# wwPDB EM Validation Summary Report (i)

Dec 17, 2022 – 09:09 am GMT

| | | |
|---|---|---|
| PDB ID | : | 6YLX |
| EMDB ID | : | EMD-10841 |
| Title | : | pre-60S State NE1 (TAP-Flag-Nop53) |
| Authors | : | Kater, L.; Beckmann, R. |
| Deposited on | : | 2020-04-07 |
| Resolution | : | 3.90 Å(reported) |
| Based on initial models | : | 6ELZ, 3JCT, 6N8J |

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

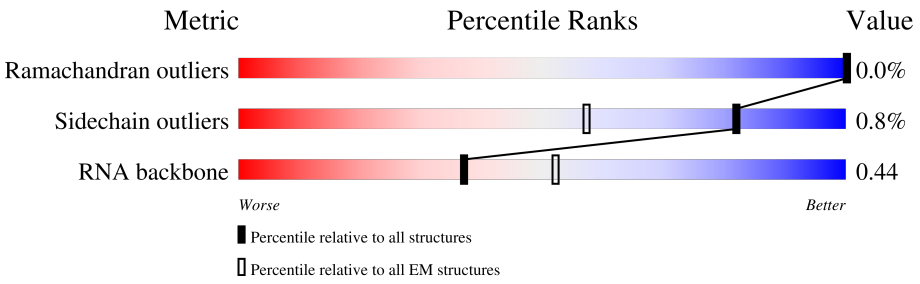
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev43 |
| MolProbity | : | 4.02b-467 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| MapQ | : | 1.9.9 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA)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

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.90 Å.

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




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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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 | B | 387 | 13% 92% 8% |
| 2 | C | 362 | • 90% 9% • |
| 3 | E | 176 | 5% 85% • 11% |
| 4 | F | 244 | • 84% 7% 9% |
| 5 | G | 256 | 10% 69% 5% 25% |
| 6 | H | 191 | 8% 94% 6% |
| 7 | K | 376 | 46% 68% • 32% |
| 8 | L | 199 | 15% 84% 10% 6% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 9 | M | 138 | 6% 93% 5% |
| 10 | N | 204 | 71% 16% 12% |
| 11 | O | 199 | 88% 11% |
| 12 | P | 184 | 8% 85% 11% |
| 13 | Q | 186 | 5% 68% 28% |
| 14 | R | 189 | 33% 79% 17% |
| 15 | S | 172 | 9% 94% 5% |
| 16 | T | 160 | 29% 34% 65% |
| 17 | U | 121 | 31% 88% 12% |
| 18 | V | 137 | 24% 96% |
| 19 | W | 236 | 44% 98% |
| 20 | X | 142 | 11% 94% 5% |
| 21 | Y | 127 | 94% 6% |
| 22 | Z | 136 | 29% 97% |
| 23 | a | 149 | 11% 58% 38% |
| 24 | b | 647 | 44% 71% 27% |
| 25 | c | 105 | 53% 92% 8% |
| 26 | d | 113 | 8% 88% 5% 5% |
| 27 | e | 130 | 5% 85% 12% |
| 28 | f | 107 | 81% 17% |
| 29 | g | 121 | 17% 85% 7% 7% |
| 30 | h | 120 | 95% |
| 31 | i | 100 | 19% 95% |
| 32 | j | 88 | 17% 81% 18% |
| 33 | k | 78 | 24% 96% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 34 | l | 51 | 69% 92% |
| 35 | n | 605 | 17% 58% 39% |
| 36 | o | 220 | 32% 57% 40% |
| 37 | q | 455 | 16% 18% 81% |
| 38 | r | 261 | 58% 82% 17% |
| 39 | s | 520 | 6% 93% |
| 40 | t | 322 | 35% 86% 11% |
| 41 | u | 199 | 19% 58% 38% |
| 42 | y | 245 | 42% 98% |
| 43 | z | 106 | 19% 52% 48% |
| 44 | 1 | 3396 | 8% 28% 37% 9% 25% |
| 45 | 2 | 158 | 15% 66% 19% |
| 46 | 6 | 232 | 12% 12% 72% |
| 47 | w | 841 | 37% 42% 57% |

# 2 Entry composition (i)

There are 47 unique types of molecules in this entry. The entry contains 118882 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 L3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 1 | B | 386 | 3081 | 1956 | 584 | 533 | 8 | 0 | 0 |

- Molecule 2 is a protein called 60S ribosomal protein L4-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 2 | C | 361 | 2749 | 1730 | 522 | 494 | 3 | 0 | 0 |

- Molecule 3 is a protein called 60S ribosomal protein L6-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 3 | E | 156 | 1239 | 800 | 222 | 216 | 1 | 0 | 0 |

- Molecule 4 is a protein called 60S ribosomal protein L7-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 4 | F | 222 | 1784 | 1151 | 324 | 308 | 1 | 0 | 0 |

- Molecule 5 is a protein called 60S ribosomal protein L8-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 5 | G | 192 | 1515 | 974 | 267 | 272 | 2 | 0 | 0 |

- Molecule 6 is a protein called 60S ribosomal protein L9-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 6 | H | 191 | 1518 | 963 | 274 | 277 | 4 | 0 | 0 |

- Molecule 7 is a protein called Proteasome-interacting protein CIC1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 7 | K | 256 | 2064 | 1332 | 342 | 387 | 3 | 0 | 0 |

- Molecule 8 is a protein called 60S ribosomal protein L13-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 8 | L | 187 | 1499 | 934 | 307 | 258 | 0 | 0 |

- Molecule 9 is a protein called 60S ribosomal protein L14-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 9 | M | 137 | 1059 | 678 | 200 | 179 | 2 | 0 | 0 |

- Molecule 10 is a protein called 60S ribosomal protein L15-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 10 | N | 180 | 1543 | 968 | 325 | 249 | 1 | 0 | 0 |

- Molecule 11 is a protein called 60S ribosomal protein L16-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 11 | O | 197 | 1555 | 1003 | 289 | 262 | 1 | 0 | 0 |

- Molecule 12 is a protein called 60S ribosomal protein L17-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 12 | P | 176 | 1397 | 868 | 279 | 250 | 0 | 0 |

- Molecule 13 is a protein called 60S ribosomal protein L18-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 13 | Q | 134 | 1035 | 659 | 196 | 179 | 1 | 0 | 0 |

- Molecule 14 is a protein called 60S ribosomal protein L19-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 14 | R | 156 | 1258 | 781 | 265 | 212 | 0 | 0 |

- Molecule 15 is a protein called 60S ribosomal protein L20-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 15 | S | 171 | 1437 | 925 | 266 | 243 | 3 | 0 | 0 |

- Molecule 16 is a protein called 60S ribosomal protein L21-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 16 | T | 56 | 434 | 268 | 86 | 79 | 1 | 0 | 0 |

- Molecule 17 is a protein called 60S ribosomal protein L22-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 17 | U | 106 | 844 | 545 | 138 | 161 | 0 | 0 |

- Molecule 18 is a protein called 60S ribosomal protein L23-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 18 | V | 136 | 1003 | 628 | 189 | 179 | 7 | 0 | 0 |

- Molecule 19 is a protein called Ribosome assembly factor MRT4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 19 | W | 234 | 1885 | 1194 | 323 | 362 | 6 | 0 | 0 |

- Molecule 20 is a protein called 60S ribosomal protein L25.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 20 | X | 141 | 1100 | 705 | 196 | 197 | 2 | 0 | 0 |

- Molecule 21 is a protein called 60S ribosomal protein L26-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 21 | Y | 126 | 993 | 625 | 192 | 176 | 0 | 0 |

- Molecule 22 is a protein called 60S ribosomal protein L27-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 22 | Z | 135 | 1092 | 710 | 202 | 180 | 0 | 0 |

- Molecule 23 is a protein called 60S ribosomal protein L28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 23 | a | 93 | 735 | 479 | 130 | 125 | 1 | 0 | 0 |

- Molecule 24 is a protein called Nucleolar GTP-binding protein 1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 24 | b | 470 | 3814 | 2424 | 663 | 709 | 18 | 0 | 0 |

- Molecule 25 is a protein called 60S ribosomal protein L30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 25 | c | 97 | 743 | 479 | 124 | 139 | 1 | 0 | 0 |

- Molecule 26 is a protein called 60S ribosomal protein L31-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 26 | d | 107 | 873 | 553 | 165 | 154 | 1 | 0 | 0 |

- Molecule 27 is a protein called 60S ribosomal protein L32.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 27 | e | 127 | 1020 | 647 | 205 | 167 | 1 | 0 | 0 |

- Molecule 28 is a protein called 60S ribosomal protein L33-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 28 | f | 106 | 850 | 540 | 165 | 144 | 1 | 0 | 0 |

- Molecule 29 is a protein called 60S ribosomal protein L34-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 29 | g | 112 | 881 | 546 | 179 | 152 | 4 | 0 | 0 |

- Molecule 30 is a protein called 60S ribosomal protein L35-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 30 | h | 119 | 969 | 615 | 186 | 167 | 1 | 0 | 0 |

- Molecule 31 is a protein called 60S ribosomal protein L36-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 31 | i | 99 | 771 | 481 | 156 | 132 | 2 | 0 | 0 |

- Molecule 32 is a protein called 60S ribosomal protein L37-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 32 | j | 87 | 681 | 414 | 148 | 114 | 5 | 0 | 0 |

- Molecule 33 is a protein called 60S ribosomal protein L38.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 33 | k | 77 | 612 | 391 | 115 | 106 | 0 | 0 |

- Molecule 34 is a protein called 60S ribosomal protein L39.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 34 | l | 50 | 436 | 272 | 97 | 65 | 2 | 0 | 0 |

- Molecule 35 is a protein called Pescadillo homolog.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 35 | n | 371 | 3030 | 1963 | 523 | 534 | 10 | 0 | 0 |

- Molecule 36 is a protein called Ribosome biogenesis protein 15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 36 | o | 133 | 1107 | 716 | 198 | 189 | 4 | 0 | 0 |

- Molecule 37 is a protein called Ribosome biogenesis protein NOP53.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 37 | q | 87 | 723 | 450 | 129 | 143 | 1 | 0 | 0 |

- Molecule 38 is a protein called Ribosome biogenesis protein NSA2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 38 | r | 217 | 1760 | 1110 | 334 | 309 | 7 | 0 | 0 |

- Molecule 39 is a protein called Nuclear GTP-binding protein NUG1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 39 | s | 36 | 301 | 184 | 69 | 46 | 2 | 0 | 0 |

- Molecule 40 is a protein called Ribosome biogenesis protein RLP7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 40 | t | 287 | 2306 | 1459 | 427 | 417 | 3 | 0 | 0 |

- Molecule 41 is a protein called Ribosome biogenesis protein RLP24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 41 | u | 123 | 1040 | 652 | 211 | 168 | 9 | 0 | 0 |

- Molecule 42 is a protein called Eukaryotic translation initiation factor 6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 42 | y | 244 | 1849 | 1146 | 319 | 377 | 7 | 0 | 0 |

- Molecule 43 is a protein called UPF0642 protein YBL028C.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 43 | z | 55 | 444 | 273 | 88 | 83 | 0 | 0 |

- Molecule 44 is a RNA chain called 25S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 44 | 1 | 2534 | 54232 | 24220 | 9799 | 17679 | 2534 | 0 | 0 |

- Molecule 45 is a RNA chain called 5.8S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 45 | 2 | 158 | 3353 | 1500 | 586 | 1109 | 158 | 0 | 0 |

- Molecule 46 is a RNA chain called ITS2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 46 | 6 | 65 | 1370 | 614 | 228 | 463 | 65 | 0 | 0 |

- Molecule 47 is a protein called 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase.

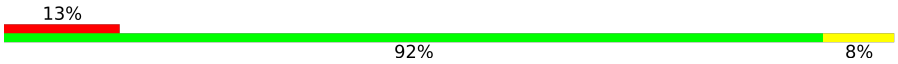
| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 47 | w | 360 | 2898 | 1860 | 507 | 516 | 15 | 0 | 0 |

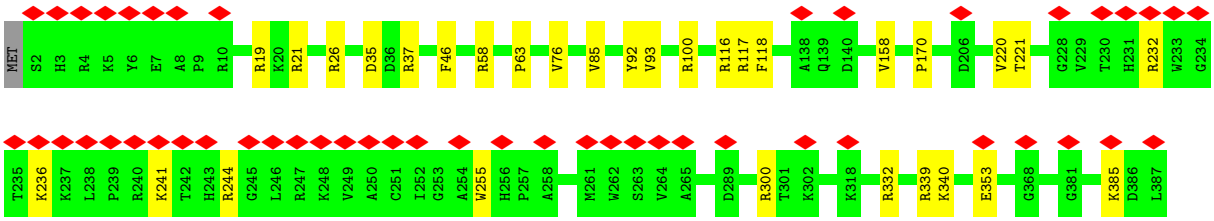
# 3 Residue-property plots (i)

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 L3

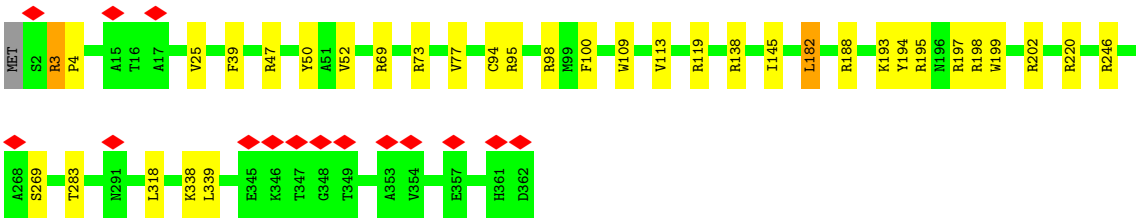
Chain B:



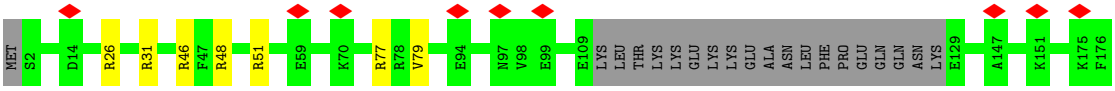

- Molecule 2: 60S ribosomal protein L4-A

Chain C:



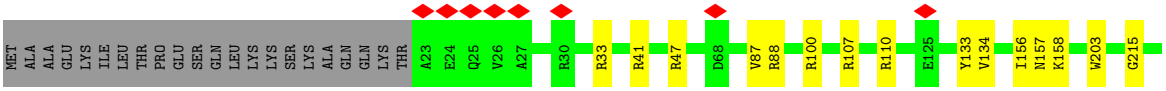

- Molecule 3: 60S ribosomal protein L6-A

Chain E:



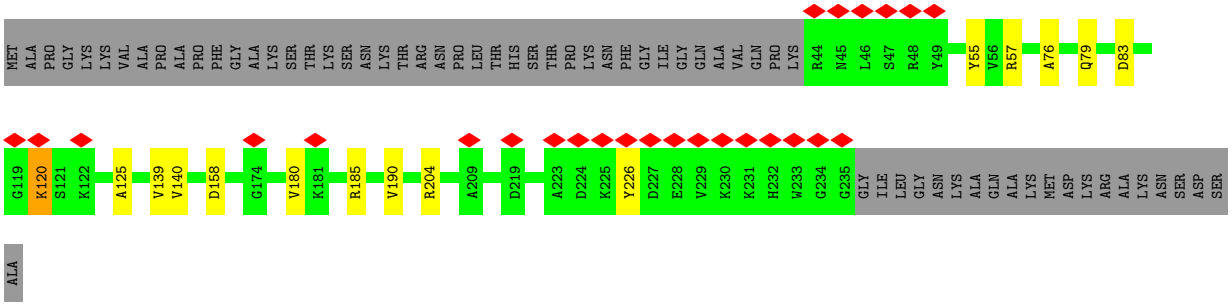

- Molecule 4: 60S ribosomal protein L7-A

Chain F:



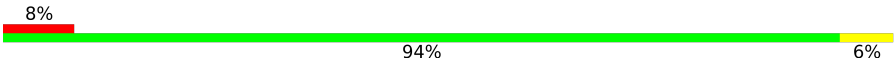
• Molecule 5: 60S ribosomal protein L8-A

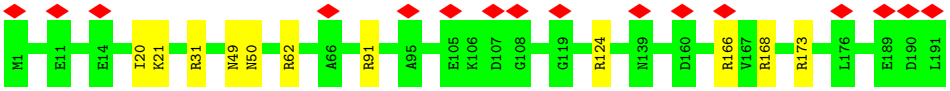
Chain G:




• Molecule 6: 60S ribosomal protein L9-A

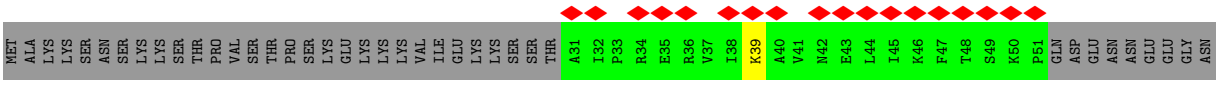
Chain H:

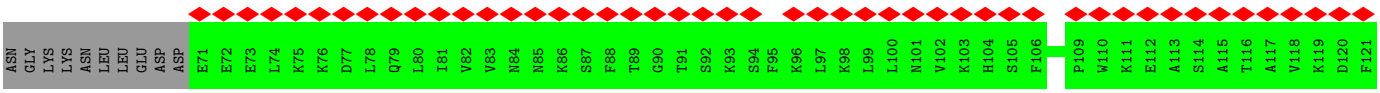


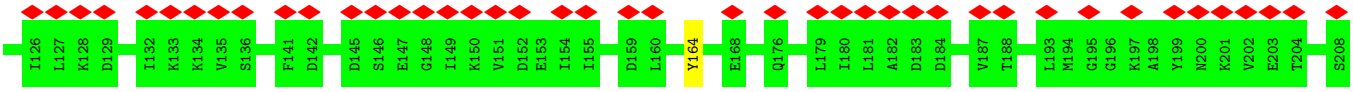



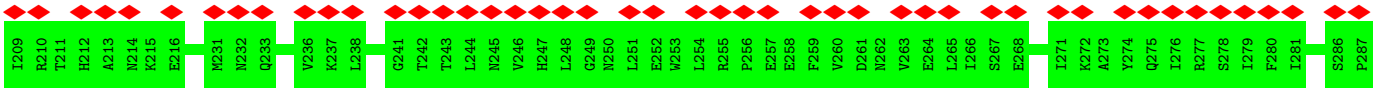

• Molecule 7: Proteasome-interacting protein CIC1

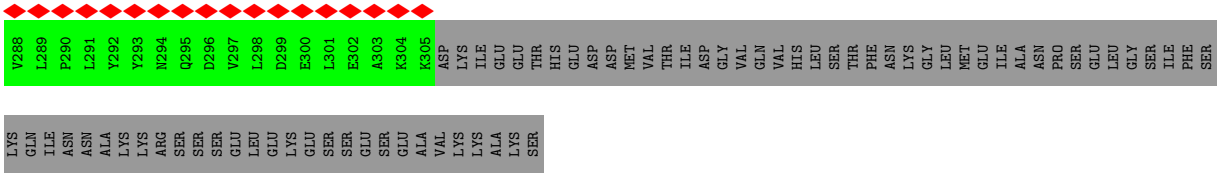
Chain K:



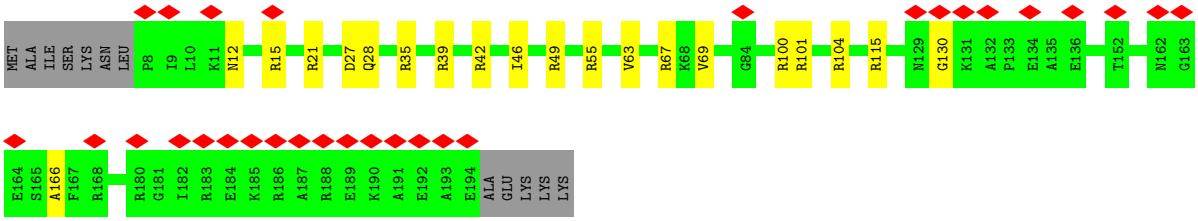



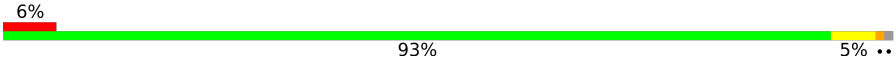

• Molecule 8: 60S ribosomal protein L13-A

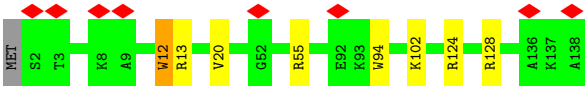
Chain L:




- Molecule 9: 60S ribosomal protein L14-A

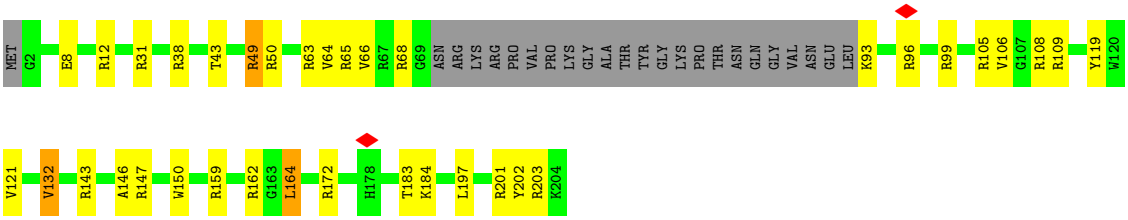
Chain M:



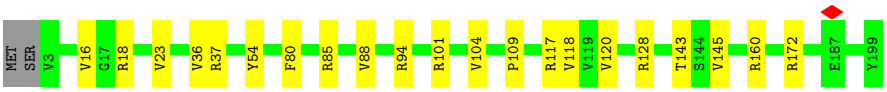

- Molecule 10: 60S ribosomal protein L15-A

Chain N:



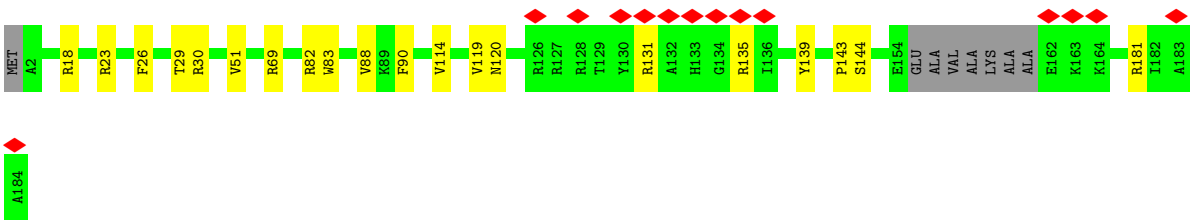

- Molecule 11: 60S ribosomal protein L16-A

Chain O:



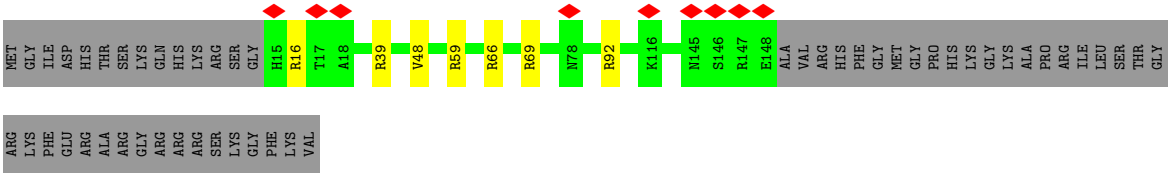

- Molecule 12: 60S ribosomal protein L17-A

Chain P:



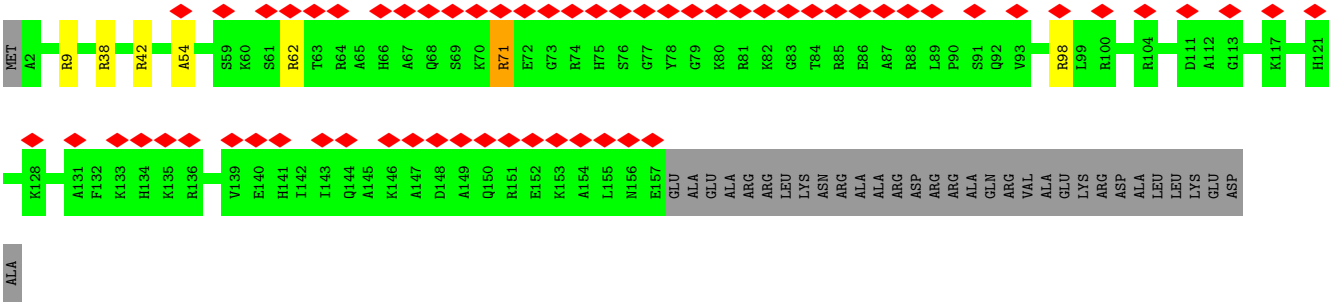

- Molecule 13: 60S ribosomal protein L18-A

Chain Q:



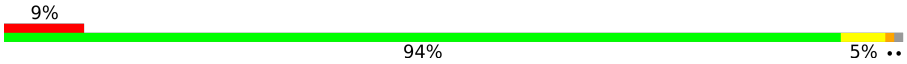

- Molecule 14: 60S ribosomal protein L19-A

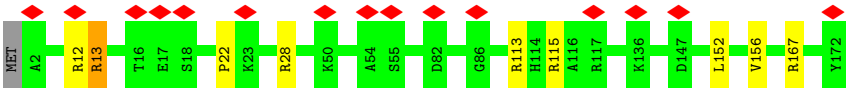
Chain R:




- Molecule 15: 60S ribosomal protein L20-A

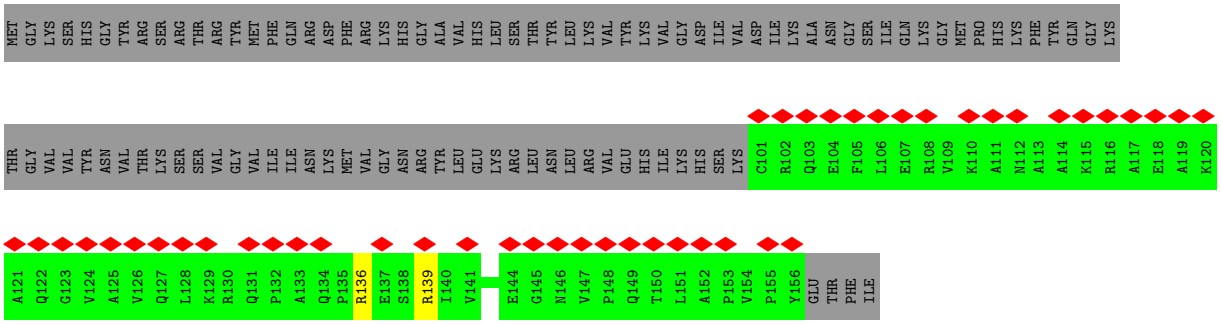
Chain S:



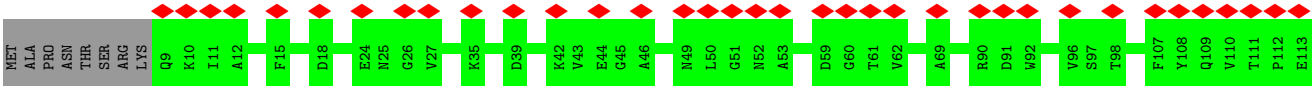

- Molecule 16: 60S ribosomal protein L21-A

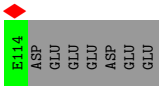
Chain T:




- Molecule 17: 60S ribosomal protein L22-A

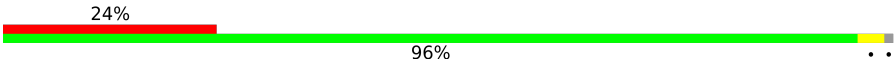
Chain U:

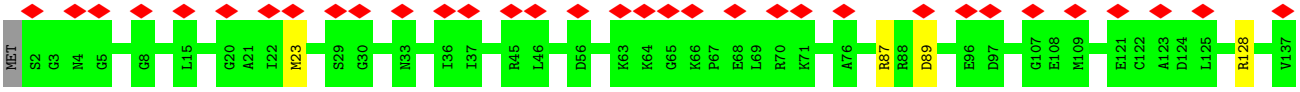





- Molecule 18: 60S ribosomal protein L23-A

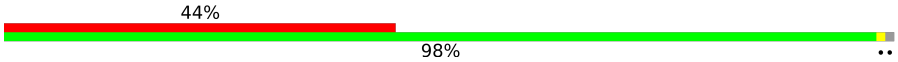
Chain V:

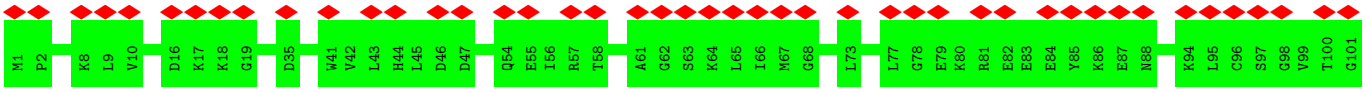


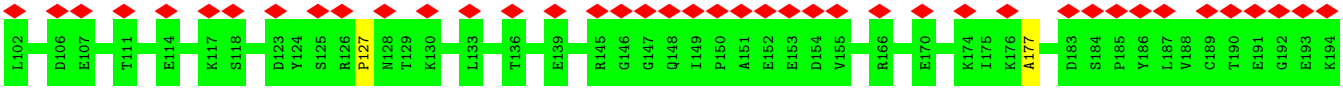



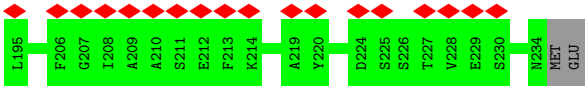

- Molecule 19: Ribosome assembly factor MRT4

Chain W:



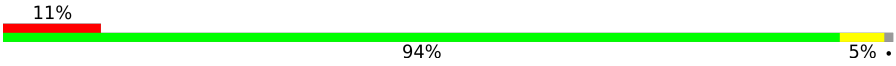



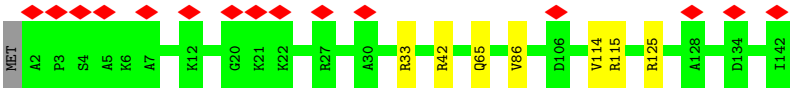




- Molecule 20: 60S ribosomal protein L25

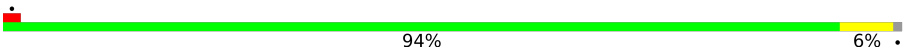
Chain X:

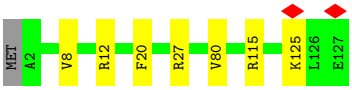



- Molecule 21: 60S ribosomal protein L26-A

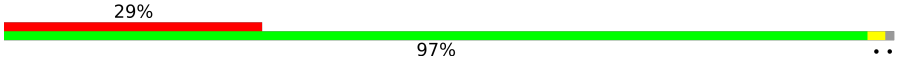
Chain Y:

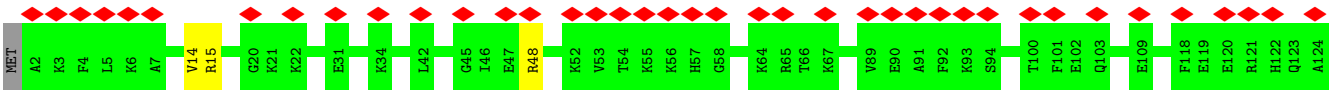



- Molecule 22: 60S ribosomal protein L27-A

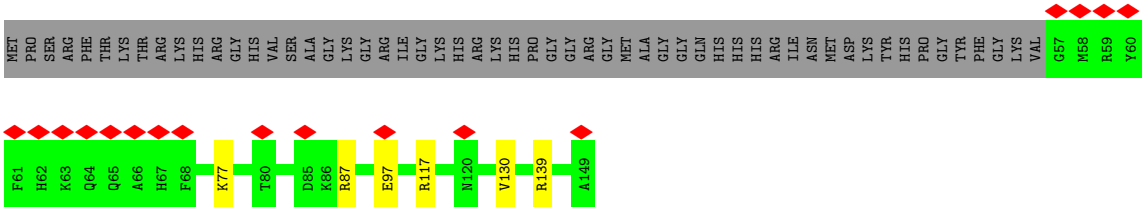
Chain Z:



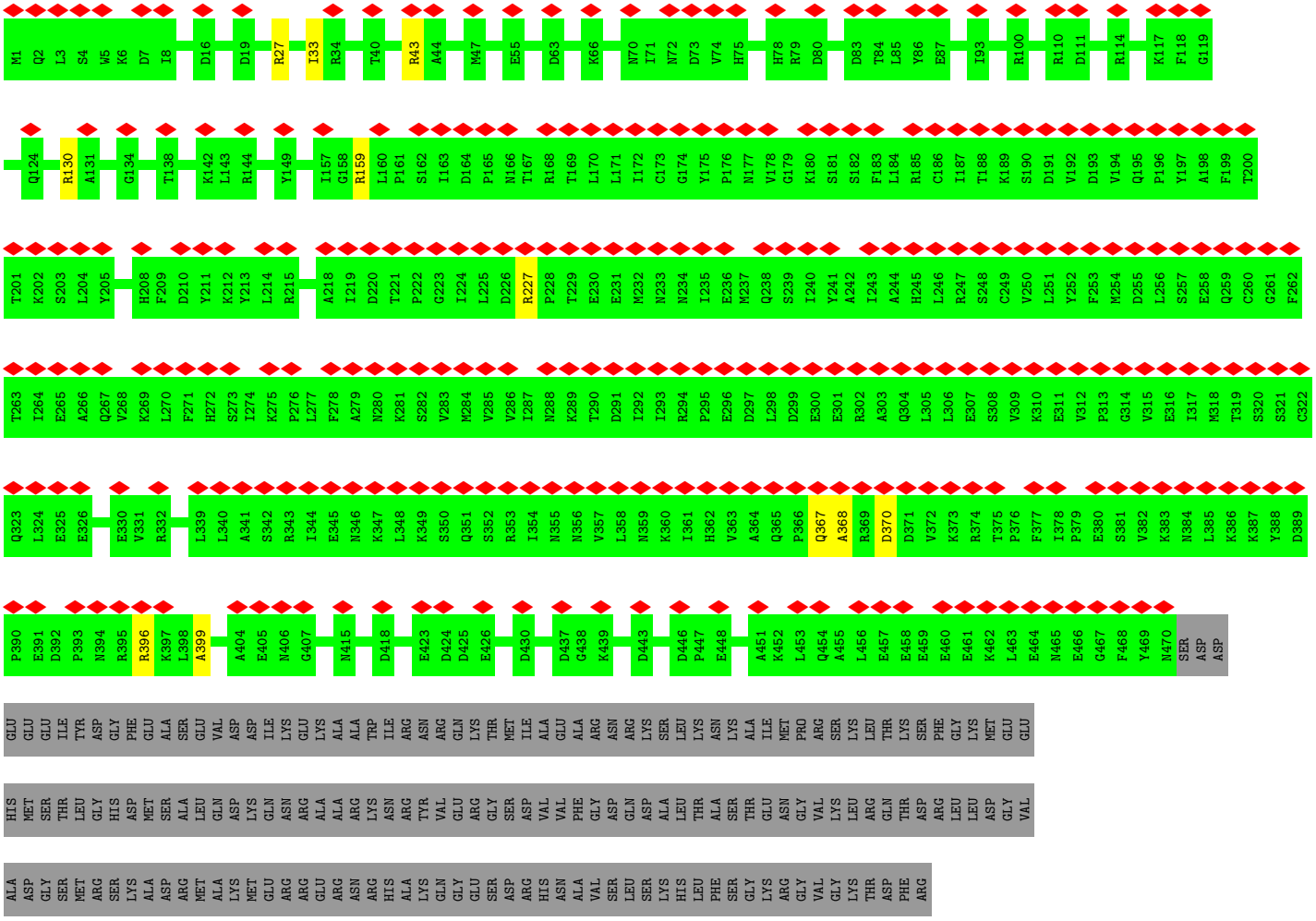
• Molecule 23: 60S ribosomal protein L28

Chain a:



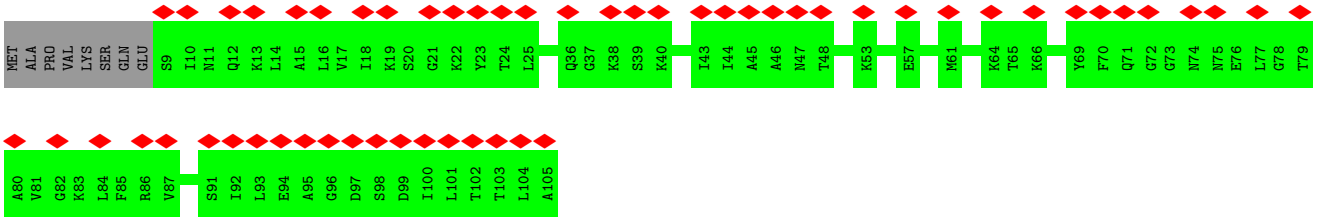

• Molecule 24: Nucleolar GTP-binding protein 1

Chain b:



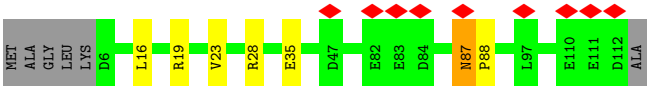

• Molecule 25: 60S ribosomal protein L30

Chain c: 53% 92% 8%



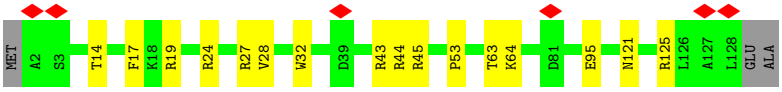

- Molecule 26: 60S ribosomal protein L31-A

Chain d: 8% 88% 5% 5%



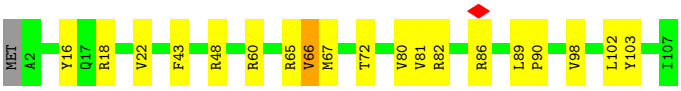

- Molecule 27: 60S ribosomal protein L32

Chain e: 5% 85% 12%



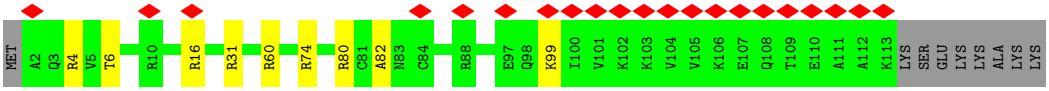

- Molecule 28: 60S ribosomal protein L33-A

Chain f: 81% 17%



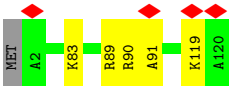

- Molecule 29: 60S ribosomal protein L34-A

Chain g: 17% 85% 7% 7%



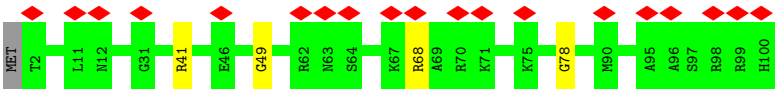

- Molecule 30: 60S ribosomal protein L35-A

Chain h: 95%

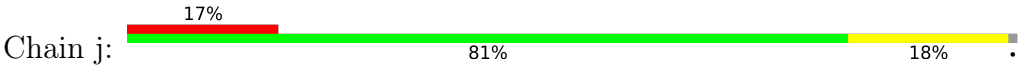


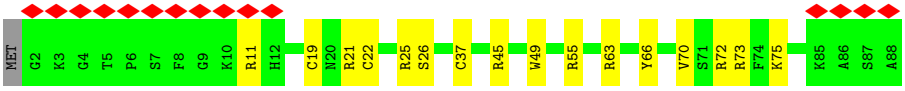

- Molecule 31: 60S ribosomal protein L36-A

Chain i: 19% 95%

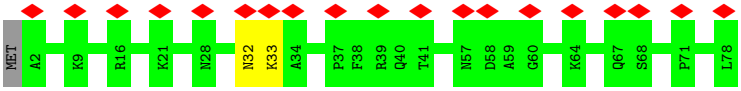



- Molecule 32: 60S ribosomal protein L37-A

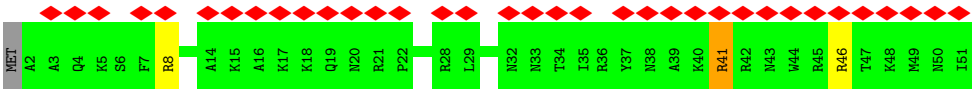


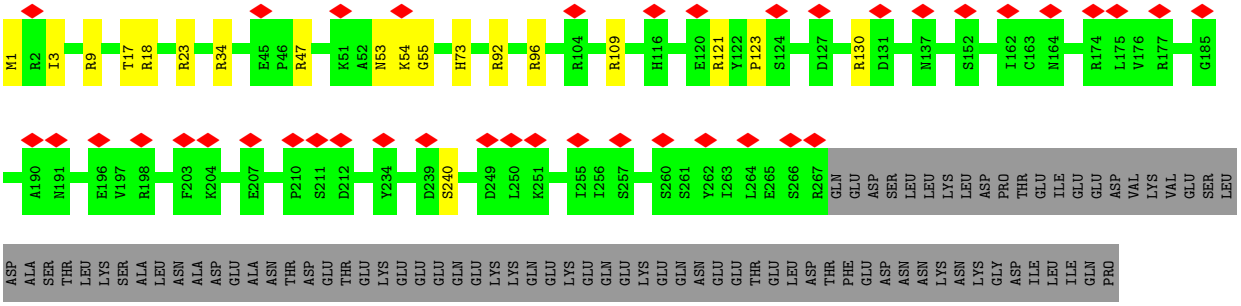

- Molecule 33: 60S ribosomal protein L38

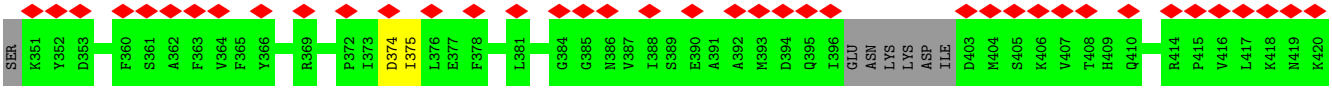


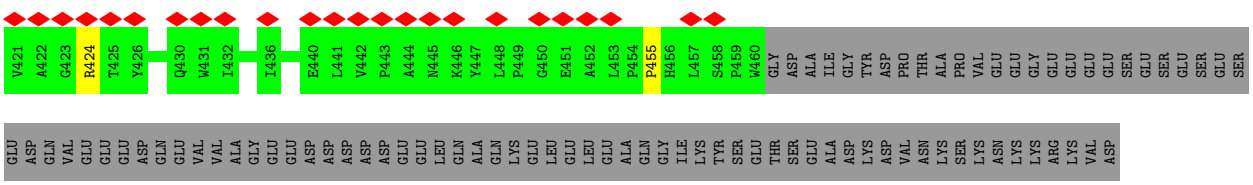

- Molecule 34: 60S ribosomal protein L39




- Molecule 35: Pescadillo homolog

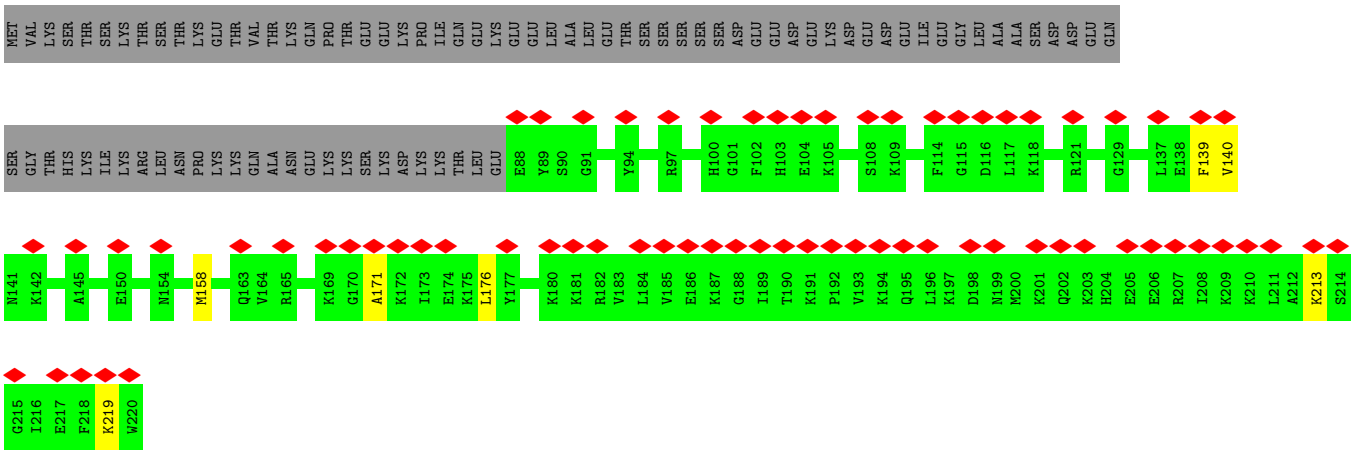


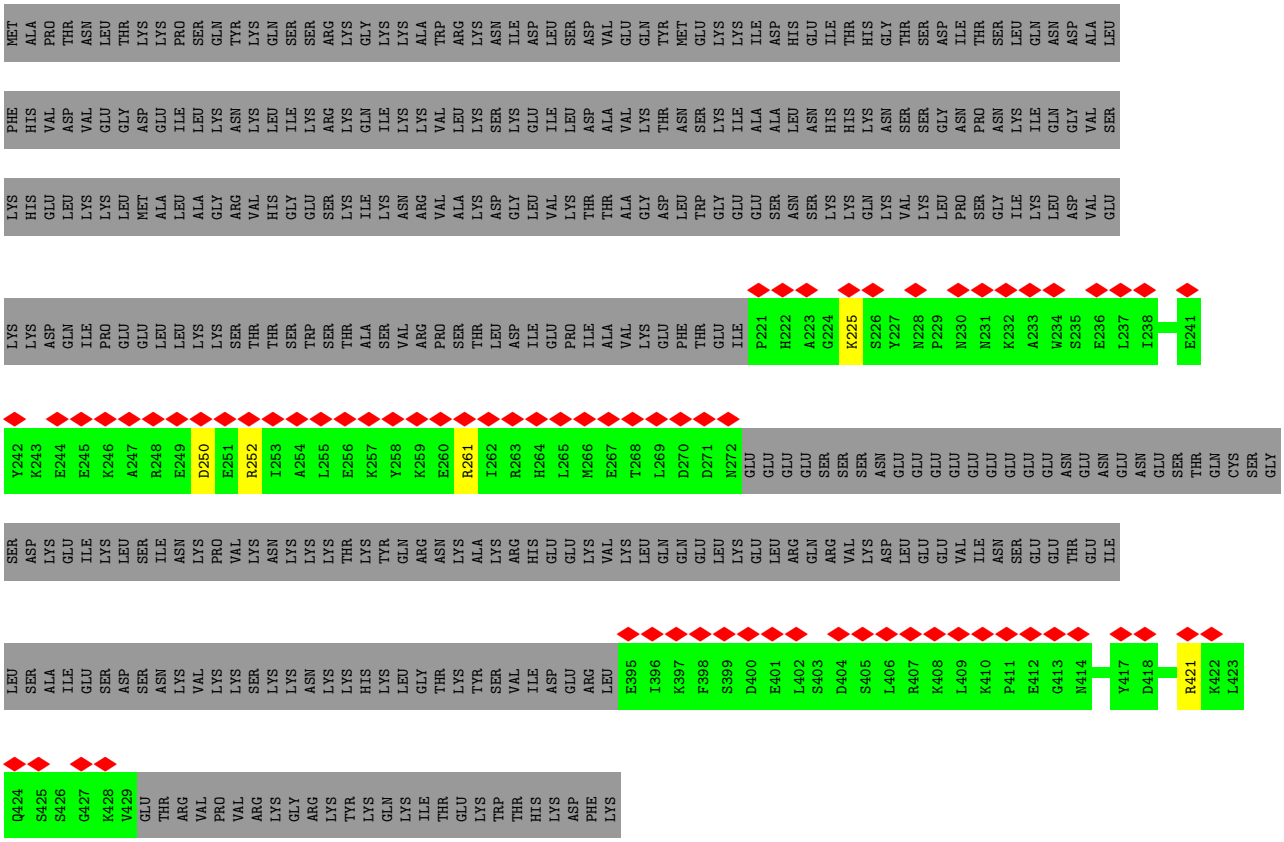
- Molecule 36: Ribosome biogenesis protein 15

Chain o:



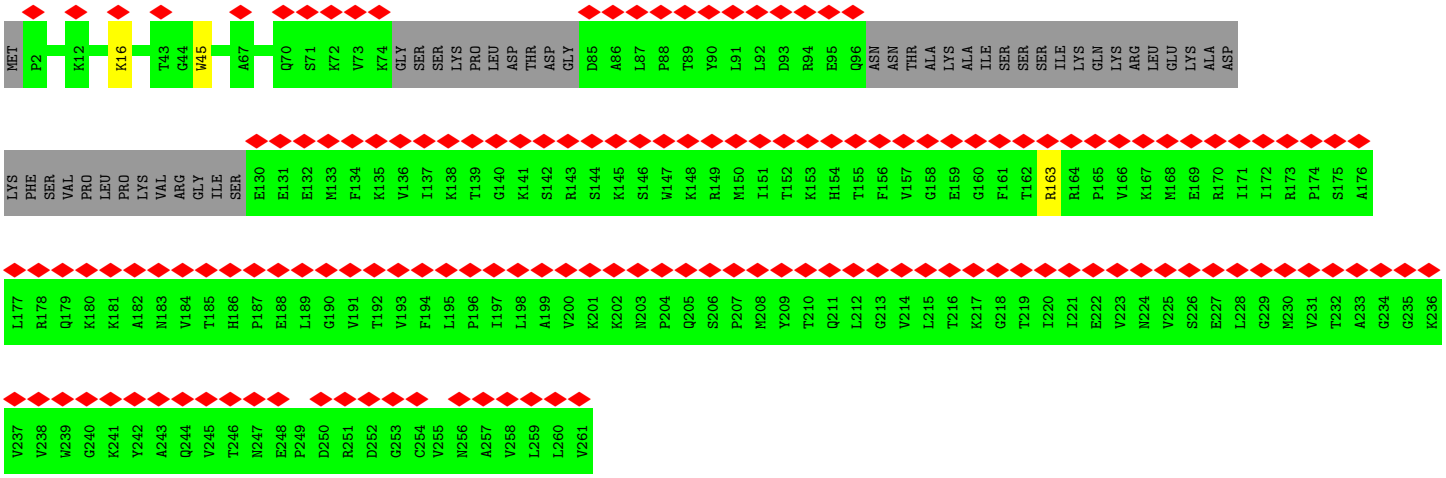

- Molecule 37: Ribosome biogenesis protein NOP53

Chain q:



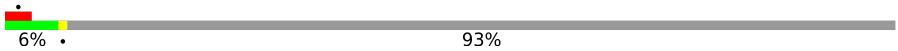

- Molecule 38: Ribosome biogenesis protein NSA2

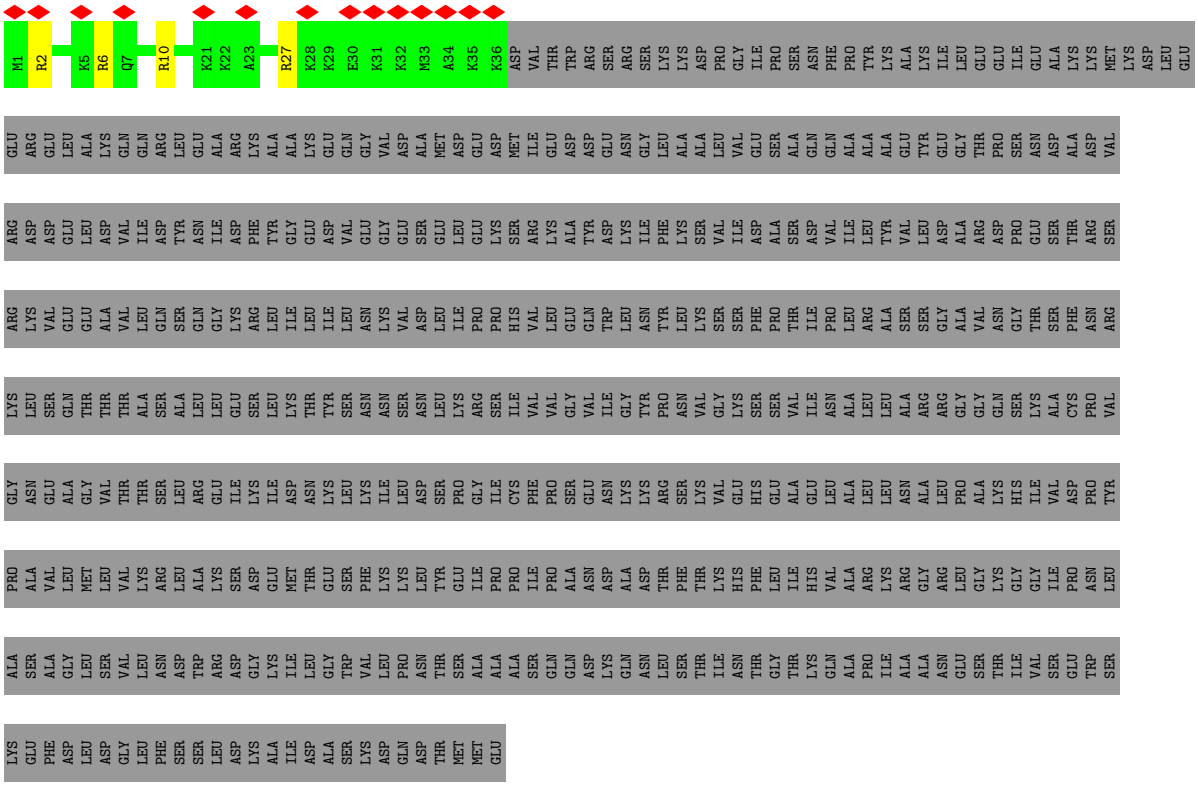
Chain r:




- Molecule 39: Nuclear GTP-binding protein NUG1

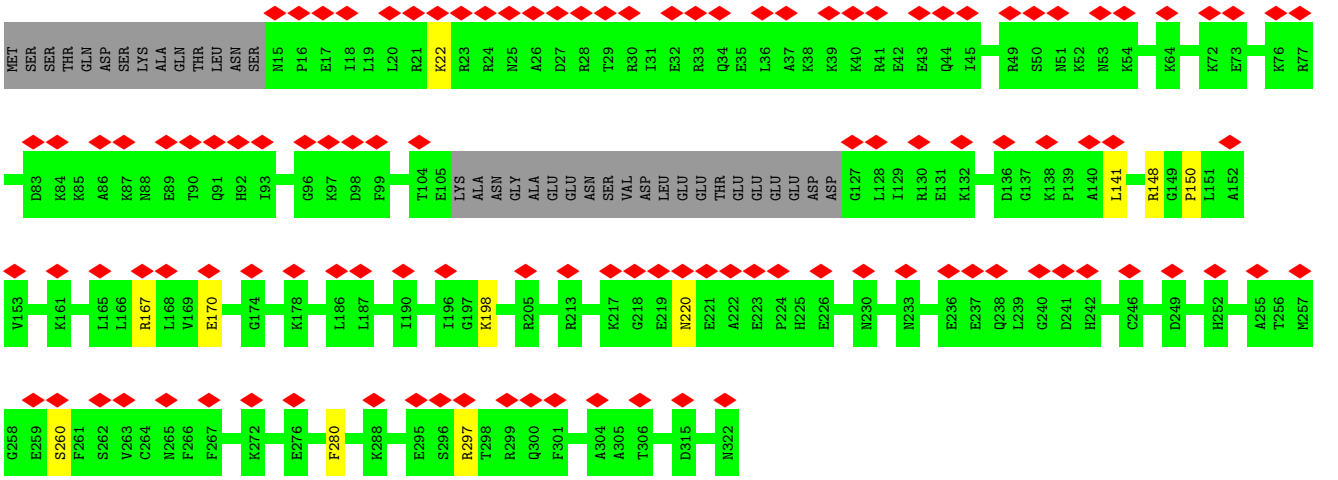
Chain s:



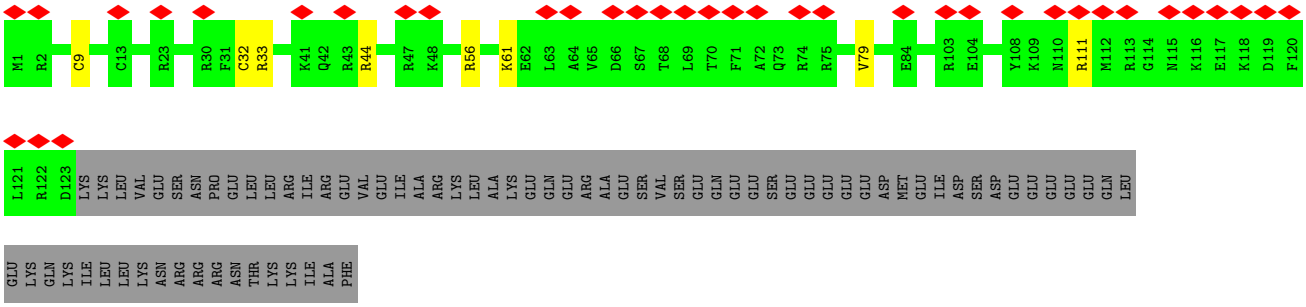

- Molecule 40: Ribosome biogenesis protein RLP7

Chain t:



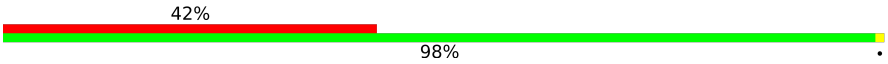

- Molecule 41: Ribosome biogenesis protein RLP24

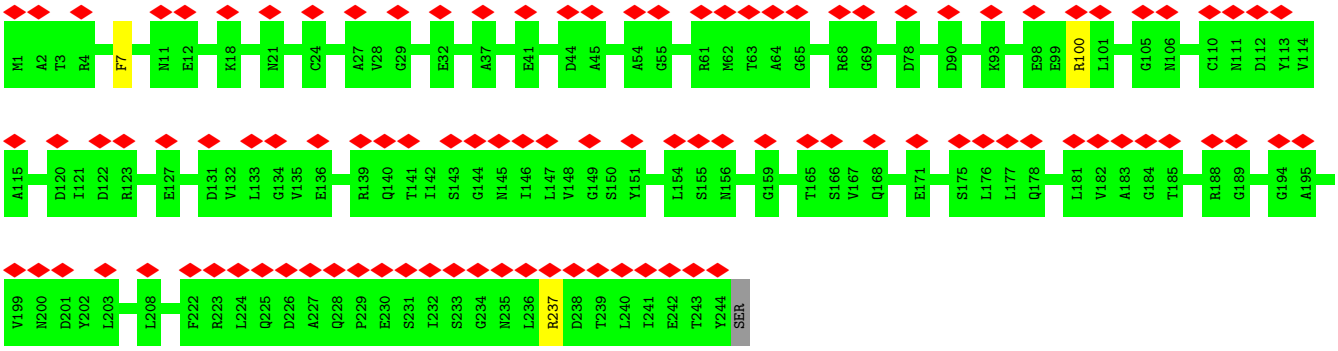
Chain u:




- Molecule 42: Eukaryotic translation initiation factor 6

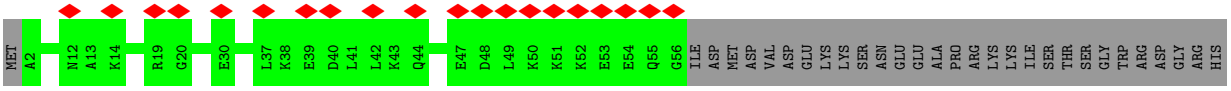
Chain y:




- Molecule 43: UPF0642 protein YBL028C

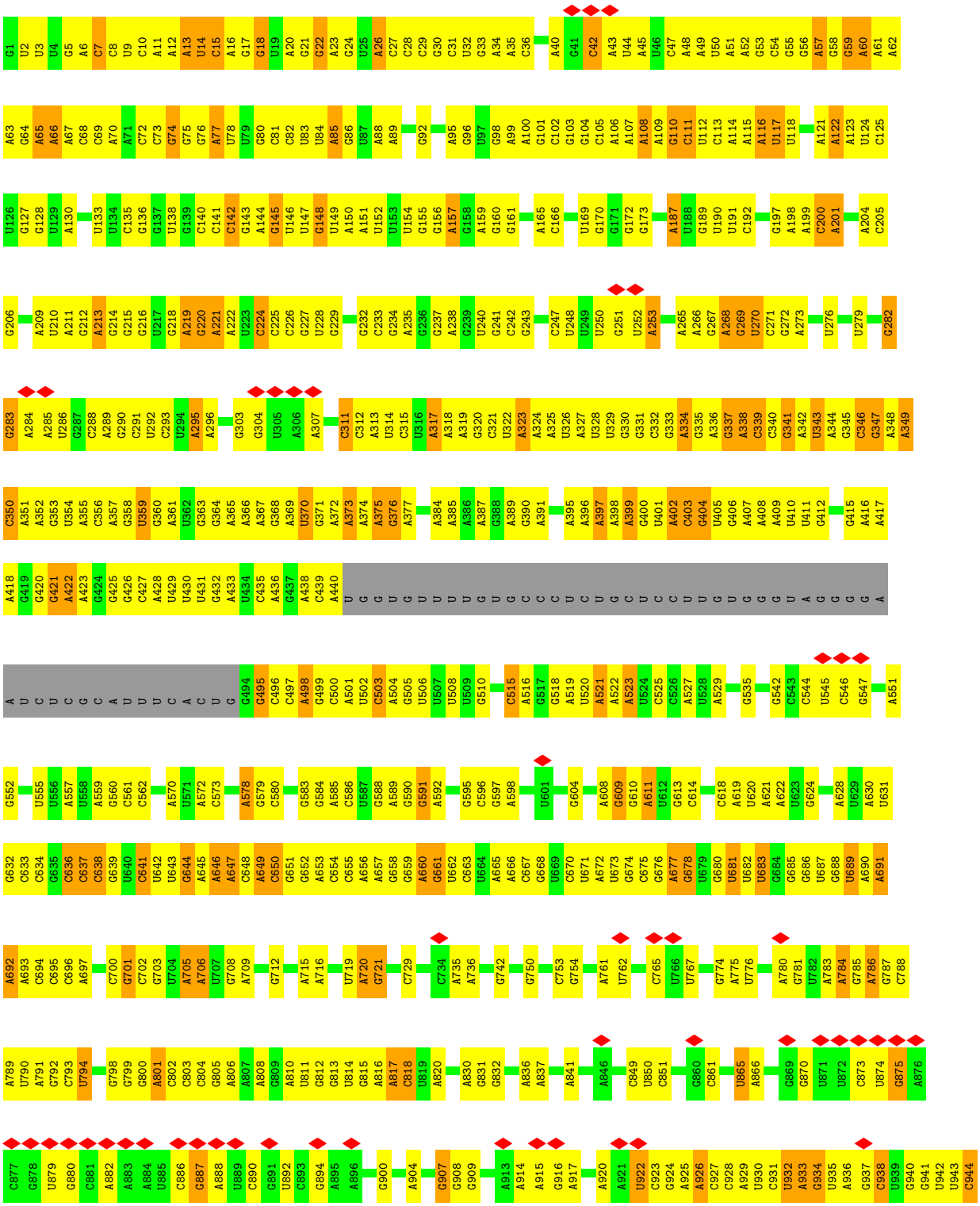
Chain z:

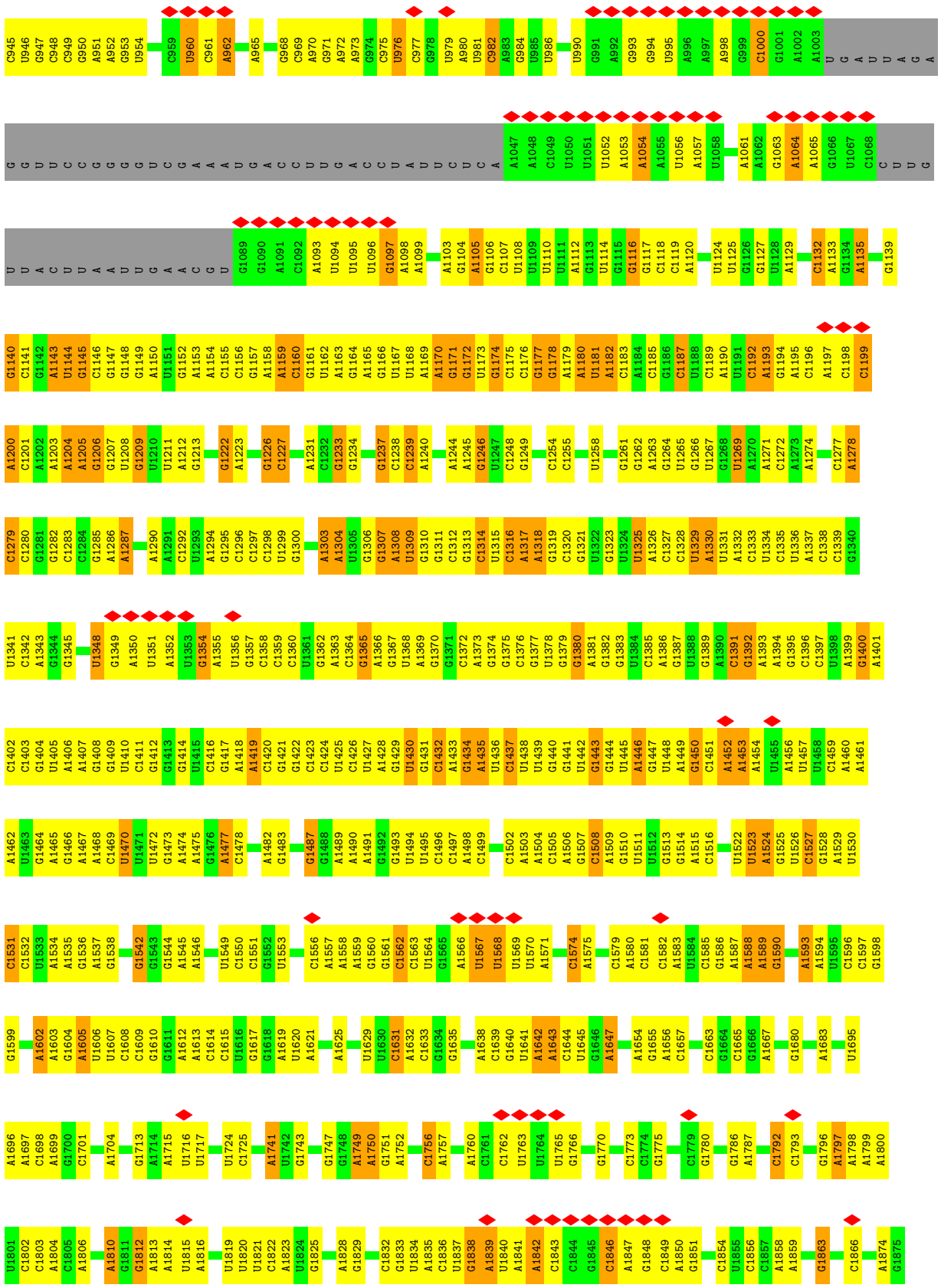


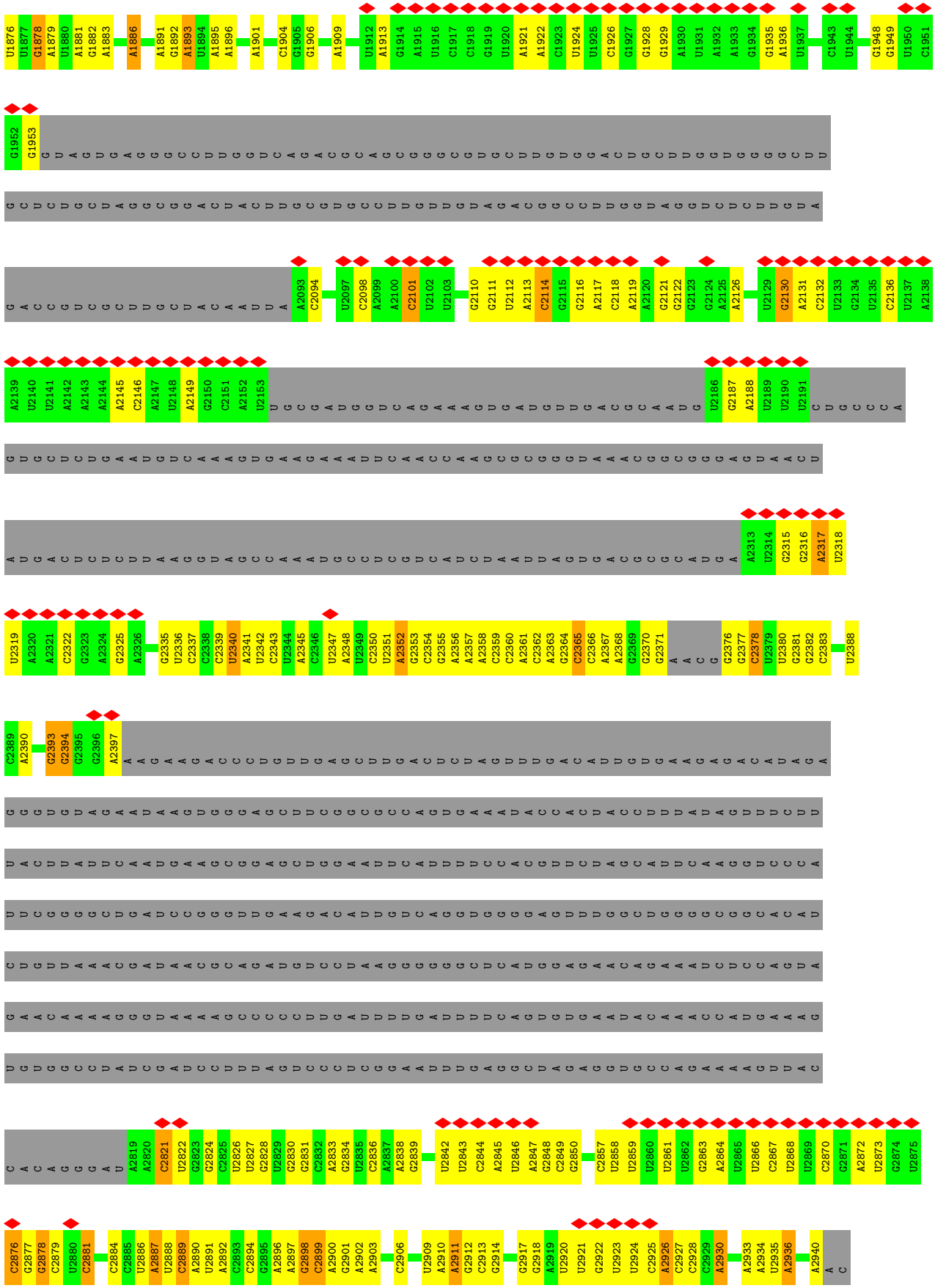
HIS THR TYR LYS LYS ALA LYS LEU MET LYS GLN SER LYS LYS LYS THR SER PHE THR ARG PHE

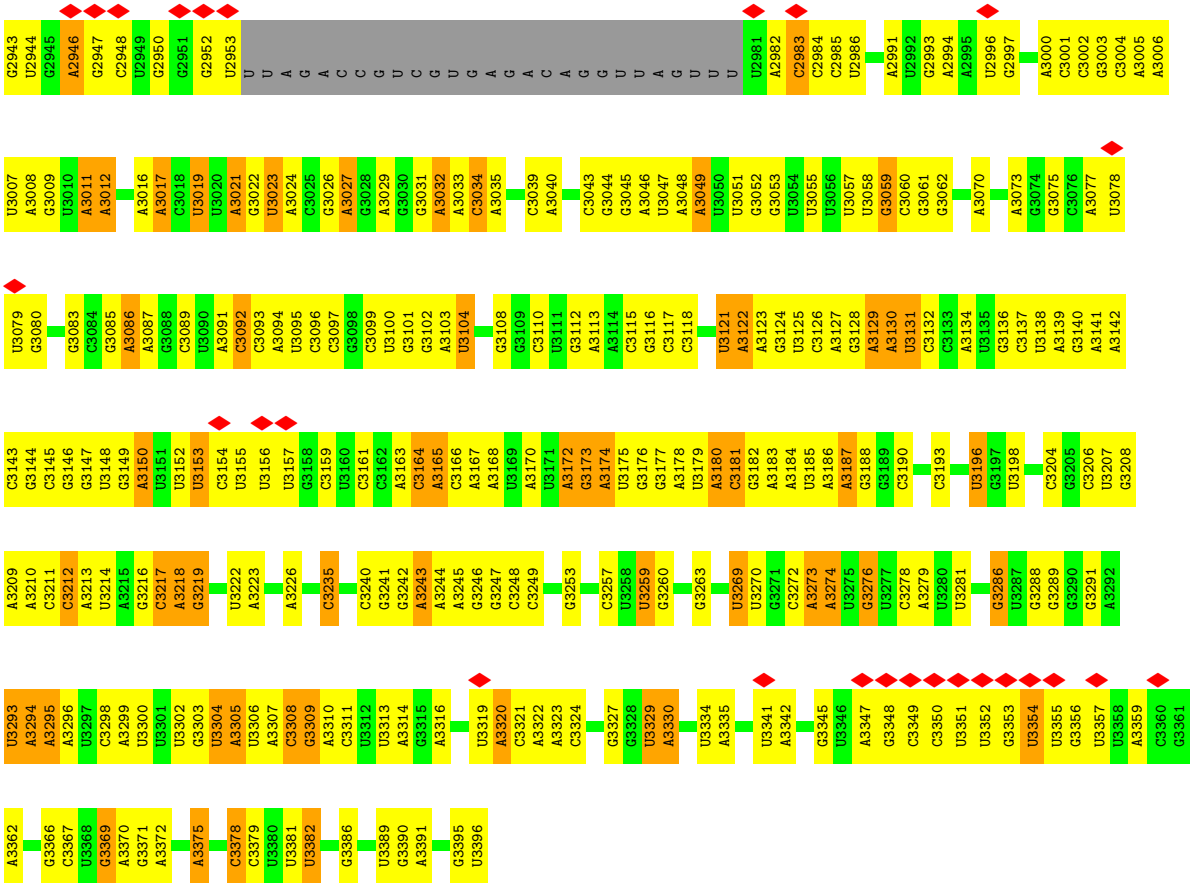
- Molecule 44: 25S rRNA

Chain 1: 8% 28% 37% 9% 25%




C945 U946 G947 C948 C949 G950 A951 A952 G953 U954 C959 U960 C961 A962 A965 G968 C969 A970 G971 A972 A973 G974 C975 U976 C977 G978 U979 A980 U981 C982 A983 G984 U985 U986 U990 G991 A992 G993 G994 U995 A996 A997 A998 G999 C1000 G1001 A1002 A1003 U G A U U A G A
G U G U U C C G G G G U C G A A A U G A C C U U U G A C U A U U C U C A A1047 A1048 C1049 U1050 U1051 U1052 A1053 A1054 A1055 U1056 A1057 U1058 A1061 A1062 G1063 A1064 A1065 G1066 U1067 C1068 C U U G
U U A C U U A A U U G A A C U G U G1089 G1090 A1091 C1092 A1093 U1094 U1095 U1096 G1097 A1098 A1099 A1103 G1104 A1105 G1106 C1107 U1108 U1109 U1110 U1111 A1112 G1113 U1114 C1115 G1116 G1117 C1118 C1119 A1120 U1124 U1125 C1126 G1127 U1128 A1129 C1132 A1133 G1134 A1135 G1139
G1140 C1141 G1142 A1143 U1144 G1145 C1146 G1147 G1148 G1149 A1150 U1151 G1152 A1153 A1154 C1155 C1156 G1157 A1158 A1159 C1160 G1161 U1162 A1163 G1164 A1165 G1166 U1167 U1168 A1169 A1170 G1171 G1172 U1173 G1174 C1175 C1176 G1177 G1178 A1179 A1180 U1181 A1182 C1183 A1184 C1185 G1186 C1187 U1188 C1189 A1190 U1191 C1192 A1193 G1194 A1195 C1196 A1197 C1198 C1199
A1200 C1201 A1202 A1203 A1204 A1205 G1206 G1207 U1208 G1209 U1210 U1211 A1212 G1213 G1222 A1223 G1226 C1227 A1231 U1232 G1233 G1234 G1237 C1238 C1239 A1240 A1244 A1245 G1246 U1247 C1248 G1249 C1254 C1255 U1258 G1261 G1262 A1263 G1264 U1265 G1266 U1267 G1268 U1269 A1270 A1271 C1272 A1273 A1274 C1277 A1278
C1279 C1280 G1281 G1282 C1283 C1284 G1285 A1286 A1287 A1290 A1291 C1292 U1293 A1294 G1295 C1296 C1297 C1298 U1299 G1300 A1303 A1304 U1305 G1306 G1307 A1308 U1309 G1310 G1311 C1312 G1313 C1314 U1315 C1316 A1317 A1318 G1319 C1320 G1321 U1322 G1323 U1324 U1325 A1326 C1327 C1328 U1329 A1330 U1331 A1332 C1333 U1334 C1335 U1336 A1337 C1338 G1340
U1341 C1342 A1343 G1344 G1345 U1348 G1349 A1350 U1351 A1352 U1353 G1354 A1355 U1356 G1357 C1358 C1359 C1360 U1361 C1362 A1363 C1364 G1365 A1366 G1367 U1368 A1369 G1370 G1371 C1372 A1373 G1374 G1375 C1376 G1377 U1378 G1379 G1380 A1381 G1382 G1383 U1384 C1385 A1386 G1387 U1388 G1389 A1390 C1391 G1392 A1393 A1394 G1395 C1396 C1397 U1398 A1399 G1400 A1401
C1402 C1403 G1404 U1405 A1406 A1407 G1408 G1409 U1410 C1411 G1412 G1413 G1414 U1415 C1416 G1417 A1418 A1419 C1420 G1421 G1422 C1423 C1424 U1425 C1426 U1427 A1428 G1429 U1430 G1431 C1432 A1433 G1434 A1435 U1436 C1437 U1438 U1439 G1440 G1441 U1442 G1443 G1444 U1445 A1446 G1447 U1448 A1449 G1450 C1451 A1452 A1453 A1454 U1455 A1456 U1457 U1458 C1459 A1460 A1461
A1462 U1463 G1464 A1465 G1466 A1467 A1468 C1469 U1470 U1471 U1472 G1473 A1474 A1475 G1476 A1477 C1478 A1482 G1483 G1487 G1488 A1489 A1490 A1491 G1492 G1493 A1494 U1495 C1496 C1497 A1498 C1499 C1502 A1503 A1504 C1505 A1506 G1507 C1508 A1509 G1510 U1511 U1512 G1513 G1514 A1515 C1516 U1522 U1523 A1524 G1525 U1526 C1527 G1528 A1529 U1530
C1531 C1532 U1533 A1534 A1535 G1536 A1537 G1538 G1542 G1543 G1544 A1545 A1546 U1549 C1550 C1551 G1552 U1553 C1556 A1557 A1558 A1559 G1560 G1561 C1562 C1563 U1564 G1565 A1566 U1567 U1568 U1569 U1570 A1571 C1574 A1575 C1579 A1580 C1581 C1582 A1583 U1584 C1585 G1586 A1587 A1588 A1589 G1590 A1593 A1594 U1595 C1596 C1597 G1598
G1599 A1602 A1603 G1604 A1605 U1606 U1607 C1608 C1609 G1610 G1611 A1612 A1613 C1614 C1615 U1616 G1617 G1618 A1619 U1620 A1621 A1625 U1629 U1630 C1631 A1632 C1633 G1634 G1635 A1638 C1639 G1640 U1641 A1642 A1643 C1644 U1645 G1646 A1647 A1654 G1655 A1656 C1657 C1663 G1664 C1665 G1666 A1667 G1680 A1683 U1695
A1696 A1697 C1698 A1699 G1700 C1701 A1704 G1713 A1714 A1715 U1716 U1717 U1724 C1725 A1741 U1742 G1743 G1747 G1748 A1749 A1750 G1751 A1752 C1756 A1757 A1760 C1761 C1762 U1763 U1764 U1765 G1766 G1770 C1773 C1774 G1775 C1779 G1780 G1786 A1787 C1792 C1793 G1796 A1797 A1798 A1799 A1800
U1801 C1802 C1803 A1804 C1805 A1806 A1810 G1811 G1812 A1813 A1814 U1815 A1816 U1819 U1820 U1821 C1822 A1823 U1824 G1825 A1828 G1829 C1832 G1833 U1834 A1835 C1836 U1837 G1838 A1839 U1840 A1841 A1842 C1843 C1844 G1845 C1846 A1847 G1848 C1849 A1850 G1851 C1854 U1855 C1856 C1857 A1858 A1859 G1863 C1866 A1874 G1875


U1876 U1877 G1878 A1879 U1880 A1881 G1882 A1883 A1886 A1891 G1892 A1893 U1894 A1895 A1896 A1901 C1904 G1905 G1906 A1909 U1912 A1913 G1914 A1915 U1916 C1917 C1918 G1919 U1920 A1921 A1922 C1923 U1924 U1925 C1926 G1927 G1928 G1929 A1930 U1931 A1932 A1933 G1934 G1935 A1936 U1937 C1943 U1944 G1948 G1949 U1950 C1951
G1952 G1953
A2093 C2094 U2097 C2098 A2099 A2100 C2101 U2102 U2103 G2110 G2111 U2112 A2113 C2114 G2115 G2116 A2117 C2118 A2119 A2120 G2121 G2122 G2123 G2124 A2125 A2126 U2129 G2130 A2131 C2132 U2133 G2134 U2135 C2136 U2137 A2138
A2139 U2140 U2141 A2142 A2143 A2144 A2145 C2146 A2147 U2148 A2149 G2150 C2151 A2152 U2153 U2186 G2187 A2188 U2189 U2190 U2191
A2313 U2314 G2315 G2316 A2317 U2318
U2319 A2320 A2321 C2322 G2323 A2324 G2325 A2326 G2335 U2336 C2337 C2338 C2339 U2340 A2341 U2342 C2343 U2344 A2345 C2346 U2347 A2348 U2349 C2350 U2351 A2352 G2353 C2354 G2355 A2356 A2357 A2358 C2359 C2360 A2361 C2362 A2363 G2364 C2365 C2366 A2367 A2368 G2369 G2370 G2371 G2376 G2377 C2378 U2379 U2380 G2381 G2382 C2383 U2388
C2389 A2390 G2393 G2394 G2395 G2396 A2397
A2819 A2820 C2821 U2822 G2823 G2824 C2825 U2826 U2827 G2828 U2829 G2830 G2831 C2832 A2833 G2834 U2835 C2836 A2837 A2838 G2839 U2842 U2843 C2844 A2845 U2846 A2847 G2848 G2849 G2850 C2857 U2858 U2859 U2860 U2861 U2862 G2863 A2864 U2865 U2866 C2867 U2868 U2869 C2870 G2871 A2872 U2873 G2874 U2875
C2876 G2877 G2878 C2879 U2880 C2881 C2884 C2885 U2886 A2887 U2888 C2889 A2890 U2891 A2892 C2893 C2894 G2895 A2896 A2897 G2898 C2899 A2900 G2901 A2902 A2903 C2906 U2909 A2910 A2911 G2912 C2913 G2914 G2917 G2918 A2919 U2920 U2921 G2922 U2923 U2924 C2925 A2926 C2927 C2928 C2929 A2930 A2933 A2934 U2935 A2936 A2940

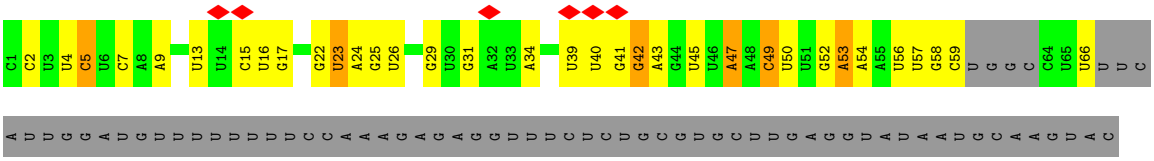


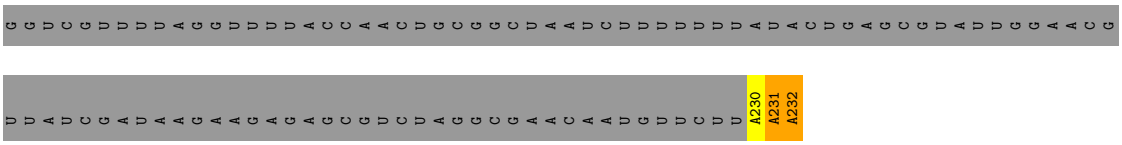
- Molecule 45: 5.8S rRNA

Chain 2: 15% 66% 19%

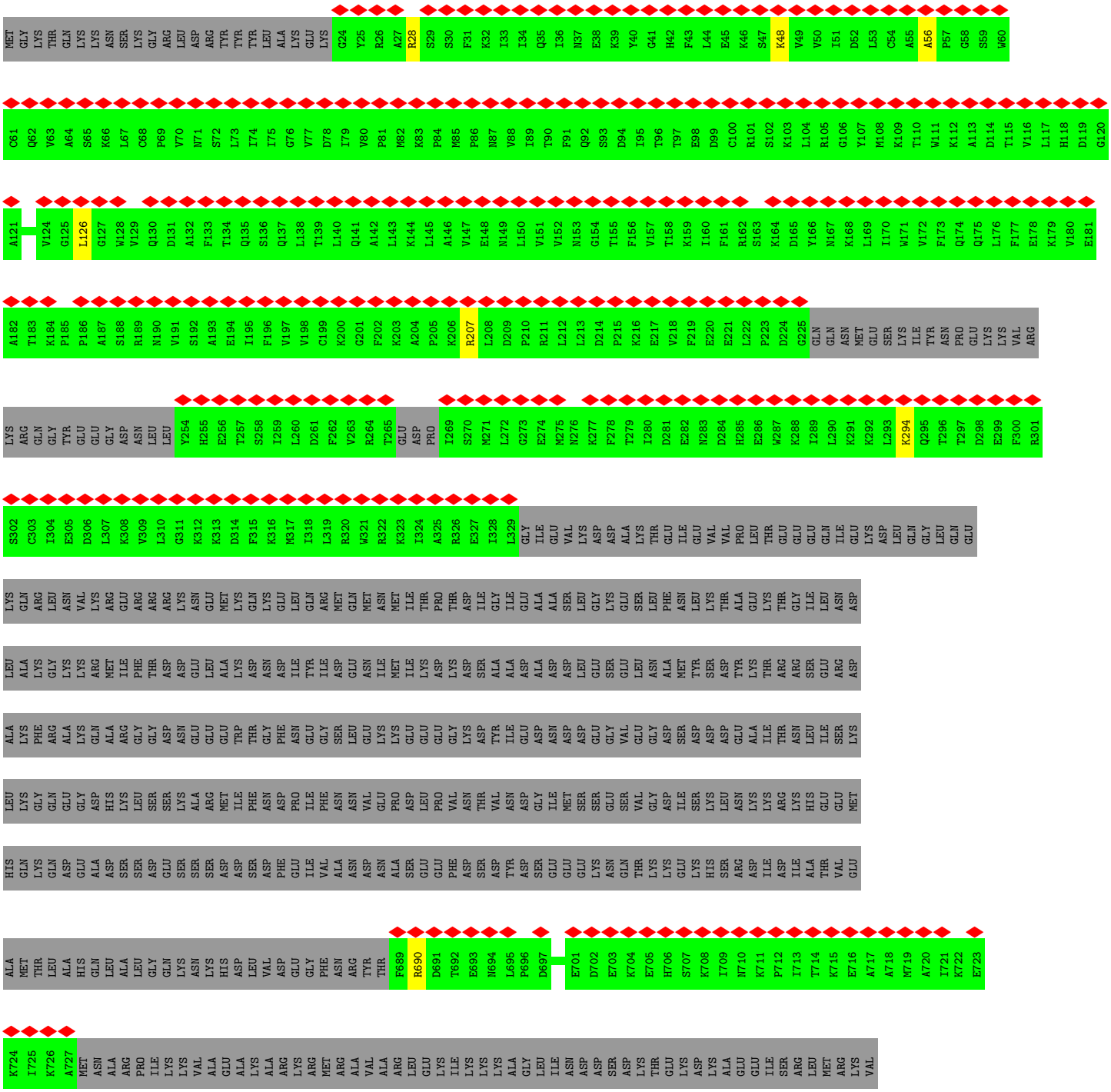
- Molecule 46: ITS2

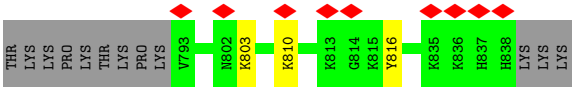
Chain 6: 12% 12% 72%





• Molecule 47: 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase




THR
LYS
LYS
PRO
LYS
THR
LYS
PRO
LYS
V793
N802
K803
K810
K813
G814
K815
Y816
K835
K836
H837
H838
LYS
LYS
LYS

# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, C1 | Depositor |
| Number of particles used | 29163 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | NONE | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/Å^2$) | 24 | 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 | 0.483 | Depositor |
| Minimum map value | -0.257 | Depositor |
| Average map value | -0.000 | Depositor |
| Map value standard deviation | 0.013 | Depositor |
| Recommended contour level | 0.055 | Depositor |
| Map size (Å) | 416.25598, 416.25598, 416.25598 | wwPDB |
| Map dimensions | 384, 384, 384 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.084, 1.084, 1.084 | Depositor |

# 5 Model quality (i)

## 5.1 Standard geometry (i)

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 | B | 1.10 | 6/3152 (0.2%) | 1.05 | 15/4239 (0.4%) |
| 2 | C | 1.33 | 14/2801 (0.5%) | 1.10 | 22/3792 (0.6%) |
| 3 | E | 0.95 | 0/1260 | 0.96 | 9/1694 (0.5%) |
| 4 | F | 1.23 | 5/1821 (0.3%) | 1.00 | 10/2451 (0.4%) |
| 5 | G | 0.91 | 5/1542 (0.3%) | 0.92 | 3/2083 (0.1%) |
| 6 | H | 0.86 | 0/1539 | 0.95 | 8/2073 (0.4%) |
| 7 | K | 0.47 | 0/2098 | 0.75 | 0/2830 |
| 8 | L | 1.08 | 2/1524 (0.1%) | 1.12 | 13/2046 (0.6%) |
| 9 | M | 1.04 | 3/1074 (0.3%) | 0.98 | 6/1446 (0.4%) |
| 10 | N | 1.49 | 12/1575 (0.8%) | 1.28 | 29/2106 (1.4%) |
| 11 | O | 1.51 | 13/1585 (0.8%) | 1.11 | 13/2128 (0.6%) |
| 12 | P | 1.35 | 12/1419 (0.8%) | 1.06 | 9/1904 (0.5%) |
| 13 | Q | 1.10 | 1/1050 (0.1%) | 1.06 | 8/1419 (0.6%) |
| 14 | R | 0.69 | 0/1275 | 0.91 | 7/1702 (0.4%) |
| 15 | S | 1.01 | 1/1473 (0.1%) | 1.01 | 9/1980 (0.5%) |
| 16 | T | 0.44 | 0/440 | 0.93 | 2/594 (0.3%) |
| 17 | U | 0.56 | 0/861 | 0.73 | 0/1167 |
| 18 | V | 0.68 | 0/1018 | 0.89 | 2/1369 (0.1%) |
| 19 | W | 0.50 | 0/1918 | 0.81 | 0/2586 |
| 20 | X | 1.18 | 3/1116 (0.3%) | 0.93 | 4/1503 (0.3%) |
| 21 | Y | 1.17 | 2/1004 (0.2%) | 1.06 | 7/1341 (0.5%) |
| 22 | Z | 0.54 | 0/1118 | 0.78 | 2/1497 (0.1%) |
| 23 | a | 0.80 | 0/751 | 0.96 | 3/1013 (0.3%) |
| 24 | b | 0.57 | 1/3885 (0.0%) | 0.85 | 6/5242 (0.1%) |
| 25 | c | 0.43 | 0/751 | 0.72 | 0/1008 |
| 26 | d | 1.00 | 1/887 (0.1%) | 0.98 | 4/1191 (0.3%) |
| 27 | e | 1.40 | 7/1041 (0.7%) | 1.09 | 10/1394 (0.7%) |
| 28 | f | 1.72 | 7/868 (0.8%) | 1.25 | 12/1168 (1.0%) |
| 29 | g | 0.80 | 0/891 | 1.07 | 8/1191 (0.7%) |
| 30 | h | 1.12 | 0/978 | 1.03 | 2/1301 (0.2%) |
| 31 | i | 0.73 | 0/778 | 0.91 | 2/1034 (0.2%) |
| 32 | j | 1.49 | 8/696 (1.1%) | 1.34 | 10/923 (1.1%) |
| 33 | k | 0.64 | 0/618 | 0.89 | 0/826 |
| 34 | l | 0.69 | 0/443 | 1.12 | 4/588 (0.7%) |

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | #\|Z\| >5 | RMSZ | #\|Z\| >5 |
| 35 | n | 0.74 | 0/3101 | 0.91 | 12/4187 (0.3%) |
| 36 | o | 0.55 | 0/1129 | 0.84 | 0/1502 |
| 37 | q | 0.47 | 0/733 | 0.90 | 4/977 (0.4%) |
| 38 | r | 0.63 | 0/1789 | 0.91 | 3/2389 (0.1%) |
| 39 | s | 0.70 | 0/301 | 1.15 | 3/386 (0.8%) |
| 40 | t | 0.54 | 0/2333 | 0.89 | 3/3128 (0.1%) |
| 41 | u | 0.72 | 0/1061 | 0.99 | 6/1410 (0.4%) |
| 42 | y | 0.52 | 0/1872 | 0.79 | 2/2548 (0.1%) |
| 43 | z | 0.58 | 0/445 | 0.89 | 0/585 |
| 44 | 1 | 1.93 | 1801/60703 (3.0%) | 1.96 | 3153/94630 (3.3%) |
| 45 | 2 | 2.45 | 221/3746 (5.9%) | 2.31 | 330/5832 (5.7%) |
| 46 | 6 | 0.96 | 1/1527 (0.1%) | 1.50 | 26/2371 (1.1%) |
| 47 | w | 0.46 | 0/2952 | 0.76 | 0/3965 |
| All | All | 1.55 | 2126/126942 (1.7%) | 1.61 | 3781/184739 (2.0%) |

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

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|---|---|---|---|
| 1 | B | 0 | 7 |
| 2 | C | 0 | 6 |
| 4 | F | 0 | 2 |
| 5 | G | 0 | 5 |
| 6 | H | 0 | 3 |
| 7 | K | 0 | 1 |
| 8 | L | 0 | 5 |
| 9 | M | 0 | 1 |
| 10 | N | 0 | 1 |
| 12 | P | 0 | 1 |
| 14 | R | 0 | 1 |
| 15 | S | 0 | 2 |
| 18 | V | 0 | 1 |
| 19 | W | 0 | 2 |
| 20 | X | 0 | 1 |
| 23 | a | 0 | 2 |
| 24 | b | 0 | 3 |
| 26 | d | 0 | 1 |
| 27 | e | 0 | 1 |
| 28 | f | 0 | 2 |
| 29 | g | 0 | 2 |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|---|---|---|---|
| 30 | h | 0 | 3 |
| 31 | i | 0 | 2 |
| 33 | k | 0 | 2 |
| 35 | n | 0 | 11 |
| 36 | o | 0 | 5 |
| 37 | q | 0 | 1 |
| 38 | r | 0 | 1 |
| 39 | s | 0 | 1 |
| 40 | t | 0 | 5 |
| 41 | u | 0 | 2 |
| 42 | y | 0 | 1 |
| 47 | w | 0 | 2 |
| All | All | 0 | 86 |

The worst 5 of 2126 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 44 | 1 | 346 | C | N1-C6 | -13.06 | 1.29 | 1.37 |
| 44 | 1 | 945 | C | C4-C5 | -12.55 | 1.32 | 1.43 |
| 44 | 1 | 1437 | C | C4-C5 | -12.42 | 1.33 | 1.43 |
| 44 | 1 | 1332 | A | N7-C5 | -12.41 | 1.31 | 1.39 |
| 44 | 1 | 407 | A | N9-C4 | -12.35 | 1.30 | 1.37 |

The worst 5 of 3781 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 44 | 1 | 630 | A | N1-C6-N6 | 17.03 | 128.82 | 118.60 |
| 44 | 1 | 630 | A | C5-C6-N6 | -16.99 | 110.11 | 123.70 |
| 44 | 1 | 1363 | A | C5-C6-N6 | -16.56 | 110.45 | 123.70 |
| 44 | 1 | 630 | A | C4-C5-N7 | 16.19 | 118.79 | 110.70 |
| 44 | 1 | 1159 | A | C5-C6-N6 | -15.59 | 111.23 | 123.70 |

There are no chirality outliers.

5 of 86 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 1 | B | 170 | PRO | Peptide |
| 1 | B | 221 | THR | Peptide |
| 1 | B | 241 | LYS | Peptide |
| 1 | B | 35 | ASP | Peptide |
| 1 | B | 37 | ARG | 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 | B | 384/387 (99%) | 363 (94%) | 21 (6%) | 0 | 100 | 100 |
| 2 | C | 359/362 (99%) | 338 (94%) | 20 (6%) | 1 (0%) | 41 | 75 |
| 3 | E | 152/176 (86%) | 150 (99%) | 2 (1%) | 0 | 100 | 100 |
| 4 | F | 220/244 (90%) | 206 (94%) | 14 (6%) | 0 | 100 | 100 |
| 5 | G | 190/256 (74%) | 183 (96%) | 7 (4%) | 0 | 100 | 100 |
| 6 | H | 189/191 (99%) | 182 (96%) | 6 (3%) | 1 (0%) | 29 | 67 |
| 7 | K | 252/376 (67%) | 242 (96%) | 10 (4%) | 0 | 100 | 100 |
| 8 | L | 185/199 (93%) | 176 (95%) | 8 (4%) | 1 (0%) | 29 | 67 |
| 9 | M | 135/138 (98%) | 133 (98%) | 2 (2%) | 0 | 100 | 100 |
| 10 | N | 176/204 (86%) | 167 (95%) | 9 (5%) | 0 | 100 | 100 |
| 11 | O | 195/199 (98%) | 191 (98%) | 4 (2%) | 0 | 100 | 100 |
| 12 | P | 172/184 (94%) | 167 (97%) | 5 (3%) | 0 | 100 | 100 |
| 13 | Q | 132/186 (71%) | 132 (100%) | 0 | 0 | 100 | 100 |
| 14 | R | 154/189 (82%) | 152 (99%) | 2 (1%) | 0 | 100 | 100 |
| 15 | S | 169/172 (98%) | 165 (98%) | 4 (2%) | 0 | 100 | 100 |
| 16 | T | 54/160 (34%) | 53 (98%) | 1 (2%) | 0 | 100 | 100 |
| 17 | U | 104/121 (86%) | 103 (99%) | 1 (1%) | 0 | 100 | 100 |
| 18 | V | 134/137 (98%) | 133 (99%) | 1 (1%) | 0 | 100 | 100 |
| 19 | W | 232/236 (98%) | 229 (99%) | 3 (1%) | 0 | 100 | 100 |
| 20 | X | 139/142 (98%) | 136 (98%) | 3 (2%) | 0 | 100 | 100 |
| 21 | Y | 124/127 (98%) | 122 (98%) | 2 (2%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 22 | Z | 133/136 (98%) | 132 (99%) | 1 (1%) | 0 | 100 | 100 |
| 23 | a | 91/149 (61%) | 87 (96%) | 4 (4%) | 0 | 100 | 100 |
| 24 | b | 468/647 (72%) | 451 (96%) | 17 (4%) | 0 | 100 | 100 |
| 25 | c | 95/105 (90%) | 95 (100%) | 0 | 0 | 100 | 100 |
| 26 | d | 105/113 (93%) | 103 (98%) | 2 (2%) | 0 | 100 | 100 |
| 27 | e | 125/130 (96%) | 123 (98%) | 2 (2%) | 0 | 100 | 100 |
| 28 | f | 104/107 (97%) | 102 (98%) | 2 (2%) | 0 | 100 | 100 |
| 29 | g | 110/121 (91%) | 107 (97%) | 3 (3%) | 0 | 100 | 100 |
| 30 | h | 117/120 (98%) | 110 (94%) | 7 (6%) | 0 | 100 | 100 |
| 31 | i | 97/100 (97%) | 94 (97%) | 3 (3%) | 0 | 100 | 100 |
| 32 | j | 85/88 (97%) | 82 (96%) | 3 (4%) | 0 | 100 | 100 |
| 33 | k | 75/78 (96%) | 74 (99%) | 1 (1%) | 0 | 100 | 100 |
| 34 | l | 48/51 (94%) | 47 (98%) | 1 (2%) | 0 | 100 | 100 |
| 35 | n | 365/605 (60%) | 339 (93%) | 26 (7%) | 0 | 100 | 100 |
| 36 | o | 131/220 (60%) | 123 (94%) | 8 (6%) | 0 | 100 | 100 |
| 37 | q | 83/455 (18%) | 80 (96%) | 3 (4%) | 0 | 100 | 100 |
| 38 | r | 211/261 (81%) | 200 (95%) | 11 (5%) | 0 | 100 | 100 |
| 39 | s | 34/520 (6%) | 31 (91%) | 3 (9%) | 0 | 100 | 100 |
| 40 | t | 283/322 (88%) | 267 (94%) | 16 (6%) | 0 | 100 | 100 |
| 41 | u | 121/199 (61%) | 115 (95%) | 6 (5%) | 0 | 100 | 100 |
| 42 | y | 242/245 (99%) | 240 (99%) | 2 (1%) | 0 | 100 | 100 |
| 43 | z | 53/106 (50%) | 52 (98%) | 1 (2%) | 0 | 100 | 100 |
| 47 | w | 350/841 (42%) | 347 (99%) | 3 (1%) | 0 | 100 | 100 |
| All | All | 7377/10105 (73%) | 7124 (97%) | 250 (3%) | 3 (0%) | 100 | 100 |

All (3) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | C | 339 | LEU |
| 8 | L | 63 | VAL |
| 6 | H | 50 | ASN |

### 5.3.2 Protein sidechains (i)

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

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 1 | B | 322/323 (100%) | 316 (98%) | 6 (2%) | 57 | 75 |
| 2 | C | 288/289 (100%) | 286 (99%) | 2 (1%) | 84 | 90 |
| 3 | E | 134/153 (88%) | 133 (99%) | 1 (1%) | 84 | 90 |
| 4 | F | 186/205 (91%) | 186 (100%) | 0 | 100 | 100 |
| 5 | G | 159/208 (76%) | 156 (98%) | 3 (2%) | 57 | 75 |
| 6 | H | 171/171 (100%) | 171 (100%) | 0 | 100 | 100 |
| 7 | K | 236/346 (68%) | 235 (100%) | 1 (0%) | 91 | 94 |
| 8 | L | 149/159 (94%) | 148 (99%) | 1 (1%) | 84 | 90 |
| 9 | M | 108/109 (99%) | 107 (99%) | 1 (1%) | 78 | 87 |
| 10 | N | 156/176 (89%) | 151 (97%) | 5 (3%) | 39 | 63 |
| 11 | O | 160/162 (99%) | 159 (99%) | 1 (1%) | 86 | 91 |
| 12 | P | 142/146 (97%) | 141 (99%) | 1 (1%) | 84 | 90 |
| 13 | Q | 110/151 (73%) | 110 (100%) | 0 | 100 | 100 |
| 14 | R | 129/154 (84%) | 128 (99%) | 1 (1%) | 81 | 89 |
| 15 | S | 155/156 (99%) | 155 (100%) | 0 | 100 | 100 |
| 16 | T | 45/137 (33%) | 45 (100%) | 0 | 100 | 100 |
| 17 | U | 93/107 (87%) | 93 (100%) | 0 | 100 | 100 |
| 18 | V | 104/105 (99%) | 103 (99%) | 1 (1%) | 76 | 86 |
| 19 | W | 211/213 (99%) | 211 (100%) | 0 | 100 | 100 |
| 20 | X | 117/118 (99%) | 117 (100%) | 0 | 100 | 100 |
| 21 | Y | 109/110 (99%) | 108 (99%) | 1 (1%) | 78 | 87 |
| 22 | Z | 115/116 (99%) | 114 (99%) | 1 (1%) | 78 | 87 |
| 23 | a | 76/119 (64%) | 75 (99%) | 1 (1%) | 69 | 82 |
| 24 | b | 424/573 (74%) | 423 (100%) | 1 (0%) | 93 | 96 |
| 25 | c | 81/88 (92%) | 81 (100%) | 0 | 100 | 100 |
| 26 | d | 94/97 (97%) | 92 (98%) | 2 (2%) | 53 | 73 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 27 | e | 109/111 (98%) | 107 (98%) | 2 (2%) | 59 | 77 |
| 28 | f | 90/91 (99%) | 89 (99%) | 1 (1%) | 73 | 84 |
| 29 | g | 95/103 (92%) | 94 (99%) | 1 (1%) | 73 | 84 |
| 30 | h | 104/105 (99%) | 104 (100%) | 0 | 100 | 100 |
| 31 | i | 81/82 (99%) | 81 (100%) | 0 | 100 | 100 |
| 32 | j | 70/71 (99%) | 69 (99%) | 1 (1%) | 67 | 81 |
| 33 | k | 68/69 (99%) | 68 (100%) | 0 | 100 | 100 |
| 34 | l | 45/46 (98%) | 44 (98%) | 1 (2%) | 52 | 71 |
| 35 | n | 334/548 (61%) | 333 (100%) | 1 (0%) | 92 | 95 |
| 36 | o | 118/199 (59%) | 116 (98%) | 2 (2%) | 60 | 78 |
| 37 | q | 80/420 (19%) | 80 (100%) | 0 | 100 | 100 |
| 38 | r | 191/229 (83%) | 191 (100%) | 0 | 100 | 100 |
| 39 | s | 32/445 (7%) | 32 (100%) | 0 | 100 | 100 |
| 40 | t | 256/287 (89%) | 253 (99%) | 3 (1%) | 71 | 83 |
| 41 | u | 108/180 (60%) | 107 (99%) | 1 (1%) | 78 | 87 |
| 42 | y | 210/211 (100%) | 210 (100%) | 0 | 100 | 100 |
| 43 | z | 48/95 (50%) | 48 (100%) | 0 | 100 | 100 |
| 47 | w | 319/745 (43%) | 311 (98%) | 8 (2%) | 47 | 69 |
| All | All | 6432/8728 (74%) | 6381 (99%) | 51 (1%) | 82 | 89 |

5 of 51 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 26 | d | 16 | LEU |
| 34 | l | 41 | ARG |
| 47 | w | 810 | LYS |
| 26 | d | 23 | VAL |
| 28 | f | 72 | THR |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 24 | b | 454 | GLN |
| 42 | y | 82 | GLN |
| 30 | h | 59 | ASN |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 41 | u | 110 | ASN |
| 27 | e | 121 | ASN |

### 5.3.3 RNA (i)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|---|---|---|---|---|
| 44 | 1 | 2523/3396 (74%) | 688 (27%) | 34 (1%) |
| 45 | 2 | 157/158 (99%) | 46 (29%) | 3 (1%) |
| 46 | 6 | 63/232 (27%) | 29 (46%) | 0 |
| All | All | 2743/3786 (72%) | 763 (27%) | 37 (1%) |

5 of 763 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 44 | 1 | 2 | U |
| 44 | 1 | 3 | U |
| 44 | 1 | 7 | C |
| 44 | 1 | 13 | A |
| 44 | 1 | 14 | U |

5 of 37 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 44 | 1 | 2317 | A |
| 45 | 2 | 73 | U |
| 44 | 1 | 2920 | U |
| 44 | 1 | 3350 | C |
| 44 | 1 | 761 | A |

## 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 |
|---|---|---|
| 28 | f | 1 |

All chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|---|---|---|---|---|---|---|
| 1 | f | 102:LEU | C | 103:TYR | N | 1.16 |

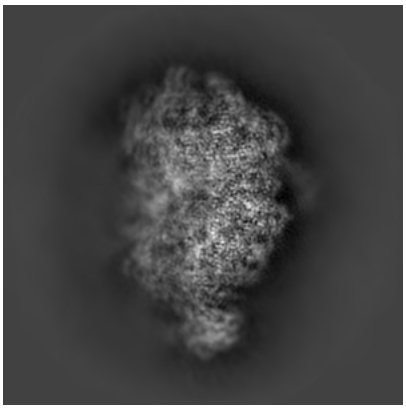
# 6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-10841. These allow visual inspection of the internal detail of the map and identification of artifacts.

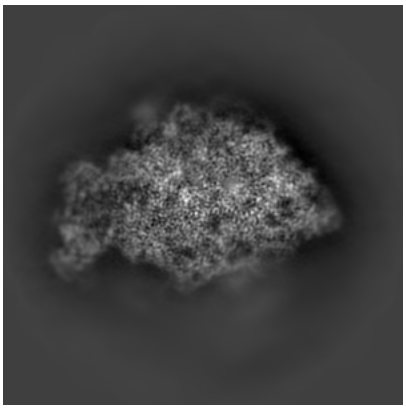
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

## 6.1 Orthogonal projections (i)

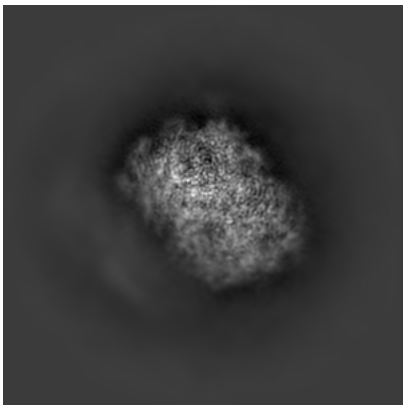
### 6.1.1 Primary map



X

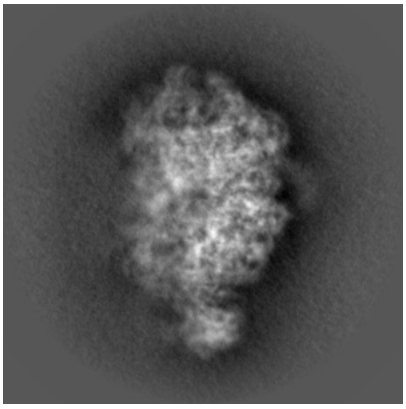


Y

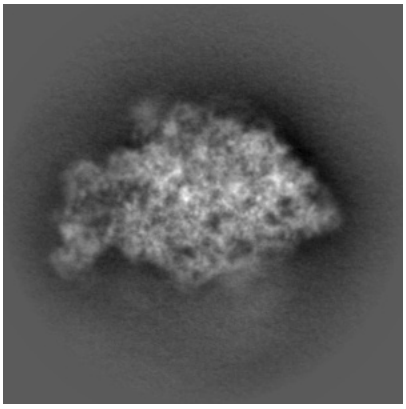


Z

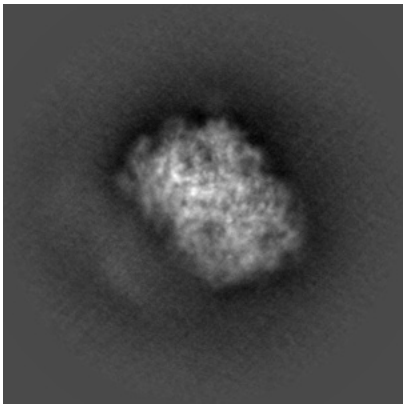
### 6.1.2 Raw map



X



Y

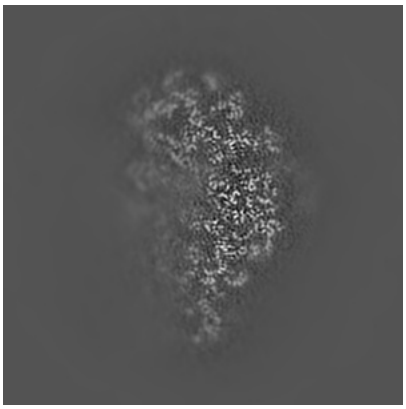


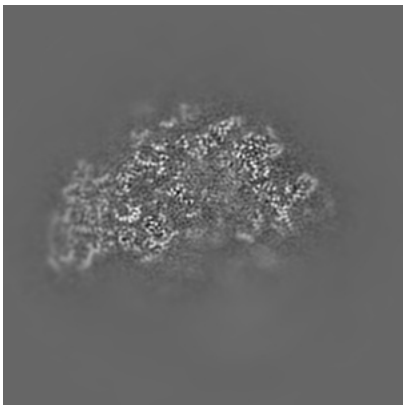
Z

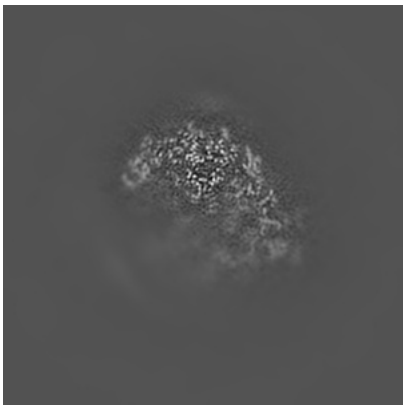
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices (i)

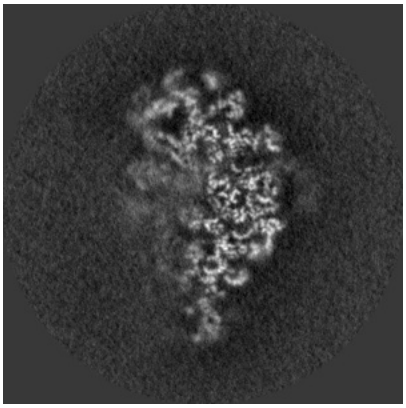
### 6.2.1 Primary map

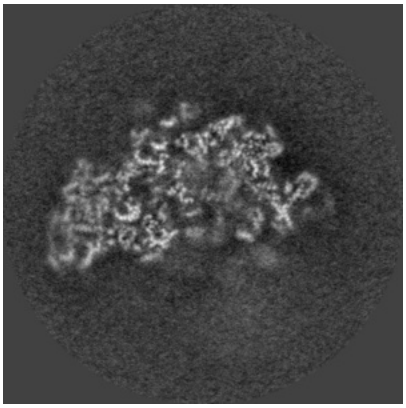

X Index: 192

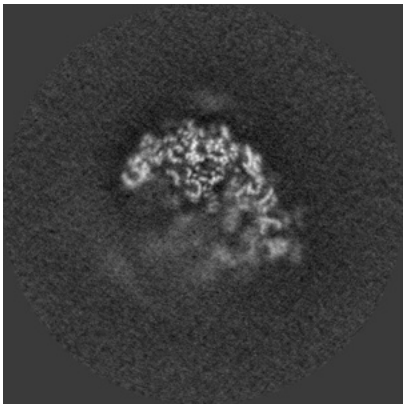

Y Index: 192


Z Index: 192

### 6.2.2 Raw map


X Index: 192

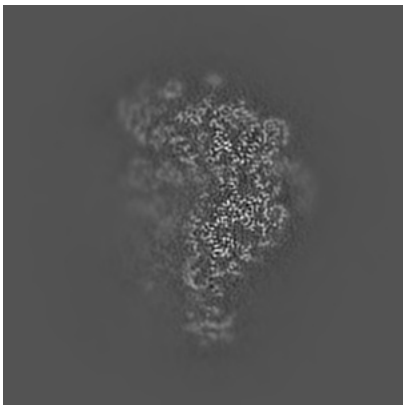

Y Index: 192


Z Index: 192

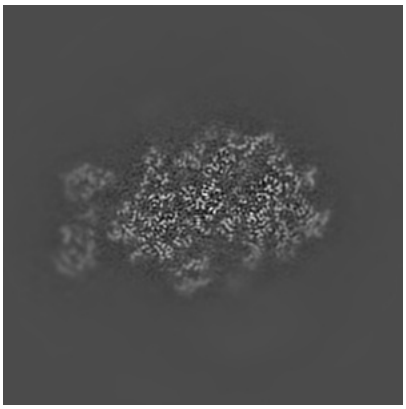
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices (i)

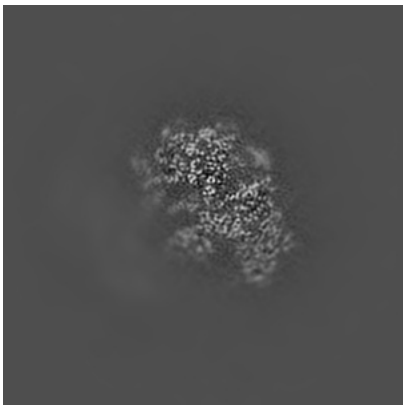
### 6.3.1 Primary map



X Index: 201

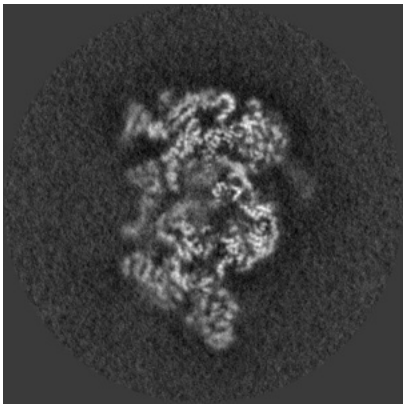


Y Index: 216

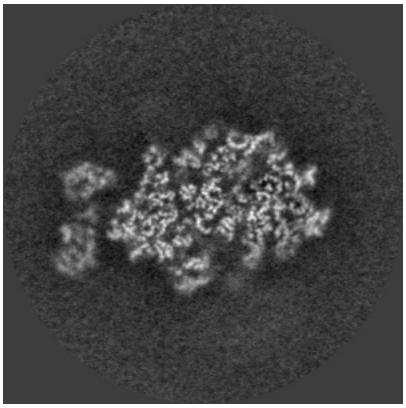


Z Index: 245

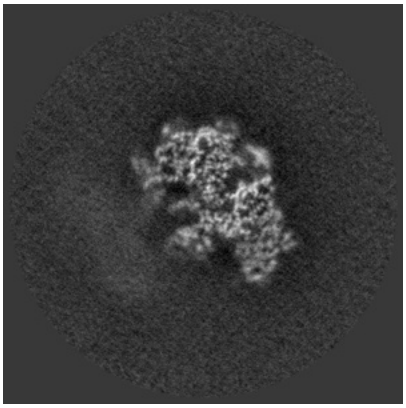
### 6.3.2 Raw map



X Index: 217



Y Index: 216



Z Index: 244

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 0.055. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 Raw map

X Y Z

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

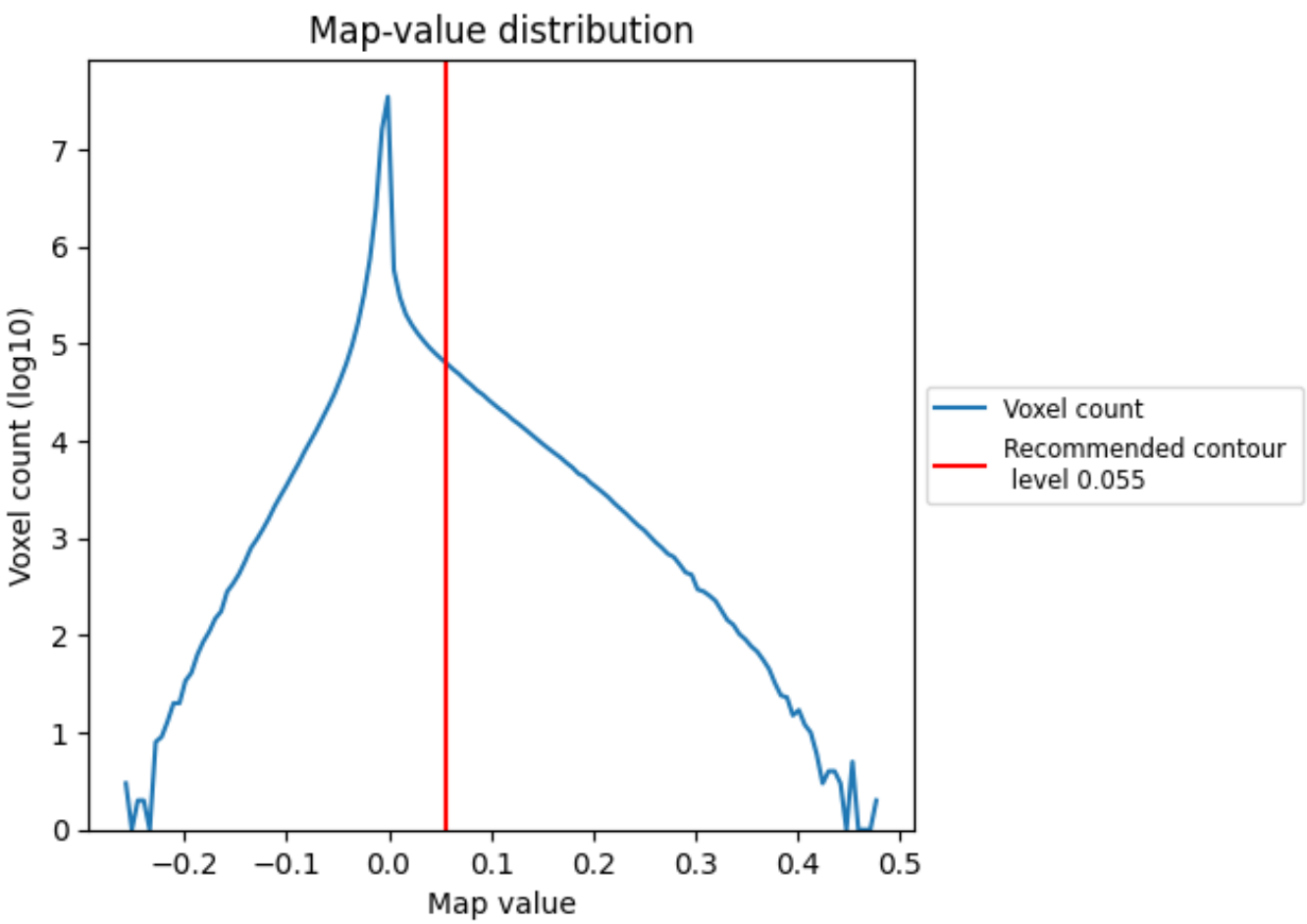
## 6.5 Mask visualisation (i)

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

# 7 Map analysis (i)

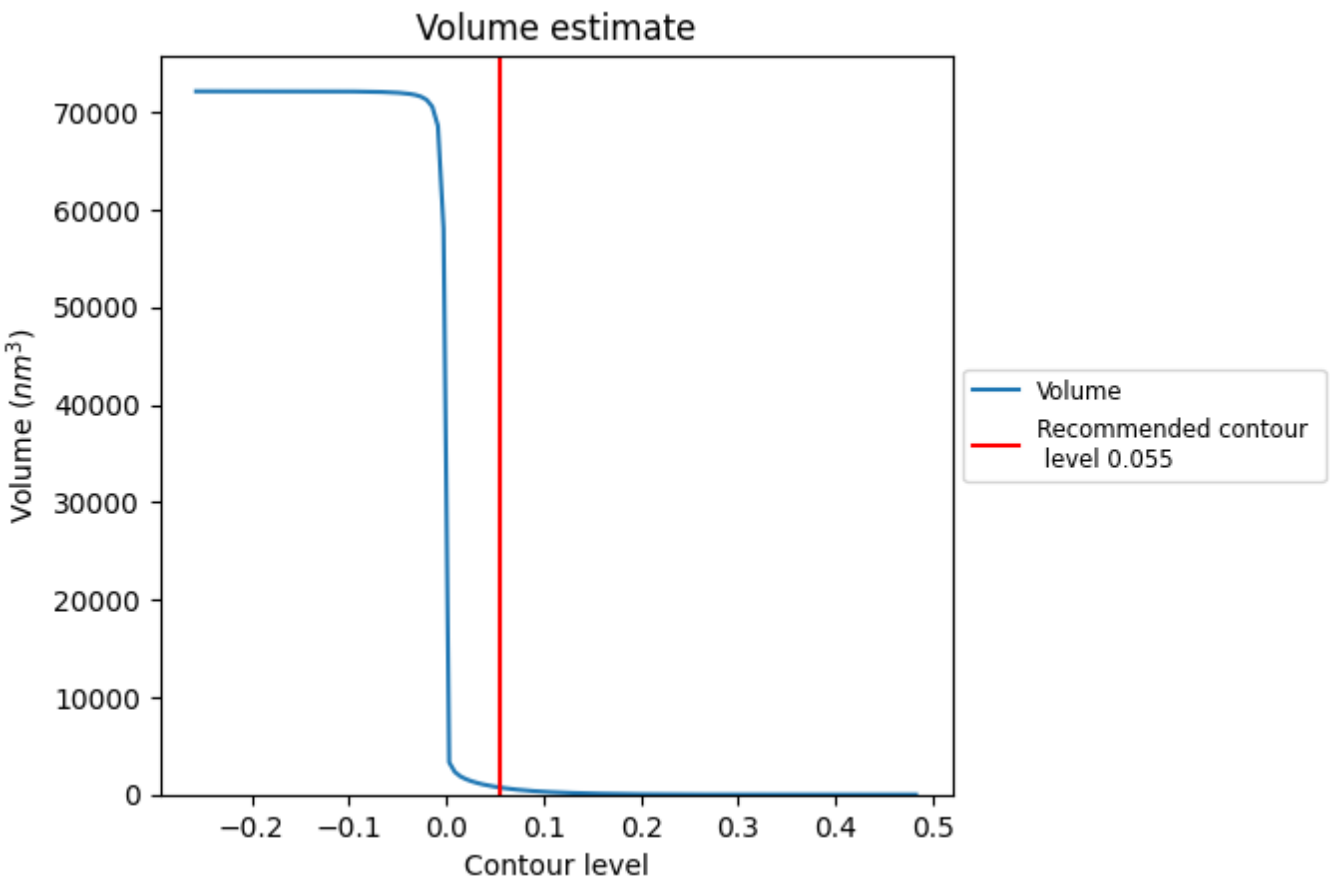
This section contains the results of statistical analysis of the map.

## 7.1 Map-value distribution (i)




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

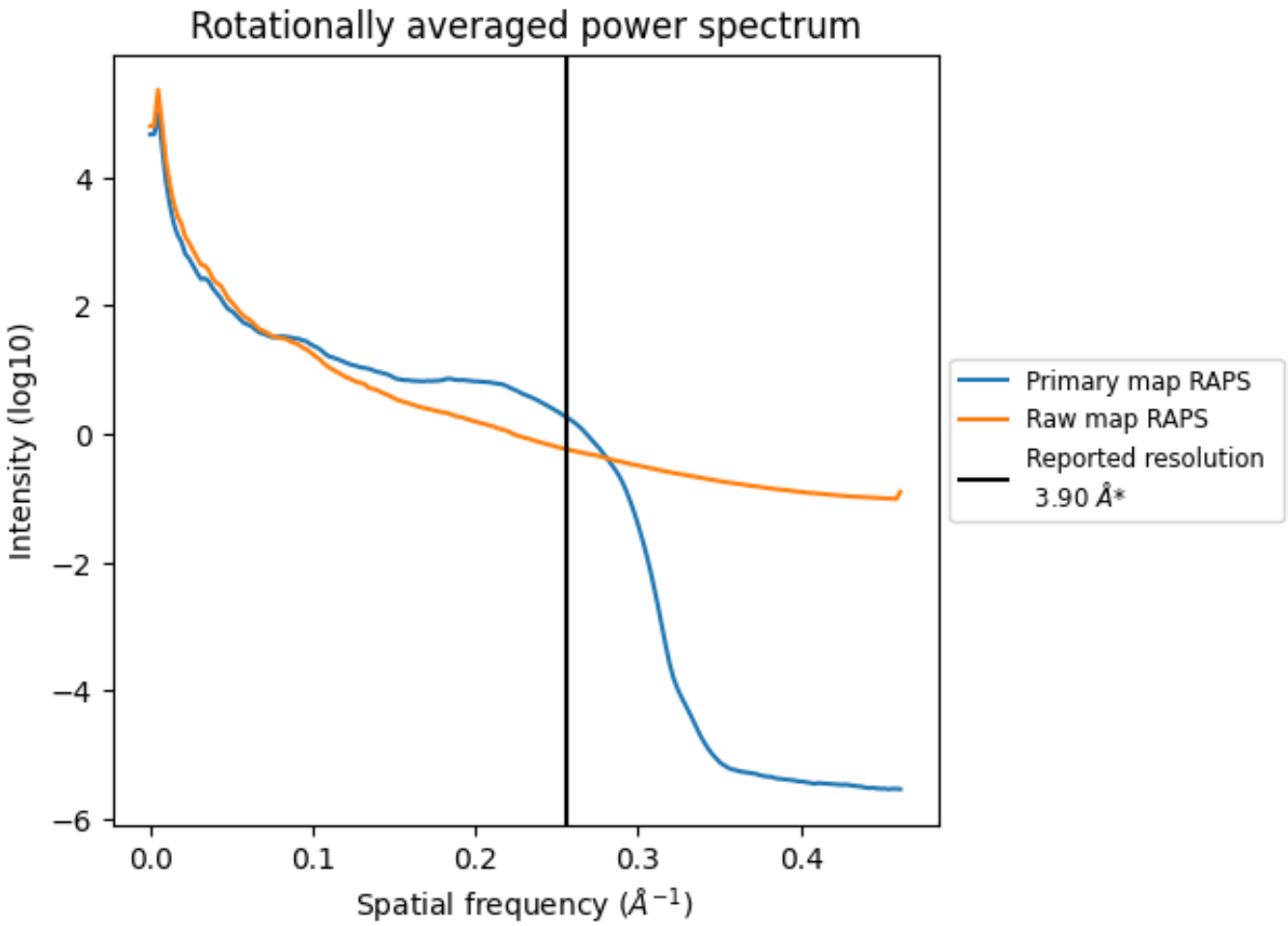
## 7.2 Volume estimate (i)




The volume at the recommended contour level is 727 $nm^3$; this corresponds to an approximate mass of 656 kDa.

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

## 7.3 Rotationally averaged power spectrum (i)

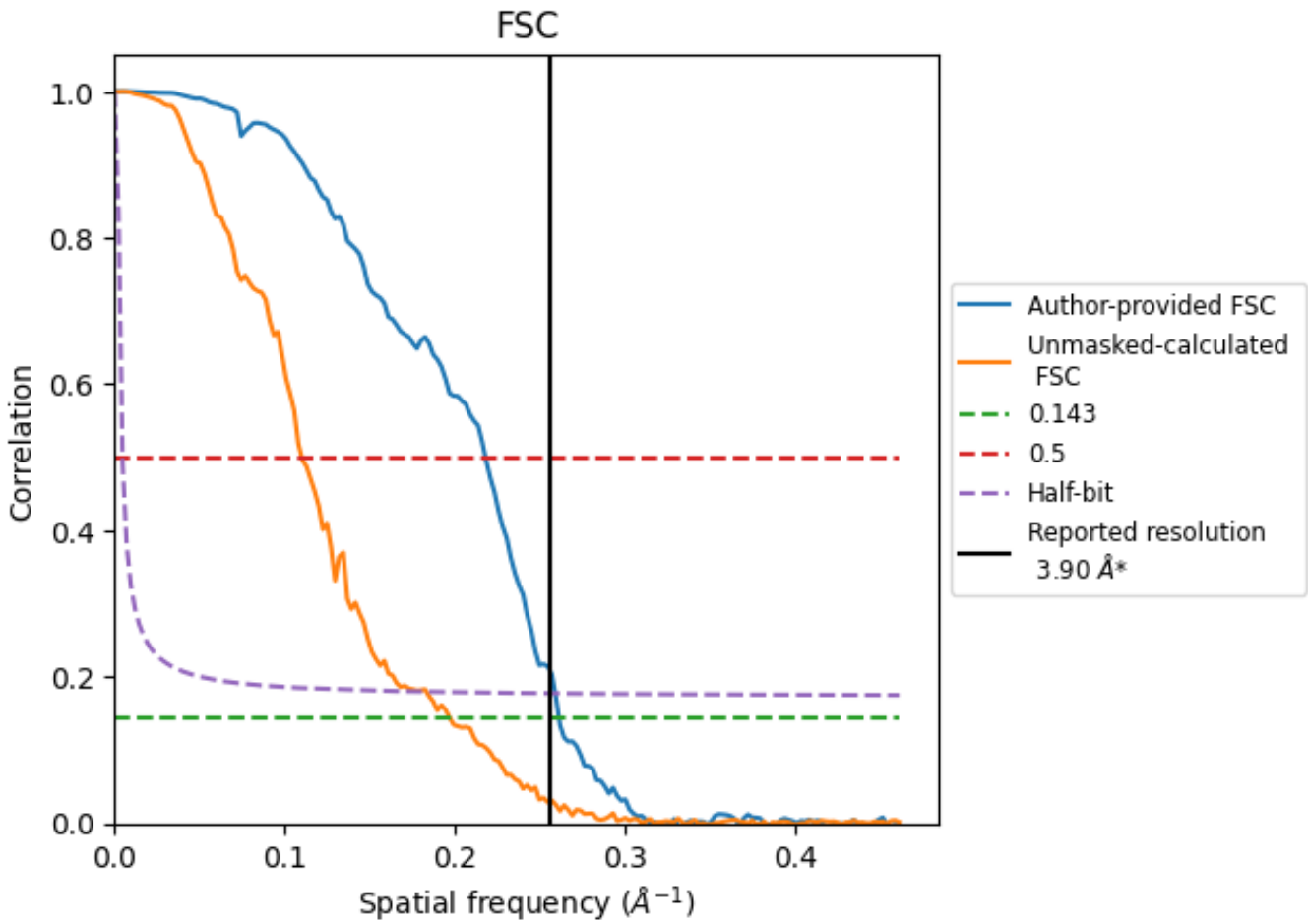



*Reported resolution corresponds to spatial frequency of 0.256 Å$^{-1}$

# 8 Fourier-Shell correlation (i)

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

## 8.1 FSC (i)




*Reported resolution corresponds to spatial frequency of 0.256 Å$^{-1}$

## 8.2 Resolution estimates (i)

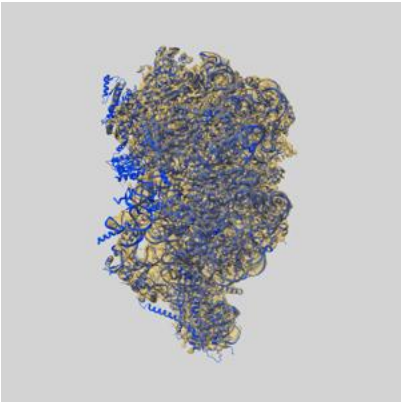
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---|---|---|---|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 3.90 | - | - |
| Author-provided FSC curve | 3.83 | 4.59 | 3.86 |
| Unmasked-calculated* | 5.07 | 9.08 | 5.45 |

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.07 differs from the reported value 3.9 by more than 10 %

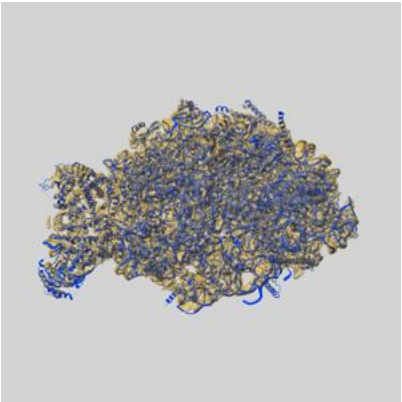
# 9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-10841 and PDB model 6YLX. Per-residue inclusion information can be found in section 3 on page 12.

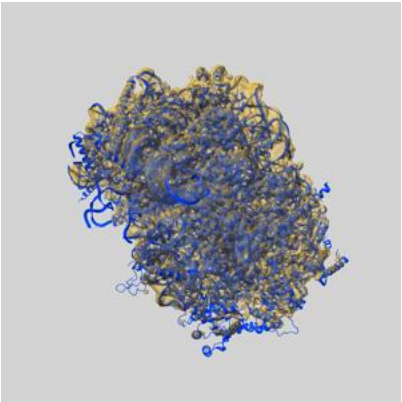
## 9.1 Map-model overlay (i)



X



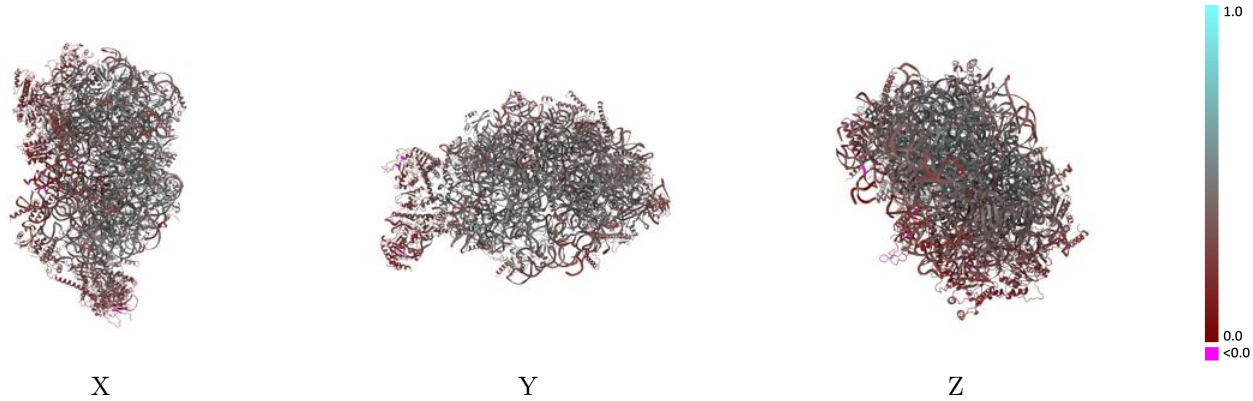
Y



Z

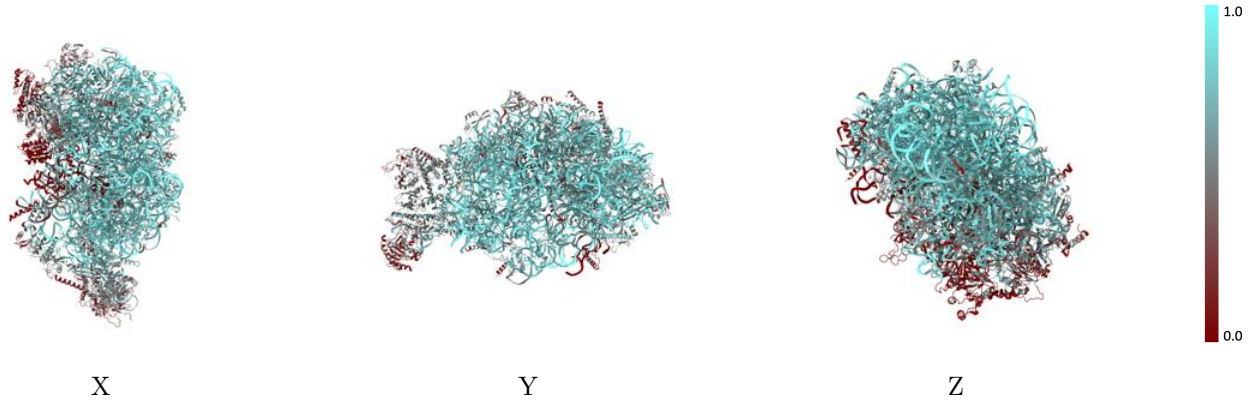
The images above show the 3D surface view of the map at the recommended contour level 0.055 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



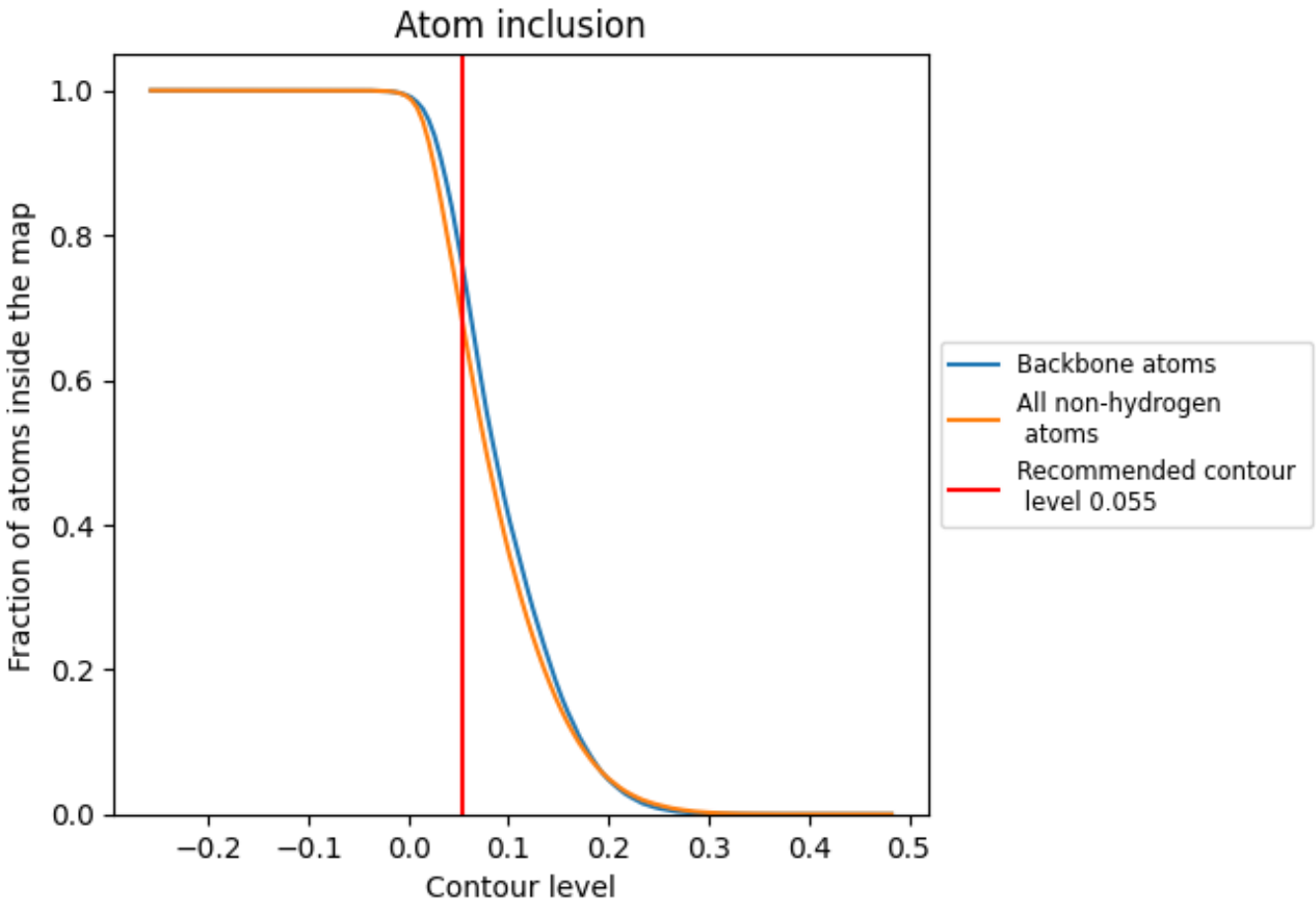

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.055).

## 9.4 Atom inclusion (i)




At the recommended contour level, 75% of all backbone atoms, 67% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.055) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|---|---|---|
| All | 0.6732 | 0.3840 |
| 1 | 0.7889 | 0.3960 |
| 2 | 0.8917 | 0.4560 |
| 6 | 0.6832 | 0.3070 |
| B | 0.6806 | 0.4290 |
| C | 0.7748 | 0.4690 |
| E | 0.7246 | 0.4280 |
| F | 0.7773 | 0.4300 |
| G | 0.6424 | 0.3890 |
| H | 0.6866 | 0.4150 |
| K | 0.2694 | 0.2150 |
| L | 0.6909 | 0.4310 |
| M | 0.7607 | 0.4410 |
| N | 0.8020 | 0.4900 |
| O | 0.8058 | 0.4790 |
| P | 0.7617 | 0.4590 |
| Q | 0.7507 | 0.4440 |
| R | 0.4546 | 0.3430 |
| S | 0.7066 | 0.4280 |
| T | 0.1876 | 0.3110 |
| U | 0.4614 | 0.3320 |
| V | 0.5393 | 0.3800 |
| W | 0.4072 | 0.2770 |
| X | 0.7078 | 0.4430 |
| Y | 0.7805 | 0.4720 |
| Z | 0.5033 | 0.3200 |
| a | 0.6194 | 0.3960 |
| b | 0.3232 | 0.2730 |
| c | 0.3406 | 0.2580 |
| d | 0.7037 | 0.4430 |
| e | 0.8008 | 0.4980 |
| f | 0.8392 | 0.5110 |
| g | 0.5810 | 0.3980 |
| h | 0.7413 | 0.4570 |
| i | 0.5933 | 0.3700 |

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| Chain | Atom inclusion | Q-score |
|---|---|---|
| j | 0.7496 | 0.4660 |
| k | 0.5409 | 0.3910 |
| l | 0.2795 | 0.3650 |
| n | 0.5325 | 0.3380 |
| o | 0.3760 | 0.2480 |
| q | 0.1926 | 0.2420 |
| r | 0.2483 | 0.2720 |
| s | 0.4775 | 0.4100 |
| t | 0.4623 | 0.3010 |
| u | 0.5326 | 0.3480 |
| w | 0.1113 | 0.2630 |
| y | 0.4430 | 0.2890 |
| z | 0.4562 | 0.3770 |