



## wwPDB EM Validation Summary Report ⓘ

Sep 28, 2024 – 07:25 pm BST

PDB ID : 6HCJ  
EMDB ID : EMD-0194  
Title : Structure of the rabbit 80S ribosome on globin mRNA in the rotated state with A/P and P/E tRNAs  
Authors : Juszkievicz, S.; Chandrasekaran, V.; Lin, Z.; Kraatz, S.; Ramakrishnan, V.; Hegde, R.S.  
Deposited on : 2018-08-15  
Resolution : 3.80 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](mailto: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:

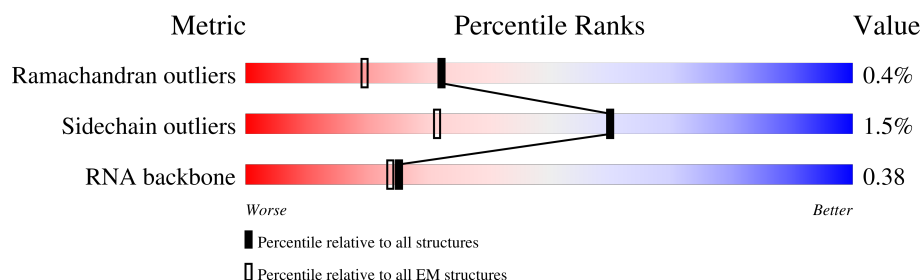
EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

# 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 3.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



| Metric                | Whole archive<br>(#Entries) | EM structures<br>(#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  $\geq 3$ , 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   | 51    | 3635   |                  |
| 2   | 71    | 120    |                  |
| 3   | 81    | 156    |                  |
| 4   | A2    | 1869   |                  |
| 5   | B2    | 295    |                  |
| 6   | C2    | 264    |                  |
| 7   | D2    | 293    |                  |
| 8   | E2    | 243    |                  |

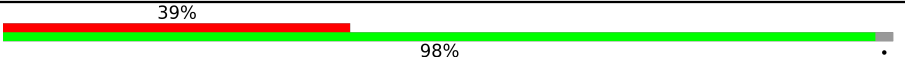


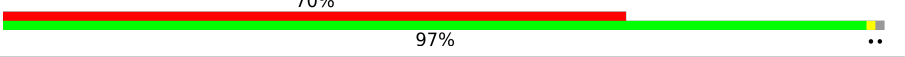
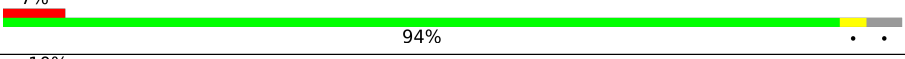
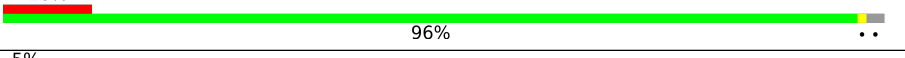
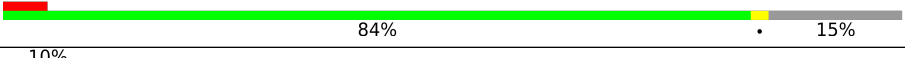
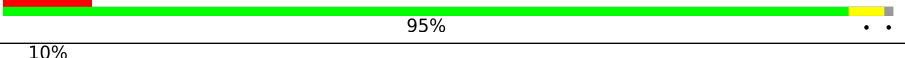
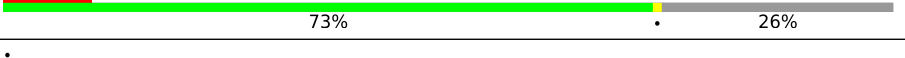


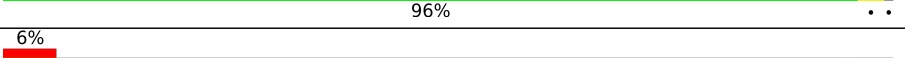
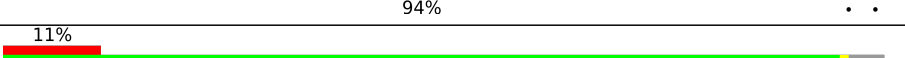
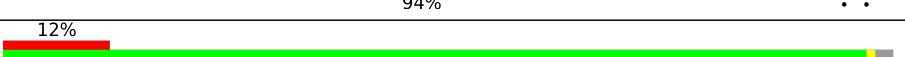
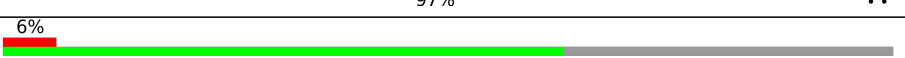
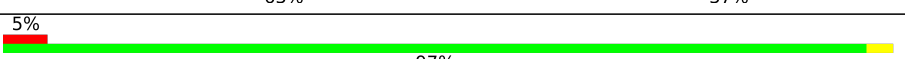
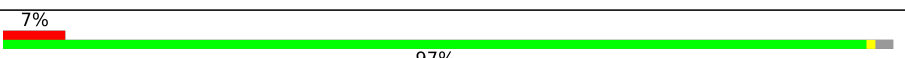
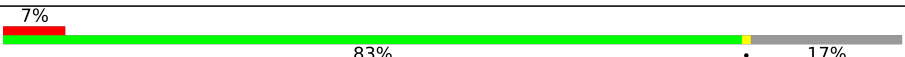
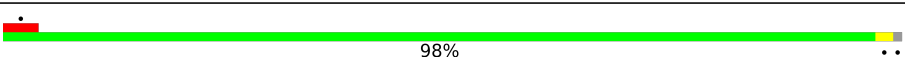

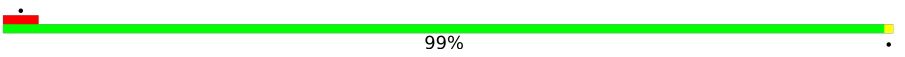
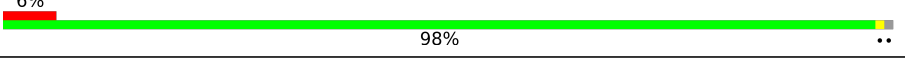

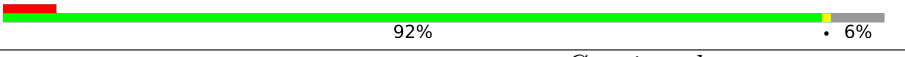

Continued on next page...

Continued from previous page...

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 9   | F2    | 263    |                  |
| 10  | G2    | 204    |                  |
| 11  | H2    | 249    |                  |
| 12  | I2    | 194    |                  |
| 13  | J2    | 208    |                  |
| 14  | K2    | 194    |                  |
| 15  | L2    | 165    |                  |
| 16  | M2    | 158    |                  |
| 17  | N2    | 132    |                  |
| 18  | O2    | 151    |                  |
| 19  | P2    | 168    |                  |
| 20  | Q2    | 145    |                  |
| 21  | R2    | 146    |                  |
| 22  | S2    | 135    |                  |
| 23  | T2    | 152    |                  |
| 24  | U2    | 145    |                  |
| 25  | V2    | 119    |                  |
| 26  | W2    | 83     |                  |
| 27  | X2    | 130    |                  |
| 28  | Y2    | 143    |                  |
| 29  | Z2    | 130    |                  |
| 30  | a2    | 125    |                  |
| 31  | b2    | 115    |                  |
| 32  | c2    | 84     |                  |
| 33  | d2    | 69     |                  |

Continued on next page...

Continued from previous page...

| Mol | Chain | Length | Quality of chain   |
|-----|-------|--------|--|
| 34  | e2    | 56     |    |
| 35  | f2    | 133    |    |
| 36  | g2    | 156    |    |
| 37  | h2    | 317    |    |
| 38  | A3    | 257    |    |
| 39  | B3    | 403    |    |
| 40  | C3    | 425    |    |
| 41  | D3    | 297    |    |
| 42  | E3    | 291    |    |
| 43  | F3    | 247    |    |
| 44  | G3    | 319    |    |
| 45  | H3    | 192    |   |
| 46  | I3    | 214    |  |
| 47  | J3    | 178    |  |
| 48  | L3    | 211    |  |
| 49  | M3    | 218    |  |
| 50  | N3    | 204    |  |
| 51  | O3    | 203    |  |
| 52  | P3    | 184    |  |
| 53  | Q3    | 188    |  |
| 54  | R3    | 196    |  |
| 55  | S3    | 176    |  |
| 56  | T3    | 160    |  |
| 57  | U3    | 128    |  |
| 58  | V3    | 140    |  |



Continued on next page...

Continued from previous page...

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 59  | X3    | 156    |                  |
| 60  | Y3    | 145    |                  |
| 61  | Z3    | 136    |                  |
| 62  | a3    | 148    |                  |
| 63  | b3    | 245    |                  |
| 64  | c3    | 115    |                  |
| 65  | d3    | 125    |                  |
| 66  | e3    | 135    |                  |
| 67  | f3    | 110    |                  |
| 68  | g3    | 117    |                  |
| 69  | h3    | 123    |                  |
| 70  | i3    | 105    |                  |
| 71  | j3    | 97     |                  |
| 72  | k3    | 70     |                  |
| 73  | l3    | 51     |                  |
| 74  | m3    | 102    |                  |
| 75  | n3    | 25     |                  |
| 76  | o3    | 106    |                  |
| 77  | p3    | 92     |                  |
| 78  | r3    | 137    |                  |
| 79  | q3    | 74     |                  |
| 80  | t3    | 318    |                  |
| 81  | u3    | 165    |                  |
| 82  | v3    | 22     |                  |
| 83  | 33    | 75     |                  |

Continued on next page...

*Continued from previous page...*

| Mol | Chain | Length | Quality of chain   |
|-----|-------|--------|--|
| 84  | w3    | 217    | 100%   |
|     |       |        |  96% . |
| 85  | 1     | 22     | 95%  |
|     |       |        |  100%  |

## 2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 219683 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 28S ribosomal RNA.

| Mol | Chain | Residues | Atoms |       |       |       |      | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|-------|------|---------|-------|
| 1   | 51    | 3635     | Total | C     | N     | O     | P    | 0       | 0     |
|     |       |          | 77827 | 34654 | 14241 | 25297 | 3635 |         |       |

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

| Mol | Chain | Residues | Atoms |      |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 2   | 71    | 120      | Total | C    | N   | O   | P   | 0       | 0     |
|     |       |          | 2558  | 1141 | 456 | 842 | 119 |         |       |

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

| Mol | Chain | Residues | Atoms |      |     |      |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|------|-----|---------|-------|
| 3   | 81    | 151      | Total | C    | N   | O    | P   | 0       | 0     |
|     |       |          | 3208  | 1432 | 564 | 1062 | 150 |         |       |

- Molecule 4 is a RNA chain called 18S ribosomal RNA.

| Mol | Chain | Residues | Atoms |       |      |       |      | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|-------|
| 4   | A2    | 1740     | Total | C     | N    | O     | P    | 0       | 0     |
|     |       |          | 37141 | 16578 | 6668 | 12156 | 1739 |         |       |

- Molecule 5 is a protein called uS2.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 5   | B2    | 217      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1710  | 1086 | 300 | 316 | 8 |         |       |

- Molecule 6 is a protein called 40S ribosomal protein S3a.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 6   | C2    | 213      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 1729  | 1098 | 309 | 308 | 14 |         |       |

- Molecule 7 is a protein called uS5.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 7   | D2    | 221      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1716  | 1111 | 295 | 301 | 9 |         |       |

- Molecule 8 is a protein called uS3.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 8   | E2    | 228      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1765  | 1125 | 316 | 316 | 8 |         |       |

- Molecule 9 is a protein called eS4.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 9   | F2    | 262      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 2076  | 1324 | 386 | 358 | 8 |         |       |

- Molecule 10 is a protein called Ribosomal protein S5.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 10  | G2    | 185      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1471  | 921 | 277 | 266 | 7 |         |       |

- Molecule 11 is a protein called 40S ribosomal protein S6.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 11  | H2    | 237      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1923  | 1200 | 387 | 329 | 7 |         |       |

- Molecule 12 is a protein called 40S ribosomal protein S7.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 12  | I2    | 185      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1488  | 952 | 271 | 264 | 1 |         |       |

- Molecule 13 is a protein called eS8.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 13  | J2    | 206      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1686  | 1058 | 332 | 291 | 5 |         |       |

- Molecule 14 is a protein called Ribosomal protein S9 (Predicted).



| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 14  | K2    | 185      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1525  | 969 | 306 | 248 | 2 |         |       |

- Molecule 15 is a protein called eS10.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 15  | L2    | 96       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 810   | 530 | 143 | 131 | 6 |         |       |

- Molecule 16 is a protein called Ribosomal protein S11.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 16  | M2    | 143      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1175  | 749 | 222 | 198 | 6 |         |       |

- Molecule 17 is a protein called 40S ribosomal protein S12.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 17  | N2    | 117      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 908   | 570 | 161 | 169 | 8 |         |       |

- Molecule 18 is a protein called uS15.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 18  | O2    | 149      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1202  | 770 | 228 | 203 | 1 |         |       |

- Molecule 19 is a protein called uS11.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 19  | P2    | 136      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1016  | 621 | 199 | 190 | 6 |         |       |

- Molecule 20 is a protein called uS19.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 20  | Q2    | 120      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 997   | 635 | 187 | 168 | 7 |         |       |

- Molecule 21 is a protein called Ribosomal protein S16.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 21  | R2    | 142      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1128  | 717 | 213 | 195 | 3 |         |       |

- Molecule 22 is a protein called eS17.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 22  | S2    | 132      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1068  | 670 | 199 | 195 | 4 |         |       |

- Molecule 23 is a protein called uS13.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 23  | T2    | 144      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1190  | 746 | 241 | 202 | 1 |         |       |

- Molecule 24 is a protein called eS19.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 24  | U2    | 141      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1097  | 688 | 211 | 195 | 3 |         |       |

- Molecule 25 is a protein called uS10.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 25  | V2    | 100      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 795   | 498 | 152 | 141 | 4 |         |       |

- Molecule 26 is a protein called eS21.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 26  | W2    | 83       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 636   | 393 | 117 | 121 | 5 |         |       |

- Molecule 27 is a protein called Ribosomal protein S15a.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 27  | X2    | 129      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1034  | 659 | 193 | 176 | 6 |         |       |

- Molecule 28 is a protein called uS12.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 28  | Y2    | 141      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1098  | 693 | 219 | 183 | 3 |         |       |

- Molecule 29 is a protein called eS24.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 29  | Z2    | 124      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1011  | 640 | 198 | 168 | 5 |         |       |

- Molecule 30 is a protein called eS25.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 30  | a2    | 75       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 598   | 382 | 111 | 104 | 1 |         |       |

- Molecule 31 is a protein called eS26.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 31  | b2    | 101      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 814   | 507 | 170 | 132 | 5 |         |       |

- Molecule 32 is a protein called 40S ribosomal protein S27.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 32  | c2    | 83       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 651   | 408 | 121 | 115 | 7 |         |       |

- Molecule 33 is a protein called Ribosomal protein S28.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 33  | d2    | 62       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 488   | 297 | 97 | 92 | 2 |         |       |

- Molecule 34 is a protein called uS14.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 34  | e2    | 55       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 459   | 286 | 94 | 74 | 5 |         |       |

- Molecule 35 is a protein called 40S ribosomal protein S30.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 35  | f2    | 55       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 443   | 274 | 97 | 71 | 1 |         |       |

- Molecule 36 is a protein called Ribosomal protein S27a.

| Mol | Chain | Residues | Atoms |     |     |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 36  | g2    | 68       | Total | C   | N   | O  | S | 0       | 0     |
|     |       |          | 555   | 351 | 103 | 94 | 7 |         |       |

- Molecule 37 is a protein called RACK1.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 37  | h2    | 313      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2436  | 1535 | 424 | 465 | 12 |         |       |

- Molecule 38 is a protein called Ribosomal protein L8.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 38  | A3    | 248      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1898  | 1189 | 389 | 314 | 6 |         |       |

- Molecule 39 is a protein called uL3.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 39  | B3    | 394      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 3172  | 2020 | 597 | 542 | 13 |         |       |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment               | Reference  |
|-------|---------|----------|--------|-----------------------|------------|
| B3    | 1       | MET      | -      | initiating methionine | UNP G1TL06 |

- Molecule 40 is a protein called uL4.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 40  | C3    | 362      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2883  | 1812 | 577 | 480 | 14 |         |       |

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

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 41  | D3    | 293      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2391  | 1512 | 438 | 427 | 14 |         |       |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment               | Reference  |
|-------|---------|----------|--------|-----------------------|------------|
| D3    | 1       | MET      | -      | initiating methionine | UNP G1SYJ6 |

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

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 42  | E3    | 216      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1729  | 1115 | 329 | 282 | 3 |         |       |

- Molecule 43 is a protein called uL30.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 43  | F3    | 225      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1875  | 1205 | 358 | 303 | 9 |         |       |

There are 4 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment  | Reference  |
|-------|---------|----------|--------|----------|------------|
| F3    | 61      | ARG      | GLY    | conflict | UNP G1TUB1 |
| F3    | 93      | ARG      | GLY    | conflict | UNP G1TUB1 |
| F3    | 131     | MET      | VAL    | conflict | UNP G1TUB1 |
| F3    | 153     | ILE      | VAL    | conflict | UNP G1TUB1 |

- Molecule 44 is a protein called eL8.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 44  | G3    | 233      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1879  | 1199 | 361 | 315 | 4 |         |       |

- Molecule 45 is a protein called uL6.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 45  | H3    | 190      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1516  | 954 | 284 | 272 | 6 |         |       |

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

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 46  | I3    | 205      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 1664  | 1056 | 321 | 274 | 13 |         |       |

- Molecule 47 is a protein called Ribosomal protein L11.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 47  | J3    | 170      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1362  | 861 | 254 | 241 | 6 |         |       |

- Molecule 48 is a protein called eL13.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 48  | L3    | 207      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1674  | 1047 | 348 | 275 | 4 |         |       |

- Molecule 49 is a protein called Ribosomal protein L14.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 49  | M3    | 138      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1137  | 727 | 221 | 182 | 7 |         |       |

- Molecule 50 is a protein called Ribosomal protein L15.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 50  | N3    | 203      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1701  | 1072 | 359 | 266 | 4 |         |       |

- Molecule 51 is a protein called uL13.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 51  | O3    | 199      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1630  | 1051 | 319 | 255 | 5 |         |       |

- Molecule 52 is a protein called uL22.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 52  | P3    | 153      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1242  | 777 | 241 | 215 | 9 |         |       |

- Molecule 53 is a protein called eL18.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 53  | Q3    | 187      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1515  | 946 | 315 | 250 | 4 |         |       |

- Molecule 54 is a protein called eL19.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 54  | R3    | 180      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1508  | 933 | 328 | 238 | 9 |         |       |

- Molecule 55 is a protein called eL20.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 55  | S3    | 176      | Total | C   | N   | O   | S  | 0       | 0     |
|     |       |          | 1462  | 930 | 285 | 236 | 11 |         |       |

- Molecule 56 is a protein called eL21.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 56  | T3    | 159      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1298  | 823 | 252 | 217 | 6 |         |       |

- Molecule 57 is a protein called eL22.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 57  | U3    | 99       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 809   | 519 | 141 | 147 | 2 |         |       |

- Molecule 58 is a protein called Ribosomal protein L23.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 58  | V3    | 131      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 979   | 618 | 184 | 172 | 5 |         |       |

- Molecule 59 is a protein called uL23.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 59  | X3    | 118      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 967   | 618 | 181 | 167 | 1 |         |       |

- Molecule 60 is a protein called Ribosomal protein L26.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 60  | Y3    | 132      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1102  | 692 | 223 | 184 | 3 |         |       |

- Molecule 61 is a protein called 60S ribosomal protein L27.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 61  | Z3    | 135      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1107  | 714 | 208 | 182 | 3 |         |       |

- Molecule 62 is a protein called uL15.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 62  | a3    | 147      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1162  | 734 | 239 | 185 | 4 |         |       |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment               | Reference  |
|-------|---------|----------|--------|-----------------------|------------|
| a3    | 1       | MET      | -      | initiating methionine | UNP G1SNY0 |

- Molecule 63 is a protein called eL29.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 63  | b3    | 104      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 848   | 527 | 189 | 129 | 3 |         |       |

- Molecule 64 is a protein called eL30.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 64  | c3    | 98       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 761   | 481 | 134 | 140 | 6 |         |       |

- Molecule 65 is a protein called eL31.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 65  | d3    | 107      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 888   | 560 | 171 | 155 | 2 |         |       |

- Molecule 66 is a protein called eL32.



| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 66  | e3    | 128      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1053  | 667 | 216 | 165 | 5 |         |       |

- Molecule 67 is a protein called eL33.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 67  | f3    | 109      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 876   | 555 | 174 | 143 | 4 |         |       |

- Molecule 68 is a protein called eL34.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 68  | g3    | 114      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 906   | 566 | 187 | 147 | 6 |         |       |

- Molecule 69 is a protein called uL29.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 69  | h3    | 122      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1013  | 640 | 204 | 168 | 1 |         |       |

- Molecule 70 is a protein called 60S ribosomal protein L36.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 70  | i3    | 102      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 830   | 520 | 176 | 129 | 5 |         |       |

- Molecule 71 is a protein called Ribosomal protein L37.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 71  | j3    | 86       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 705   | 434 | 155 | 111 | 5 |         |       |

- Molecule 72 is a protein called eL38.

| Mol | Chain | Residues | Atoms |     |     |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 72  | k3    | 69       | Total | C   | N   | O  | S | 0       | 0     |
|     |       |          | 569   | 366 | 103 | 99 | 1 |         |       |

- Molecule 73 is a protein called eL39.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 73  | l3    | 50       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 447   | 286 | 96 | 64 | 1 |         |       |

- Molecule 74 is a protein called eL40.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 74  | m3    | 52       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 429   | 266 | 90 | 67 | 6 |         |       |

- Molecule 75 is a protein called eL41.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 75  | n3    | 25       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 239   | 145 | 64 | 27 | 3 |         |       |

- Molecule 76 is a protein called eL42.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 76  | o3    | 104      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 851   | 533 | 174 | 138 | 6 |         |       |

- Molecule 77 is a protein called eL43.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 77  | p3    | 91       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 708   | 445 | 136 | 120 | 7 |         |       |

- Molecule 78 is a protein called eL28.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 78  | r3    | 124      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 994   | 616 | 205 | 167 | 6 |         |       |

- Molecule 79 is a RNA chain called A/P RNA.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 79  | q3    | 74       | Total | C   | N   | O   | P  | 0       | 0     |
|     |       |          | 1579  | 705 | 285 | 516 | 73 |         |       |

- Molecule 80 is a protein called uL10.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 80  | t3    | 196      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1507  | 959 | 263 | 276 | 9 |         |       |

- Molecule 81 is a protein called Ribosomal protein L12.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 81  | u3    | 153      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1160  | 722 | 218 | 217 | 3 |         |       |

- Molecule 82 is a RNA chain called mRNA.

| Mol | Chain | Residues | Atoms |     |    |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|----|---------|-------|
| 82  | v3    | 22       | Total | C   | N  | O   | P  | 0       | 0     |
|     |       |          | 463   | 207 | 77 | 157 | 22 |         |       |

- Molecule 83 is a RNA chain called P/E tRNA.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 83  | 33    | 75       | Total | C   | N   | O   | P  | 0       | 0     |
|     |       |          | 1604  | 717 | 298 | 515 | 74 |         |       |

- Molecule 84 is a protein called uL1.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 84  | w3    | 217      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1741  | 1113 | 312 | 307 | 9 |         |       |

- Molecule 85 is a protein called nascent chain.

| Mol | Chain | Residues | Atoms |    |    |    | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|---------|-------|
| 85  | 1     | 22       | Total | C  | N  | O  | 0       | 0     |
|     |       |          | 110   | 66 | 22 | 22 |         |       |

- Molecule 86 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms |     | AltConf |
|-----|-------|----------|-------|-----|---------|
| 86  | 51    | 200      | Total | Mg  | 0       |
|     |       |          | 200   | 200 |         |
| 86  | 71    | 6        | Total | Mg  | 0       |
|     |       |          | 6     | 6   |         |
| 86  | 81    | 6        | Total | Mg  | 0       |
|     |       |          | 6     | 6   |         |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Residues | Atoms       |          | AltConf |
|-----|-------|----------|-------------|----------|---------|
| 86  | A2    | 76       | Total<br>76 | Mg<br>76 | 0       |
| 86  | G2    | 1        | Total<br>1  | Mg<br>1  | 0       |
| 86  | b2    | 1        | Total<br>1  | Mg<br>1  | 0       |
| 86  | g2    | 1        | Total<br>1  | Mg<br>1  | 0       |
| 86  | B3    | 2        | Total<br>2  | Mg<br>2  | 0       |
| 86  | D3    | 1        | Total<br>1  | Mg<br>1  | 0       |
| 86  | N3    | 1        | Total<br>1  | Mg<br>1  | 0       |
| 86  | P3    | 1        | Total<br>1  | Mg<br>1  | 0       |
| 86  | V3    | 1        | Total<br>1  | Mg<br>1  | 0       |
| 86  | a3    | 1        | Total<br>1  | Mg<br>1  | 0       |
| 86  | e3    | 1        | Total<br>1  | Mg<br>1  | 0       |
| 86  | q3    | 1        | Total<br>1  | Mg<br>1  | 0       |

- Molecule 87 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms      |         | AltConf |
|-----|-------|----------|------------|---------|---------|
| 87  | b2    | 1        | Total<br>1 | Zn<br>1 | 0       |
| 87  | e2    | 1        | Total<br>1 | Zn<br>1 | 0       |
| 87  | g2    | 1        | Total<br>1 | Zn<br>1 | 0       |
| 87  | g3    | 1        | Total<br>1 | Zn<br>1 | 0       |
| 87  | j3    | 1        | Total<br>1 | Zn<br>1 | 0       |
| 87  | m3    | 1        | Total<br>1 | Zn<br>1 | 0       |
| 87  | o3    | 1        | Total<br>1 | Zn<br>1 | 0       |

*Continued on next page...*

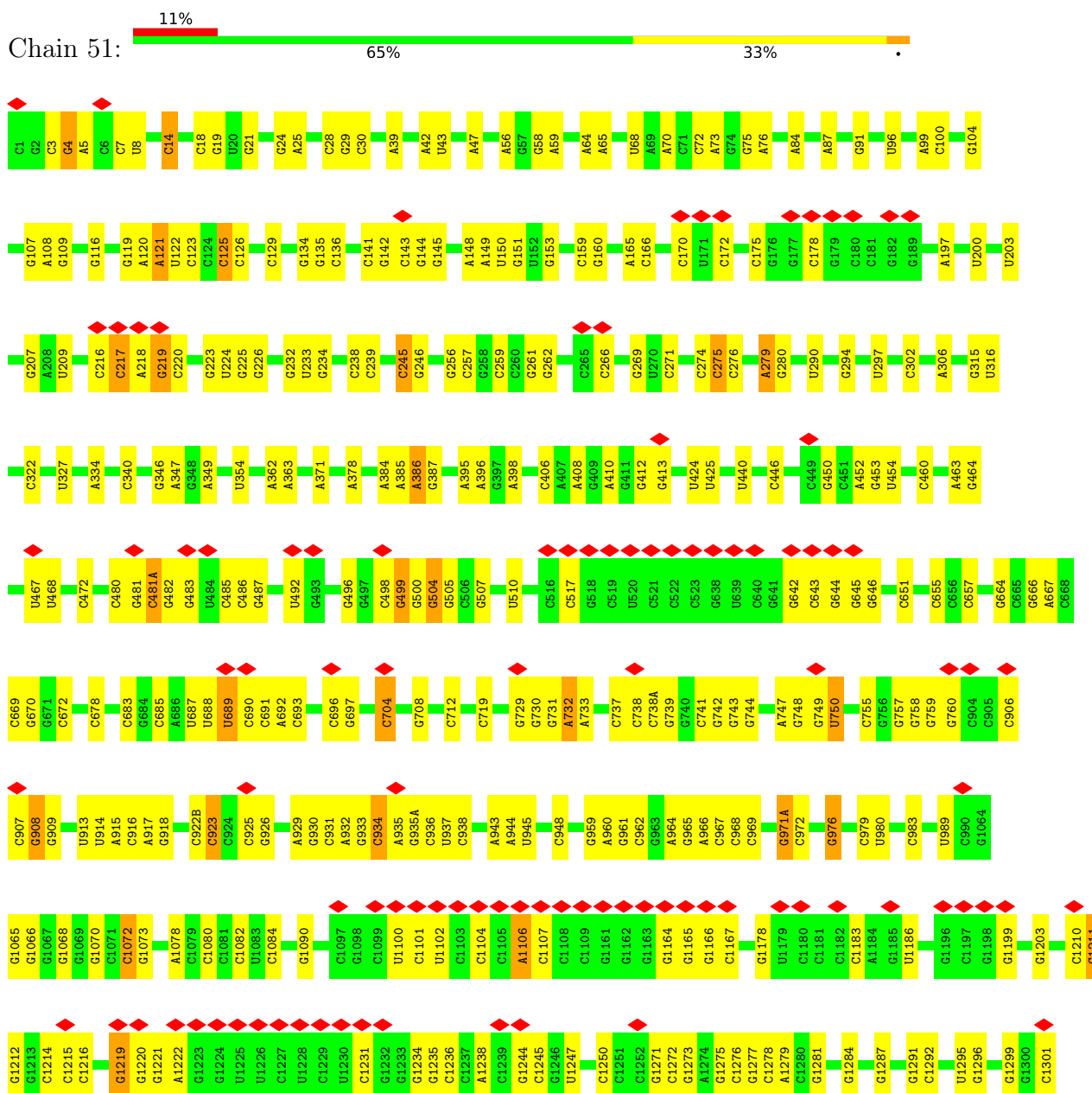
*Continued from previous page...*

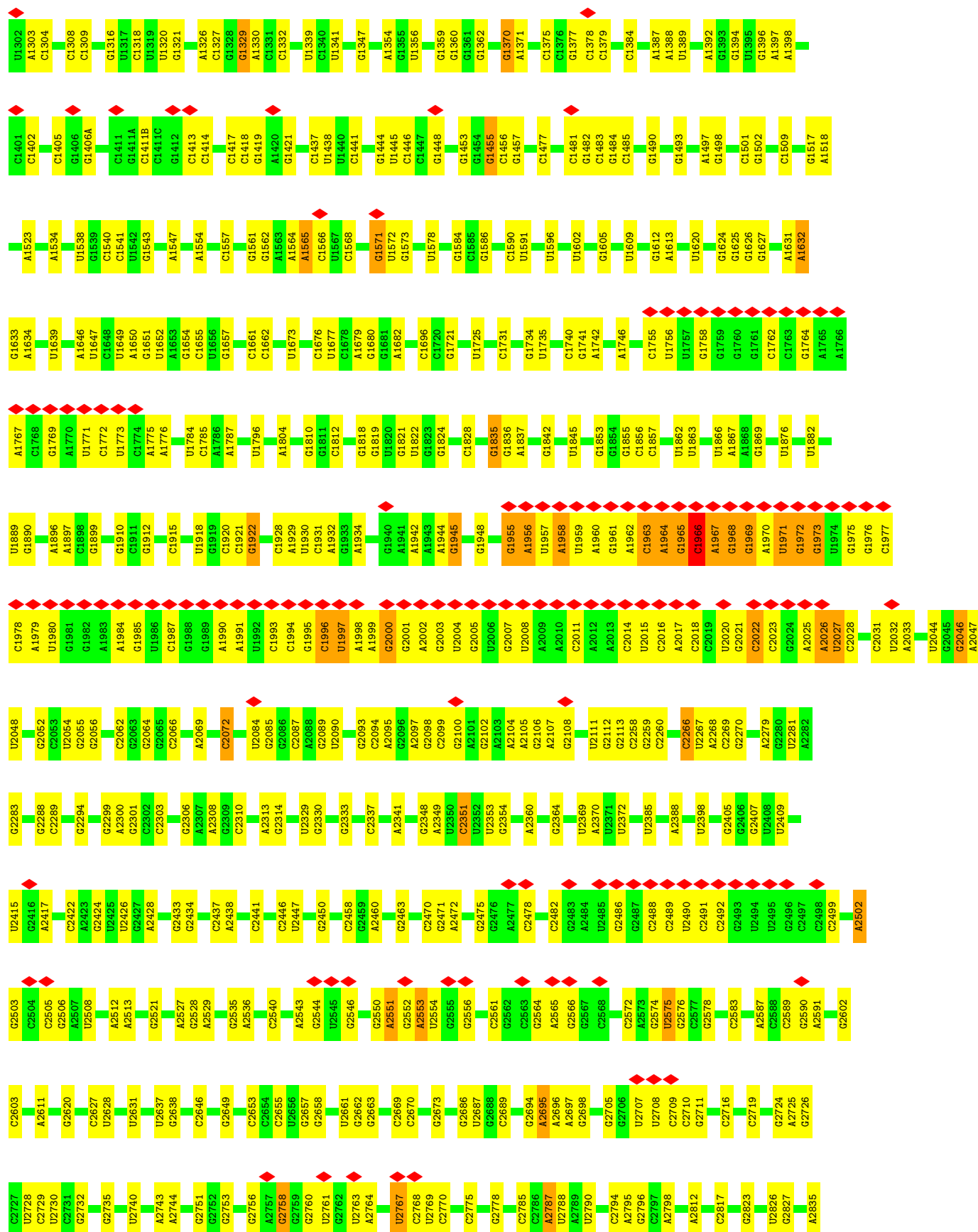
| Mol | Chain | Residues | Atoms |    | AltConf |
|-----|-------|----------|-------|----|---------|
|     |       |          | Total | Zn |         |
| 87  | p3    | 1        | 1     | 1  | 0       |

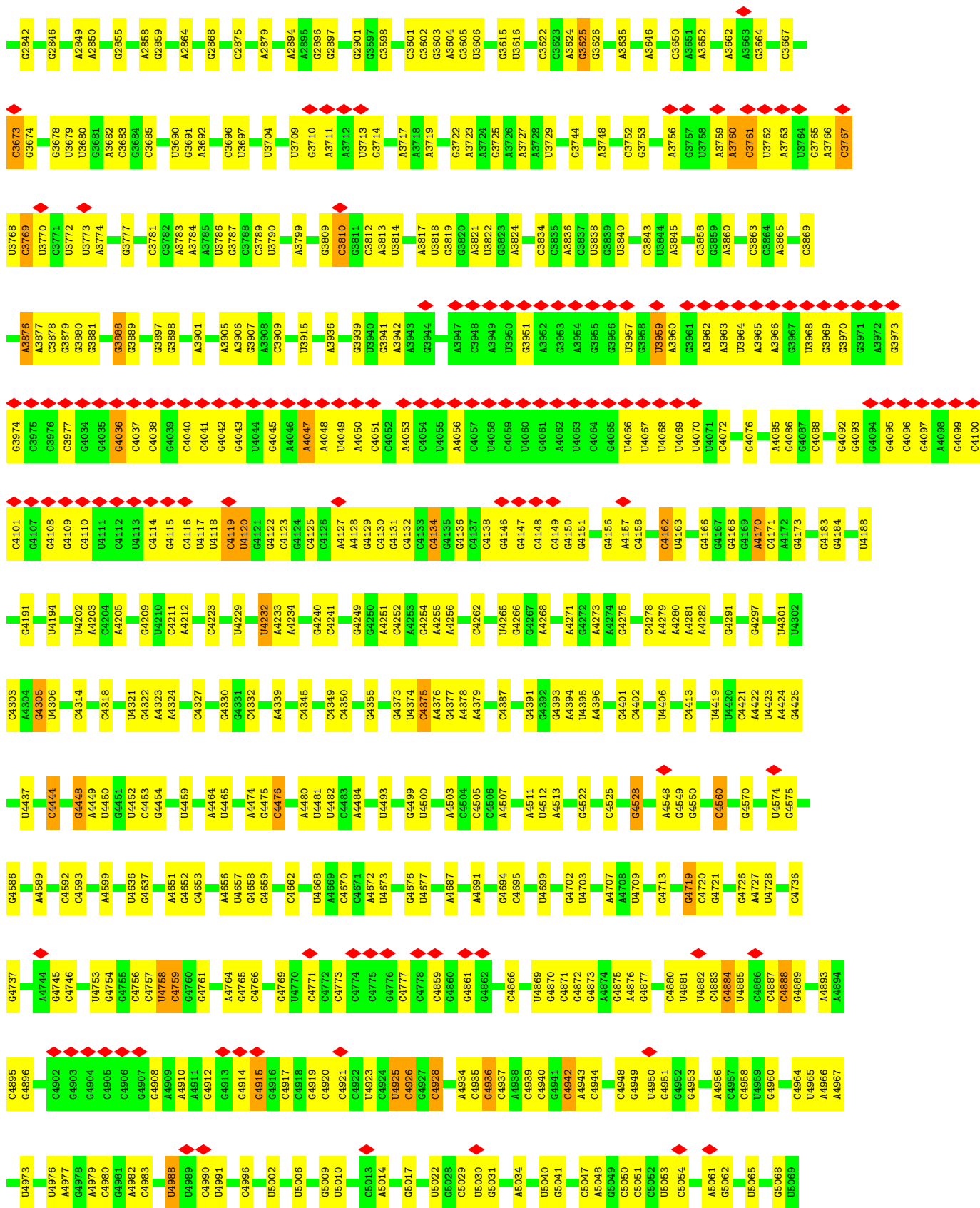
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: 28S ribosomal RNA



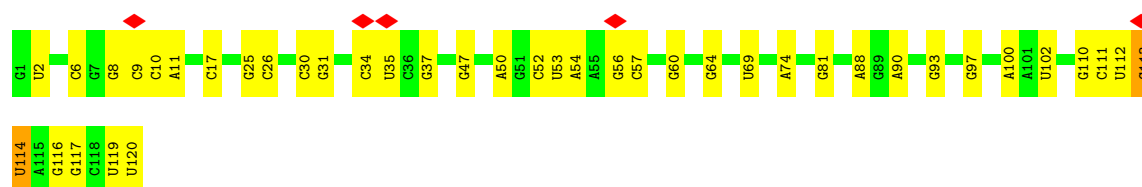




- Molecule 2: 5S ribosomal RNA

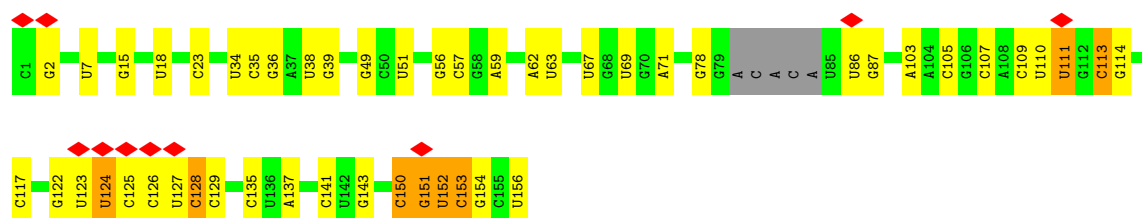


Chain 71:  66% 32%



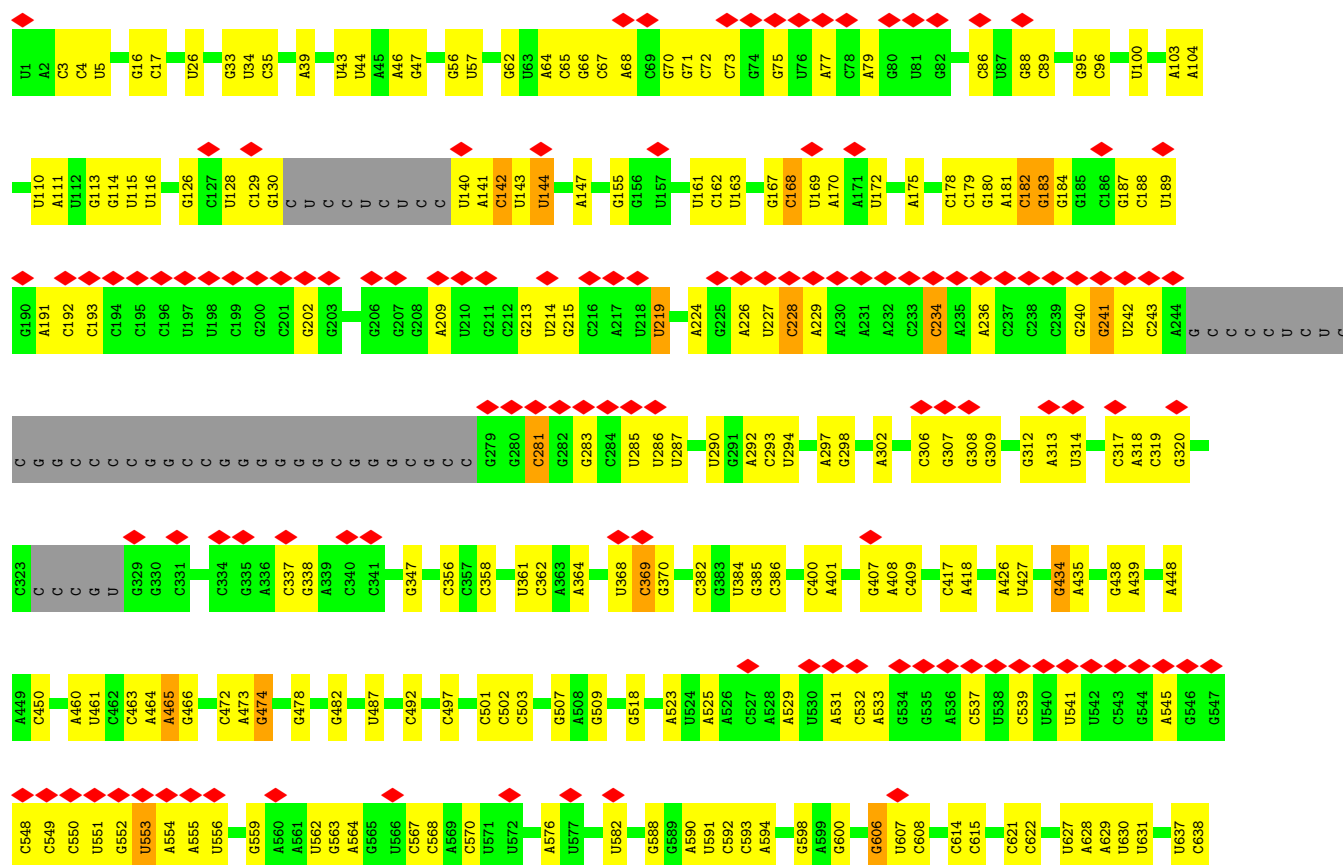
• Molecule 3: 5.8S ribosomal RNA

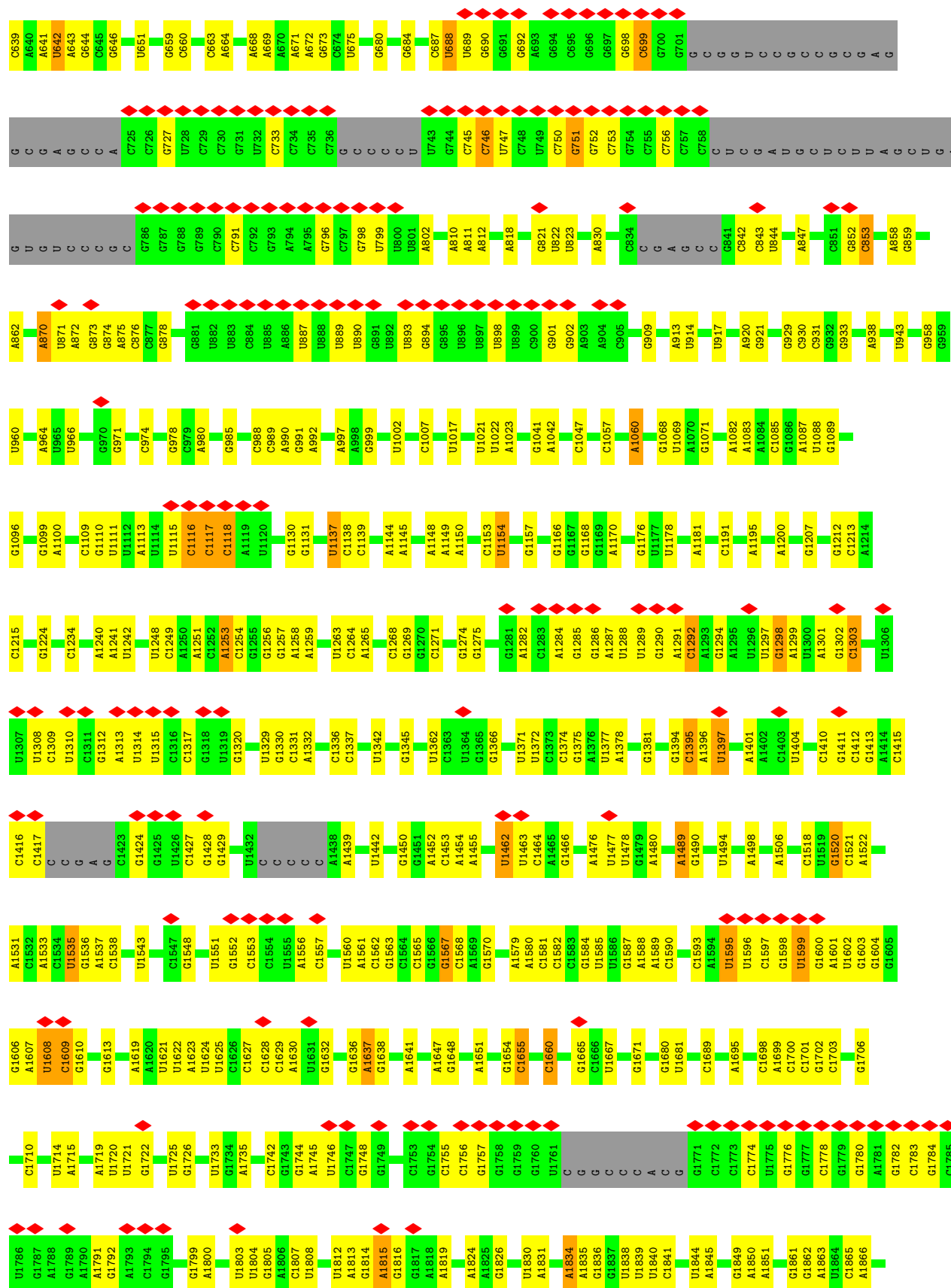
Chain 81:  6% 65% 27% 5%



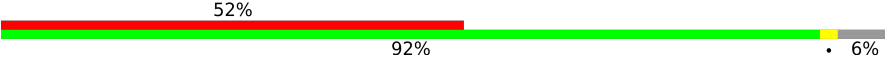
• Molecule 4: 18S ribosomal RNA

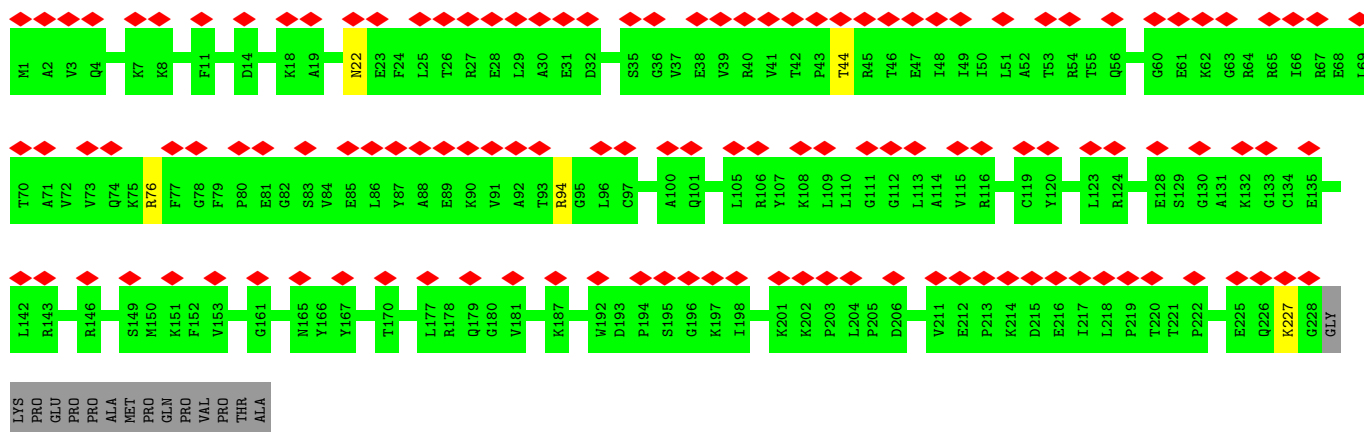
Chain A2:  16% 60% 31% 7%





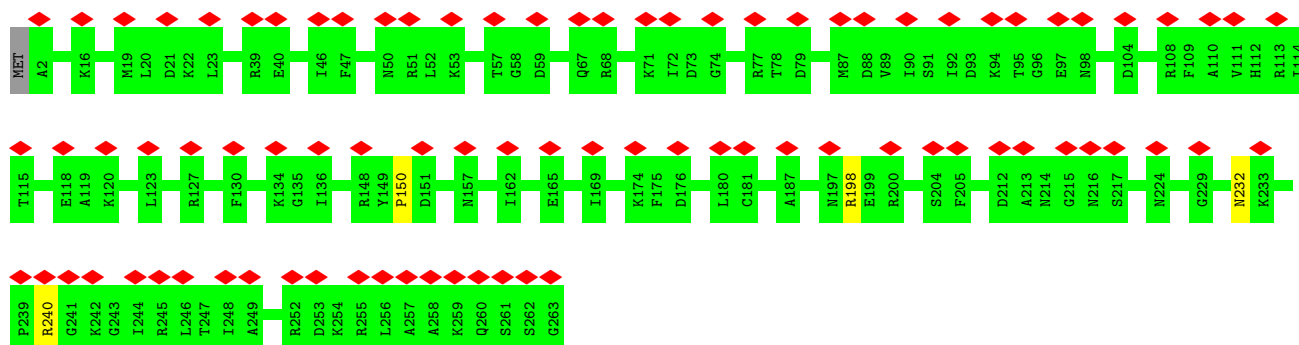


Chain E2: 




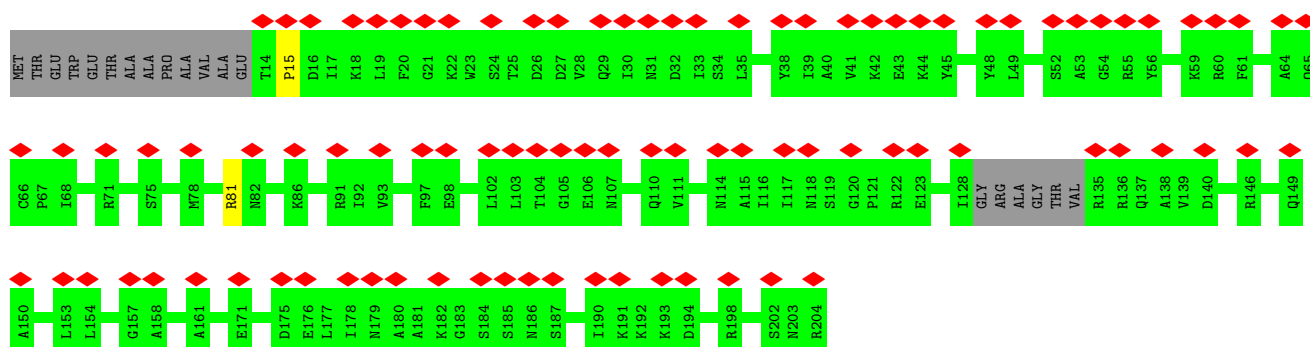
• Molecule 9: eS4

Chain F2: 




• Molecule 10: Ribosomal protein S5

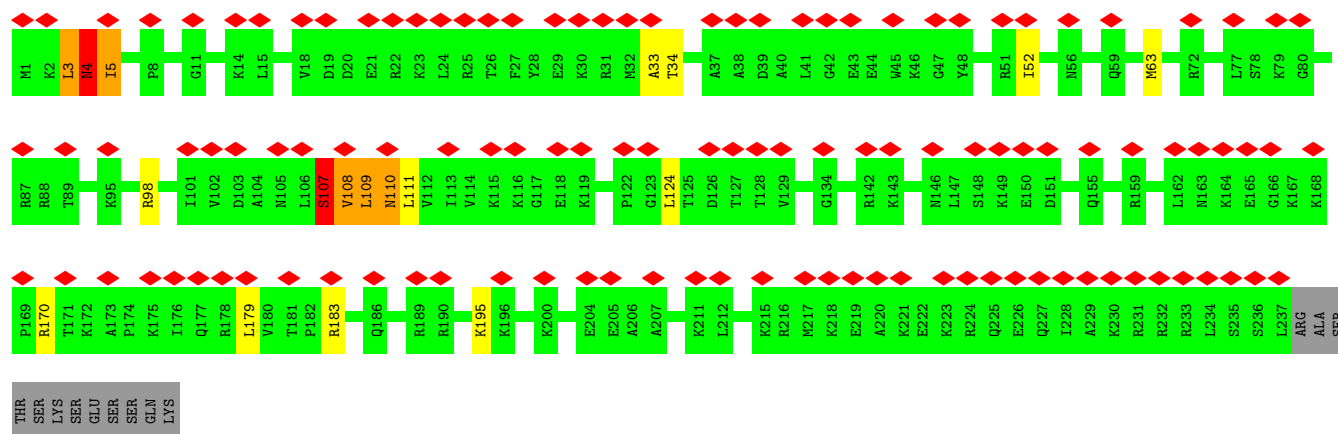
Chain G2: 



• Molecule 11: 40S ribosomal protein S6

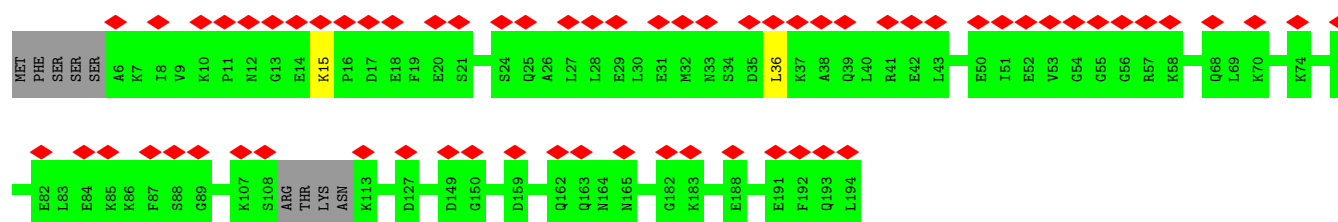
Chain H2: 





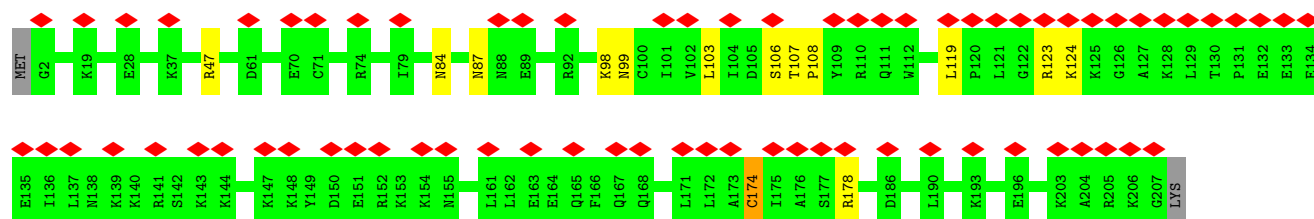
• Molecule 12: 40S ribosomal protein S7

Chain I2: 34% 94% 5%



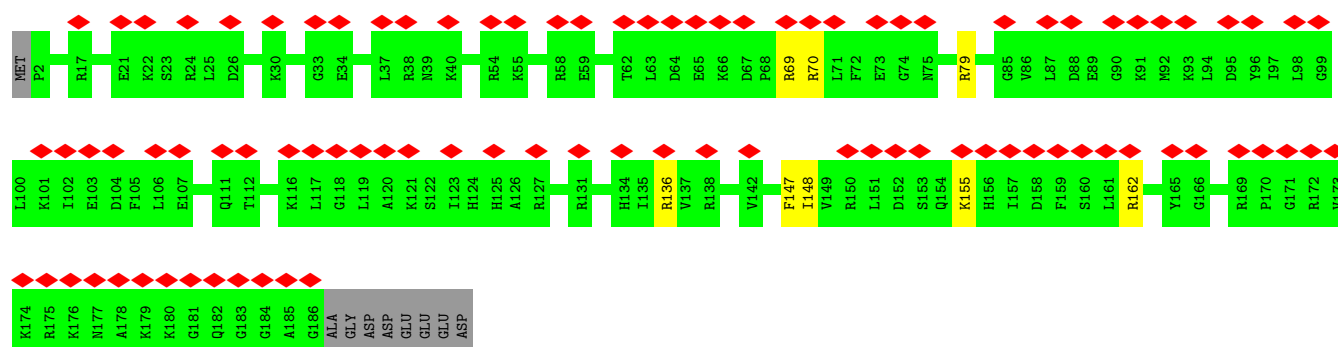
• Molecule 13: eS8

Chain J2: 34% 92% 6%

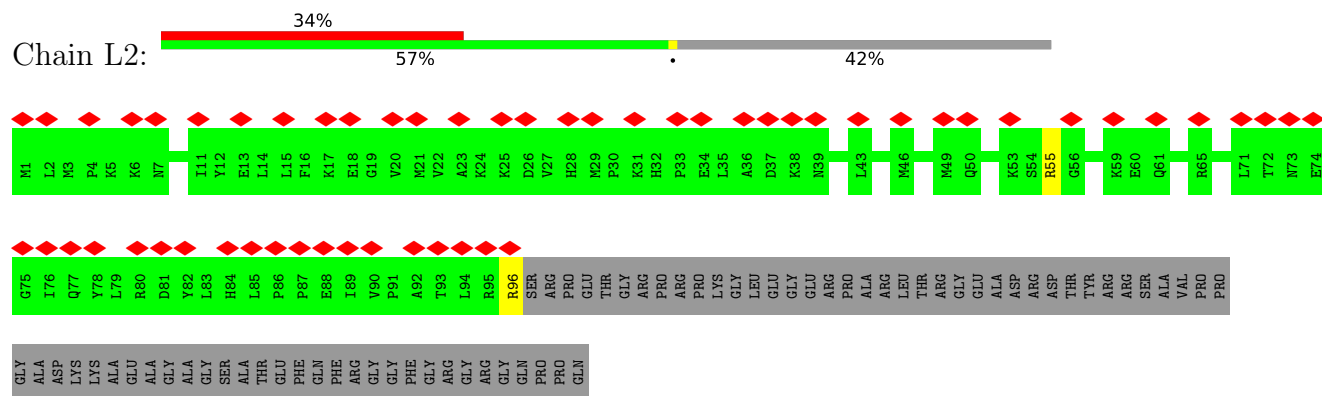


• Molecule 14: Ribosomal protein S9 (Predicted)

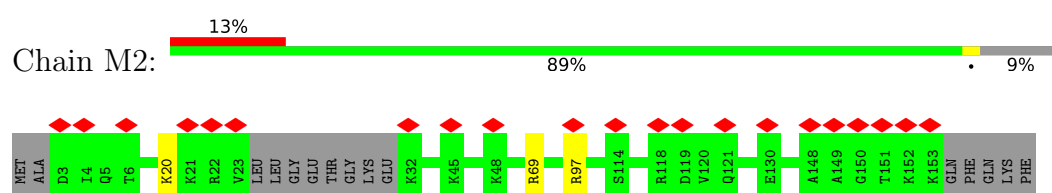
Chain K2: 47% 91% 5%



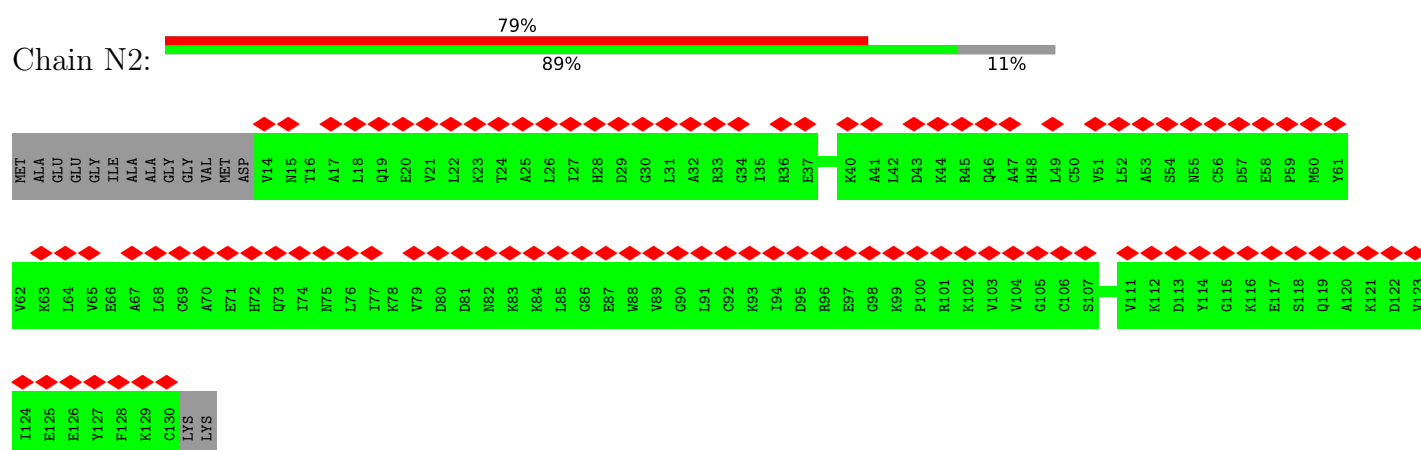
- Molecule 15: eS10



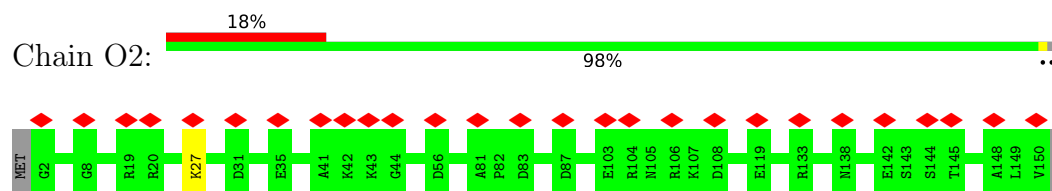
- Molecule 16: Ribosomal protein S11



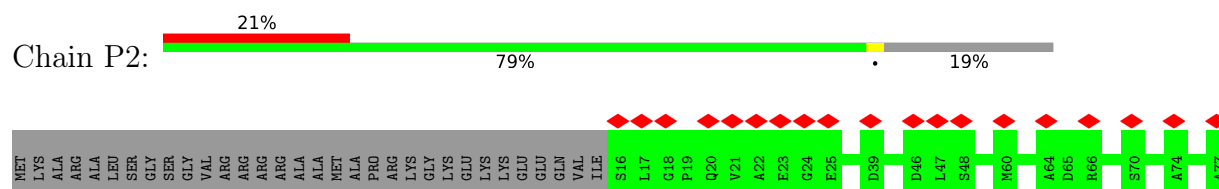
- Molecule 17: 40S ribosomal protein S12



- Molecule 18: uS15

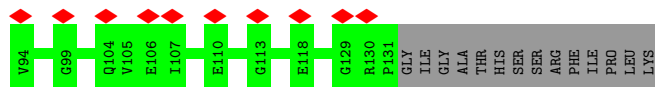
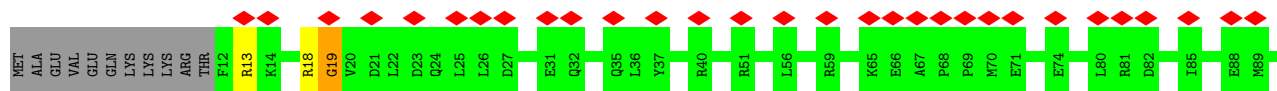
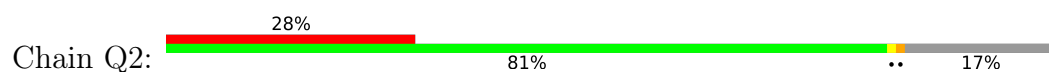


- Molecule 19: uS11

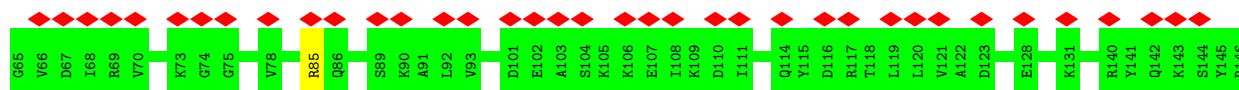
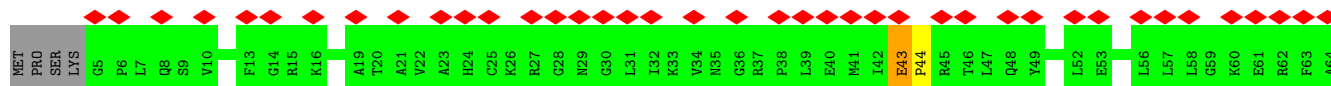




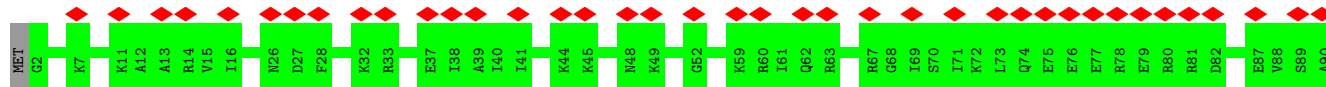
- Molecule 20: uS19



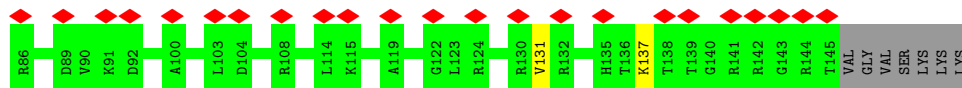
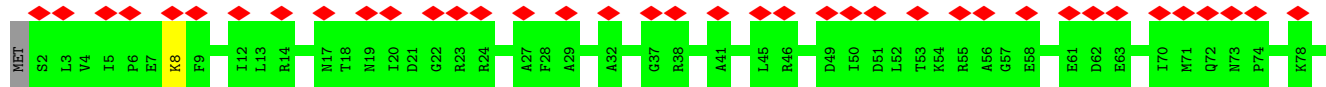
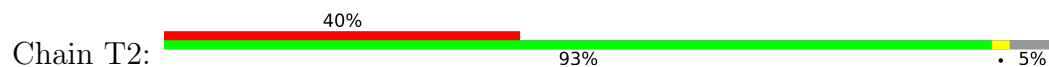
- Molecule 21: Ribosomal protein S16



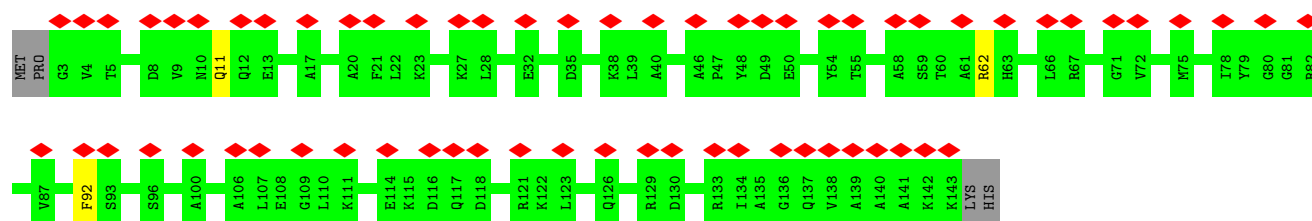
- Molecule 22: eS17



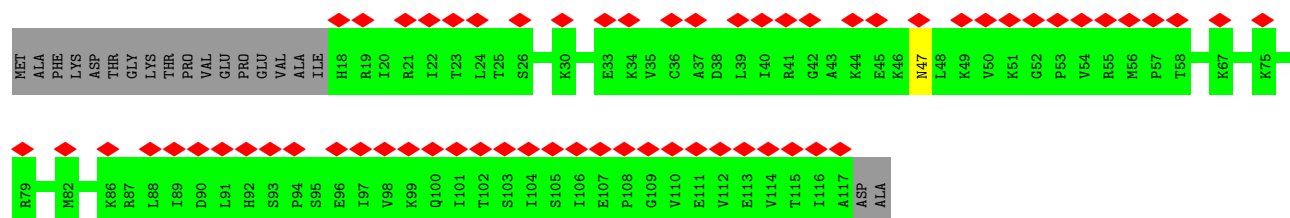
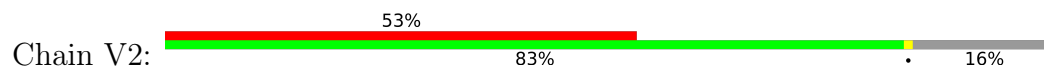
- Molecule 23: uS13



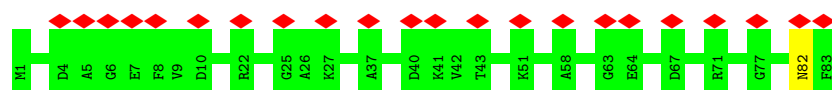
- Molecule 24: eS19



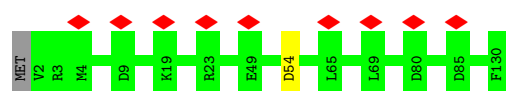
• Molecule 25: uS10



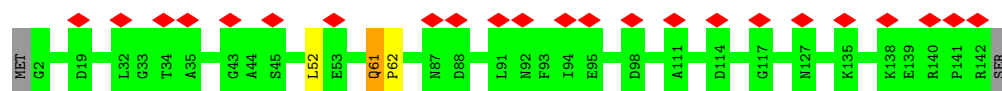
• Molecule 26: eS21



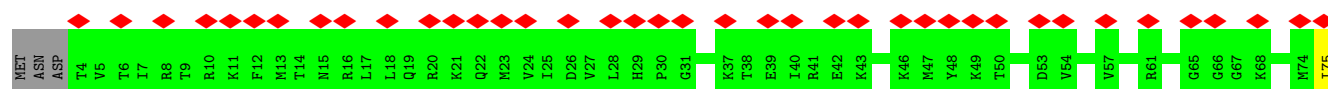
• Molecule 27: Ribosomal protein S15a



• Molecule 28: uS12



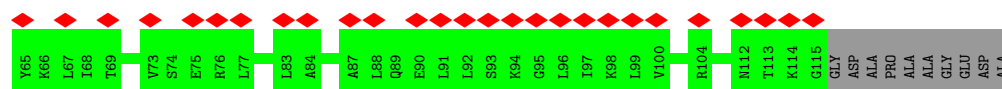
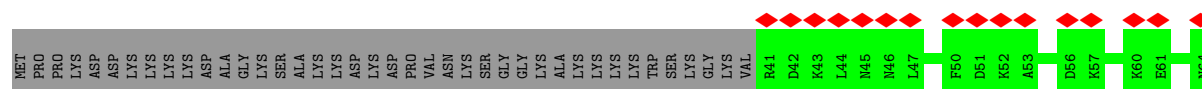
• Molecule 29: eS24



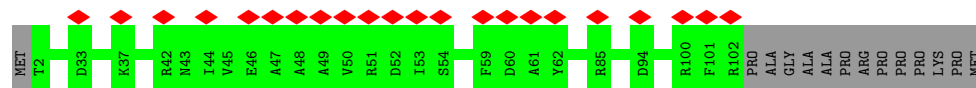
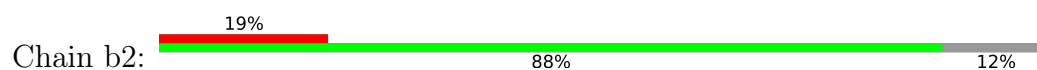




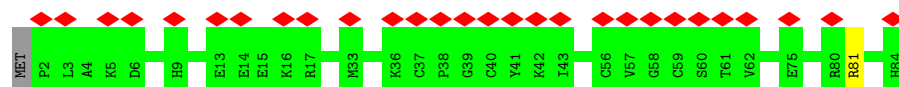
- Molecule 30: eS25



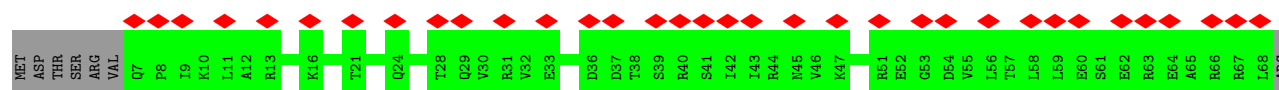
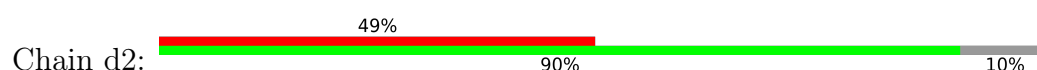
- Molecule 31: eS26



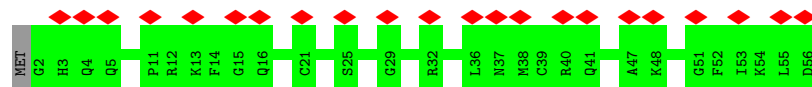
- Molecule 32: 40S ribosomal protein S27



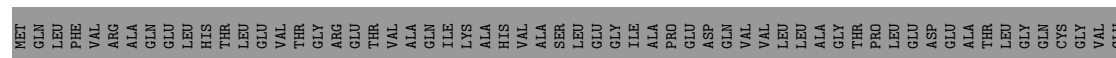
- Molecule 33: Ribosomal protein S28



- Molecule 34: uS14

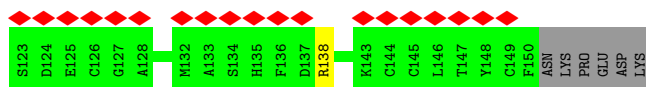
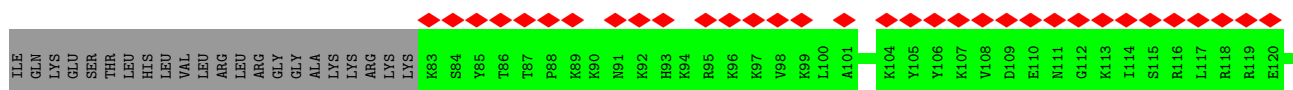


- Molecule 35: 40S ribosomal protein S30

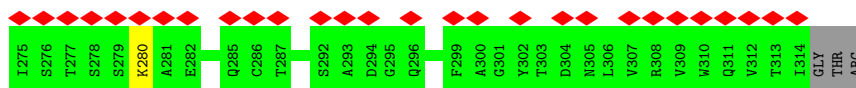
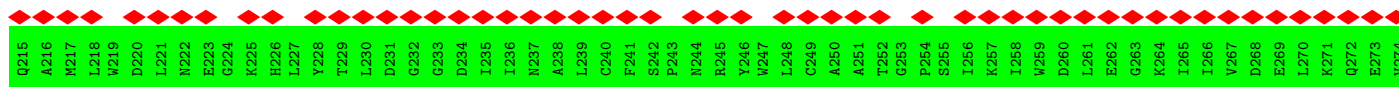
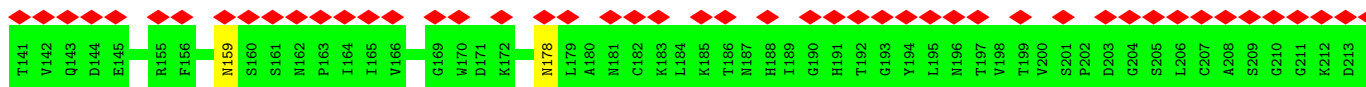
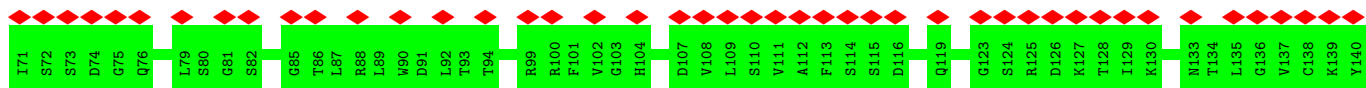
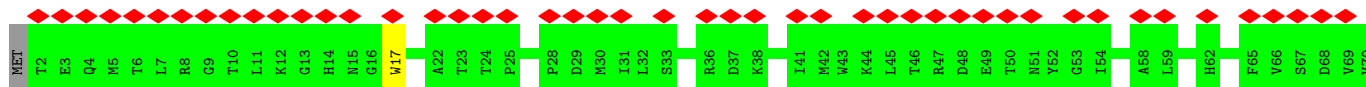
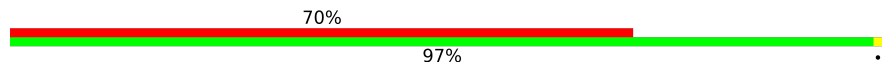




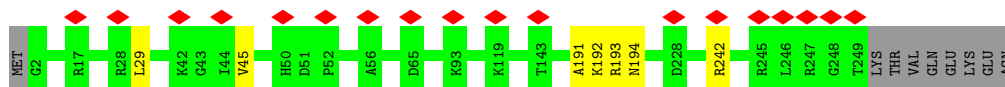
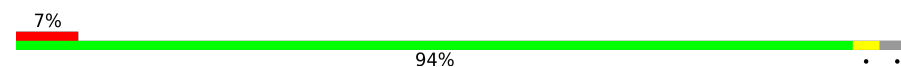
- Chain g2:



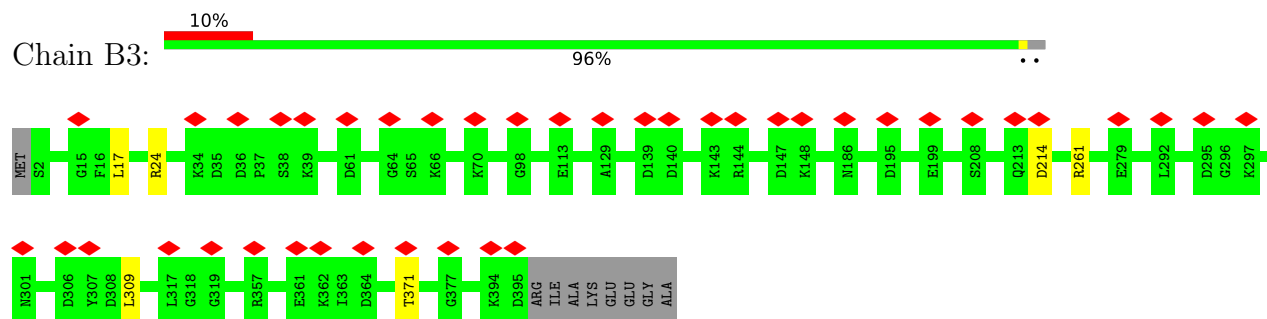
- Chain h2:



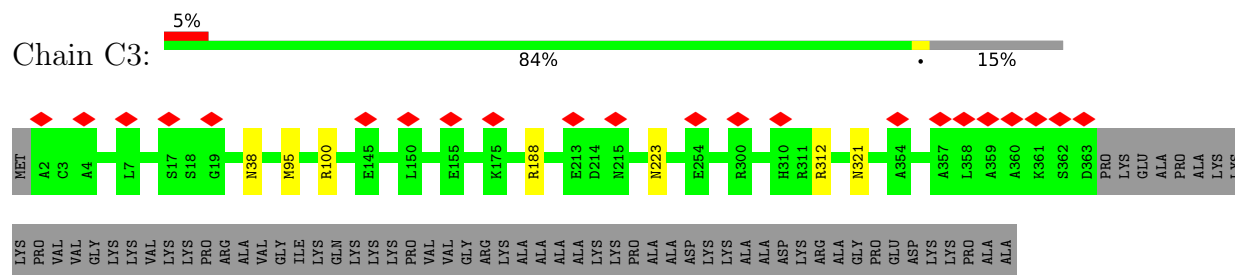
- Chain A3:



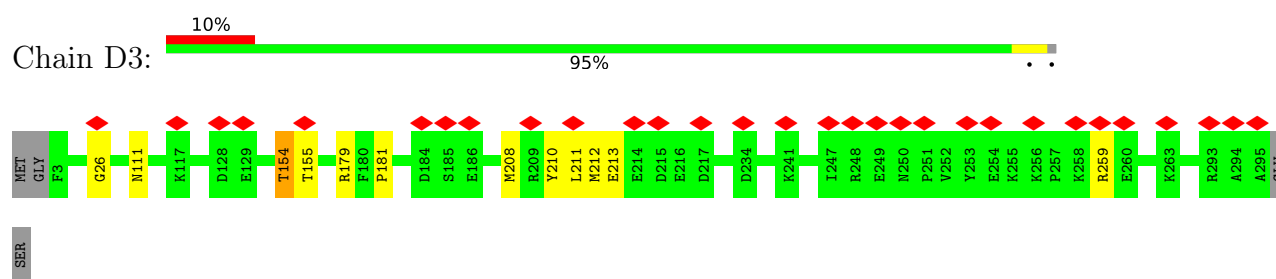
- Molecule 39: uL3



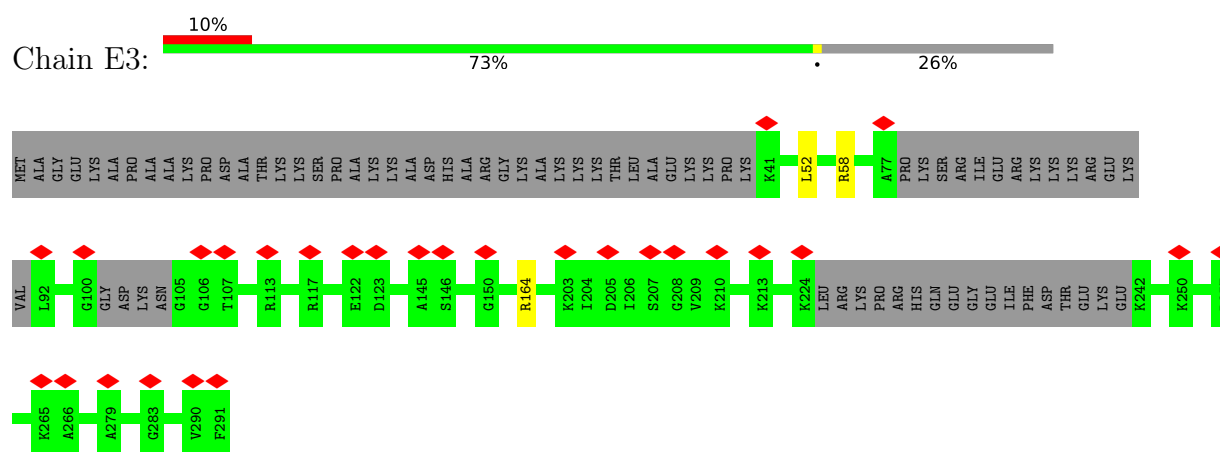
- Molecule 40: uL4



- Molecule 41: 60S ribosomal protein L5

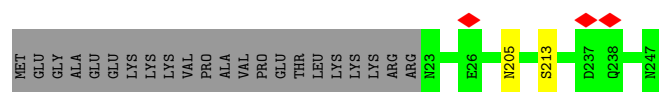


- Molecule 42: 60S ribosomal protein L6

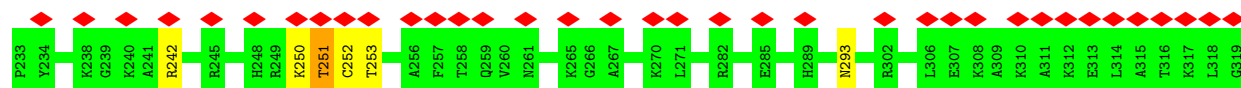
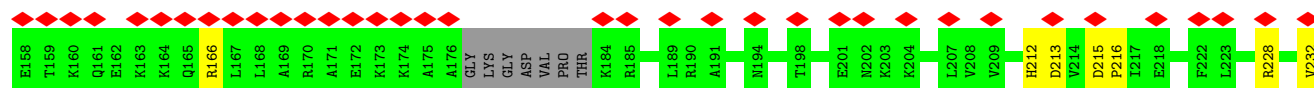
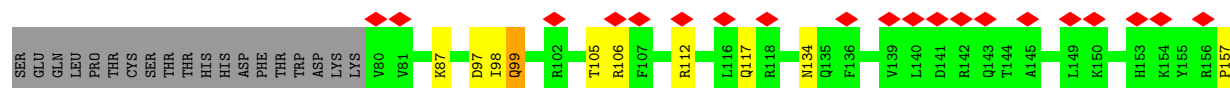
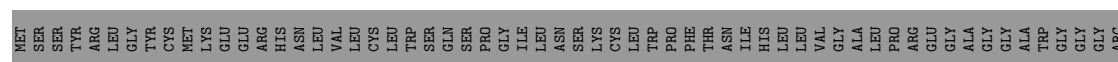


- Molecule 43: uL30

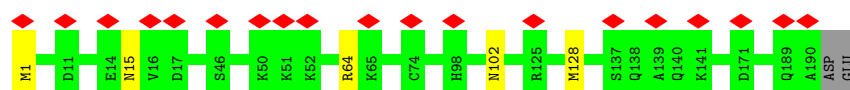




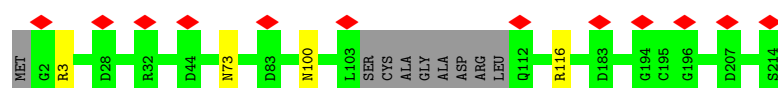
• Molecule 44: eL8



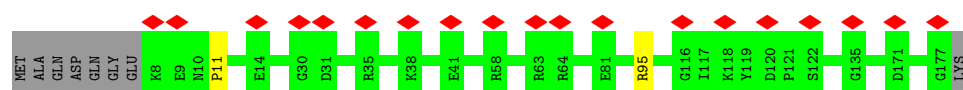
• Molecule 45: uL6



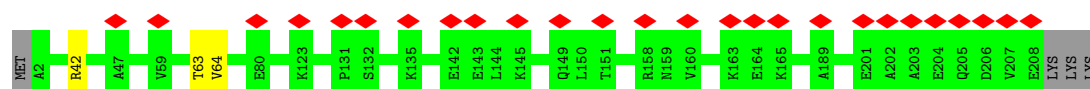
• Molecule 46: 60S ribosomal protein L10



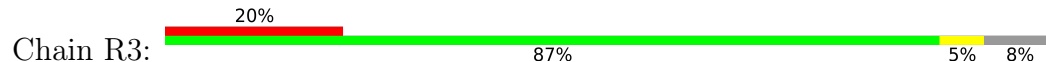
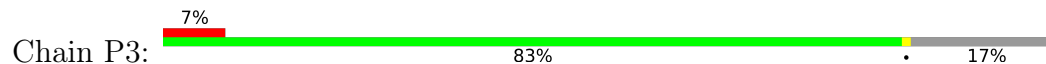
• Molecule 47: Ribosomal protein L11



• Molecule 48: eL13

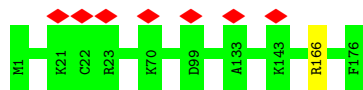


- Chain M3: 



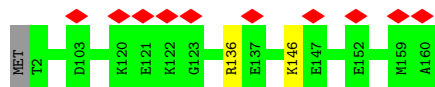
- Molecule 55: eL20

Chain S3:  99%




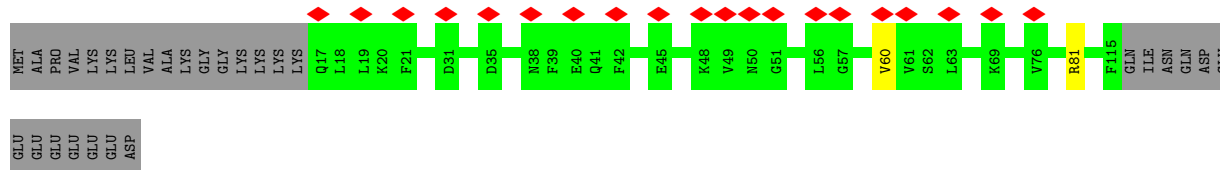
- Molecule 56: eL21

Chain T3:  98%



- Molecule 57: eL22

Chain U3:  76% 23%




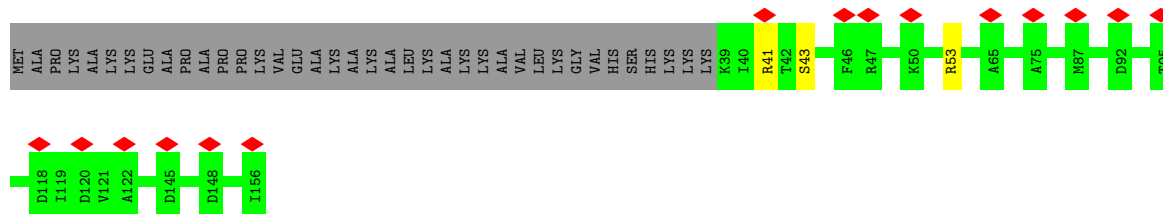
- Molecule 58: Ribosomal protein L23

Chain V3:  92% 6%



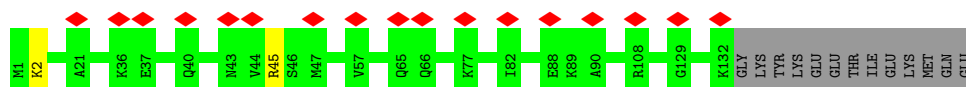
- Molecule 59: uL23

Chain X3:  74% 24%



- Molecule 60: Ribosomal protein L26

Chain Y3:  90% 9%



- 
- Figure 1: Distribution of 2000 genes across 15 categories. The chart shows the number of genes in each category, with red diamonds indicating specific genes of interest.
- | Category | Gene Count | Gene of Interest |
|----------|------------|------------------|
| MET      | 1          |                  |
| G2       | 1          |                  |
| M5       | 1          |                  |
| T33      | 1          |                  |
| S34      | 1          |                  |
| D35      | 1          |                  |
| Y38      | 1          |                  |
| G45      | 1          |                  |
| I46      | 1          |                  |
| D47      | 1          |                  |
| T54      | 1          |                  |
| A55      | 1          |                  |
| A56      | 1          |                  |
| M57      | 1          |                  |
| K64      | 1          |                  |
| S70      | 1          |                  |
| R84      | 1          |                  |
| Y85      | 1          |                  |
| P90      | 1          |                  |
| L91      | 1          |                  |
| L91      | 1          |                  |
| D92      | 1          |                  |
| K93      | 1          |                  |
| D99      | 1          |                  |
| R102     | 1          |                  |
| A105     | 1          |                  |
| R112     | 1          |                  |
| V116     | 1          |                  |
| E119     | 1          |                  |
| K126     | 1          |                  |
| E126     | 1          |                  |

- 
- Diagram illustrating the 14 amino acid residues of the 14-3-3 protein. The residues are arranged in a sequence, with MET at the N-terminus and A148 at the C-terminus. The residues are color-coded: MET is grey, P2 is green, S3 is green, R4 is yellow, D76 is green, E84 is green, R87 is green, A91 is green, K92 is green, N93 is green, K94 is green, D102 is green, R105 is green, K116 is green, A143 is green, and A148 is green. Red diamonds are placed above the residues D76, E84, R87, A91, K92, N93, K94, D102, R105, K116, A143, and A148.

- |     |    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |      |      |      |      |     |     |     |     |     |     |     |     |     |     |
|-----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | A2 | R25 | S26 | K33 | K51 | M57 | N60 | N61 | A62 | M65 | A66 | A67 | R68 | A69 | E70 | A71 | T72 | K73 | A74 | L75 | V76 | LYS | PRO | LYS | GLU | VAL | LYS | PRO | LYS | THR | ILE | PRO | LYS | GLY | V89 | S90 | R91 | R107 | R114 | G115 | L116 | R117 | LEU | SER | ARG | PRO | GLN | THR | LYS | ALA | LYS | ALA |
|-----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| LYS | THR | GLU | PRO | GLN | ILE | LYS | GLY | LYS | VAL | ALA | LYS | ALA | GLN | GLN | ILE | LYS | ALA | ALA | ALA | GLU | THR | LYS | PRO | LYS | GLN | GLN | GLY | LYS | PRO |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

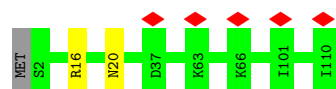
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| LYS | ALA | GLN | ALA | GLY | LYS | PRO | LYS | ALA | GLN | ALA | GLY | THR | LYS | PRO | LYS | LYS | ALA | GLN | ALA | THR | PRO | ALA | VAL | PRO | ALA | GLN | ALA | PRO | PRO | LYS | GLY |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

- 
- The diagram illustrates the arrangement of amino acid residues in the protein sequence from MET to LYS. The residues are grouped into three main regions: a grey region (MET-VAL, ALA-ALA, LYS-LYS, THR-THR, LYS), a yellow region (C52-P53), and another grey region (G100-D101, S102-D103, R106-S107, MET-PRO, GLU-GLN, THR-THR, GLY-GLU, LYS). Red diamonds indicate specific residues: VAL, ALA, LYS, THR, C52, P53, G100, D101, S102, D103, R106, and S107.

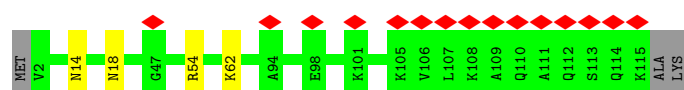
- 
- | Category | Count |
|----------|-------|
| MET      | 1     |
| ALA      | 1     |
| PRO      | 1     |
| ALA      | 1     |
| LYS      | 1     |
| LYS      | 1     |
| GLY      | 1     |
| GLY      | 1     |
| GLU      | 1     |
| LYS      | 1     |
| LYS      | 1     |
| LYS      | 1     |
| GLY      | 1     |
| ARG      | 1     |
| SER      | 1     |
| ALA      | 1     |
| ILE      | 1     |
| N18      | 1     |
| K31      | 1     |
| E94      | 1     |
| D95      | 1     |
| E96      | 1     |
| D97      | 1     |
| S98      | 1     |
| P99      | 1     |
| D123     | 1     |
| E124     | 1     |
| ASN      | 1     |

- 

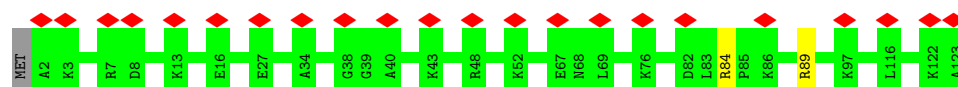
- 
- WORLD WIDE  
PDB  
PROTEIN DATA BANK



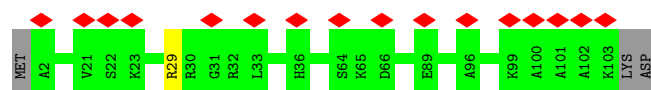
- Molecule 68: eL34



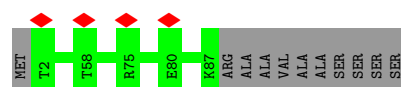
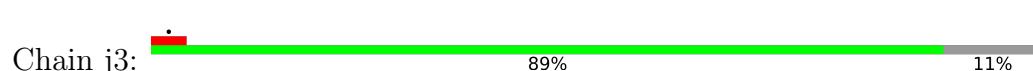
- Molecule 69: uL29



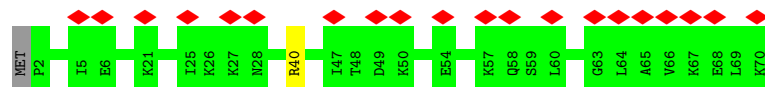
- Molecule 70: 60S ribosomal protein L36



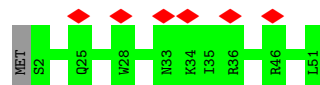
- Molecule 71: Ribosomal protein L37



- Molecule 72: eL38



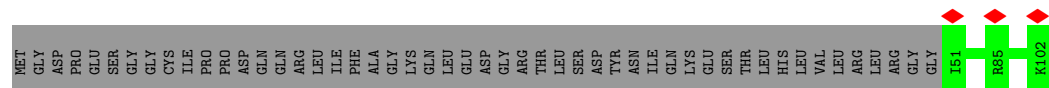
- Molecule 73: eL39





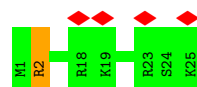
- Molecule 74: eL40

Chain m3:  51% 49%



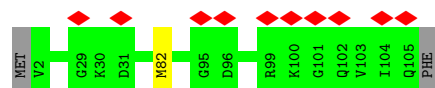
- Molecule 75: eL41

Chain n3:  16% 96%



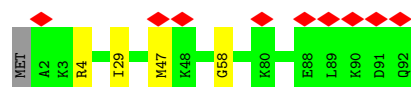
- Molecule 76: eL42

Chain o3:  9% 97%




- Molecule 77: eL43

Chain p3:  10% 95%




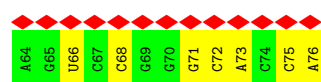
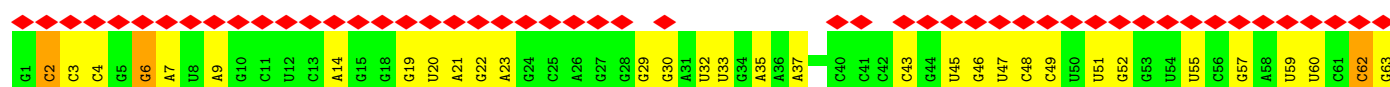
- Molecule 78: eL28

Chain r3:  7% 89% 9%



- Molecule 79: A/P RNA

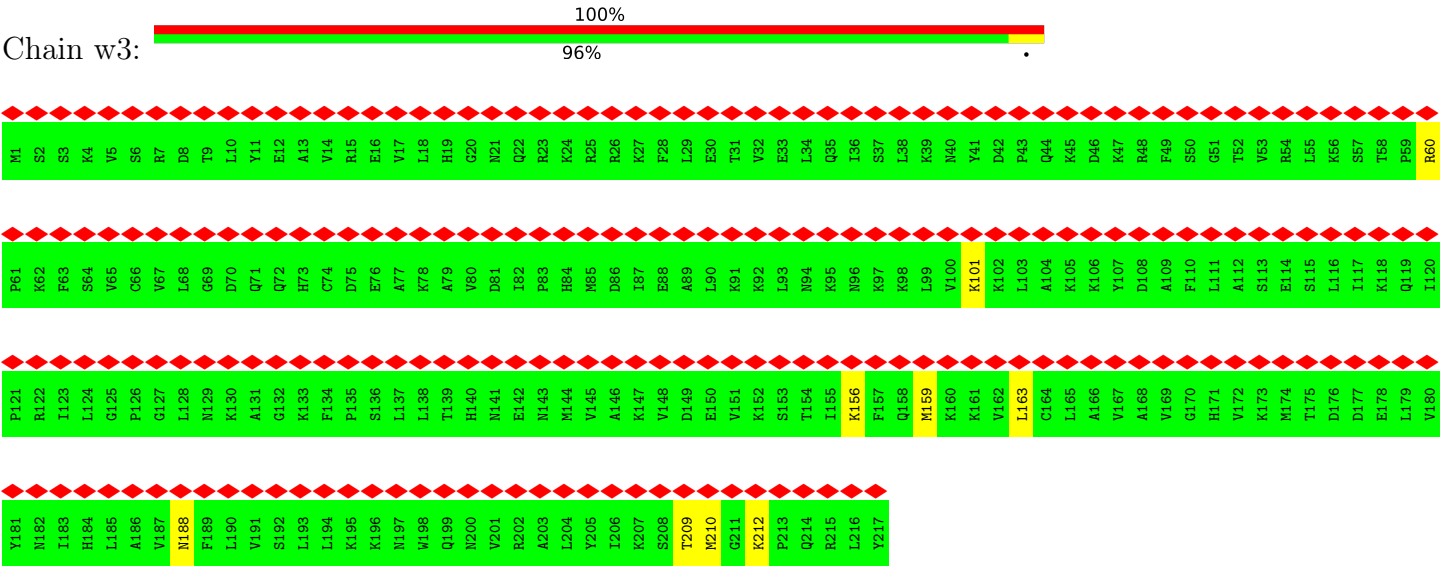
Chain q3:  85% 47% 49%



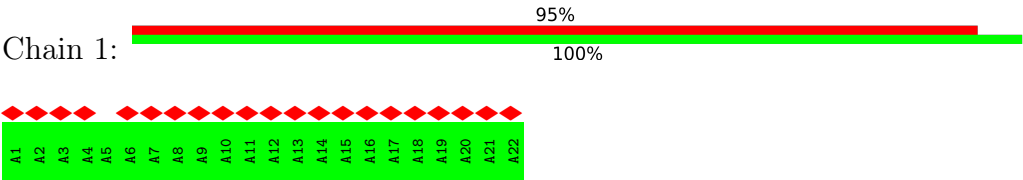
- Molecule 80: uL10



● Molecule 84: uL1



● Molecule 85: nascent chain



## 4 Experimental information

| Property                             | Value                                   | Source    |
|--------------------------------------|---|-----------|
| EM reconstruction method             | SINGLE PARTICLE                         | Depositor |
| Imposed symmetry                     | POINT, C1                               | Depositor |
| Number of particles used             | 98611                                   | 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 ( $e^-/\text{\AA}^2$ ) | 1.79                                    | Depositor |
| Minimum defocus (nm)                 | Not provided                            |           |
| Maximum defocus (nm)                 | Not provided                            |           |
| Magnification                        | Not provided                            |           |
| Image detector                       | FEI FALCON III (4k x 4k)                | Depositor |
| Maximum map value                    | 1.111                                   | Depositor |
| Minimum map value                    | -0.731                                  | Depositor |
| Average map value                    | 0.001                                   | Depositor |
| Map value standard deviation         | 0.033                                   | Depositor |
| Recommended contour level            | 0.12                                    | Depositor |
| Map size (Å)                         | 541.12, 541.12, 541.12                  | wwPDB     |
| Map dimensions                       | 356, 356, 356                           | wwPDB     |
| Map angles (°)                       | 90.0, 90.0, 90.0                        | wwPDB     |
| Pixel spacing (Å)                    | 1.52, 1.52, 1.52                        | Depositor |

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

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   | 51    | 1.66         | 16/87039 (0.0%) | 1.29        | 419/135714 (0.3%) |
| 2   | 71    | 0.76         | 0/2858          | 1.00        | 4/4455 (0.1%)     |
| 3   | 81    | 4.86         | 13/3581 (0.4%)  | 1.67        | 40/5577 (0.7%)    |
| 4   | A2    | 0.62         | 0/41516         | 1.07        | 200/64670 (0.3%)  |
| 5   | B2    | 0.34         | 0/1747          | 0.58        | 0/2374            |
| 6   | C2    | 0.35         | 0/1756          | 0.57        | 0/2350            |
| 7   | D2    | 0.39         | 0/1753          | 0.58        | 0/2369            |
| 8   | E2    | 0.33         | 0/1793          | 0.59        | 0/2413            |
| 9   | F2    | 0.32         | 0/2118          | 0.58        | 0/2849            |
| 10  | G2    | 0.32         | 0/1492          | 0.59        | 0/2005            |
| 11  | H2    | 0.32         | 0/1946          | 0.78        | 6/2590 (0.2%)     |
| 12  | I2    | 0.30         | 0/1510          | 0.60        | 1/2022 (0.0%)     |
| 13  | J2    | 0.36         | 0/1715          | 0.71        | 3/2287 (0.1%)     |
| 14  | K2    | 0.37         | 0/1550          | 0.65        | 0/2069            |
| 15  | L2    | 0.34         | 0/834           | 0.62        | 0/1125            |
| 16  | M2    | 0.36         | 0/1195          | 0.55        | 0/1597            |
| 17  | N2    | 0.31         | 0/918           | 0.67        | 0/1233            |
| 18  | O2    | 0.32         | 0/1226          | 0.54        | 0/1649            |
| 19  | P2    | 0.36         | 0/1029          | 0.58        | 0/1380            |
| 20  | Q2    | 0.35         | 0/1017          | 0.58        | 0/1358            |
| 21  | R2    | 0.34         | 0/1146          | 0.57        | 0/1534            |
| 22  | S2    | 0.29         | 0/1082          | 0.53        | 0/1452            |
| 23  | T2    | 0.35         | 0/1208          | 0.64        | 0/1618            |
| 24  | U2    | 0.37         | 0/1115          | 0.62        | 0/1493            |
| 25  | V2    | 0.32         | 0/805           | 0.57        | 0/1081            |
| 26  | W2    | 0.33         | 0/643           | 0.56        | 0/860             |
| 27  | X2    | 0.37         | 0/1051          | 0.57        | 0/1406            |
| 28  | Y2    | 0.35         | 0/1116          | 0.59        | 1/1490 (0.1%)     |
| 29  | Z2    | 0.34         | 0/1028          | 0.60        | 0/1366            |
| 30  | a2    | 0.30         | 0/604           | 0.63        | 0/810             |
| 31  | b2    | 0.37         | 0/828           | 0.57        | 0/1109            |
| 32  | c2    | 0.30         | 0/665           | 0.55        | 0/891             |

| Mol | Chain | Bond lengths |               | Bond angles |               |
|-----|-------|--------------|---------------|-------------|---------------|
|     |       | RMSZ         | # Z  >5       | RMSZ        | # Z  >5       |
| 33  | d2    | 0.30         | 0/490         | 0.56        | 0/656         |
| 34  | e2    | 0.38         | 0/470         | 0.54        | 0/623         |
| 35  | f2    | 0.30         | 0/447         | 0.50        | 0/587         |
| 36  | g2    | 0.35         | 0/567         | 0.63        | 0/753         |
| 37  | h2    | 0.32         | 0/2493        | 0.63        | 1/3394 (0.0%) |
| 38  | A3    | 0.44         | 0/1936        | 0.68        | 1/2596 (0.0%) |
| 39  | B3    | 0.43         | 0/3240        | 0.61        | 3/4339 (0.1%) |
| 40  | C3    | 0.43         | 0/2937        | 0.59        | 0/3946        |
| 41  | D3    | 0.41         | 0/2437        | 0.59        | 0/3264        |
| 42  | E3    | 0.39         | 0/1762        | 0.61        | 1/2362 (0.0%) |
| 43  | F3    | 0.47         | 1/1911 (0.1%) | 0.60        | 0/2549        |
| 44  | G3    | 2.74         | 1/1909 (0.1%) | 0.81        | 2/2566 (0.1%) |
| 45  | H3    | 0.38         | 0/1535        | 0.58        | 0/2063        |
| 46  | I3    | 0.40         | 0/1702        | 0.54        | 0/2272        |
| 47  | J3    | 0.38         | 0/1385        | 0.60        | 0/1852        |
| 48  | L3    | 0.42         | 0/1705        | 0.59        | 0/2283        |
| 49  | M3    | 0.45         | 0/1158        | 0.58        | 0/1547        |
| 50  | N3    | 0.49         | 0/1746        | 0.62        | 0/2338        |
| 51  | O3    | 0.43         | 0/1662        | 0.60        | 0/2222        |
| 52  | P3    | 0.44         | 0/1268        | 0.55        | 0/1700        |
| 53  | Q3    | 0.43         | 0/1539        | 0.61        | 0/2054        |
| 54  | R3    | 0.43         | 0/1524        | 0.75        | 2/2013 (0.1%) |
| 55  | S3    | 0.45         | 0/1501        | 0.59        | 0/2012        |
| 56  | T3    | 0.44         | 0/1326        | 0.53        | 0/1770        |
| 57  | U3    | 0.38         | 0/823         | 0.62        | 0/1104        |
| 58  | V3    | 0.39         | 0/993         | 0.58        | 0/1332        |
| 59  | X3    | 0.36         | 0/984         | 0.63        | 1/1323 (0.1%) |
| 60  | Y3    | 0.42         | 0/1119        | 0.56        | 0/1488        |
| 61  | Z3    | 0.42         | 0/1130        | 0.63        | 0/1507        |
| 62  | a3    | 0.43         | 0/1191        | 0.56        | 0/1590        |
| 63  | b3    | 1.87         | 1/861 (0.1%)  | 0.62        | 2/1138 (0.2%) |
| 64  | c3    | 0.37         | 0/771         | 0.57        | 0/1034        |
| 65  | d3    | 0.41         | 0/903         | 0.58        | 0/1216        |
| 66  | e3    | 0.43         | 0/1071        | 0.60        | 1/1429 (0.1%) |
| 67  | f3    | 0.47         | 0/895         | 0.63        | 0/1198        |
| 68  | g3    | 0.43         | 0/916         | 0.65        | 0/1220        |
| 69  | h3    | 2.07         | 2/1021 (0.2%) | 1.10        | 4/1348 (0.3%) |
| 70  | i3    | 0.34         | 0/841         | 0.61        | 0/1112        |
| 71  | j3    | 0.43         | 0/720         | 0.60        | 0/952         |
| 72  | k3    | 0.34         | 0/575         | 0.63        | 0/761         |
| 73  | l3    | 0.39         | 0/459         | 0.53        | 0/608         |
| 74  | m3    | 0.38         | 0/435         | 0.54        | 0/575         |
| 75  | n3    | 0.38         | 0/240         | 0.70        | 0/305         |

| Mol | Chain | Bond lengths |                  | Bond angles |                   |
|-----|-------|--------------|------------------|-------------|-------------------|
|     |       | RMSZ         | # Z  >5          | RMSZ        | # Z  >5           |
| 76  | o3    | 0.42         | 0/864            | 0.57        | 0/1140            |
| 77  | p3    | 0.43         | 0/718            | 0.71        | 1/953 (0.1%)      |
| 78  | r3    | 0.44         | 0/1010           | 0.60        | 0/1354            |
| 79  | q3    | 0.44         | 0/1762           | 1.19        | 21/2739 (0.8%)    |
| 80  | t3    | 0.54         | 1/1530 (0.1%)    | 0.97        | 10/2064 (0.5%)    |
| 81  | u3    | 0.30         | 0/1174           | 0.67        | 0/1582            |
| 82  | v3    | 0.60         | 0/515            | 1.24        | 4/799 (0.5%)      |
| 83  | 33    | 0.46         | 0/1795           | 0.98        | 2/2798 (0.1%)     |
| 84  | w3    | 0.29         | 0/1769           | 0.64        | 1/2371 (0.0%)     |
| 85  | 1     | 0.24         | 0/109            | 0.31        | 0/151             |
| All | All   | 1.27         | 35/235728 (0.0%) | 1.05        | 731/346148 (0.2%) |

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 1   | 51    | 0                   | 1                   |
| 5   | B2    | 0                   | 1                   |
| 8   | E2    | 0                   | 1                   |
| 11  | H2    | 0                   | 8                   |
| 13  | J2    | 0                   | 4                   |
| 14  | K2    | 0                   | 1                   |
| 20  | Q2    | 0                   | 2                   |
| 21  | R2    | 0                   | 1                   |
| 23  | T2    | 0                   | 1                   |
| 27  | X2    | 0                   | 1                   |
| 28  | Y2    | 0                   | 1                   |
| 38  | A3    | 0                   | 1                   |
| 44  | G3    | 0                   | 10                  |
| 50  | N3    | 0                   | 4                   |
| 54  | R3    | 0                   | 1                   |
| 57  | U3    | 0                   | 1                   |
| 61  | Z3    | 0                   | 3                   |
| 63  | b3    | 0                   | 1                   |
| 64  | c3    | 0                   | 1                   |
| 66  | e3    | 0                   | 1                   |
| 67  | f3    | 0                   | 1                   |
| 69  | h3    | 0                   | 1                   |
| 75  | n3    | 0                   | 1                   |
| 77  | p3    | 0                   | 1                   |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 80  | t3    | 0                   | 8                   |
| 84  | w3    | 0                   | 2                   |
| All | All   | 0                   | 59                  |

The worst 5 of 35 bond length outliers are listed below:

| Mol | Chain | Res  | Type | Atoms | Z      | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|-------|--------|-------------|----------|
| 1   | 51    | 1244 | G    | N7-C5 | 223.92 | 2.73        | 1.39     |
| 1   | 51    | 1244 | G    | C8-N7 | 220.37 | 2.63        | 1.30     |
| 1   | 51    | 1244 | G    | N9-C8 | 179.65 | 2.63        | 1.37     |
| 1   | 51    | 1244 | G    | N9-C4 | 159.88 | 2.65        | 1.38     |
| 1   | 51    | 1244 | G    | C5-C4 | 151.21 | 2.44        | 1.38     |

The worst 5 of 731 bond angle outliers are listed below:

| Mol | Chain | Res  | Type | Atoms    | Z       | Observed(°) | Ideal(°) |
|-----|-------|------|------|----------|---------|-------------|----------|
| 1   | 51    | 1966 | C    | C6-N1-C2 | -202.29 | 39.38       | 120.30   |
| 1   | 51    | 1966 | C    | N1-C2-N3 | -112.99 | 40.11       | 119.20   |
| 1   | 51    | 1966 | C    | N3-C2-O2 | 44.23   | 152.86      | 121.90   |
| 1   | 51    | 1966 | C    | C4-C5-C6 | -43.75  | 95.53       | 117.40   |
| 1   | 51    | 1966 | C    | N3-C4-C5 | -37.03  | 107.09      | 121.90   |

There are no chirality outliers.

5 of 59 planarity outliers are listed below:

| Mol | Chain | Res  | Type | Group     |
|-----|-------|------|------|-----------|
| 1   | 51    | 1966 | C    | Sidechain |
| 5   | B2    | 42   | LYS  | Peptide   |
| 8   | E2    | 44   | THR  | Peptide   |
| 11  | H2    | 3    | LEU  | Peptide   |
| 11  | H2    | 4    | ASN  | Peptide   |

## 5.2 Too-close contacts

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



## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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 |     |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 5   | B2    | 215/295 (73%) | 190 (88%) | 25 (12%) | 0        | 100         | 100 |
| 6   | C2    | 211/264 (80%) | 191 (90%) | 20 (10%) | 0        | 100         | 100 |
| 7   | D2    | 219/293 (75%) | 202 (92%) | 17 (8%)  | 0        | 100         | 100 |
| 8   | E2    | 226/243 (93%) | 206 (91%) | 20 (9%)  | 0        | 100         | 100 |
| 9   | F2    | 260/263 (99%) | 233 (90%) | 26 (10%) | 1 (0%)   | 30          | 63  |
| 10  | G2    | 181/204 (89%) | 164 (91%) | 16 (9%)  | 1 (1%)   | 22          | 55  |
| 11  | H2    | 235/249 (94%) | 185 (79%) | 44 (19%) | 6 (3%)   | 4           | 28  |
| 12  | I2    | 181/194 (93%) | 167 (92%) | 14 (8%)  | 0        | 100         | 100 |
| 13  | J2    | 204/208 (98%) | 167 (82%) | 35 (17%) | 2 (1%)   | 13          | 44  |
| 14  | K2    | 183/194 (94%) | 157 (86%) | 25 (14%) | 1 (0%)   | 25          | 58  |
| 15  | L2    | 94/165 (57%)  | 84 (89%)  | 10 (11%) | 0        | 100         | 100 |
| 16  | M2    | 139/158 (88%) | 130 (94%) | 9 (6%)   | 0        | 100         | 100 |
| 17  | N2    | 115/132 (87%) | 97 (84%)  | 18 (16%) | 0        | 100         | 100 |
| 18  | O2    | 147/151 (97%) | 141 (96%) | 6 (4%)   | 0        | 100         | 100 |
| 19  | P2    | 134/168 (80%) | 122 (91%) | 12 (9%)  | 0        | 100         | 100 |
| 20  | Q2    | 118/145 (81%) | 105 (89%) | 12 (10%) | 1 (1%)   | 16          | 49  |
| 21  | R2    | 140/146 (96%) | 127 (91%) | 11 (8%)  | 2 (1%)   | 9           | 37  |
| 22  | S2    | 130/135 (96%) | 120 (92%) | 10 (8%)  | 0        | 100         | 100 |
| 23  | T2    | 142/152 (93%) | 116 (82%) | 25 (18%) | 1 (1%)   | 19          | 52  |
| 24  | U2    | 139/145 (96%) | 121 (87%) | 16 (12%) | 2 (1%)   | 9           | 37  |
| 25  | V2    | 98/119 (82%)  | 91 (93%)  | 7 (7%)   | 0        | 100         | 100 |
| 26  | W2    | 81/83 (98%)   | 74 (91%)  | 7 (9%)   | 0        | 100         | 100 |
| 27  | X2    | 127/130 (98%) | 118 (93%) | 9 (7%)   | 0        | 100         | 100 |
| 28  | Y2    | 139/143 (97%) | 125 (90%) | 12 (9%)  | 2 (1%)   | 9           | 37  |
| 29  | Z2    | 122/130 (94%) | 107 (88%) | 15 (12%) | 0        | 100         | 100 |

Continued on next page...

*Continued from previous page...*

| Mol | Chain | Analysed      | Favoured  | Allowed  | Outliers | Percentiles |     |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 30  | a2    | 73/125 (58%)  | 65 (89%)  | 8 (11%)  | 0        | 100         | 100 |
| 31  | b2    | 99/115 (86%)  | 92 (93%)  | 7 (7%)   | 0        | 100         | 100 |
| 32  | c2    | 81/84 (96%)   | 76 (94%)  | 5 (6%)   | 0        | 100         | 100 |
| 33  | d2    | 60/69 (87%)   | 58 (97%)  | 2 (3%)   | 0        | 100         | 100 |
| 34  | e2    | 53/56 (95%)   | 48 (91%)  | 5 (9%)   | 0        | 100         | 100 |
| 35  | f2    | 53/133 (40%)  | 48 (91%)  | 5 (9%)   | 0        | 100         | 100 |
| 36  | g2    | 66/156 (42%)  | 53 (80%)  | 13 (20%) | 0        | 100         | 100 |
| 37  | h2    | 311/317 (98%) | 253 (81%) | 58 (19%) | 0        | 100         | 100 |
| 38  | A3    | 246/257 (96%) | 200 (81%) | 44 (18%) | 2 (1%)   | 16          | 49  |
| 39  | B3    | 392/403 (97%) | 352 (90%) | 40 (10%) | 0        | 100         | 100 |
| 40  | C3    | 360/425 (85%) | 329 (91%) | 31 (9%)  | 0        | 100         | 100 |
| 41  | D3    | 291/297 (98%) | 256 (88%) | 31 (11%) | 4 (1%)   | 9           | 37  |
| 42  | E3    | 208/291 (72%) | 192 (92%) | 16 (8%)  | 0        | 100         | 100 |
| 43  | F3    | 223/247 (90%) | 204 (92%) | 19 (8%)  | 0        | 100         | 100 |
| 44  | G3    | 227/319 (71%) | 188 (83%) | 35 (15%) | 4 (2%)   | 7           | 34  |
| 45  | H3    | 188/192 (98%) | 176 (94%) | 12 (6%)  | 0        | 100         | 100 |
| 46  | I3    | 201/214 (94%) | 179 (89%) | 22 (11%) | 0        | 100         | 100 |
| 47  | J3    | 168/178 (94%) | 152 (90%) | 15 (9%)  | 1 (1%)   | 22          | 55  |
| 48  | L3    | 205/211 (97%) | 185 (90%) | 18 (9%)  | 2 (1%)   | 13          | 44  |
| 49  | M3    | 136/218 (62%) | 124 (91%) | 12 (9%)  | 0        | 100         | 100 |
| 50  | N3    | 201/204 (98%) | 179 (89%) | 22 (11%) | 0        | 100         | 100 |
| 51  | O3    | 197/203 (97%) | 182 (92%) | 15 (8%)  | 0        | 100         | 100 |
| 52  | P3    | 151/184 (82%) | 143 (95%) | 8 (5%)   | 0        | 100         | 100 |
| 53  | Q3    | 185/188 (98%) | 169 (91%) | 16 (9%)  | 0        | 100         | 100 |
| 54  | R3    | 178/196 (91%) | 156 (88%) | 21 (12%) | 1 (1%)   | 22          | 55  |
| 55  | S3    | 174/176 (99%) | 159 (91%) | 14 (8%)  | 1 (1%)   | 22          | 55  |
| 56  | T3    | 157/160 (98%) | 143 (91%) | 14 (9%)  | 0        | 100         | 100 |
| 57  | U3    | 97/128 (76%)  | 79 (81%)  | 18 (19%) | 0        | 100         | 100 |
| 58  | V3    | 129/140 (92%) | 119 (92%) | 10 (8%)  | 0        | 100         | 100 |
| 59  | X3    | 116/156 (74%) | 98 (84%)  | 17 (15%) | 1 (1%)   | 14          | 45  |
| 60  | Y3    | 130/145 (90%) | 122 (94%) | 8 (6%)   | 0        | 100         | 100 |

*Continued on next page...*

Continued from previous page...

| Mol | Chain | Analysed          | Favoured    | Allowed    | Outliers | Percentiles |     |
|-----|-------|-------------------|-------------|------------|----------|-------------|-----|
| 61  | Z3    | 133/136 (98%)     | 114 (86%)   | 17 (13%)   | 2 (2%)   | 8           | 37  |
| 62  | a3    | 145/148 (98%)     | 134 (92%)   | 11 (8%)    | 0        | 100         | 100 |
| 63  | b3    | 100/245 (41%)     | 94 (94%)    | 6 (6%)     | 0        | 100         | 100 |
| 64  | c3    | 96/115 (84%)      | 84 (88%)    | 11 (12%)   | 1 (1%)   | 13          | 44  |
| 65  | d3    | 105/125 (84%)     | 96 (91%)    | 9 (9%)     | 0        | 100         | 100 |
| 66  | e3    | 126/135 (93%)     | 115 (91%)   | 11 (9%)    | 0        | 100         | 100 |
| 67  | f3    | 107/110 (97%)     | 95 (89%)    | 12 (11%)   | 0        | 100         | 100 |
| 68  | g3    | 112/117 (96%)     | 101 (90%)   | 11 (10%)   | 0        | 100         | 100 |
| 69  | h3    | 120/123 (98%)     | 113 (94%)   | 7 (6%)     | 0        | 100         | 100 |
| 70  | i3    | 100/105 (95%)     | 90 (90%)    | 10 (10%)   | 0        | 100         | 100 |
| 71  | j3    | 84/97 (87%)       | 74 (88%)    | 10 (12%)   | 0        | 100         | 100 |
| 72  | k3    | 67/70 (96%)       | 53 (79%)    | 14 (21%)   | 0        | 100         | 100 |
| 73  | l3    | 48/51 (94%)       | 42 (88%)    | 6 (12%)    | 0        | 100         | 100 |
| 74  | m3    | 50/102 (49%)      | 47 (94%)    | 3 (6%)     | 0        | 100         | 100 |
| 75  | n3    | 23/25 (92%)       | 20 (87%)    | 2 (9%)     | 1 (4%)   | 2           | 20  |
| 76  | o3    | 102/106 (96%)     | 93 (91%)    | 9 (9%)     | 0        | 100         | 100 |
| 77  | p3    | 89/92 (97%)       | 71 (80%)    | 17 (19%)   | 1 (1%)   | 12          | 42  |
| 78  | r3    | 122/137 (89%)     | 110 (90%)   | 12 (10%)   | 0        | 100         | 100 |
| 80  | t3    | 194/318 (61%)     | 154 (79%)   | 39 (20%)   | 1 (0%)   | 25          | 58  |
| 81  | u3    | 151/165 (92%)     | 126 (83%)   | 25 (17%)   | 0        | 100         | 100 |
| 84  | w3    | 215/217 (99%)     | 183 (85%)   | 30 (14%)   | 2 (1%)   | 14          | 45  |
| 85  | 1     | 20/22 (91%)       | 19 (95%)    | 1 (5%)     | 0        | 100         | 100 |
| All | All   | 11645/13457 (86%) | 10347 (89%) | 1255 (11%) | 43 (0%)  | 32          | 63  |

5 of 43 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 11  | H2    | 34  | THR  |
| 11  | H2    | 108 | VAL  |
| 11  | H2    | 109 | LEU  |
| 23  | T2    | 137 | LYS  |
| 41  | D3    | 213 | GLU  |

### 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 |     |
|-----|-------|----------------|------------|----------|-------------|-----|
| 5   | B2    | 180/245 (74%)  | 179 (99%)  | 1 (1%)   | 84          | 88  |
| 6   | C2    | 194/231 (84%)  | 191 (98%)  | 3 (2%)   | 60          | 74  |
| 7   | D2    | 187/225 (83%)  | 186 (100%) | 1 (0%)   | 86          | 90  |
| 8   | E2    | 189/202 (94%)  | 185 (98%)  | 4 (2%)   | 48          | 66  |
| 9   | F2    | 224/225 (100%) | 221 (99%)  | 3 (1%)   | 65          | 76  |
| 10  | G2    | 158/170 (93%)  | 157 (99%)  | 1 (1%)   | 84          | 88  |
| 11  | H2    | 207/218 (95%)  | 200 (97%)  | 7 (3%)   | 32          | 55  |
| 12  | I2    | 165/174 (95%)  | 164 (99%)  | 1 (1%)   | 84          | 88  |
| 13  | J2    | 178/180 (99%)  | 172 (97%)  | 6 (3%)   | 32          | 55  |
| 14  | K2    | 161/168 (96%)  | 155 (96%)  | 6 (4%)   | 29          | 53  |
| 15  | L2    | 87/136 (64%)   | 85 (98%)   | 2 (2%)   | 45          | 63  |
| 16  | M2    | 130/142 (92%)  | 127 (98%)  | 3 (2%)   | 45          | 63  |
| 17  | N2    | 99/108 (92%)   | 99 (100%)  | 0        | 100         | 100 |
| 18  | O2    | 130/131 (99%)  | 129 (99%)  | 1 (1%)   | 79          | 84  |
| 19  | P2    | 106/130 (82%)  | 103 (97%)  | 3 (3%)   | 38          | 59  |
| 20  | Q2    | 109/130 (84%)  | 108 (99%)  | 1 (1%)   | 75          | 82  |
| 21  | R2    | 117/121 (97%)  | 116 (99%)  | 1 (1%)   | 75          | 82  |
| 22  | S2    | 119/121 (98%)  | 119 (100%) | 0        | 100         | 100 |
| 23  | T2    | 125/132 (95%)  | 124 (99%)  | 1 (1%)   | 79          | 84  |
| 24  | U2    | 111/115 (96%)  | 110 (99%)  | 1 (1%)   | 75          | 82  |
| 25  | V2    | 92/107 (86%)   | 91 (99%)   | 1 (1%)   | 70          | 79  |
| 26  | W2    | 67/67 (100%)   | 66 (98%)   | 1 (2%)   | 60          | 74  |
| 27  | X2    | 112/113 (99%)  | 112 (100%) | 0        | 100         | 100 |
| 28  | Y2    | 113/115 (98%)  | 113 (100%) | 0        | 100         | 100 |
| 29  | Z2    | 107/112 (96%)  | 104 (97%)  | 3 (3%)   | 38          | 59  |
| 30  | a2    | 66/103 (64%)   | 66 (100%)  | 0        | 100         | 100 |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Analysed       | Rotameric  | Outliers | Percentiles |     |
|-----|-------|----------------|------------|----------|-------------|-----|
| 31  | b2    | 88/98 (90%)    | 88 (100%)  | 0        | 100         | 100 |
| 32  | c2    | 75/76 (99%)    | 74 (99%)   | 1 (1%)   | 65          | 76  |
| 33  | d2    | 55/62 (89%)    | 55 (100%)  | 0        | 100         | 100 |
| 34  | e2    | 48/49 (98%)    | 48 (100%)  | 0        | 100         | 100 |
| 35  | f2    | 46/106 (43%)   | 44 (96%)   | 2 (4%)   | 25          | 49  |
| 36  | g2    | 61/140 (44%)   | 60 (98%)   | 1 (2%)   | 58          | 73  |
| 37  | h2    | 272/275 (99%)  | 269 (99%)  | 3 (1%)   | 70          | 79  |
| 38  | A3    | 190/199 (96%)  | 187 (98%)  | 3 (2%)   | 58          | 73  |
| 39  | B3    | 342/348 (98%)  | 339 (99%)  | 3 (1%)   | 75          | 82  |
| 40  | C3    | 302/347 (87%)  | 295 (98%)  | 7 (2%)   | 45          | 63  |
| 41  | D3    | 247/250 (99%)  | 238 (96%)  | 9 (4%)   | 30          | 54  |
| 42  | E3    | 190/251 (76%)  | 188 (99%)  | 2 (1%)   | 70          | 79  |
| 43  | F3    | 196/215 (91%)  | 195 (100%) | 1 (0%)   | 86          | 90  |
| 44  | G3    | 200/272 (74%)  | 192 (96%)  | 8 (4%)   | 27          | 50  |
| 45  | H3    | 169/171 (99%)  | 164 (97%)  | 5 (3%)   | 36          | 58  |
| 46  | I3    | 175/181 (97%)  | 171 (98%)  | 4 (2%)   | 45          | 63  |
| 47  | J3    | 143/149 (96%)  | 142 (99%)  | 1 (1%)   | 81          | 86  |
| 48  | L3    | 172/176 (98%)  | 171 (99%)  | 1 (1%)   | 84          | 88  |
| 49  | M3    | 117/161 (73%)  | 117 (100%) | 0        | 100         | 100 |
| 50  | N3    | 171/172 (99%)  | 169 (99%)  | 2 (1%)   | 67          | 77  |
| 51  | O3    | 171/173 (99%)  | 168 (98%)  | 3 (2%)   | 54          | 71  |
| 52  | P3    | 134/163 (82%)  | 133 (99%)  | 1 (1%)   | 81          | 86  |
| 53  | Q3    | 164/165 (99%)  | 161 (98%)  | 3 (2%)   | 54          | 71  |
| 54  | R3    | 159/175 (91%)  | 154 (97%)  | 5 (3%)   | 35          | 56  |
| 55  | S3    | 157/157 (100%) | 157 (100%) | 0        | 100         | 100 |
| 56  | T3    | 139/140 (99%)  | 137 (99%)  | 2 (1%)   | 62          | 75  |
| 57  | U3    | 89/114 (78%)   | 88 (99%)   | 1 (1%)   | 70          | 79  |
| 58  | V3    | 101/107 (94%)  | 99 (98%)   | 2 (2%)   | 50          | 68  |
| 59  | X3    | 106/134 (79%)  | 105 (99%)  | 1 (1%)   | 75          | 82  |
| 60  | Y3    | 123/135 (91%)  | 121 (98%)  | 2 (2%)   | 58          | 73  |
| 61  | Z3    | 117/118 (99%)  | 117 (100%) | 0        | 100         | 100 |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Analysed          | Rotameric  | Outliers | Percentiles |     |
|-----|-------|-------------------|------------|----------|-------------|-----|
| 62  | a3    | 119/120 (99%)     | 118 (99%)  | 1 (1%)   | 79          | 84  |
| 63  | b3    | 84/184 (46%)      | 83 (99%)   | 1 (1%)   | 67          | 77  |
| 64  | c3    | 84/98 (86%)       | 84 (100%)  | 0        | 100         | 100 |
| 65  | d3    | 98/110 (89%)      | 96 (98%)   | 2 (2%)   | 50          | 68  |
| 66  | e3    | 114/121 (94%)     | 113 (99%)  | 1 (1%)   | 75          | 82  |
| 67  | f3    | 88/89 (99%)       | 87 (99%)   | 1 (1%)   | 70          | 79  |
| 68  | g3    | 98/100 (98%)      | 94 (96%)   | 4 (4%)   | 26          | 50  |
| 69  | h3    | 109/110 (99%)     | 109 (100%) | 0        | 100         | 100 |
| 70  | i3    | 86/89 (97%)       | 85 (99%)   | 1 (1%)   | 67          | 77  |
| 71  | j3    | 73/80 (91%)       | 73 (100%)  | 0        | 100         | 100 |
| 72  | k3    | 64/65 (98%)       | 63 (98%)   | 1 (2%)   | 58          | 73  |
| 73  | l3    | 47/48 (98%)       | 47 (100%)  | 0        | 100         | 100 |
| 74  | m3    | 48/90 (53%)       | 48 (100%)  | 0        | 100         | 100 |
| 75  | n3    | 24/24 (100%)      | 24 (100%)  | 0        | 100         | 100 |
| 76  | o3    | 92/94 (98%)       | 91 (99%)   | 1 (1%)   | 70          | 79  |
| 77  | p3    | 74/75 (99%)       | 73 (99%)   | 1 (1%)   | 62          | 75  |
| 78  | r3    | 108/121 (89%)     | 106 (98%)  | 2 (2%)   | 52          | 69  |
| 80  | t3    | 164/258 (64%)     | 159 (97%)  | 5 (3%)   | 36          | 58  |
| 81  | u3    | 126/137 (92%)     | 126 (100%) | 0        | 100         | 100 |
| 84  | w3    | 195/196 (100%)    | 191 (98%)  | 4 (2%)   | 48          | 66  |
| All | All   | 10147/11409 (89%) | 9998 (98%) | 149 (2%) | 60          | 74  |

5 of 149 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 54  | R3    | 173 | ARG  |
| 80  | t3    | 197 | SER  |
| 58  | V3    | 48  | ARG  |
| 68  | g3    | 14  | ASN  |
| 29  | Z2    | 75  | ILE  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 96 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 43  | F3    | 118 | ASN  |
| 52  | P3    | 25  | HIS  |
| 43  | F3    | 205 | ASN  |
| 46  | I3    | 73  | ASN  |
| 54  | R3    | 36  | ASN  |

### 5.3.3 RNA ⓘ

| Mol | Chain | Analysed        | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 1   | 51    | 3594/3635 (98%) | 1186 (32%)        | 44 (1%)         |
| 2   | 71    | 119/120 (99%)   | 40 (33%)          | 0               |
| 3   | 81    | 149/156 (95%)   | 46 (30%)          | 1 (0%)          |
| 4   | A2    | 1717/1869 (91%) | 578 (33%)         | 23 (1%)         |
| 79  | q3    | 70/74 (94%)     | 35 (50%)          | 0               |
| 82  | v3    | 21/22 (95%)     | 14 (66%)          | 0               |
| 83  | 33    | 74/75 (98%)     | 17 (22%)          | 1 (1%)          |
| All | All   | 5744/5951 (96%) | 1916 (33%)        | 69 (1%)         |

5 of 1916 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 51    | 3   | C    |
| 1   | 51    | 4   | G    |
| 1   | 51    | 5   | A    |
| 1   | 51    | 7   | C    |
| 1   | 51    | 8   | U    |

5 of 69 RNA pucker outliers are listed below:

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 4   | A2    | 751  | G    |
| 4   | A2    | 870  | A    |
| 4   | A2    | 1489 | A    |
| 1   | 51    | 2266 | C    |
| 1   | 51    | 2259 | G    |

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 308 ligands modelled in this entry, 308 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 1   | 51    | 32               |
| 4   | A2    | 12               |
| 79  | q3    | 3                |
| 44  | G3    | 1                |
| 43  | F3    | 1                |

The worst 5 of 49 chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1     | 51    | 2113:G    | O3'    | 2258:C    | P      | 42.01        |
| 1     | 51    | 1252:C    | O3'    | 1271:G    | P      | 37.73        |
| 1     | 51    | 990:C     | O3'    | 1064:G    | P      | 18.57        |
| 1     | 51    | 1696:C    | O3'    | 1720:C    | P      | 18.37        |
| 1     | 51    | 1109:C    | O3'    | 1161:G    | P      | 18.08        |



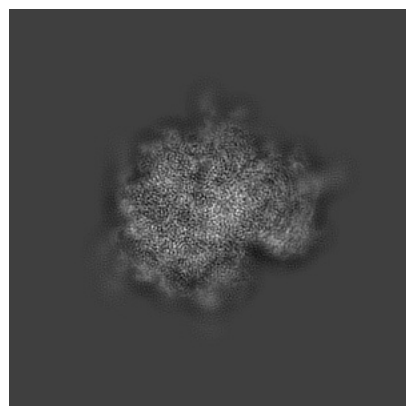
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0194. These allow visual inspection of the internal detail of the map and identification of artifacts.

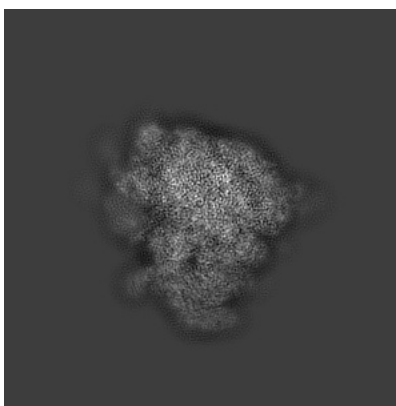
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

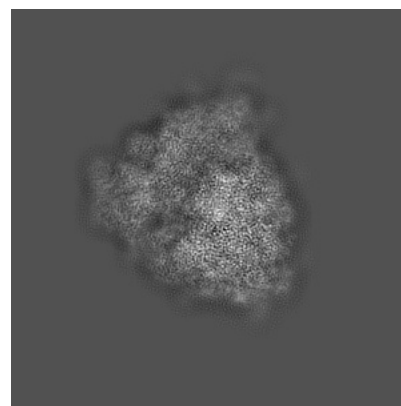
#### 6.1.1 Primary map



X

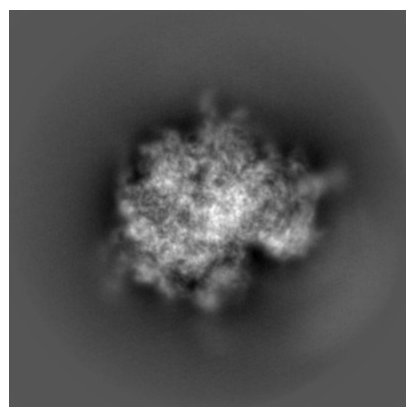


Y

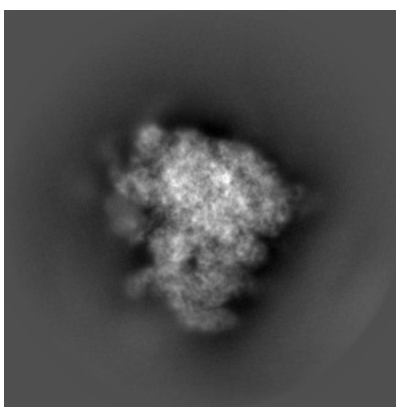


Z

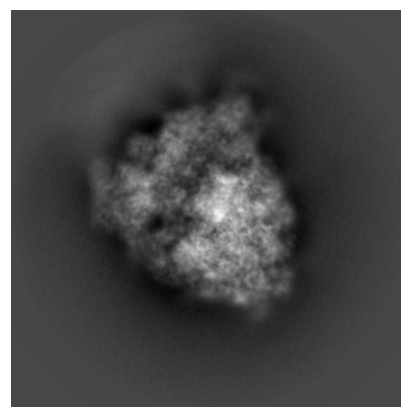
#### 6.1.2 Raw map



X



Y

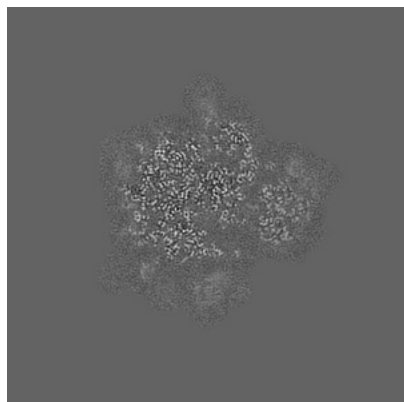


Z

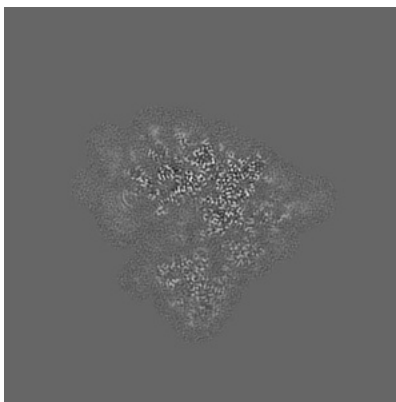
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

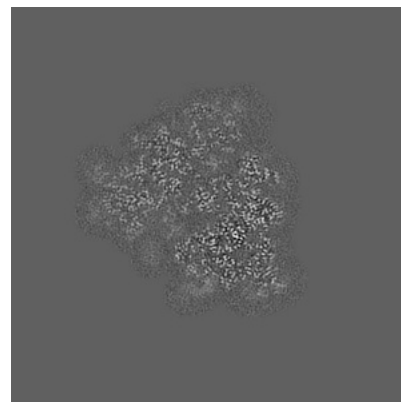
### 6.2.1 Primary map



X Index: 178

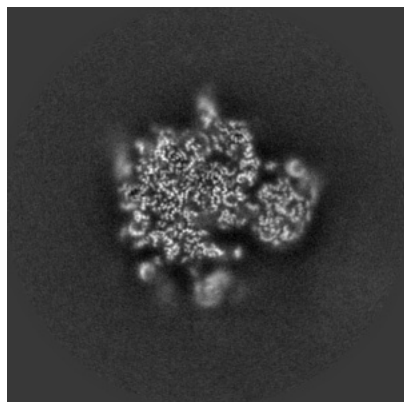


Y Index: 178

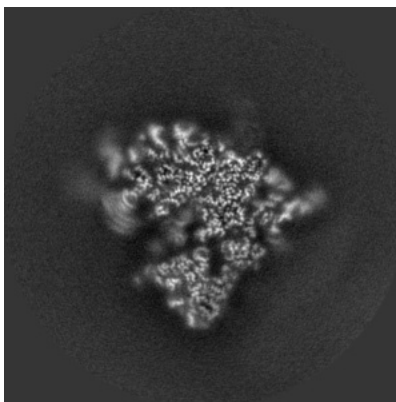


Z Index: 178

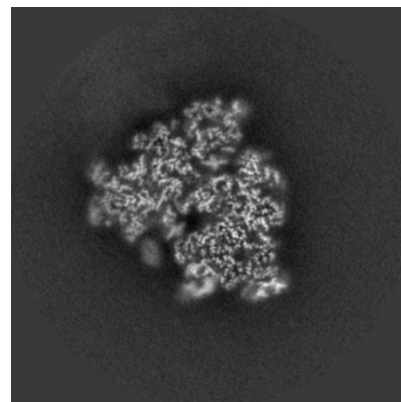
### 6.2.2 Raw map



X Index: 178



Y Index: 178

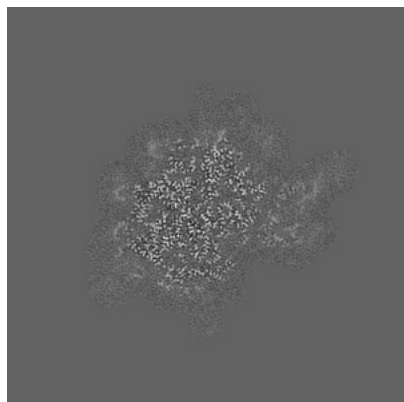


Z Index: 178

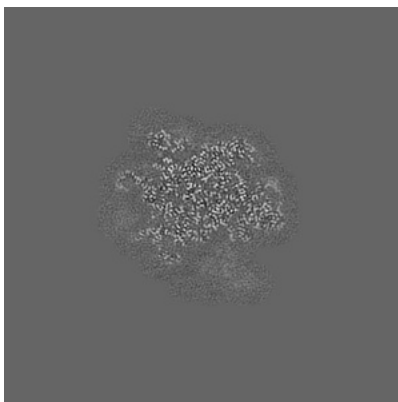
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

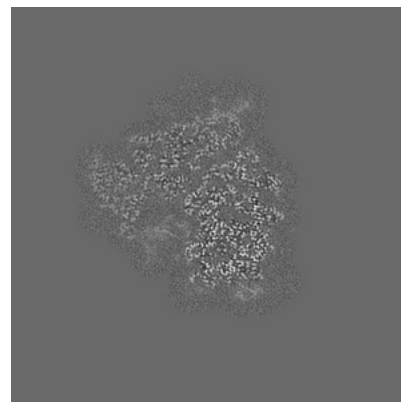
### 6.3.1 Primary map



X Index: 204

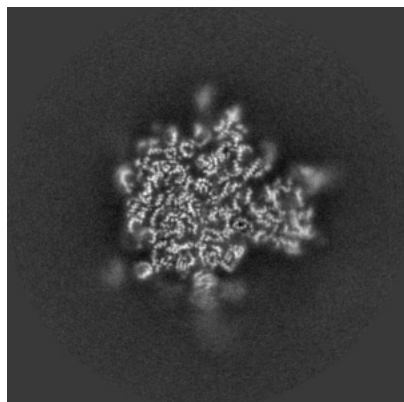


Y Index: 143

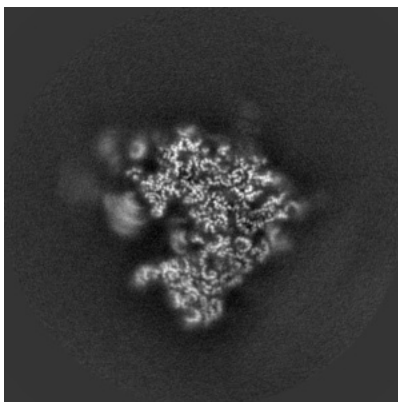


Z Index: 186

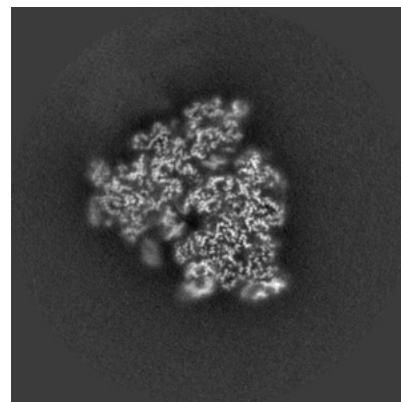
### 6.3.2 Raw map



X Index: 188



Y Index: 185

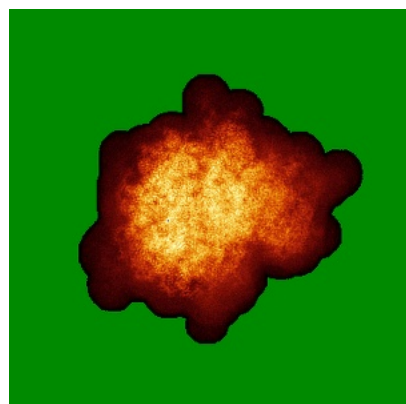


Z Index: 179

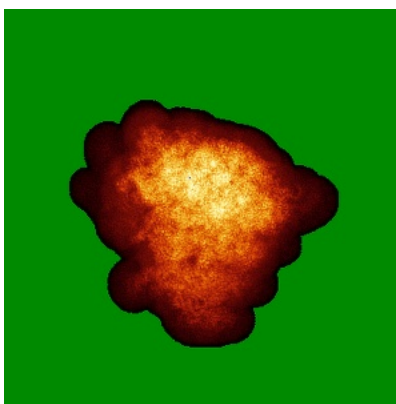
The images above show the largest variance slices of the map in three orthogonal directions.

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

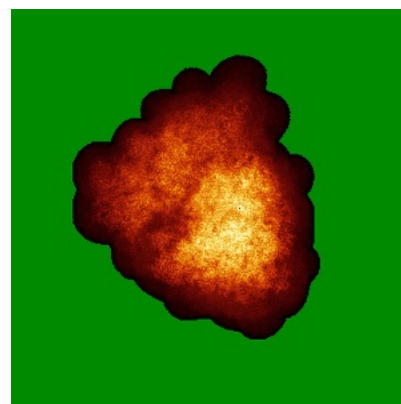
### 6.4.1 Primary map



X

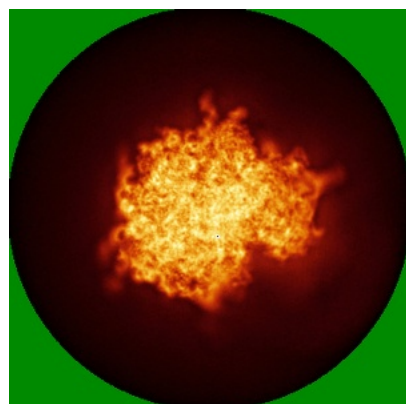


Y

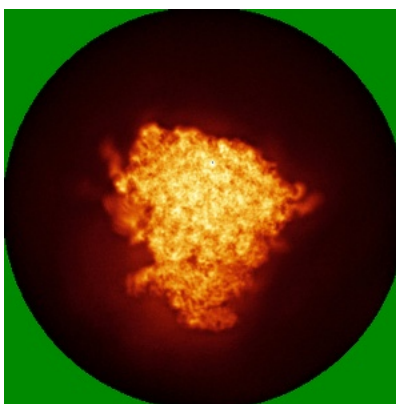


Z

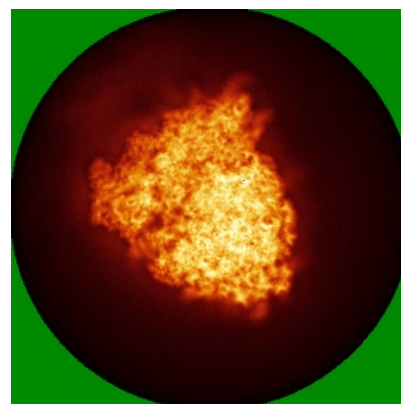
### 6.4.2 Raw map



X



Y

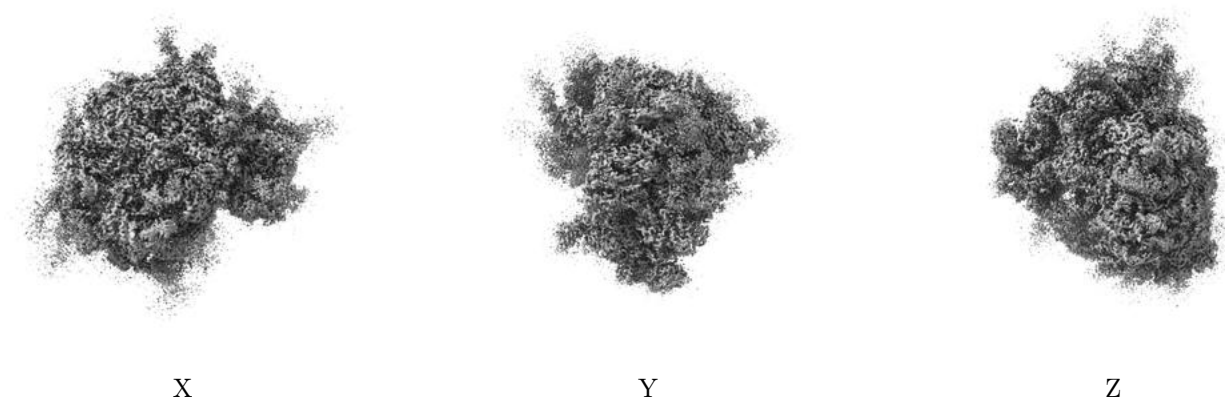


Z

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 0.12. 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.

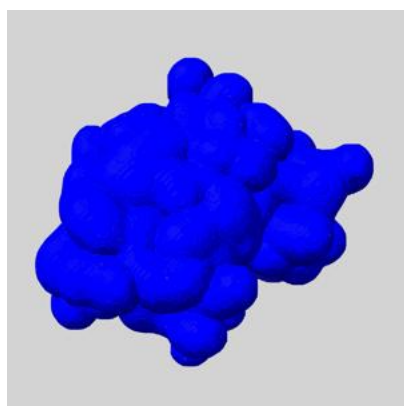
## 6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

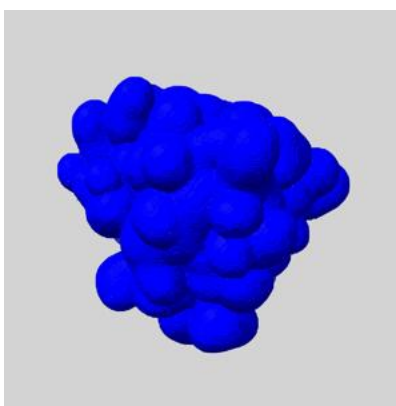
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

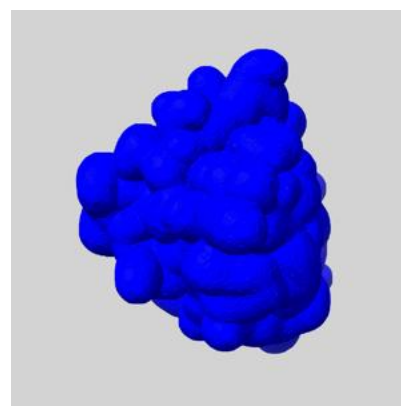
### 6.6.1 emd\_0194\_msk\_1.map [i](#)



X



Y

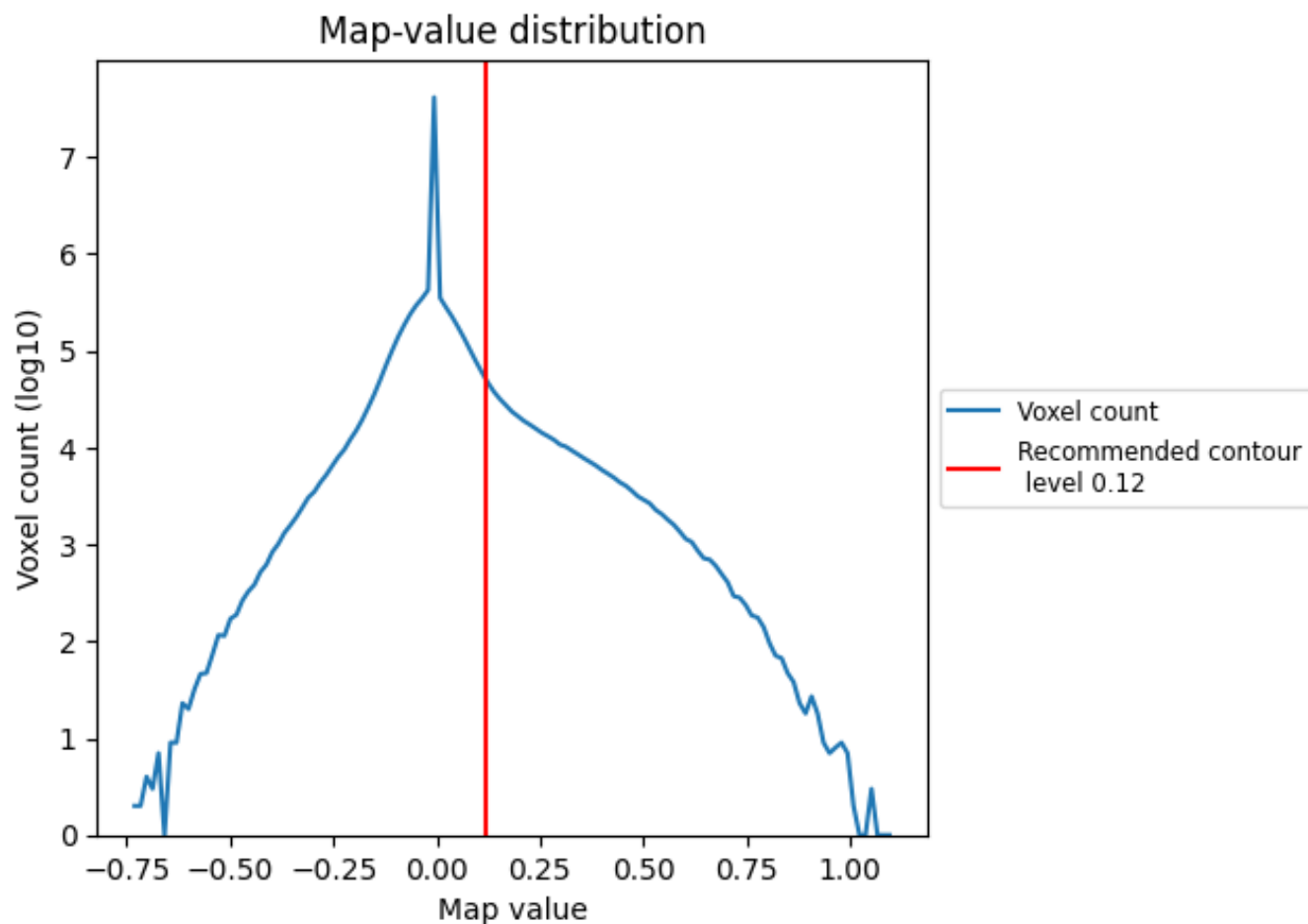


Z

## 7 Map analysis [i](#)

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

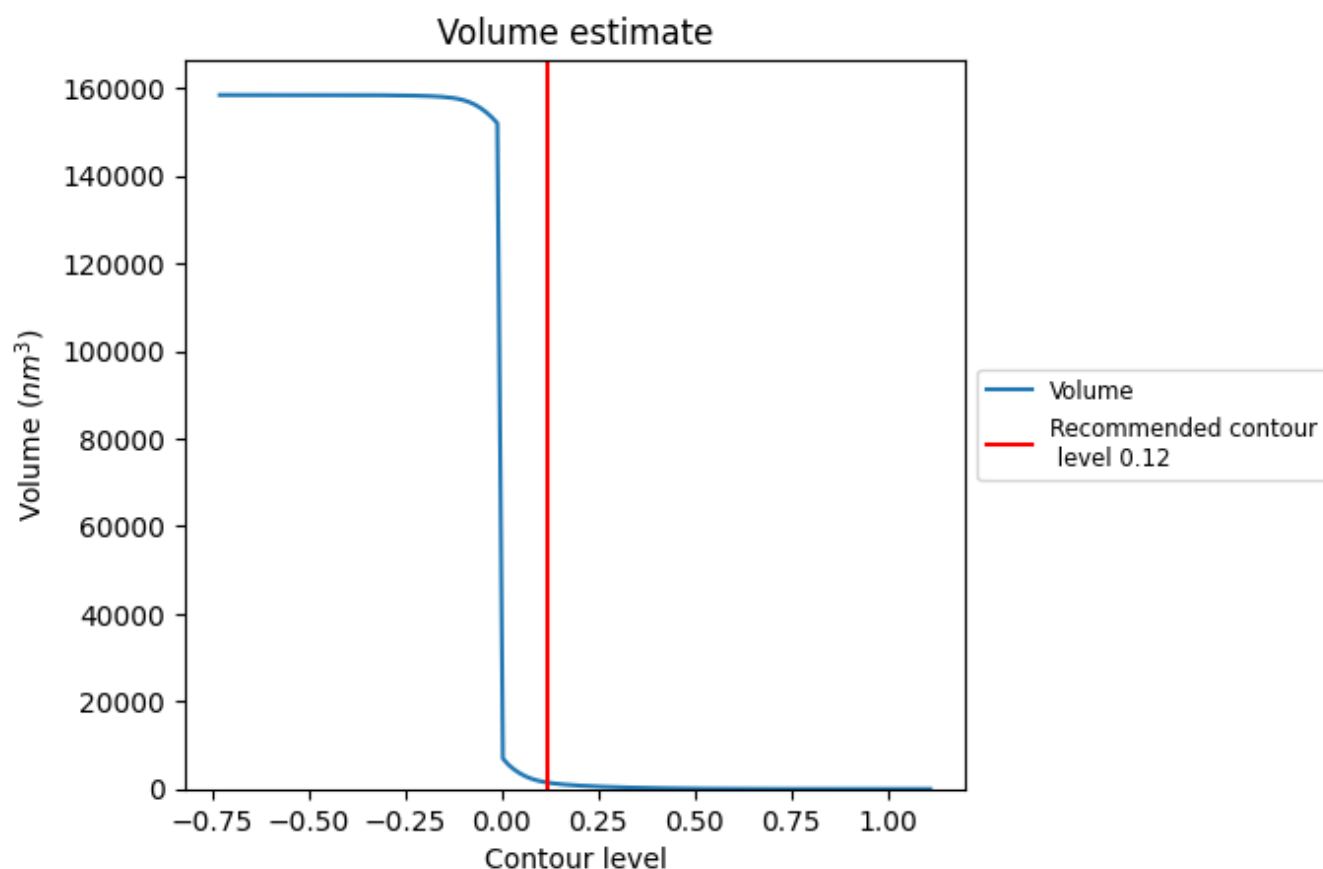
### 7.1 Map-value distribution [i](#)



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](#)

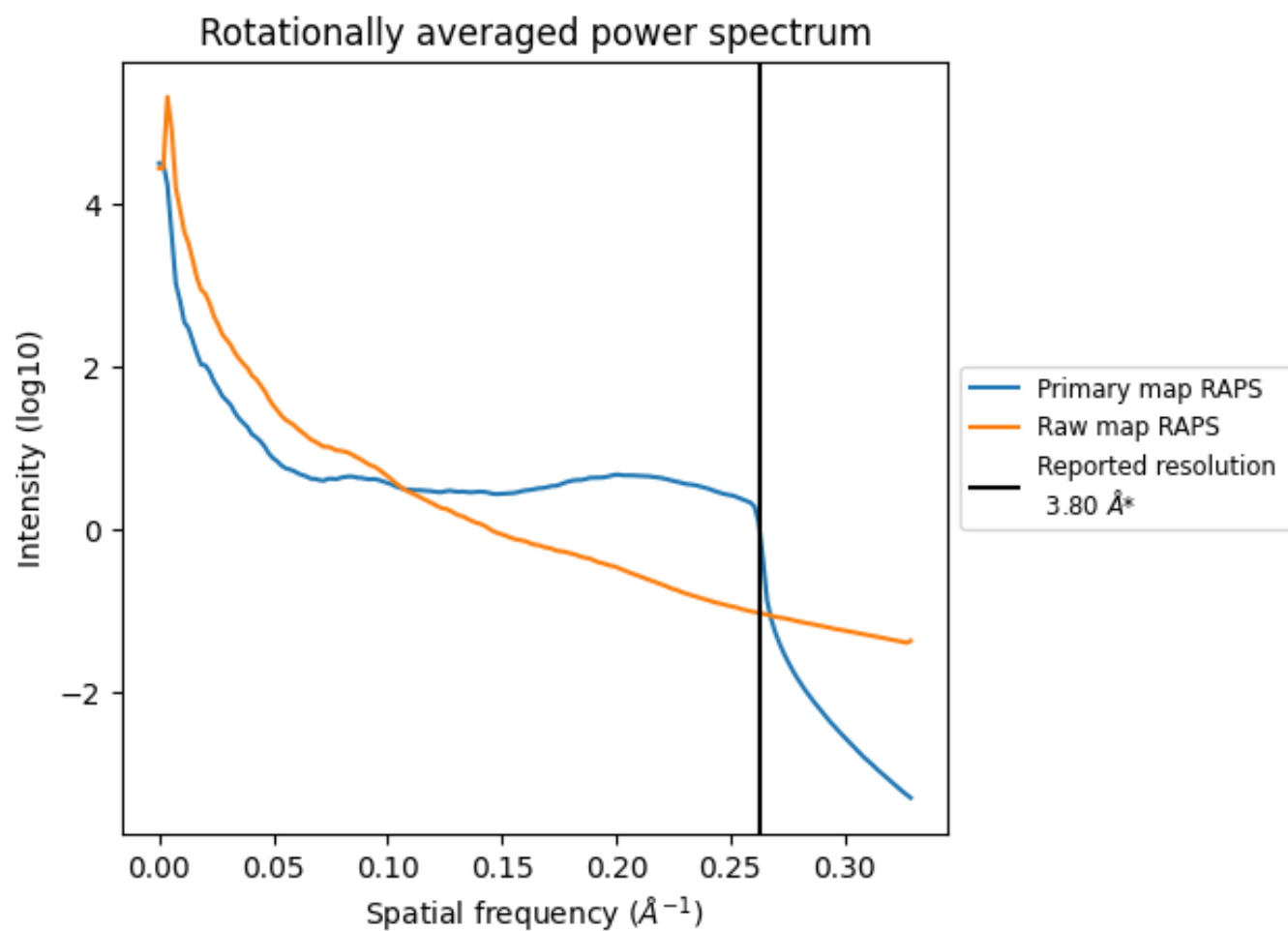


The volume at the recommended contour level is 1440 nm<sup>3</sup>; this corresponds to an approximate mass of 1301 kDa.

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 ⓘ

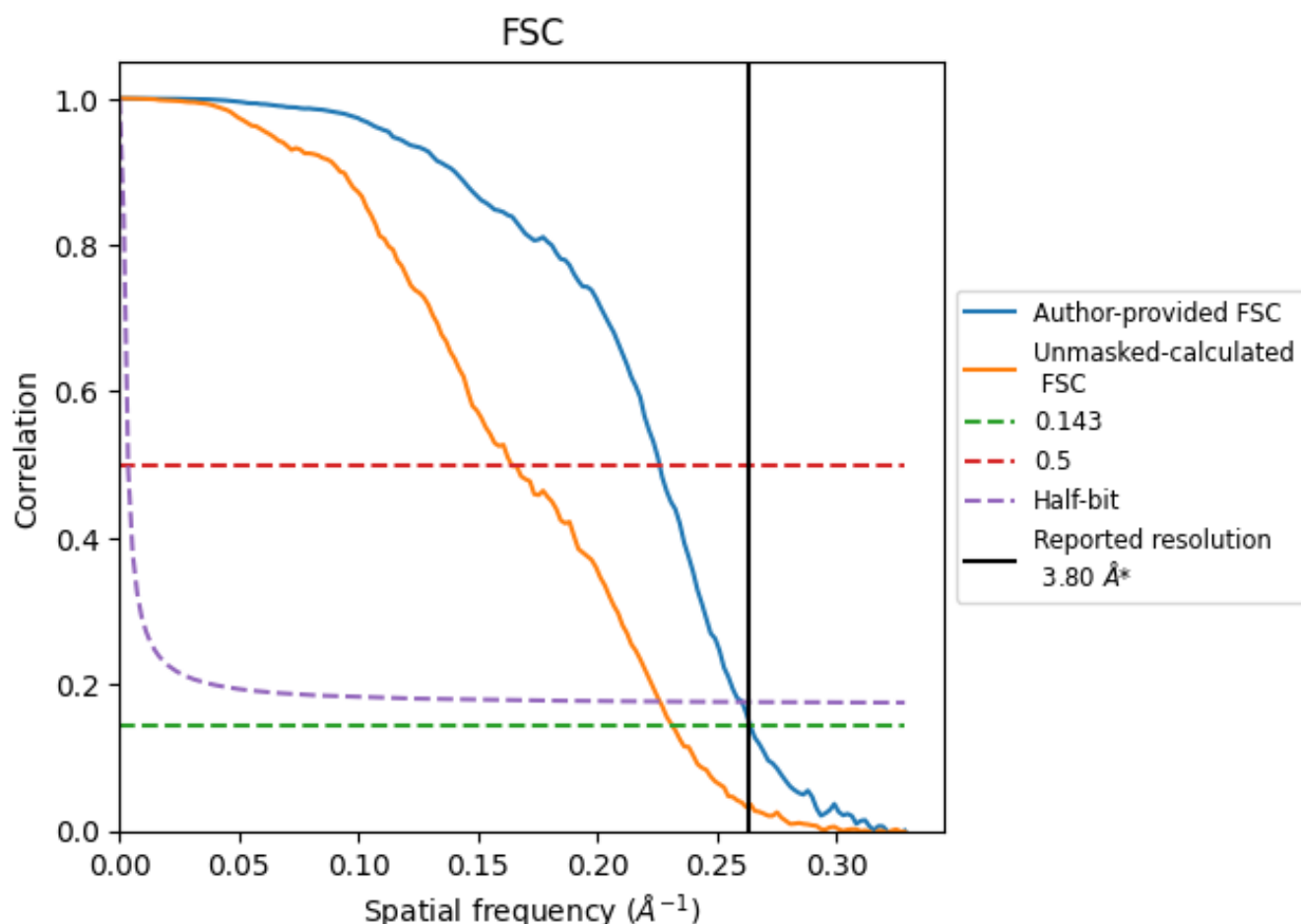


\*Reported resolution corresponds to spatial frequency of 0.263 Å<sup>-1</sup>

## 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  $0.263 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [i](#)

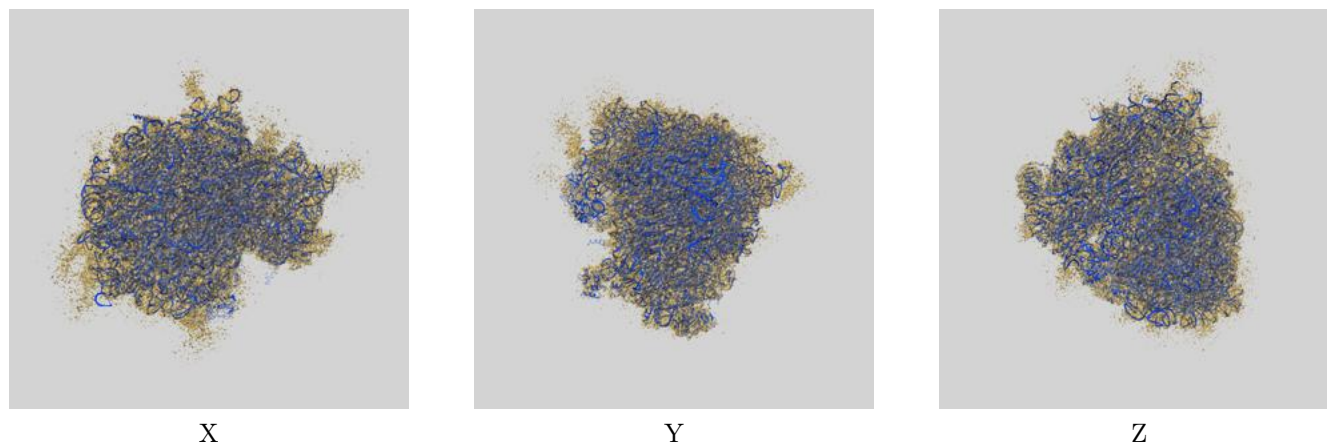
| Resolution estimate (Å)   | Estimation criterion (FSC cut-off) |      |          |
|---------------------------|------------------------------------|------|----------|
|                           | 0.143                              | 0.5  | Half-bit |
| Reported by author        | 3.80                               | -    | -        |
| Author-provided FSC curve | 3.79                               | 4.42 | 3.84     |
| Unmasked-calculated*      | 4.32                               | 6.09 | 4.42     |

\*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 4.32 differs from the reported value 3.8 by more than 10 %

## 9 Map-model fit [i](#)

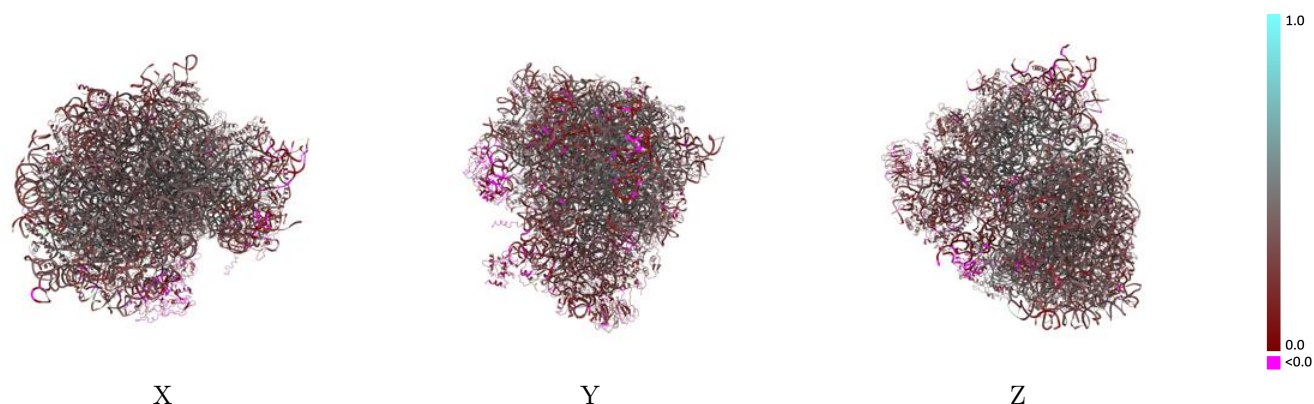
This section contains information regarding the fit between EMDB map EMD-0194 and PDB model 6HCJ. Per-residue inclusion information can be found in [section 3](#) on [page 22](#).

### 9.1 Map-model overlay [i](#)



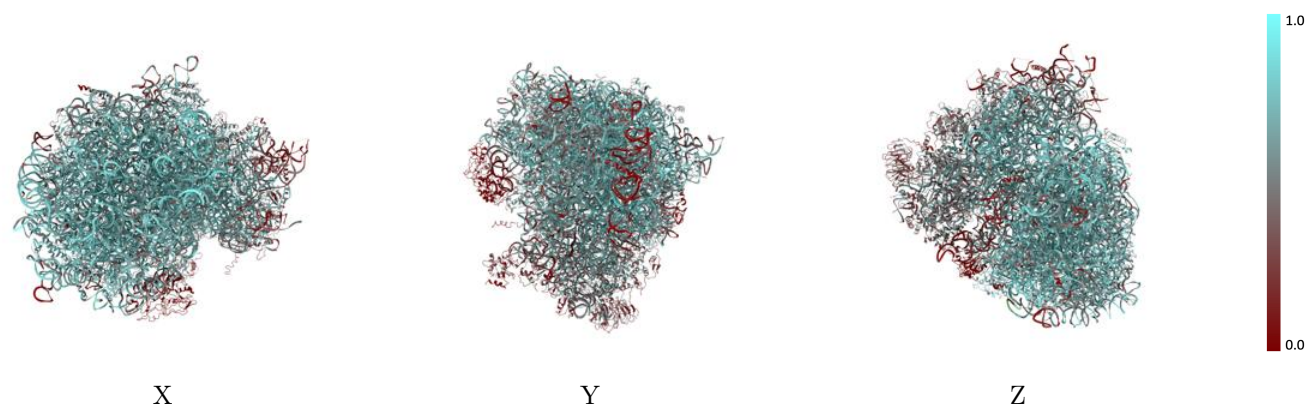
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



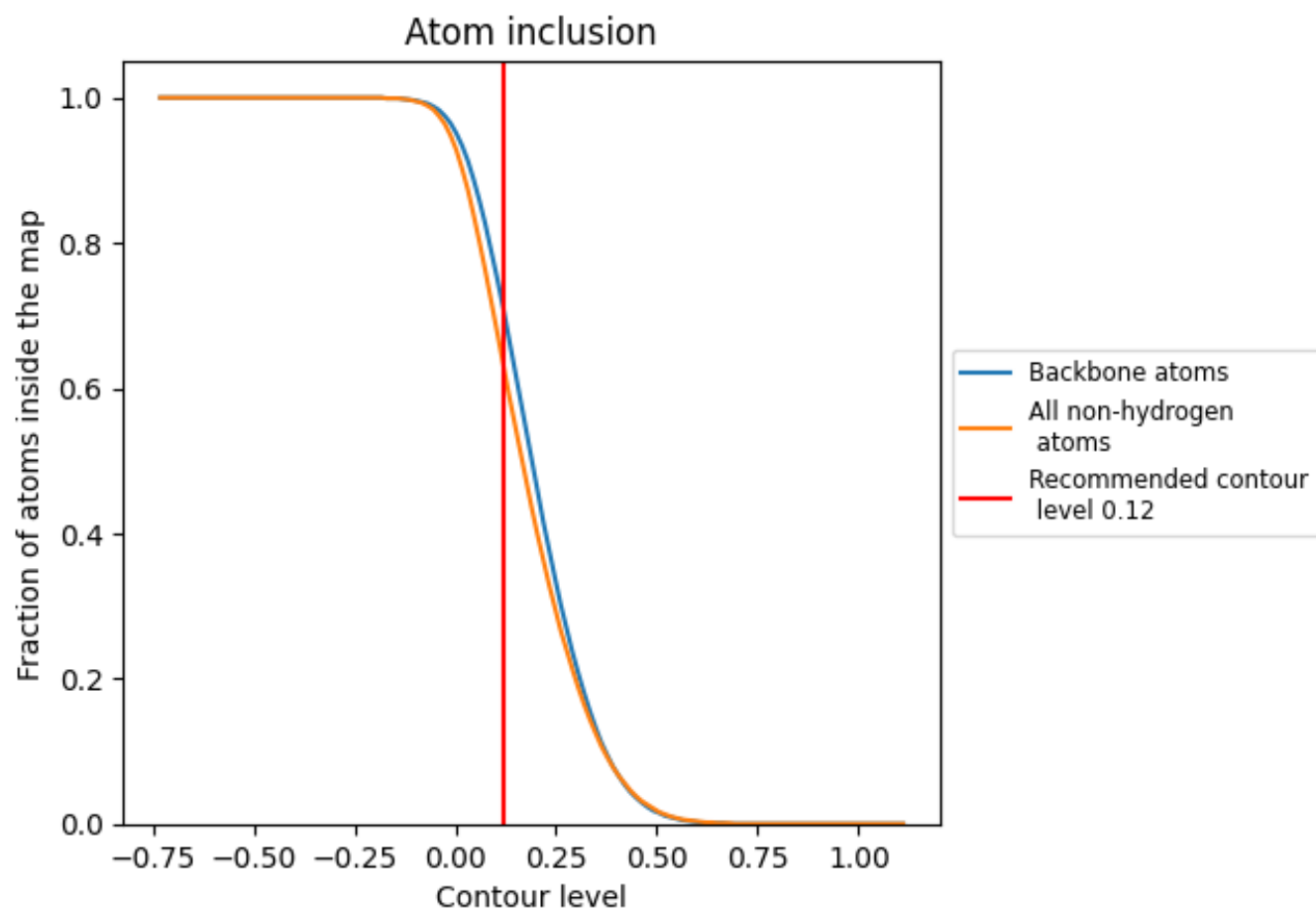
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.12).







































































## 9.4 Atom inclusion ⓘ



At the recommended contour level, 71% of all backbone atoms, 63% 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 (0.12) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion   | Q-score  |
|-------|--|--|
| All   |  0.6300   |  0.3350   |
| 1     |  0.0820   |  0.2160   |
| 33    |  0.4770   |  0.2550   |
| 51    |  0.7360   |  0.3730   |
| 71    |  0.8200   |  0.4150   |
| 81    |  0.7360   |  0.3320   |
| A2    |  0.6230   |  0.3160   |
| A3    |  0.6980   |  0.4090   |
| B2    |  0.4900   |  0.2870   |
| B3    |  0.6630   |  0.3370   |
| C2    |  0.5110   |  0.3100   |
| C3    |  0.6980   |  0.3660   |
| D2    |  0.5450   |  0.3290   |
| D3    |  0.6820   |  0.3870   |
| E2    |  0.3730  |  0.2380  |
| E3    |  0.6310 |  0.3010 |
| F2    |  0.5010 |  0.3240 |
| F3    |  0.7670 |  0.4470 |
| G2    |  0.4110 |  0.2270 |
| G3    |  0.4800 |  0.2190 |
| H2    |  0.4090 |  0.2480 |
| H3    |  0.6290 |  0.3250 |
| I2    |  0.4910 |  0.3540 |
| I3    |  0.7050 |  0.4330 |
| J2    |  0.5000 |  0.3240 |
| J3    |  0.6330 |  0.3810 |
| K2    |  0.4100 |  0.2300 |
| L2    |  0.3630 |  0.1830 |
| L3    |  0.6340 |  0.3270 |
| M2    |  0.6110 |  0.4170 |
| M3    |  0.6510 |  0.3150 |
| N2    |  0.1600 |  0.1160 |
| N3    |  0.7030 |  0.3700 |
| O2    |  0.6060 |  0.4180 |
| O3    |  0.6870 |  0.3580 |



*Continued on next page...*



















*Continued from previous page...*

| Chain | Atom inclusion   | Q-score  |
|-------|--|--|
| P2    |  0.5280   |  0.3240   |
| P3    |  0.6790   |  0.3390   |
| Q2    |  0.5020   |  0.2860   |
| Q3    |  0.7390   |  0.4420   |
| R2    |  0.3970   |  0.2220   |
| R3    |  0.5930   |  0.3340   |
| S2    |  0.4040   |  0.2650   |
| S3    |  0.7250   |  0.4160   |
| T2    |  0.4640   |  0.2530   |
| T3    |  0.7080   |  0.4530   |
| U2    |  0.4420   |  0.2300   |
| U3    |  0.5450   |  0.2730   |
| V2    |  0.3240   |  0.2050   |
| V3    |  0.7030   |  0.4350   |
| W2    |  0.5240   |  0.3320   |
| X2    |  0.6500   |  0.4080   |
| X3    |  0.5990   |  0.3030   |
| Y2    |  0.6010  |  0.3900  |
| Y3    |  0.6160 |  0.2830 |
| Z2    |  0.4020 |  0.2320 |
| Z3    |  0.6240 |  0.3430 |
| a2    |  0.3720 |  0.2350 |
| a3    |  0.7430 |  0.4280 |
| b2    |  0.5700 |  0.3520 |
| b3    |  0.6220 |  0.3920 |
| c2    |  0.4980 |  0.3560 |
| c3    |  0.6340 |  0.4010 |
| d2    |  0.3400 |  0.2220 |
| d3    |  0.6650 |  0.3570 |
| e2    |  0.5070 |  0.2840 |
| e3    |  0.7190 |  0.3850 |
| f2    |  0.3610 |  0.2600 |
| f3    |  0.7090 |  0.3550 |
| g2    |  0.2490 |  0.1930 |
| g3    |  0.6490 |  0.3710 |
| h2    |  0.2910 |  0.1950 |
| h3    |  0.5760 |  0.2790 |
| i3    |  0.5840 |  0.3070 |
| j3    |  0.7280 |  0.3960 |
| k3    |  0.5530 |  0.3140 |
| l3    |  0.7000 |  0.3790 |
| m3    |  0.6660 |  0.3670 |

*Continued on next page...*



*Continued from previous page...*

| Chain | Atom inclusion   | Q-score  |
|-------|--|--|
| n3    |  0.6560 |  0.3890 |
| o3    |  0.6680 |  0.4180 |
| p3    |  0.6810 |  0.4240 |
| q3    |  0.2010 |  0.2000 |
| r3    |  0.6950 |  0.3490 |
| t3    |  0.0270 |  0.0290 |
| u3    |  0.0250 |  0.0320 |
| v3    |  0.3260 |  0.2070 |
| w3    |  0.0220 |  0.0340 |