



wwPDB EM Validation Summary Report ⓘ

Feb 10, 2025 – 09:13 PM EST

PDB ID : 8UT0
EMDB ID : EMD-42525
Title : Eukaryotic 80S ribosome with Reh1, eIF5A and A/P site tRNA
Authors : Yelland, J.N.; Taylor, D.W.; Johnson, A.W.
Deposited on : 2023-10-30
Resolution : 3.22 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.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

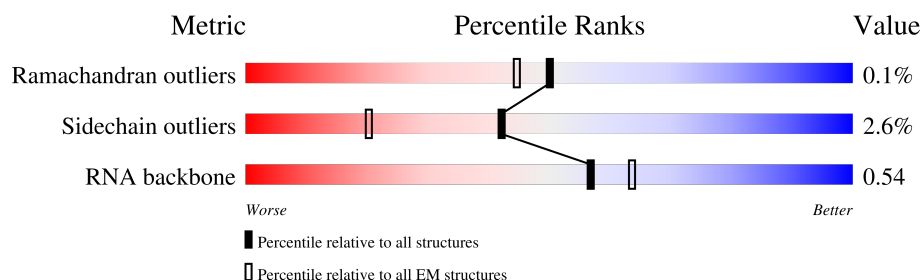
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.22 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.



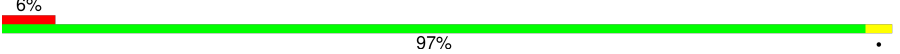
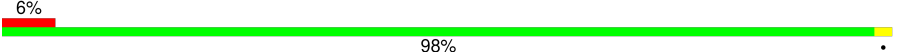
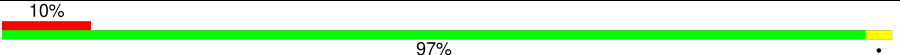
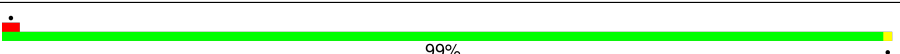

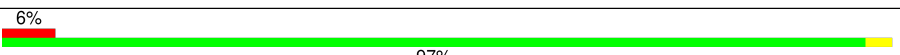
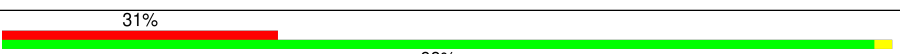
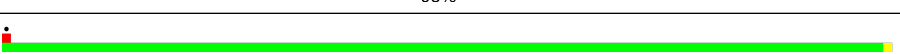
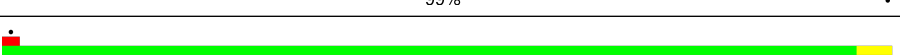
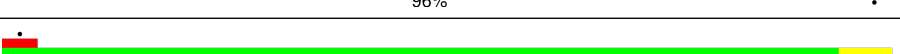
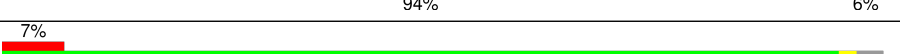
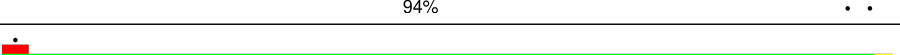
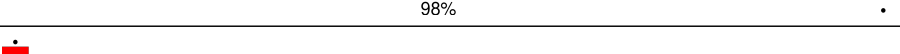
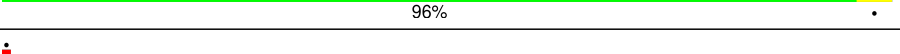
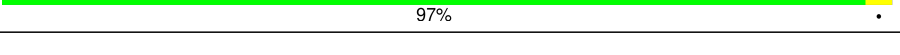
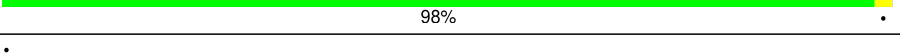
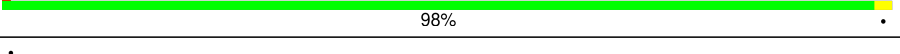
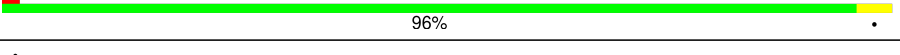
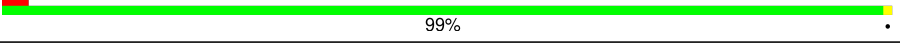
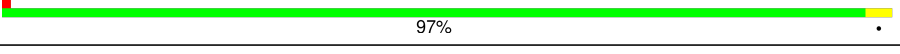
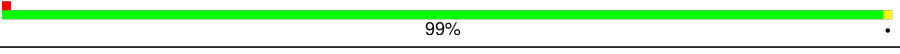
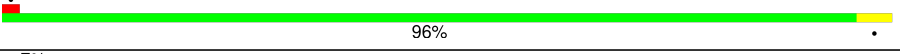
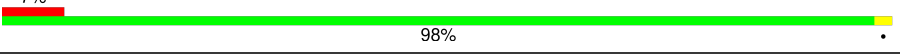
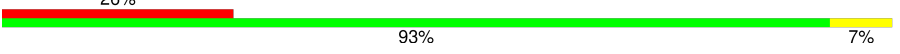
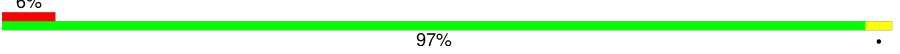
| Metric | Whole archive (#Entries) | EM structures (#Entries) |
|-----------------------|-----------------------------|-----------------------------|
| Ramachandran outliers | 207382 | 16835 |
| Sidechain outliers | 206894 | 16415 |
| RNA backbone | 6643 | 2191 |

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 | 2 | 1800 | |
| 2 | SP | 206 | |
| 3 | SQ | 232 | |
| 4 | SE | 117 | |
| 5 | SR | 216 | |
| 6 | SA | 222 | |
| 7 | SS | 258 | |
| 8 | SB | 206 | |

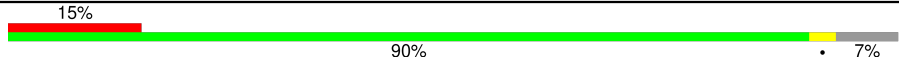

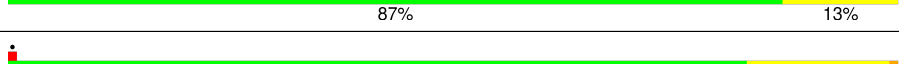
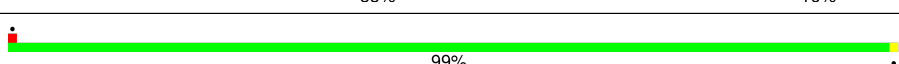
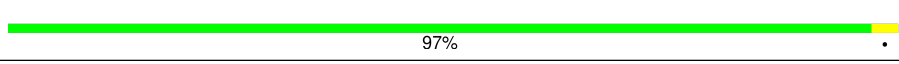
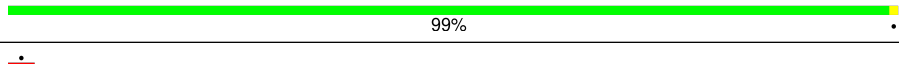
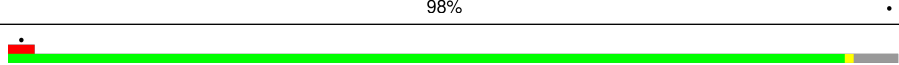
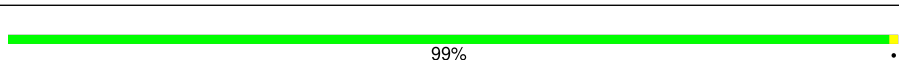
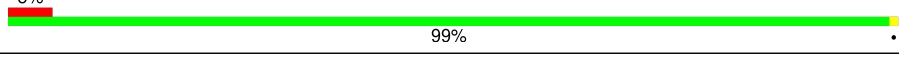
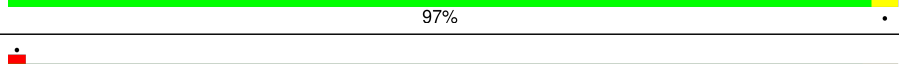
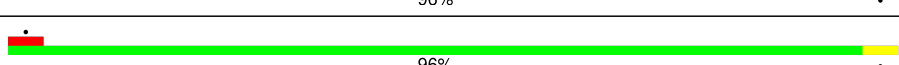
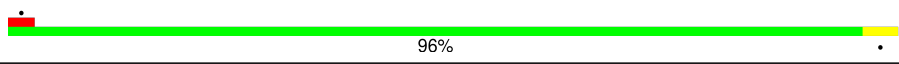
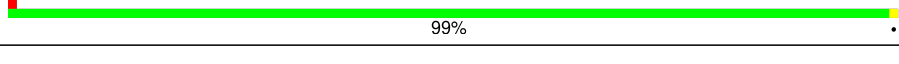
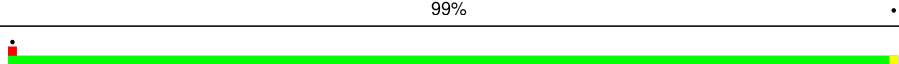
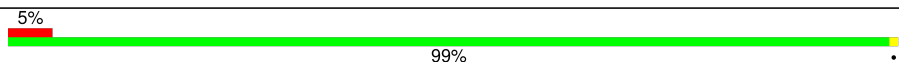
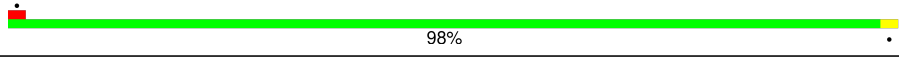
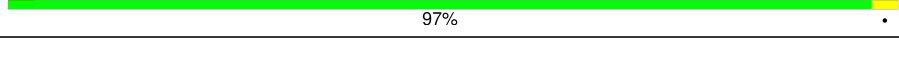
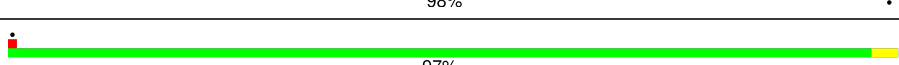
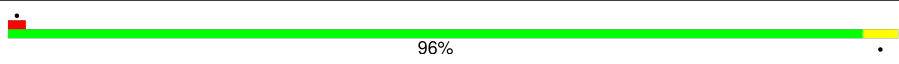
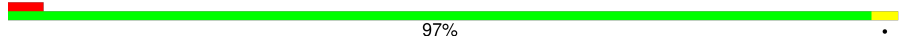



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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 9 | ST | 228 |  |
| 10 | SU | 184 |  |
| 11 | SV | 187 |  |
| 12 | SW | 184 |  |
| 13 | SC | 92 |  |
| 14 | SX | 142 |  |
| 15 | SD | 121 |  |
| 16 | SY | 150 |  |
| 17 | SZ | 127 |  |
| 18 | SF | 141 |  |
| 19 | SG | 125 |  |
| 20 | SH | 145 |  |
| 21 | SI | 143 |  |
| 22 | SJ | 100 |  |
| 23 | Sa | 87 |  |
| 24 | Sb | 129 |  |
| 25 | Sc | 144 |  |
| 26 | Sd | 134 |  |
| 27 | Se | 97 |  |
| 28 | Sf | 81 |  |
| 29 | SM | 53 |  |
| 30 | Sg | 57 |  |
| 31 | SN | 73 |  |
| 32 | SO | 312 |  |
| 33 | SL | 63 |  |

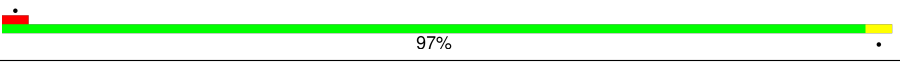

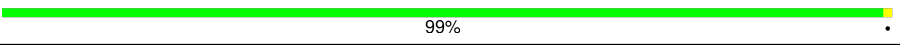
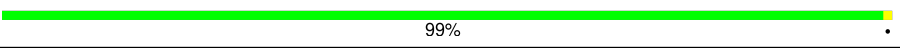
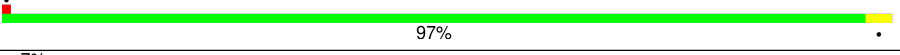
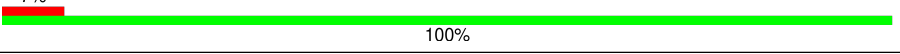
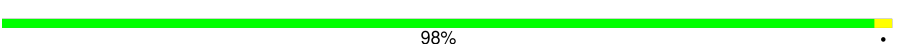
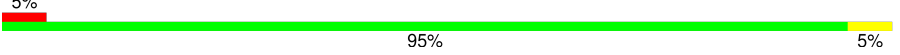
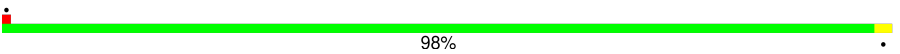
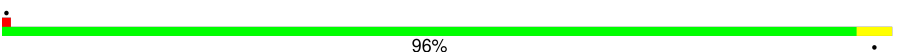
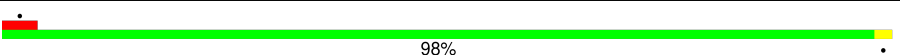
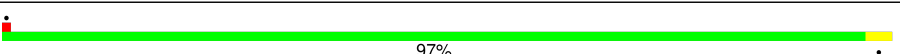
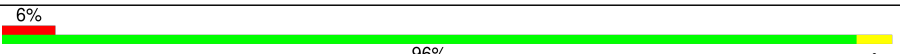
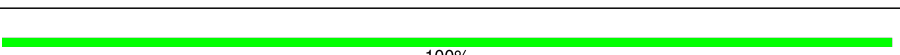
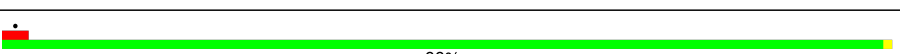
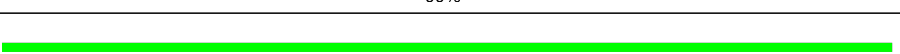
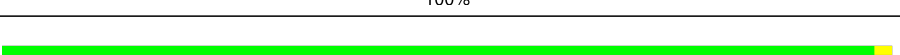
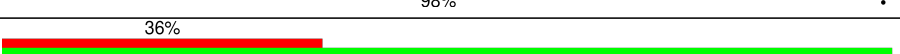
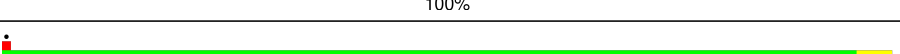
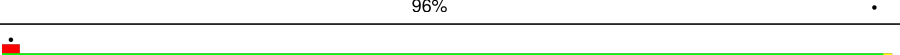
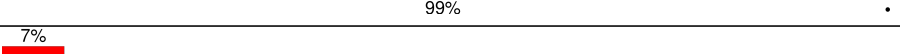
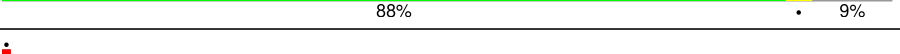
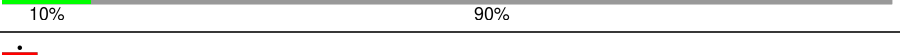


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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 34 | AA | 102 |  |
| 35 | A | 3394 |  |
| 36 | B | 121 |  |
| 37 | C | 158 |  |
| 38 | LD | 251 |  |
| 39 | LE | 386 |  |
| 40 | LF | 361 |  |
| 41 | LG | 294 |  |
| 42 | LH | 175 |  |
| 43 | LI | 222 |  |
| 44 | LJ | 233 |  |
| 45 | LK | 191 |  |
| 46 | LL | 218 |  |
| 47 | LM | 169 |  |
| 48 | LN | 193 |  |
| 49 | LO | 136 |  |
| 50 | LP | 203 |  |
| 51 | LQ | 197 |  |
| 52 | LR | 183 |  |
| 53 | LS | 185 |  |
| 54 | LT | 188 |  |
| 55 | LU | 171 |  |
| 56 | LV | 159 |  |
| 57 | LW | 100 | |
| 58 | LX | 136 | |

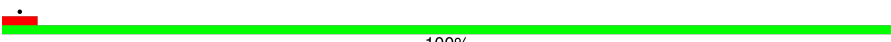
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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|---|
| 59 | LY | 65 |  97% |
| 60 | LZ | 121 |  100% |
| 61 | La | 125 |  99% |
| 62 | Lb | 135 |  99% |
| 63 | Lc | 148 |  97% |
| 64 | Ld | 58 |  100% |
| 65 | Le | 96 |  98% |
| 66 | Lf | 109 |  95% 5% |
| 67 | Lg | 127 |  98% |
| 68 | Lh | 106 |  96% |
| 69 | Li | 112 |  98% |
| 70 | Lj | 119 |  97% |
| 71 | Lk | 99 |  96% |
| 72 | Ll | 81 |  100% |
| 73 | Lm | 77 |  99% |
| 74 | Ln | 50 |  100% |
| 75 | Lo | 52 |  98% |
| 76 | Lp | 25 |  36% 100% |
| 77 | Lq | 103 |  96% |
| 78 | Lr | 91 |  99% |
| 79 | Ls | 157 |  88% 9% |
| 80 | z | 588 |  10% 90% |
| 81 | m | 76 |  66% 32% |
| 82 | n | 75 |  75% 23% |
| 83 | D | 10 |  60% 40% |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 84 | E | 210 |  100% |

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 205193 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 RNA chain called 18S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|-------|
| 1 | 2 | 1771 | Total | C | N | O | P | 0 | 0 |
| | | | 37739 | 16872 | 6683 | 12413 | 1771 | | |

- Molecule 2 is a protein called 40S ribosomal protein S0-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 2 | SP | 206 | Total | C | N | O | S | 0 | 0 |
| | | | 1603 | 1030 | 284 | 287 | 2 | | |

- Molecule 3 is a protein called 40S ribosomal protein S1-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 3 | SQ | 226 | Total | C | N | O | S | 0 | 0 |
| | | | 1798 | 1139 | 330 | 325 | 4 | | |

- Molecule 4 is a protein called 40S ribosomal protein S15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 4 | SE | 117 | Total | C | N | O | S | 0 | 0 |
| | | | 916 | 583 | 171 | 155 | 7 | | |

- Molecule 5 is a protein called 40S ribosomal protein S2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 5 | SR | 216 | Total | C | N | O | S | 0 | 0 |
| | | | 1626 | 1042 | 287 | 295 | 2 | | |

- Molecule 6 is a protein called 40S ribosomal protein S3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 6 | SA | 222 | Total | C | N | O | S | 0 | 0 |
| | | | 1729 | 1098 | 312 | 313 | 6 | | |

- Molecule 7 is a protein called 40S ribosomal protein S4-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 7 | SS | 258 | Total | C | N | O | S | 0 | 0 |
| | | | 2056 | 1308 | 387 | 358 | 3 | | |

- Molecule 8 is a protein called 40S ribosomal protein S5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 8 | SB | 206 | Total | C | N | O | S | 0 | 0 |
| | | | 1605 | 1005 | 299 | 298 | 3 | | |

- Molecule 9 is a protein called 40S ribosomal protein S6-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 9 | ST | 228 | Total | C | N | O | S | 0 | 0 |
| | | | 1815 | 1138 | 351 | 323 | 3 | | |

- Molecule 10 is a protein called 40S ribosomal protein S7-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 10 | SU | 184 | Total | C | N | O | 0 | 0 |
| | | | 1473 | 946 | 263 | 264 | | |

- Molecule 11 is a protein called 40S ribosomal protein S8-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 11 | SV | 187 | Total | C | N | O | S | 0 | 0 |
| | | | 1476 | 916 | 295 | 263 | 2 | | |

- Molecule 12 is a protein called 40S ribosomal protein S9-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 12 | SW | 184 | Total | C | N | O | S | 0 | 0 |
| | | | 1479 | 935 | 285 | 258 | 1 | | |

- Molecule 13 is a protein called 40S ribosomal protein S10-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 13 | SC | 92 | Total | C | N | O | S | 0 | 0 |
| | | | 754 | 489 | 122 | 141 | 2 | | |

- Molecule 14 is a protein called 40S ribosomal protein S11-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 14 | SX | 142 | Total | C | N | O | S | 0 | 0 |
| | | | 1142 | 733 | 217 | 189 | 3 | | |

- Molecule 15 is a protein called 40S ribosomal protein S12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 15 | SD | 121 | Total | C | N | O | S | 0 | 0 |
| | | | 875 | 551 | 153 | 169 | 2 | | |

- Molecule 16 is a protein called 40S ribosomal protein S13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 16 | SY | 150 | Total | C | N | O | S | 0 | 0 |
| | | | 1192 | 759 | 224 | 207 | 2 | | |

- Molecule 17 is a protein called 40S ribosomal protein S14-B.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 17 | SZ | 127 | Total | C | N | O | S | 0 | 0 |
| | | | 923 | 568 | 185 | 167 | 3 | | |

- Molecule 18 is a protein called 40S ribosomal protein S16-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 18 | SF | 141 | Total | C | N | O | | 0 | 0 |
| | | | 1105 | 708 | 203 | 194 | | | |

- Molecule 19 is a protein called 40S ribosomal protein S17-B.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 19 | SG | 121 | Total | C | N | O | S | 0 | 0 |
| | | | 948 | 596 | 179 | 171 | 2 | | |

- Molecule 20 is a protein called 40S ribosomal protein S18-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 20 | SH | 145 | Total | C | N | O | S | 0 | 0 |
| | | | 1188 | 741 | 237 | 208 | 2 | | |

- Molecule 21 is a protein called 40S ribosomal protein S19-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 21 | SI | 143 | Total | C | N | O | S | 0 | 0 |
| | | | 1112 | 694 | 208 | 208 | 2 | | |

- Molecule 22 is a protein called 40S ribosomal protein S20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 22 | SJ | 100 | Total | C | N | O | S | 0 | 0 |
| | | | 797 | 506 | 144 | 146 | 1 | | |

- Molecule 23 is a protein called 40S ribosomal protein S21-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 23 | Sa | 87 | Total | C | N | O | S | 0 | 0 |
| | | | 673 | 415 | 125 | 131 | 2 | | |

- Molecule 24 is a protein called 40S ribosomal protein S22-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 24 | Sb | 129 | Total | C | N | O | S | 0 | 0 |
| | | | 1021 | 650 | 188 | 180 | 3 | | |

- Molecule 25 is a protein called 40S ribosomal protein S23-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 25 | Sc | 144 | Total | C | N | O | S | 0 | 0 |
| | | | 1121 | 708 | 220 | 191 | 2 | | |

- Molecule 26 is a protein called 40S ribosomal protein S24-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 26 | Sd | 134 | Total | C | N | O | 0 | 0 |
| | | | 1032 | 651 | 195 | 186 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 27 | Se | 97 | Total | C | N | O | S | 0 | 0 |
| | | | 765 | 473 | 160 | 127 | 5 | | |

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

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

- Molecule 29 is a protein called 40S ribosomal protein S29-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 29 | SM | 53 | Total | C | N | O | S | 0 | 0 |
| | | | 443 | 275 | 92 | 72 | 4 | | |

- Molecule 30 is a protein called 40S ribosomal protein S30-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 30 | Sg | 57 | Total | C | N | O | S | 0 | 0 |
| | | | 451 | 284 | 93 | 73 | 1 | | |

- Molecule 31 is a protein called 40S ribosomal protein S31.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 31 | SN | 73 | Total | C | N | O | S | 0 | 0 |
| | | | 556 | 352 | 105 | 95 | 4 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|----------------|
| SN | 97 | ALA | LYS | conflict | UNP A0A6A5PU37 |

- Molecule 32 is a protein called 40S ribosomal protein ASC1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 32 | SO | 312 | Total | C | N | O | S | 0 | 0 |
| | | | 2383 | 1514 | 409 | 452 | 8 | | |

- Molecule 33 is a protein called 40S ribosomal protein S28-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 33 | SL | 63 | Total | C | N | O | S | 0 | 0 |
| | | | 491 | 303 | 96 | 91 | 1 | | |

- Molecule 34 is a protein called 40S ribosomal protein S25-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 34 | AA | 95 | Total | C | N | O | 0 | 0 |
| | | | 737 | 466 | 139 | 132 | | |

- Molecule 35 is a RNA chain called 25S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|-------|------|---------|-------|
| 35 | A | 3184 | Total | C | N | O | P | 0 | 0 |
| | | | 68091 | 30415 | 12259 | 22233 | 3184 | | |

- Molecule 36 is a RNA chain called 5S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 36 | B | 121 | Total | C | N | O | P | 0 | 0 |
| | | | 2579 | 1152 | 461 | 845 | 121 | | |

- Molecule 37 is a RNA chain called 5.8S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|------|-----|---------|-------|
| 37 | C | 158 | Total | C | N | O | P | 0 | 0 |
| | | | 3353 | 1500 | 586 | 1109 | 158 | | |

- Molecule 38 is a protein called 60S ribosomal protein L2-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 38 | LD | 251 | Total | C | N | O | S | 0 | 0 |
| | | | 1899 | 1182 | 385 | 331 | 1 | | |

- Molecule 39 is a protein called 60S ribosomal protein L3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 39 | LE | 386 | Total | C | N | O | S | 0 | 0 |
| | | | 3079 | 1954 | 584 | 533 | 8 | | |

- Molecule 40 is a protein called 60S ribosomal protein L4-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 40 | LF | 361 | Total | C | N | O | S | 0 | 0 |
| | | | 2749 | 1730 | 522 | 494 | 3 | | |

- Molecule 41 is a protein called 60S ribosomal protein L5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 41 | LG | 294 | Total | C | N | O | S | 0 | 0 |
| | | | 2351 | 1484 | 410 | 455 | 2 | | |

- Molecule 42 is a protein called 60S ribosomal protein L6-B.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 42 | LH | 167 | Total | C | N | O | | 0 | 0 |
| | | | 1307 | 843 | 234 | 230 | | | |

- Molecule 43 is a protein called 60S ribosomal protein L7-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 43 | LI | 222 | Total | C | N | O | S | 0 | 0 |
| | | | 1784 | 1151 | 324 | 308 | 1 | | |

- Molecule 44 is a protein called 60S ribosomal protein L8-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 44 | LJ | 233 | Total | C | N | O | S | 0 | 0 |
| | | | 1804 | 1151 | 323 | 327 | 3 | | |

- Molecule 45 is a protein called 60S ribosomal protein L9-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 45 | LK | 191 | Total | C | N | O | S | 0 | 0 |
| | | | 1508 | 957 | 274 | 273 | 4 | | |

- Molecule 46 is a protein called 60S ribosomal protein L10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 46 | LL | 218 | Total | C | N | O | S | 0 | 0 |
| | | | 1764 | 1117 | 334 | 306 | 7 | | |

- Molecule 47 is a protein called 60S ribosomal protein L11-B.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 47 | LM | 169 | Total | C | N | O | S | 0 | 0 |
| | | | 1346 | 843 | 252 | 247 | 4 | | |

- Molecule 48 is a protein called 60S ribosomal protein L13-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 48 | LN | 193 | Total | C | N | O | 0 | 0 |
| | | | 1543 | 962 | 315 | 266 | | |

- Molecule 49 is a protein called 60S ribosomal protein L14-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 49 | LO | 136 | Total | C | N | O | S | 0 |
| | | | 1053 | 675 | 199 | 177 | 2 | 0 |

- Molecule 50 is a protein called 60S ribosomal protein L15-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 50 | LP | 203 | Total | C | N | O | S | 0 |
| | | | 1720 | 1077 | 361 | 281 | 1 | 0 |

- Molecule 51 is a protein called 60S ribosomal protein L16-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 51 | LQ | 197 | Total | C | N | O | S | 0 |
| | | | 1555 | 1003 | 289 | 262 | 1 | 0 |

- Molecule 52 is a protein called 60S ribosomal protein L17-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 52 | LR | 183 | Total | C | N | O | 0 | 0 |
| | | | 1416 | 879 | 284 | 253 | | |

- Molecule 53 is a protein called 60S ribosomal protein L18-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 53 | LS | 185 | Total | C | N | O | S | 0 |
| | | | 1441 | 908 | 290 | 241 | 2 | 0 |

- Molecule 54 is a protein called 60S ribosomal protein L19-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 54 | LT | 188 | Total | C | N | O | 0 | 0 |
| | | | 1515 | 932 | 323 | 260 | | |

- Molecule 55 is a protein called 60S ribosomal protein L20-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 55 | LU | 171 | Total | C | N | O | S | 0 | 0 |
| | | | 1437 | 925 | 266 | 243 | 3 | | |

- Molecule 56 is a protein called 60S ribosomal protein L21-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 56 | LV | 159 | Total | C | N | O | S | 0 | 0 |
| | | | 1272 | 802 | 245 | 221 | 4 | | |

- Molecule 57 is a protein called 60S ribosomal protein L22-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 57 | LW | 100 | Total | C | N | O | S | 0 | 0 |
| | | | 796 | 516 | 131 | 149 | | | |

- Molecule 58 is a protein called 60S ribosomal protein L23-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 58 | LX | 136 | Total | C | N | O | S | 0 | 0 |
| | | | 1003 | 628 | 189 | 179 | 7 | | |

- Molecule 59 is a protein called 60S ribosomal protein L24-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 59 | LY | 65 | Total | C | N | O | S | 0 | 0 |
| | | | 528 | 339 | 104 | 84 | 1 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 60 | LZ | 121 | Total | C | N | O | S | 0 | 0 |
| | | | 964 | 620 | 169 | 173 | 2 | | |

- Molecule 61 is a protein called 60S ribosomal protein L26-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 61 | La | 125 | Total | C | N | O | S | 0 | 0 |
| | | | 984 | 620 | 191 | 173 | | | |

- Molecule 62 is a protein called 60S ribosomal protein L27-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 62 | Lb | 135 | Total | C | N | O | 0 | 0 |
| | | | 1080 | 701 | 199 | 180 | | |

- Molecule 63 is a protein called 60S ribosomal protein L28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 63 | Lc | 148 | Total | C | N | O | S | 0 | 0 |
| | | | 1169 | 747 | 231 | 188 | 3 | | |

- Molecule 64 is a protein called 60S ribosomal protein L29.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---------|-------|
| 64 | Ld | 58 | Total | C | N | O | 0 | 0 |
| | | | 462 | 289 | 100 | 73 | | |

- Molecule 65 is a protein called 60S ribosomal protein L30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 65 | Le | 96 | Total | C | N | O | S | 0 | 0 |
| | | | 737 | 476 | 123 | 137 | 1 | | |

- Molecule 66 is a protein called 60S ribosomal protein L31-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 66 | Lf | 109 | Total | C | N | O | S | 0 | 0 |
| | | | 876 | 556 | 167 | 152 | 1 | | |

- Molecule 67 is a protein called 60S ribosomal protein L32.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 67 | Lg | 127 | Total | C | N | O | S | 0 | 0 |
| | | | 1017 | 644 | 205 | 167 | 1 | | |

- Molecule 68 is a protein called 60S ribosomal protein L33-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 68 | Lh | 106 | Total | C | N | O | S | 0 | 0 |
| | | | 850 | 540 | 165 | 144 | 1 | | |

- Molecule 69 is a protein called 60S ribosomal protein L34-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 69 | Li | 112 | Total | C | N | O | S | 0 | 0 |
| | | | 880 | 545 | 179 | 152 | 4 | | |

- Molecule 70 is a protein called 60S ribosomal protein L35-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 70 | Lj | 119 | Total | C | N | O | S | 0 | 0 |
| | | | 969 | 615 | 186 | 167 | 1 | | |

- Molecule 71 is a protein called 60S ribosomal protein L36-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 71 | Lk | 99 | Total | C | N | O | S | 0 | 0 |
| | | | 766 | 478 | 154 | 132 | 2 | | |

- Molecule 72 is a protein called 60S ribosomal protein L37-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 72 | Ll | 81 | Total | C | N | O | S | 0 | 0 |
| | | | 645 | 393 | 141 | 106 | 5 | | |

- Molecule 73 is a protein called 60S ribosomal protein L38.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 73 | Lm | 77 | Total | C | N | O | 0 | 0 |
| | | | 612 | 391 | 115 | 106 | | |

- Molecule 74 is a protein called 60S ribosomal protein L39.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 74 | Ln | 50 | Total | C | N | O | S | 0 | 0 |
| | | | 436 | 272 | 97 | 65 | 2 | | |

- Molecule 75 is a protein called 60S ribosomal protein L40-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 75 | Lo | 52 | Total | C | N | O | S | 0 | 0 |
| | | | 410 | 254 | 86 | 65 | 5 | | |

- Molecule 76 is a protein called 60S ribosomal protein L41-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 76 | Lp | 25 | Total | C | N | O | S | 0 | 0 |
| | | | 229 | 139 | 62 | 27 | 1 | | |

- Molecule 77 is a protein called 60S ribosomal protein L42-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 77 | Lq | 103 | Total | C | N | O | S | 0 | 0 |
| | | | 824 | 517 | 167 | 135 | 5 | | |

- Molecule 78 is a protein called 60S ribosomal protein L43-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 78 | Lr | 91 | Total | C | N | O | S | 0 | 0 |
| | | | 694 | 429 | 138 | 121 | 6 | | |

- Molecule 79 is a protein called Translation factor eIF5A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 79 | Ls | 143 | Total | C | N | O | S | 0 | 0 |
| | | | 1081 | 672 | 181 | 219 | 9 | | |

- Molecule 80 is a protein called Cytoplasmic 60S subunit biogenesis factor REH1 (N-terminal 3xFLAG tag).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 80 | z | 57 | Total | C | N | O | S | 0 | 0 |
| | | | 480 | 295 | 96 | 86 | 3 | | |

- Molecule 81 is a RNA chain called A site tRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 81 | m | 76 | Total | C | N | O | P | 0 | 0 |
| | | | 1611 | 721 | 281 | 534 | 75 | | |

- Molecule 82 is a RNA chain called P site initiator tRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 82 | n | 75 | Total | C | N | O | P | 0 | 0 |
| | | | 1606 | 716 | 297 | 518 | 75 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|-----------|
| n | 10 | A | G | conflict | GB 176433 |

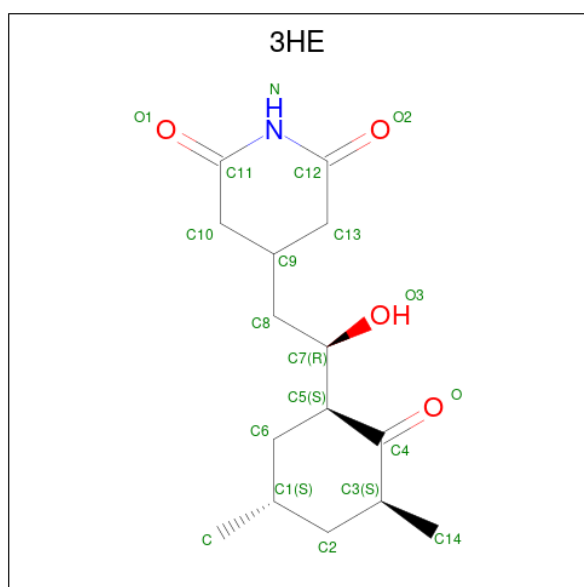
- Molecule 83 is a RNA chain called Messenger RNA (5'-R(P*AP*AP*UP*AP*UP*GP*AP*AP*AP*A)-3').

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|---------|-------|
| 83 | D | 10 | Total | C | N | O | P | |
| | | | 213 | 98 | 44 | 61 | 10 | |
| | | | | | | | 0 | 0 |

- Molecule 84 is a protein called 60S ribosomal protein L1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 84 | E | 210 | Total | C | N | O | | |
| | | | 1051 | 630 | 210 | 211 | | |
| | | | | | | | 0 | 0 |

- Molecule 85 is 4-{(2R)-2-[(1S,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (three-letter code: 3HE) (formula: C₁₅H₂₃NO₄).

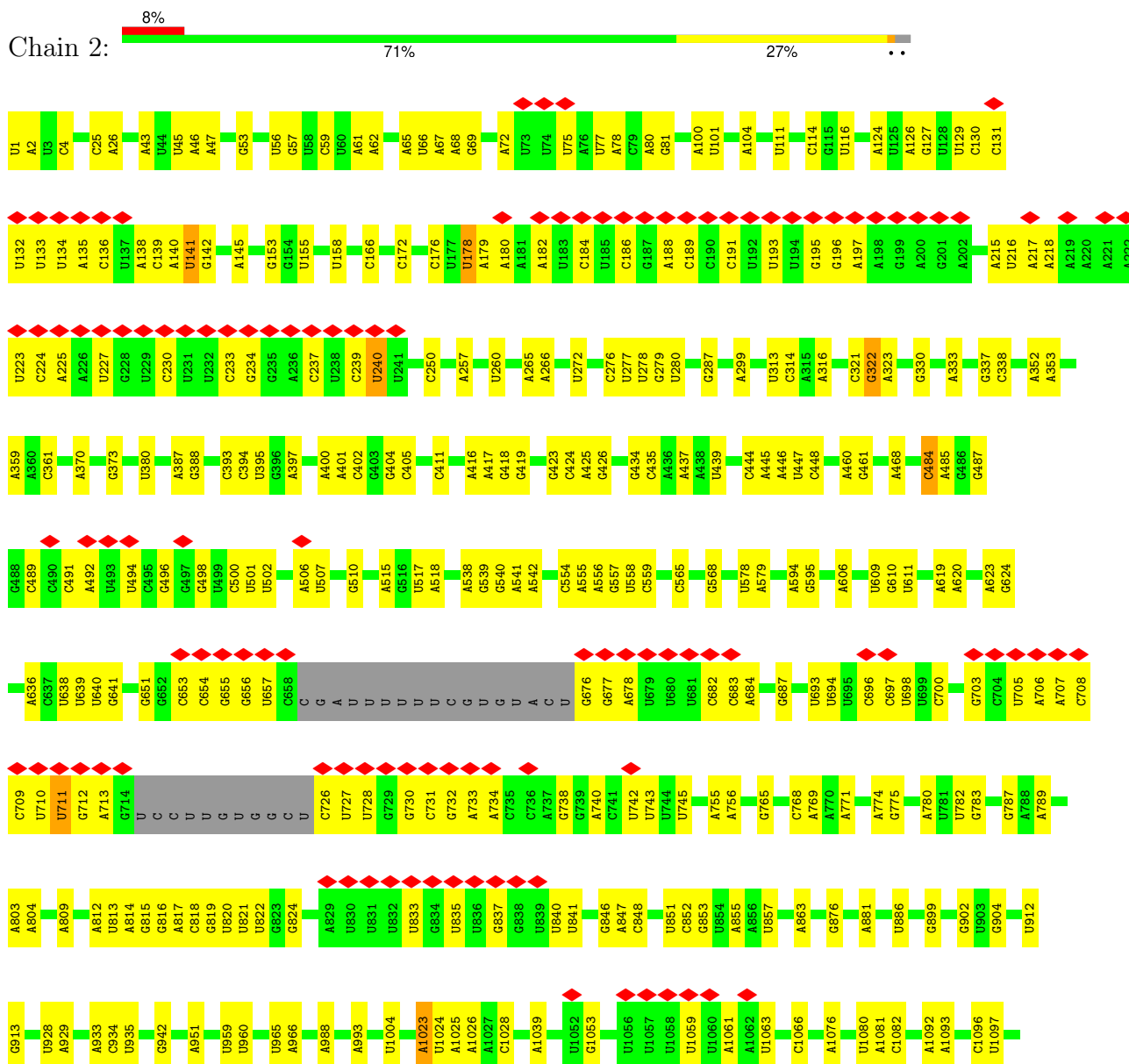


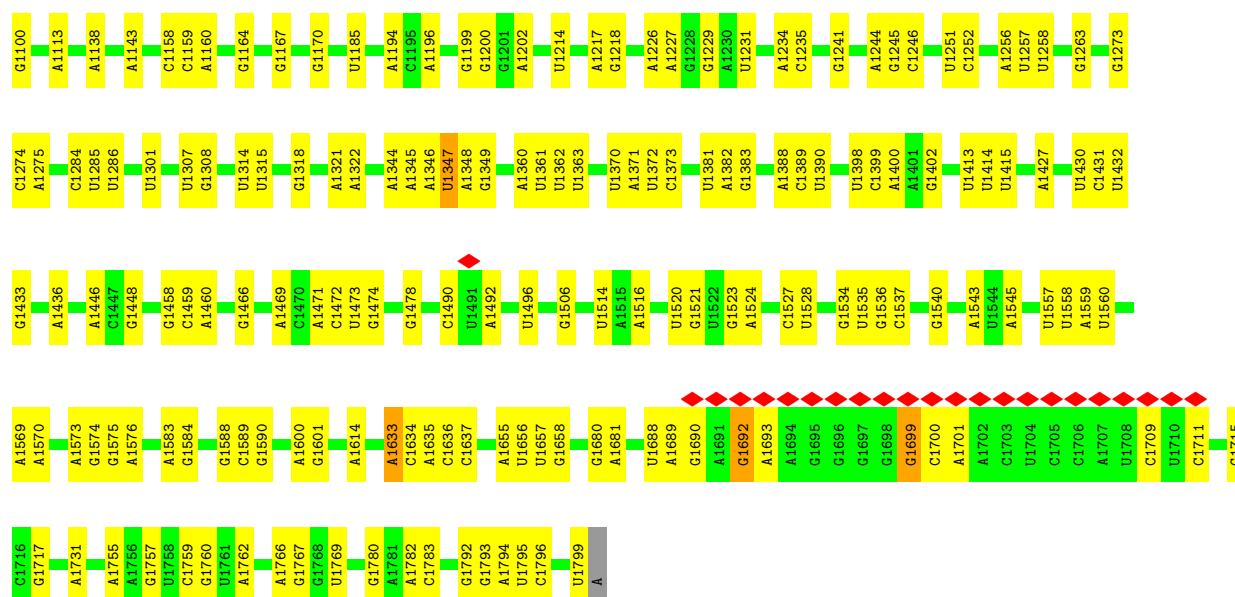
| Mol | Chain | Residues | Atoms | | | | AltConf |
|-----|-------|----------|-------|----|---|---|---------|
| 85 | A | 1 | Total | C | N | O | |
| | | | 20 | 15 | 1 | 4 | |
| | | | | | | | 0 |

3 Residue-property plots

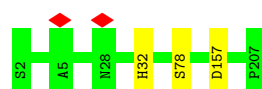
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 18S rRNA

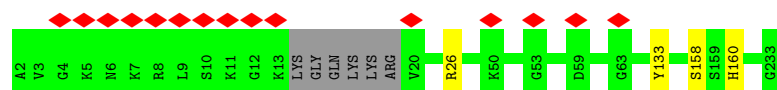




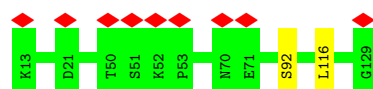
- Molecule 2: 40S ribosomal protein S0-A



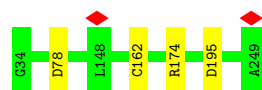
- Molecule 3: 40S ribosomal protein S1-A



- Molecule 4: 40S ribosomal protein S15



- Molecule 5: 40S ribosomal protein S2



- Molecule 6: 40S ribosomal protein S3

Chain SA:  97%



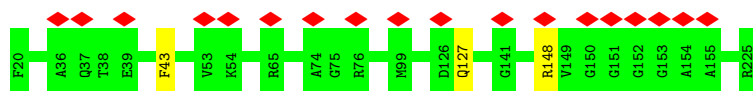
- Molecule 7: 40S ribosomal protein S4-A

Chain SS:  98%



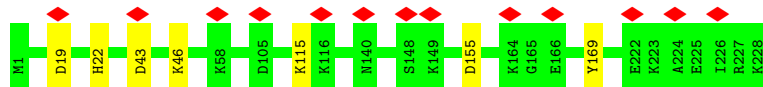
- Molecule 8: 40S ribosomal protein S5

Chain SB:  99%



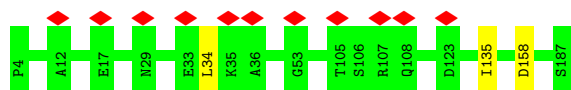
- Molecule 9: 40S ribosomal protein S6-A

Chain ST:  97%



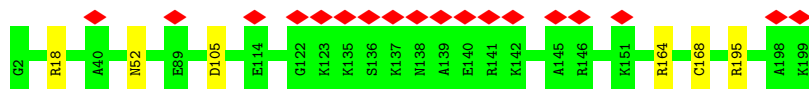
- Molecule 10: 40S ribosomal protein S7-A

Chain SU:  98%



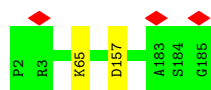
- Molecule 11: 40S ribosomal protein S8-A

Chain SV:  97%

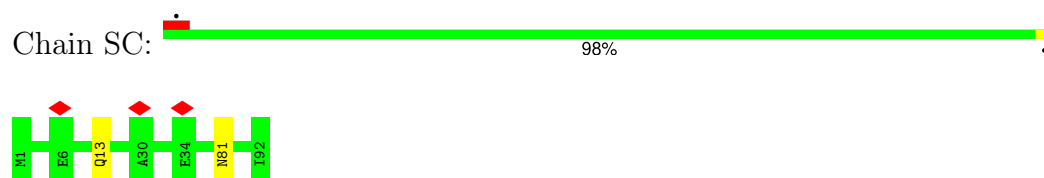


- Molecule 12: 40S ribosomal protein S9-A

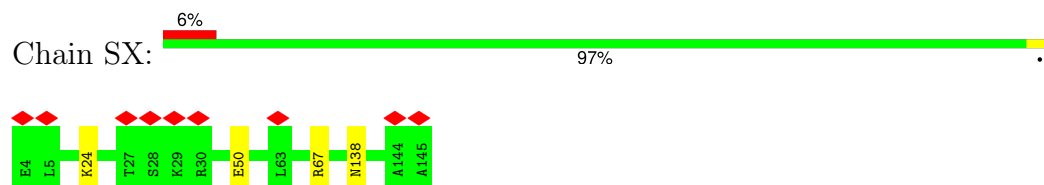
Chain SW:  99%



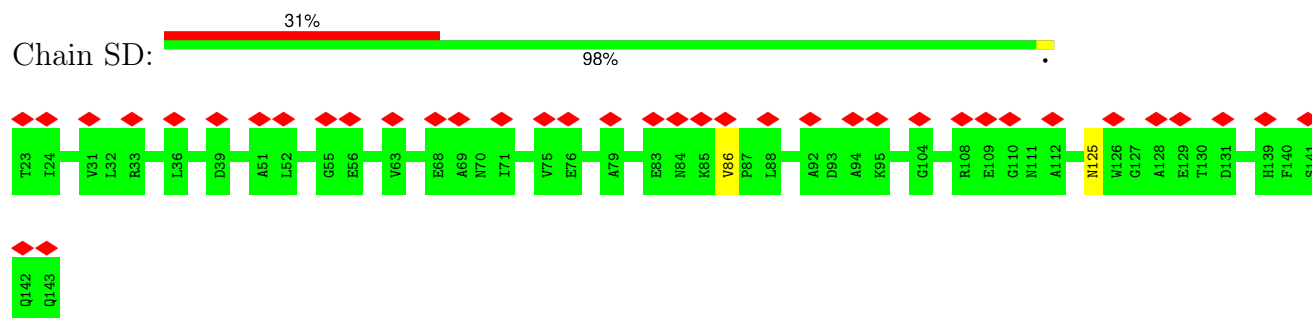
- Molecule 13: 40S ribosomal protein S10-A



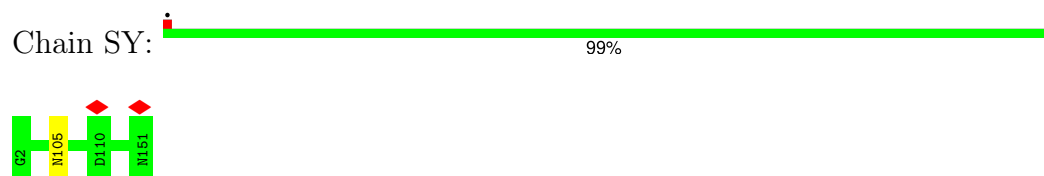
- Molecule 14: 40S ribosomal protein S11-A



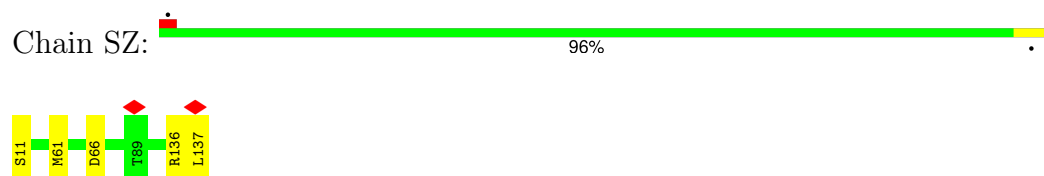
- Molecule 15: 40S ribosomal protein S12



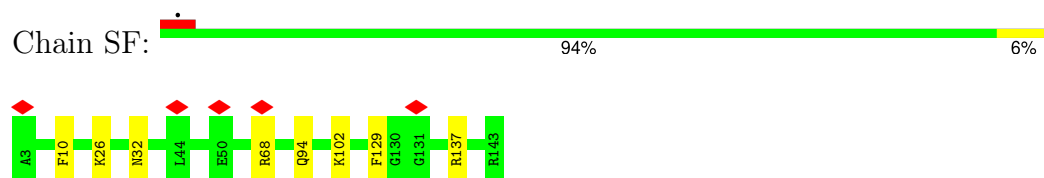
- Molecule 16: 40S ribosomal protein S13



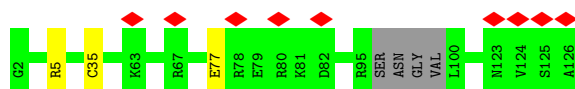
- Molecule 17: 40S ribosomal protein S14-B



- Molecule 18: 40S ribosomal protein S16-A



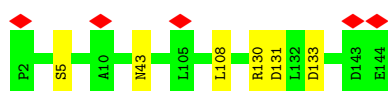
- Molecule 19: 40S ribosomal protein S17-B



- Molecule 20: 40S ribosomal protein S18-A



- Molecule 21: 40S ribosomal protein S19-A



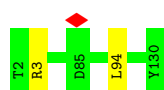
- Molecule 22: 40S ribosomal protein S20



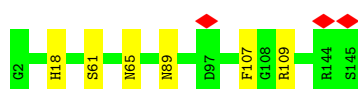
- Molecule 23: 40S ribosomal protein S21-A



- Molecule 24: 40S ribosomal protein S22-A

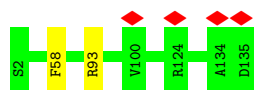


- Molecule 25: 40S ribosomal protein S23-A



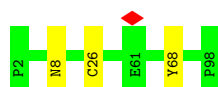
- Molecule 26: 40S ribosomal protein S24-A

Chain Sd:  99%



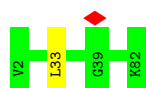
- Molecule 27: 40S ribosomal protein S26-B

Chain Se:  97%



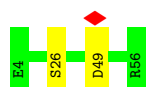
- Molecule 28: 40S ribosomal protein S27-A

Chain Sf:  99%



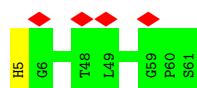
- Molecule 29: 40S ribosomal protein S29-A

Chain SM:  96%



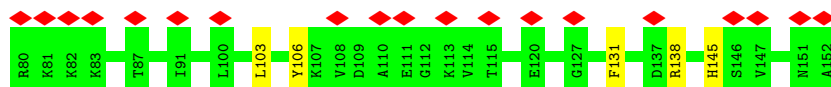
- Molecule 30: 40S ribosomal protein S30-A

Chain Sg:  98%



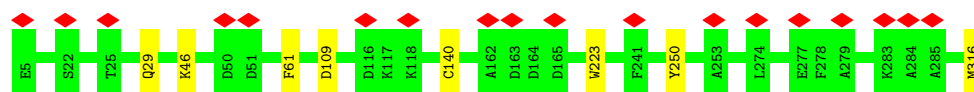
- Molecule 31: 40S ribosomal protein S31

Chain SN:  93%

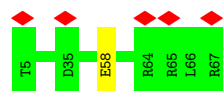


- Molecule 32: 40S ribosomal protein ASC1

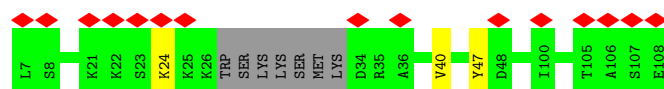
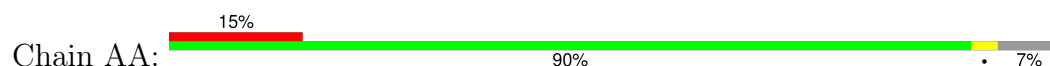
Chain SO:  97%



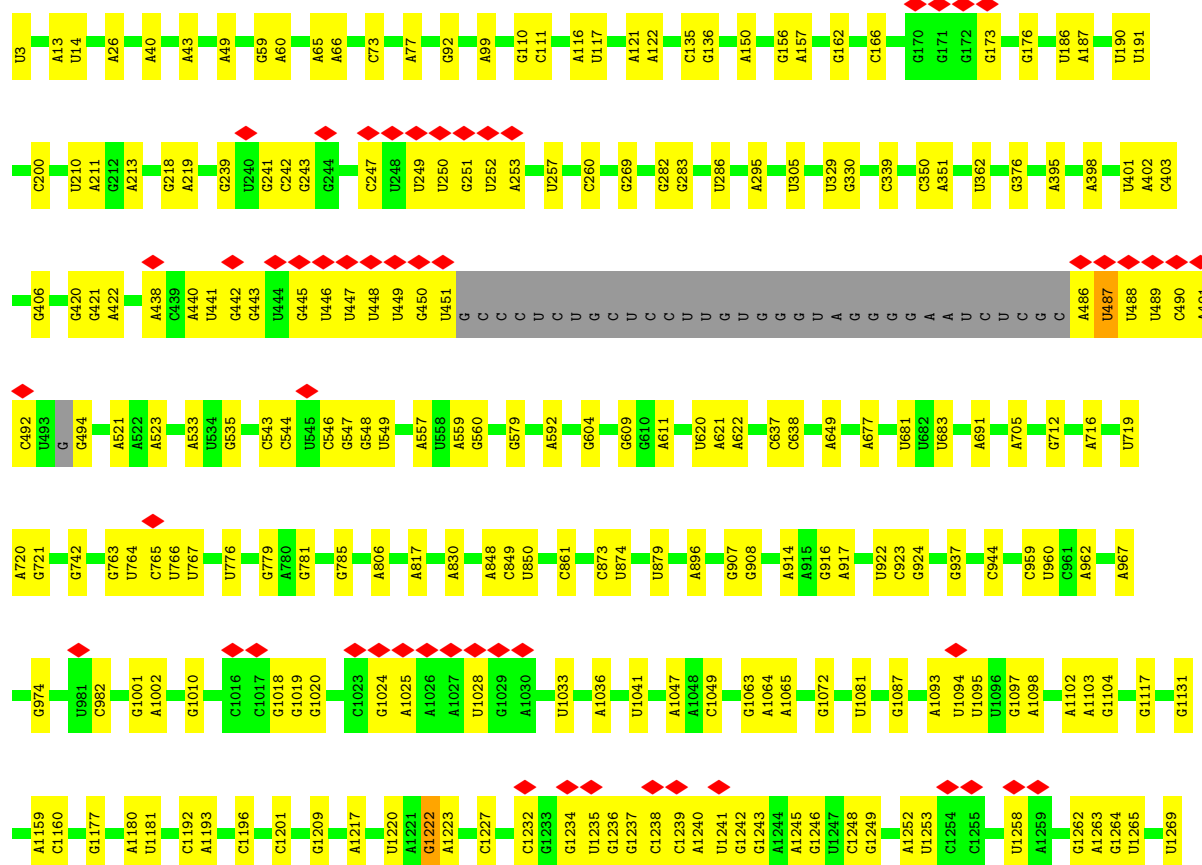
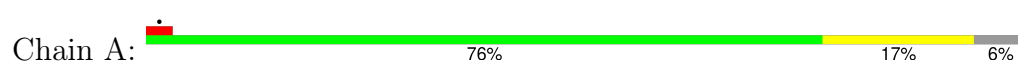
- Molecule 33: 40S ribosomal protein S28-A

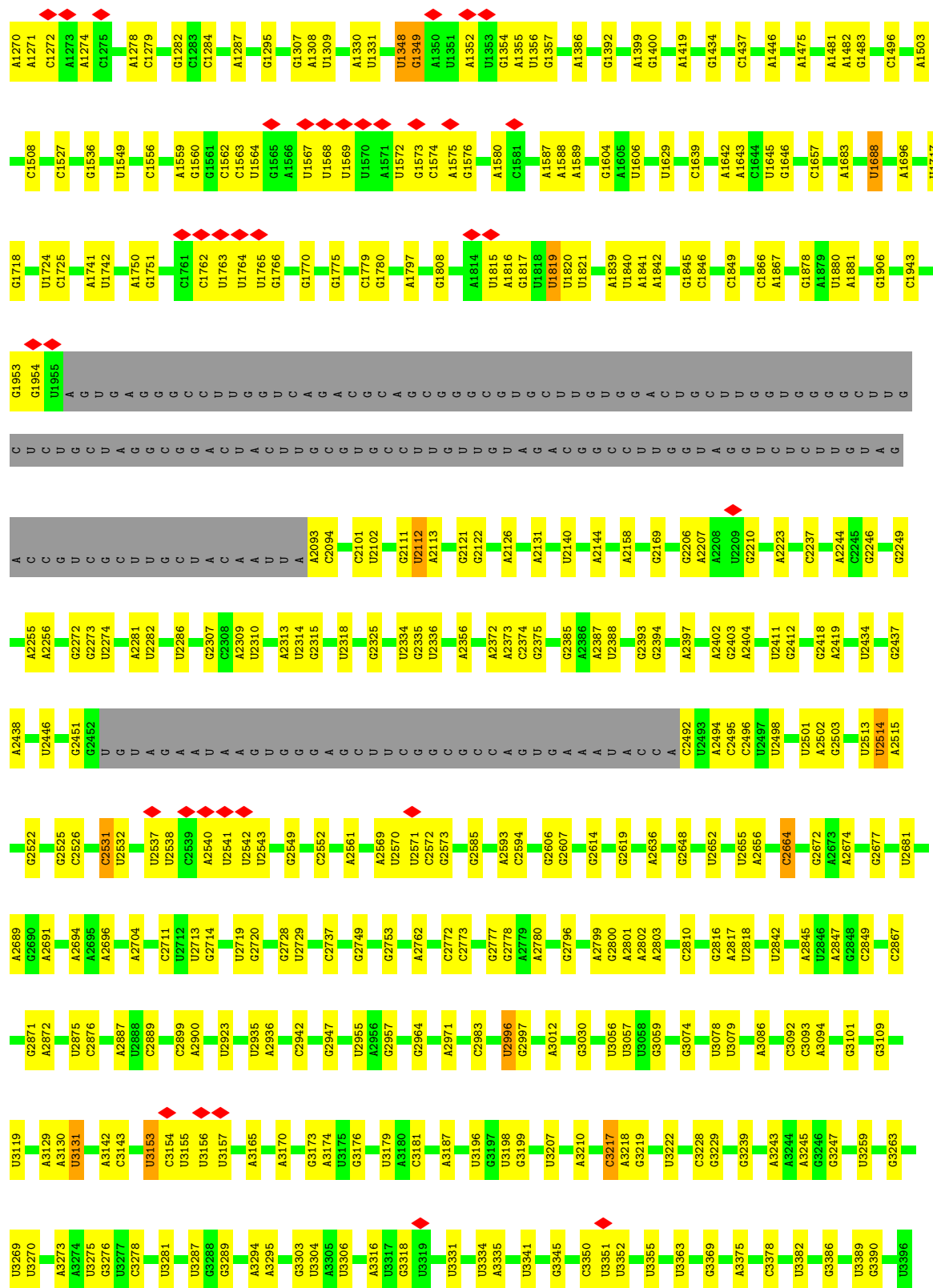


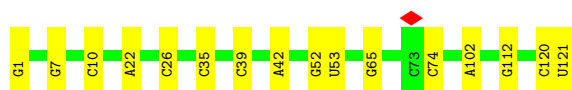
- Molecule 34: 40S ribosomal protein S25-A



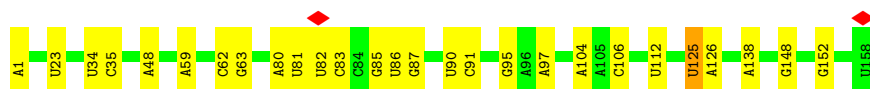
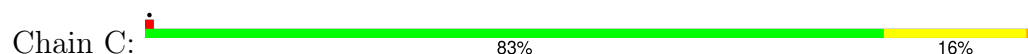
- Molecule 35: 25S rRNA







- Molecule 37: 5.8S rRNA



- Molecule 38: 60S ribosomal protein L2-A



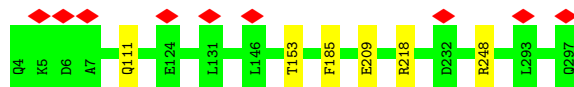
- Molecule 39: 60S ribosomal protein L3



- Molecule 40: 60S ribosomal protein L4-A



- Molecule 41: 60S ribosomal protein L5

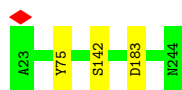


- Molecule 42: 60S ribosomal protein L6-B



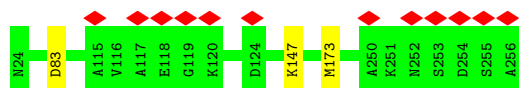
- Molecule 43: 60S ribosomal protein L7-A

Chain LI:  99%



- Molecule 44: 60S ribosomal protein L8-A

Chain LJ:  99%



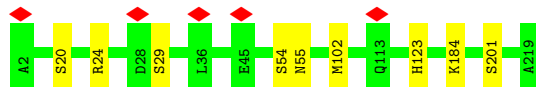
- Molecule 45: 60S ribosomal protein L9-A

Chain LK:  97%



- Molecule 46: 60S ribosomal protein L10

Chain LL:  96%



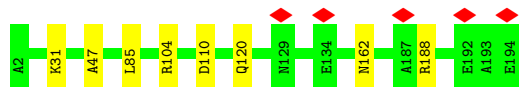
- Molecule 47: 60S ribosomal protein L11-B

Chain LM:  96%



- Molecule 48: 60S ribosomal protein L13-A

Chain LN:  96%



- Molecule 49: 60S ribosomal protein L14-A

Chain LO:  99%



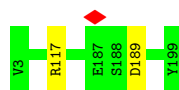
- Molecule 50: 60S ribosomal protein L15-A

Chain LP:  99%



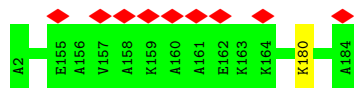
- Molecule 51: 60S ribosomal protein L16-A

Chain LQ:  99%



- Molecule 52: 60S ribosomal protein L17-A

Chain LR:  5% 99%



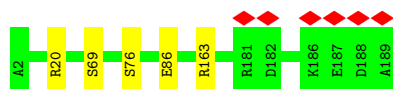
- Molecule 53: 60S ribosomal protein L18-A

Chain LS:  98%



- Molecule 54: 60S ribosomal protein L19-A

Chain LT:  97%



- Molecule 55: 60S ribosomal protein L20-A

Chain LU:  98%



- Molecule 56: 60S ribosomal protein L21-A

Chain LV:  97%



- Molecule 57: 60S ribosomal protein L22-A

Chain LW: 96%



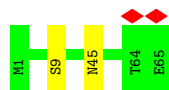
- Molecule 58: 60S ribosomal protein L23-A

Chain LX: 97%



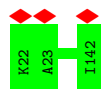
- Molecule 59: 60S ribosomal protein L24-A

Chain LY: 97%



- Molecule 60: 60S ribosomal protein L25

Chain LZ: 100%



- Molecule 61: 60S ribosomal protein L26-A

Chain La: 99%



- Molecule 62: 60S ribosomal protein L27-A

Chain Lb: 99%



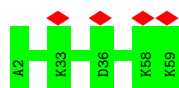
- Molecule 63: 60S ribosomal protein L28

Chain Lc:  97%



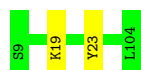
- Molecule 64: 60S ribosomal protein L29

Chain Ld:  100%



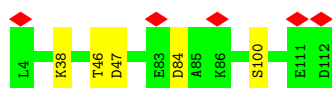
- Molecule 65: 60S ribosomal protein L30

Chain Le:  98%



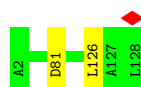
- Molecule 66: 60S ribosomal protein L31-A

Chain Lf:  95%



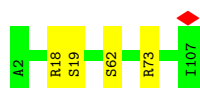
- Molecule 67: 60S ribosomal protein L32

Chain Lg:  98%



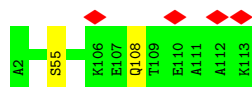
- Molecule 68: 60S ribosomal protein L33-A

Chain Lh:  96%



- Molecule 69: 60S ribosomal protein L34-A

Chain Li:  98%



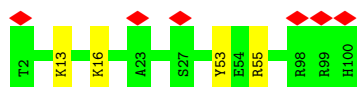
- Molecule 70: 60S ribosomal protein L35-A

Chain Lj:  97%



- Molecule 71: 60S ribosomal protein L36-A

Chain Lk:  96%



- Molecule 72: 60S ribosomal protein L37-A

Chain Ll:  100%

There are no outlier residues recorded for this chain.

- Molecule 73: 60S ribosomal protein L38

Chain Lm:  99%



- Molecule 74: 60S ribosomal protein L39

Chain Ln:  100%

There are no outlier residues recorded for this chain.

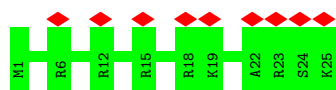
- Molecule 75: 60S ribosomal protein L40-A

Chain Lo:  98%



- Molecule 76: 60S ribosomal protein L41-A

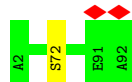
Chain Lp:  100%



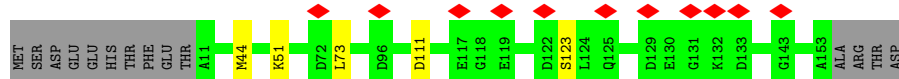
- Molecule 77: 60S ribosomal protein L42-A



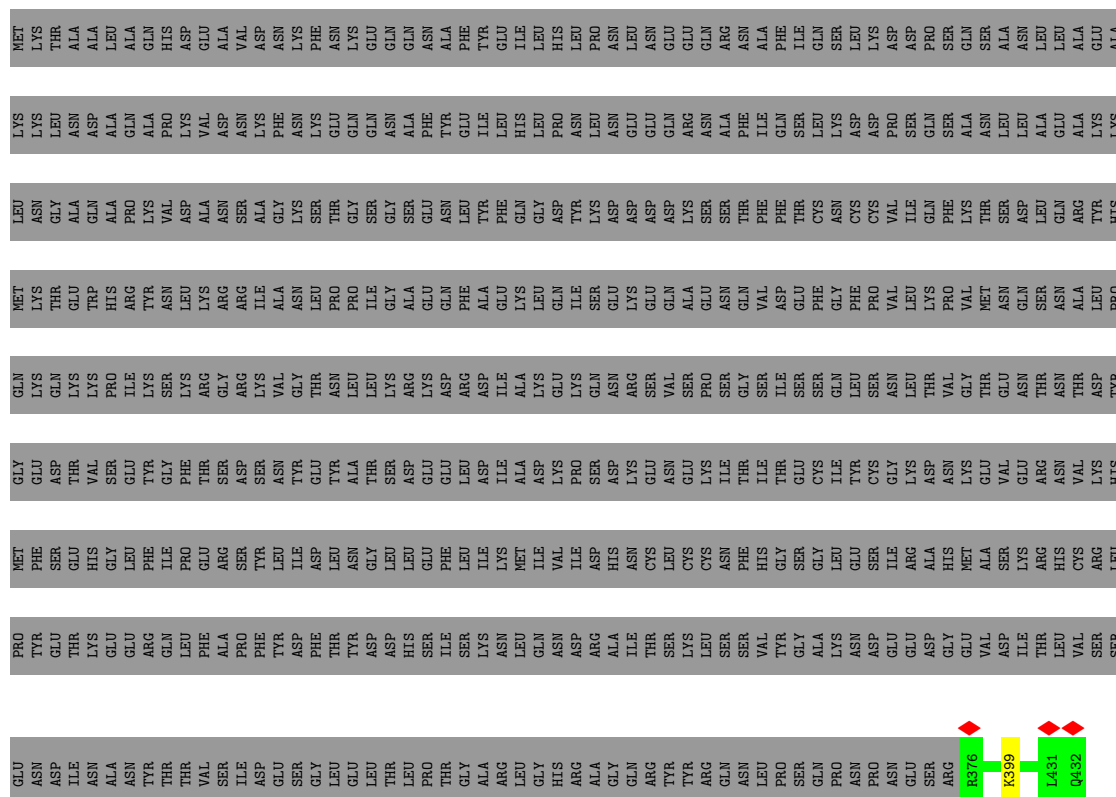
- Molecule 78: 60S ribosomal protein L43-A



- Molecule 79: Translation factor eIF5A

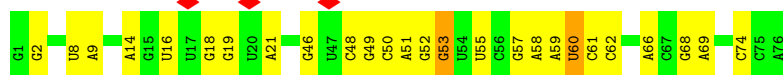


- Molecule 80: Cytoplasmic 60S subunit biogenesis factor REH1 (N-terminal 3xFLAG tag)



- Molecule 81: A site tRNA

Chain m:  66% 32%



- Molecule 82: P site initiator tRNA

Chain n:  75% 23%



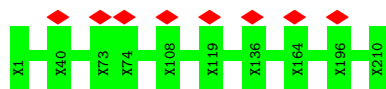
- Molecule 83: Messenger RNA (5'-R(P*AP*AP*UP*AP*UP*GP*AP*AP*AP*A)-3')

Chain D:  60% 40%



- Molecule 84: 60S ribosomal protein L1

Chain E:  100%



4 Experimental information

| Property | Value | Source |
|--------------------------------------|---|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 23734 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 70 | Depositor |
| Minimum defocus (nm) | 1000 | Depositor |
| Maximum defocus (nm) | 2500 | Depositor |
| Magnification | Not provided | |
| Image detector | GATAN K3 (6k x 4k) | Depositor |
| Maximum map value | 0.629 | Depositor |
| Minimum map value | -0.337 | Depositor |
| Average map value | -0.001 | Depositor |
| Map value standard deviation | 0.027 | Depositor |
| Recommended contour level | 0.0875 | Depositor |
| Map size (\AA) | 524.88, 524.88, 524.88 | wwPDB |
| Map dimensions | 648, 648, 648 | wwPDB |
| Map angles ($^\circ$) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (\AA) | 0.81, 0.81, 0.81 | Depositor |

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5CT, 3HE

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 | 2 | 0.65 | 0/42211 | 0.89 | 34/65773 (0.1%) |
| 2 | SP | 0.36 | 0/1644 | 0.54 | 0/2249 |
| 3 | SQ | 0.34 | 0/1823 | 0.56 | 0/2447 |
| 4 | SE | 0.33 | 0/936 | 0.58 | 0/1259 |
| 5 | SR | 0.39 | 0/1656 | 0.55 | 0/2251 |
| 6 | SA | 0.34 | 0/1754 | 0.60 | 0/2361 |
| 7 | SS | 0.39 | 0/2097 | 0.59 | 0/2823 |
| 8 | SB | 0.33 | 0/1625 | 0.60 | 0/2197 |
| 9 | ST | 0.33 | 0/1839 | 0.60 | 0/2460 |
| 10 | SU | 0.33 | 0/1498 | 0.60 | 1/2019 (0.0%) |
| 11 | SV | 0.39 | 0/1501 | 0.61 | 0/2006 |
| 12 | SW | 0.34 | 0/1504 | 0.61 | 0/2016 |
| 13 | SC | 0.40 | 0/772 | 0.55 | 0/1044 |
| 14 | SX | 0.45 | 0/1168 | 0.62 | 0/1575 |
| 15 | SD | 0.27 | 0/883 | 0.52 | 0/1199 |
| 16 | SY | 0.36 | 0/1215 | 0.55 | 0/1638 |
| 17 | SZ | 0.35 | 0/934 | 0.61 | 0/1257 |
| 18 | SF | 0.36 | 0/1125 | 0.60 | 0/1510 |
| 19 | SG | 0.32 | 0/957 | 0.62 | 0/1283 |
| 20 | SH | 0.34 | 0/1207 | 0.60 | 0/1623 |
| 21 | SI | 0.34 | 0/1130 | 0.57 | 0/1517 |
| 22 | SJ | 0.34 | 0/807 | 0.56 | 0/1091 |
| 23 | Sa | 0.39 | 0/682 | 0.60 | 0/921 |
| 24 | Sb | 0.42 | 0/1038 | 0.59 | 0/1395 |
| 25 | Sc | 0.40 | 0/1139 | 0.58 | 0/1518 |
| 26 | Sd | 0.38 | 0/1046 | 0.58 | 0/1401 |
| 27 | Se | 0.37 | 0/778 | 0.60 | 0/1042 |
| 28 | Sf | 0.36 | 0/620 | 0.56 | 0/838 |
| 29 | SM | 0.40 | 0/453 | 0.59 | 0/602 |
| 30 | Sg | 0.34 | 0/459 | 0.60 | 0/611 |
| 31 | SN | 0.33 | 0/567 | 0.67 | 1/764 (0.1%) |
| 32 | SO | 0.31 | 0/2436 | 0.59 | 0/3318 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|---------|-------------|------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 33 | SL | 0.34 | 0/493 | 0.70 | 0/663 |
| 34 | AA | 0.31 | 0/744 | 0.58 | 0/991 |
| 35 | A | 0.77 | 0/76214 | 0.88 | 42/118821 (0.0%) |
| 36 | B | 0.62 | 0/2883 | 0.84 | 1/4491 (0.0%) |
| 37 | C | 0.83 | 0/3746 | 0.85 | 2/5832 (0.0%) |
| 38 | LD | 0.45 | 0/1933 | 0.62 | 0/2598 |
| 39 | LE | 0.45 | 0/3150 | 0.58 | 0/4236 |
| 40 | LF | 0.42 | 0/2801 | 0.57 | 0/3792 |
| 41 | LG | 0.36 | 0/2400 | 0.57 | 0/3239 |
| 42 | LH | 0.39 | 0/1329 | 0.54 | 0/1794 |
| 43 | LI | 0.41 | 0/1821 | 0.53 | 0/2451 |
| 44 | LJ | 0.39 | 0/1836 | 0.56 | 0/2481 |
| 45 | LK | 0.40 | 0/1529 | 0.60 | 0/2060 |
| 46 | LL | 0.41 | 0/1801 | 0.60 | 0/2416 |
| 47 | LM | 0.35 | 0/1367 | 0.64 | 0/1834 |
| 48 | LN | 0.40 | 0/1568 | 0.61 | 1/2106 (0.0%) |
| 49 | LO | 0.36 | 0/1068 | 0.56 | 0/1438 |
| 50 | LP | 0.48 | 0/1757 | 0.64 | 0/2354 |
| 51 | LQ | 0.43 | 0/1585 | 0.55 | 0/2128 |
| 52 | LR | 0.44 | 0/1439 | 0.58 | 0/1938 |
| 53 | LS | 0.39 | 0/1465 | 0.61 | 0/1965 |
| 54 | LT | 0.38 | 0/1532 | 0.58 | 0/2043 |
| 55 | LU | 0.44 | 0/1473 | 0.57 | 0/1980 |
| 56 | LV | 0.39 | 0/1296 | 0.56 | 0/1739 |
| 57 | LW | 0.41 | 0/812 | 0.62 | 1/1099 (0.1%) |
| 58 | LX | 0.45 | 0/1018 | 0.60 | 0/1369 |
| 59 | LY | 0.41 | 0/540 | 0.54 | 0/717 |
| 60 | LZ | 0.47 | 0/979 | 0.58 | 0/1321 |
| 61 | La | 0.41 | 0/995 | 0.55 | 0/1329 |
| 62 | Lb | 0.44 | 0/1106 | 0.54 | 0/1485 |
| 63 | Lc | 0.42 | 0/1200 | 0.62 | 0/1607 |
| 64 | Ld | 0.31 | 0/473 | 0.48 | 0/629 |
| 65 | Le | 0.43 | 0/745 | 0.53 | 0/1001 |
| 66 | Lf | 0.42 | 0/890 | 0.59 | 0/1196 |
| 67 | Lg | 0.42 | 0/1038 | 0.60 | 0/1390 |
| 68 | Lh | 0.48 | 0/868 | 0.61 | 0/1168 |
| 69 | Li | 0.48 | 0/890 | 0.62 | 0/1189 |
| 70 | Lj | 0.39 | 0/978 | 0.57 | 0/1301 |
| 71 | Lk | 0.33 | 0/772 | 0.60 | 0/1026 |
| 72 | Ll | 0.46 | 0/660 | 0.62 | 0/875 |
| 73 | Lm | 0.38 | 0/618 | 0.61 | 0/826 |
| 74 | Ln | 0.43 | 0/443 | 0.65 | 0/588 |
| 75 | Lo | 0.38 | 0/416 | 0.56 | 0/553 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|-----------------|-------------|------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 76 | Lp | 0.30 | 0/230 | 0.68 | 0/296 |
| 77 | Lq | 0.41 | 0/836 | 0.60 | 0/1104 |
| 78 | Lr | 0.44 | 0/701 | 0.60 | 0/934 |
| 79 | Ls | 0.33 | 0/1080 | 0.60 | 1/1452 (0.1%) |
| 80 | z | 0.38 | 0/483 | 0.61 | 0/640 |
| 81 | m | 0.58 | 0/1799 | 1.02 | 3/2801 (0.1%) |
| 82 | n | 1.15 | 1/1796 (0.1%) | 1.00 | 6/2799 (0.2%) |
| 83 | D | 0.68 | 0/240 | 1.02 | 0/368 |
| All | All | 0.62 | 1/219340 (0.0%) | 0.79 | 93/322461 (0.0%) |

All (1) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|-------|-------------|----------|
| 82 | n | 16 | U | O3'-P | 42.52 | 2.12 | 1.61 |

The worst 5 of 93 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|-----------|--------|-------------|----------|
| 82 | n | 16 | U | P-O3'-C3' | -17.22 | 99.04 | 119.70 |
| 35 | A | 2094 | C | N3-C2-O2 | -10.12 | 114.81 | 121.90 |
| 82 | n | 16 | U | C5-C4-O4 | 8.83 | 131.19 | 125.90 |
| 35 | A | 2094 | C | N1-C2-O2 | 7.89 | 123.63 | 118.90 |
| 35 | A | 3278 | C | N1-C2-O2 | 7.59 | 123.45 | 118.90 |

There are no chirality outliers.

There are no planarity outliers.

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 | |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 2 | SP | 204/206 (99%) | 188 (92%) | 16 (8%) | 0 | 100 | 100 |
| 3 | SQ | 222/232 (96%) | 208 (94%) | 14 (6%) | 0 | 100 | 100 |
| 4 | SE | 115/117 (98%) | 108 (94%) | 7 (6%) | 0 | 100 | 100 |
| 5 | SR | 214/216 (99%) | 207 (97%) | 6 (3%) | 1 (0%) | 25 | 59 |
| 6 | SA | 220/222 (99%) | 209 (95%) | 11 (5%) | 0 | 100 | 100 |
| 7 | SS | 256/258 (99%) | 236 (92%) | 20 (8%) | 0 | 100 | 100 |
| 8 | SB | 204/206 (99%) | 193 (95%) | 11 (5%) | 0 | 100 | 100 |
| 9 | ST | 226/228 (99%) | 216 (96%) | 10 (4%) | 0 | 100 | 100 |
| 10 | SU | 182/184 (99%) | 173 (95%) | 8 (4%) | 1 (0%) | 25 | 59 |
| 11 | SV | 183/187 (98%) | 174 (95%) | 9 (5%) | 0 | 100 | 100 |
| 12 | SW | 182/184 (99%) | 177 (97%) | 5 (3%) | 0 | 100 | 100 |
| 13 | SC | 90/92 (98%) | 86 (96%) | 4 (4%) | 0 | 100 | 100 |
| 14 | SX | 140/142 (99%) | 125 (89%) | 15 (11%) | 0 | 100 | 100 |
| 15 | SD | 119/121 (98%) | 106 (89%) | 12 (10%) | 1 (1%) | 16 | 50 |
| 16 | SY | 148/150 (99%) | 138 (93%) | 10 (7%) | 0 | 100 | 100 |
| 17 | SZ | 125/127 (98%) | 121 (97%) | 4 (3%) | 0 | 100 | 100 |
| 18 | SF | 139/141 (99%) | 134 (96%) | 5 (4%) | 0 | 100 | 100 |
| 19 | SG | 117/125 (94%) | 110 (94%) | 7 (6%) | 0 | 100 | 100 |
| 20 | SH | 143/145 (99%) | 140 (98%) | 3 (2%) | 0 | 100 | 100 |
| 21 | SI | 141/143 (99%) | 138 (98%) | 3 (2%) | 0 | 100 | 100 |
| 22 | SJ | 98/100 (98%) | 97 (99%) | 1 (1%) | 0 | 100 | 100 |
| 23 | Sa | 85/87 (98%) | 80 (94%) | 5 (6%) | 0 | 100 | 100 |
| 24 | Sb | 127/129 (98%) | 120 (94%) | 7 (6%) | 0 | 100 | 100 |
| 25 | Sc | 142/144 (99%) | 137 (96%) | 5 (4%) | 0 | 100 | 100 |
| 26 | Sd | 132/134 (98%) | 126 (96%) | 6 (4%) | 0 | 100 | 100 |
| 27 | Se | 95/97 (98%) | 94 (99%) | 1 (1%) | 0 | 100 | 100 |
| 28 | Sf | 79/81 (98%) | 75 (95%) | 4 (5%) | 0 | 100 | 100 |
| 29 | SM | 51/53 (96%) | 50 (98%) | 1 (2%) | 0 | 100 | 100 |
| 30 | Sg | 55/57 (96%) | 46 (84%) | 9 (16%) | 0 | 100 | 100 |
| 31 | SN | 71/73 (97%) | 61 (86%) | 10 (14%) | 0 | 100 | 100 |
| 32 | SO | 310/312 (99%) | 289 (93%) | 21 (7%) | 0 | 100 | 100 |
| 33 | SL | 61/63 (97%) | 58 (95%) | 3 (5%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|----------|-------------|-----|
| 34 | AA | 91/102 (89%) | 78 (86%) | 12 (13%) | 1 (1%) | 12 | 43 |
| 38 | LD | 249/251 (99%) | 231 (93%) | 18 (7%) | 0 | 100 | 100 |
| 39 | LE | 384/386 (100%) | 364 (95%) | 20 (5%) | 0 | 100 | 100 |
| 40 | LF | 359/361 (99%) | 344 (96%) | 15 (4%) | 0 | 100 | 100 |
| 41 | LG | 292/294 (99%) | 281 (96%) | 11 (4%) | 0 | 100 | 100 |
| 42 | LH | 163/175 (93%) | 152 (93%) | 11 (7%) | 0 | 100 | 100 |
| 43 | LI | 220/222 (99%) | 213 (97%) | 7 (3%) | 0 | 100 | 100 |
| 44 | LJ | 231/233 (99%) | 222 (96%) | 9 (4%) | 0 | 100 | 100 |
| 45 | LK | 189/191 (99%) | 181 (96%) | 8 (4%) | 0 | 100 | 100 |
| 46 | LL | 216/218 (99%) | 202 (94%) | 13 (6%) | 1 (0%) | 25 | 59 |
| 47 | LM | 167/169 (99%) | 159 (95%) | 8 (5%) | 0 | 100 | 100 |
| 48 | LN | 191/193 (99%) | 174 (91%) | 16 (8%) | 1 (0%) | 25 | 59 |
| 49 | LO | 134/136 (98%) | 129 (96%) | 5 (4%) | 0 | 100 | 100 |
| 50 | LP | 201/203 (99%) | 189 (94%) | 12 (6%) | 0 | 100 | 100 |
| 51 | LQ | 195/197 (99%) | 190 (97%) | 5 (3%) | 0 | 100 | 100 |
| 52 | LR | 181/183 (99%) | 168 (93%) | 13 (7%) | 0 | 100 | 100 |
| 53 | LS | 183/185 (99%) | 168 (92%) | 14 (8%) | 1 (0%) | 25 | 59 |
| 54 | LT | 186/188 (99%) | 183 (98%) | 3 (2%) | 0 | 100 | 100 |
| 55 | LU | 169/171 (99%) | 158 (94%) | 11 (6%) | 0 | 100 | 100 |
| 56 | LV | 157/159 (99%) | 150 (96%) | 7 (4%) | 0 | 100 | 100 |
| 57 | LW | 98/100 (98%) | 86 (88%) | 12 (12%) | 0 | 100 | 100 |
| 58 | LX | 134/136 (98%) | 131 (98%) | 3 (2%) | 0 | 100 | 100 |
| 59 | LY | 63/65 (97%) | 59 (94%) | 4 (6%) | 0 | 100 | 100 |
| 60 | LZ | 119/121 (98%) | 112 (94%) | 7 (6%) | 0 | 100 | 100 |
| 61 | La | 123/125 (98%) | 122 (99%) | 1 (1%) | 0 | 100 | 100 |
| 62 | Lb | 133/135 (98%) | 130 (98%) | 3 (2%) | 0 | 100 | 100 |
| 63 | Lc | 146/148 (99%) | 134 (92%) | 11 (8%) | 1 (1%) | 19 | 53 |
| 64 | Ld | 56/58 (97%) | 50 (89%) | 6 (11%) | 0 | 100 | 100 |
| 65 | Le | 94/96 (98%) | 94 (100%) | 0 | 0 | 100 | 100 |
| 66 | Lf | 107/109 (98%) | 102 (95%) | 5 (5%) | 0 | 100 | 100 |
| 67 | Lg | 125/127 (98%) | 120 (96%) | 5 (4%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-------------------|-------------|----------|----------|-------------|-----|
| 68 | Lh | 104/106 (98%) | 102 (98%) | 2 (2%) | 0 | 100 | 100 |
| 69 | Li | 110/112 (98%) | 107 (97%) | 3 (3%) | 0 | 100 | 100 |
| 70 | Lj | 117/119 (98%) | 112 (96%) | 3 (3%) | 2 (2%) | 7 | 35 |
| 71 | Lk | 97/99 (98%) | 90 (93%) | 7 (7%) | 0 | 100 | 100 |
| 72 | Ll | 79/81 (98%) | 74 (94%) | 5 (6%) | 0 | 100 | 100 |
| 73 | Lm | 75/77 (97%) | 73 (97%) | 2 (3%) | 0 | 100 | 100 |
| 74 | Ln | 48/50 (96%) | 47 (98%) | 1 (2%) | 0 | 100 | 100 |
| 75 | Lo | 50/52 (96%) | 49 (98%) | 1 (2%) | 0 | 100 | 100 |
| 76 | Lp | 23/25 (92%) | 23 (100%) | 0 | 0 | 100 | 100 |
| 77 | Lq | 101/103 (98%) | 93 (92%) | 8 (8%) | 0 | 100 | 100 |
| 78 | Lr | 89/91 (98%) | 83 (93%) | 6 (7%) | 0 | 100 | 100 |
| 79 | Ls | 140/157 (89%) | 129 (92%) | 11 (8%) | 0 | 100 | 100 |
| 80 | z | 55/588 (9%) | 53 (96%) | 2 (4%) | 0 | 100 | 100 |
| All | All | 11120/11853 (94%) | 10531 (95%) | 579 (5%) | 10 (0%) | 50 | 79 |

5 of 10 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 34 | AA | 40 | VAL |
| 48 | LN | 47 | ALA |
| 15 | SD | 86 | VAL |
| 63 | Lc | 40 | HIS |
| 5 | SR | 174 | ARG |

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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 | |
|-----|-------|---------------|-----------|----------|-------------|----|
| 2 | SP | 170/173 (98%) | 167 (98%) | 3 (2%) | 54 | 75 |
| 3 | SQ | 200/205 (98%) | 196 (98%) | 4 (2%) | 50 | 73 |
| 4 | SE | 95/98 (97%) | 93 (98%) | 2 (2%) | 48 | 72 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|-------------|----|
| 5 | SR | 175/175 (100%) | 172 (98%) | 3 (2%) | 56 | 77 |
| 6 | SA | 182/182 (100%) | 176 (97%) | 6 (3%) | 33 | 62 |
| 7 | SS | 220/220 (100%) | 214 (97%) | 6 (3%) | 40 | 67 |
| 8 | SB | 172/173 (99%) | 169 (98%) | 3 (2%) | 56 | 77 |
| 9 | ST | 189/195 (97%) | 182 (96%) | 7 (4%) | 29 | 60 |
| 10 | SU | 163/165 (99%) | 162 (99%) | 1 (1%) | 84 | 91 |
| 11 | SV | 148/149 (99%) | 142 (96%) | 6 (4%) | 26 | 57 |
| 12 | SW | 156/157 (99%) | 154 (99%) | 2 (1%) | 65 | 81 |
| 13 | SC | 78/85 (92%) | 76 (97%) | 2 (3%) | 41 | 68 |
| 14 | SX | 126/127 (99%) | 122 (97%) | 4 (3%) | 34 | 63 |
| 15 | SD | 88/98 (90%) | 87 (99%) | 1 (1%) | 70 | 84 |
| 16 | SY | 127/127 (100%) | 126 (99%) | 1 (1%) | 79 | 89 |
| 17 | SZ | 90/96 (94%) | 85 (94%) | 5 (6%) | 17 | 49 |
| 18 | SF | 117/117 (100%) | 109 (93%) | 8 (7%) | 13 | 42 |
| 19 | SG | 101/113 (89%) | 98 (97%) | 3 (3%) | 36 | 64 |
| 20 | SH | 127/128 (99%) | 124 (98%) | 3 (2%) | 44 | 69 |
| 21 | SI | 115/115 (100%) | 109 (95%) | 6 (5%) | 19 | 50 |
| 22 | SJ | 93/93 (100%) | 90 (97%) | 3 (3%) | 34 | 63 |
| 23 | Sa | 71/74 (96%) | 69 (97%) | 2 (3%) | 38 | 66 |
| 24 | Sb | 110/110 (100%) | 108 (98%) | 2 (2%) | 54 | 75 |
| 25 | Sc | 119/119 (100%) | 113 (95%) | 6 (5%) | 20 | 52 |
| 26 | Sd | 102/112 (91%) | 100 (98%) | 2 (2%) | 50 | 73 |
| 27 | Se | 82/83 (99%) | 79 (96%) | 3 (4%) | 29 | 60 |
| 28 | Sf | 70/70 (100%) | 69 (99%) | 1 (1%) | 62 | 80 |
| 29 | SM | 47/47 (100%) | 45 (96%) | 2 (4%) | 25 | 55 |
| 30 | Sg | 48/49 (98%) | 47 (98%) | 1 (2%) | 48 | 72 |
| 31 | SN | 56/63 (89%) | 52 (93%) | 4 (7%) | 12 | 40 |
| 32 | SO | 250/257 (97%) | 242 (97%) | 8 (3%) | 34 | 63 |
| 33 | SL | 55/56 (98%) | 54 (98%) | 1 (2%) | 54 | 75 |
| 34 | AA | 76/83 (92%) | 74 (97%) | 2 (3%) | 41 | 68 |
| 38 | LD | 190/193 (98%) | 187 (98%) | 3 (2%) | 58 | 78 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|------------|----------|-------------|-----|
| 39 | LE | 321/322 (100%) | 311 (97%) | 10 (3%) | 35 | 64 |
| 40 | LF | 288/288 (100%) | 283 (98%) | 5 (2%) | 56 | 77 |
| 41 | LG | 241/243 (99%) | 235 (98%) | 6 (2%) | 42 | 69 |
| 42 | LH | 139/154 (90%) | 137 (99%) | 2 (1%) | 62 | 80 |
| 43 | LI | 186/186 (100%) | 183 (98%) | 3 (2%) | 58 | 78 |
| 44 | LJ | 187/191 (98%) | 184 (98%) | 3 (2%) | 58 | 78 |
| 45 | LK | 168/171 (98%) | 163 (97%) | 5 (3%) | 36 | 64 |
| 46 | LL | 185/185 (100%) | 177 (96%) | 8 (4%) | 25 | 55 |
| 47 | LM | 145/147 (99%) | 138 (95%) | 7 (5%) | 21 | 53 |
| 48 | LN | 154/154 (100%) | 148 (96%) | 6 (4%) | 27 | 58 |
| 49 | LO | 107/107 (100%) | 105 (98%) | 2 (2%) | 52 | 74 |
| 50 | LP | 175/175 (100%) | 172 (98%) | 3 (2%) | 56 | 77 |
| 51 | LQ | 160/160 (100%) | 158 (99%) | 2 (1%) | 65 | 81 |
| 52 | LR | 138/145 (95%) | 137 (99%) | 1 (1%) | 81 | 90 |
| 53 | LS | 150/150 (100%) | 147 (98%) | 3 (2%) | 50 | 73 |
| 54 | LT | 152/153 (99%) | 147 (97%) | 5 (3%) | 33 | 62 |
| 55 | LU | 155/155 (100%) | 151 (97%) | 4 (3%) | 41 | 68 |
| 56 | LV | 135/136 (99%) | 131 (97%) | 4 (3%) | 36 | 64 |
| 57 | LW | 87/87 (100%) | 84 (97%) | 3 (3%) | 32 | 61 |
| 58 | LX | 104/104 (100%) | 100 (96%) | 4 (4%) | 28 | 59 |
| 59 | LY | 54/57 (95%) | 52 (96%) | 2 (4%) | 29 | 60 |
| 60 | LZ | 104/105 (99%) | 104 (100%) | 0 | 100 | 100 |
| 61 | La | 108/108 (100%) | 107 (99%) | 1 (1%) | 75 | 87 |
| 62 | Lb | 112/115 (97%) | 111 (99%) | 1 (1%) | 75 | 87 |
| 63 | Lc | 117/118 (99%) | 113 (97%) | 4 (3%) | 32 | 61 |
| 64 | Ld | 46/46 (100%) | 46 (100%) | 0 | 100 | 100 |
| 65 | Le | 81/81 (100%) | 79 (98%) | 2 (2%) | 42 | 69 |
| 66 | Lf | 92/96 (96%) | 87 (95%) | 5 (5%) | 18 | 50 |
| 67 | Lg | 108/109 (99%) | 106 (98%) | 2 (2%) | 52 | 74 |
| 68 | Lh | 90/90 (100%) | 86 (96%) | 4 (4%) | 24 | 55 |
| 69 | Li | 95/95 (100%) | 93 (98%) | 2 (2%) | 48 | 72 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-----------------|------------|----------|-------------|-----|
| 70 | Lj | 104/104 (100%) | 103 (99%) | 1 (1%) | 73 | 86 |
| 71 | Lk | 80/81 (99%) | 76 (95%) | 4 (5%) | 20 | 52 |
| 72 | Ll | 67/67 (100%) | 67 (100%) | 0 | 100 | 100 |
| 73 | Lm | 68/68 (100%) | 67 (98%) | 1 (2%) | 60 | 79 |
| 74 | Ln | 45/45 (100%) | 45 (100%) | 0 | 100 | 100 |
| 75 | Lo | 45/47 (96%) | 44 (98%) | 1 (2%) | 47 | 71 |
| 76 | Lp | 22/23 (96%) | 22 (100%) | 0 | 100 | 100 |
| 77 | Lq | 87/88 (99%) | 83 (95%) | 4 (5%) | 23 | 54 |
| 78 | Lr | 71/71 (100%) | 70 (99%) | 1 (1%) | 62 | 80 |
| 79 | Ls | 118/132 (89%) | 115 (98%) | 3 (2%) | 42 | 69 |
| 80 | z | 52/523 (10%) | 51 (98%) | 1 (2%) | 52 | 74 |
| All | All | 9351/9989 (94%) | 9110 (97%) | 241 (3%) | 42 | 68 |

5 of 241 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 38 | LD | 149 | ARG |
| 68 | Lh | 62 | SER |
| 44 | LJ | 147 | LYS |
| 68 | Lh | 18 | ARG |
| 78 | Lr | 72 | SER |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 38 | LD | 24 | GLN |
| 80 | z | 403 | GLN |
| 46 | LL | 112 | GLN |
| 80 | z | 402 | GLN |
| 65 | Le | 75 | ASN |

5.3.3 RNA ⓘ

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 1 | 2 | 1768/1800 (98%) | 447 (25%) | 60 (3%) |
| 35 | A | 3180/3394 (93%) | 560 (17%) | 38 (1%) |

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| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 36 | B | 120/121 (99%) | 13 (10%) | 2 (1%) |
| 37 | C | 157/158 (99%) | 25 (15%) | 1 (0%) |
| 81 | m | 75/76 (98%) | 26 (34%) | 0 |
| 82 | n | 74/75 (98%) | 18 (24%) | 0 |
| 83 | D | 9/10 (90%) | 4 (44%) | 1 (11%) |
| All | All | 5383/5634 (95%) | 1093 (20%) | 102 (1%) |

5 of 1093 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | 2 | 2 | A |
| 1 | 2 | 4 | C |
| 1 | 2 | 25 | C |
| 1 | 2 | 26 | A |
| 1 | 2 | 43 | A |

5 of 102 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 1 | 2 | 1636 | C |
| 35 | A | 1097 | G |
| 36 | B | 120 | C |
| 1 | 2 | 1688 | U |
| 35 | A | 719 | U |

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

1 non-standard protein/DNA/RNA residue is 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 | $\# Z > 2$ |
| 79 | 5CT | Ls | 51 | 79 | 13,14,15 | 0.72 | 0 | 8,15,17 | 1.76 | 2 (25%) |

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 |
|-----|------|-------|-----|------|---------|------------|-------|
| 79 | 5CT | Ls | 51 | 79 | - | 1/13/14/16 | - |

There are no bond length outliers.

All (2) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|-------|-------------|----------|
| 79 | Ls | 51 | 5CT | C4-C3-C2 | -3.76 | 105.54 | 113.47 |
| 79 | Ls | 51 | 5CT | C1-NZ-CE | -2.35 | 108.24 | 113.38 |

There are no chirality outliers.

All (1) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|-----|-------|-----|------|-------------|
| 79 | Ls | 51 | 5CT | C2-C3-C4-N1 |

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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 | $\# Z > 2$ |
| 85 | 3HE | A | 3401 | - | 21,21,21 | 0.60 | 0 | 23,30,30 | 0.87 | 0 |

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 |
|-----|------|-------|------|------|---------|-----------|---------|
| 85 | 3HE | A | 3401 | - | - | 0/8/36/36 | 0/2/2/2 |

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 |
|-----|-------|------------------|
| 11 | SV | 1 |
| 82 | n | 1 |

All chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1 | SV | 123:LYS | C | 135:LYS | N | 20.35 |
| 1 | n | 16:U | O3' | 18:G | P | 2.12 |

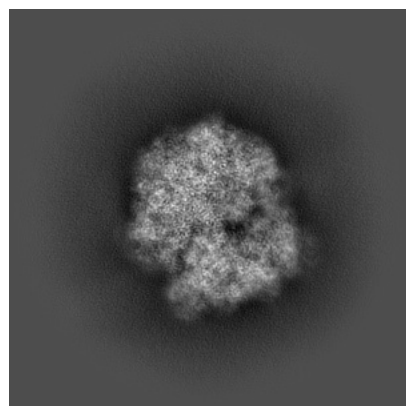
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42525. These allow visual inspection of the internal detail of the map and identification of artifacts.

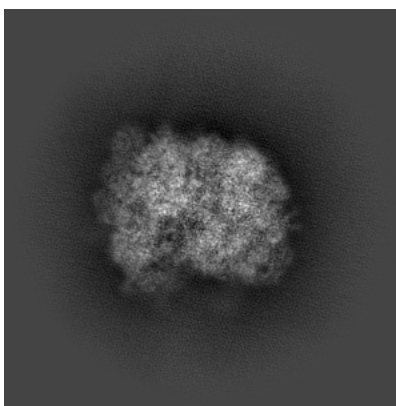
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

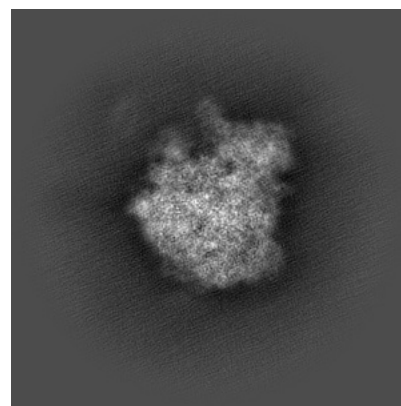
6.1.1 Primary map



X

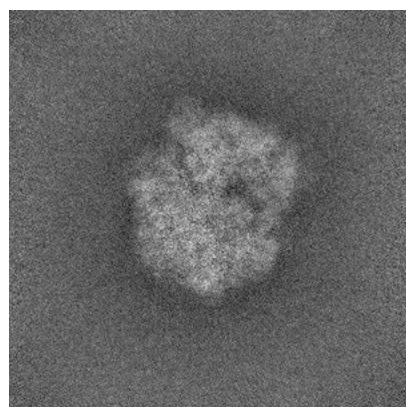


Y

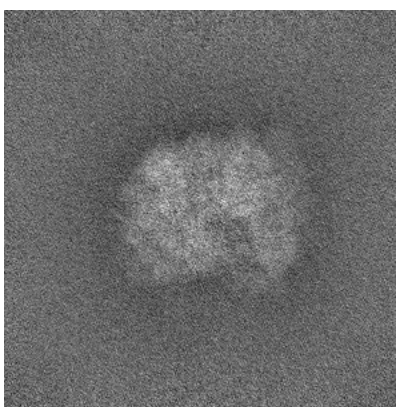


Z

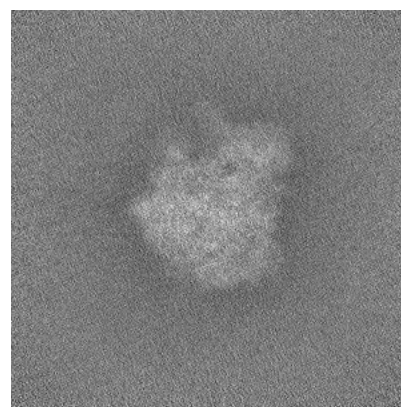
6.1.2 Raw map



X



Y

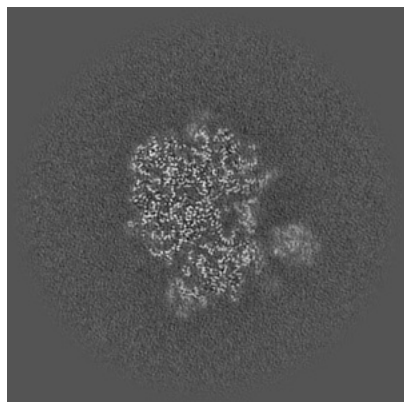


Z

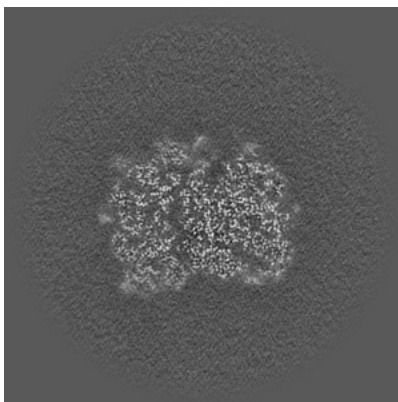
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

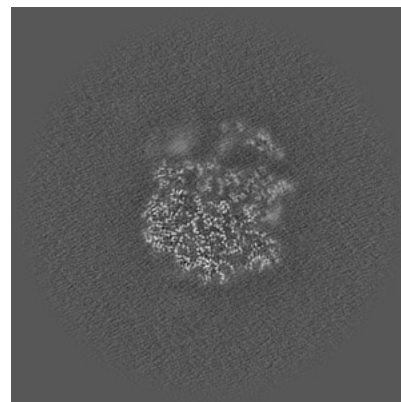
6.2.1 Primary map



X Index: 324

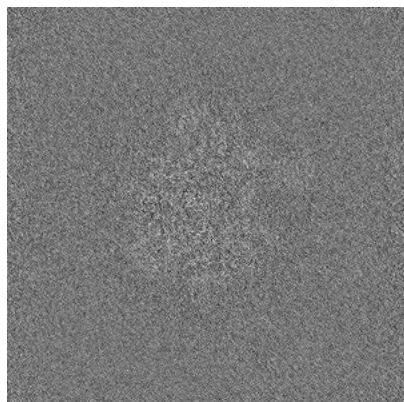


Y Index: 324

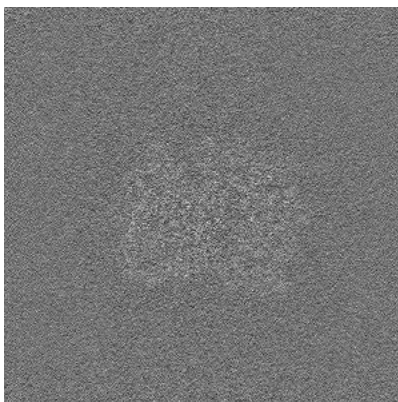


Z Index: 324

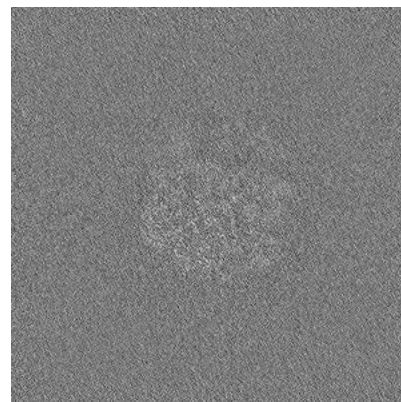
6.2.2 Raw map



X Index: 324



Y Index: 324

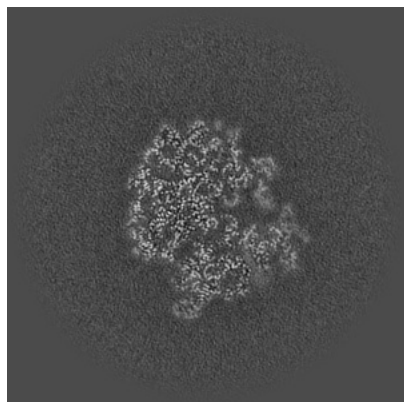


Z Index: 324

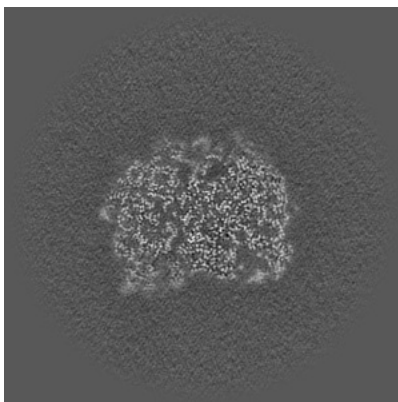
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

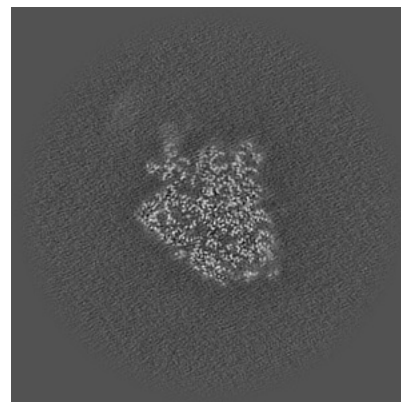
6.3.1 Primary map



X Index: 343

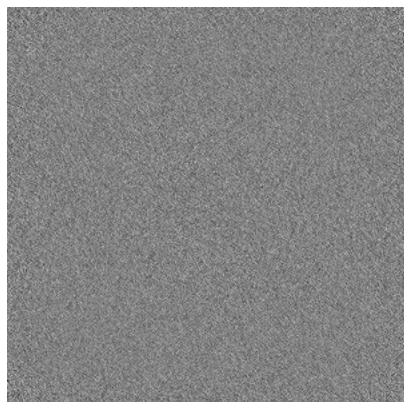


Y Index: 319

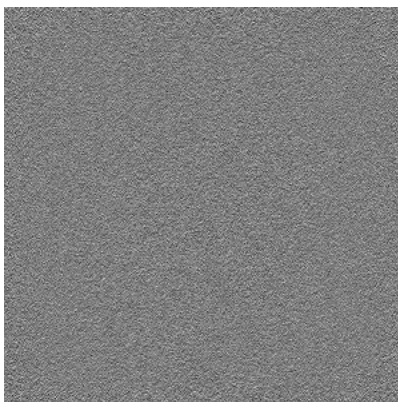


Z Index: 366

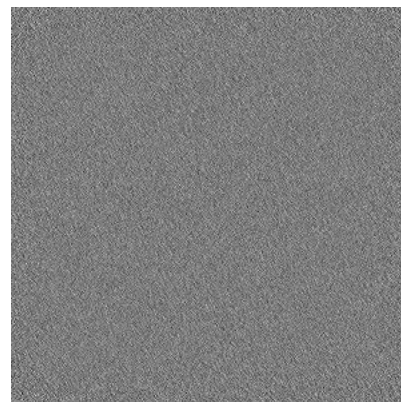
6.3.2 Raw map



X Index: 0



Y Index: 0

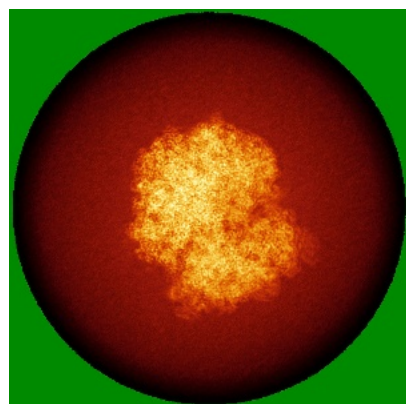


Z Index: 0

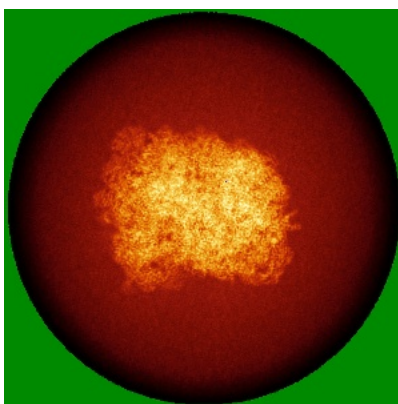
The images above show the largest variance slices of the map in three orthogonal directions.

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

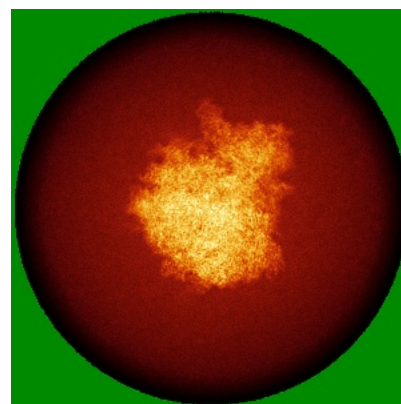
6.4.1 Primary map



X

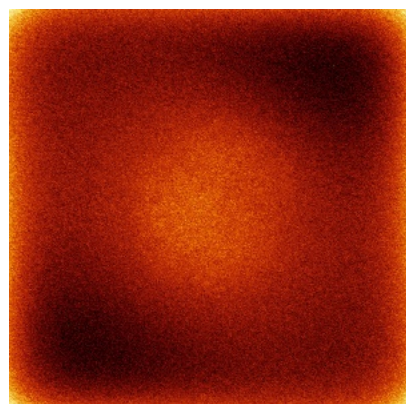


Y

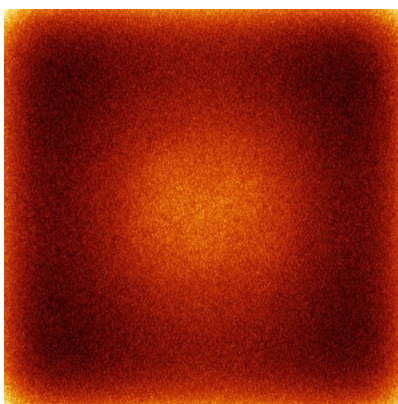


Z

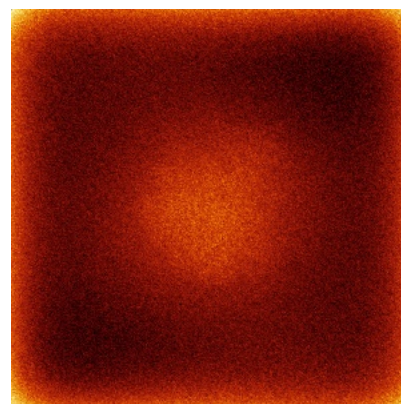
6.4.2 Raw map



X



Y

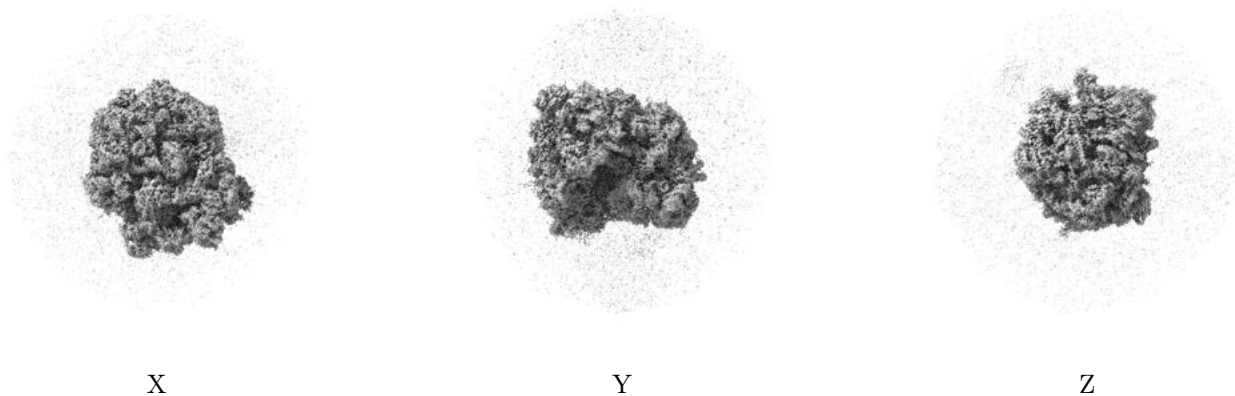


Z

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.

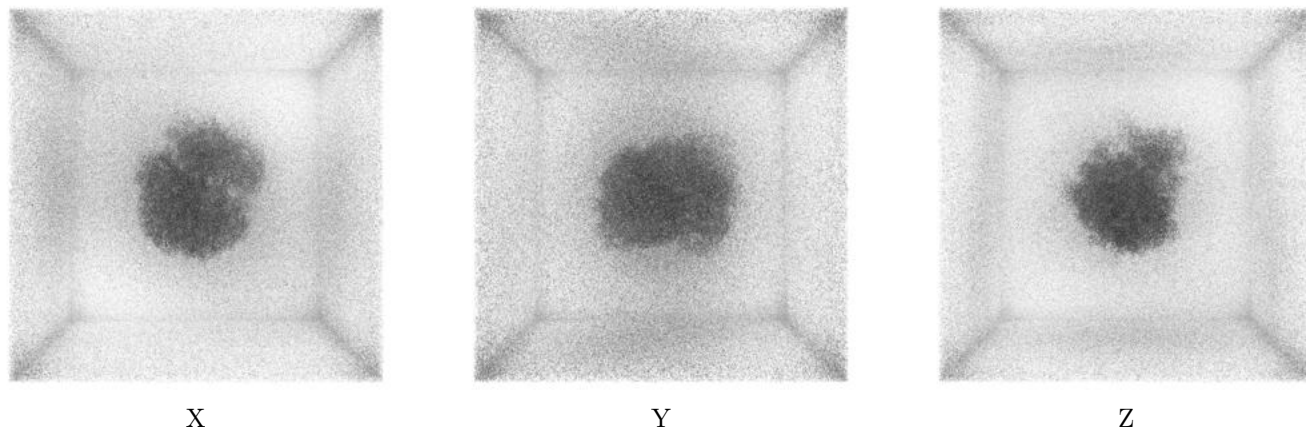
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0875. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

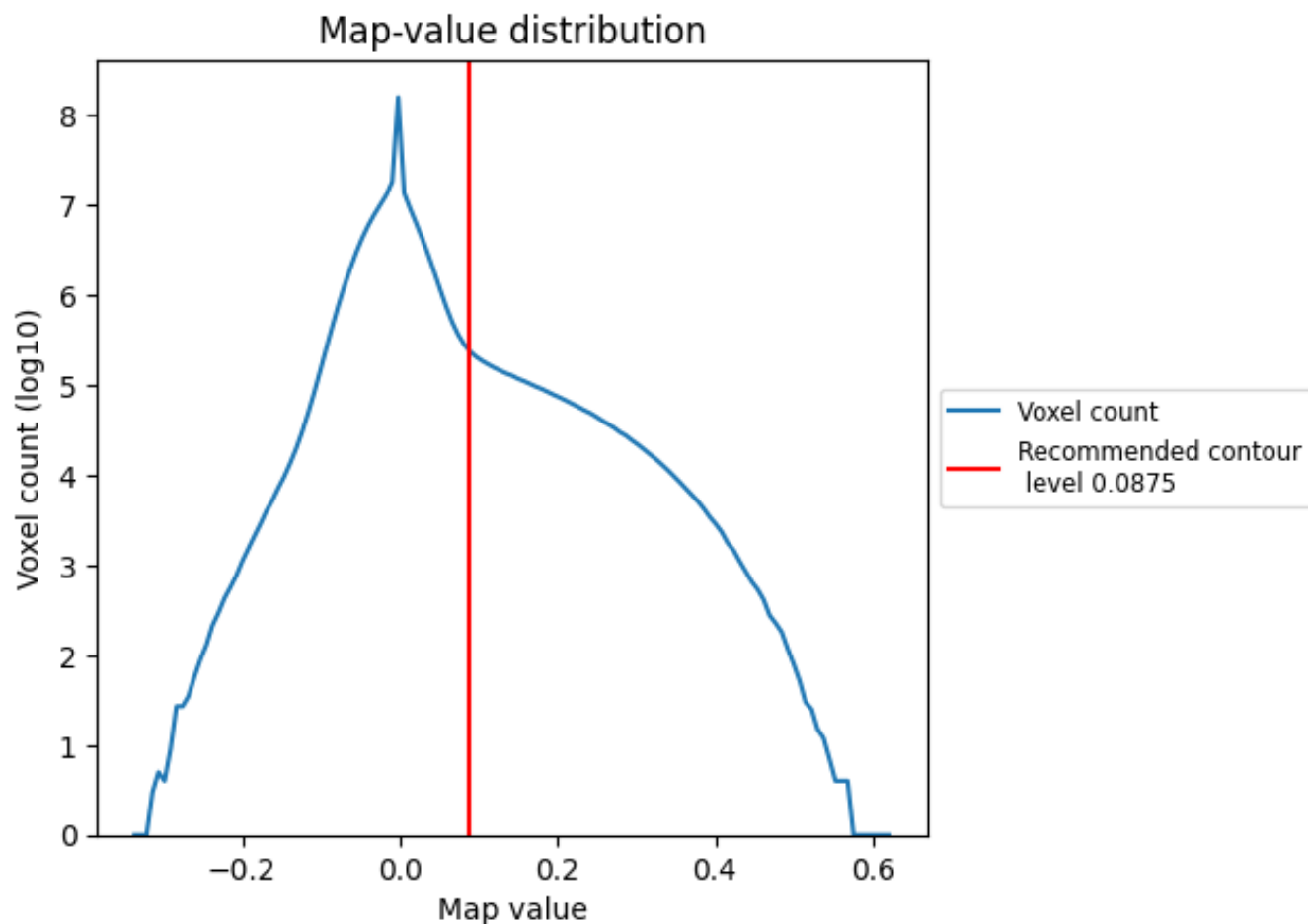
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

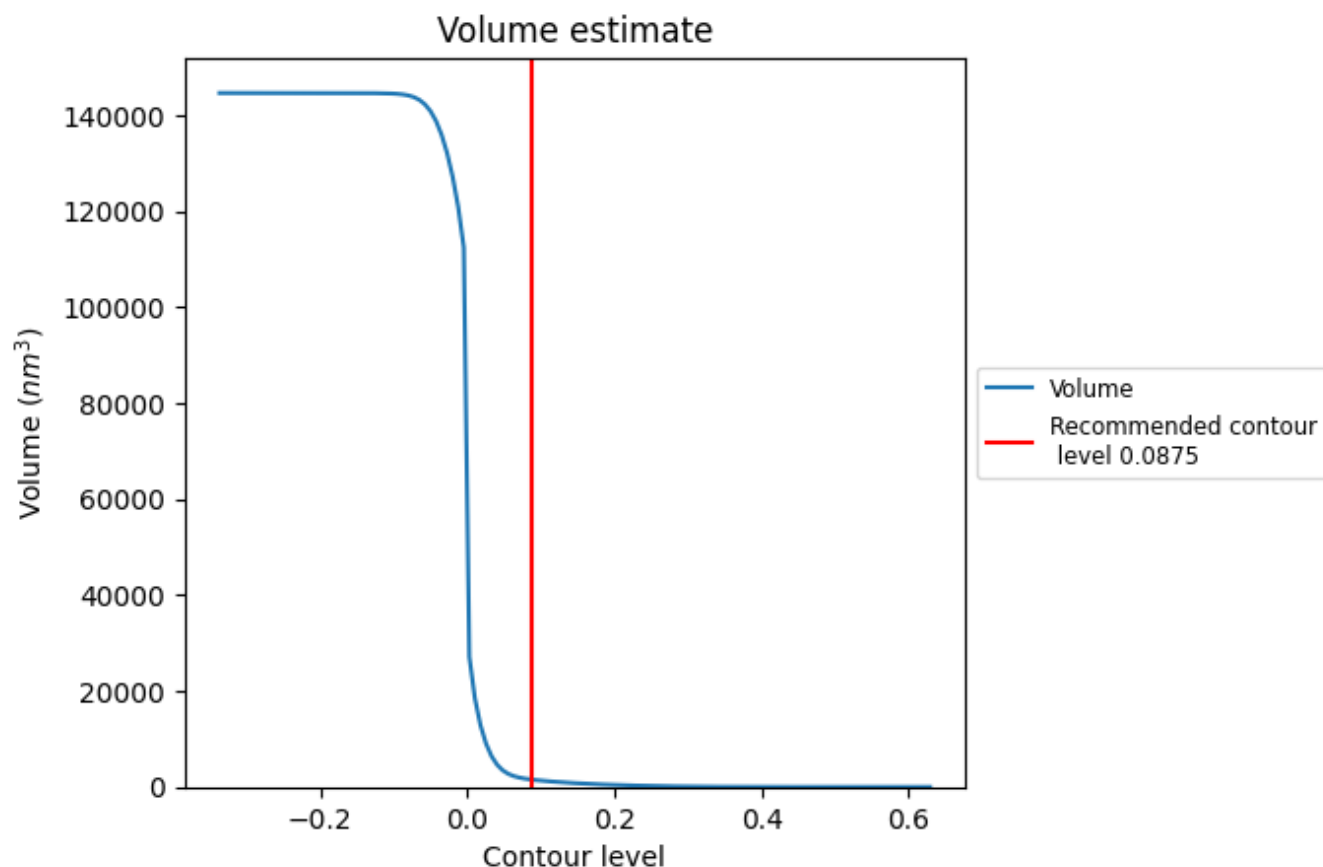
This section contains the results of statistical analysis of the map.

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.

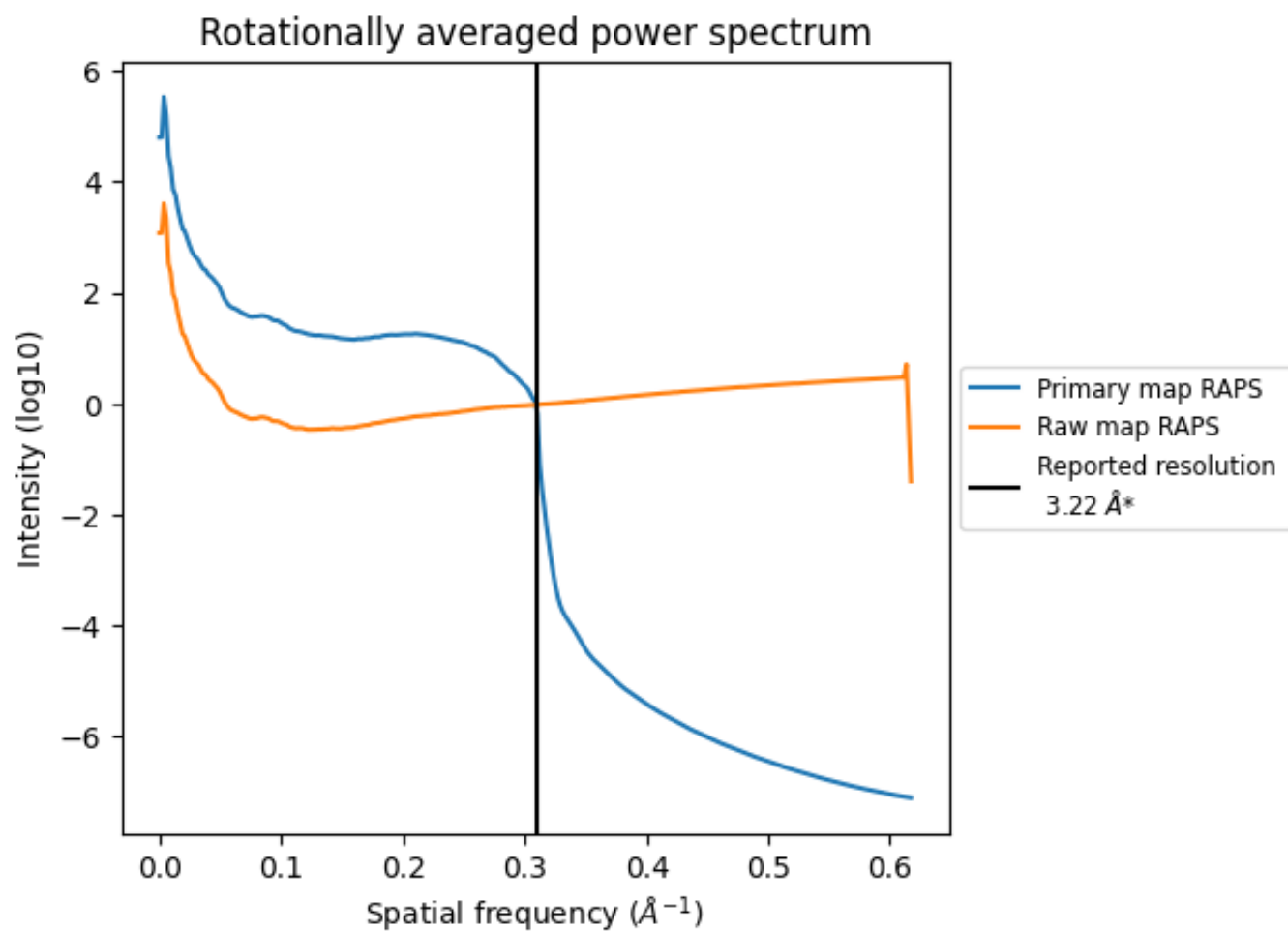
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1531 nm³; this corresponds to an approximate mass of 1383 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 ⓘ

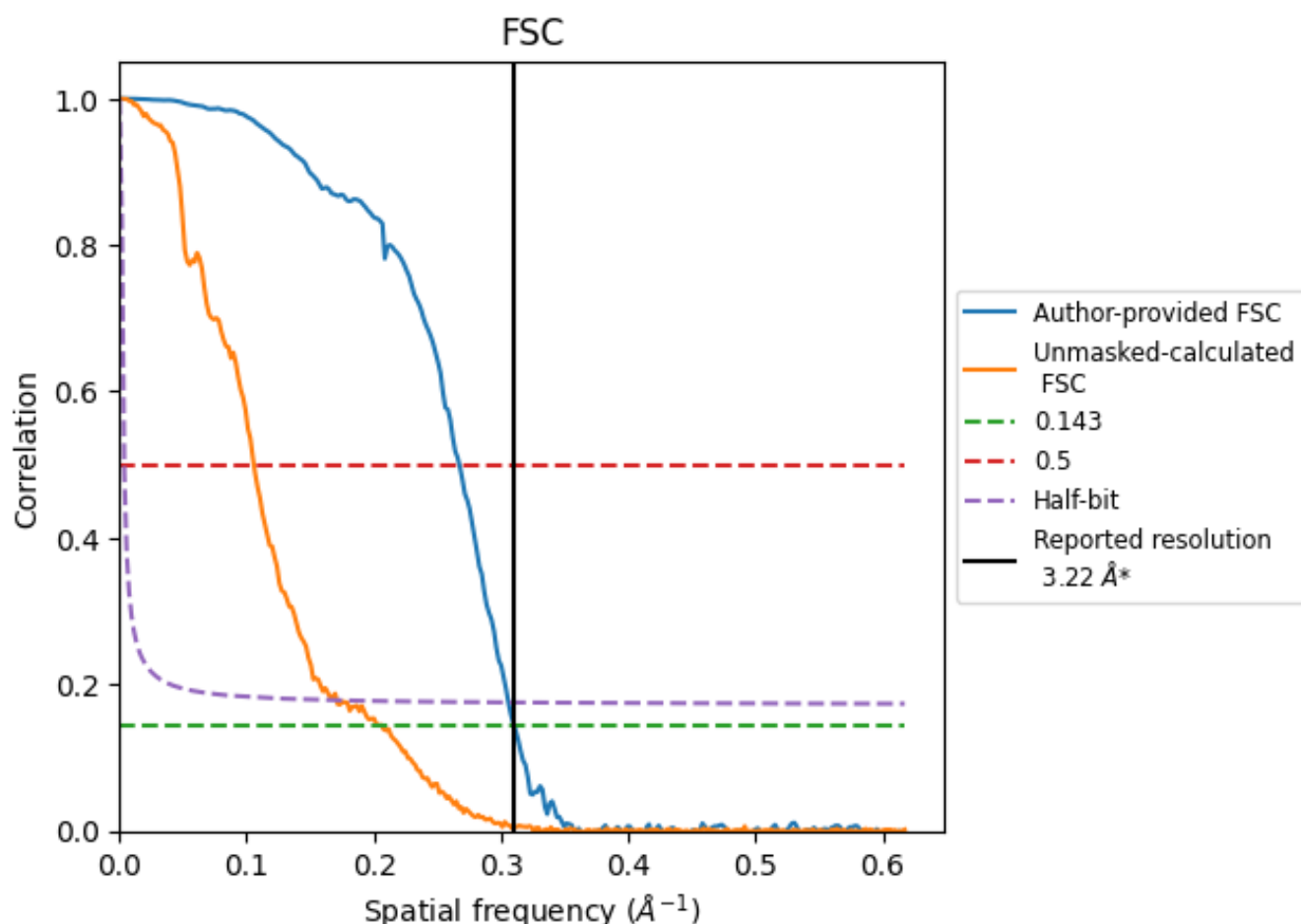


*Reported resolution corresponds to spatial frequency of 0.311 \AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.311 \AA^{-1}

8.2 Resolution estimates [i](#)

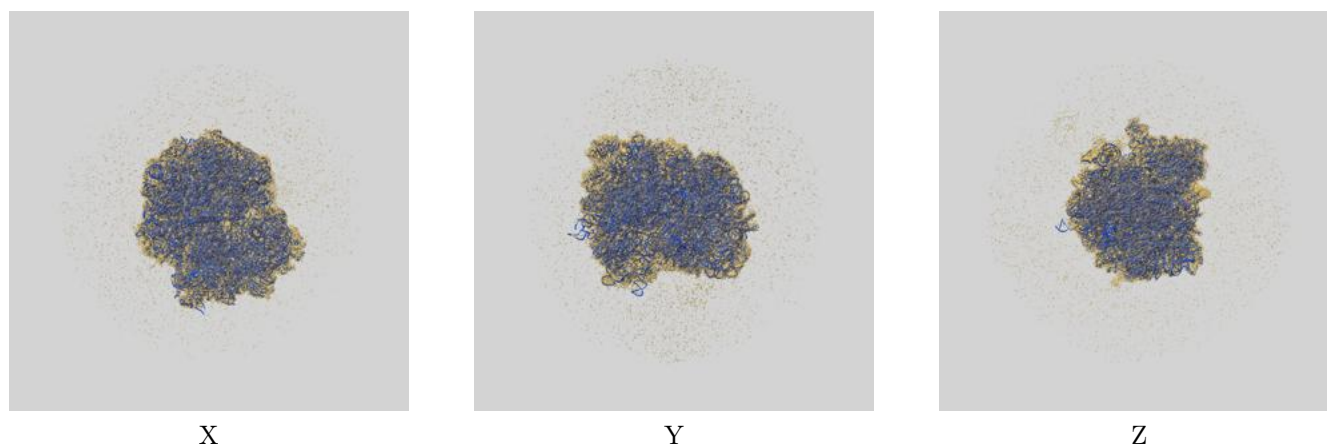
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---------------------------|------------------------------------|------|----------|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 3.22 | - | - |
| Author-provided FSC curve | 3.22 | 3.74 | 3.27 |
| Unmasked-calculated* | 4.85 | 9.47 | 5.85 |

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.85 differs from the reported value 3.22 by more than 10 %

9 Map-model fit [i](#)

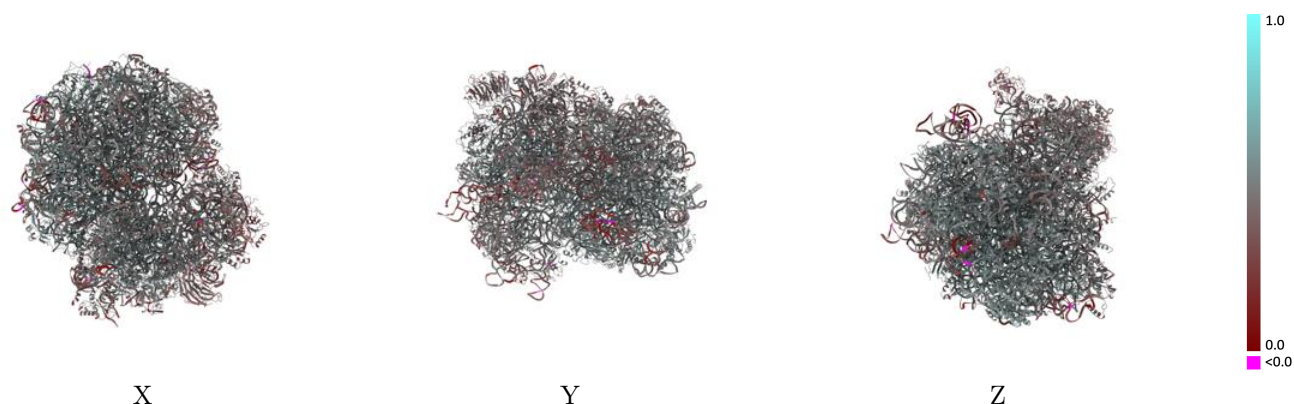
This section contains information regarding the fit between EMDB map EMD-42525 and PDB model 8UT0. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



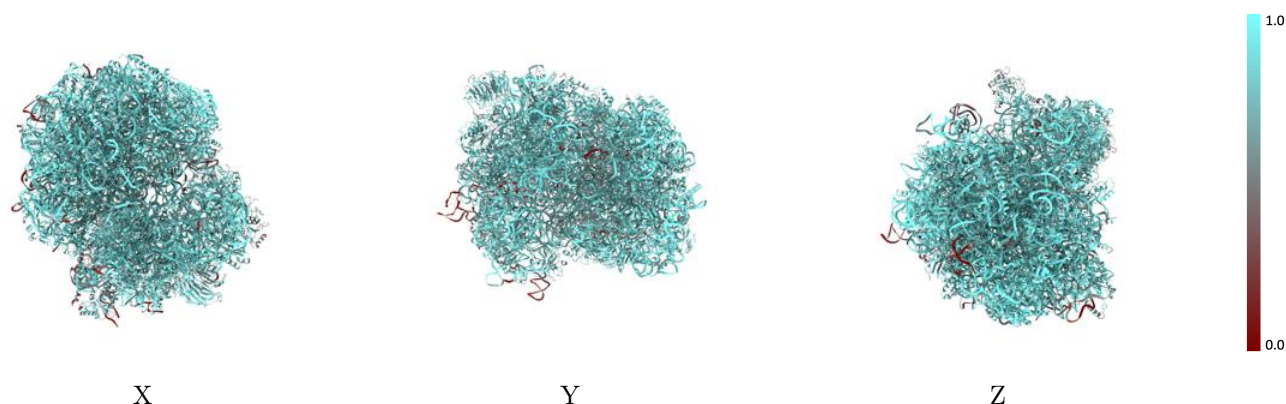
The images above show the 3D surface view of the map at the recommended contour level 0.0875 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



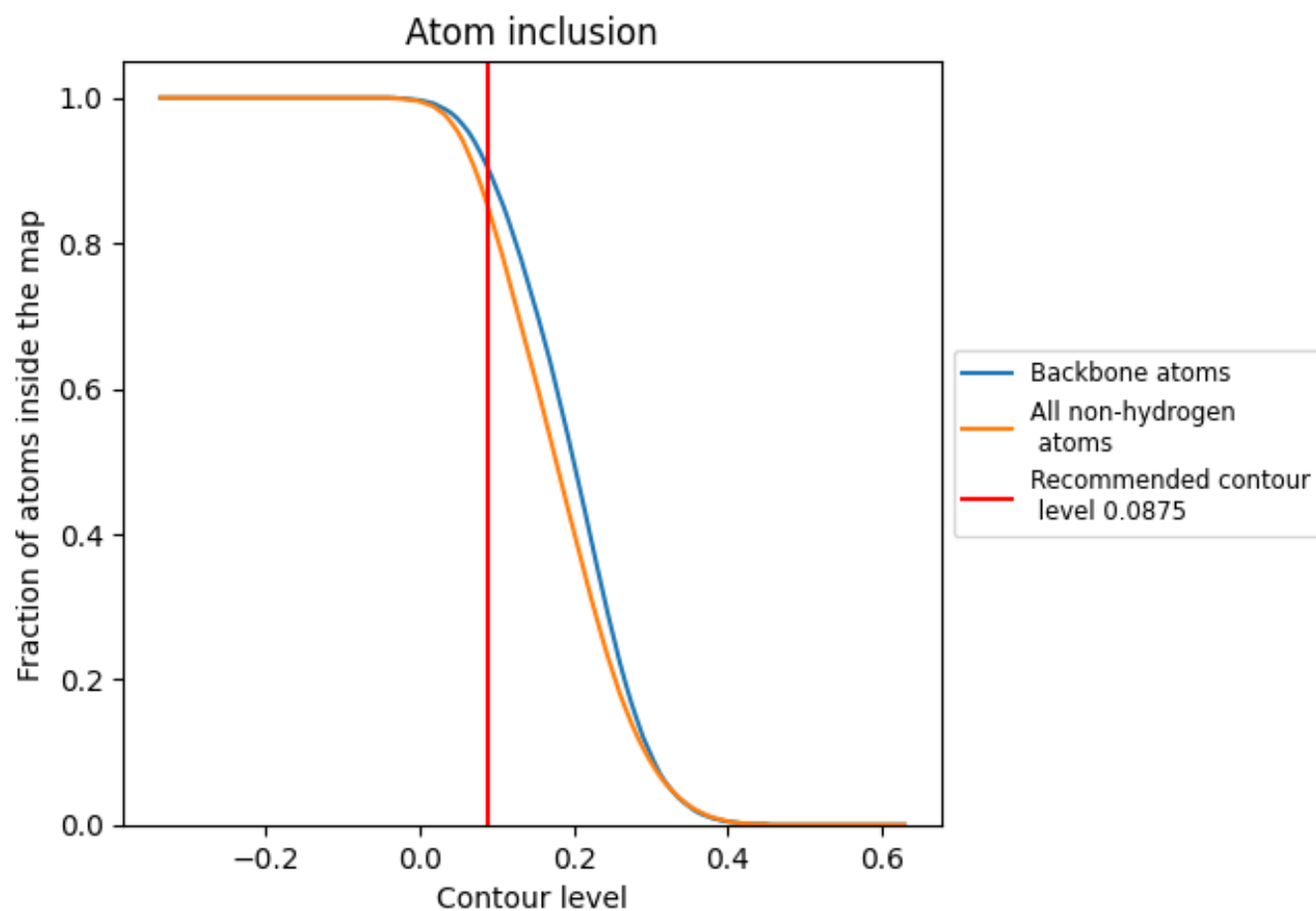
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0875).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 85% 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 (0.0875) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| All |  0.8530 |  0.4730 |
| 2 |  0.8450 |  0.4340 |
| A |  0.9010 |  0.4750 |
| AA |  0.6400 |  0.4220 |
| B |  0.9520 |  0.4600 |
| C |  0.9390 |  0.5020 |
| D |  0.9110 |  0.4860 |
| E |  0.8600 |  0.4560 |
| LD |  0.8300 |  0.5460 |
| LE |  0.8680 |  0.5260 |
| LF |  0.8760 |  0.5310 |
| LG |  0.8340 |  0.4450 |
| LH |  0.8530 |  0.5010 |
| LI |  0.8530 |  0.5110 |
| LJ |  0.8140 |  0.4870 |
| LK |  0.8370 |  0.5030 |
| LL |  0.7960 |  0.5050 |
| LM |  0.7770 |  0.4490 |
| LN |  0.8510 |  0.5030 |
| LO |  0.8630 |  0.5000 |
| LP |  0.8550 |  0.5350 |
| LQ |  0.8550 |  0.5210 |
| LR |  0.8640 |  0.5360 |
| LS |  0.8620 |  0.5150 |
| LT |  0.8190 |  0.5110 |
| LU |  0.8380 |  0.5140 |
| LV |  0.8190 |  0.5020 |
| LW |  0.8170 |  0.4740 |
| LX |  0.7760 |  0.5250 |
| LY |  0.8380 |  0.5390 |
| LZ |  0.8540 |  0.5340 |
| La |  0.8940 |  0.5420 |
| Lb |  0.8740 |  0.5130 |
| Lc |  0.8720 |  0.5170 |
| Ld |  0.7720 |  0.4920 |



















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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| Le |  0.8620 |  0.5100 |
| Lf |  0.8620 |  0.5190 |
| Lg |  0.8610 |  0.5460 |
| Lh |  0.8500 |  0.5440 |
| Li |  0.8310 |  0.5290 |
| Lj |  0.8800 |  0.5300 |
| Lk |  0.7920 |  0.4610 |
| Ll |  0.9030 |  0.5570 |
| Lm |  0.8280 |  0.5030 |
| Ln |  0.9040 |  0.5580 |
| Lo |  0.8310 |  0.5370 |
| Lp |  0.5480 |  0.4930 |
| Lq |  0.8100 |  0.4980 |
| Lr |  0.8010 |  0.5430 |
| Ls |  0.6590 |  0.4950 |
| SA |  0.7580 |  0.4660 |
| SB |  0.7050 |  0.4290 |
| SC |  0.8310 |  0.4390 |
| SD |  0.5530 |  0.2860 |
| SE |  0.7620 |  0.4310 |
| SF |  0.7910 |  0.4420 |
| SG |  0.7850 |  0.4390 |
| SH |  0.7890 |  0.4460 |
| SI |  0.8060 |  0.4300 |
| SJ |  0.7520 |  0.4340 |
| SL |  0.7150 |  0.4370 |
| SM |  0.8590 |  0.4830 |
| SN |  0.5560 |  0.3040 |
| SO |  0.7630 |  0.3940 |
| SP |  0.8380 |  0.4860 |
| SQ |  0.7510 |  0.4650 |
| SR |  0.8260 |  0.5180 |
| SS |  0.8140 |  0.4960 |
| ST |  0.7730 |  0.4350 |
| SU |  0.7720 |  0.4520 |
| SV |  0.7720 |  0.4740 |
| SW |  0.8180 |  0.4810 |
| SX |  0.8030 |  0.5080 |
| SY |  0.8170 |  0.5020 |
| SZ |  0.7740 |  0.4770 |
| Sa |  0.8620 |  0.5140 |
| Sb |  0.8440 |  0.5310 |

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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| Sc |  0.7810 |  0.5350 |
| Sd |  0.8010 |  0.4560 |
| Se |  0.8420 |  0.5050 |
| Sf |  0.8290 |  0.4820 |
| Sg |  0.7630 |  0.4830 |
| m |  0.8410 |  0.3990 |
| n |  0.8410 |  0.4460 |
| z |  0.7630 |  0.4980 |