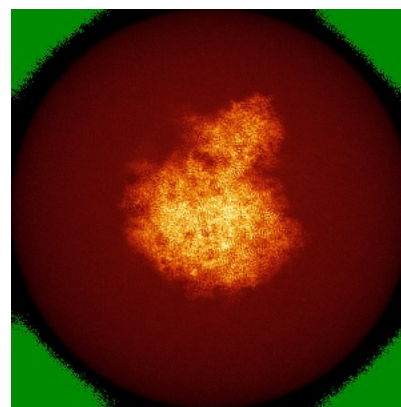
6.4.1 Primary map



X



Y

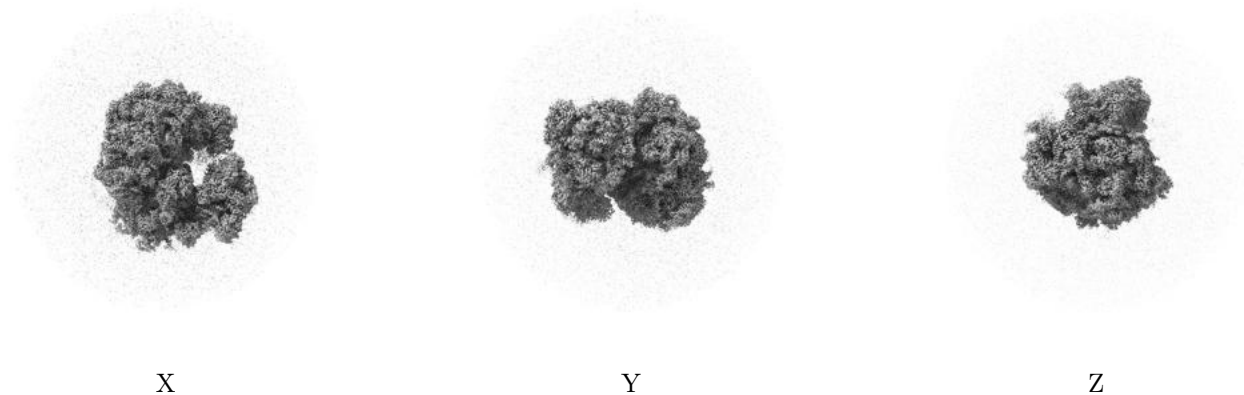


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

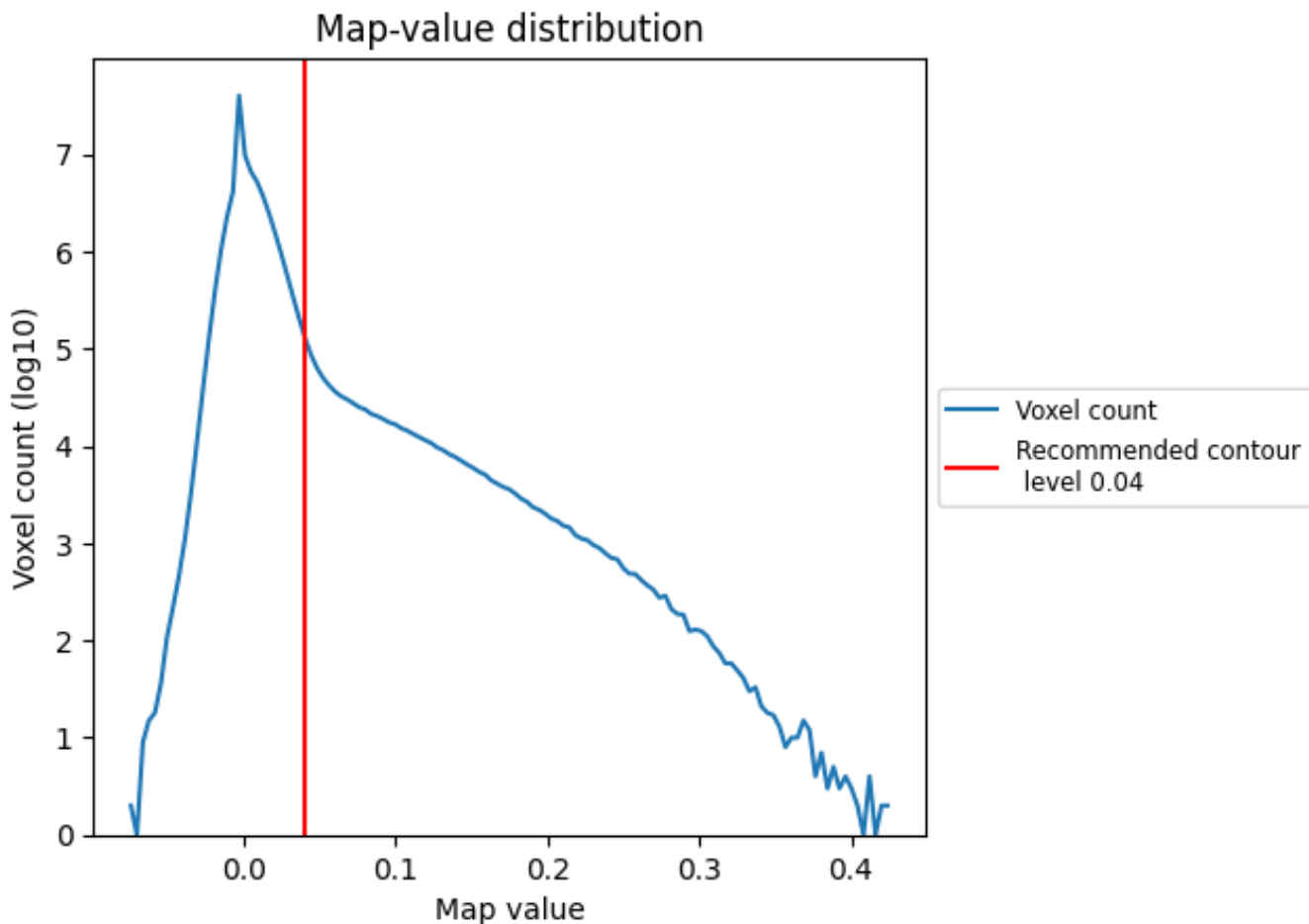
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

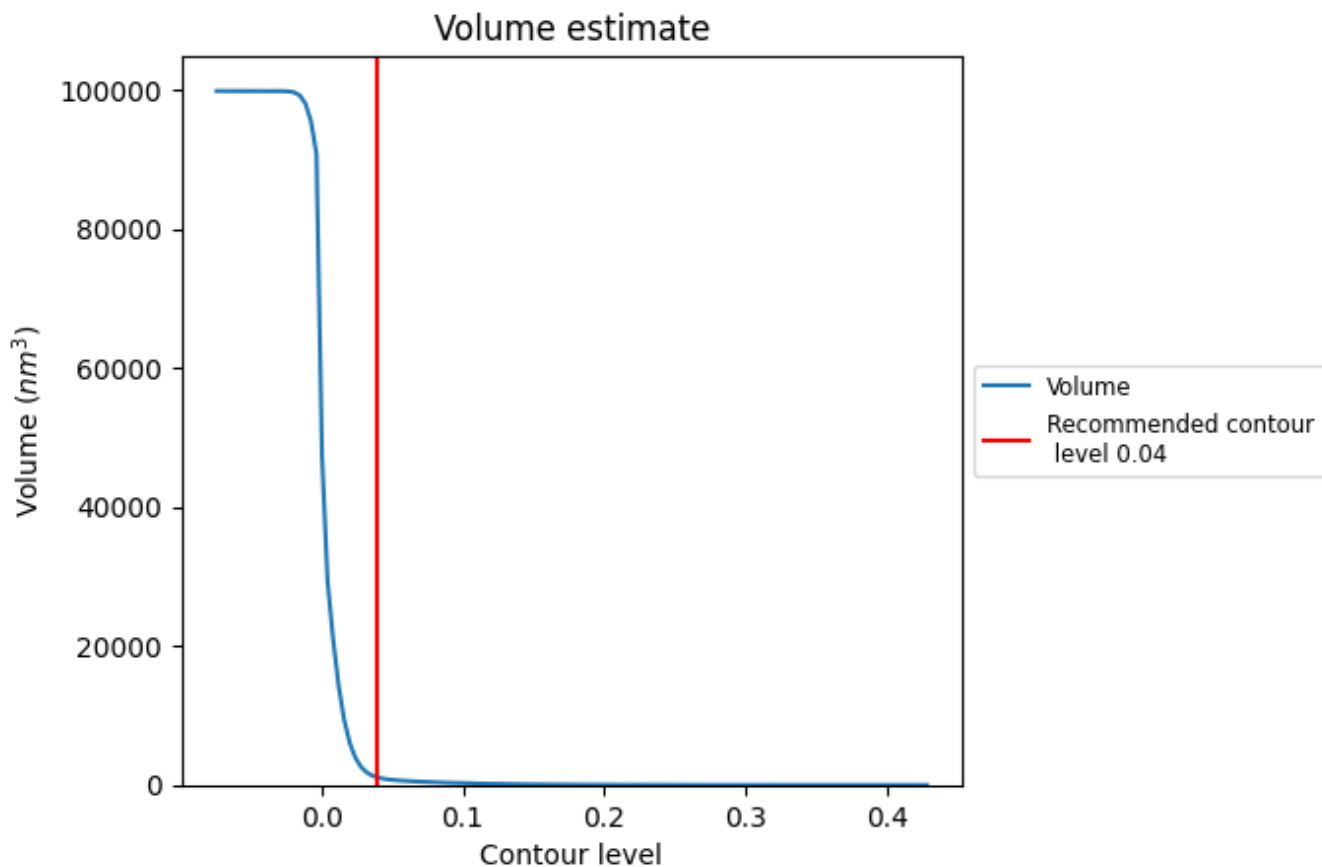
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

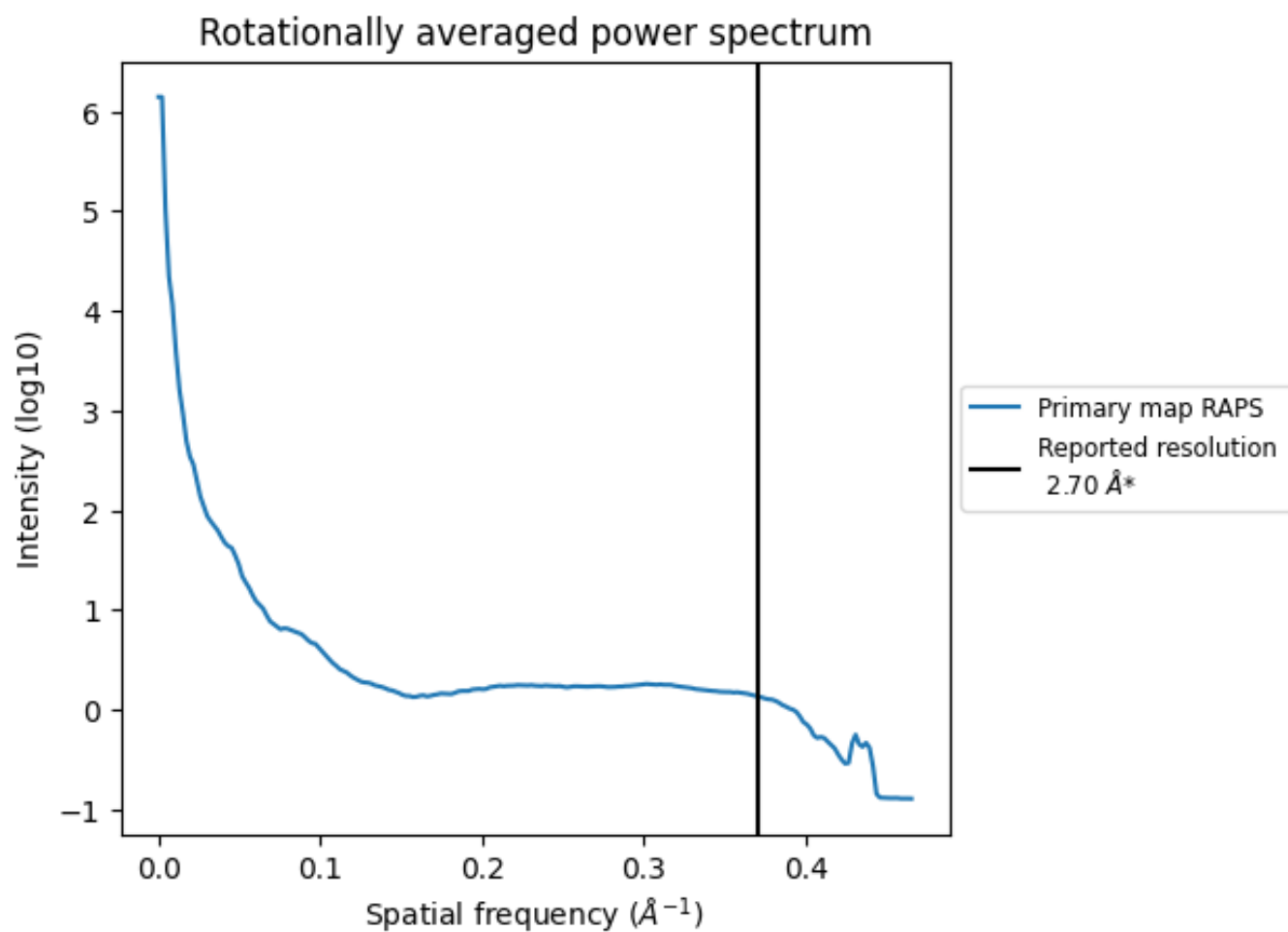
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1070 nm^3 ; this corresponds to an approximate mass of 967 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum i



*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

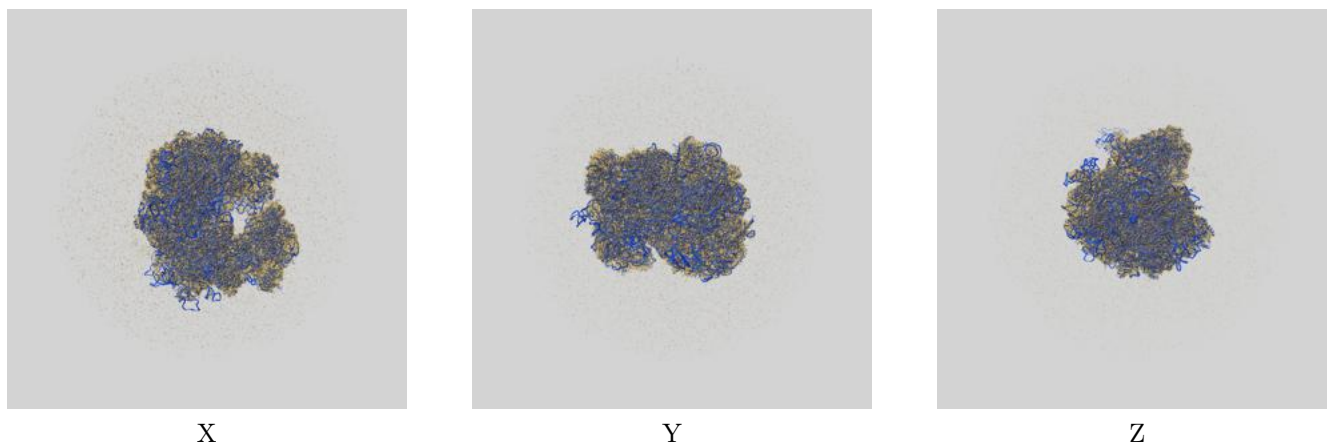
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

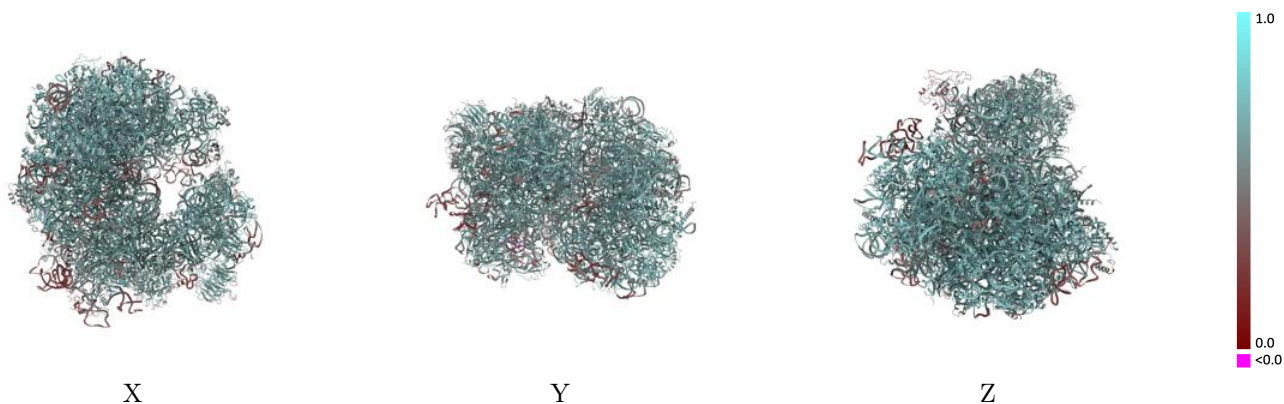
This section contains information regarding the fit between EMDB map EMD-23935 and PDB model 7MPJ. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



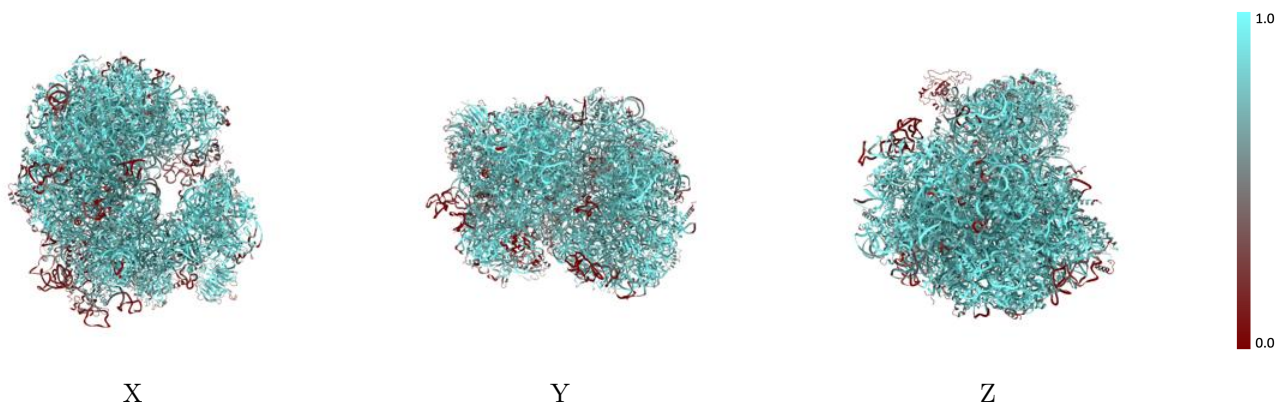
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



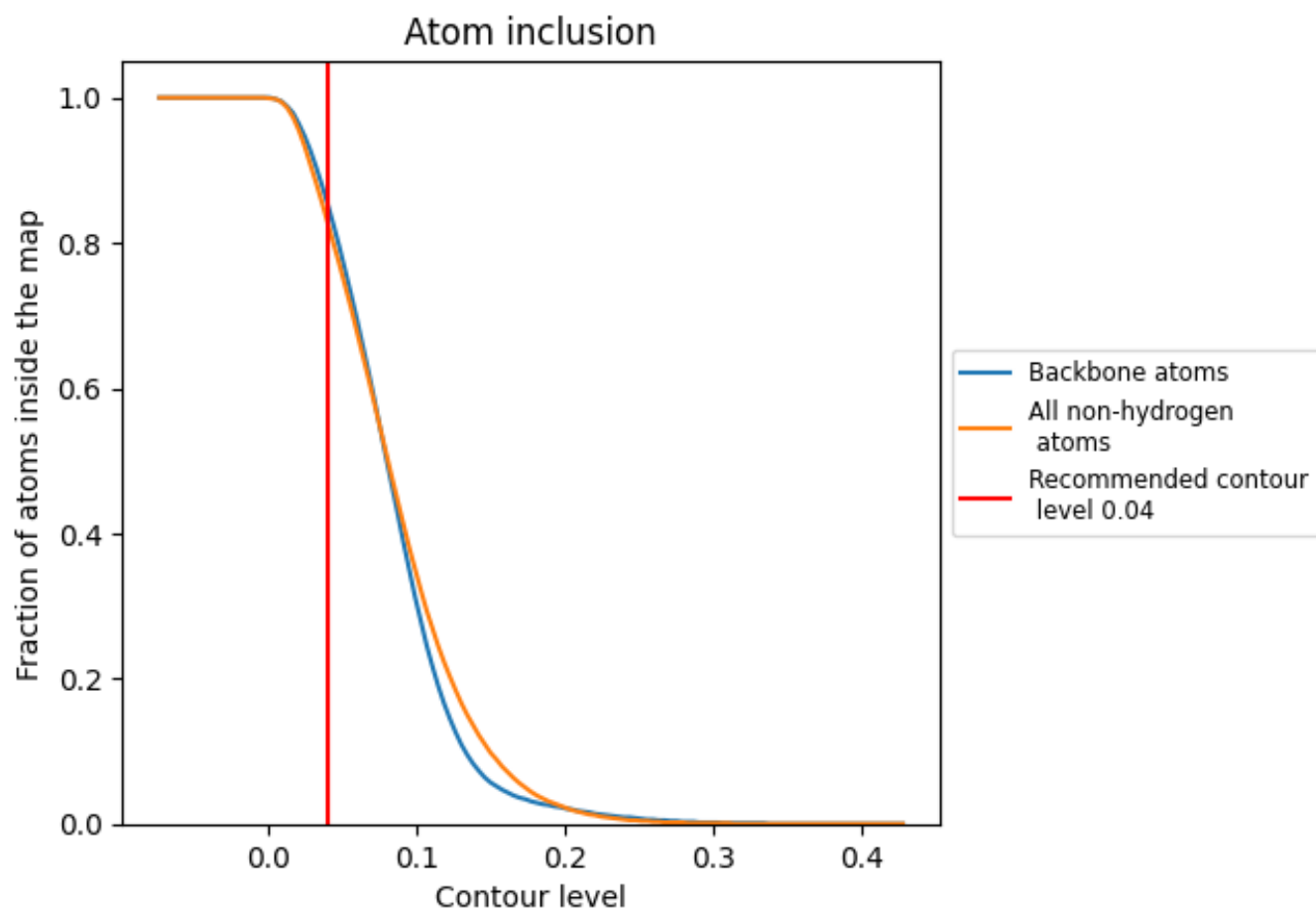
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.04).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 82% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (0.04) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| All |  0.8250 |  0.6130 |
| A1 |  0.8730 |  0.6280 |
| A3 |  0.9310 |  0.6380 |
| A4 |  0.9270 |  0.6530 |
| AA |  0.9060 |  0.6730 |
| AB |  0.8890 |  0.6730 |
| AC |  0.8710 |  0.6580 |
| AD |  0.7290 |  0.5920 |
| AE |  0.7460 |  0.6180 |
| AF |  0.8780 |  0.6680 |
| AG |  0.7570 |  0.6170 |
| AH |  0.8040 |  0.6440 |
| AI |  0.7560 |  0.6150 |
| AJ |  0.5280 |  0.5080 |
| AL |  0.8330 |  0.6550 |
| AM |  0.8350 |  0.6630 |
| AN |  0.9520 |  0.6790 |
| AO |  0.9070 |  0.6800 |
| AP |  0.8480 |  0.6560 |
| AQ |  0.9080 |  0.6730 |
| AR |  0.7230 |  0.5860 |
| AS |  0.8750 |  0.6700 |
| AT |  0.8330 |  0.6390 |
| AU |  0.6380 |  0.5700 |
| AV |  0.8480 |  0.6520 |
| AW |  0.8440 |  0.6570 |
| AX |  0.8360 |  0.6490 |
| AY |  0.8460 |  0.6490 |
| AZ |  0.7370 |  0.6050 |
| Aa |  0.8980 |  0.6630 |
| Ab |  0.7410 |  0.5910 |
| Ac |  0.7200 |  0.5870 |
| Ad |  0.7940 |  0.6310 |
| Ae |  0.8820 |  0.6690 |
| Af |  0.9260 |  0.6940 |









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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| Ag |  0.8390 |  0.6390 |
| Ah |  0.8240 |  0.6340 |
| Ai |  0.7650 |  0.6030 |
| Aj |  0.9330 |  0.6870 |
| Ak |  0.5640 |  0.5270 |
| Al |  0.9040 |  0.6620 |
| Am |  0.8190 |  0.6530 |
| An |  0.6180 |  0.5650 |
| Ao |  0.7690 |  0.6180 |
| Ap |  0.8210 |  0.6440 |
| B5 |  0.8240 |  0.5850 |
| BA |  0.7650 |  0.5780 |
| BB |  0.7100 |  0.5630 |
| BC |  0.8260 |  0.6080 |
| BD |  0.7580 |  0.5820 |
| BE |  0.8250 |  0.6130 |
| BF |  0.8140 |  0.6000 |
| BG |  0.6500 |  0.5590 |
| BH |  0.5360 |  0.5090 |
| BI |  0.7810 |  0.5920 |
| BJ |  0.8000 |  0.5980 |
| BK |  0.7110 |  0.5390 |
| BL |  0.7440 |  0.5970 |
| BM |  0.0470 |  0.3070 |
| BN |  0.7920 |  0.6020 |
| BO |  0.7850 |  0.5780 |
| BP |  0.7220 |  0.5690 |
| BQ |  0.8840 |  0.6360 |
| BR |  0.6380 |  0.5330 |
| BS |  0.7950 |  0.5900 |
| BT |  0.8820 |  0.6260 |
| BU |  0.6380 |  0.5420 |
| BV |  0.8000 |  0.5950 |
| BW |  0.8980 |  0.6380 |
| BX |  0.8360 |  0.6150 |
| BY |  0.7770 |  0.5970 |
| BZ |  0.7580 |  0.5740 |
| Ba |  0.8320 |  0.5940 |
| Bb |  0.7110 |  0.5690 |
| Bc |  0.7340 |  0.5710 |
| Bd |  0.9120 |  0.6510 |
| Be |  0.6500 |  0.5650 |

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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| Bf |  0.0880 |  0.2970 |
| Bg |  0.7720 |  0.5850 |
| Bh |  0.3310 |  0.4820 |