



## wwPDB EM Validation Summary Report ⓘ

Dec 12, 2022 – 06:06 am GMT

PDB ID : 6XU8  
EMDB ID : EMD-10624  
Title : Drosophila melanogaster Ovary 80S ribosome  
Authors : Hopes, T.; Agapiou, M.; Norris, K.; McCarthy, C.G.P.; OConnell, M.J.;  
Fontana, J.; Aspden, J.L.  
Deposited on : 2020-01-17  
Resolution : 3.00 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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

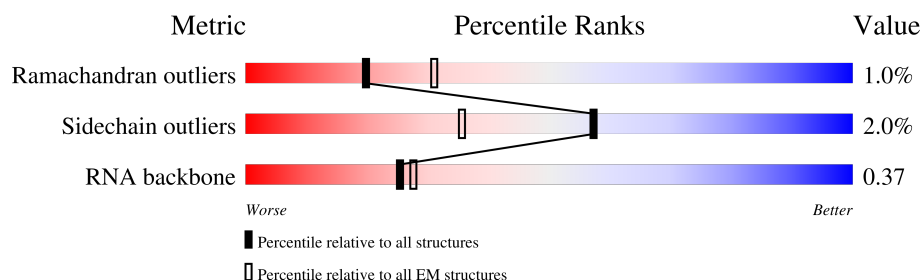
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.00 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.



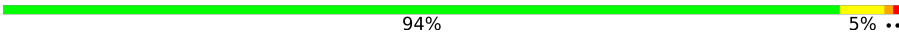
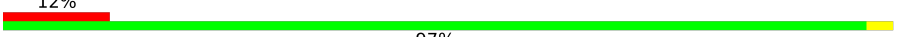

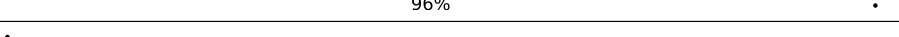


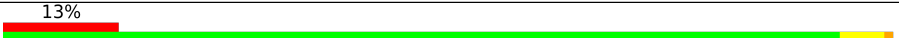
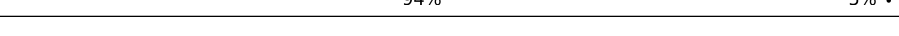
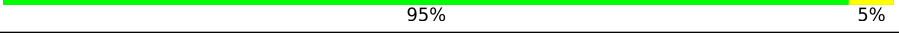
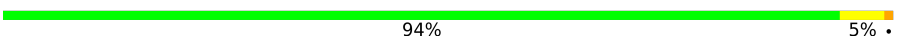

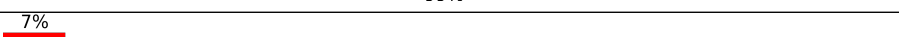

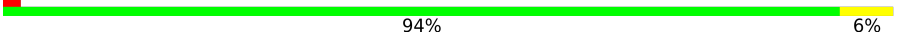



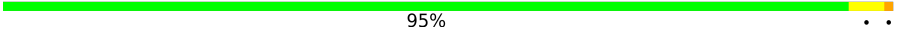
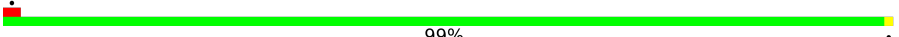

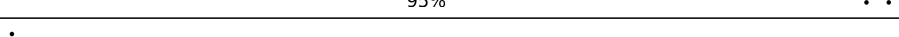



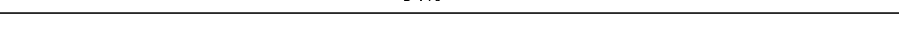
| Metric                | Whole archive<br>(#Entries) | EM structures<br>(#Entries) |
|-----------------------|-----------------------------|-----------------------------|
| Ramachandran outliers | 154571                      | 4023                        |
| Sidechain outliers    | 154315                      | 3826                        |
| RNA backbone          | 4643                        | 859                         |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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   | CO    | 205    |                  |
| 2   | CL    | 210    |                  |
| 3   | CV    | 134    |                  |
| 4   | CM    | 159    |                  |
| 5   | Ca    | 149    |                  |
| 6   | CN    | 203    |                  |
| 7   | CI    | 217    |                  |
| 8   | CD    | 290    |                  |

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| Mol | Chain | Length | Quality of chain  |
|-----|-------|--------|---|
| 9   | CQ    | 187    |  94% 5% ..    |
| 10  | CR    | 203    |  12% 97% .    |
| 11  | CA    | 253    |  96% .        |
| 12  | CS    | 173    |  85% 14% .    |
| 13  | CT    | 158    |  92% 7% .     |
| 14  | CP    | 185    |  13% 94% 5% . |
| 15  | CX    | 120    |  95% 5%       |
| 16  | CY    | 131    |  94% 5% .     |
| 17  | CZ    | 134    |  99% .        |
| 18  | Cr    | 134    |  7% 82% 17% . |
| 19  | Ch    | 123    |  94% 6%       |
| 20  | Cb    | 75     |  88% 11% .    |
| 21  | CB    | 414    |  91% 8%       |
| 22  | CF    | 226    |  95% ..       |
| 23  | Cc    | 100    |  99% .       |
| 24  | Ce    | 132    |  95% ..     |
| 25  | Cf    | 157    |  84% 15% .  |
| 26  | Ci    | 113    |  90% 10%    |
| 27  | Ck    | 70     |  94% ..     |
| 28  | Cl    | 50     |  98% .      |
| 29  | CC    | 392    |  91% 8% .   |
| 30  | Cm    | 52     |  92% 6% .   |
| 31  | Cn    | 25     |  96% .      |
| 32  | Cp    | 91     |  95% 5%     |
| 33  | Co    | 104    |  93% 7%     |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 34  | CJ    | 182    |                  |
| 35  | CH    | 190    |                  |
| 36  | CE    | 228    |                  |
| 37  | CG    | 241    |                  |
| 38  | A9    | 30     |                  |
| 39  | A7    | 120    |                  |
| 40  | A8    | 123    |                  |
| 41  | Ag    | 318    |                  |
| 42  | AU    | 102    |                  |
| 43  | AO    | 127    |                  |
| 44  | AX    | 143    |                  |
| 45  | AM    | 119    |                  |
| 46  | Ad    | 52     |                  |
| 47  | AN    | 150    |                  |
| 48  | AL    | 155    |                  |
| 49  | AR    | 120    |                  |
| 50  | AP    | 124    |                  |
| 51  | AB    | 220    |                  |
| 52  | AA    | 218    |                  |
| 53  | AV    | 82     |                  |
| 54  | AY    | 126    |                  |
| 55  | AZ    | 74     |                  |
| 56  | Aa    | 107    |                  |
| 57  | Ab    | 84     |                  |
| 58  | AD    | 227    |                  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 59  | Ae    | 58     |                  |
| 60  | Af    | 80     |                  |
| 61  | AJ    | 181    |                  |
| 62  | AE    | 261    |                  |
| 63  | AC    | 227    |                  |
| 64  | AG    | 231    |                  |
| 65  | AH    | 194    |                  |
| 66  | AI    | 207    |                  |
| 67  | AQ    | 148    |                  |
| 68  | Cz    | 217    |                  |
| 69  | A5    | 3703   |                  |
| 70  | B2    | 1936   |                  |
| 71  | AW    | 129    |                  |
| 72  | AT    | 126    |                  |
| 73  | AK    | 90     |                  |
| 74  | AF    | 189    |                  |
| 75  | Ac    | 62     |                  |
| 76  | CU    | 99     |                  |
| 77  | Cj    | 87     |                  |
| 78  | CW    | 60     |                  |
| 79  | Cg    | 103    |                  |
| 80  | Cd    | 107    |                  |
| 81  | AS    | 136    |                  |

## 2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 216955 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 60S ribosomal protein L13a.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 1   | CO    | 205      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1668  | 1063 | 331 | 268 | 6 |         |       |

- Molecule 2 is a protein called 60S ribosomal protein L13.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 2   | CL    | 210      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1695  | 1066 | 342 | 284 | 3 |         |       |

- Molecule 3 is a protein called 60S ribosomal protein L23.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 3   | CV    | 134      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 998   | 629 | 190 | 173 | 6 |         |       |

- Molecule 4 is a protein called 60S ribosomal protein L14.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 4   | CM    | 159      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1302  | 826 | 256 | 218 | 2 |         |       |

- Molecule 5 is a protein called 60S ribosomal protein L27a.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 5   | Ca    | 149      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1204  | 769 | 242 | 189 | 4 |         |       |

- Molecule 6 is a protein called 60S ribosomal protein L15.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 6   | CN    | 203      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1710  | 1072 | 362 | 271 | 5 |         |       |

- Molecule 7 is a protein called 60S ribosomal protein L10.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 7   | CI    | 217      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 1785  | 1125 | 343 | 304 | 13 |         |       |

- Molecule 8 is a protein called 60S ribosomal protein L5.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 8   | CD    | 290      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 2334  | 1471 | 434 | 423 | 6 |         |       |

- Molecule 9 is a protein called 60S ribosomal protein L18.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 9   | CQ    | 187      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1518  | 957 | 306 | 251 | 4 |         |       |

- Molecule 10 is a protein called 60S ribosomal protein L19.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 10  | CR    | 203      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1683  | 1047 | 350 | 277 | 9 |         |       |

- Molecule 11 is a protein called 60S ribosomal protein L8.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 11  | CA    | 253      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1935  | 1206 | 395 | 326 | 8 |         |       |

- Molecule 12 is a protein called 60S ribosomal protein L18a.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 12  | CS    | 173      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1454  | 935 | 275 | 240 | 4 |         |       |

- Molecule 13 is a protein called RE62581p.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 13  | CT    | 158      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1297  | 829 | 253 | 212 | 3 |         |       |

- Molecule 14 is a protein called 60S ribosomal protein L17.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 14  | CP    | 185      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1505  | 928 | 305 | 263 | 9 |         |       |

- Molecule 15 is a protein called IP17216p.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 15  | CX    | 120      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 984   | 625 | 192 | 165 | 2 |         |       |

- Molecule 16 is a protein called GEO07453p1.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 16  | CY    | 131      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1078  | 676 | 224 | 176 | 2 |         |       |

- Molecule 17 is a protein called 60S ribosomal protein L27.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 17  | CZ    | 134      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1115  | 723 | 209 | 180 | 3 |         |       |

- Molecule 18 is a protein called 60S ribosomal protein L28.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 18  | Cr    | 134      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 1051  | 670 | 205 | 176 |         |       |

- Molecule 19 is a protein called FI02809p.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 19  | Ch    | 123      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1015  | 646 | 202 | 164 | 3 |         |       |

- Molecule 20 is a protein called 60S ribosomal protein L29.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 20  | Cb    | 75       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 619   | 378 | 133 | 107 | 1 |         |       |

- Molecule 21 is a protein called 60S ribosomal protein L3.



| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 21  | CB    | 414      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 3287  | 2083 | 621 | 565 | 18 |         |       |

- Molecule 22 is a protein called 60S ribosomal protein L7.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 22  | CF    | 226      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1895  | 1216 | 368 | 308 | 3 |         |       |

- Molecule 23 is a protein called RE25263p.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 23  | Cc    | 100      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 770   | 486 | 132 | 147 | 5 |         |       |

- Molecule 24 is a protein called 60S ribosomal protein L32.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 24  | Ce    | 132      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1110  | 698 | 230 | 177 | 5 |         |       |

- Molecule 25 is a protein called GEO07455p1.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 25  | Cf    | 157      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1244  | 781 | 255 | 203 | 5 |         |       |

- Molecule 26 is a protein called 60S ribosomal protein L36.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 26  | Ci    | 113      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 934   | 585 | 193 | 153 | 3 |         |       |

- Molecule 27 is a protein called 60S ribosomal protein L38.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 27  | Ck    | 70       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 576   | 366 | 108 | 100 | 2 |         |       |

- Molecule 28 is a protein called 60S ribosomal protein L39.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 28  | Cl    | 50       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 437   | 276 | 98 | 63 |         |       |

- Molecule 29 is a protein called 60S ribosomal protein L4.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 29  | CC    | 392      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 3109  | 1959 | 622 | 522 | 6 |         |       |

- Molecule 30 is a protein called Ubiquitin-60S ribosomal protein L40.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 30  | Cm    | 52       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 429   | 267 | 89 | 67 | 6 |         |       |

- Molecule 31 is a protein called 60S ribosomal protein L41.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 31  | Cn    | 25       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 236   | 143 | 63 | 27 | 3 |         |       |

- Molecule 32 is a protein called 60S ribosomal protein L37a.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 32  | Cp    | 91       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 710   | 441 | 140 | 122 | 7 |         |       |

- Molecule 33 is a protein called TA01007p.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 33  | Co    | 104      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 874   | 548 | 180 | 138 | 8 |         |       |

- Molecule 34 is a protein called 60S ribosomal protein L11.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 34  | CJ    | 182      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1468  | 926 | 278 | 258 | 6 |         |       |

- Molecule 35 is a protein called 60S ribosomal protein L9.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 35  | CH    | 190      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1499  | 947 | 265 | 278 | 9 |         |       |

- Molecule 36 is a protein called Ribosomal protein L6, isoform A.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 36  | CE    | 228      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1845  | 1185 | 351 | 305 | 4 |         |       |

- Molecule 37 is a protein called 60S ribosomal protein L7a.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 37  | CG    | 241      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1936  | 1237 | 368 | 327 | 4 |         |       |

- Molecule 38 is a RNA chain called 2S ribosomal RNA.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 38  | A9    | 30       | Total | C   | N   | O   | P  | 0       | 0     |
|     |       |          | 639   | 286 | 111 | 213 | 29 |         |       |

- Molecule 39 is a RNA chain called 5S ribosomal RNA.

| Mol | Chain | Residues | Atoms |      |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 39  | A7    | 120      | Total | C    | N   | O   | P   | 0       | 0     |
|     |       |          | 2554  | 1141 | 456 | 838 | 119 |         |       |

- Molecule 40 is a RNA chain called 5.8S ribosomal RNA.

| Mol | Chain | Residues | Atoms |      |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 40  | A8    | 123      | Total | C    | N   | O   | P   | 0       | 0     |
|     |       |          | 2621  | 1173 | 474 | 852 | 122 |         |       |

- Molecule 41 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 41  | Ag    | 318      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2511  | 1577 | 444 | 480 | 10 |         |       |

- Molecule 42 is a protein called 40S ribosomal protein S20.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 42  | AU    | 102      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 815   | 505 | 161 | 145 | 4 |         |       |

- Molecule 43 is a protein called 40S ribosomal protein S14a.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 43  | AO    | 127      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 953   | 587 | 185 | 177 | 4 |         |       |

- Molecule 44 is a protein called 40S ribosomal protein S23.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 44  | AX    | 143      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1131  | 712 | 226 | 191 | 2 |         |       |

- Molecule 45 is a protein called 40S ribosomal protein S12.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 45  | AM    | 119      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 924   | 582 | 165 | 171 | 6 |         |       |

- Molecule 46 is a protein called 40S ribosomal protein S29.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 46  | Ad    | 52       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 433   | 269 | 87 | 72 | 5 |         |       |

- Molecule 47 is a protein called 40S ribosomal protein S13.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 47  | AN    | 150      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1202  | 767 | 229 | 203 | 3 |         |       |

- Molecule 48 is a protein called 40S ribosomal protein S11.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 48  | AL    | 155      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1274  | 803 | 254 | 211 | 6 |         |       |

- Molecule 49 is a protein called 40S ribosomal protein S17.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 49  | AR    | 120      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 981   | 618 | 183 | 176 | 4 |         |       |

- Molecule 50 is a protein called GEO07301p1.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 50  | AP    | 124      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1016  | 652 | 189 | 169 | 6 |         |       |

- Molecule 51 is a protein called 40S ribosomal protein S3a.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 51  | AB    | 220      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1798  | 1138 | 328 | 324 | 8 |         |       |

- Molecule 52 is a protein called 40S ribosomal protein SA.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 52  | AA    | 218      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1737  | 1113 | 298 | 321 | 5 |         |       |

- Molecule 53 is a protein called 40S ribosomal protein S21.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 53  | AV    | 82       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 617   | 373 | 114 | 125 | 5 |         |       |

There are 13 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment  | Reference  |
|-------|---------|----------|--------|----------|------------|
| AV    | 2       | GLN      | GLU    | conflict | UNP O76927 |
| AV    | 8       | PHE      | ASN    | conflict | UNP O76927 |
| AV    | 25      | GLY      | HIS    | conflict | UNP O76927 |
| AV    | 32      | ILE      | VAL    | conflict | UNP O76927 |
| AV    | 34      | MET      | LEU    | conflict | UNP O76927 |
| AV    | 35      | ASN      | SER    | conflict | UNP O76927 |
| AV    | 36      | VAL      | ILE    | conflict | UNP O76927 |
| AV    | 58      | ALA      | GLU    | conflict | UNP O76927 |
| AV    | 68      | SER      | CYS    | conflict | UNP O76927 |
| AV    | 70      | LEU      | VAL    | conflict | UNP O76927 |
| AV    | 75      | ALA      | LYS    | conflict | UNP O76927 |
| AV    | 79      | VAL      | ILE    | conflict | UNP O76927 |

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| Chain | Residue | Modelled | Actual | Comment  | Reference  |
|-------|---------|----------|--------|----------|------------|
| AV    | 80      | SER      | THR    | conflict | UNP O76927 |

- Molecule 54 is a protein called 40S ribosomal protein S24.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 54  | AY    | 126      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1016  | 644 | 196 | 171 | 5 |         |       |

- Molecule 55 is a protein called 40S ribosomal protein S25.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 55  | AZ    | 74       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 608   | 390 | 112 | 106 |   |         |       |

- Molecule 56 is a protein called 40S ribosomal protein S26.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 56  | Aa    | 107      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 867   | 539 | 182 | 140 | 6 |         |       |

- Molecule 57 is a protein called 40S ribosomal protein S27.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 57  | Ab    | 84       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 653   | 412 | 123 | 110 | 8 |         |       |

- Molecule 58 is a protein called 40S ribosomal protein S3.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 58  | AD    | 227      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 1782  | 1127 | 319 | 326 | 10 |         |       |

- Molecule 59 is a protein called 40S ribosomal protein S30.

| Mol | Chain | Residues | Atoms |     |     |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 59  | Ae    | 58       | Total | C   | N   | O  | S | 0       | 0     |
|     |       |          | 469   | 289 | 105 | 75 |   |         |       |

- Molecule 60 is a protein called Ubiquitin-40S ribosomal protein S27a.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 60  | Af    | 80       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 659   | 417 | 128 | 109 | 5 |         |       |

- Molecule 61 is a protein called 40S ribosomal protein S9.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 61  | AJ    | 181      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1503  | 957 | 298 | 247 | 1 |         |       |

- Molecule 62 is a protein called 40S ribosomal protein S4.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 62  | AE    | 261      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 2054  | 1314 | 380 | 353 | 7 |         |       |

- Molecule 63 is a protein called 40S ribosomal protein S2.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 63  | AC    | 227      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1746  | 1126 | 302 | 311 | 7 |         |       |

- Molecule 64 is a protein called 40S ribosomal protein S6.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 64  | AG    | 231      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1866  | 1172 | 372 | 315 | 7 |         |       |

- Molecule 65 is a protein called 40S ribosomal protein S7.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 65  | AH    | 194      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1566  | 1006 | 278 | 281 | 1 |         |       |

- Molecule 66 is a protein called 40S ribosomal protein S8.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 66  | AI    | 207      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1665  | 1037 | 329 | 296 | 3 |         |       |

- Molecule 67 is a protein called 40S ribosomal protein S16.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 67  | AQ    | 148      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1183  | 753 | 223 | 204 | 3 |         |       |

- Molecule 68 is a protein called 60S ribosomal protein L10a-2.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 68  | Cz    | 217      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 1702  | 1084 | 303 | 305 | 10 |         |       |

- Molecule 69 is a RNA chain called 28S ribosomal RNA.

| Mol | Chain | Residues | Atoms |       |       |       |      | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|-------|------|---------|-------|
| 69  | A5    | 3703     | Total | C     | N     | O     | P    | 0       | 0     |
|     |       |          | 77093 | 34436 | 13555 | 25401 | 3701 |         |       |

- Molecule 70 is a RNA chain called 18S ribosomal RNA.

| Mol | Chain | Residues | Atoms |       |      |       |      | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|-------|
| 70  | B2    | 1936     | Total | C     | N    | O     | P    | 0       | 0     |
|     |       |          | 39355 | 17526 | 6780 | 13114 | 1935 |         |       |

- Molecule 71 is a protein called 40S ribosomal protein S15Aa.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 71  | AW    | 129      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1028  | 656 | 189 | 176 | 7 |         |       |

- Molecule 72 is a protein called 40S ribosomal protein S19a.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 72  | AT    | 126      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1000  | 635 | 192 | 170 | 3 |         |       |

There are 13 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment  | Reference  |
|-------|---------|----------|--------|----------|------------|
| AT    | ?       | -        | GLU    | deletion | UNP P39018 |
| AT    | ?       | -        | HIS    | deletion | UNP P39018 |
| AT    | ?       | -        | ALA    | deletion | UNP P39018 |
| AT    | ?       | -        | ARG    | deletion | UNP P39018 |
| AT    | ?       | -        | LEU    | deletion | UNP P39018 |
| AT    | ?       | -        | VAL    | deletion | UNP P39018 |

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| Chain | Residue | Modelled | Actual | Comment  | Reference  |
|-------|---------|----------|--------|----------|------------|
| AT    | ?       | -        | GLU    | deletion | UNP P39018 |
| AT    | ?       | -        | LYS    | deletion | UNP P39018 |
| AT    | ?       | -        | HIS    | deletion | UNP P39018 |
| AT    | ?       | -        | PRO    | deletion | UNP P39018 |
| AT    | ?       | -        | ASP    | deletion | UNP P39018 |
| AT    | ?       | -        | GLY    | deletion | UNP P39018 |
| AT    | ?       | -        | GLY    | deletion | UNP P39018 |

- Molecule 73 is a protein called 40S ribosomal protein S10b.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 73  | AK    | 90       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 760   | 500 | 130 | 127 | 3 |         |       |

- Molecule 74 is a protein called 40S ribosomal protein S5b.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 74  | AF    | 189      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1481  | 925 | 283 | 266 | 7 |         |       |

- Molecule 75 is a protein called 40S ribosomal protein S28.

| Mol | Chain | Residues | Atoms |     |     |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 75  | Ac    | 62       | Total | C   | N   | O  | S | 0       | 0     |
|     |       |          | 498   | 307 | 100 | 89 | 2 |         |       |

- Molecule 76 is a protein called 60S ribosomal protein L22.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 76  | CU    | 99       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 825   | 530 | 144 | 149 | 2 |         |       |

- Molecule 77 is a protein called Probable 60S ribosomal protein L37-A.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 77  | Cj    | 87       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 704   | 430 | 154 | 115 | 5 |         |       |

- Molecule 78 is a protein called 60S ribosomal protein L24.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 78  | CW    | 60       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 503   | 326 | 95 | 78 | 4 |         |       |

- Molecule 79 is a protein called 60S ribosomal protein L34.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 79  | Cg    | 103      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 844   | 525 | 176 | 138 | 5 |         |       |

- Molecule 80 is a protein called 60S ribosomal protein L31.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 80  | Cd    | 107      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 893   | 556 | 176 | 159 | 2 |         |       |

- Molecule 81 is a protein called 40S ribosomal protein S18.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 81  | AS    | 136      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1117  | 701 | 216 | 197 | 3 |         |       |

### 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.

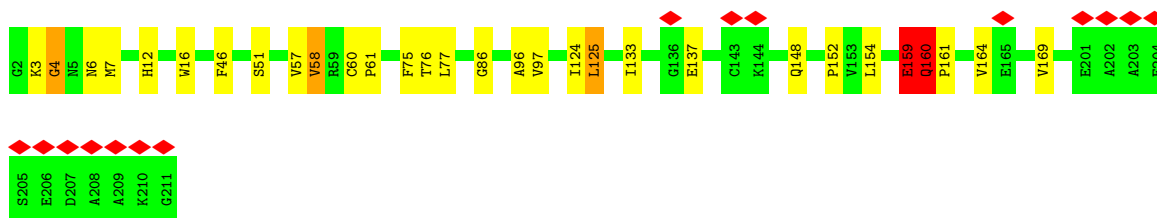
- Molecule 1: 60S ribosomal protein L13a

Chain CO:  94% 5%



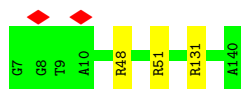
- Molecule 2: 60S ribosomal protein L13

Chain CL:  7% 86% 12% ..



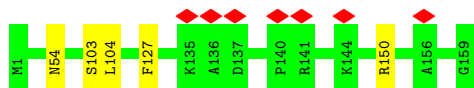
- Molecule 3: 60S ribosomal protein L23

Chain CV:  98%



- Molecule 4: 60S ribosomal protein L14

Chain CM:  97%



- Molecule 5: 60S ribosomal protein L27a

Chain Ca:  92% 7%



- Molecule 6: 60S ribosomal protein L15

Chain CN: 91% 8% .



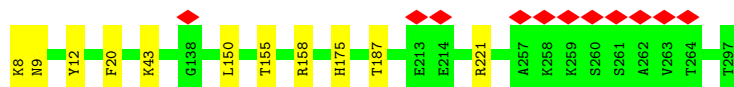
- Molecule 7: 60S ribosomal protein L10

Chain CI: 6% 96% .



- Molecule 8: 60S ribosomal protein L5

Chain CD: 96% .



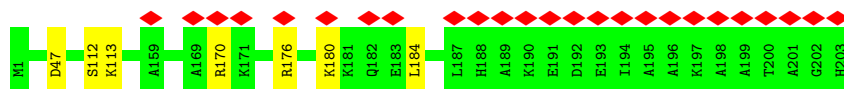
- Molecule 9: 60S ribosomal protein L18

Chain CQ: 94% 5% ..



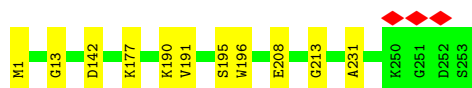
- Molecule 10: 60S ribosomal protein L19

Chain CR: 12% 97% .




- Molecule 11: 60S ribosomal protein L8

Chain CA: 96% .



- Molecule 12: 60S ribosomal protein L18a

Chain CS:  85% 14%



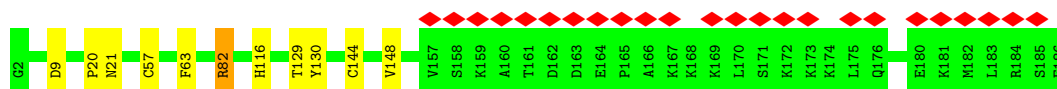
- Molecule 13: RE62581p

Chain CT:  92% 7%



- Molecule 14: 60S ribosomal protein L17

Chain CP:  13% 94% 5%



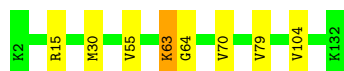
- Molecule 15: IP17216p

Chain CX:  95% 5%



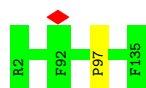
- Molecule 16: GEO07453p1

Chain CY:  94% 5%




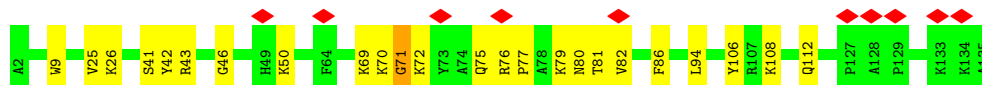
- Molecule 17: 60S ribosomal protein L27

Chain CZ:  99%



- Molecule 18: 60S ribosomal protein L28

Chain Cr:  7% 82% 17%




- Molecule 19: FI02809p

Chain Ch:  94% 6%



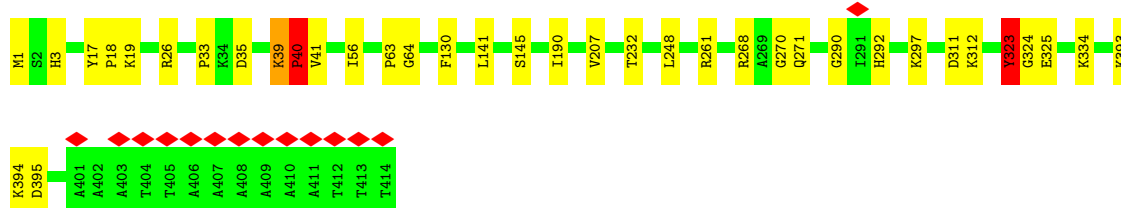
- Molecule 20: 60S ribosomal protein L29

Chain Cb:  88% 11%



- Molecule 21: 60S ribosomal protein L3

Chain CB:  91% 8%



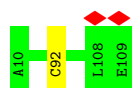
- Molecule 22: 60S ribosomal protein L7

Chain CF:  95%



- Molecule 23: RE25263p

Chain Cc:  99%




- Molecule 24: 60S ribosomal protein L32

Chain Ce:  95%



- Molecule 25: GEO07455p1

Chain Cf:  84% 15%



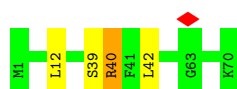
- Molecule 26: 60S ribosomal protein L36

Chain Ci:  90% 10%



- Molecule 27: 60S ribosomal protein L38

Chain Ck:  94%



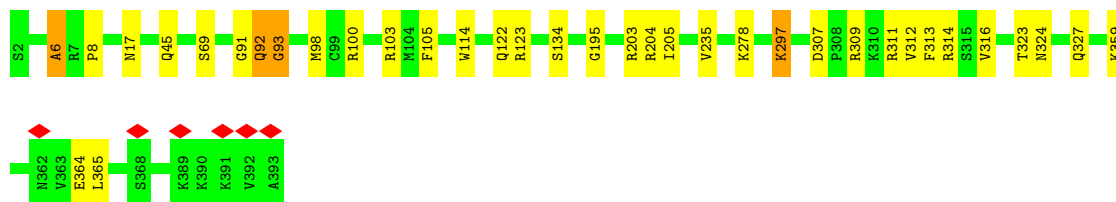
- Molecule 28: 60S ribosomal protein L39

Chain Cl:  98%



- Molecule 29: 60S ribosomal protein L4

Chain CC:  91% 8%



- Molecule 30: Ubiquitin-60S ribosomal protein L40

Chain Cm:  92% 6%

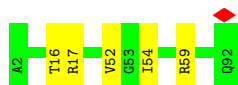


- Molecule 31: 60S ribosomal protein L41

Chain Cn:  96%



- Molecule 32: 60S ribosomal protein L37a



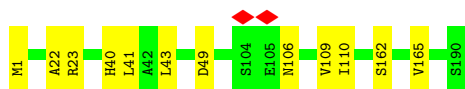
- Molecule 33: TA01007p



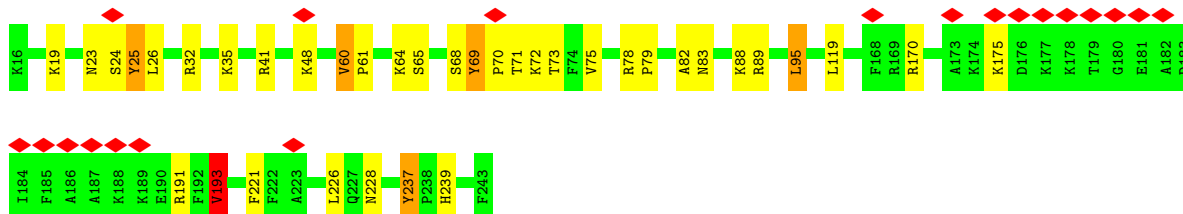
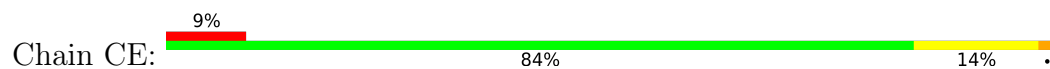
- Molecule 34: 60S ribosomal protein L11



- Molecule 35: 60S ribosomal protein L9



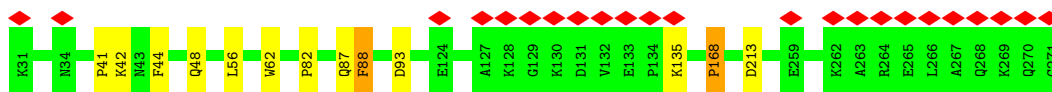
- Molecule 36: Ribosomal protein L6, isoform A



- Molecule 37: 60S ribosomal protein L7a







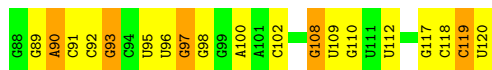
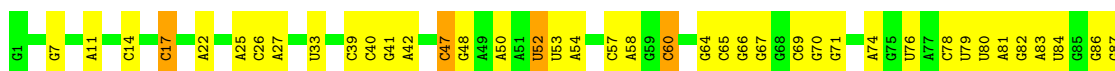
• Molecule 38: 2S ribosomal RNA

Chain A9: 53% 37% 10%



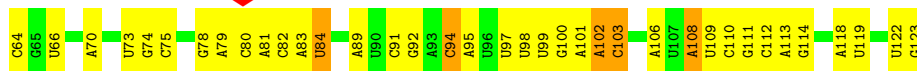
• Molecule 39: 5S ribosomal RNA

Chain A7: 51% 42% 8%



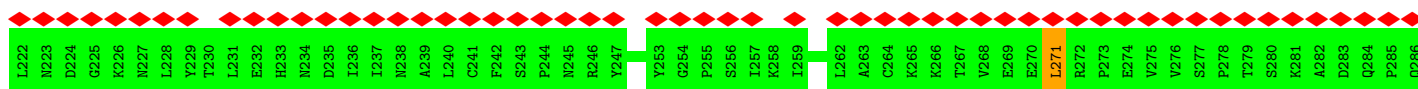
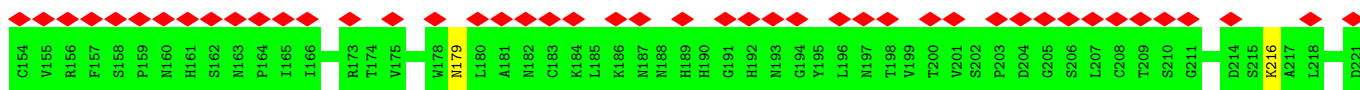
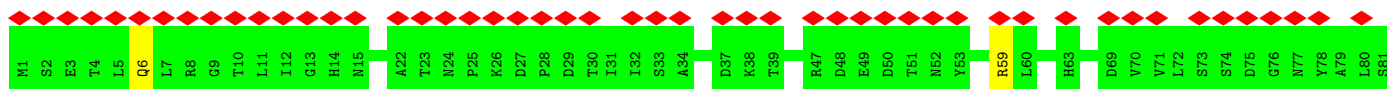
• Molecule 40: 5.8S ribosomal RNA

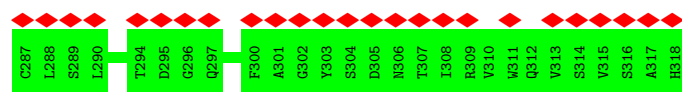
Chain A8: 31% 56% 13%



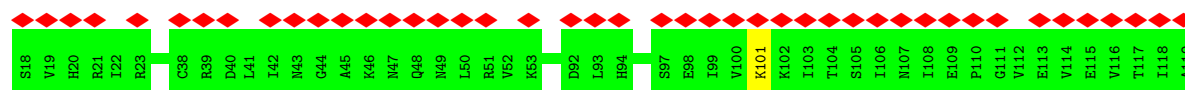
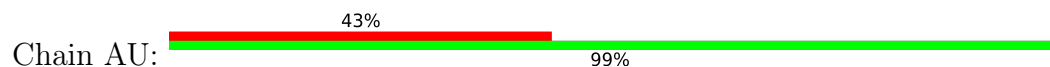
• Molecule 41: Guanine nucleotide-binding protein subunit beta-like protein

Chain Ag: 68% 97%

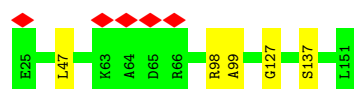




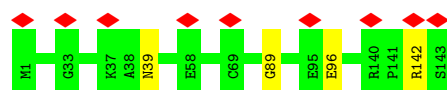
- Molecule 42: 40S ribosomal protein S20



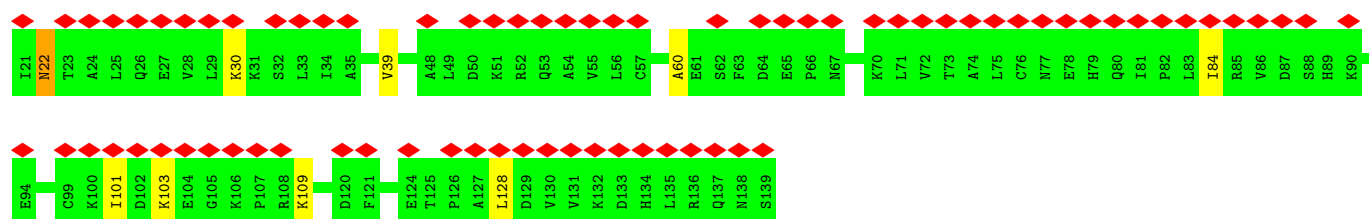
- Molecule 43: 40S ribosomal protein S14a



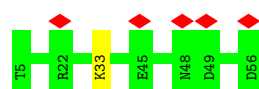
- Molecule 44: 40S ribosomal protein S23



- Molecule 45: 40S ribosomal protein S12

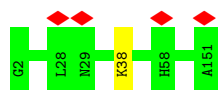


- Molecule 46: 40S ribosomal protein S29

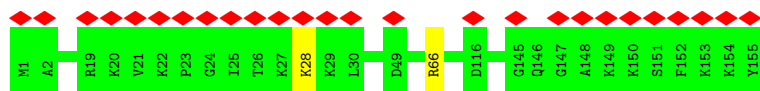


- Molecule 47: 40S ribosomal protein S13

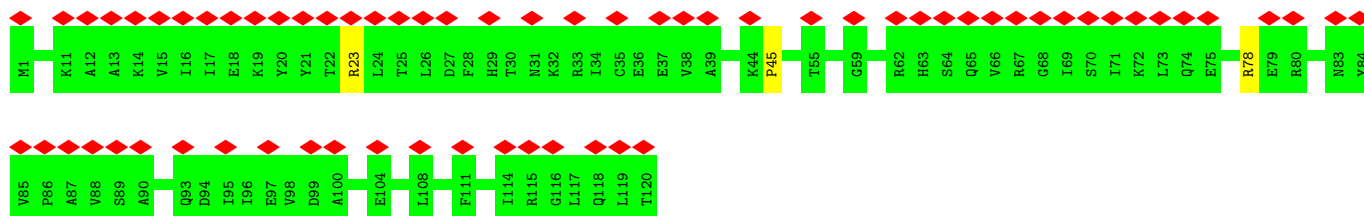




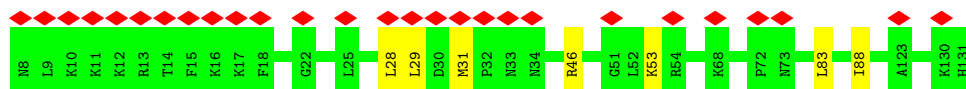
- Molecule 48: 40S ribosomal protein S11



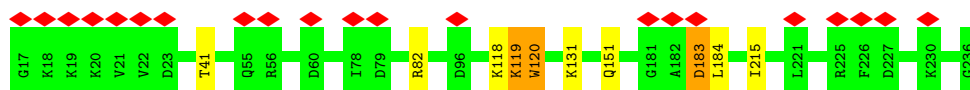
- Molecule 49: 40S ribosomal protein S17



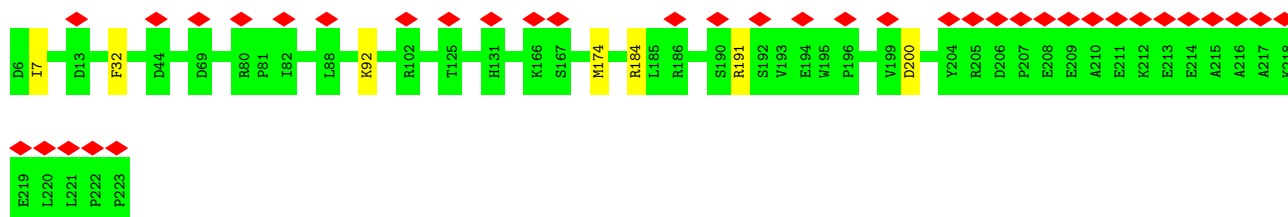
- Molecule 50: GEO07301p1



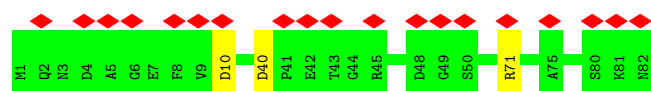
- Molecule 51: 40S ribosomal protein S3a



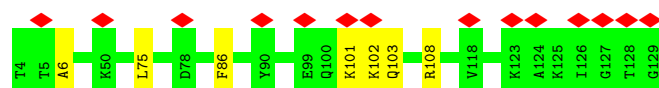
- Molecule 52: 40S ribosomal protein SA



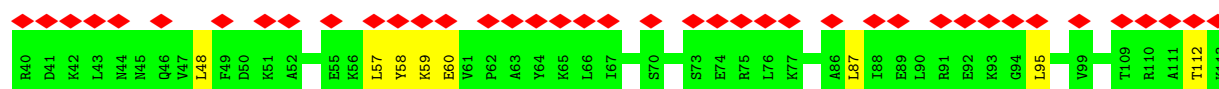
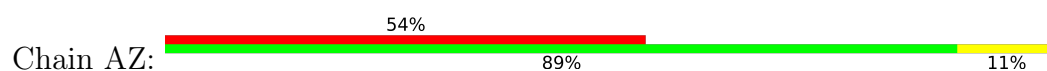
- Molecule 53: 40S ribosomal protein S21



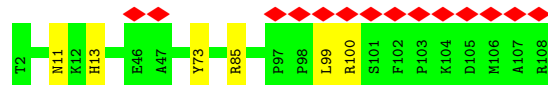
- Molecule 54: 40S ribosomal protein S24



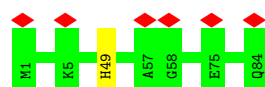
- Molecule 55: 40S ribosomal protein S25



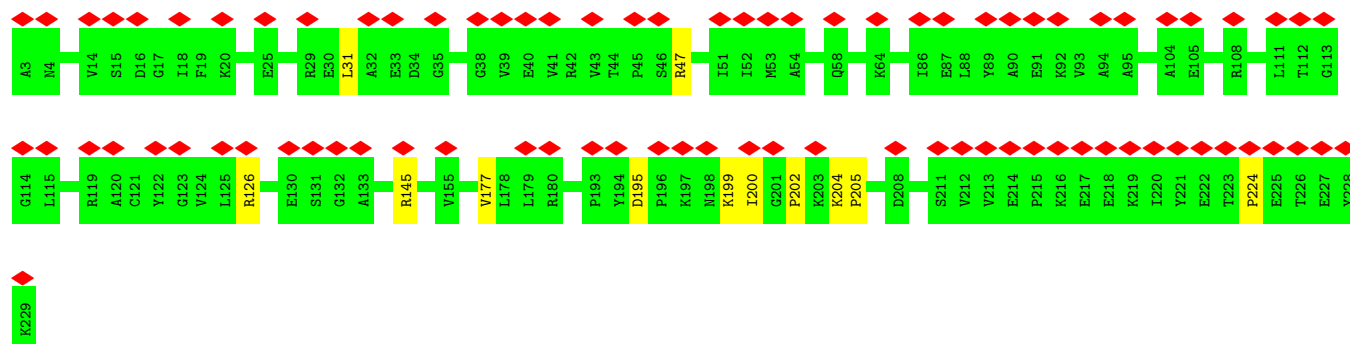
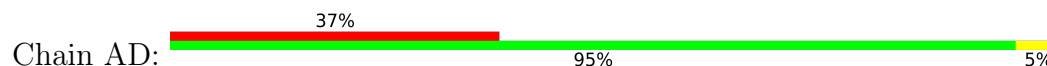
- Molecule 56: 40S ribosomal protein S26



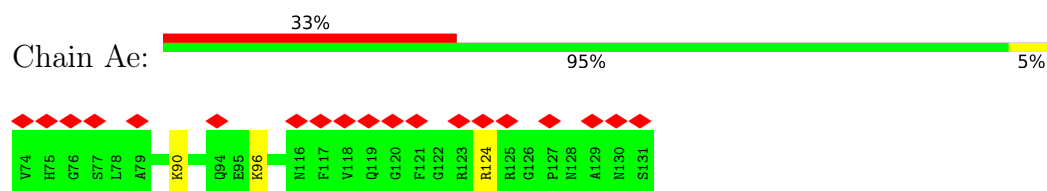
- Molecule 57: 40S ribosomal protein S27



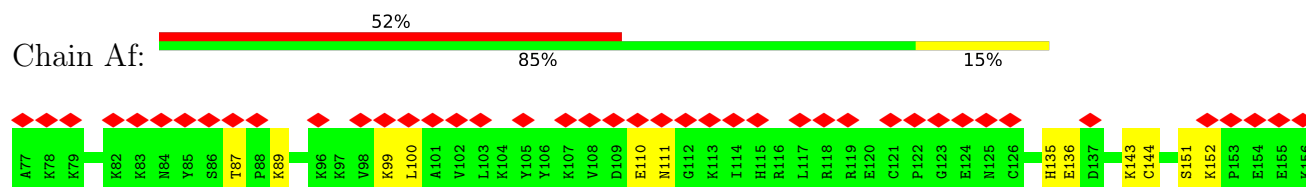
- Molecule 58: 40S ribosomal protein S3



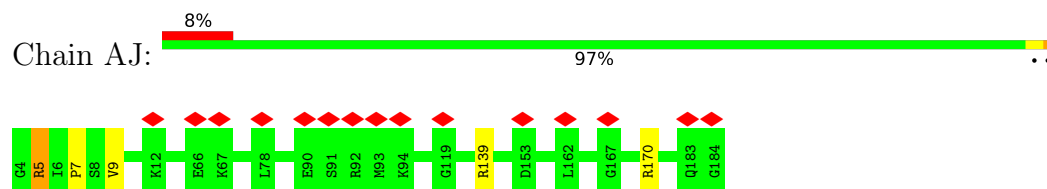
- Molecule 59: 40S ribosomal protein S30



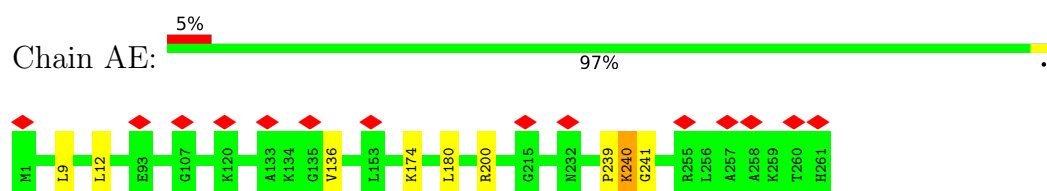
- Molecule 60: Ubiquitin-40S ribosomal protein S27a



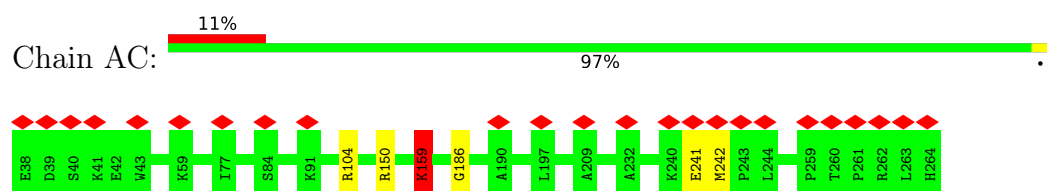
- Molecule 61: 40S ribosomal protein S9



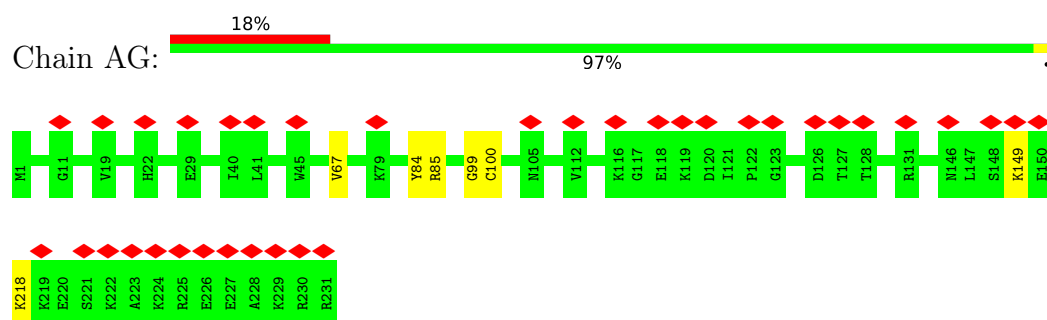
- Molecule 62: 40S ribosomal protein S4



- Molecule 63: 40S ribosomal protein S2

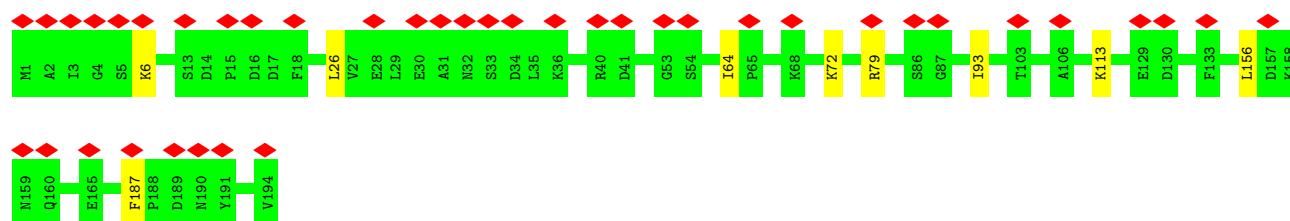


- Molecule 64: 40S ribosomal protein S6



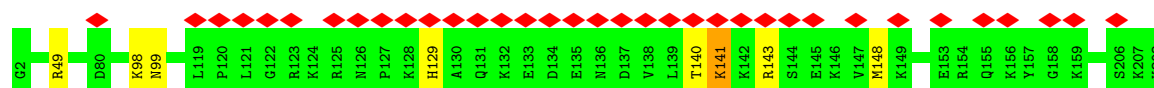
- Molecule 65: 40S ribosomal protein S7

Chain AH: 

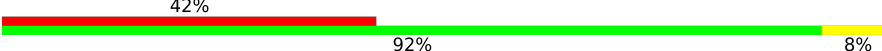


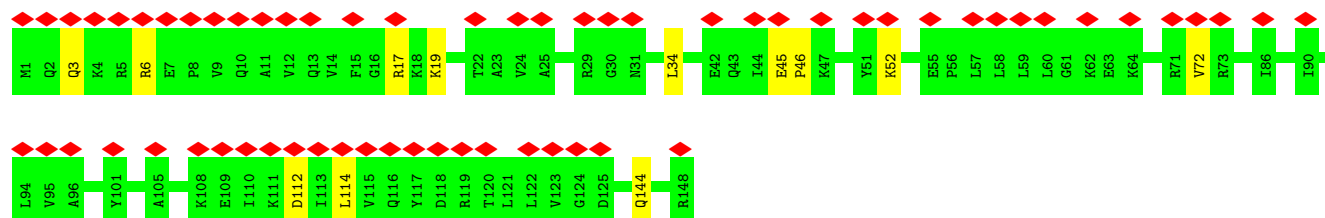
- Molecule 66: 40S ribosomal protein S8

Chain AI: 



- Molecule 67: 40S ribosomal protein S16

Chain AQ: 



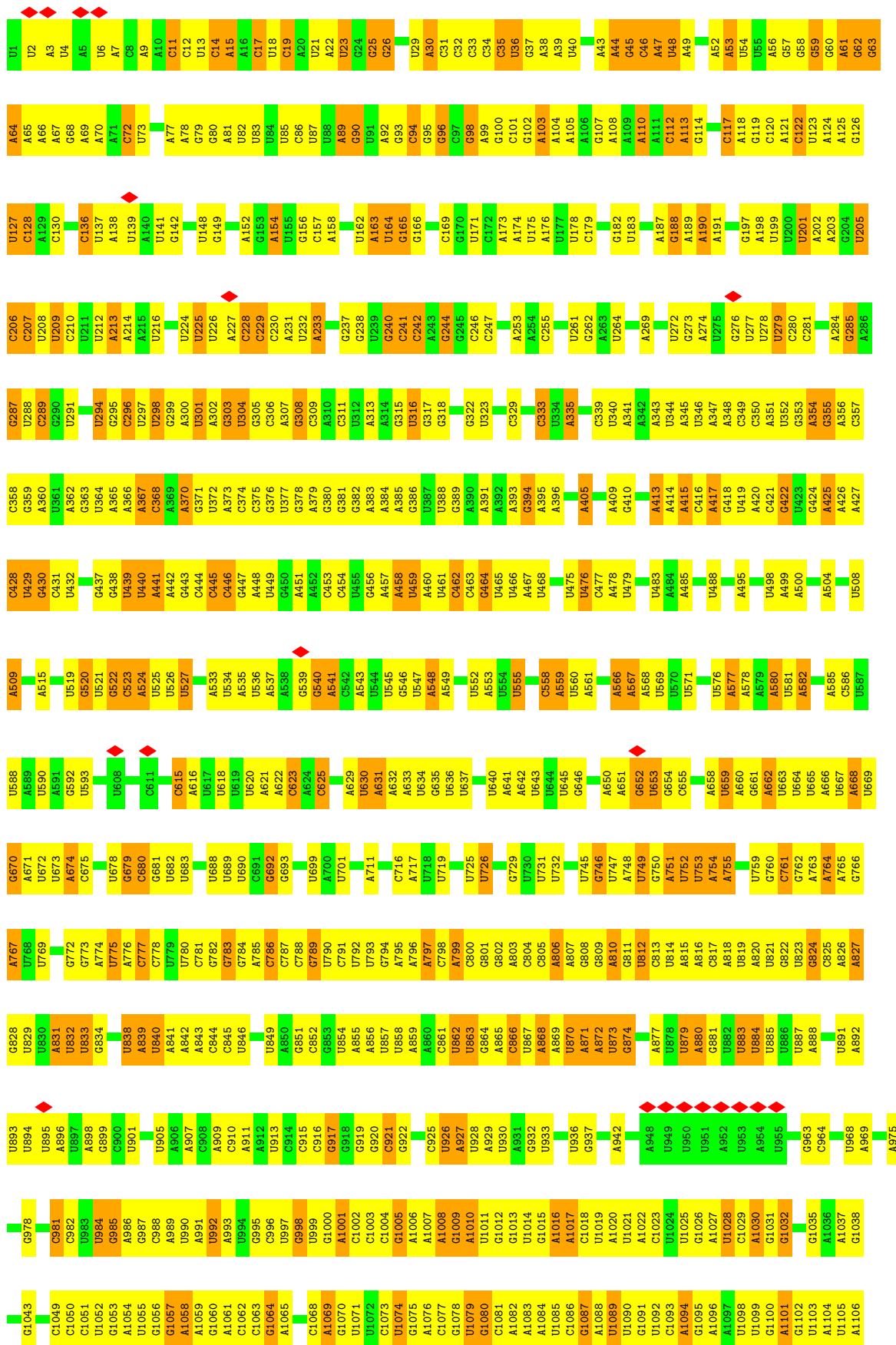
- Molecule 68: 60S ribosomal protein L10a-2

Chain Cz: 



- Molecule 69: 28S ribosomal RNA

Chain A5: 

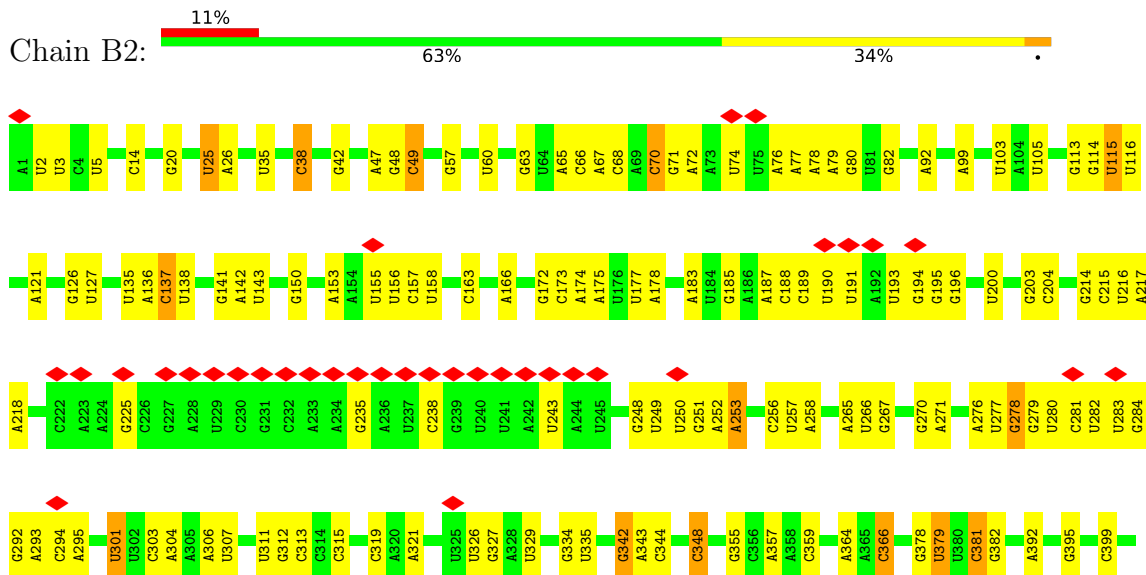


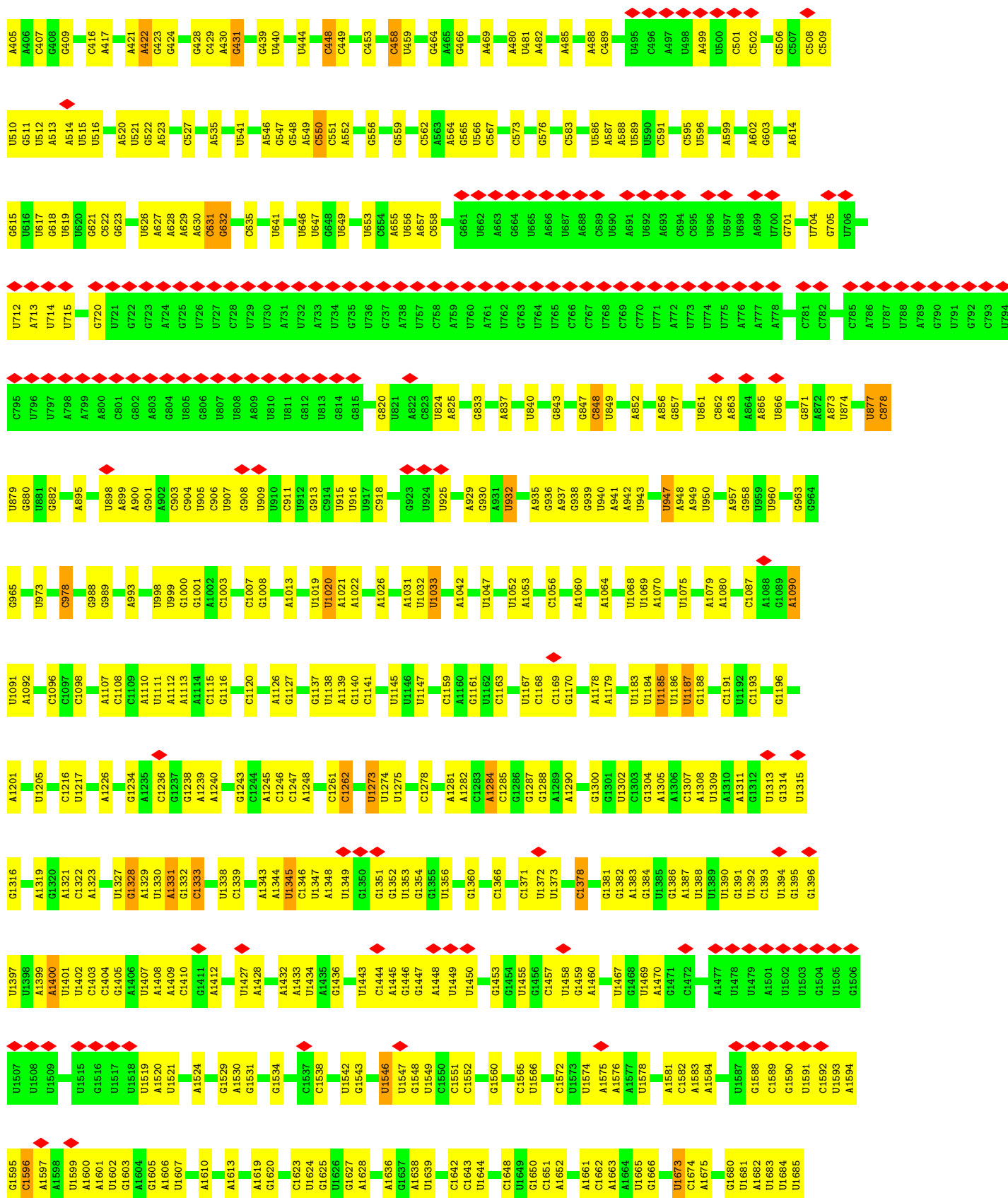


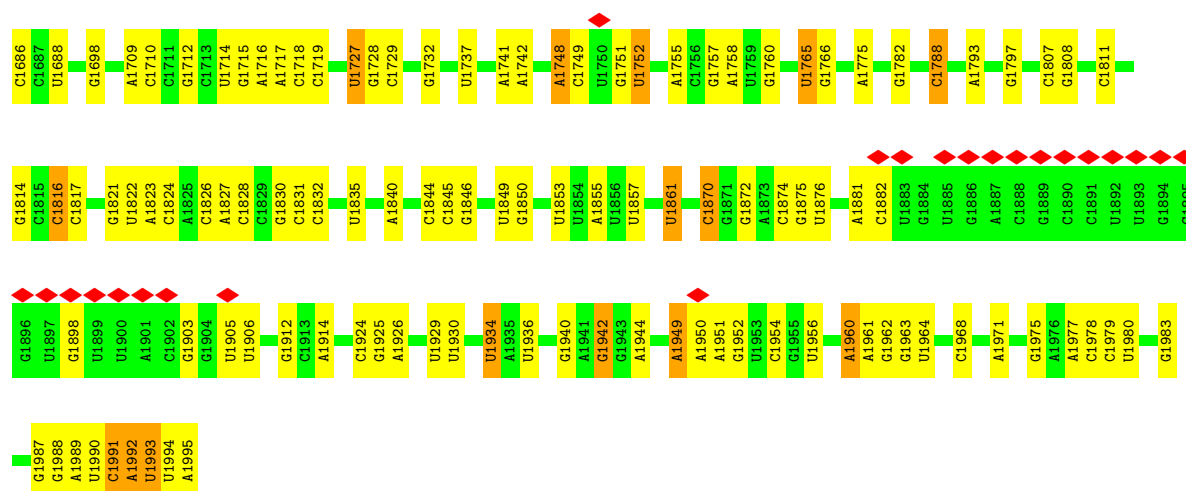


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|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| C2152 | C2153 | C2154 | A2155 | U2156 | U2157 | U2158 | C2159 | C2160 | C2161 | C2162 | C2163 | C2164 | C2165 | U2166 | C2167 | U2168 | U2169 | C2170 | U2171 | C2172 | C2173 | A2174 | A2175 | C2176 | C2177 | U2178 | A2181 | C2182 | A2183 | C2184 | U2185 | C2186 | U2187 | C2188 | U2189 | A2190 | C2191 | U2192 | C2193 | C2194 | A2195 | U2196 | A2197 | C2198 | A2199 | A2200 | U2201 | A2202 | A2203 | U2204 | C2205 | U2206 | A2207 | C2208 | C2209 | U2210 | C2211 | A2212 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       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|       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| G2213 | G2214 | G2215 | A2216 | C2217 | C2218 | U2219 | C2220 | C2221 | C2222 | C2223 | A2224 | C2225 | A2226 | U2227 | U2228 | A2229 | C2230 | A2231 | U2232 | C2233 | C2234 | C2235 | C2236 | C2237 | C2238 | U2239 | U2240 | U2241 | C2242 | C2243 | C2244 | C2245 | A2246 | U2247 | A2248 | C2249 | U2250 | U2251 | U2252 | C2253 | C2254 | C2255 | C2256 | U2257 | U2258 | C2259 | U2260 | U2261 | C2262 | C2263 | U2264 | C2265 | C2266 | U2267 | C2268 | A2269 | C2270 | A2271 | U2272 | A2273 | C2274 | U2275 | C2276 | C2277 | U2278 | C2279 | C2280 | U2281 | U2282 | C2283 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       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|       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| A2284 | U2285 | U2286 | C2287 | C2288 | C2289 | A2290 | A2291 | C2292 | C2293 | U2294 | C2295 | U2296 | C2297 | C2298 | C2299 | C2300 | C2301 | C2302 | C2303 | C2304 | C2305 | C2306 | C2307 | C2308 | C2309 | C2310 | C2311 | C2312 | C2313 | C2314 | C2315 | C2316 | C2317 | C2318 | C2319 | C2320 | C2321 | C2322 | C2323 | C2324 | C2325 | C2326 | C2327 | C2328 | C2329 | C2330 | C2331 | C2332 | C2333 | C2334 | C2335 | C2336 | C2337 | C2338 | C2339 | C2340 | C2341 | C2342 | C2343 | C2344 | C2345 | C2346 | C2347 | C2348 | C2349 | C2350 | C2351 | C2352 | C2353 | C2354 | C2355 | C2356 | C2357 | C2358 | C2359 | C2360 | C2361 | C2362 | C2363 | C2364 | C2365 | C2366 | C2367 | C2368 | C2369 | C2370 | C2371 | C2372 | C2373 | C2374 | C2375 | C2376 | C2377 | C2378 | C2379 | C2380 | C2381 | C2382 | C2383 | C2384 | C2385 | C2386 | C2387 | C2388 | C2389 | C2390 | C2391 | C2392 | C2393 | C2394 | C2395 | C2396 | C2397 | C2398 | C2399 | C2400 | C2401 | C2402 | C2403 | C2404 | C2405 | C2406 | C2407 | C2408 | C2409 | C2410 | C2411 | C2412 | C2413 | C2414 | C2415 | C2416 | C2417 | C2418 | C2419 | C2420 | C2421 | C2422 | C2423 | C2424 | C2425 | C2426 | C2427 | C2428 | C2429 | C2430 | C2431 | C2432 | C2433 | C2434 | C2435 | C2436 | C2437 | C2438 | C2439 | C2440 | C2441 | C2442 | C2443 | C2444 | C2445 | C2446 | C2447 | C2448 | C2449 | C2450 | C2451 | C2452 | C2453 | C2454 | C2455 | C2456 | C2457 | C2458 | C2459 | C2460 | C2461 | C2462 | C2463 | C2464 | C2465 | C2466 | C2467 | C2468 | C2469 | C2470 | C2471 | C2472 | C2473 | C2474 | C2475 | C2476 | C2477 | C2478 | C2479 | C2480 | C2481 | C2482 | C2483 | C2484 | C2485 | C2486 | C2487 | C2488 | C2489 | C2490 | C2491 | C2492 | C2493 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       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|       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| C2494 | C2495 | C2496 | C2497 | C2498 | C2499 | C2500 | C2501 | C2502 | C2503 | C2504 | C2505 | C2506 | C2507 | C2508 | C2509 | C2510 | C2511 | C2512 | C2513 | C2514 | C2515 | C2516 | C2517 | C2518 | C2519 | C2520 | C2521 | C2522 | C2523 | C2524 | C2525 | C2526 | C2527 | C2528 | C2529 | C2530 | C2531 | C2532 | C2533 | C2534 | C2535 | C2536 | C2537 | C2538 | C2539 | C2540 | C2541 | C2542 | C2543 | C2544 | C2545 | C2546 | C2547 | C2548 | C2549 | C2550 | C2551 | C2552 | C2553 | C2554 | C2555 | C2556 | C2557 | C2558 | C2559 | C2560 | C2561 | C2562 | C2563 | C2564 | C2565 | C2566 | C2567 | C2568 | C2569 | C2570 | C2571 | C2572 | C2573 | C2574 | C2575 | C2576 | C2577 | C2578 | C2579 | C2580 | C2581 | C2582 | C2583 | C2584 | C2585 | C2586 | C2587 | C2588 | C2589 | C2590 | C2591 | C2592 | C2593 | C2594 | C2595 | C2596 | C2597 | C2598 | C2599 | C2600 | C2601 | C2602 | C2603 | C2604 | C2605 | C2606 | C2607 | C2608 | C2609 | C2610 | C2611 | C2612 | C2613 | C2614 | C2615 | C2616 | C2617 | C2618 | C2619 | C2620 | C2621 | C2622 | C2623 | C2624 | C2625 | C2626 | C2627 | C2628 | C2629 | C2630 | C2631 | C2632 | C2633 | C2634 | C2635 | C2636 | C2637 | C2638 | C2639 | C2640 | C2641 | C2642 | C2643 | C2644 | C2645 | C2646 | C2647 | C2648 | C2649 | C2650 | C2651 | C2652 | C2653 | C2654 | C2655 | C2656 | C2657 | C2658 | C2659 | C2660 | C2661 | C2662 | C2663 | C2664 | C2665 | C2666 | C2667 | C2668 | C2669 | C2670 | C2671 | C2672 | C2673 | C2674 | C2675 | C2676 | C2677 | C2678 | C2679 | C2680 | C2681 | C2682 | C2683 | C2684 | C2685 | C2686 | C2687 | C2688 | C2689 | C2690 | C2691 | C2692 | C2693 | C2694 | C2695 | C2696 | C2697 | C2698 | C2699 | C2700 | C2701 | C2702 | C2703 | C2704 | C2705 | C2706 | C2707 | C2708 | C2709 | C2710 | C2711 | C2712 | C2713 | C2714 | C2715 | C2716 | C2717 | C2718 | C2719 | C2720 | C2721 | C2722 | C2723 | C2724 | C2725 | C2726 | C2727 | C2728 | C2729 | C2730 | C2731 | C2732 | C2733 | C2734 | C2735 | C2736 | C2737 | C2738 | C2739 | C2740 | C2741 | C2742 | C2743 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| C2869 | C2870 | C2871 | C2872 | C2873 | C2874 | C2875 | C2876 | C2877 | C2878 | C2879 | C2880 | C2881 | C2882 | C2883 | C2884 | C2885 | C2886 | C2887 | C2888 | C2889 | C2890 | C2891 | C2892 | C2893 | C2894 | C2895 | C2896 | C2897 | C2898 | C2899 | C2900 | C2901 | C2902 | C2903 | C2904 | C2905 | C2906 | C2907 | C2908 | C2909 | C2910 | C2911 | C2912 | C2913 | C2914 | C2915 | C2916 | C2917 | C2918 | C2919 | C2920 | C2921 | C2922 | C2923 | C2924 | C2925 | C2926 | C2927 | C2928 | C2929 | C2930 | C2931 | C2932 | C2933 | C2934 | C2935 | C2936 | C2937 | C2938 | C2939 | C2940 | C2941 | C2942 | C2943 | C2944 | C2945 | C2946 | C2947 | C2948 | C2949 | C2950 | C2951 | C2952 | C2953 | C2954 | C2955 | C2956 | C2957 | C2958 | C2959 | C2960 | C2961 | C2962 | C2963 | C2964 | C2965 | C2966 | C2967 | C2968 | C2969 | C2970 | C2971 | C2972 | C2973 | C2974 | C2975 | C2976 | C2977 | C2978 | C2979 | C2980 | C2981 | C2982 | C2983 | C2984 | C2985 | C2986 | C2987 | C2988 | C2989 | C2990 | C2991 | C2992 | C2993 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| C3119 | C3120 | C3121 | C3122 | C3123 | C3124 | C3125 | C3126 | C3127 | C3128 | C3129 | C3130 | C3131 | C3132 | C3133 | C3134 | C3135 | C3136 | C3137 | C3138 | C3139 | C3140 |
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| U3266 | U3267 | U3268 | U3269 | U3270 | U3271 | U3272 | U3273 | U3274 | U3275 | U3276 | U3277 | U3278 | U3279 | U3280 | U3281 | U3282 | U3283 | U3284 | U3285 | U3286 | U3287 | U3288 | U3289 | U3290 | U3291 | U3292 | U3293 | U3294 | U3295 | U3296 | U3297 | U3298 | U3299 | U3300 | U3301 | U3302 | U3303 | U3304 | U3305 | U3306 | U3307 | U3308 | U3309 | U3310 | U3311 | U3312 | U3313 | U3314 | U3315 | U3316 | U3317 | U3318 | U3319 | U3320 | U3321 | U3322 | U3323 | U3324 | U3325 | U3326 | U3327 | U3328 | U3329 | U3330 | U3331 | U3332 | U3333 | U3334 | U3335 | U3336 | U3337 | U3338 | U3339 | U3340 | U3341 | U3342 | U3343 | U3344 | U3345 | U3346 | U3347 | U3348 | U3349 | U3350 | U3351 | U3352 | U3353 | U3354 | U3355 | U3356 | U3357 | U3358 | U3359 | U3360 | U3361 | U3362 | U3363 | U3364 | U3365 | U3366 | U3367 | U3368 | U3369 | U3370 | U3371 | U3372 | U3373 | U3374 | U3375 | U3376 | U3377 | U3378 | U3379 | U3380 | U3381 | U3382 | U3383 | U3384 | U3385 | U3386 | U3387 | U3388 | U3389 | U3390 | U3391 | U3392 | U3393 | U3394 | U3395 | U3396 | U3397 | U3398 | U3399 | U3400 | U3401 | U3402 | U3403 | U3404 | U3405 | U3406 | U3407 | U3408 | U3409 | U3410 | U3411 | U3412 | U3413 | U3414 | U3415 | U3416 | U3417 | U3418 | U3419 | U3420 | U3421 | U3422 | U3423 | U3424 | U3425 | U3426 | U3427 | U3428 | U3429 | U3430 | U3431 | U3432 | U3433 | U3434 | U3435 | U3436 | U3437 | U3438 | U3439 | U3440 | U3441 | U3442 | U3443 | U3444 | U3445 | U3446 | U3447 | U3448 | U3449 | U3450 | U3451 | U3452 | U3453 | U3454 | U3455 | U3456 | U3457 | U3458 | U3459 | U3460 | U3461 | U3462 | U3463 | U3464 | U3465 | U3466 | U3467 | U3468 | U3469 | U3470 | U34   |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |

- Molecule 70: 18S ribosomal RNA

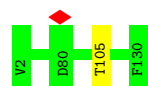






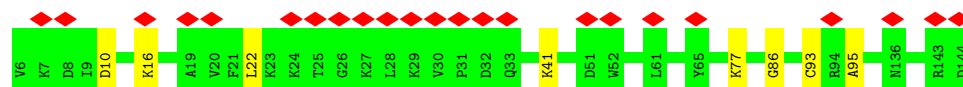
- Molecule 71: 40S ribosomal protein S15Aa

Chain AW: 99%



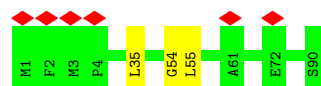
- Molecule 72: 40S ribosomal protein S19a

Chain AT: 18% 94% 6%



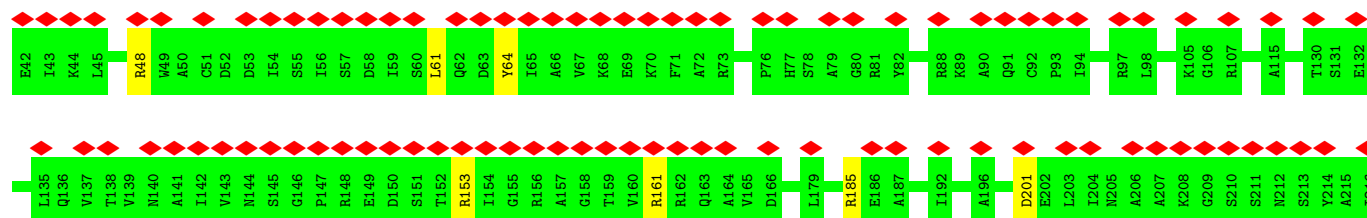
- Molecule 73: 40S ribosomal protein S10b

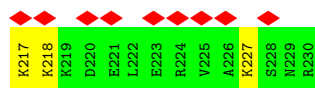
Chain AK: 7% 97% 5%



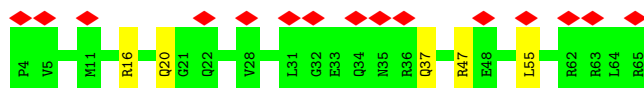
- Molecule 74: 40S ribosomal protein S5b

Chain AF: 53% 95% 5%

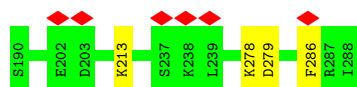




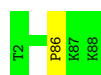
- Molecule 75: 40S ribosomal protein S28



- Molecule 76: 60S ribosomal protein L22



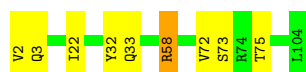
- Molecule 77: Probable 60S ribosomal protein L37-A



- Molecule 78: 60S ribosomal protein L24



- Molecule 79: 60S ribosomal protein L34

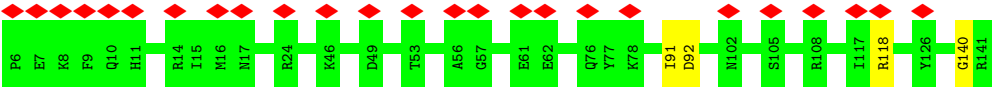


- Molecule 80: 60S ribosomal protein L31



- Molecule 81: 40S ribosomal protein S18





## 4 Experimental information

| Property                             | Value                           | Source    |
|--------------------------------------|---------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE                 | Depositor |
| Imposed symmetry                     | POINT, C1                       | Depositor |
| Number of particles used             | 185913                          | Depositor |
| Resolution determination method      | FSC 0.143 CUT-OFF               | Depositor |
| CTF correction method                | PHASE FLIPPING ONLY             | Depositor |
| Microscope                           | FEI TITAN KRIOS                 | Depositor |
| Voltage (kV)                         | 300                             | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 80                              | Depositor |
| Minimum defocus (nm)                 | Not provided                    |           |
| Maximum defocus (nm)                 | Not provided                    |           |
| Magnification                        | Not provided                    |           |
| Image detector                       | FEI FALCON II (4k x 4k)         | Depositor |
| Maximum map value                    | 0.861                           | Depositor |
| Minimum map value                    | -0.593                          | Depositor |
| Average map value                    | 0.000                           | Depositor |
| Map value standard deviation         | 0.023                           | Depositor |
| Recommended contour level            | 0.035                           | Depositor |
| Map size ( $\text{\AA}$ )            | 426.00003, 426.00003, 426.00003 | wwPDB     |
| Map dimensions                       | 400, 400, 400                   | wwPDB     |
| Map angles ( $^\circ$ )              | 90.0, 90.0, 90.0                | wwPDB     |
| Pixel spacing ( $\text{\AA}$ )       | 1.065, 1.065, 1.065             | Depositor |

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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   | CO    | 0.89         | 0/1700        | 0.90        | 5/2277 (0.2%) |
| 2   | CL    | 0.74         | 1/1726 (0.1%) | 1.02        | 5/2308 (0.2%) |
| 3   | CV    | 0.77         | 0/1014        | 0.79        | 1/1362 (0.1%) |
| 4   | CM    | 0.67         | 0/1326        | 0.77        | 0/1780        |
| 5   | Ca    | 0.98         | 1/1235 (0.1%) | 1.00        | 5/1640 (0.3%) |
| 6   | CN    | 1.02         | 4/1750 (0.2%) | 0.99        | 2/2335 (0.1%) |
| 7   | CI    | 0.53         | 1/1827 (0.1%) | 0.66        | 1/2447 (0.0%) |
| 8   | CD    | 0.61         | 0/2379        | 0.68        | 1/3196 (0.0%) |
| 9   | CQ    | 0.96         | 1/1544 (0.1%) | 0.93        | 3/2069 (0.1%) |
| 10  | CR    | 0.61         | 0/1703        | 0.67        | 1/2255 (0.0%) |
| 11  | CA    | 0.84         | 1/1970 (0.1%) | 0.83        | 3/2635 (0.1%) |
| 12  | CS    | 0.85         | 0/1491        | 1.00        | 4/1998 (0.2%) |
| 13  | CT    | 0.83         | 1/1326 (0.1%) | 0.85        | 3/1773 (0.2%) |
| 14  | CP    | 0.92         | 2/1529 (0.1%) | 0.87        | 2/2042 (0.1%) |
| 15  | CX    | 0.66         | 0/1001        | 0.84        | 3/1348 (0.2%) |
| 16  | CY    | 0.79         | 0/1094        | 0.81        | 2/1456 (0.1%) |
| 17  | CZ    | 0.51         | 0/1141        | 0.67        | 0/1517        |
| 18  | Cr    | 0.88         | 2/1069 (0.2%) | 1.13        | 3/1432 (0.2%) |
| 19  | Ch    | 0.65         | 0/1024        | 0.78        | 0/1353        |
| 20  | Cb    | 0.62         | 0/628         | 0.95        | 1/832 (0.1%)  |
| 21  | CB    | 0.79         | 1/3356 (0.0%) | 0.91        | 8/4494 (0.2%) |
| 22  | CF    | 0.90         | 0/1931        | 0.84        | 4/2587 (0.2%) |
| 23  | Cc    | 0.55         | 0/779         | 0.64        | 0/1048        |
| 24  | Ce    | 1.04         | 1/1132 (0.1%) | 0.94        | 2/1508 (0.1%) |
| 25  | Cf    | 0.92         | 2/1270 (0.2%) | 1.07        | 4/1696 (0.2%) |
| 26  | Ci    | 0.58         | 0/944         | 0.89        | 3/1250 (0.2%) |
| 27  | Ck    | 0.60         | 0/583         | 0.79        | 2/774 (0.3%)  |
| 28  | Cl    | 0.89         | 0/445         | 0.89        | 1/589 (0.2%)  |
| 29  | CC    | 0.91         | 1/3163 (0.0%) | 0.95        | 8/4253 (0.2%) |
| 30  | Cm    | 0.57         | 0/435         | 0.78        | 0/575         |
| 31  | Cn    | 0.57         | 0/237         | 0.74        | 1/300 (0.3%)  |
| 32  | Cp    | 0.85         | 0/719         | 0.87        | 0/954         |
| 33  | Co    | 0.76         | 0/887         | 0.88        | 1/1162 (0.1%) |
| 34  | CJ    | 0.42         | 0/1494        | 0.76        | 3/2001 (0.1%) |



| Mol | Chain | Bond lengths |                   | Bond angles |                    |
|-----|-------|--------------|-------------------|-------------|--------------------|
|     |       | RMSZ         | # Z  >5           | RMSZ        | # Z  >5            |
| 35  | CH    | 0.61         | 0/1519            | 0.80        | 3/2042 (0.1%)      |
| 36  | CE    | 0.65         | 1/1883 (0.1%)     | 0.97        | 5/2514 (0.2%)      |
| 37  | CG    | 0.58         | 1/1968 (0.1%)     | 0.77        | 0/2637             |
| 38  | A9    | 1.48         | 2/714 (0.3%)      | 1.50        | 18/1112 (1.6%)     |
| 39  | A7    | 1.53         | 15/2854 (0.5%)    | 1.51        | 59/4447 (1.3%)     |
| 40  | A8    | 1.93         | 42/2932 (1.4%)    | 1.72        | 96/4568 (2.1%)     |
| 41  | Ag    | 0.32         | 0/2574            | 0.70        | 3/3506 (0.1%)      |
| 42  | AU    | 0.31         | 0/825             | 0.64        | 0/1111             |
| 43  | AO    | 0.35         | 0/965             | 0.70        | 0/1295             |
| 44  | AX    | 0.36         | 0/1152            | 0.69        | 0/1540             |
| 45  | AM    | 0.34         | 0/937             | 0.79        | 2/1260 (0.2%)      |
| 46  | Ad    | 0.33         | 0/443             | 0.64        | 0/589              |
| 47  | AN    | 0.38         | 0/1225            | 0.63        | 0/1641             |
| 48  | AL    | 0.45         | 0/1296            | 0.64        | 0/1725             |
| 49  | AR    | 0.34         | 0/993             | 0.74        | 0/1333             |
| 50  | AP    | 0.32         | 0/1036            | 0.76        | 3/1383 (0.2%)      |
| 51  | AB    | 0.33         | 0/1825            | 0.69        | 1/2448 (0.0%)      |
| 52  | AA    | 0.33         | 0/1777            | 0.64        | 0/2422             |
| 53  | AV    | 0.34         | 0/622             | 0.64        | 0/835              |
| 54  | AY    | 0.30         | 0/1032            | 0.69        | 1/1373 (0.1%)      |
| 55  | AZ    | 0.33         | 0/616             | 0.85        | 3/826 (0.4%)       |
| 56  | Aa    | 0.41         | 0/883             | 0.69        | 0/1184             |
| 57  | Ab    | 0.30         | 0/668             | 0.65        | 0/898              |
| 58  | AD    | 0.31         | 0/1808            | 0.71        | 1/2427 (0.0%)      |
| 59  | Ae    | 0.31         | 0/475             | 0.65        | 0/625              |
| 60  | Af    | 0.33         | 0/672             | 0.74        | 1/887 (0.1%)       |
| 61  | AJ    | 0.32         | 0/1526            | 0.64        | 1/2037 (0.0%)      |
| 62  | AE    | 0.34         | 0/2096            | 0.67        | 2/2819 (0.1%)      |
| 63  | AC    | 0.37         | 0/1785            | 0.70        | 1/2415 (0.0%)      |
| 64  | AG    | 0.32         | 0/1891            | 0.67        | 1/2519 (0.0%)      |
| 65  | AH    | 0.32         | 0/1593            | 0.68        | 2/2145 (0.1%)      |
| 66  | AI    | 0.41         | 0/1689            | 0.80        | 1/2250 (0.0%)      |
| 67  | AQ    | 0.33         | 0/1202            | 0.79        | 3/1608 (0.2%)      |
| 68  | Cz    | 0.33         | 0/1727            | 0.75        | 3/2308 (0.1%)      |
| 69  | A5    | 1.84         | 1826/86147 (2.1%) | 1.78        | 3112/134004 (2.3%) |
| 70  | B2    | 0.69         | 4/43887 (0.0%)    | 1.11        | 255/68161 (0.4%)   |
| 71  | AW    | 0.37         | 0/1046            | 0.60        | 0/1402             |
| 72  | AT    | 0.29         | 0/1019            | 0.66        | 0/1367             |
| 73  | AK    | 0.33         | 0/786             | 0.78        | 3/1064 (0.3%)      |
| 74  | AF    | 0.33         | 0/1501            | 0.70        | 1/2017 (0.0%)      |
| 75  | Ac    | 0.36         | 0/502             | 0.75        | 1/670 (0.1%)       |
| 76  | CU    | 0.45         | 0/838             | 0.79        | 1/1123 (0.1%)      |
| 77  | Cj    | 1.06         | 0/717             | 0.85        | 0/950              |

| Mol | Chain | Bond lengths |                    | Bond angles |                    |
|-----|-------|--------------|--------------------|-------------|--------------------|
|     |       | RMSZ         | # Z  >5            | RMSZ        | # Z  >5            |
| 78  | CW    | 0.68         | 0/515              | 0.77        | 0/683              |
| 79  | Cg    | 0.80         | 0/855              | 0.84        | 2/1142 (0.2%)      |
| 80  | Cd    | 0.27         | 0/908              | 0.46        | 0/1221             |
| 81  | AS    | 0.28         | 0/1135             | 0.67        | 2/1521 (0.1%)      |
| All | All   | 1.26         | 1910/232911 (0.8%) | 1.34        | 3669/341300 (1.1%) |

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   | CO    | 0                   | 9                   |
| 2   | CL    | 0                   | 14                  |
| 4   | CM    | 0                   | 2                   |
| 5   | Ca    | 0                   | 5                   |
| 6   | CN    | 0                   | 7                   |
| 7   | CI    | 0                   | 5                   |
| 8   | CD    | 0                   | 5                   |
| 9   | CQ    | 0                   | 5                   |
| 10  | CR    | 0                   | 3                   |
| 11  | CA    | 0                   | 4                   |
| 12  | CS    | 0                   | 11                  |
| 13  | CT    | 0                   | 8                   |
| 14  | CP    | 0                   | 3                   |
| 16  | CY    | 0                   | 2                   |
| 18  | Cr    | 0                   | 15                  |
| 19  | Ch    | 0                   | 5                   |
| 20  | Cb    | 0                   | 4                   |
| 21  | CB    | 0                   | 18                  |
| 22  | CF    | 0                   | 4                   |
| 24  | Ce    | 0                   | 3                   |
| 25  | Cf    | 0                   | 11                  |
| 26  | Ci    | 0                   | 7                   |
| 27  | Ck    | 0                   | 2                   |
| 29  | CC    | 0                   | 15                  |
| 30  | Cm    | 0                   | 2                   |
| 33  | Co    | 0                   | 3                   |
| 34  | CJ    | 0                   | 4                   |
| 35  | CH    | 0                   | 4                   |
| 36  | CE    | 0                   | 25                  |
| 37  | CG    | 0                   | 9                   |

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| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 43  | AO    | 0                   | 4                   |
| 44  | AX    | 0                   | 1                   |
| 45  | AM    | 0                   | 3                   |
| 46  | Ad    | 0                   | 1                   |
| 50  | AP    | 0                   | 3                   |
| 51  | AB    | 0                   | 4                   |
| 52  | AA    | 0                   | 2                   |
| 53  | AV    | 0                   | 2                   |
| 54  | AY    | 0                   | 1                   |
| 55  | AZ    | 0                   | 4                   |
| 56  | Aa    | 0                   | 2                   |
| 57  | Ab    | 0                   | 1                   |
| 58  | AD    | 0                   | 6                   |
| 59  | Ae    | 0                   | 1                   |
| 60  | Af    | 0                   | 10                  |
| 61  | AJ    | 0                   | 4                   |
| 62  | AE    | 0                   | 1                   |
| 63  | AC    | 0                   | 2                   |
| 64  | AG    | 0                   | 2                   |
| 65  | AH    | 0                   | 3                   |
| 66  | AI    | 0                   | 2                   |
| 67  | AQ    | 0                   | 5                   |
| 68  | Cz    | 0                   | 2                   |
| 72  | AT    | 0                   | 3                   |
| 74  | AF    | 0                   | 2                   |
| 75  | Ac    | 0                   | 1                   |
| 76  | CU    | 0                   | 1                   |
| 78  | CW    | 0                   | 1                   |
| 79  | Cg    | 0                   | 1                   |
| 80  | Cd    | 0                   | 1                   |
| All | All   | 0                   | 290                 |

The worst 5 of 1910 bond length outliers are listed below:

| Mol | Chain | Res  | Type | Atoms | Z      | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|-------|--------|-------------|----------|
| 69  | A5    | 1313 | A    | N9-C4 | -13.10 | 1.29        | 1.37     |
| 69  | A5    | 1795 | A    | C5-C6 | -12.81 | 1.29        | 1.41     |
| 69  | A5    | 1689 | G    | N7-C5 | -12.62 | 1.31        | 1.39     |
| 69  | A5    | 1686 | A    | N9-C4 | -11.02 | 1.31        | 1.37     |
| 69  | A5    | 754  | A    | N9-C4 | -10.88 | 1.31        | 1.37     |

The worst 5 of 3669 bond angle outliers are listed below:

| Mol | Chain | Res  | Type | Atoms     | Z      | Observed(°) | Ideal(°) |
|-----|-------|------|------|-----------|--------|-------------|----------|
| 69  | A5    | 1699 | A    | N1-C6-N6  | -37.41 | 96.15       | 118.60   |
| 69  | A5    | 3472 | A    | C8-N9-C4  | -20.68 | 97.53       | 105.80   |
| 69  | A5    | 1699 | A    | C5-C6-N6  | 20.58  | 140.17      | 123.70   |
| 69  | A5    | 840  | U    | O5'-P-OP1 | -19.48 | 87.32       | 110.70   |
| 69  | A5    | 33   | C    | C6-N1-C2  | -17.17 | 113.43      | 120.30   |

There are no chirality outliers.

5 of 290 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group   |
|-----|-------|-----|------|---------|
| 1   | CO    | 109 | GLY  | Peptide |
| 1   | CO    | 111 | PRO  | Peptide |
| 1   | CO    | 112 | SER  | Peptide |
| 1   | CO    | 177 | LYS  | Peptide |
| 1   | CO    | 190 | ALA  | Peptide |

## 5.2 Too-close contacts [i](#)

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

## 5.3 Torsion angles [i](#)

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

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

| Mol | Chain | Analysed      | Favoured  | Allowed  | Outliers | Percentiles |     |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 1   | CO    | 203/205 (99%) | 177 (87%) | 24 (12%) | 2 (1%)   | 15          | 53  |
| 2   | CL    | 208/210 (99%) | 154 (74%) | 42 (20%) | 12 (6%)  | 1           | 10  |
| 3   | CV    | 132/134 (98%) | 122 (92%) | 10 (8%)  | 0        | 100         | 100 |
| 4   | CM    | 157/159 (99%) | 129 (82%) | 27 (17%) | 1 (1%)   | 25          | 64  |
| 5   | Ca    | 147/149 (99%) | 113 (77%) | 33 (22%) | 1 (1%)   | 22          | 60  |
| 6   | CN    | 201/203 (99%) | 166 (83%) | 32 (16%) | 3 (2%)   | 10          | 42  |
| 7   | CI    | 215/217 (99%) | 183 (85%) | 30 (14%) | 2 (1%)   | 17          | 55  |

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| Mol | Chain | Analysed       | Favoured  | Allowed  | Outliers | Percentiles |     |
|-----|-------|----------------|-----------|----------|----------|-------------|-----|
| 8   | CD    | 288/290 (99%)  | 247 (86%) | 39 (14%) | 2 (1%)   | 22          | 60  |
| 9   | CQ    | 185/187 (99%)  | 160 (86%) | 25 (14%) | 0        | 100         | 100 |
| 10  | CR    | 201/203 (99%)  | 183 (91%) | 18 (9%)  | 0        | 100         | 100 |
| 11  | CA    | 251/253 (99%)  | 211 (84%) | 39 (16%) | 1 (0%)   | 34          | 72  |
| 12  | CS    | 171/173 (99%)  | 126 (74%) | 37 (22%) | 8 (5%)   | 2           | 14  |
| 13  | CT    | 156/158 (99%)  | 130 (83%) | 25 (16%) | 1 (1%)   | 25          | 64  |
| 14  | CP    | 183/185 (99%)  | 163 (89%) | 19 (10%) | 1 (0%)   | 29          | 68  |
| 15  | CX    | 118/120 (98%)  | 98 (83%)  | 19 (16%) | 1 (1%)   | 19          | 57  |
| 16  | CY    | 129/131 (98%)  | 112 (87%) | 16 (12%) | 1 (1%)   | 19          | 57  |
| 17  | CZ    | 132/134 (98%)  | 110 (83%) | 21 (16%) | 1 (1%)   | 19          | 57  |
| 18  | Cr    | 132/134 (98%)  | 81 (61%)  | 47 (36%) | 4 (3%)   | 4           | 24  |
| 19  | Ch    | 121/123 (98%)  | 106 (88%) | 15 (12%) | 0        | 100         | 100 |
| 20  | Cb    | 73/75 (97%)    | 59 (81%)  | 11 (15%) | 3 (4%)   | 3           | 16  |
| 21  | CB    | 412/414 (100%) | 346 (84%) | 56 (14%) | 10 (2%)  | 6           | 29  |
| 22  | CF    | 224/226 (99%)  | 199 (89%) | 20 (9%)  | 5 (2%)   | 6           | 31  |
| 23  | Cc    | 98/100 (98%)   | 94 (96%)  | 4 (4%)   | 0        | 100         | 100 |
| 24  | Ce    | 130/132 (98%)  | 118 (91%) | 11 (8%)  | 1 (1%)   | 19          | 57  |
| 25  | Cf    | 155/157 (99%)  | 113 (73%) | 36 (23%) | 6 (4%)   | 3           | 17  |
| 26  | Ci    | 111/113 (98%)  | 82 (74%)  | 28 (25%) | 1 (1%)   | 17          | 55  |
| 27  | Ck    | 68/70 (97%)    | 61 (90%)  | 7 (10%)  | 0        | 100         | 100 |
| 28  | Cl    | 48/50 (96%)    | 45 (94%)  | 3 (6%)   | 0        | 100         | 100 |
| 29  | CC    | 390/392 (100%) | 318 (82%) | 67 (17%) | 5 (1%)   | 12          | 45  |
| 30  | Cm    | 50/52 (96%)    | 43 (86%)  | 6 (12%)  | 1 (2%)   | 7           | 34  |
| 31  | Cn    | 23/25 (92%)    | 21 (91%)  | 2 (9%)   | 0        | 100         | 100 |
| 32  | Cp    | 89/91 (98%)    | 80 (90%)  | 9 (10%)  | 0        | 100         | 100 |
| 33  | Co    | 102/104 (98%)  | 82 (80%)  | 18 (18%) | 2 (2%)   | 7           | 34  |
| 34  | CJ    | 180/182 (99%)  | 149 (83%) | 30 (17%) | 1 (1%)   | 25          | 64  |
| 35  | CH    | 188/190 (99%)  | 164 (87%) | 21 (11%) | 3 (2%)   | 9           | 40  |
| 36  | CE    | 226/228 (99%)  | 157 (70%) | 62 (27%) | 7 (3%)   | 4           | 23  |
| 37  | CG    | 239/241 (99%)  | 194 (81%) | 43 (18%) | 2 (1%)   | 19          | 57  |
| 41  | Ag    | 316/318 (99%)  | 265 (84%) | 51 (16%) | 0        | 100         | 100 |

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| Mol | Chain | Analysed      | Favoured  | Allowed  | Outliers | Percentiles |     |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 42  | AU    | 100/102 (98%) | 89 (89%)  | 11 (11%) | 0        | 100         | 100 |
| 43  | AO    | 125/127 (98%) | 100 (80%) | 25 (20%) | 0        | 100         | 100 |
| 44  | AX    | 141/143 (99%) | 120 (85%) | 20 (14%) | 1 (1%)   | 22          | 60  |
| 45  | AM    | 117/119 (98%) | 85 (73%)  | 32 (27%) | 0        | 100         | 100 |
| 46  | Ad    | 50/52 (96%)   | 33 (66%)  | 17 (34%) | 0        | 100         | 100 |
| 47  | AN    | 148/150 (99%) | 137 (93%) | 11 (7%)  | 0        | 100         | 100 |
| 48  | AL    | 153/155 (99%) | 133 (87%) | 19 (12%) | 1 (1%)   | 22          | 60  |
| 49  | AR    | 118/120 (98%) | 92 (78%)  | 25 (21%) | 1 (1%)   | 19          | 57  |
| 50  | AP    | 122/124 (98%) | 96 (79%)  | 26 (21%) | 0        | 100         | 100 |
| 51  | AB    | 218/220 (99%) | 176 (81%) | 37 (17%) | 5 (2%)   | 6           | 30  |
| 52  | AA    | 216/218 (99%) | 179 (83%) | 36 (17%) | 1 (0%)   | 29          | 68  |
| 53  | AV    | 80/82 (98%)   | 67 (84%)  | 13 (16%) | 0        | 100         | 100 |
| 54  | AY    | 124/126 (98%) | 101 (82%) | 22 (18%) | 1 (1%)   | 19          | 57  |
| 55  | AZ    | 72/74 (97%)   | 56 (78%)  | 16 (22%) | 0        | 100         | 100 |
| 56  | Aa    | 105/107 (98%) | 86 (82%)  | 18 (17%) | 1 (1%)   | 15          | 53  |
| 57  | Ab    | 82/84 (98%)   | 64 (78%)  | 18 (22%) | 0        | 100         | 100 |
| 58  | AD    | 225/227 (99%) | 179 (80%) | 44 (20%) | 2 (1%)   | 17          | 55  |
| 59  | Ae    | 56/58 (97%)   | 39 (70%)  | 17 (30%) | 0        | 100         | 100 |
| 60  | Af    | 78/80 (98%)   | 57 (73%)  | 21 (27%) | 0        | 100         | 100 |
| 61  | AJ    | 179/181 (99%) | 152 (85%) | 26 (14%) | 1 (1%)   | 25          | 64  |
| 62  | AE    | 259/261 (99%) | 215 (83%) | 42 (16%) | 2 (1%)   | 19          | 57  |
| 63  | AC    | 225/227 (99%) | 188 (84%) | 35 (16%) | 2 (1%)   | 17          | 55  |
| 64  | AG    | 229/231 (99%) | 197 (86%) | 30 (13%) | 2 (1%)   | 17          | 55  |
| 65  | AH    | 192/194 (99%) | 161 (84%) | 31 (16%) | 0        | 100         | 100 |
| 66  | AI    | 205/207 (99%) | 161 (78%) | 41 (20%) | 3 (2%)   | 10          | 42  |
| 67  | AQ    | 146/148 (99%) | 116 (80%) | 29 (20%) | 1 (1%)   | 22          | 60  |
| 68  | Cz    | 215/217 (99%) | 175 (81%) | 40 (19%) | 0        | 100         | 100 |
| 71  | AW    | 127/129 (98%) | 117 (92%) | 10 (8%)  | 0        | 100         | 100 |
| 72  | AT    | 122/126 (97%) | 92 (75%)  | 29 (24%) | 1 (1%)   | 19          | 57  |
| 73  | AK    | 88/90 (98%)   | 64 (73%)  | 24 (27%) | 0        | 100         | 100 |
| 74  | AF    | 187/189 (99%) | 146 (78%) | 41 (22%) | 0        | 100         | 100 |

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| Mol | Chain | Analysed          | Favoured   | Allowed    | Outliers | Percentiles |     |
|-----|-------|-------------------|------------|------------|----------|-------------|-----|
| 75  | Ac    | 60/62 (97%)       | 49 (82%)   | 11 (18%)   | 0        | 100         | 100 |
| 76  | CU    | 97/99 (98%)       | 73 (75%)   | 23 (24%)   | 1 (1%)   | 15          | 53  |
| 77  | Cj    | 85/87 (98%)       | 74 (87%)   | 10 (12%)   | 1 (1%)   | 13          | 48  |
| 78  | CW    | 58/60 (97%)       | 53 (91%)   | 5 (9%)     | 0        | 100         | 100 |
| 79  | Cg    | 101/103 (98%)     | 90 (89%)   | 10 (10%)   | 1 (1%)   | 15          | 53  |
| 80  | Cd    | 105/107 (98%)     | 97 (92%)   | 8 (8%)     | 0        | 100         | 100 |
| 81  | AS    | 134/136 (98%)     | 117 (87%)  | 16 (12%)   | 1 (1%)   | 22          | 60  |
| All | All   | 11596/11750 (99%) | 9587 (83%) | 1892 (16%) | 117 (1%) | 20          | 53  |

5 of 117 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | CO    | 112 | SER  |
| 1   | CO    | 113 | PRO  |
| 2   | CL    | 7   | MET  |
| 2   | CL    | 148 | GLN  |
| 2   | CL    | 160 | GLN  |

### 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 |     |
|-----|-------|----------------|------------|----------|-------------|-----|
| 1   | CO    | 175/175 (100%) | 175 (100%) | 0        | 100         | 100 |
| 2   | CL    | 173/173 (100%) | 168 (97%)  | 5 (3%)   | 42          | 76  |
| 3   | CV    | 101/101 (100%) | 99 (98%)   | 2 (2%)   | 55          | 83  |
| 4   | CM    | 138/138 (100%) | 136 (99%)  | 2 (1%)   | 67          | 88  |
| 5   | Ca    | 122/122 (100%) | 121 (99%)  | 1 (1%)   | 81          | 93  |
| 6   | CN    | 174/174 (100%) | 169 (97%)  | 5 (3%)   | 42          | 76  |
| 7   | CI    | 187/187 (100%) | 187 (100%) | 0        | 100         | 100 |
| 8   | CD    | 241/241 (100%) | 238 (99%)  | 3 (1%)   | 71          | 90  |
| 9   | CQ    | 164/164 (100%) | 159 (97%)  | 5 (3%)   | 41          | 75  |

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| Mol | Chain | Analysed       | Rotameric  | Outliers | Percentiles |     |
|-----|-------|----------------|------------|----------|-------------|-----|
| 10  | CR    | 176/176 (100%) | 173 (98%)  | 3 (2%)   | 60          | 85  |
| 11  | CA    | 195/195 (100%) | 192 (98%)  | 3 (2%)   | 65          | 87  |
| 12  | CS    | 156/156 (100%) | 152 (97%)  | 4 (3%)   | 46          | 78  |
| 13  | CT    | 137/137 (100%) | 135 (98%)  | 2 (2%)   | 65          | 87  |
| 14  | CP    | 160/160 (100%) | 155 (97%)  | 5 (3%)   | 40          | 75  |
| 15  | CX    | 106/106 (100%) | 103 (97%)  | 3 (3%)   | 43          | 77  |
| 16  | CY    | 116/116 (100%) | 112 (97%)  | 4 (3%)   | 37          | 72  |
| 17  | CZ    | 121/121 (100%) | 121 (100%) | 0        | 100         | 100 |
| 18  | Cr    | 112/112 (100%) | 110 (98%)  | 2 (2%)   | 59          | 85  |
| 19  | Ch    | 112/112 (100%) | 110 (98%)  | 2 (2%)   | 59          | 85  |
| 20  | Cb    | 67/67 (100%)   | 65 (97%)   | 2 (3%)   | 41          | 75  |
| 21  | CB    | 349/349 (100%) | 342 (98%)  | 7 (2%)   | 55          | 83  |
| 22  | CF    | 200/200 (100%) | 198 (99%)  | 2 (1%)   | 76          | 91  |
| 23  | Cc    | 84/84 (100%)   | 83 (99%)   | 1 (1%)   | 71          | 90  |
| 24  | Ce    | 120/120 (100%) | 119 (99%)  | 1 (1%)   | 81          | 93  |
| 25  | Cf    | 123/123 (100%) | 119 (97%)  | 4 (3%)   | 38          | 73  |
| 26  | Ci    | 100/100 (100%) | 100 (100%) | 0        | 100         | 100 |
| 27  | Ck    | 65/65 (100%)   | 64 (98%)   | 1 (2%)   | 65          | 87  |
| 28  | Cl    | 45/45 (100%)   | 45 (100%)  | 0        | 100         | 100 |
| 29  | CC    | 323/323 (100%) | 311 (96%)  | 12 (4%)  | 34          | 70  |
| 30  | Cm    | 48/48 (100%)   | 46 (96%)   | 2 (4%)   | 30          | 66  |
| 31  | Cn    | 23/23 (100%)   | 23 (100%)  | 0        | 100         | 100 |
| 32  | Cp    | 74/74 (100%)   | 69 (93%)   | 5 (7%)   | 16          | 48  |
| 33  | Co    | 94/94 (100%)   | 93 (99%)   | 1 (1%)   | 73          | 90  |
| 34  | CJ    | 155/155 (100%) | 154 (99%)  | 1 (1%)   | 86          | 95  |
| 35  | CH    | 169/169 (100%) | 167 (99%)  | 2 (1%)   | 71          | 90  |
| 36  | CE    | 197/197 (100%) | 190 (96%)  | 7 (4%)   | 35          | 70  |
| 37  | CG    | 210/210 (100%) | 207 (99%)  | 3 (1%)   | 67          | 88  |
| 41  | Ag    | 280/280 (100%) | 272 (97%)  | 8 (3%)   | 42          | 76  |
| 42  | AU    | 95/95 (100%)   | 94 (99%)   | 1 (1%)   | 73          | 90  |
| 43  | AO    | 98/98 (100%)   | 97 (99%)   | 1 (1%)   | 76          | 91  |

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| Mol | Chain | Analysed       | Rotameric  | Outliers | Percentiles |     |
|-----|-------|----------------|------------|----------|-------------|-----|
| 44  | AX    | 116/116 (100%) | 114 (98%)  | 2 (2%)   | 60          | 85  |
| 45  | AM    | 104/104 (100%) | 99 (95%)   | 5 (5%)   | 25          | 62  |
| 46  | Ad    | 45/45 (100%)   | 45 (100%)  | 0        | 100         | 100 |
| 47  | AN    | 130/130 (100%) | 129 (99%)  | 1 (1%)   | 81          | 93  |
| 48  | AL    | 138/138 (100%) | 137 (99%)  | 1 (1%)   | 84          | 94  |
| 49  | AR    | 108/108 (100%) | 106 (98%)  | 2 (2%)   | 57          | 84  |
| 50  | AP    | 111/111 (100%) | 110 (99%)  | 1 (1%)   | 78          | 92  |
| 51  | AB    | 199/199 (100%) | 196 (98%)  | 3 (2%)   | 65          | 87  |
| 52  | AA    | 190/190 (100%) | 186 (98%)  | 4 (2%)   | 53          | 82  |
| 53  | AV    | 67/67 (100%)   | 66 (98%)   | 1 (2%)   | 65          | 87  |
| 54  | AY    | 105/106 (99%)  | 101 (96%)  | 4 (4%)   | 33          | 69  |
| 55  | AZ    | 67/67 (100%)   | 66 (98%)   | 1 (2%)   | 65          | 87  |
| 56  | Aa    | 94/94 (100%)   | 91 (97%)   | 3 (3%)   | 39          | 74  |
| 57  | Ab    | 72/72 (100%)   | 72 (100%)  | 0        | 100         | 100 |
| 58  | AD    | 192/192 (100%) | 189 (98%)  | 3 (2%)   | 62          | 86  |
| 59  | Ae    | 47/47 (100%)   | 45 (96%)   | 2 (4%)   | 29          | 66  |
| 60  | Af    | 70/70 (100%)   | 69 (99%)   | 1 (1%)   | 67          | 88  |
| 61  | AJ    | 161/161 (100%) | 161 (100%) | 0        | 100         | 100 |
| 62  | AE    | 220/220 (100%) | 215 (98%)  | 5 (2%)   | 50          | 80  |
| 63  | AC    | 188/188 (100%) | 185 (98%)  | 3 (2%)   | 62          | 86  |
| 64  | AG    | 200/200 (100%) | 197 (98%)  | 3 (2%)   | 65          | 87  |
| 65  | AH    | 175/175 (100%) | 171 (98%)  | 4 (2%)   | 50          | 80  |
| 66  | AI    | 175/175 (100%) | 172 (98%)  | 3 (2%)   | 60          | 85  |
| 67  | AQ    | 122/122 (100%) | 119 (98%)  | 3 (2%)   | 47          | 79  |
| 68  | Cz    | 190/190 (100%) | 185 (97%)  | 5 (3%)   | 46          | 78  |
| 71  | AW    | 113/113 (100%) | 112 (99%)  | 1 (1%)   | 78          | 92  |
| 72  | AT    | 104/104 (100%) | 100 (96%)  | 4 (4%)   | 33          | 69  |
| 73  | AK    | 81/81 (100%)   | 81 (100%)  | 0        | 100         | 100 |
| 74  | AF    | 157/157 (100%) | 150 (96%)  | 7 (4%)   | 27          | 64  |
| 75  | Ac    | 54/54 (100%)   | 51 (94%)   | 3 (6%)   | 21          | 56  |
| 76  | CU    | 92/92 (100%)   | 91 (99%)   | 1 (1%)   | 73          | 90  |

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| Mol | Chain | Analysed           | Rotameric  | Outliers | Percentiles |     |
|-----|-------|--------------------|------------|----------|-------------|-----|
| 77  | Cj    | 74/74 (100%)       | 74 (100%)  | 0        | 100         | 100 |
| 78  | CW    | 54/54 (100%)       | 53 (98%)   | 1 (2%)   | 57          | 84  |
| 79  | Cg    | 95/95 (100%)       | 88 (93%)   | 7 (7%)   | 13          | 44  |
| 80  | Cd    | 99/99 (100%)       | 93 (94%)   | 6 (6%)   | 18          | 53  |
| 81  | AS    | 122/122 (100%)     | 121 (99%)  | 1 (1%)   | 81          | 93  |
| All | All   | 10116/10117 (100%) | 9913 (98%) | 203 (2%) | 57          | 83  |

5 of 203 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 45  | AM    | 30  | LYS  |
| 59  | Ae    | 90  | LYS  |
| 80  | Cd    | 83  | VAL  |
| 47  | AN    | 38  | LYS  |
| 52  | AA    | 191 | ARG  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 81  | AS    | 73  | ASN  |
| 81  | AS    | 87  | GLN  |
| 81  | AS    | 135 | HIS  |
| 55  | AZ    | 46  | GLN  |
| 66  | AI    | 64  | ASN  |

### 5.3.3 RNA ⓘ

| Mol | Chain | Analysed        | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 38  | A9    | 29/30 (96%)     | 8 (27%)           | 1 (3%)          |
| 39  | A7    | 119/120 (99%)   | 30 (25%)          | 1 (0%)          |
| 40  | A8    | 122/123 (99%)   | 45 (36%)          | 1 (0%)          |
| 69  | A5    | 3561/3703 (96%) | 1353 (37%)        | 81 (2%)         |
| 70  | B2    | 1792/1936 (92%) | 630 (35%)         | 32 (1%)         |
| All | All   | 5623/5912 (95%) | 2066 (36%)        | 116 (2%)        |

5 of 2066 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 38  | A9    | 4   | U    |
| 38  | A9    | 9   | C    |
| 38  | A9    | 20  | U    |
| 38  | A9    | 21  | G    |
| 38  | A9    | 22  | A    |

5 of 116 RNA pucker outliers are listed below:

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 69  | A5    | 2125 | G    |
| 70  | B2    | 1673 | U    |
| 69  | A5    | 3608 | G    |
| 70  | B2    | 1595 | G    |
| 70  | B2    | 1185 | U    |

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 69  | A5    | 7                |
| 70  | B2    | 5                |
| 72  | AT    | 1                |
| 7   | CI    | 1                |

The worst 5 of 14 chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1     | AT    | 107:LEU   | C      | 121:ARG   | N      | 19.55        |
| 1     | A5    | 2293:C    | O3'    | 2390:U    | P      | 18.82        |
| 1     | A5    | 2941:G    | O3'    | 2976:A    | P      | 18.19        |
| 1     | B2    | 738:A     | O3'    | 757:U     | P      | 14.79        |
| 1     | A5    | 2406:A    | O3'    | 2452:A    | P      | 13.09        |

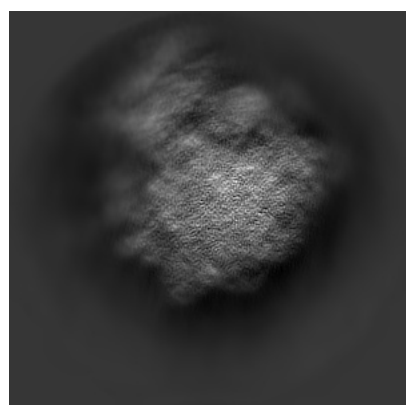
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10624. These allow visual inspection of the internal detail of the map and identification of artifacts.

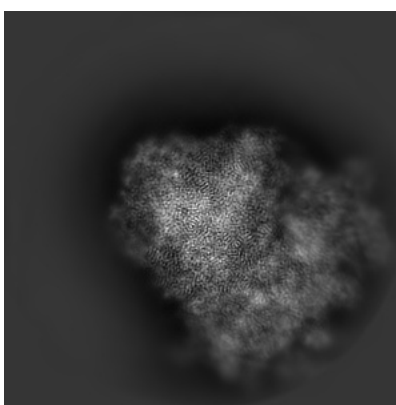
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

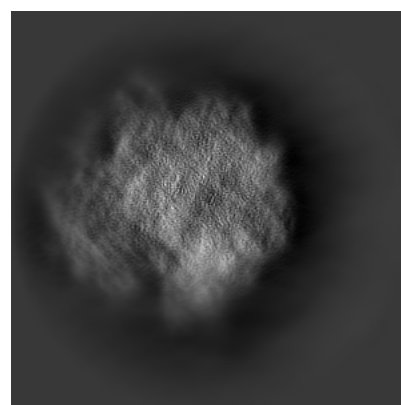
#### 6.1.1 Primary map



X



Y

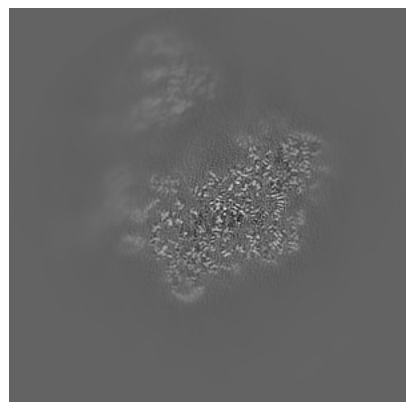


Z

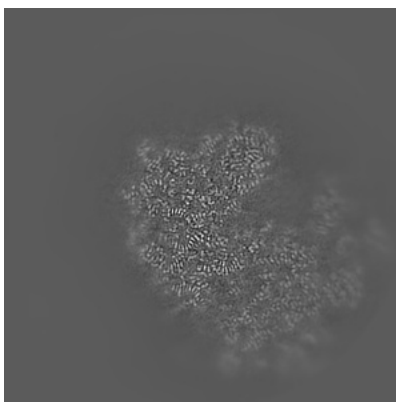
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

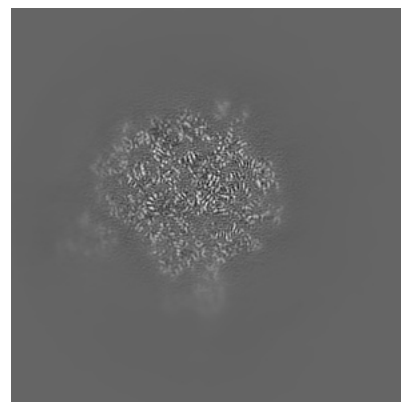
#### 6.2.1 Primary map



X Index: 200



Y Index: 200

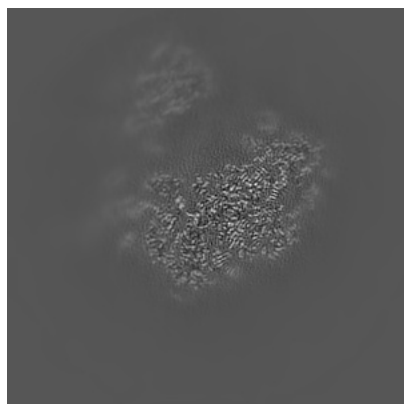


Z Index: 200

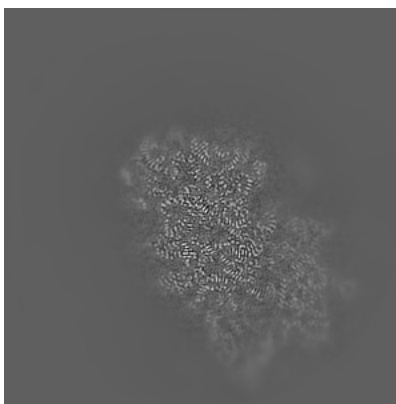
The images above show central slices of the map in three orthogonal directions.

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

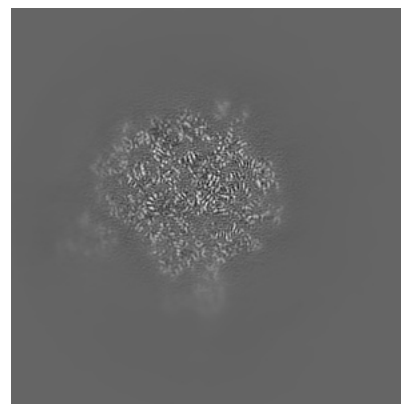
### 6.3.1 Primary map



X Index: 206



Y Index: 225



Z Index: 200

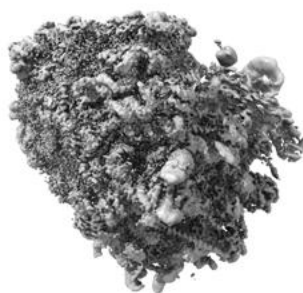
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal surface views [i](#)

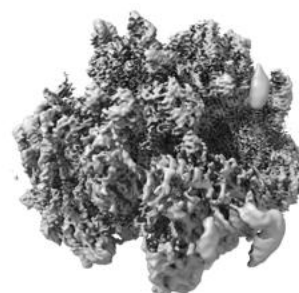
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

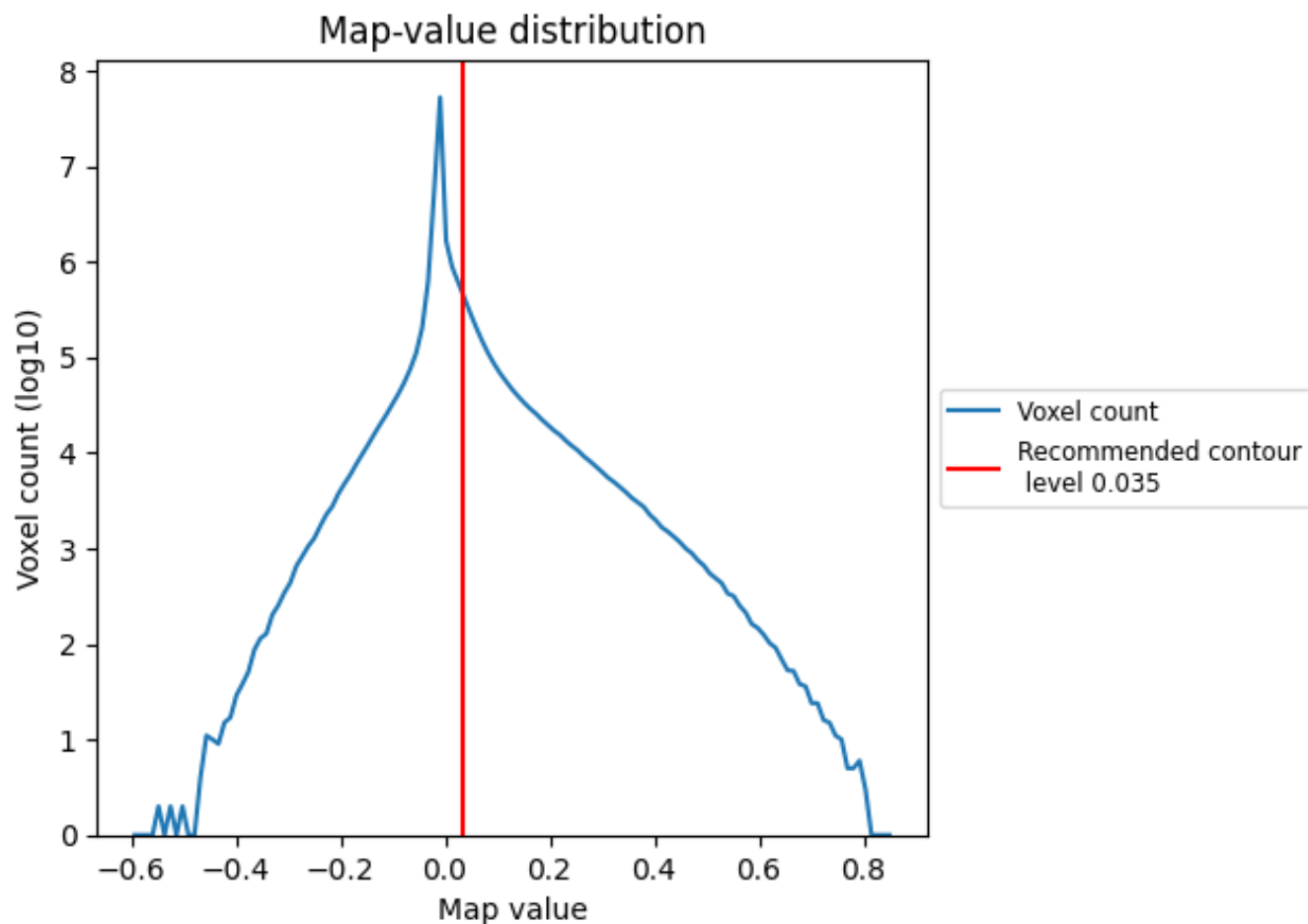
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

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

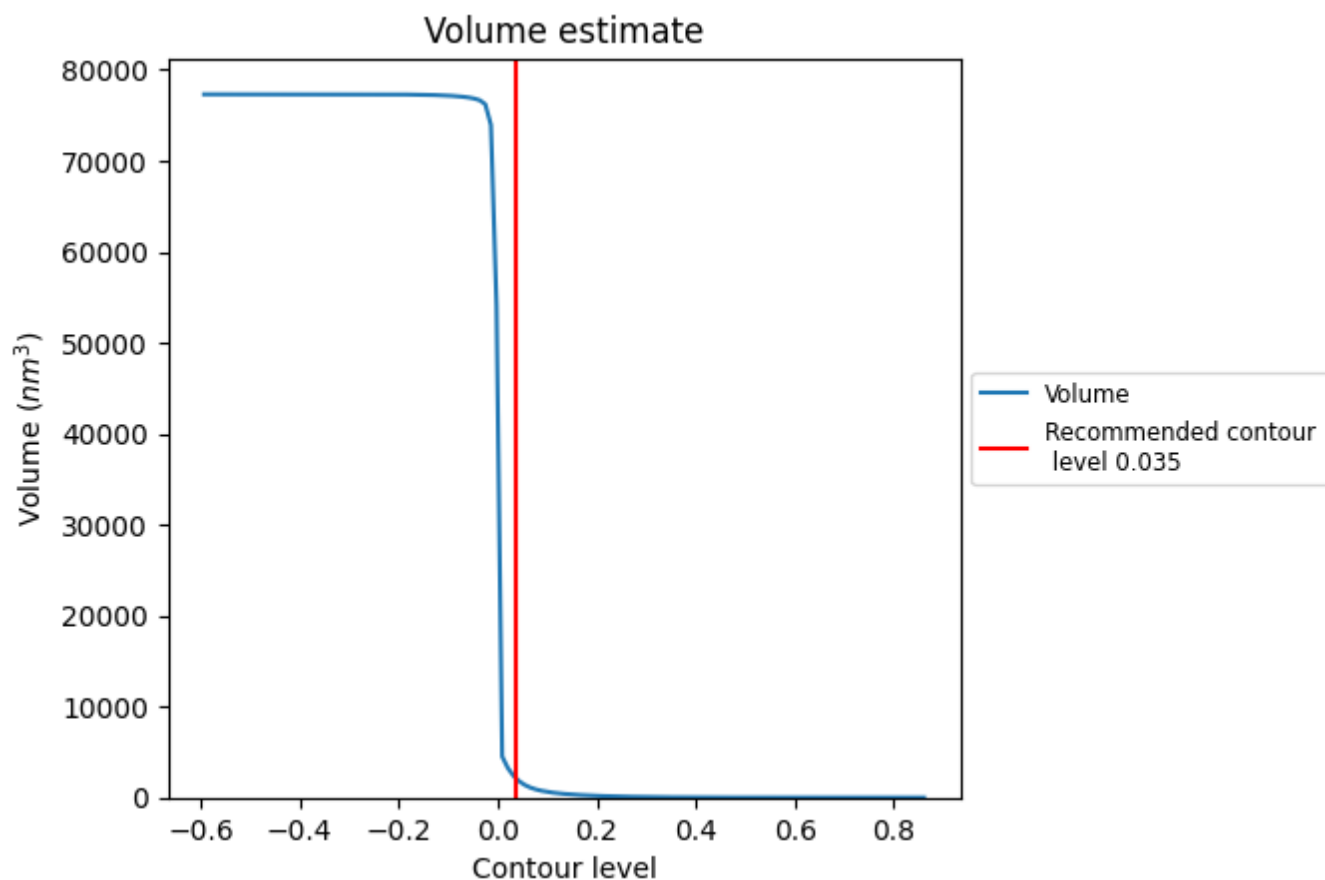
### 7.1 Map-value distribution [i](#)



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



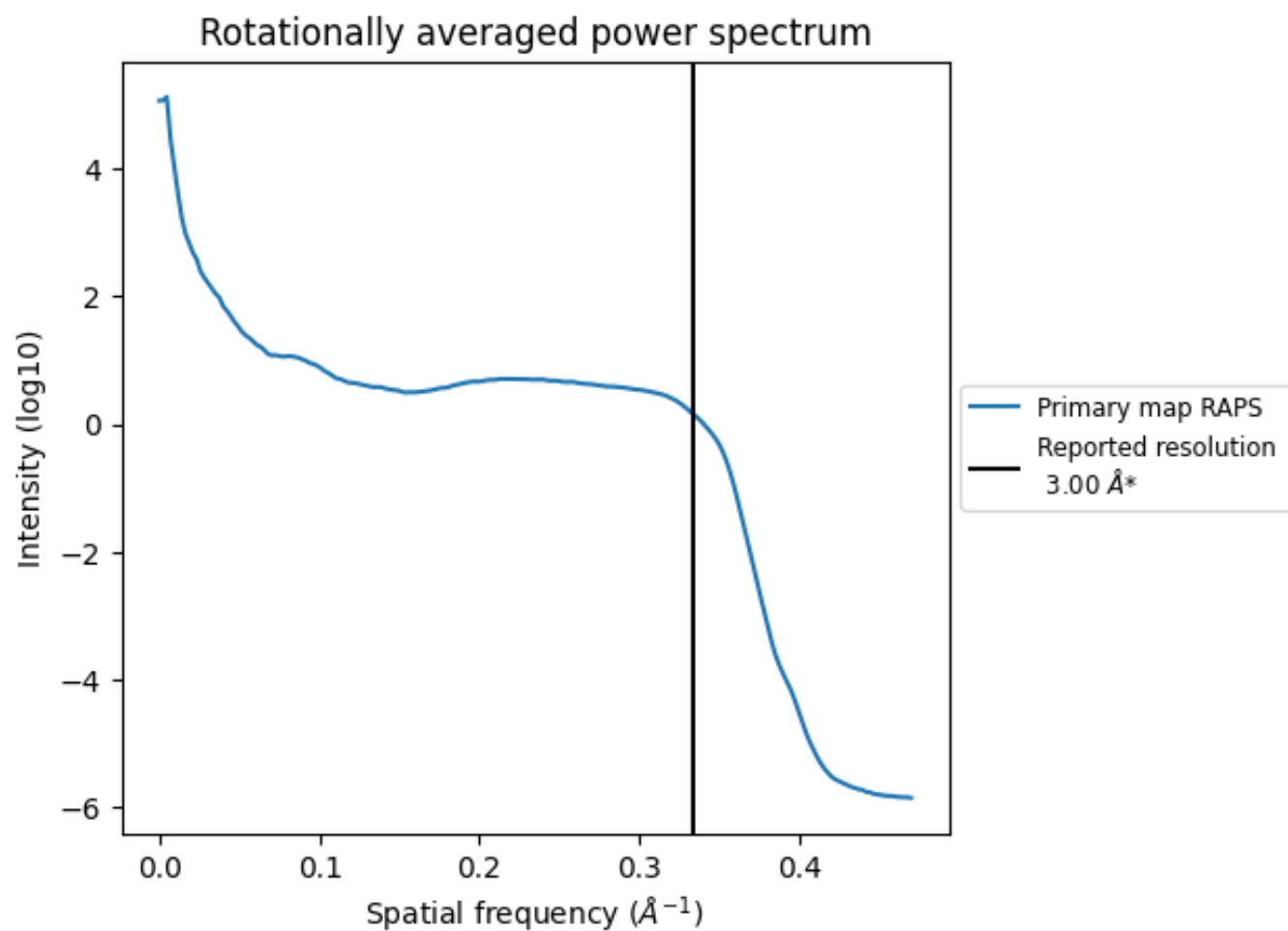
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2221 nm<sup>3</sup>; this corresponds to an approximate mass of 2007 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 ⓘ

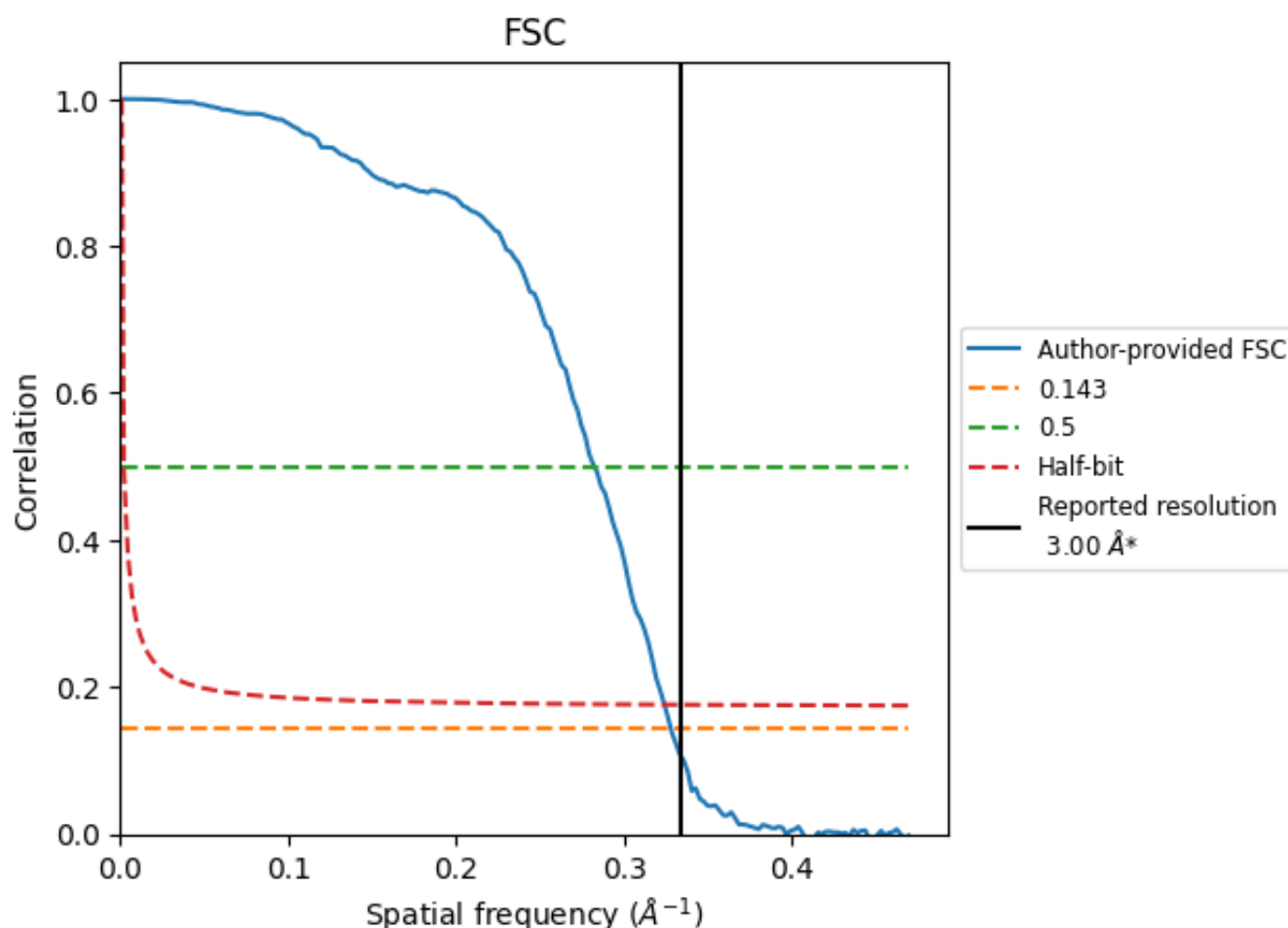


\*Reported resolution corresponds to spatial frequency of 0.333 Å<sup>-1</sup>

## 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 0.333 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

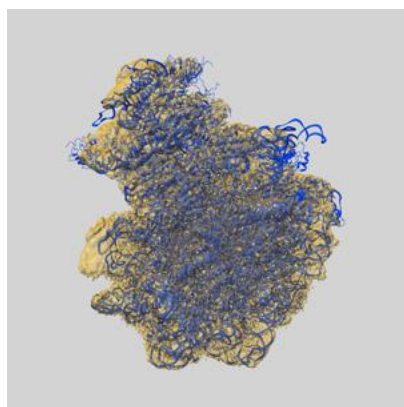
| Resolution estimate (Å)   | Estimation criterion (FSC cut-off) |      |          |
|---------------------------|------------------------------------|------|----------|
|                           | 0.143                              | 0.5  | Half-bit |
| Reported by author        | 3.00                               | -    | -        |
| Author-provided FSC curve | 3.05                               | 3.54 | 3.09     |
| Unmasked-calculated*      | -                                  | -    | -        |

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

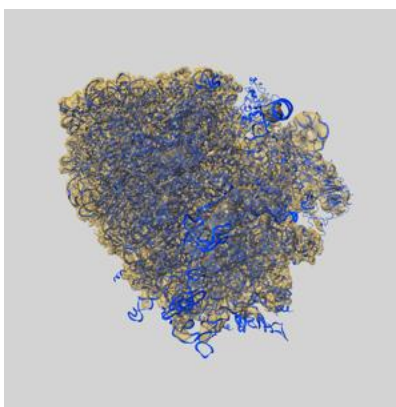
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10624 and PDB model 6XU8. Per-residue inclusion information can be found in section 3 on page 19.

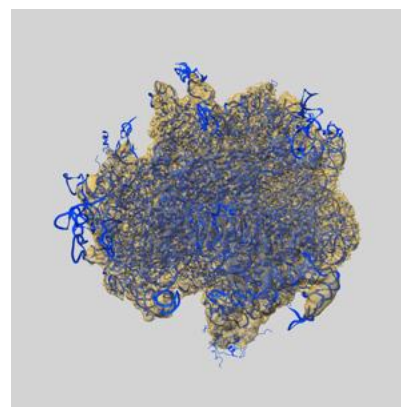
### 9.1 Map-model overlay [i](#)



X



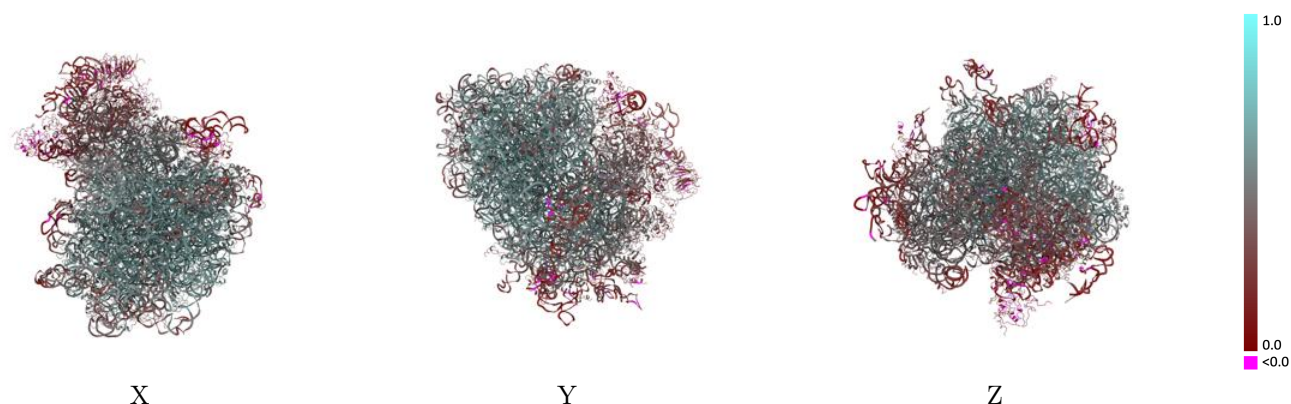
Y



Z

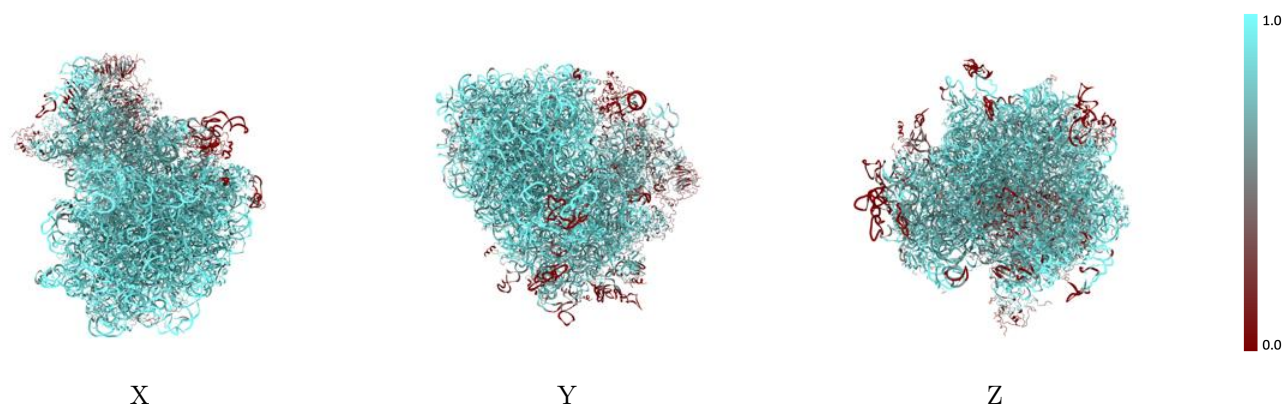
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



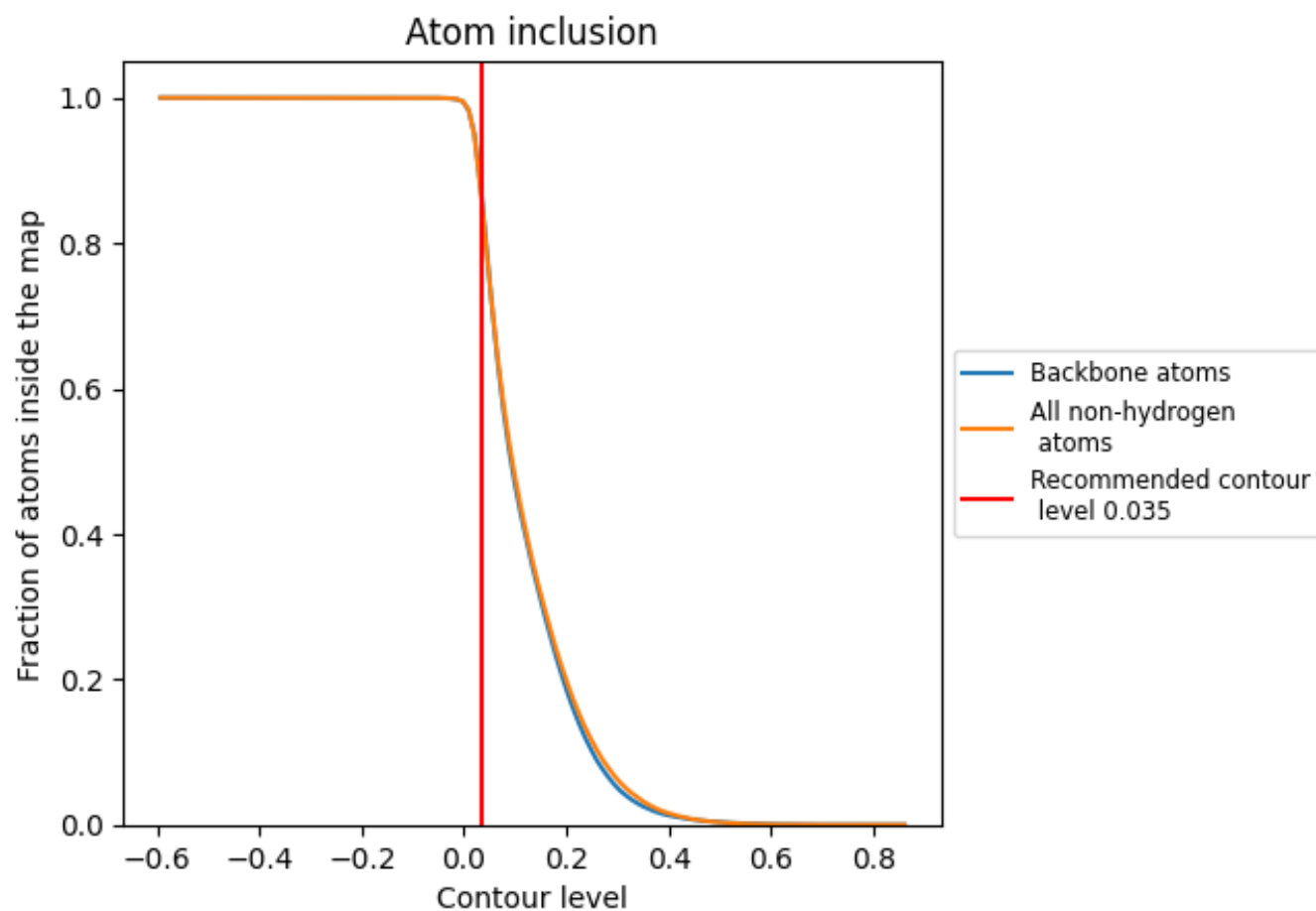
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.035).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 86% 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 (0.035) and Q-score for the entire model and for each chain.





















































































| Chain | Atom inclusion   | Q-score  |
|-------|--|--|
| All   |  0.8557   |  0.4690   |
| A5    |  0.9303   |  0.5240   |
| A7    |  0.9894   |  0.5620   |
| A8    |  0.9786   |  0.5900   |
| A9    |  0.9890   |  0.5630   |
| AA    |  0.6439   |  0.3570   |
| AB    |  0.7855   |  0.4240   |
| AC    |  0.7076   |  0.4180   |
| AD    |  0.4963   |  0.2880   |
| AE    |  0.7815   |  0.4400   |
| AF    |  0.4029   |  0.2890   |
| AG    |  0.6767   |  0.3620   |
| AH    |  0.6717   |  0.3350   |
| AI    |  0.7137   |  0.4450   |
| AJ    |  0.7858  |  0.3840  |
| AK    |  0.8306 |  0.1820 |
| AL    |  0.7307 |  0.4760 |
| AM    |  0.3337 |  0.0880 |
| AN    |  0.8366 |  0.4940 |
| AO    |  0.8011 |  0.4400 |
| AP    |  0.6411 |  0.2030 |
| AQ    |  0.4760 |  0.2430 |
| AR    |  0.3861 |  0.2720 |
| AS    |  0.6636 |  0.2790 |
| AT    |  0.6783 |  0.2550 |
| AU    |  0.4620 |  0.2850 |
| AV    |  0.6103 |  0.3970 |
| AW    |  0.8338 |  0.4890 |
| AX    |  0.7805 |  0.4840 |
| AY    |  0.7452 |  0.3580 |
| AZ    |  0.3970 |  0.2280 |
| Aa    |  0.7762 |  0.4720 |
| Ab    |  0.7903 |  0.3890 |
| Ac    |  0.5365 |  0.3050 |
| Ad    |  0.8285 |  0.3120 |



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| Chain | Atom inclusion   | Q-score  |
|-------|--|--|
| Ae    |  0.6000   |  0.3500   |
| Af    |  0.4230   |  0.0970   |
| Ag    |  0.2735   |  0.1760   |
| B2    |  0.8562   |  0.3880   |
| CA    |  0.9589   |  0.5900   |
| CB    |  0.9337   |  0.5680   |
| CC    |  0.9431   |  0.5700   |
| CD    |  0.8932   |  0.4970   |
| CE    |  0.8359   |  0.4500   |
| CF    |  0.9766   |  0.5970   |
| CG    |  0.8212   |  0.4880   |
| CH    |  0.9592   |  0.5270   |
| CI    |  0.8556   |  0.4890   |
| CJ    |  0.8406   |  0.4420   |
| CL    |  0.8713   |  0.5180   |
| CM    |  0.9020   |  0.4850   |
| CN    |  0.9673   |  0.5880   |
| CO    |  0.9583   |  0.5830   |
| CP    |  0.8399   |  0.5490   |
| CQ    |  0.9719  |  0.5970  |
| CR    |  0.8274 |  0.4900 |
| CS    |  0.9538 |  0.5590 |
| CT    |  0.9515 |  0.5600 |
| CU    |  0.8197 |  0.4670 |
| CV    |  0.9579 |  0.5910 |
| CW    |  0.9506 |  0.5770 |
| CX    |  0.9116 |  0.5480 |
| CY    |  0.9672 |  0.5800 |
| CZ    |  0.9256 |  0.5180 |
| Ca    |  0.9522 |  0.5710 |
| Cb    |  0.9332 |  0.5120 |
| Cc    |  0.9350 |  0.5380 |
| Cd    |  0.9534 |  0.5620 |
| Ce    |  0.9681 |  0.6060 |
| Cf    |  0.9069 |  0.5050 |
| Cg    |  0.9726 |  0.5870 |
| Ch    |  0.9340 |  0.5600 |
| Ci    |  0.8646 |  0.4810 |
| Cj    |  0.9777 |  0.6210 |
| Ck    |  0.8650 |  0.4890 |
| Cl    |  0.9808 |  0.6090 |
| Cm    |  0.9735 |  0.5340 |

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| Chain | Atom inclusion   | Q-score  |
|-------|--|--|
| Cn    |  0.9349 |  0.5760 |
| Co    |  0.9481 |  0.5650 |
| Cp    |  0.9561 |  0.5900 |
| Cr    |  0.8535 |  0.5020 |
| Cz    |  0.0226 |  0.1440 |