



## wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 04:02 AM UTC

PDB ID : 5WYJ / pdb\_00005wyj  
EMDB ID : EMD-6695  
Title : Cryo-EM structure of the 90S small subunit pre-ribosome (Dhr1-depleted, Enp1-TAP, state 1)  
Authors : Ye, K.; Zhu, X.; Sun, Q.  
Deposited on : 2017-01-13  
Resolution : 8.70 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](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.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

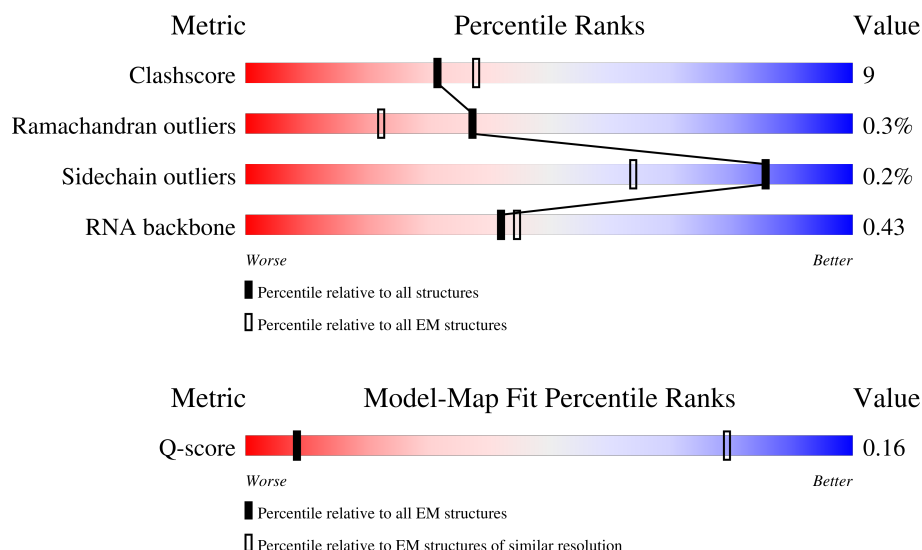
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 8.70 Å.

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



| Metric                | Whole archive<br>(#Entries) | EM structures<br>(#Entries) | Similar EM resolution<br>(#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|-----------------------------|----------------------------------------------------------|
| Clashscore            | 229148                      | 23984                       | -                                                        |
| Ramachandran outliers | 224038                      | 23583                       | -                                                        |
| Sidechain outliers    | 223484                      | 23102                       | -                                                        |
| RNA backbone          | 8273                        | 3508                        | -                                                        |
| Q-score               | -                           | 25397                       | 282 ( 8.20 - 9.20 )                                      |

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   | 3A    | 333    | <div> <div>5%</div> <div>25%</div> <div>20%</div> <div>53%</div> </div>  |
| 2   | 3B    | 327    | <div> <div>20%</div> <div>57%</div> <div>16%</div> <div>27%</div> </div> |
| 2   | 3C    | 327    | <div> <div>38%</div> <div>62%</div> <div>11%</div> <div>27%</div> </div> |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 3   | 3D    | 504    |                  |
| 4   | 3E    | 511    |                  |
| 5   | 3F    | 573    |                  |
| 6   | 3G    | 126    |                  |
| 6   | 3H    | 126    |                  |
| 7   | 5A    | 700    |                  |
| 8   | AA    | 776    |                  |
| 9   | AB    | 643    |                  |
| 10  | AC    | 713    |                  |
| 11  | AD    | 575    |                  |
| 12  | AE    | 1769   |                  |
| 13  | AF    | 513    |                  |
| 14  | AG    | 896    |                  |
| 15  | B1    | 1183   |                  |
| 16  | BA    | 923    |                  |
| 17  | BB    | 943    |                  |
| 18  | BC    | 817    |                  |
| 19  | BD    | 594    |                  |
| 20  | BE    | 939    |                  |
| 21  | CA    | 297    |                  |
| 22  | CB    | 1237   |                  |
| 23  | E1    | 252    |                  |
| 23  | E2    | 252    |                  |
| 24  | E3    | 483    |                  |
| 25  | E4    | 707    |                  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 26  | K1    | 316    |                  |
| 27  | MA    | 183    |                  |
| 28  | MB    | 290    |                  |
| 29  | MC    | 593    |                  |
| 30  | P1    | 274    |                  |
| 31  | R1    | 367    |                  |
| 32  | R2    | 1729   |                  |
| 33  | S1    | 489    |                  |
| 34  | SA    | 1812   |                  |
| 35  | SC    | 255    |                  |
| 36  | SF    | 261    |                  |
| 37  | SG    | 225    |                  |
| 38  | SH    | 236    |                  |
| 39  | SI    | 190    |                  |
| 40  | SJ    | 200    |                  |
| 41  | SK    | 197    |                  |
| 42  | SM    | 156    |                  |
| 43  | SN    | 143    |                  |
| 44  | SO    | 151    |                  |
| 45  | SP    | 137    |                  |
| 46  | SR    | 143    |                  |
| 47  | SX    | 130    |                  |
| 48  | SY    | 145    |                  |
| 49  | SZ    | 135    |                  |
| 50  | Sc    | 82     |                  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 51  | Sd    | 67     |                  |
| 52  | Sf    | 63     |                  |
| 53  | Sg    | 152    |                  |
| 54  | U1    | 554    |                  |
| 55  | U2    | 250    |                  |
| 56  | U3    | 2493   |                  |
| 57  | U4    | 189    |                  |
| 58  | U5    | 274    |                  |
| 59  | UA    | 1615   |                  |
| 60  | UB    | 987    |                  |
| 61  | UC    | 1033   |                  |

## 2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 173863 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called U3 RNA.

| Mol | Chain | Residues | Atoms |      |     |      |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|------|-----|---------|-------|
| 1   | 3A    | 157      | Total | C    | N   | O    | P   | 0       | 0     |
|     |       |          | 3327  | 1488 | 575 | 1107 | 157 |         |       |

- Molecule 2 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 2   | 3B    | 239      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 1866  | 1183 | 332 | 341 | 10 |         |       |
| 2   | 3C    | 239      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 1866  | 1183 | 332 | 341 | 10 |         |       |

- Molecule 3 is a protein called Nucleolar protein 56.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 3   | 3D    | 370      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 2915  | 1843 | 503 | 560 | 9 |         |       |

- Molecule 4 is a protein called Nucleolar protein 58.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 4   | 3E    | 382      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 2935  | 1859 | 498 | 570 | 8 |         |       |

- Molecule 5 is a protein called Ribosomal RNA-processing protein 9.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 5   | 3F    | 365      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2916  | 1871 | 506 | 529 | 10 |         |       |

- Molecule 6 is a protein called 13 kDa ribonucleoprotein-associated protein.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 6   | 3G    | 122      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 924   | 589 | 159 | 172 | 4 |         |       |
| 6   | 3H    | 122      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 924   | 589 | 159 | 172 | 4 |         |       |

- Molecule 7 is a RNA chain called 5ETS RNA.

| Mol | Chain | Residues | Atoms |      |      |      |     | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|-----|---------|-------|
| 7   | 5A    | 462      | Total | C    | N    | O    | P   | 0       | 0     |
|     |       |          | 9867  | 4406 | 1749 | 3250 | 462 |         |       |

- Molecule 8 is a protein called Utp4.

| Mol | Chain | Residues | Atoms |      |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 8   | AA    | 569      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2845  | 1707 | 569 | 569 |         |       |

- Molecule 9 is a protein called Utp5.

| Mol | Chain | Residues | Atoms |      |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 9   | AB    | 403      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2015  | 1209 | 403 | 403 |         |       |

- Molecule 10 is a protein called Utp8.

| Mol | Chain | Residues | Atoms |      |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 10  | AC    | 472      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2360  | 1416 | 472 | 472 |         |       |

- Molecule 11 is a protein called Utp9.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 11  | AD    | 101      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 505   | 303 | 101 | 101 |         |       |

- Molecule 12 is a protein called U3 small nucleolar RNA-associated protein 10,Utp10.

| Mol | Chain | Residues | Atoms |      |      |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| 12  | AE    | 1536     | Total | C    | N    | O    | S  | 0       | 0     |
|     |       |          | 9970  | 6261 | 1772 | 1918 | 19 |         |       |

- Molecule 13 is a protein called Utp15.

| Mol | Chain | Residues | Atoms |      |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 13  | AF    | 376      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 1880  | 1128 | 376 | 376 |         |       |

- Molecule 14 is a protein called Utp17.

| Mol | Chain | Residues | Atoms |      |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 14  | AG    | 612      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 3060  | 1836 | 612 | 612 |         |       |

- Molecule 15 is a protein called Ribosome biogenesis protein BMS1.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 15  | B1    | 536      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 4325  | 2801 | 758 | 746 | 20 |         |       |

- Molecule 16 is a protein called Periodic tryptophan protein 2.

| Mol | Chain | Residues | Atoms |      |      |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| 16  | BA    | 755      | Total | C    | N    | O    | S  | 0       | 0     |
|     |       |          | 6026  | 3862 | 1025 | 1123 | 16 |         |       |

- Molecule 17 is a protein called U3 small nucleolar RNA-associated protein 12.

| Mol | Chain | Residues | Atoms |      |      |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| 17  | BB    | 778      | Total | C    | N    | O    | S  | 0       | 0     |
|     |       |          | 6138  | 3931 | 1019 | 1161 | 27 |         |       |

- Molecule 18 is a protein called U3 small nucleolar RNA-associated protein 13.

| Mol | Chain | Residues | Atoms |      |      |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| 18  | BC    | 783      | Total | C    | N    | O    | S  | 0       | 0     |
|     |       |          | 6117  | 3870 | 1033 | 1187 | 27 |         |       |

- Molecule 19 is a protein called U3 small nucleolar RNA-associated protein 18.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 19  | BD    | 325      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 2539  | 1606 | 458 | 466 | 9 |         |       |

- Molecule 20 is a protein called U3 small nucleolar RNA-associated protein 21.

| Mol | Chain | Residues | Atoms |      |      |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| 20  | BE    | 753      | Total | C    | N    | O    | S  | 0       | 0     |
|     |       |          | 5936  | 3769 | 1020 | 1126 | 21 |         |       |

- Molecule 21 is a protein called Ribosomal RNA-processing protein 7.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 21  | CA    | 196      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1582  | 1016 | 259 | 300 | 7 |         |       |

- Molecule 22 is a protein called U3 small nucleolar RNA-associated protein 22.

| Mol | Chain | Residues | Atoms |      |      |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| 22  | CB    | 1098     | Total | C    | N    | O    | S  | 0       | 0     |
|     |       |          | 8870  | 5763 | 1462 | 1621 | 24 |         |       |

- Molecule 23 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 23  | E1    | 217      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 1689  | 1073 | 293 | 312 | 11 |         |       |
| 23  | E2    | 216      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 1695  | 1078 | 295 | 313 | 9  |         |       |

- Molecule 24 is a protein called Essential nuclear protein 1.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 24  | E3    | 260      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 2114  | 1378 | 359 | 374 | 3 |         |       |

- Molecule 25 is a protein called Enp2.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 25  | E4    | 285      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 1425  | 855 | 285 | 285 |         |       |

- Molecule 26 is a protein called KRR1 small subunit processome component.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 26  | K1    | 175      | Total | C   | N   | O   | S  | 0       | 0     |
|     |       |          | 1410  | 903 | 252 | 245 | 10 |         |       |

- Molecule 27 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 27  | MA    | 133      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1097  | 692 | 204 | 194 | 7 |         |       |

- Molecule 28 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 28  | MB    | 184      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1465  | 926 | 273 | 260 | 6 |         |       |

- Molecule 29 is a protein called Mpp10,U3 small nucleolar RNA-associated protein MPP10.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 29  | MC    | 46       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 307   | 193 | 52 | 62 |         |       |

- Molecule 30 is a protein called Pre-rRNA-processing protein PNO1.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 30  | P1    | 173      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1368  | 876 | 245 | 243 | 4 |         |       |

- Molecule 31 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 31  | R1    | 355      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2742  | 1756 | 466 | 509 | 11 |         |       |

- Molecule 32 is a protein called rRNA biogenesis protein RRP5.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 32  | R2    | 272      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 2228  | 1433 | 374 | 416 | 5 |         |       |

- Molecule 33 is a protein called Sof1.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 33  | S1    | 285      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 1425  | 855 | 285 | 285 |         |       |

- Molecule 34 is a RNA chain called 18S ribosomal RNA.

| Mol | Chain | Residues | Atoms |       |      |      |      | AltConf | Trace |
|-----|-------|----------|-------|-------|------|------|------|---------|-------|
| 34  | SA    | 1115     | Total | C     | N    | O    | P    | 0       | 0     |
|     |       |          | 23759 | 10623 | 4225 | 7796 | 1115 |         |       |

- Molecule 35 is a protein called 40S ribosomal protein S1-A.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 35  | SC    | 214      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1709  | 1084 | 310 | 311 | 4 |         |       |

- Molecule 36 is a protein called 40S ribosomal protein S4-A.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 36  | SF    | 237      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1881  | 1205 | 345 | 328 | 3 |         |       |

- Molecule 37 is a protein called 40S ribosomal protein S5.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 37  | SG    | 206      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1609  | 1007 | 300 | 299 | 3 |         |       |

- Molecule 38 is a protein called 40S ribosomal protein S6-A.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 38  | SH    | 174      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1369  | 856 | 262 | 248 | 3 |         |       |

- Molecule 39 is a protein called 40S ribosomal protein S7-A.

| Mol | Chain | Residues | Atoms |     |     |     |  | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 39  | SI    | 165      | Total | C   | N   | O   |  | 0       | 0     |
|     |       |          | 1322  | 856 | 227 | 239 |  |         |       |

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

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 40  | SJ    | 170      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1350  | 839 | 268 | 241 | 2 |         |       |

- Molecule 41 is a protein called 40S ribosomal protein S9-A.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 41  | SK    | 175      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1412  | 892 | 272 | 247 | 1 |         |       |

- Molecule 42 is a protein called 40S ribosomal protein S11-A.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 42  | SM    | 141      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1143  | 733 | 216 | 191 | 3 |         |       |

- Molecule 43 is a protein called 40S ribosomal protein S12.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 43  | SN    | 124      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 890   | 560 | 156 | 172 | 2 |         |       |

- Molecule 44 is a protein called 40S ribosomal protein S13.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 44  | SO    | 134      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1087  | 698 | 202 | 186 | 1 |         |       |

- Molecule 45 is a protein called 40S ribosomal protein S14-A.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 45  | SP    | 109      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 750   | 462 | 147 | 140 | 1 |         |       |

- Molecule 46 is a protein called 40S ribosomal protein S16-A.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 46  | SR    | 125      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 973   | 625 | 174 | 174 |         |       |

- Molecule 47 is a protein called 40S ribosomal protein S22-A.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 47  | SX    | 129      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1021  | 650 | 188 | 180 | 3 |         |       |

- Molecule 48 is a protein called 40S ribosomal protein S23-A.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 48  | SY    | 103      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 785   | 501 | 144 | 138 | 2 |         |       |

- Molecule 49 is a protein called 40S ribosomal protein S24-A.

| Mol | Chain | Residues | Atoms |     |     |     |  | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 49  | SZ    | 101      | Total | C   | N   | O   |  | 0       | 0     |
|     |       |          | 801   | 512 | 144 | 145 |  |         |       |

- Molecule 50 is a protein called 40S ribosomal protein S27-A.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 50  | Sc    | 79       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 595   | 371 | 108 | 111 | 5 |         |       |

- Molecule 51 is a protein called 40S ribosomal protein S28-A.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 51  | Sd    | 63       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 497   | 306 | 99 | 91 | 1 |         |       |

- Molecule 52 is a protein called 40S ribosomal protein S30-A.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 52  | Sf    | 30       | Total | C   | N  | O  |         | 0     |
|     |       |          | 251   | 162 | 50 | 39 |         | 0     |

- Molecule 53 is a protein called Ubiquitin-40S ribosomal protein S31.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 53  | Sg    | 51       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 397   | 249 | 73 | 71 | 4 |         |       |

- Molecule 54 is a protein called Utp7.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 54  | U1    | 285      | Total | C   | N   | O   |         | 0     |
|     |       |          | 1425  | 855 | 285 | 285 |         | 0     |

- Molecule 55 is a protein called Utp11.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 55  | U2    | 73       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 365   | 219 | 73 | 73 |         |       |

- Molecule 56 is a protein called Utp20.

| Mol | Chain | Residues | Atoms |      |      |      | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|---------|-------|
| 56  | U3    | 1407     | Total | C    | N    | O    | 0       | 0     |
|     |       |          | 7035  | 4221 | 1407 | 1407 |         |       |

- Molecule 57 is a protein called rRNA-processing protein FCF1.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 57  | U4    | 126      | Total | C   | N   | O   | S  | 0       | 0     |
|     |       |          | 990   | 633 | 179 | 168 | 10 |         |       |

- Molecule 58 is a protein called Ribosome biogenesis protein UTP30.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 58  | U5    | 248      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 2009  | 1285 | 357 | 359 | 8 |         |       |

- Molecule 59 is a protein called Helical domain protein.

| Mol | Chain | Residues | Atoms |      |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 59  | UA    | 338      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 1690  | 1014 | 338 | 338 |         |       |

- Molecule 60 is a protein called Helical domain protein.

| Mol | Chain | Residues | Atoms |      |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 60  | UB    | 555      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2775  | 1665 | 555 | 555 |         |       |

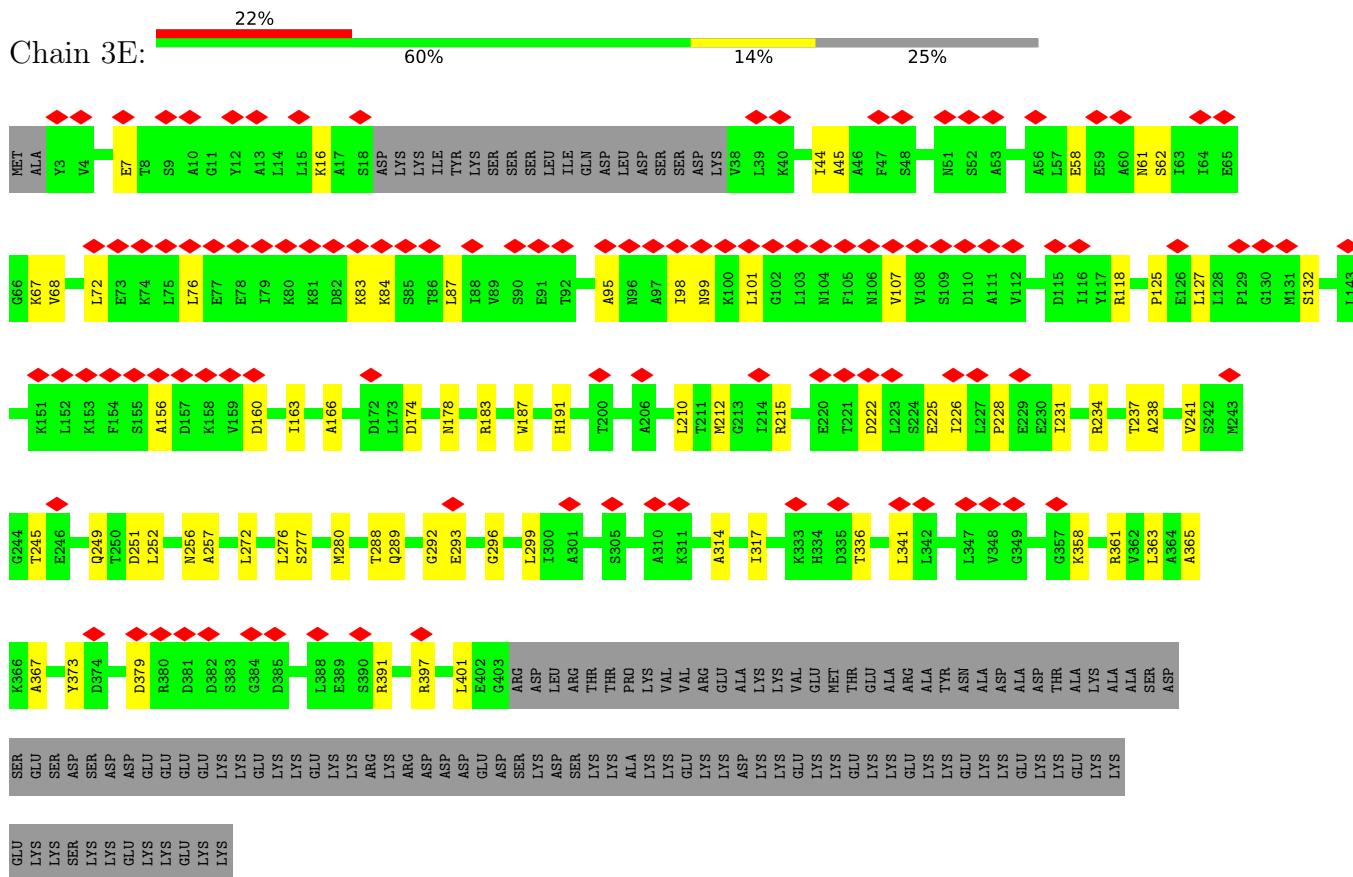
- Molecule 61 is a protein called Unassigned helices.

| Mol | Chain | Residues | Atoms |      |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 61  | UC    | 660      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 3300  | 1980 | 660 | 660 |         |       |

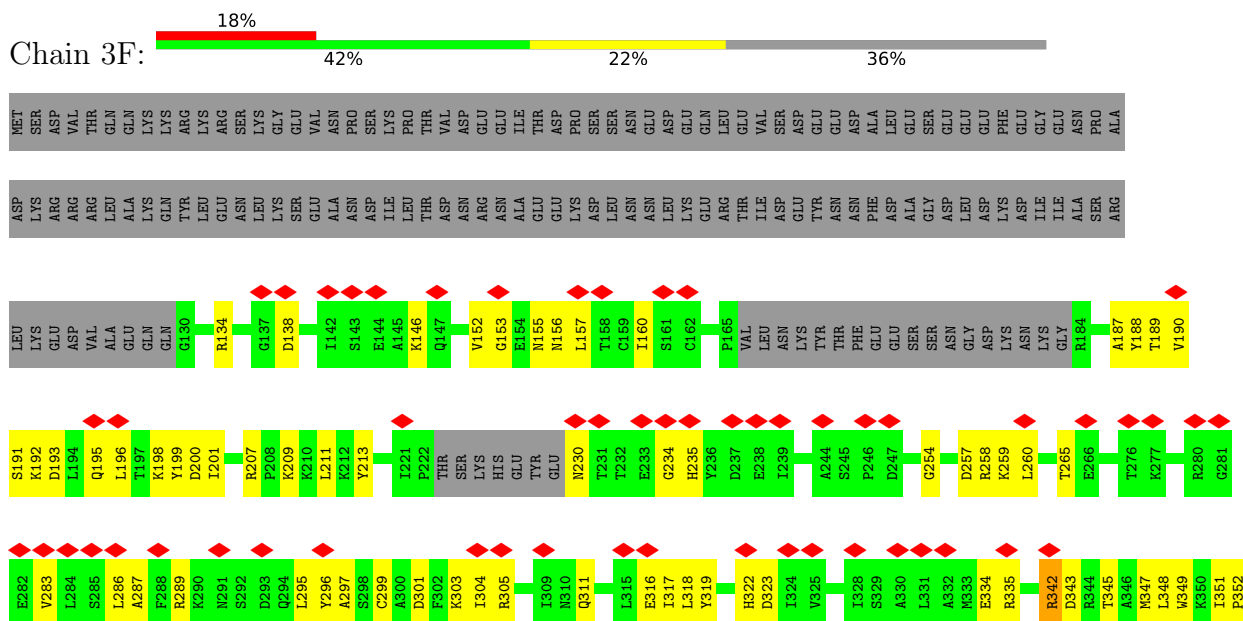


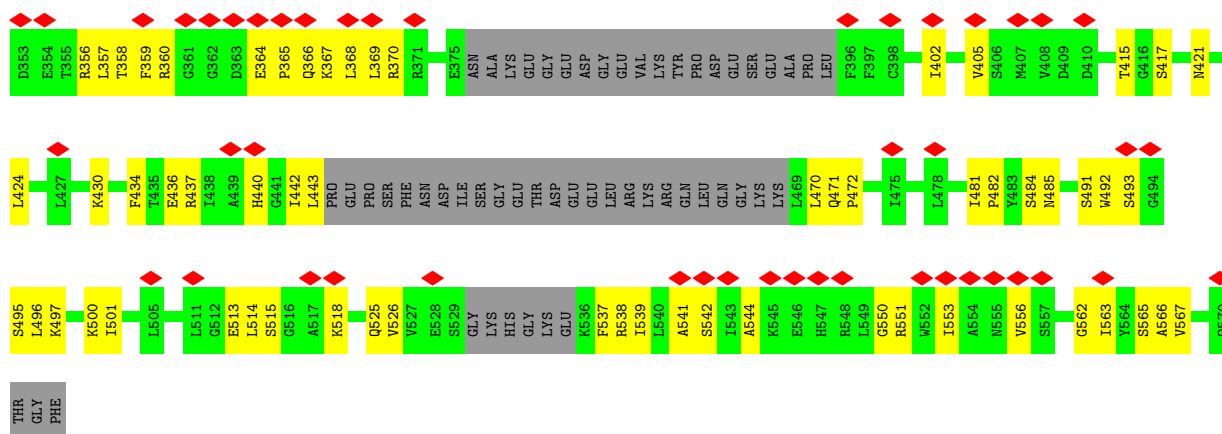


- Molecule 4: Nucleolar protein 58

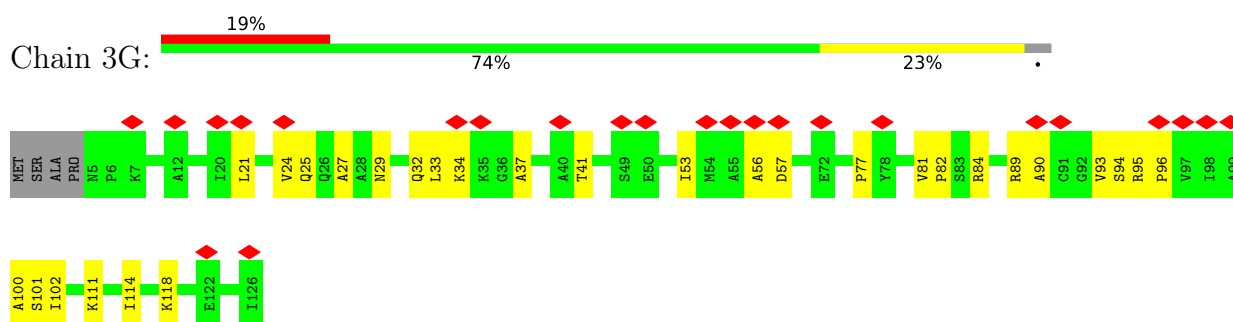


- Molecule 5: Ribosomal RNA-processing protein 9

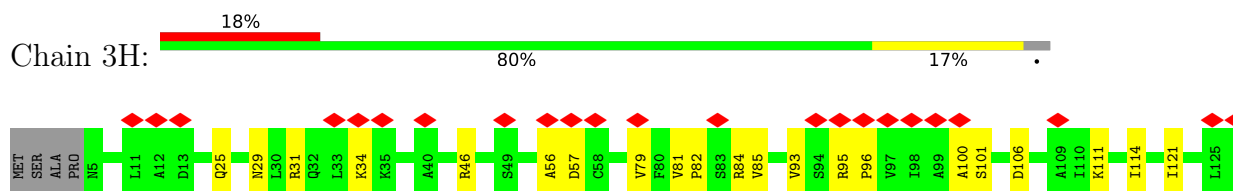




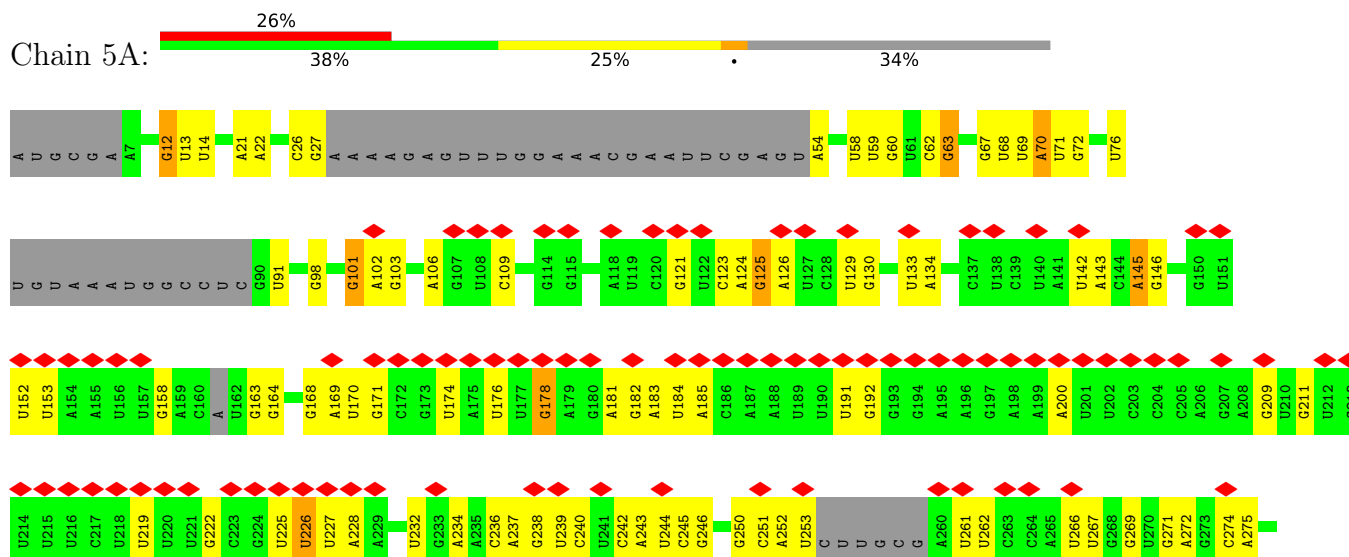
- Molecule 6: 13 kDa ribonucleoprotein-associated protein

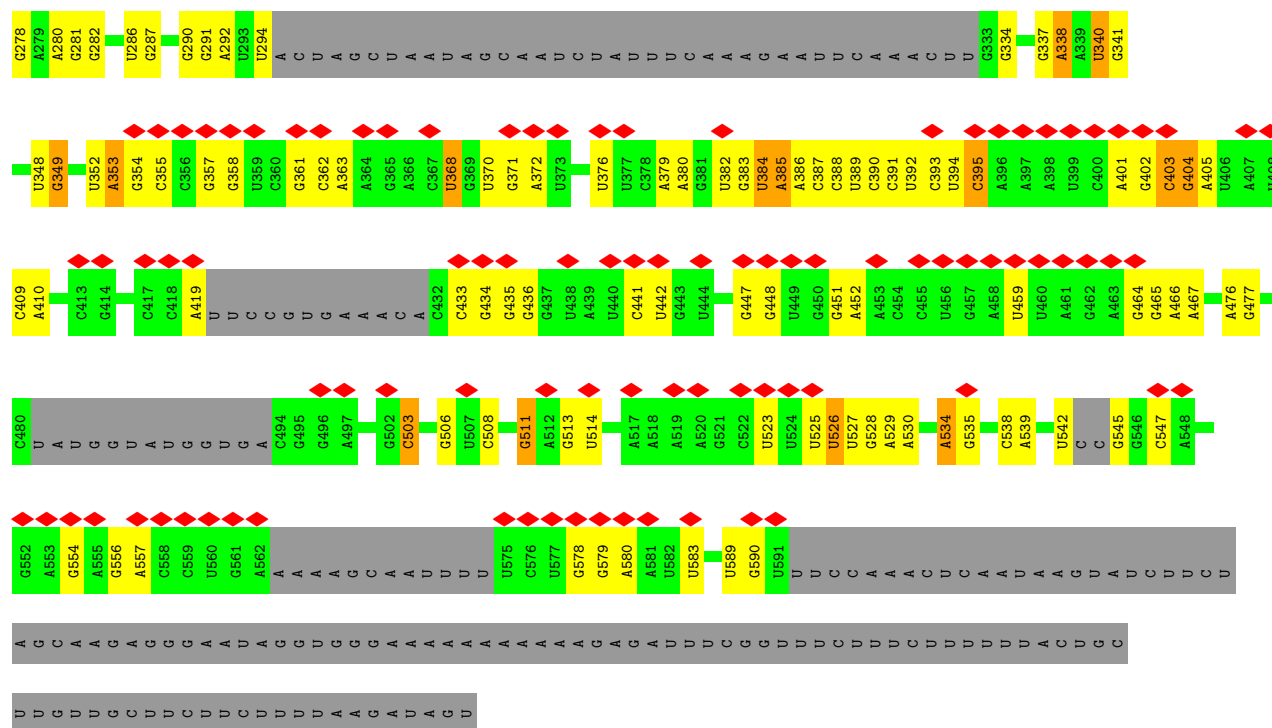


- Molecule 6: 13 kDa ribonucleoprotein-associated protein

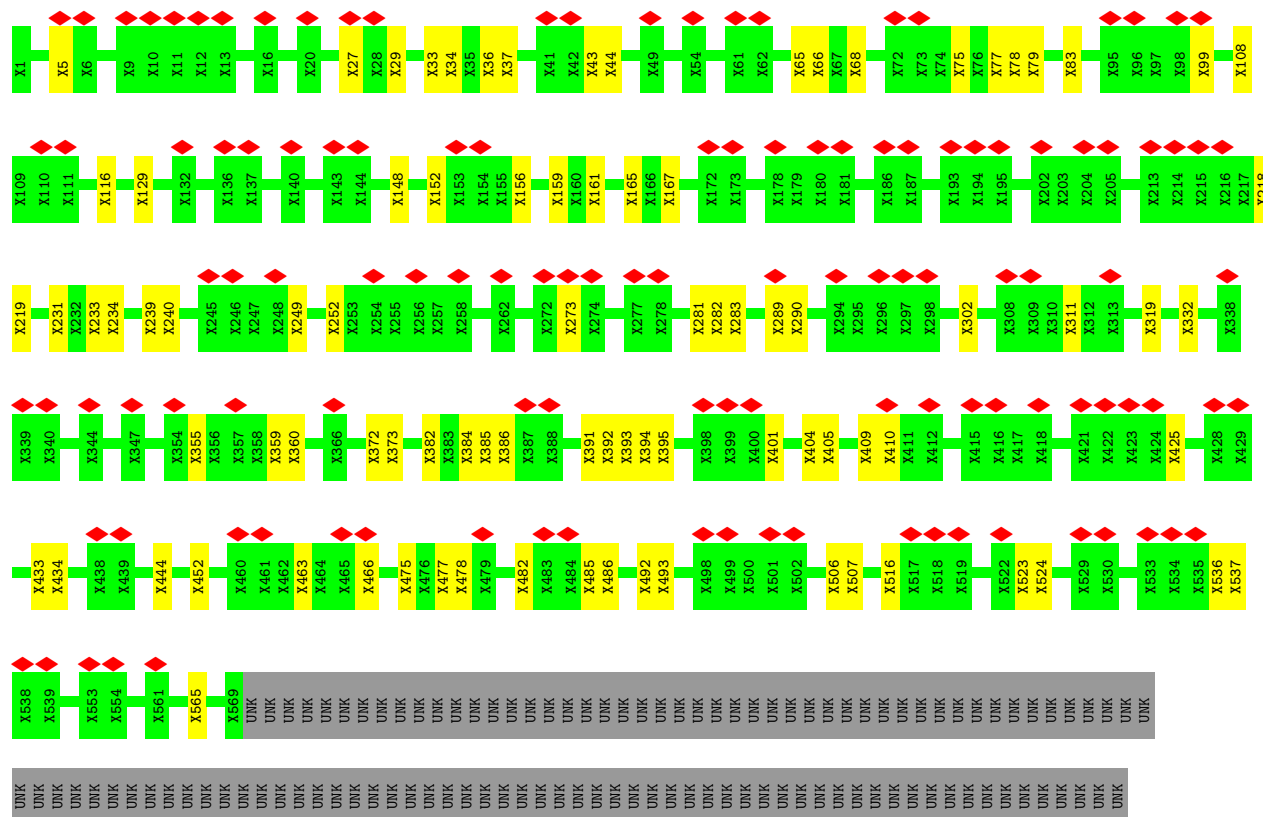


- Molecule 7: 5ETS RNA



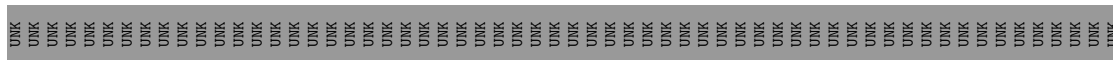


• Molecule 8: Utp4

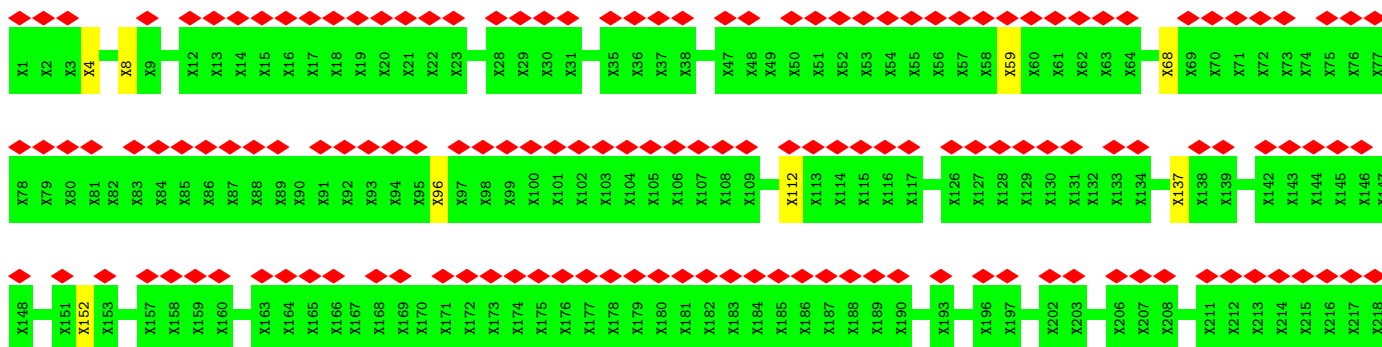


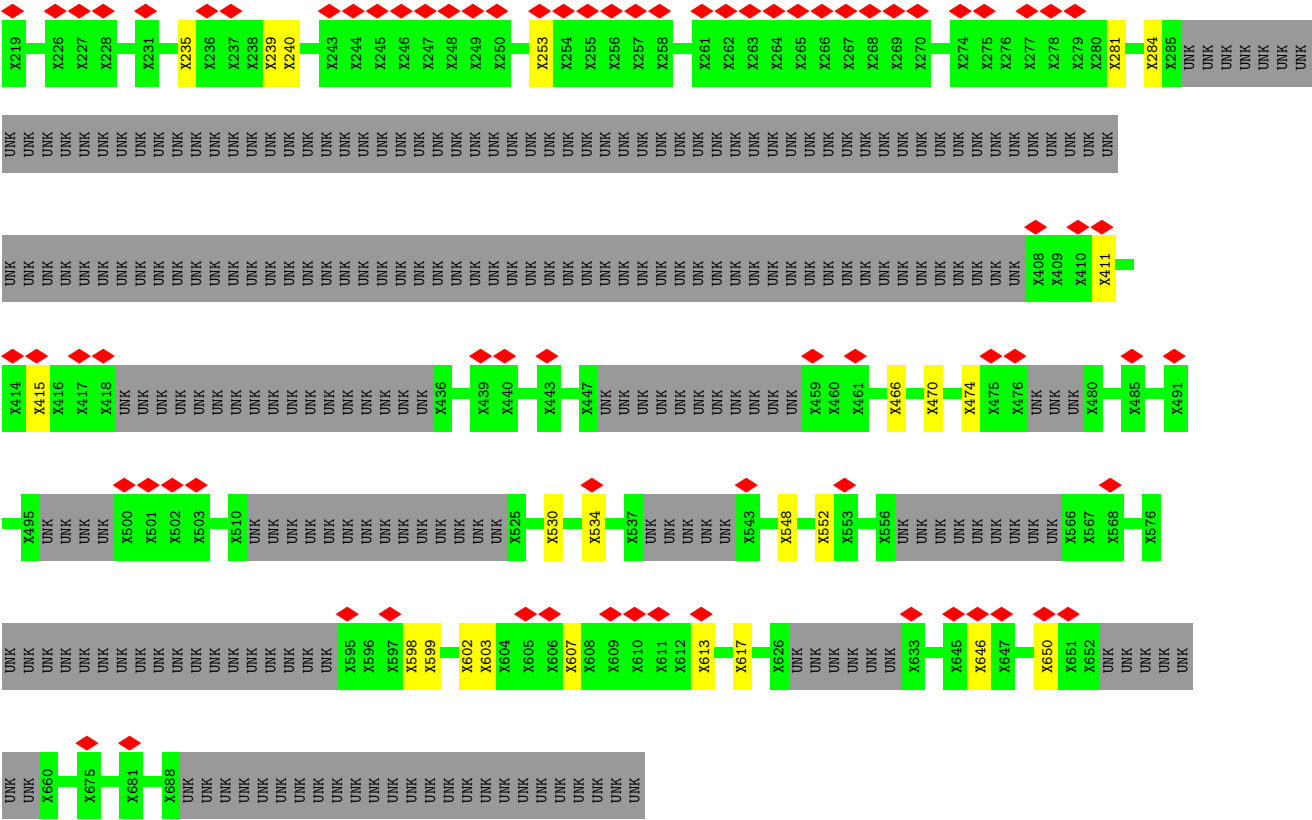
[illegible]

Chain AB: 

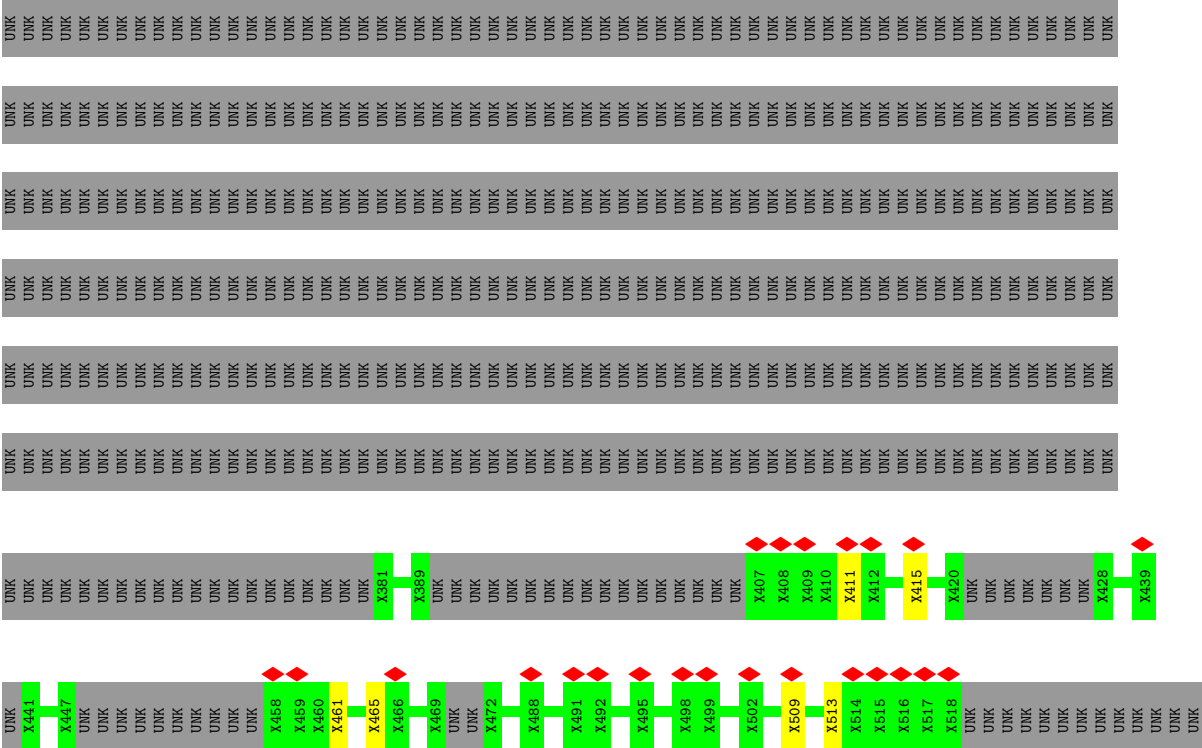


Chain AC: 

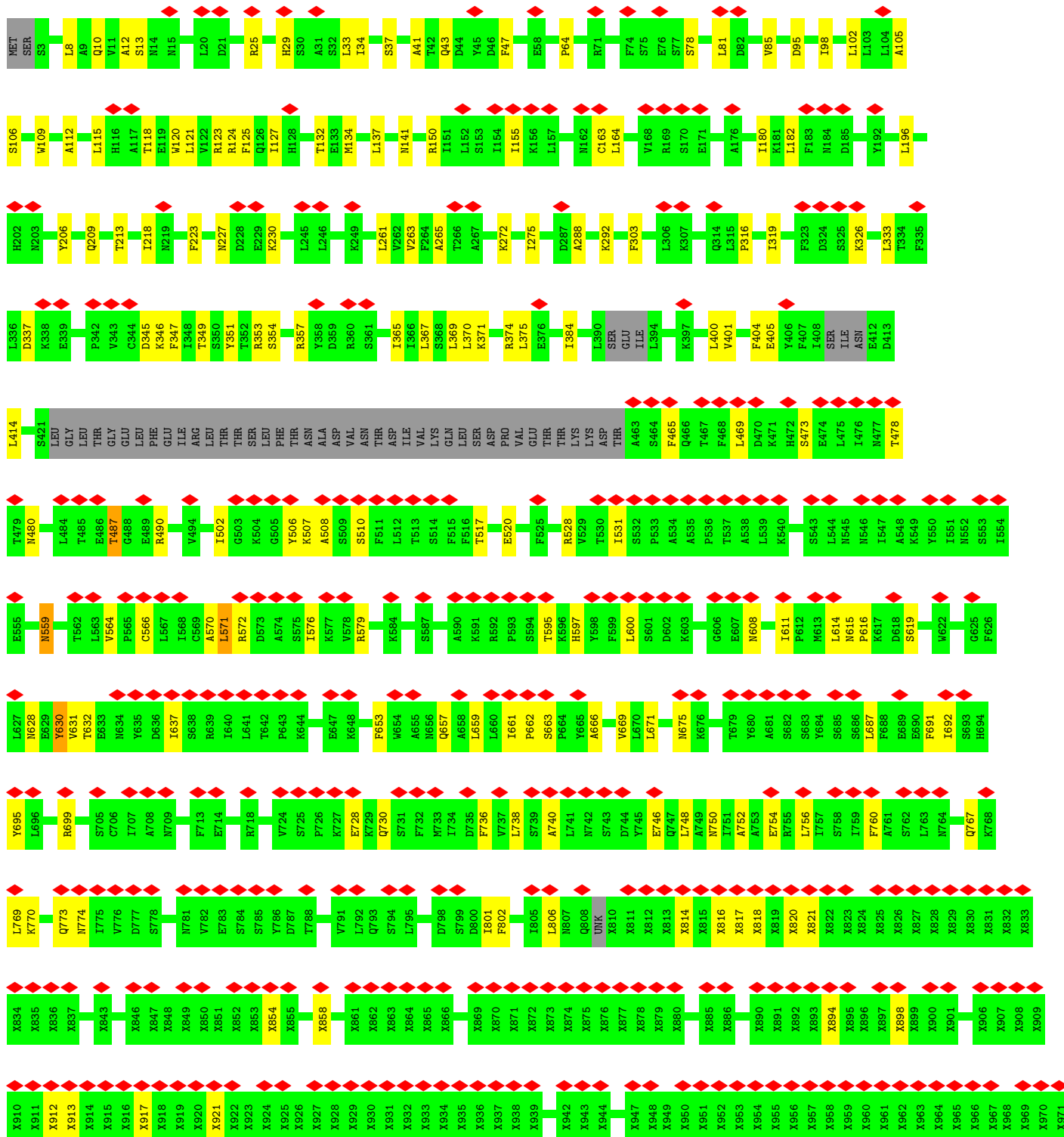
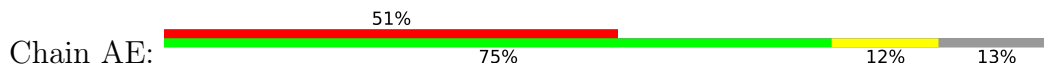




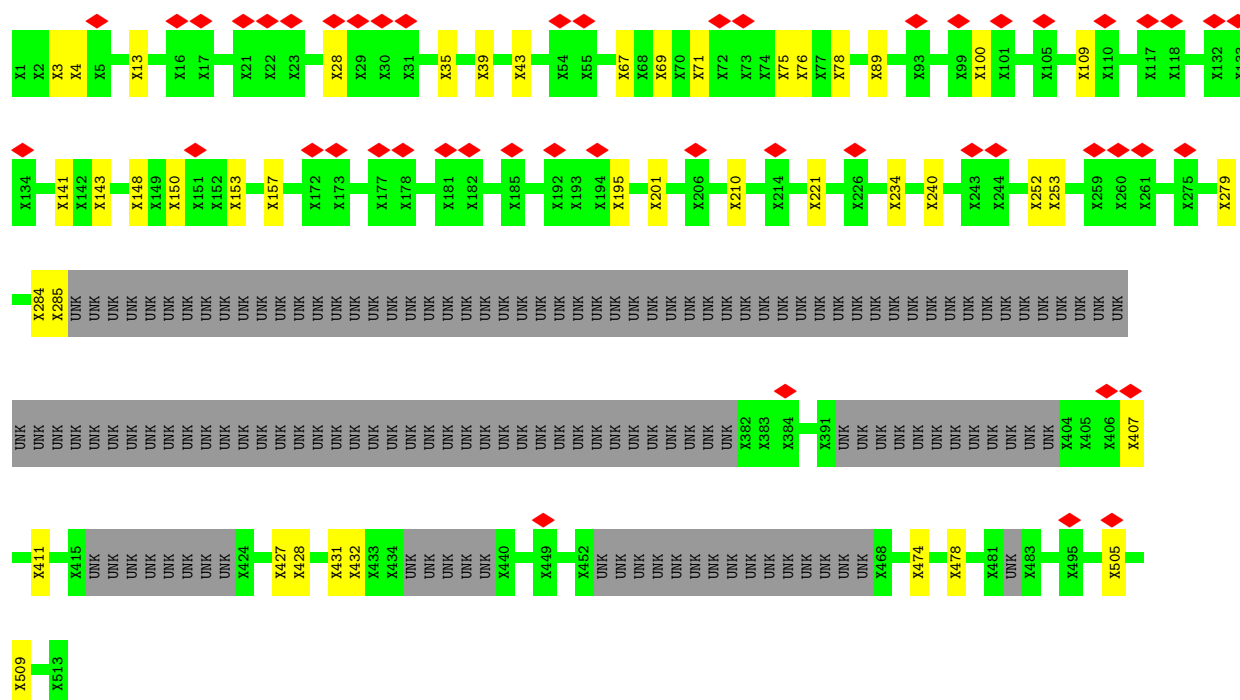
• Molecule 11: Utp9



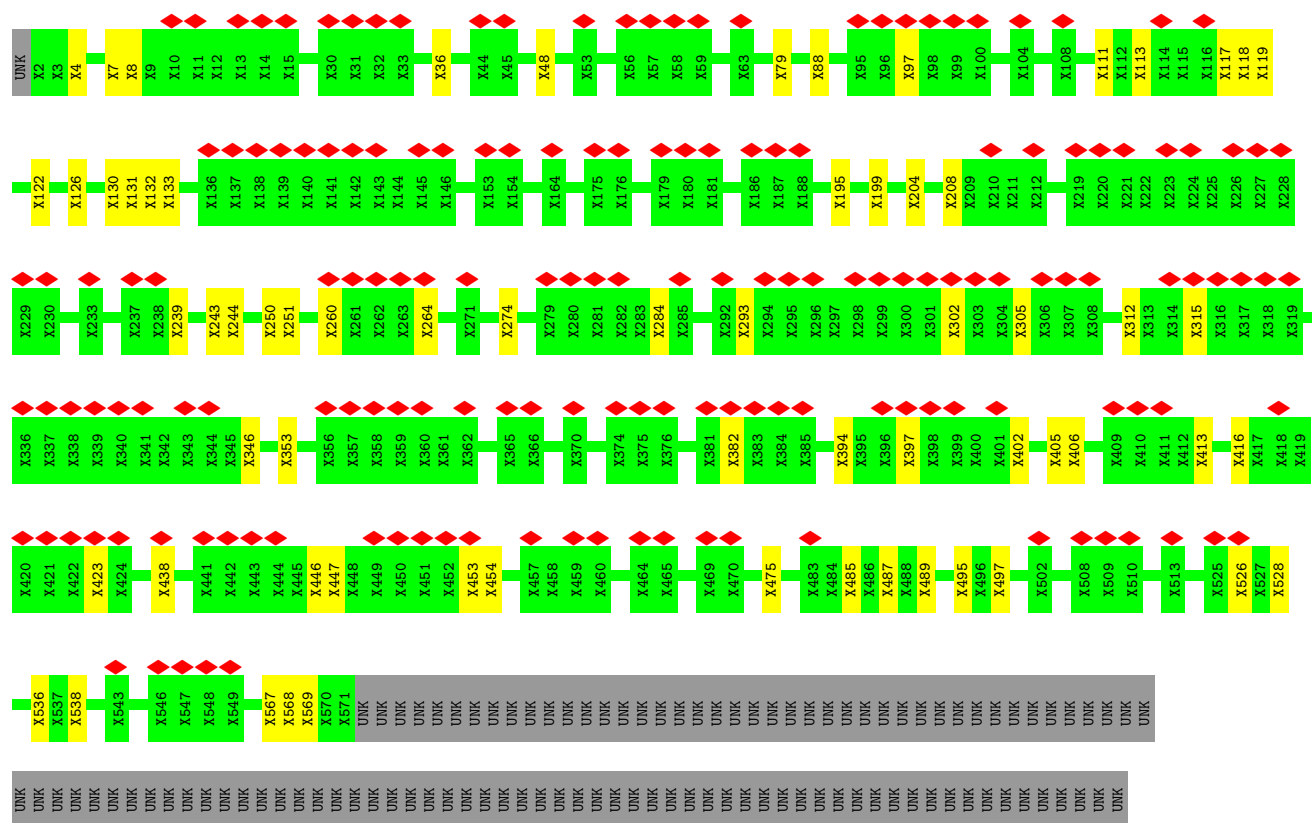
- Molecule 12: U3 small nucleolar RNA-associated protein 10,Utp10



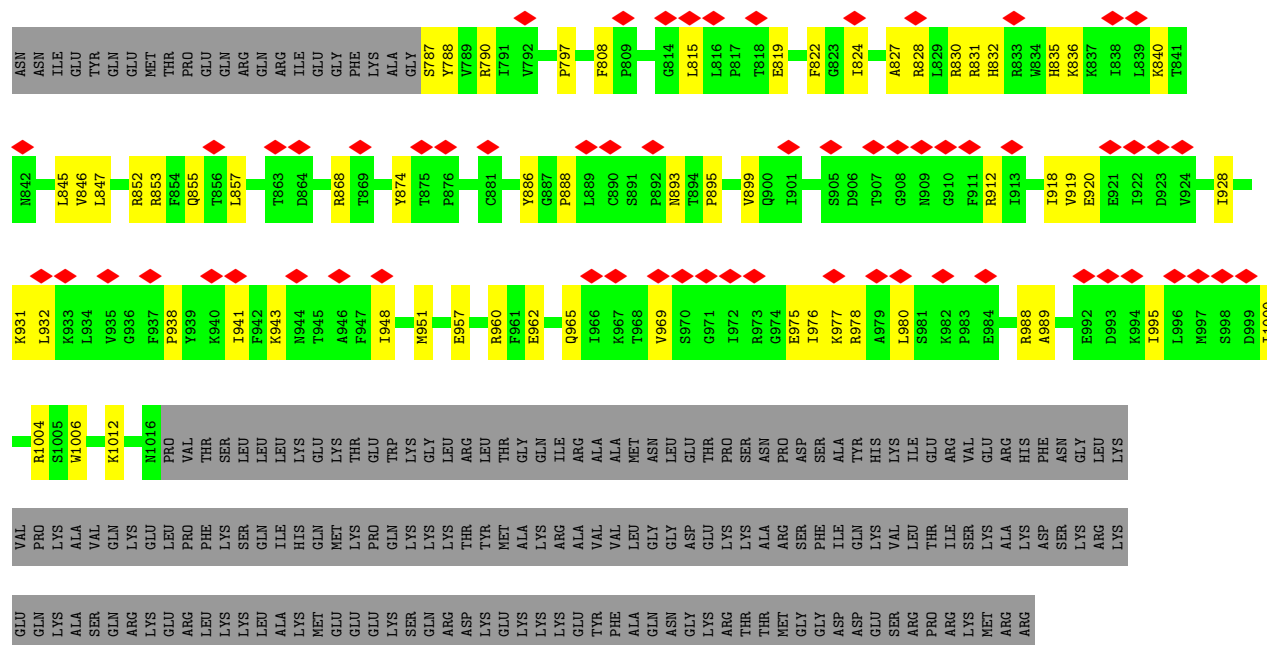




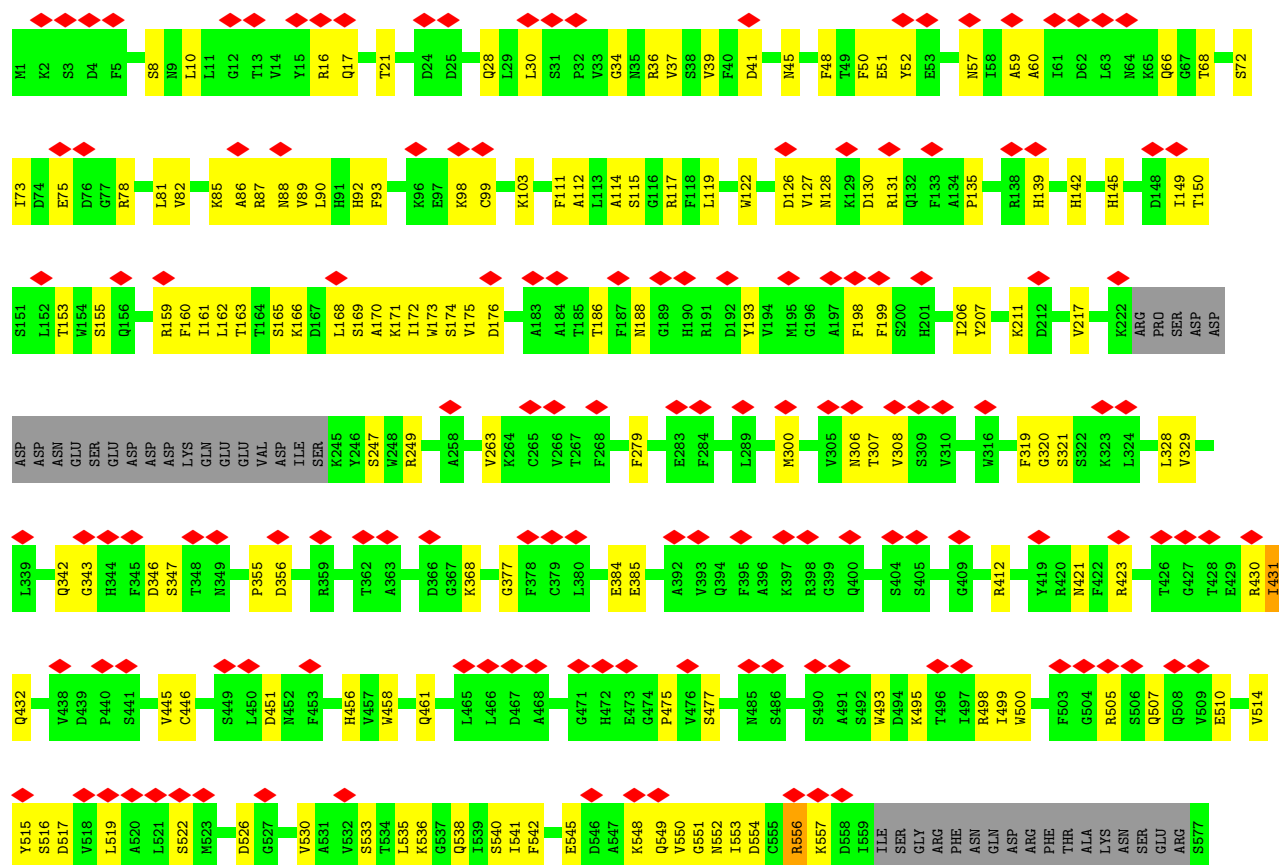
• Molecule 14: Utp17



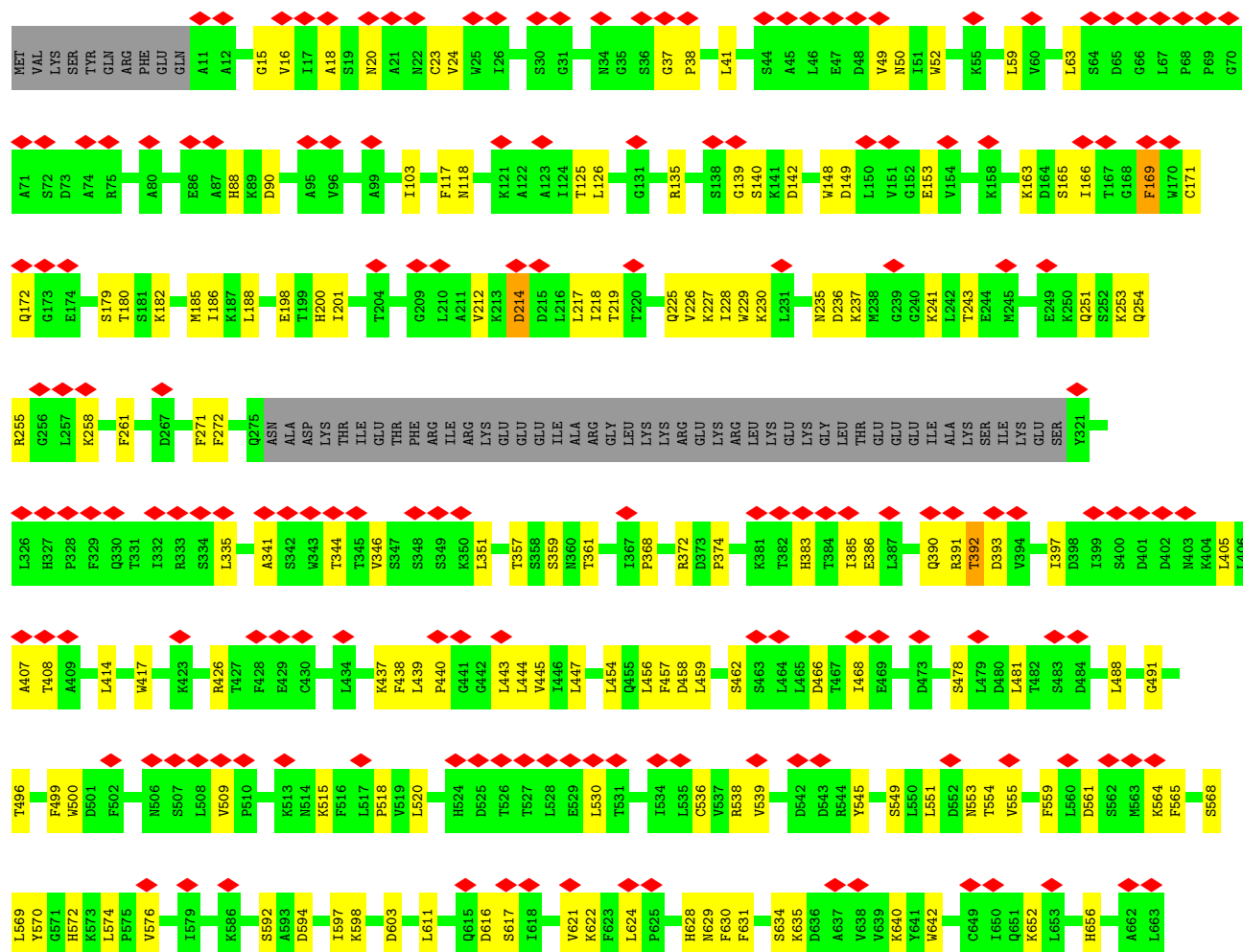


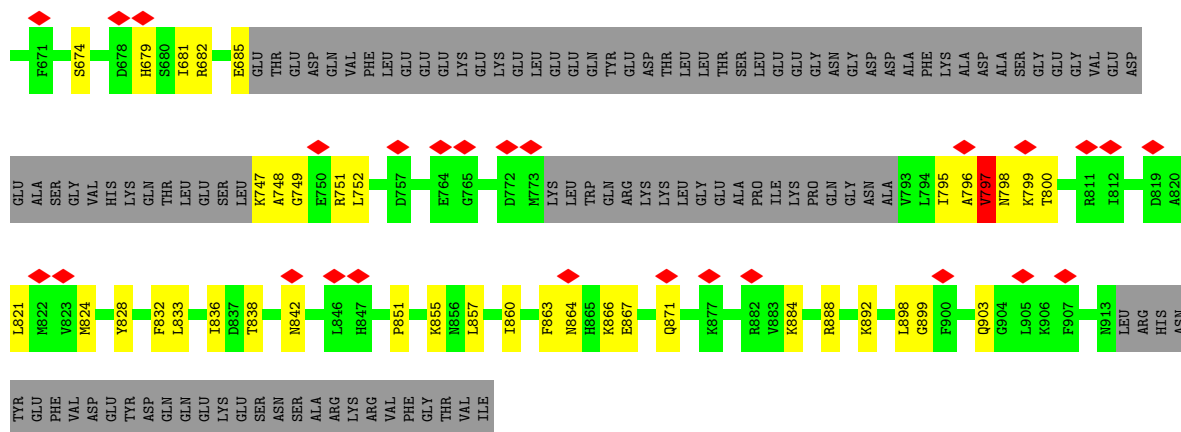


• Molecule 16: Periodic tryptophan protein 2

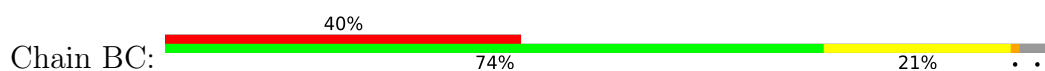


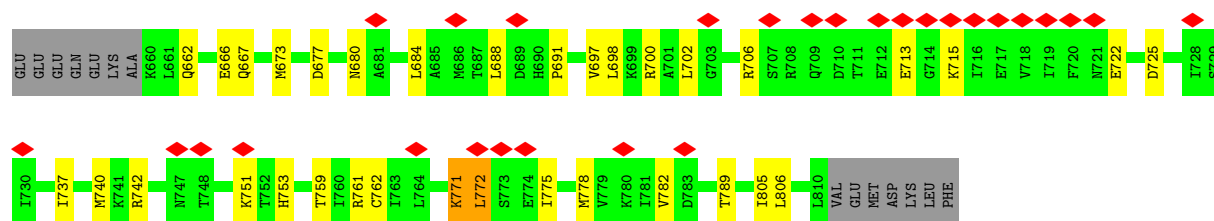
- Molecule 17: U3 small nucleolar RNA-associated protein 12



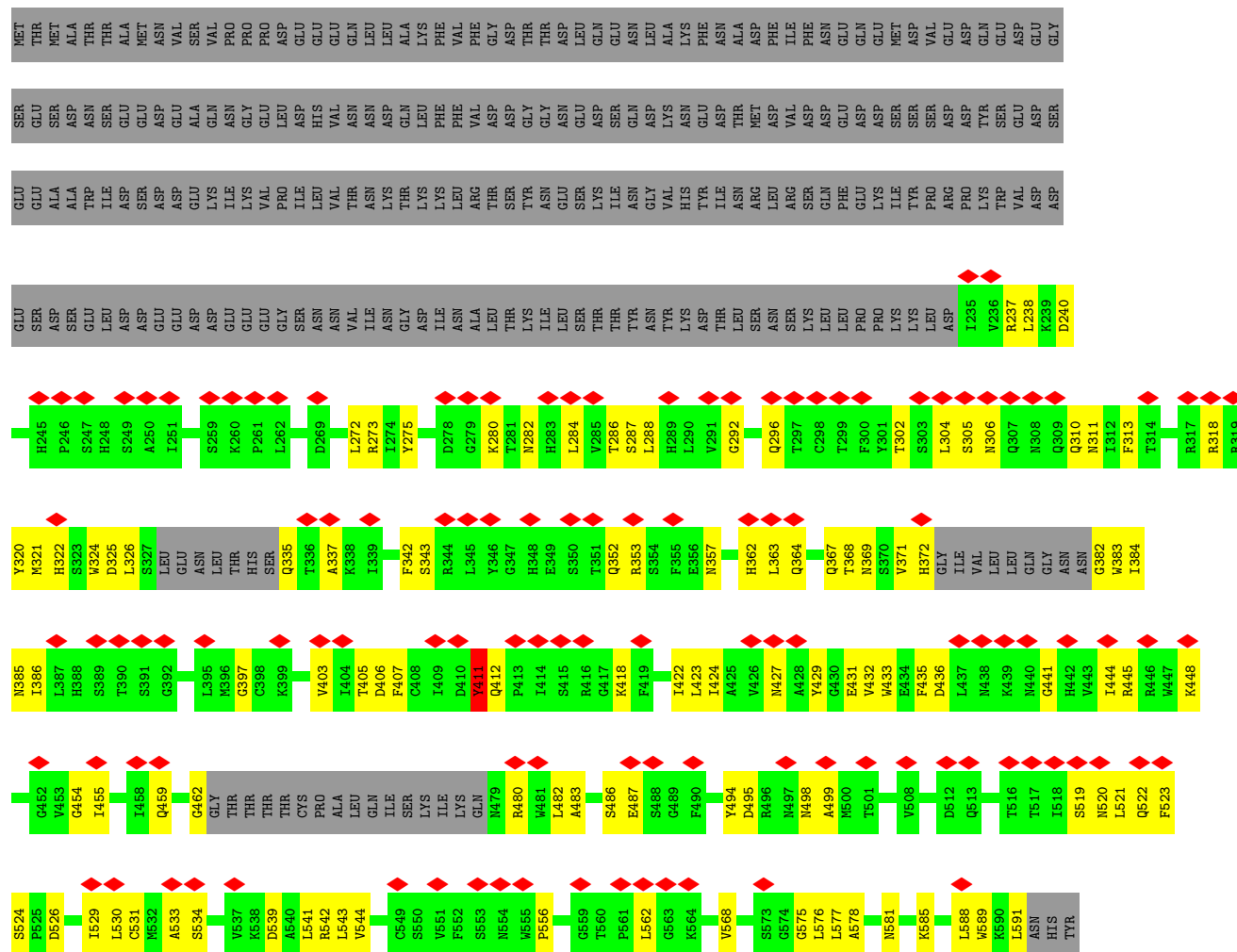


• Molecule 18: U3 small nucleolar RNA-associated protein 13

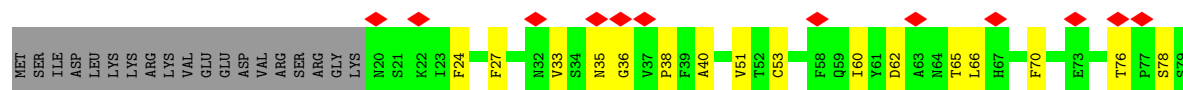


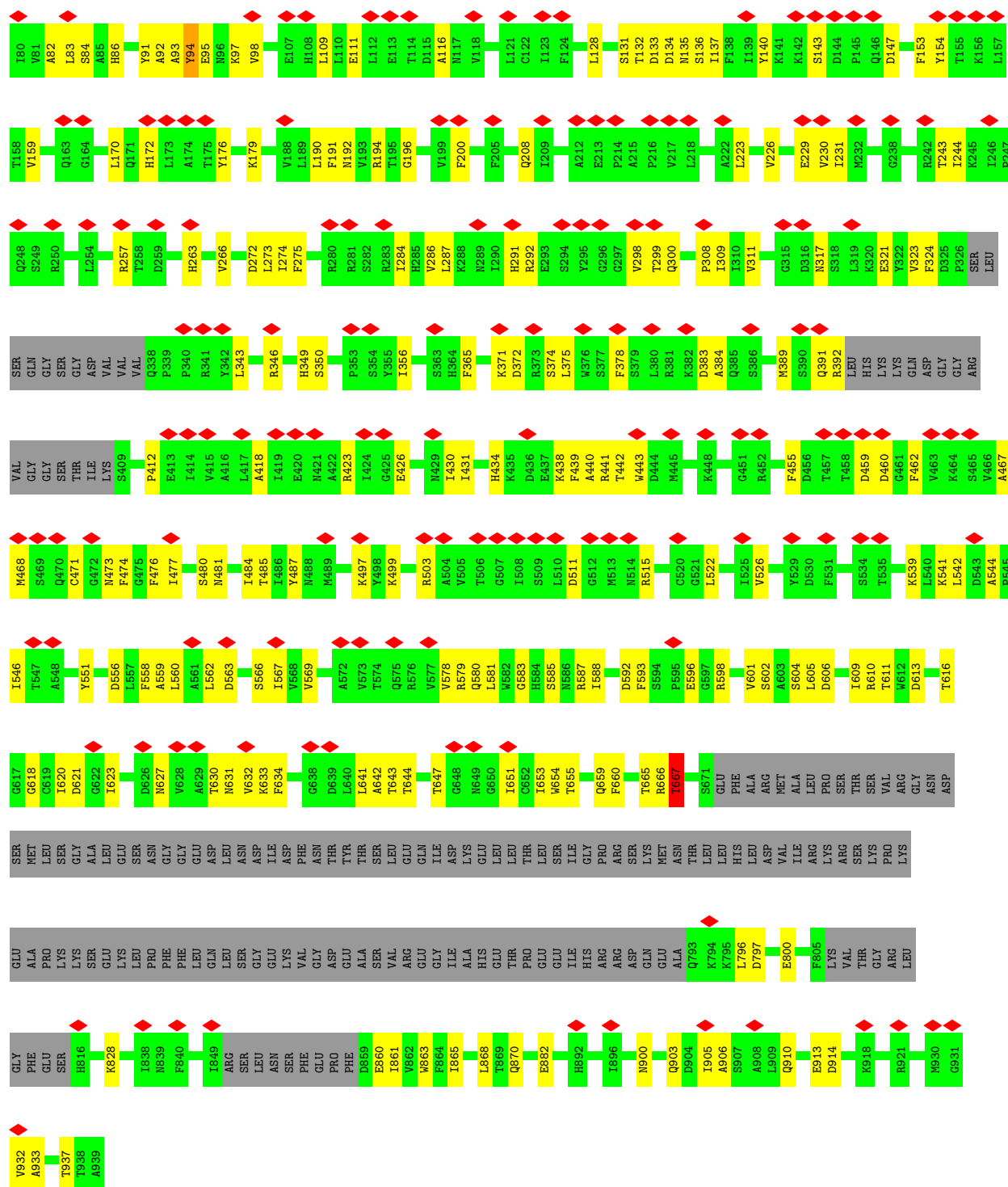


• Molecule 19: U3 small nucleolar RNA-associated protein 18

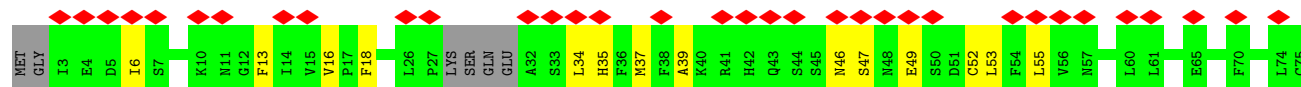


• Molecule 20: U3 small nucleolar RNA-associated protein 21

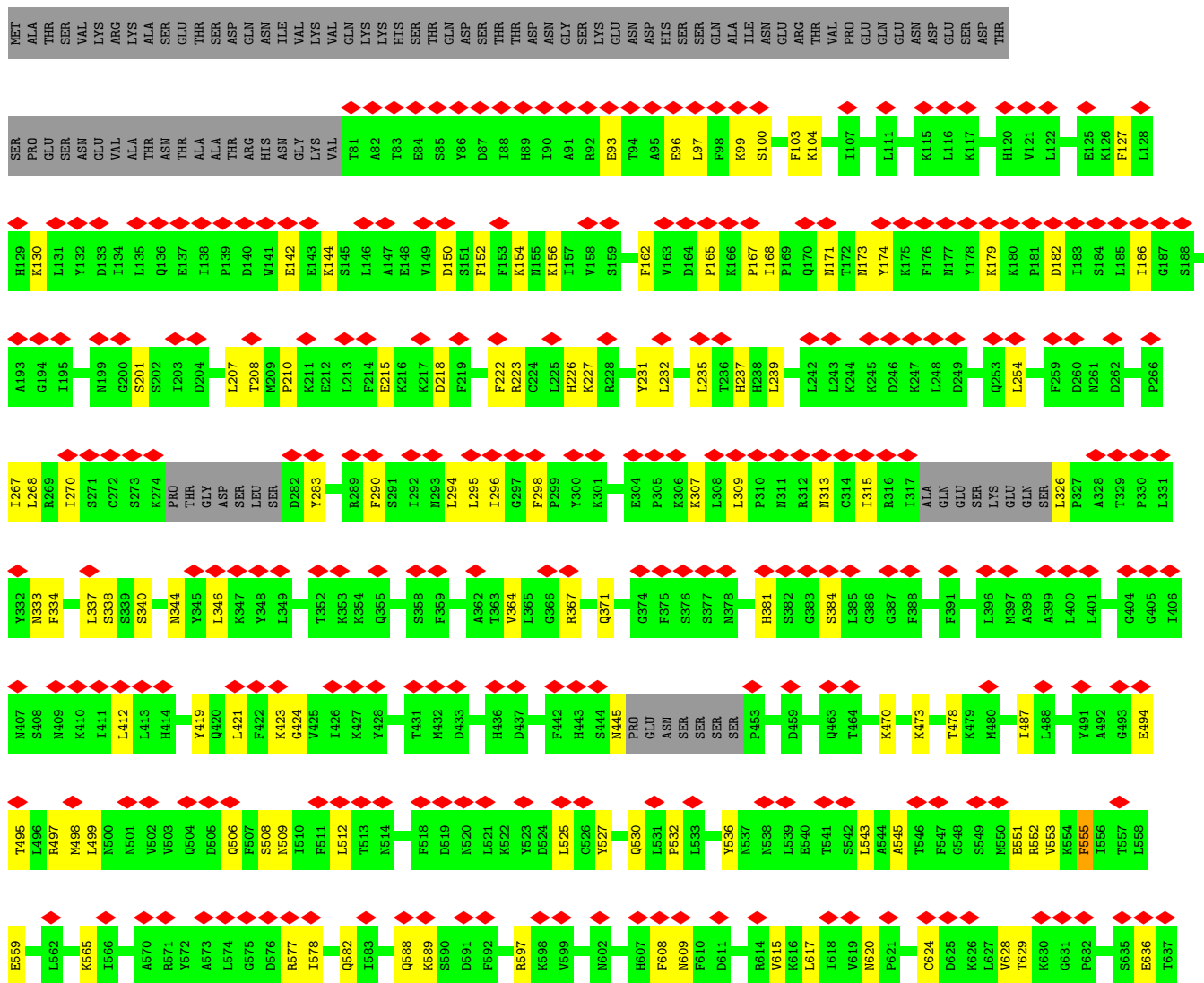


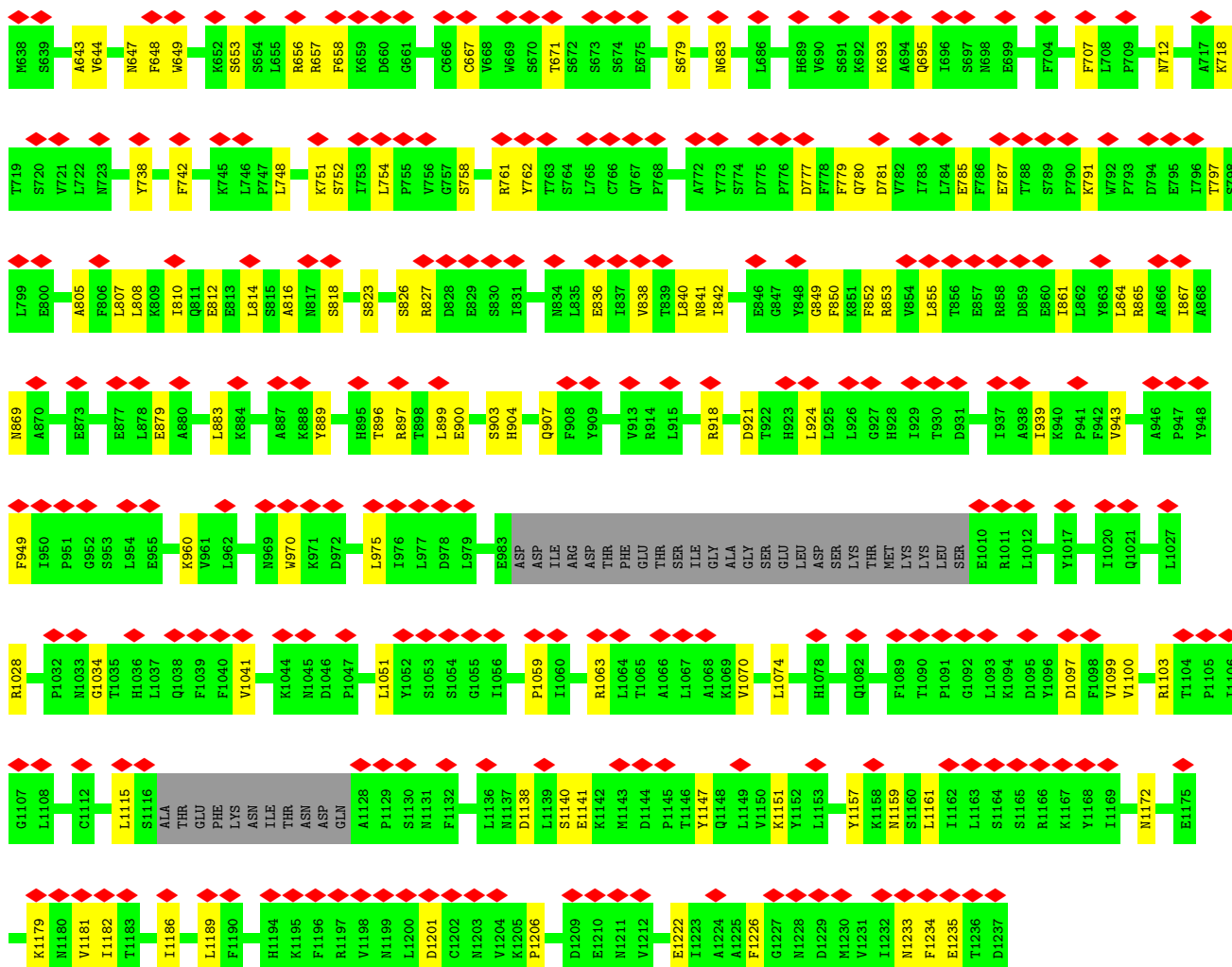


- Molecule 21: Ribosomal RNA-processing protein 7

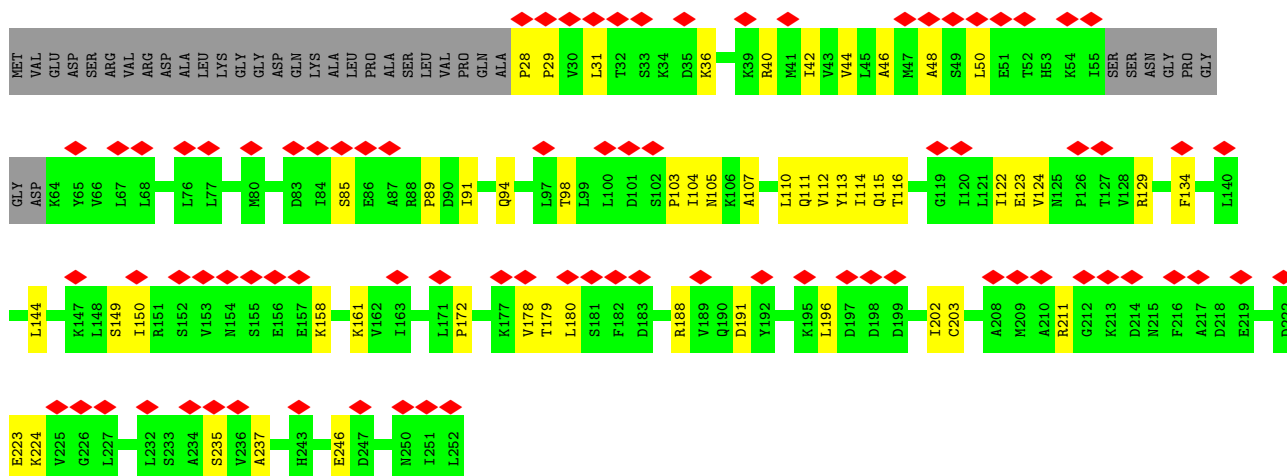


- Molecule 22: U3 small nucleolar RNA-associated protein 22



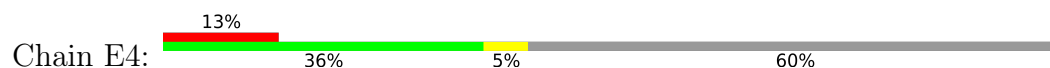


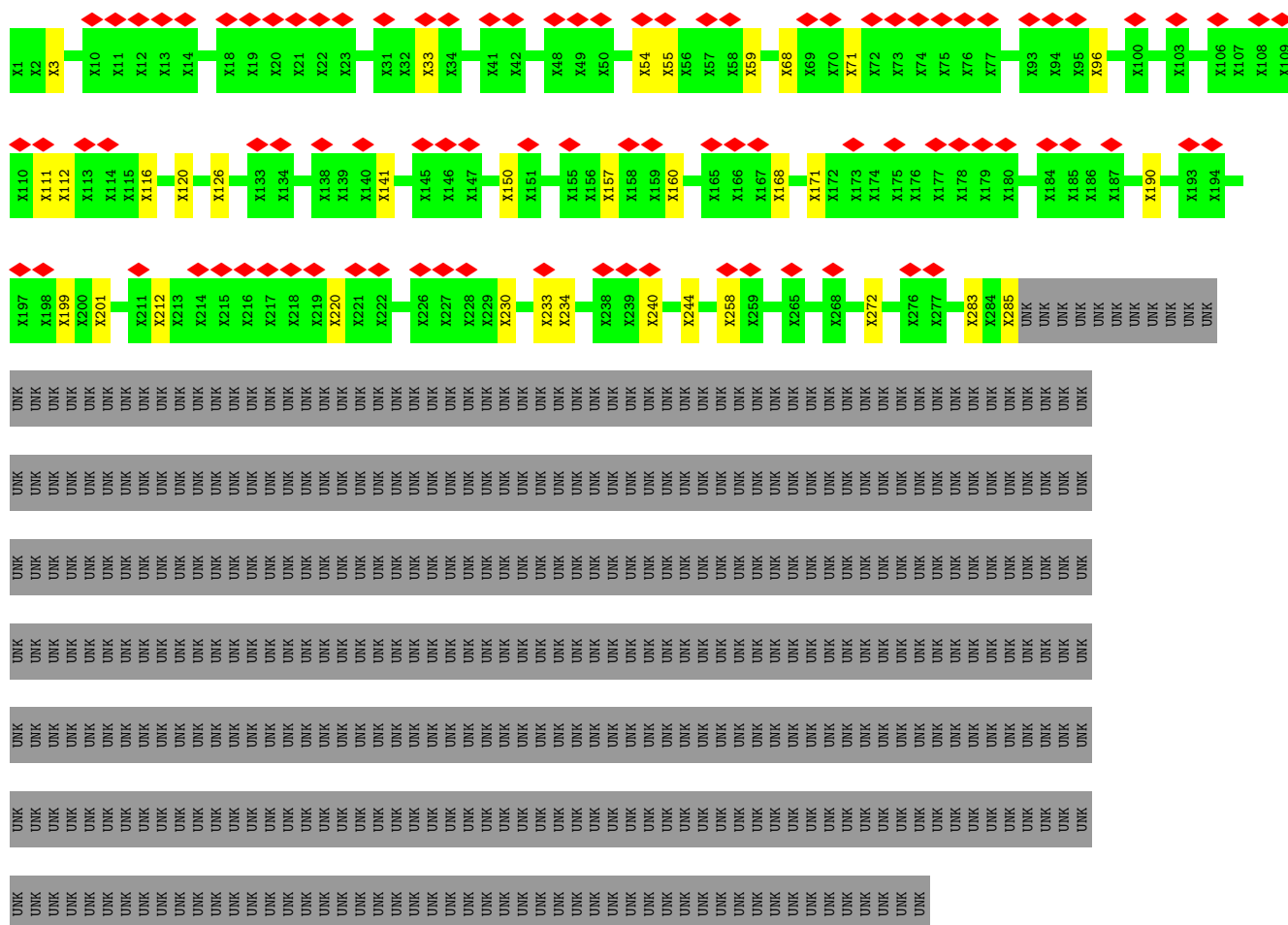
• Molecule 23: Ribosomal RNA small subunit methyltransferase NEP1



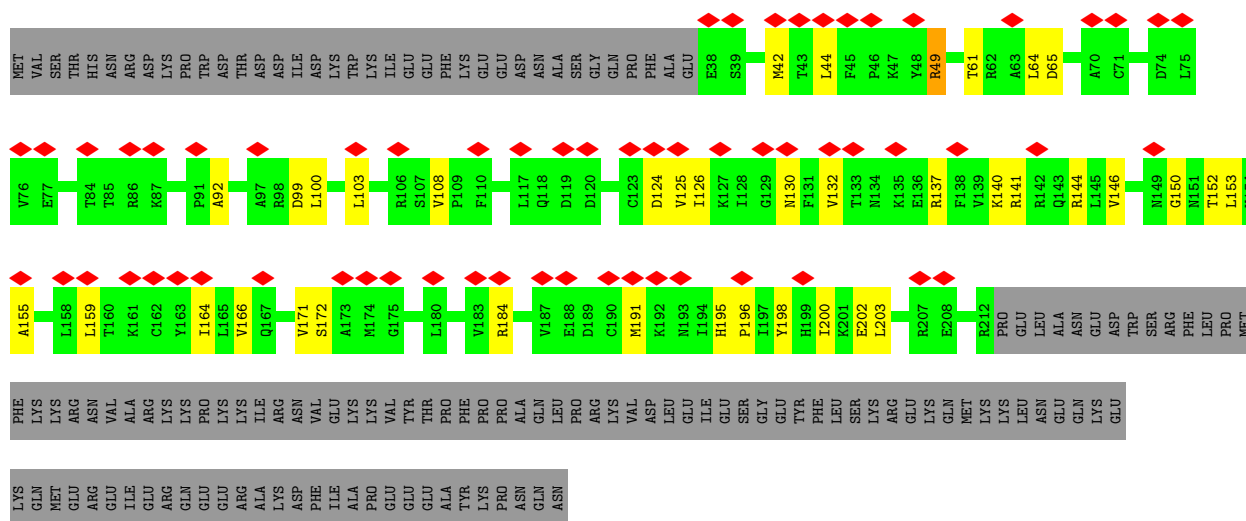
• Molecule 23: Ribosomal RNA small subunit methyltransferase NEP1

- Molecule 25: Enp2

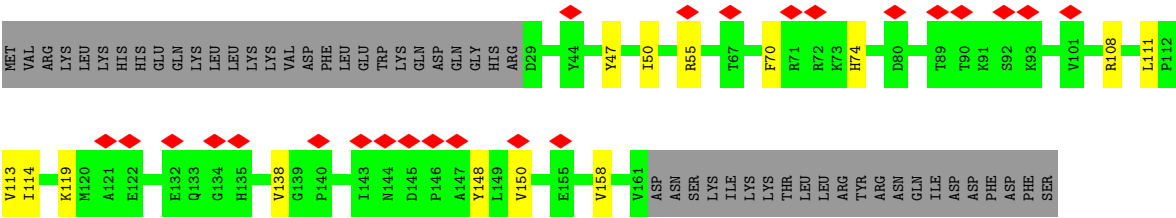




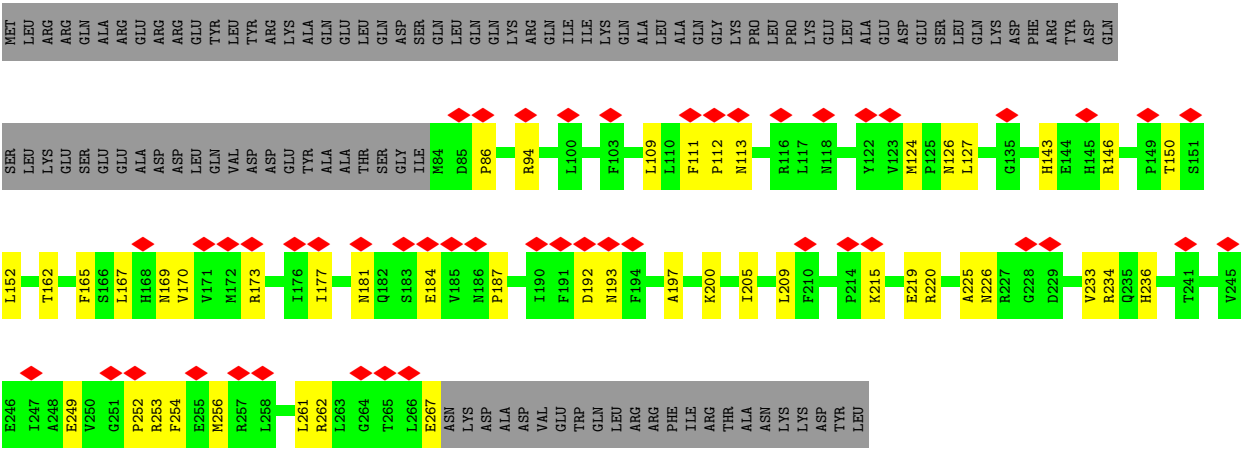
- Molecule 26: KRR1 small subunit processome component



- Molecule 27: U3 small nucleolar ribonucleoprotein protein IMP3

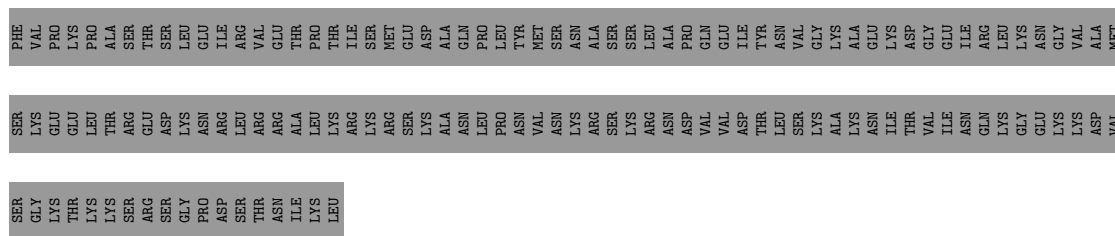


● Molecule 28: U3 small nucleolar ribonucleoprotein protein IMP4

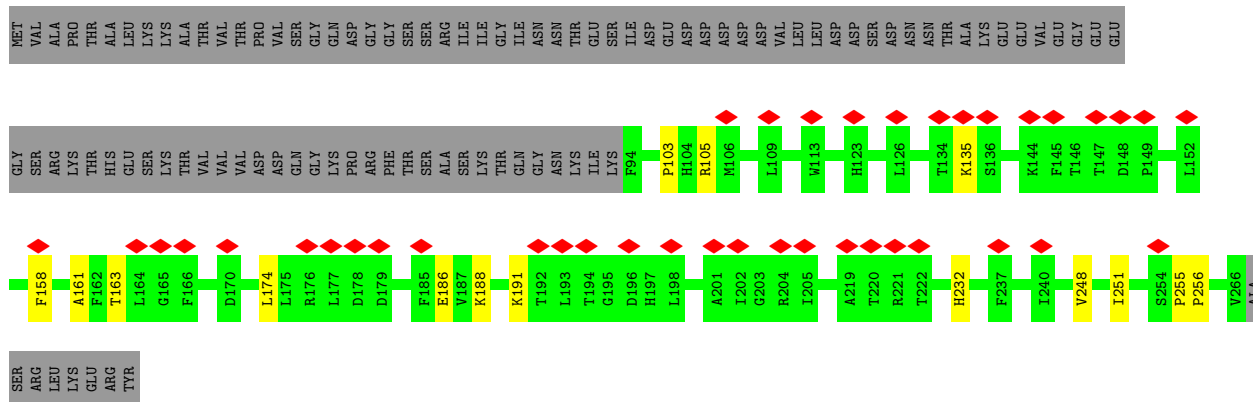


● Molecule 29: Mpp10,U3 small nucleolar RNA-associated protein MPP10

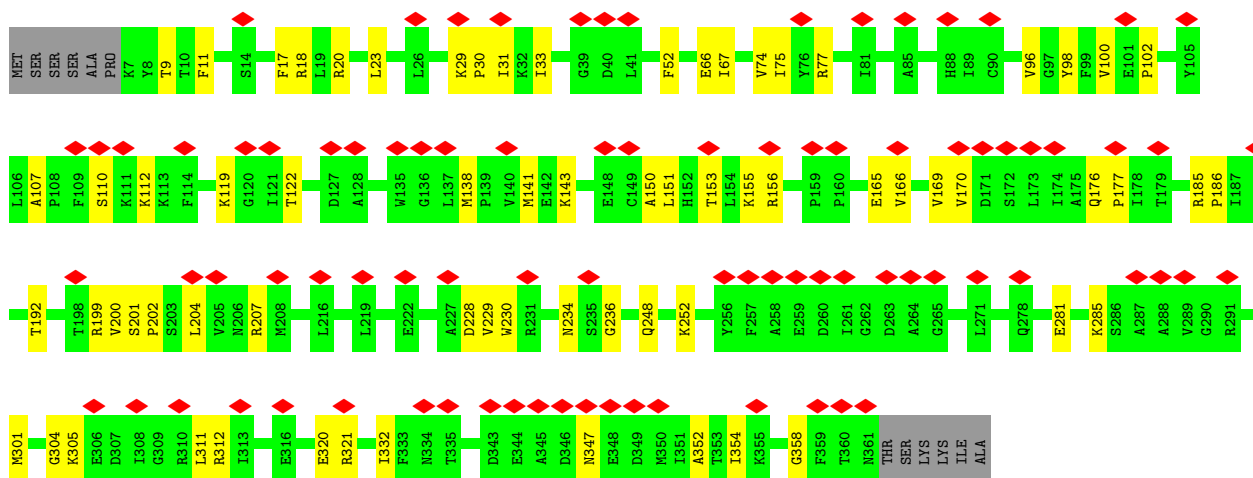
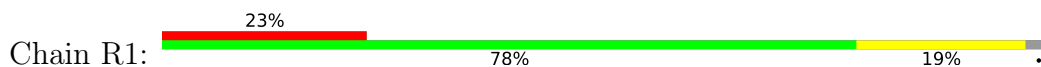




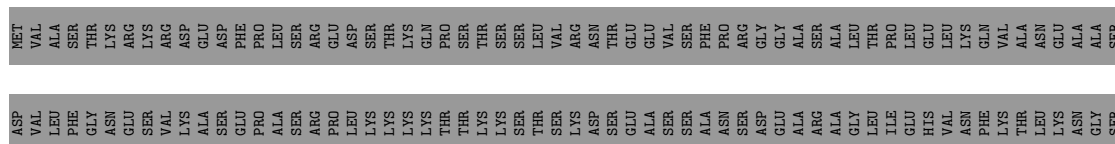
- Molecule 30: Pre-rRNA-processing protein PNO1



- Molecule 31: RNA 3'-terminal phosphate cyclase-like protein



- Molecule 32: rRNA biogenesis protein RRP5

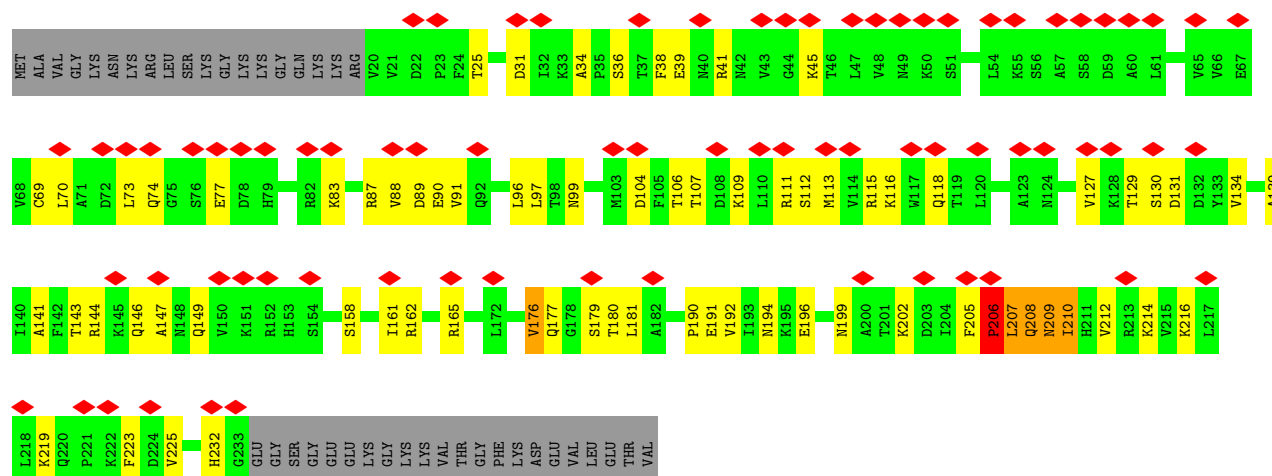


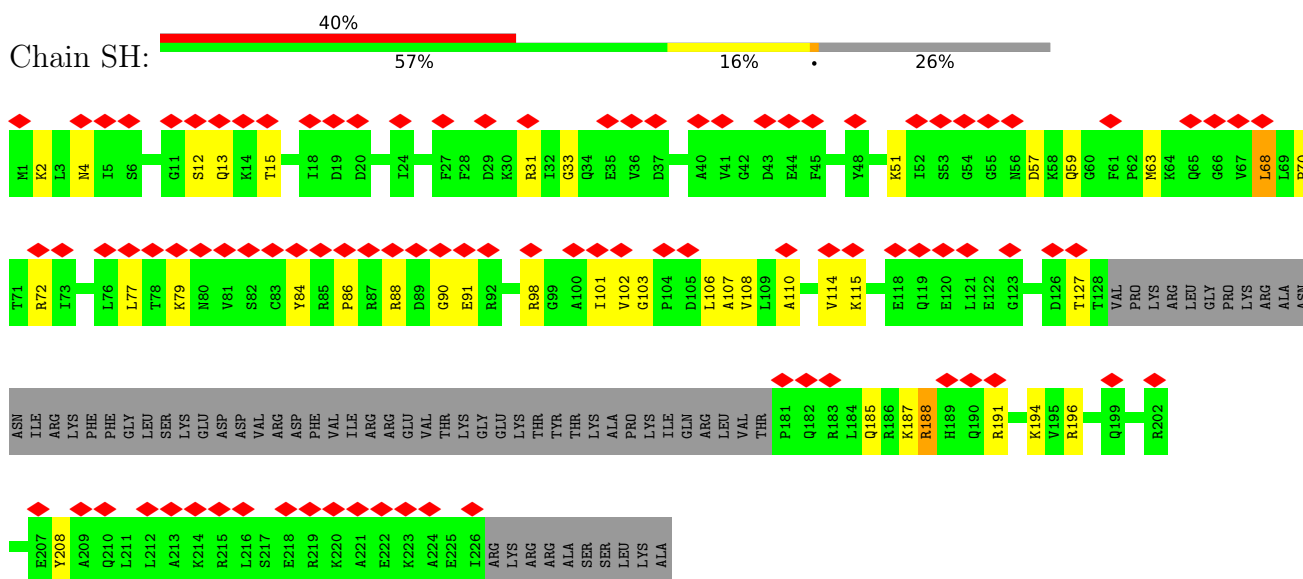




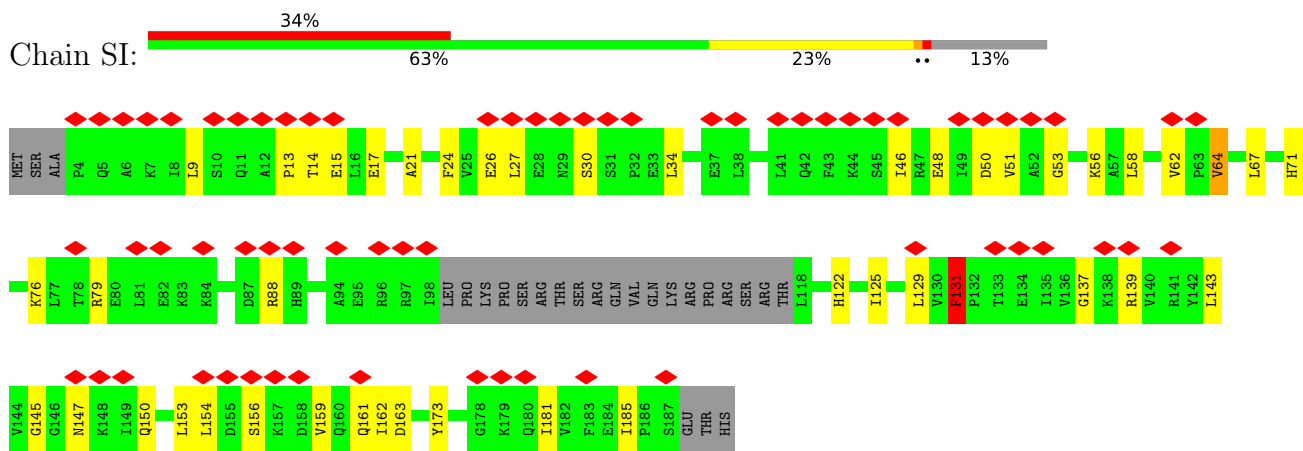




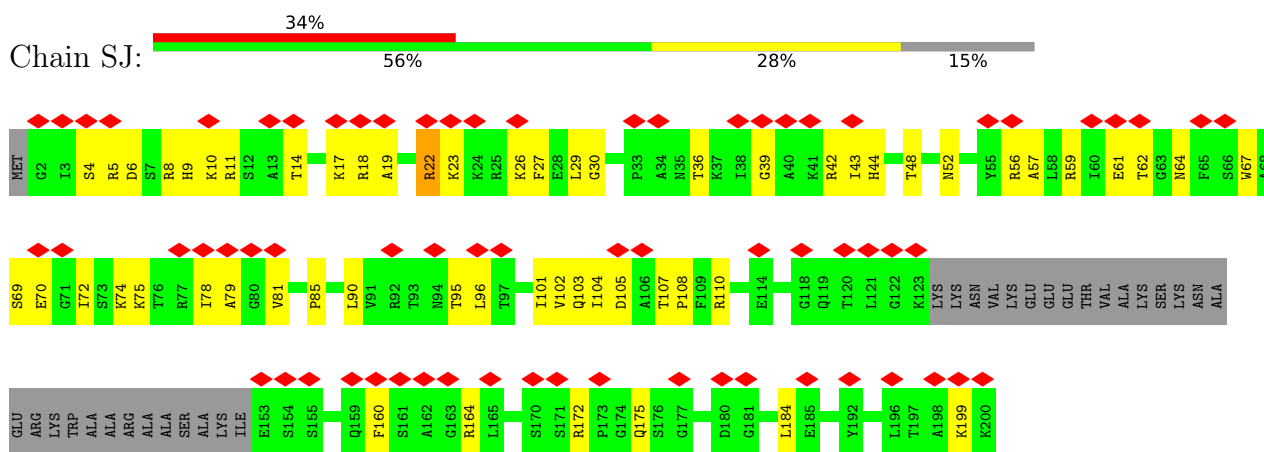




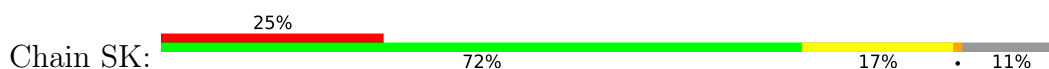
• Molecule 39: 40S ribosomal protein S7-A



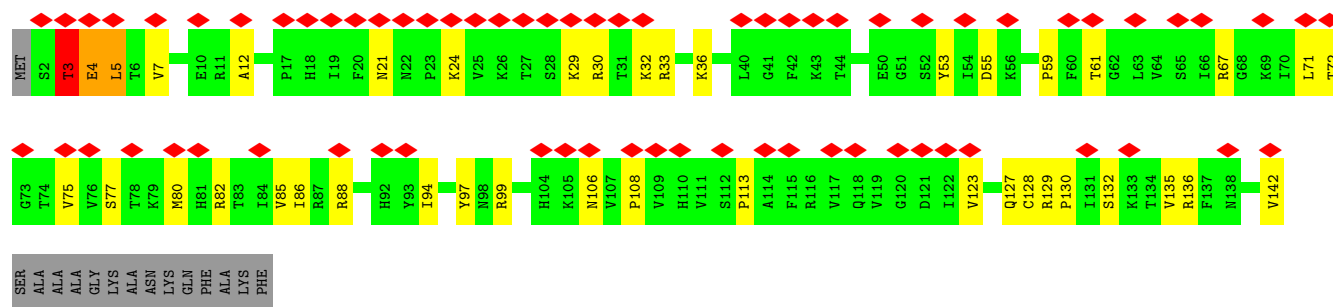
• Molecule 40: 40S ribosomal protein S8-A



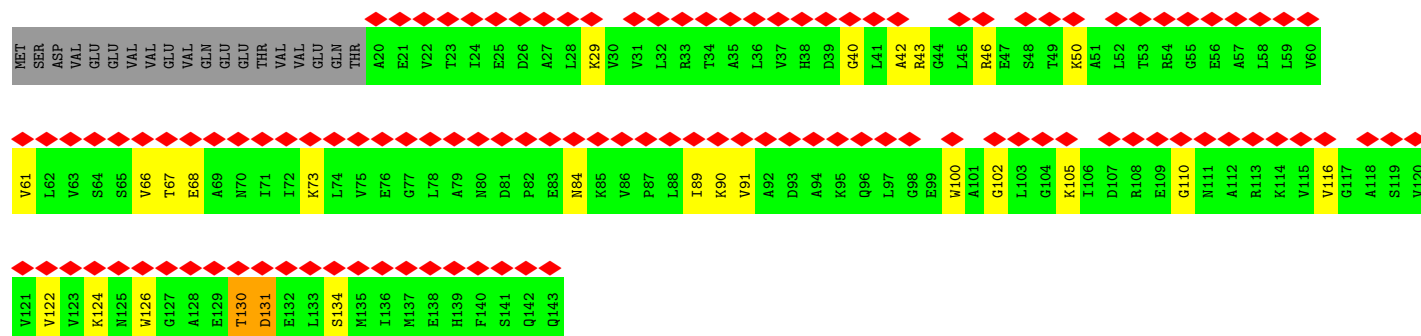
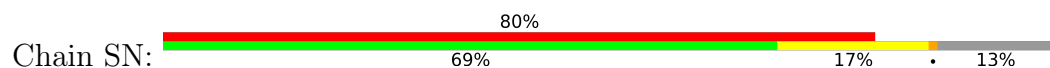
• Molecule 41: 40S ribosomal protein S9-A



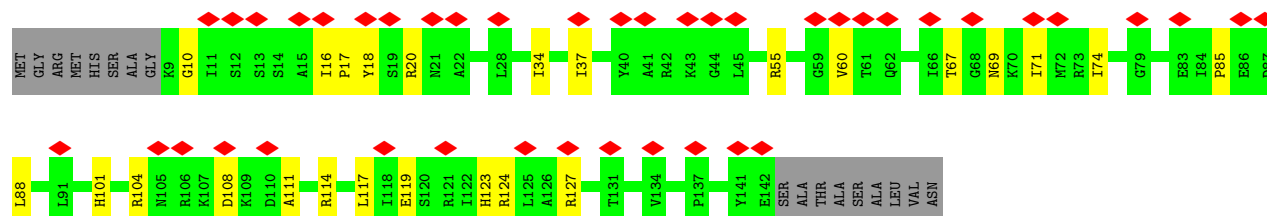
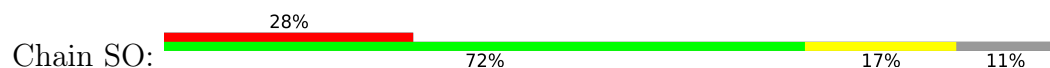
- Molecule 42: 40S ribosomal protein S11-A



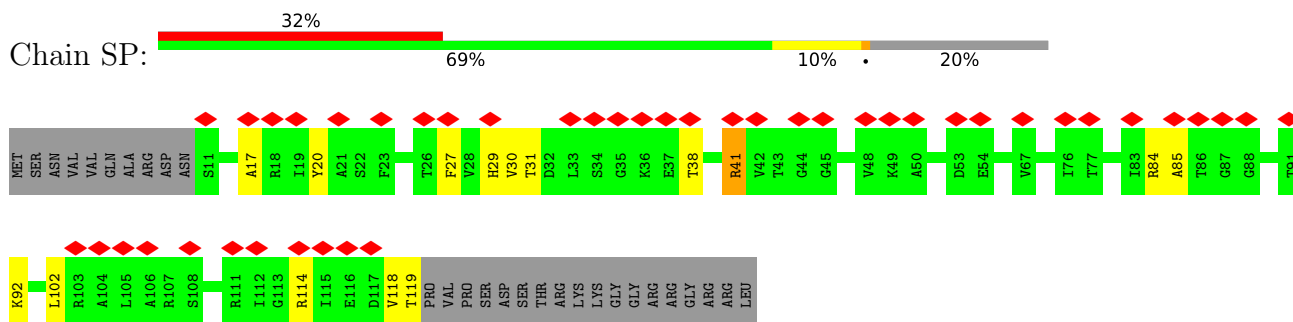
- Molecule 43: 40S ribosomal protein S12



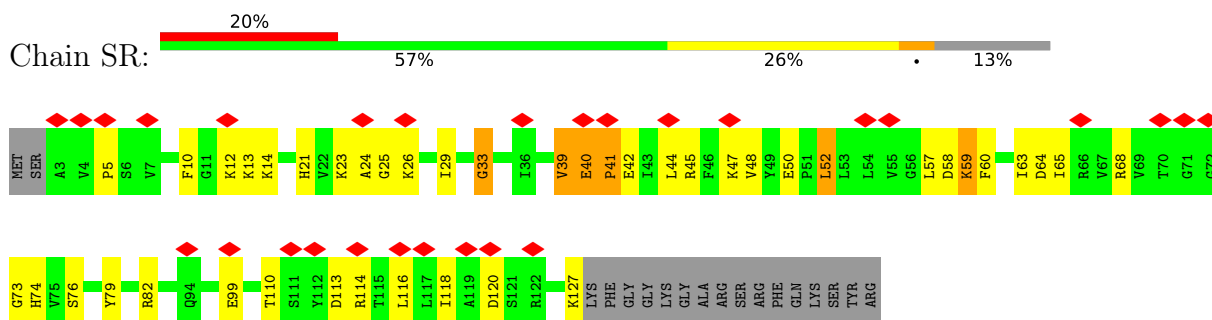
- Molecule 44: 40S ribosomal protein S13



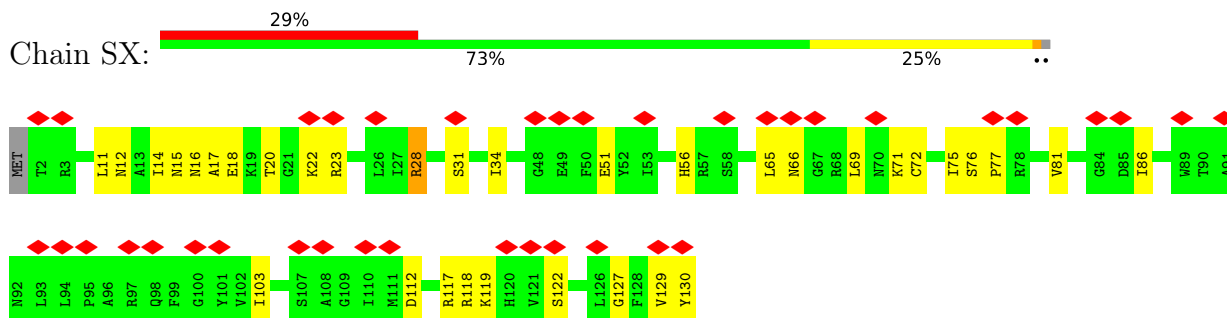
- Molecule 45: 40S ribosomal protein S14-A



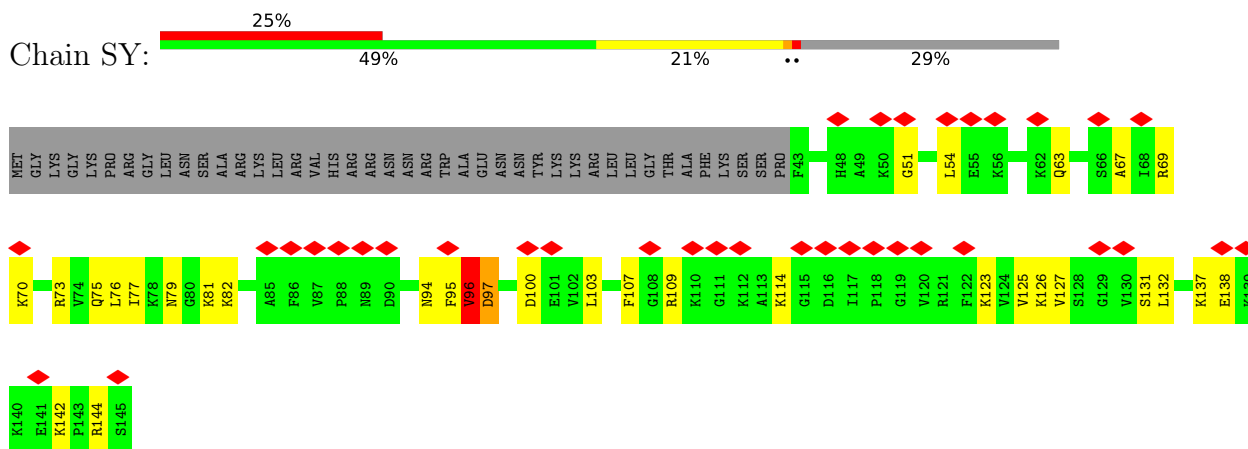
- Molecule 46: 40S ribosomal protein S16-A



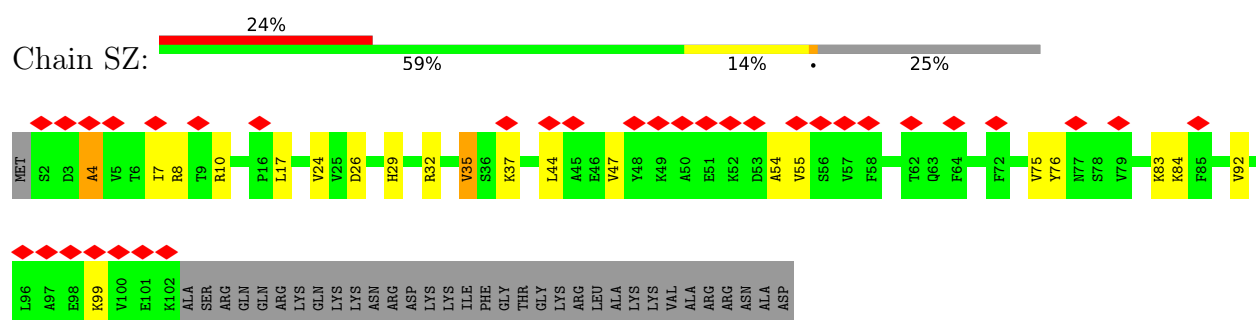
- Molecule 47: 40S ribosomal protein S22-A



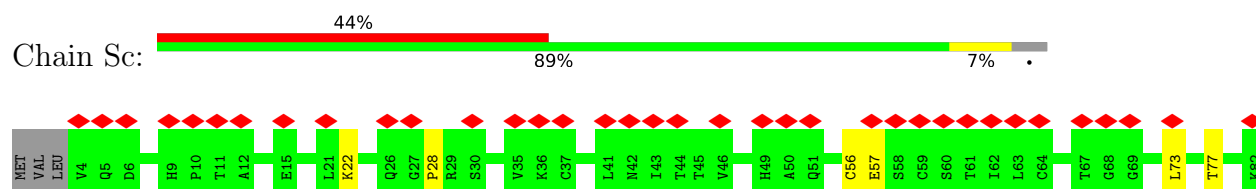
- Molecule 48: 40S ribosomal protein S23-A



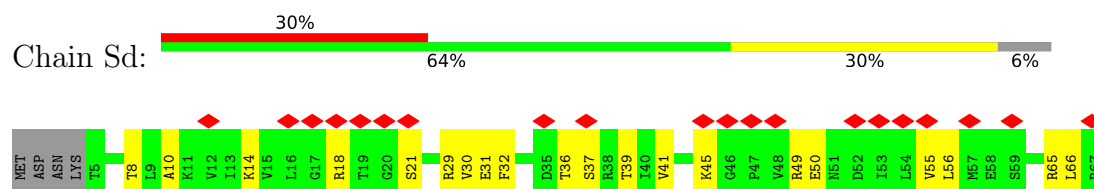
- Molecule 49: 40S ribosomal protein S24-A



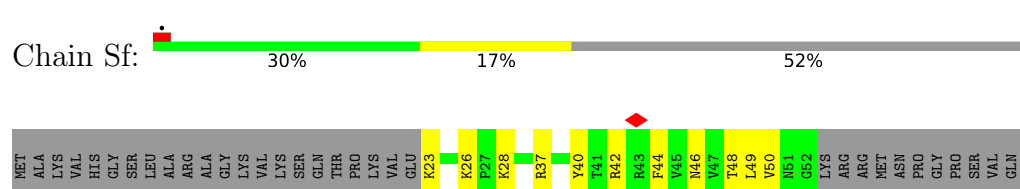
- Molecule 50: 40S ribosomal protein S27-A



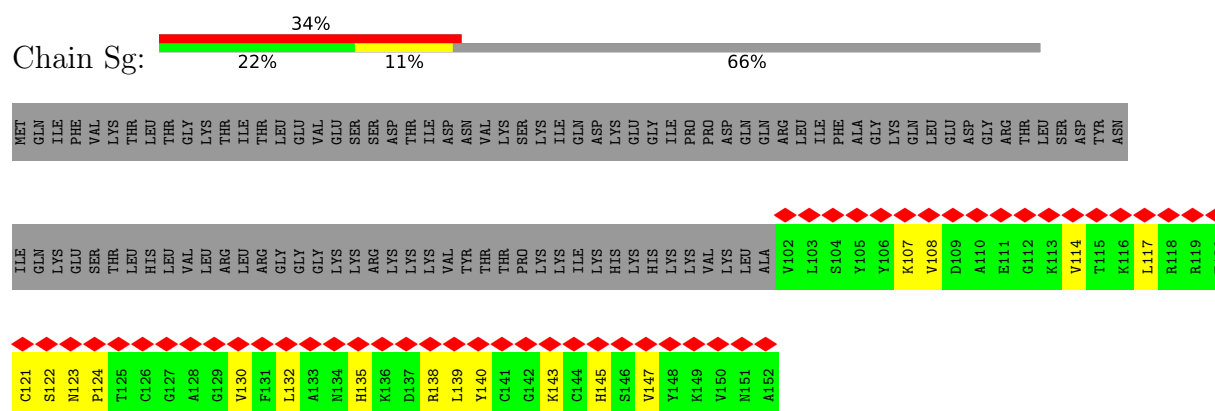
- Molecule 51: 40S ribosomal protein S28-A



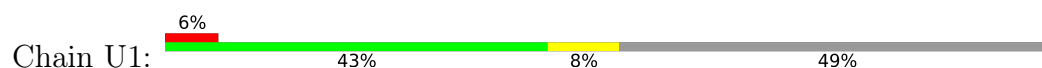
- Molecule 52: 40S ribosomal protein S30-A

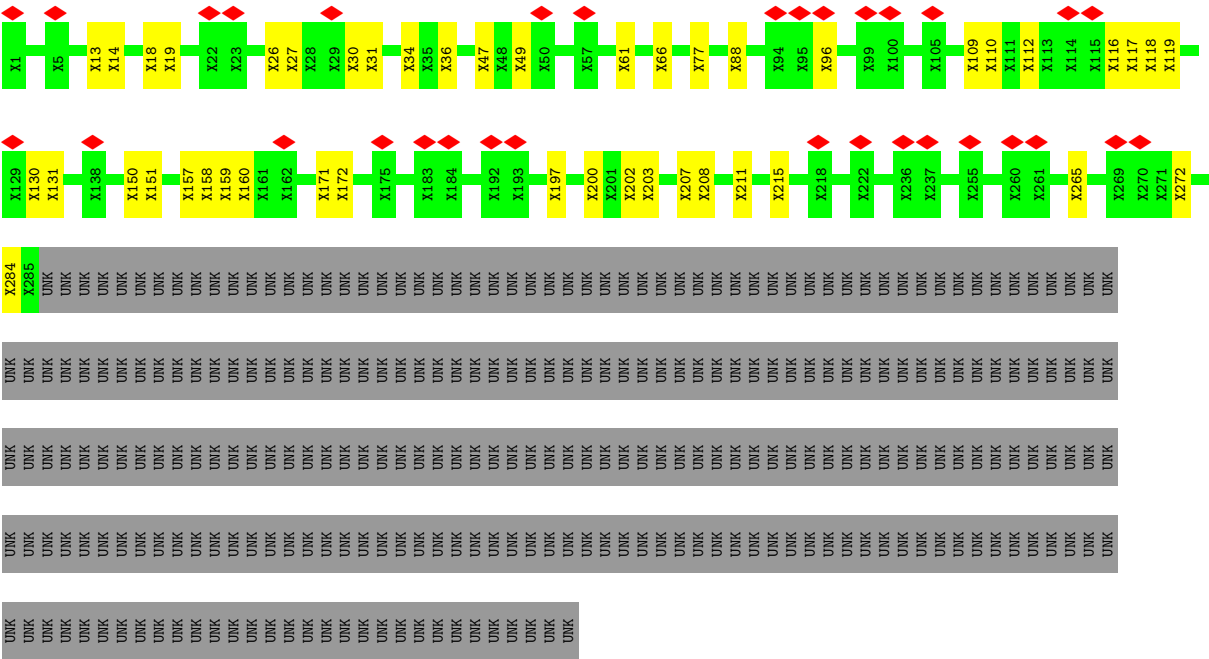


- Molecule 53: Ubiquitin-40S ribosomal protein S31



- Molecule 54: Utp7

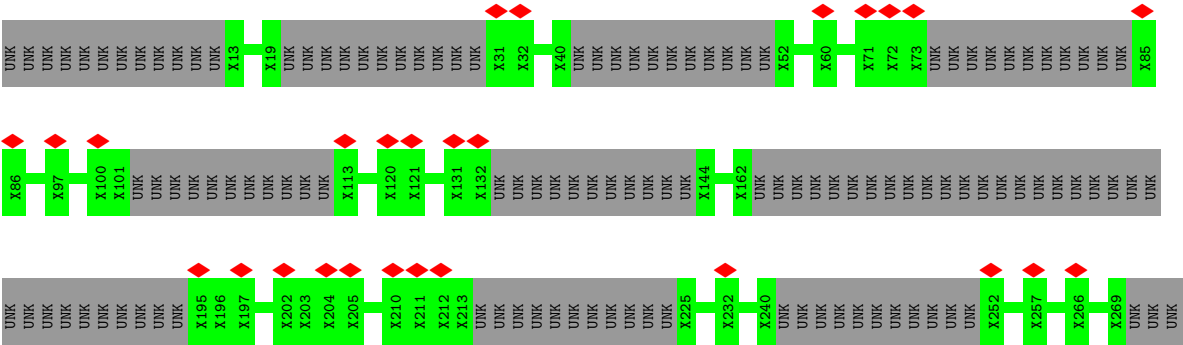




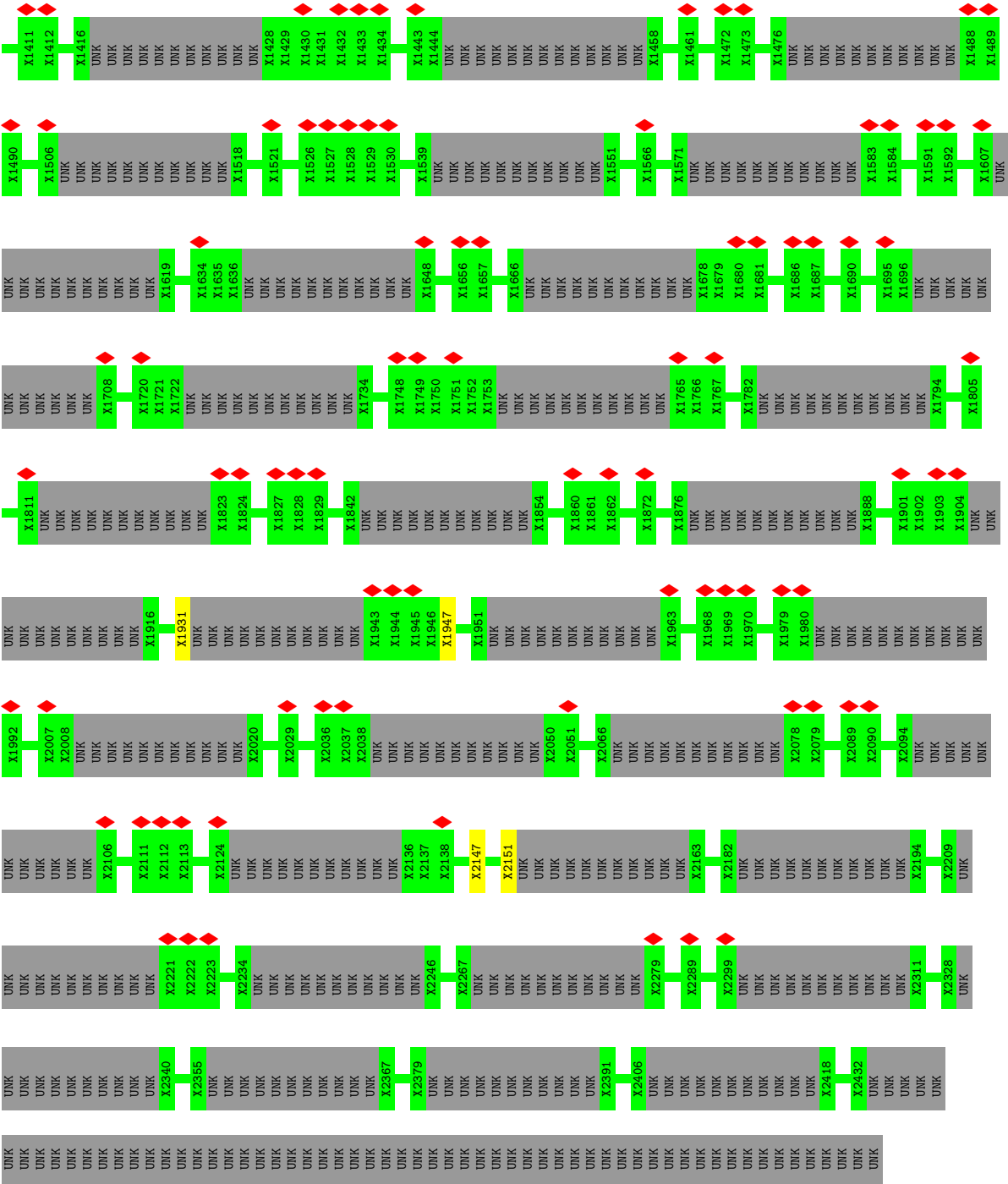
• Molecule 55: Utp11



• Molecule 56: Utp20





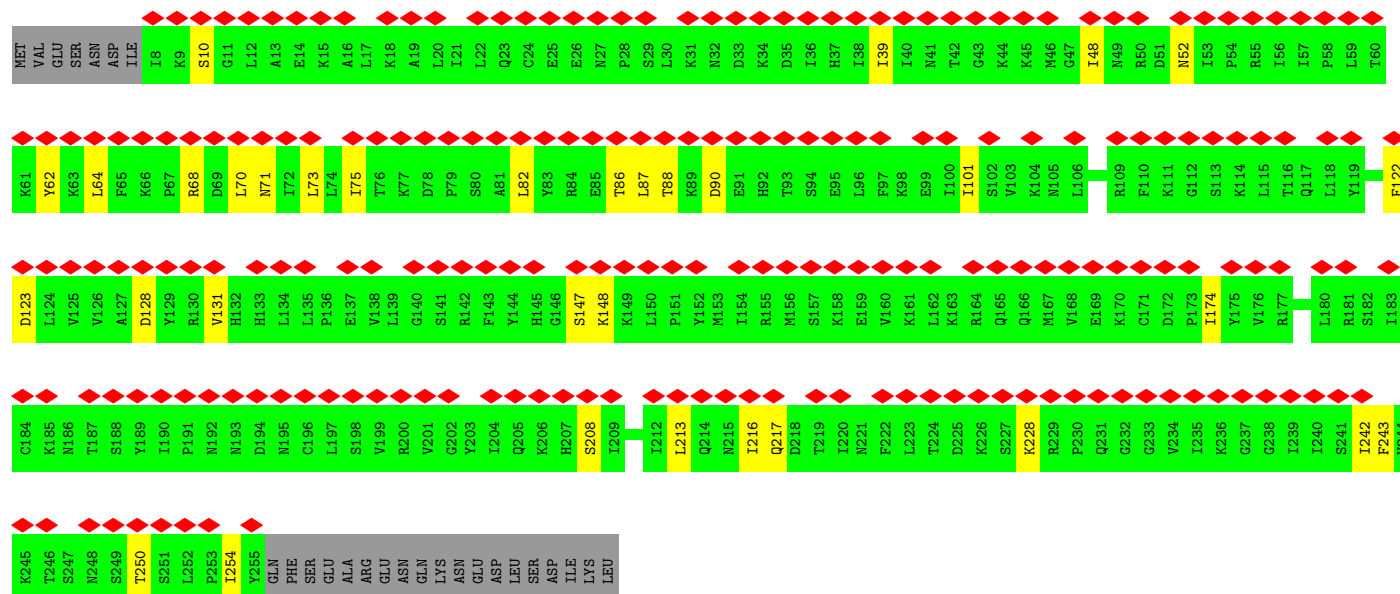
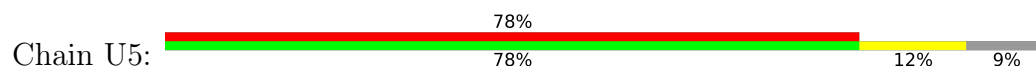


• Molecule 57: rRNA-processing protein FCF1

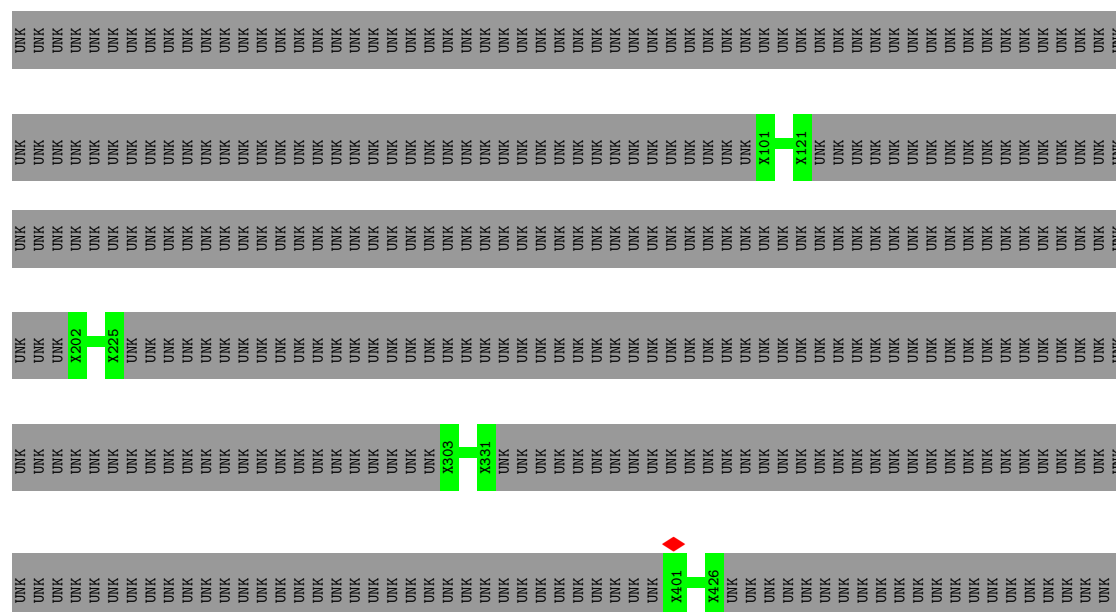


|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | GLY | LYS | ALA | LYS | LYS | THR | ARG | LYS | PHE | GLY | LEU | VAL | LYS | ARG | THR | LEU | ASN | THR | LYS | LYS | ASP | GLN | ARG | LEU | LYS | LYS | ASN | GLN | GLU | ASN | TLE | LYS | THR | LYS | GLU | ASP | PRO | GLU | THR | ARG | ASN | TLE | PRO | GLN | VAL | SER | ALA | LEU | PHE | PHE | GLN | TYR | ASN | Q57 | A58 | I59 | R60 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

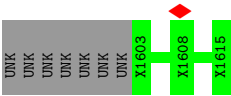
- Molecule 58: Ribosome biogenesis protein UTP30



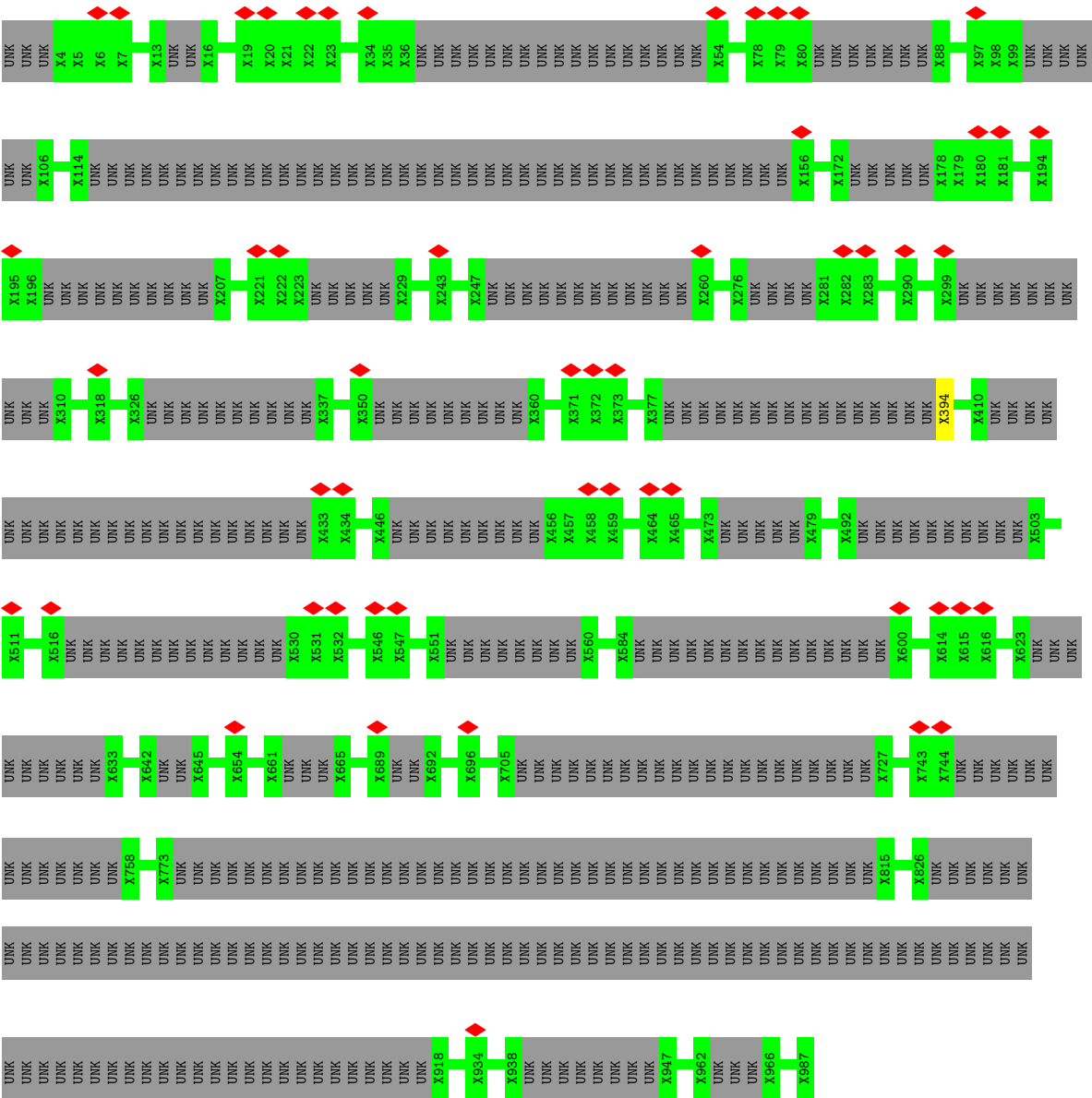
- Molecule 59: Helical domain protein



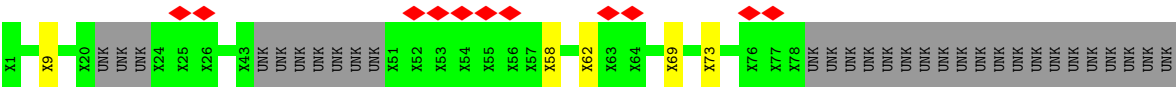


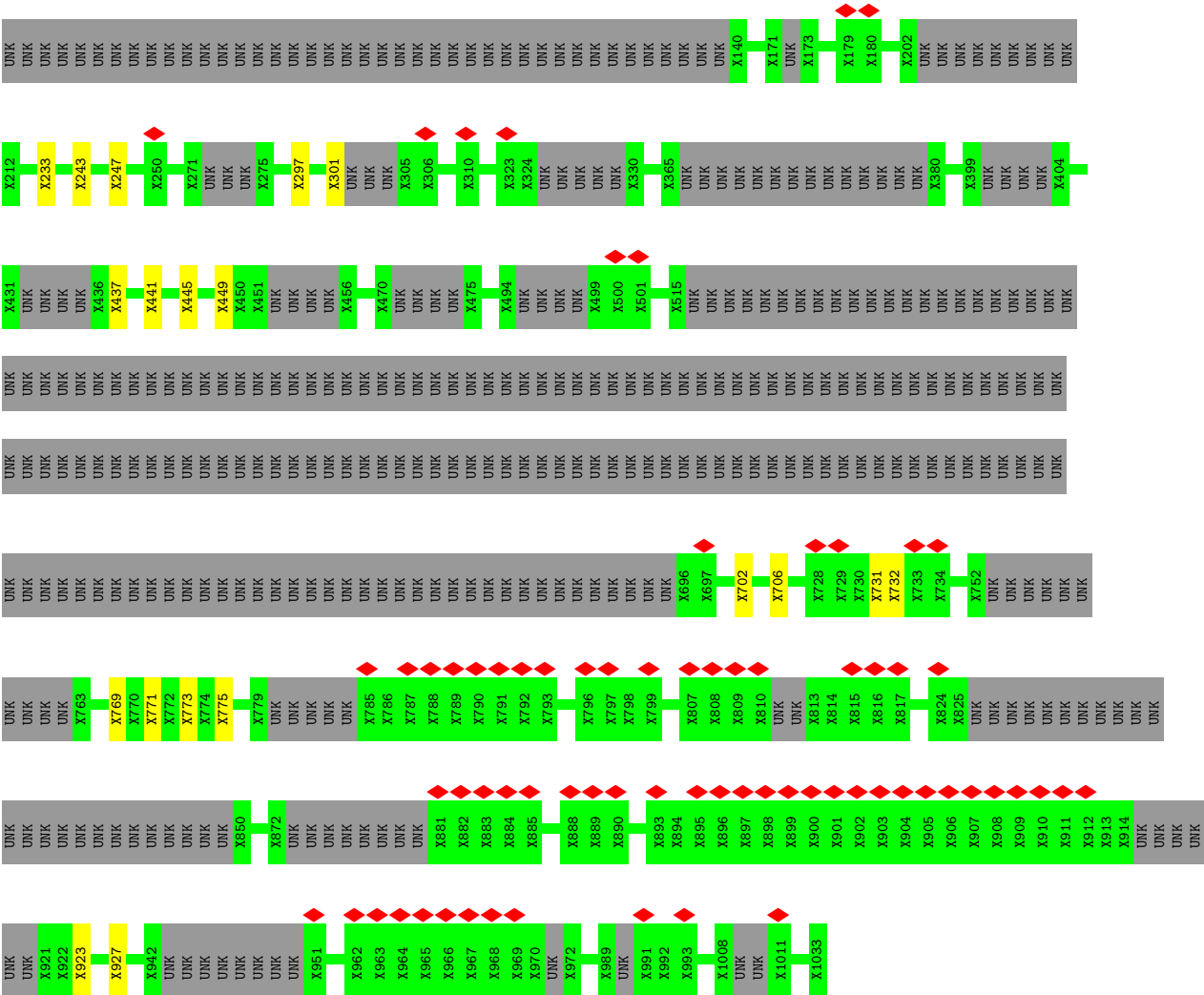


• Molecule 60: Helical domain protein



• Molecule 61: Unassigned helices





## 4 Experimental information

| Property                             | Value               | Source    |
|--------------------------------------|---------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE     | Depositor |
| Imposed symmetry                     | POINT, C1           | Depositor |
| Number of particles used             | 30995               | 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 ( $e^-/\text{\AA}^2$ ) | 40                  | Depositor |
| Minimum defocus (nm)                 | 2000                | Depositor |
| Maximum defocus (nm)                 | 4000                | Depositor |
| Magnification                        | 79545               | Depositor |
| Image detector                       | OTHER               | Depositor |
| Maximum map value                    | 0.342               | Depositor |
| Minimum map value                    | -0.265              | Depositor |
| Average map value                    | 0.000               | Depositor |
| Map value standard deviation         | 0.018               | Depositor |
| Recommended contour level            | 0.09                | Depositor |
| Map size ( $\text{\AA}$ )            | 704.0, 704.0, 704.0 | wwPDB     |
| Map dimensions                       | 400, 400, 400       | wwPDB     |
| Map angles ( $^\circ$ )              | 90.0, 90.0, 90.0    | wwPDB     |
| Pixel spacing ( $\text{\AA}$ )       | 1.76, 1.76, 1.76    | 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   | 3A    | 0.17         | 0/3710         | 0.35        | 0/5763         |
| 2   | 3B    | 0.25         | 0/1903         | 0.64        | 4/2572 (0.2%)  |
| 2   | 3C    | 0.23         | 0/1903         | 0.59        | 2/2572 (0.1%)  |
| 3   | 3D    | 0.24         | 0/2960         | 0.65        | 4/3987 (0.1%)  |
| 4   | 3E    | 0.19         | 0/2970         | 0.55        | 1/4004 (0.0%)  |
| 5   | 3F    | 0.23         | 0/2975         | 0.61        | 0/4008         |
| 6   | 3G    | 0.23         | 0/936          | 0.53        | 0/1273         |
| 6   | 3H    | 0.20         | 0/936          | 0.50        | 0/1273         |
| 7   | 5A    | 0.16         | 0/11029        | 0.34        | 0/17170        |
| 12  | AE    | 0.94         | 2/6194 (0.0%)  | 0.72        | 11/8384 (0.1%) |
| 15  | B1    | 0.25         | 0/4431         | 0.68        | 3/5988 (0.1%)  |
| 16  | BA    | 0.25         | 0/6164         | 0.68        | 6/8349 (0.1%)  |
| 17  | BB    | 0.25         | 0/6264         | 0.72        | 7/8473 (0.1%)  |
| 18  | BC    | 0.25         | 0/6226         | 0.71        | 10/8442 (0.1%) |
| 19  | BD    | 0.36         | 1/2597 (0.0%)  | 0.73        | 5/3520 (0.1%)  |
| 20  | BE    | 0.23         | 0/6056         | 0.61        | 6/8189 (0.1%)  |
| 21  | CA    | 0.18         | 0/1621         | 0.49        | 0/2196         |
| 22  | CB    | 0.18         | 0/9081         | 0.48        | 0/12283        |
| 23  | E1    | 0.17         | 0/1716         | 0.46        | 0/2319         |
| 23  | E2    | 0.19         | 0/1721         | 0.47        | 0/2323         |
| 24  | E3    | 0.25         | 0/2168         | 0.63        | 3/2942 (0.1%)  |
| 26  | K1    | 0.24         | 0/1432         | 0.61        | 2/1926 (0.1%)  |
| 27  | MA    | 0.21         | 0/1117         | 0.51        | 0/1509         |
| 28  | MB    | 0.25         | 0/1496         | 0.63        | 1/2025 (0.0%)  |
| 29  | MC    | 0.16         | 0/209          | 0.43        | 0/282          |
| 30  | P1    | 0.22         | 0/1394         | 0.61        | 0/1881         |
| 31  | R1    | 0.20         | 0/2793         | 0.49        | 2/3774 (0.1%)  |
| 32  | R2    | 0.16         | 0/2271         | 0.48        | 0/3054         |
| 34  | SA    | 0.31         | 7/26553 (0.0%) | 0.39        | 3/41320 (0.0%) |
| 35  | SC    | 0.30         | 0/1735         | 0.94        | 7/2335 (0.3%)  |
| 36  | SF    | 0.28         | 0/1920         | 0.75        | 1/2589 (0.0%)  |
| 37  | SG    | 0.32         | 0/1629         | 0.81        | 0/2202         |
| 38  | SH    | 0.23         | 0/1385         | 0.65        | 0/1851         |
| 39  | SI    | 0.31         | 0/1343         | 0.76        | 0/1808         |

| Mol | Chain | Bond lengths |                  | Bond angles |                   |
|-----|-------|--------------|------------------|-------------|-------------------|
|     |       | RMSZ         | # Z  >5          | RMSZ        | # Z  >5           |
| 40  | SJ    | 0.24         | 0/1373           | 0.76        | 2/1834 (0.1%)     |
| 41  | SK    | 0.26         | 0/1434           | 0.74        | 0/1920            |
| 42  | SM    | 0.29         | 0/1169           | 0.68        | 3/1576 (0.2%)     |
| 43  | SN    | 0.32         | 0/898            | 1.09        | 2/1220 (0.2%)     |
| 44  | SO    | 0.22         | 0/1109           | 0.66        | 0/1495            |
| 45  | SP    | 0.24         | 0/758            | 0.74        | 0/1028            |
| 46  | SR    | 0.28         | 0/990            | 1.01        | 4/1335 (0.3%)     |
| 47  | SX    | 0.23         | 0/1038           | 0.62        | 1/1395 (0.1%)     |
| 48  | SY    | 0.27         | 0/796            | 0.85        | 3/1062 (0.3%)     |
| 49  | SZ    | 0.25         | 0/814            | 0.74        | 3/1093 (0.3%)     |
| 50  | Sc    | 0.24         | 0/605            | 0.62        | 0/817             |
| 51  | Sd    | 0.22         | 0/499            | 0.64        | 0/670             |
| 52  | Sf    | 0.29         | 0/255            | 0.79        | 1/339 (0.3%)      |
| 53  | Sg    | 0.26         | 0/404            | 0.76        | 0/542             |
| 57  | U4    | 0.24         | 0/1007           | 0.63        | 0/1357            |
| 58  | U5    | 0.22         | 0/2043           | 0.62        | 3/2747 (0.1%)     |
| All | All   | 0.31         | 10/144030 (0.0%) | 0.58        | 100/203016 (0.0%) |

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 |
|-----|-------|---------------------|---------------------|
| 3   | 3D    | 0                   | 2                   |
| 5   | 3F    | 0                   | 2                   |
| 12  | AE    | 0                   | 1                   |
| 15  | B1    | 0                   | 3                   |
| 16  | BA    | 0                   | 2                   |
| 17  | BB    | 0                   | 7                   |
| 18  | BC    | 0                   | 6                   |
| 19  | BD    | 0                   | 3                   |
| 20  | BE    | 0                   | 4                   |
| 21  | CA    | 0                   | 1                   |
| 22  | CB    | 0                   | 1                   |
| 34  | SA    | 0                   | 1                   |
| 35  | SC    | 0                   | 2                   |
| 36  | SF    | 0                   | 2                   |
| 37  | SG    | 0                   | 7                   |
| 38  | SH    | 0                   | 1                   |
| 39  | SI    | 0                   | 3                   |
| 41  | SK    | 0                   | 3                   |

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| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 42  | SM    | 0                   | 1                   |
| 43  | SN    | 0                   | 4                   |
| 45  | SP    | 0                   | 1                   |
| 46  | SR    | 0                   | 3                   |
| 48  | SY    | 0                   | 1                   |
| 53  | Sg    | 0                   | 1                   |
| 58  | U5    | 0                   | 1                   |
| 61  | UC    | 0                   | 2                   |
| All | All   | 0                   | 65                  |

The worst 5 of 10 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z     | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|-------|-------------|----------|
| 12  | AE    | 571 | LEU  | CA-C  | 71.11 | 2.11        | 1.52     |
| 34  | SA    | 283 | U    | C2-N3 | 18.61 | 1.75        | 1.37     |
| 34  | SA    | 283 | U    | N3-C4 | 18.24 | 1.75        | 1.38     |
| 34  | SA    | 283 | U    | N1-C2 | 17.93 | 1.74        | 1.38     |
| 34  | SA    | 283 | U    | N1-C6 | 16.42 | 1.70        | 1.38     |

The worst 5 of 100 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms   | Z      | Observed(°) | Ideal(°) |
|-----|-------|-----|------|---------|--------|-------------|----------|
| 12  | AE    | 571 | LEU  | O-C-N   | -23.75 | 98.51       | 121.79   |
| 12  | AE    | 571 | LEU  | CB-CA-C | 14.79  | 134.94      | 112.31   |
| 46  | SR    | 40  | GLU  | CA-C-N  | 13.02  | 133.51      | 119.05   |
| 46  | SR    | 40  | GLU  | C-N-CA  | 13.02  | 133.51      | 119.05   |
| 19  | BD    | 455 | ILE  | N-CA-C  | -10.49 | 102.20      | 112.17   |

There are no chirality outliers.

5 of 65 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group   |
|-----|-------|-----|------|---------|
| 3   | 3D    | 392 | TYR  | Peptide |
| 3   | 3D    | 91  | SER  | Peptide |
| 5   | 3F    | 342 | ARG  | Peptide |
| 5   | 3F    | 437 | ARG  | Peptide |
| 12  | AE    | 64  | PRO  | Peptide |

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1   | 3A    | 3327  | 0        | 1687     | 58      | 0            |
| 2   | 3B    | 1866  | 0        | 1904     | 31      | 0            |
| 2   | 3C    | 1866  | 0        | 1904     | 21      | 0            |
| 3   | 3D    | 2915  | 0        | 2930     | 44      | 0            |
| 4   | 3E    | 2935  | 0        | 3033     | 50      | 0            |
| 5   | 3F    | 2916  | 0        | 2947     | 82      | 0            |
| 6   | 3G    | 924   | 0        | 975      | 21      | 0            |
| 6   | 3H    | 924   | 0        | 975      | 17      | 0            |
| 7   | 5A    | 9867  | 0        | 4954     | 84      | 0            |
| 8   | AA    | 2845  | 0        | 658      | 47      | 0            |
| 9   | AB    | 2015  | 0        | 454      | 19      | 0            |
| 10  | AC    | 2360  | 0        | 534      | 17      | 0            |
| 11  | AD    | 505   | 0        | 116      | 3       | 0            |
| 12  | AE    | 9970  | 0        | 7056     | 161     | 0            |
| 13  | AF    | 1880  | 0        | 425      | 23      | 0            |
| 14  | AG    | 3060  | 0        | 707      | 36      | 0            |
| 15  | B1    | 4325  | 0        | 4434     | 85      | 0            |
| 16  | BA    | 6026  | 0        | 5940     | 129     | 0            |
| 17  | BB    | 6138  | 0        | 6163     | 119     | 0            |
| 18  | BC    | 6117  | 0        | 6141     | 104     | 0            |
| 19  | BD    | 2539  | 0        | 2520     | 72      | 0            |
| 20  | BE    | 5936  | 0        | 5882     | 139     | 0            |
| 21  | CA    | 1582  | 0        | 1528     | 36      | 0            |
| 22  | CB    | 8870  | 0        | 8975     | 148     | 0            |
| 23  | E1    | 1689  | 0        | 1738     | 33      | 0            |
| 23  | E2    | 1695  | 0        | 1757     | 39      | 0            |
| 24  | E3    | 2114  | 0        | 2154     | 57      | 0            |
| 25  | E4    | 1425  | 0        | 322      | 18      | 0            |
| 26  | K1    | 1410  | 0        | 1503     | 27      | 0            |
| 27  | MA    | 1097  | 0        | 1130     | 8       | 0            |
| 28  | MB    | 1465  | 0        | 1486     | 32      | 0            |
| 29  | MC    | 307   | 0        | 231      | 1       | 0            |
| 30  | P1    | 1368  | 0        | 1436     | 9       | 0            |
| 31  | R1    | 2742  | 0        | 2829     | 43      | 0            |
| 32  | R2    | 2228  | 0        | 2228     | 17      | 0            |
| 33  | S1    | 1425  | 0        | 334      | 35      | 0            |
| 34  | SA    | 23759 | 0        | 11991    | 353     | 0            |

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| Mol | Chain | Non-H  | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|--------|----------|----------|---------|--------------|
| 35  | SC    | 1709   | 0        | 1784     | 49      | 0            |
| 36  | SF    | 1881   | 0        | 1958     | 50      | 0            |
| 37  | SG    | 1609   | 0        | 1675     | 43      | 0            |
| 38  | SH    | 1369   | 0        | 1414     | 69      | 0            |
| 39  | SI    | 1322   | 0        | 1394     | 29      | 0            |
| 40  | SJ    | 1350   | 0        | 1374     | 41      | 0            |
| 41  | SK    | 1412   | 0        | 1486     | 22      | 0            |
| 42  | SM    | 1143   | 0        | 1210     | 28      | 0            |
| 43  | SN    | 890    | 0        | 887      | 13      | 0            |
| 44  | SO    | 1087   | 0        | 1152     | 17      | 0            |
| 45  | SP    | 750    | 0        | 728      | 9       | 0            |
| 46  | SR    | 973    | 0        | 1029     | 37      | 0            |
| 47  | SX    | 1021   | 0        | 1060     | 26      | 0            |
| 48  | SY    | 785    | 0        | 840      | 22      | 0            |
| 49  | SZ    | 801    | 0        | 828      | 14      | 0            |
| 50  | Sc    | 595    | 0        | 613      | 5       | 0            |
| 51  | Sd    | 497    | 0        | 535      | 19      | 0            |
| 52  | Sf    | 251    | 0        | 277      | 18      | 0            |
| 53  | Sg    | 397    | 0        | 399      | 12      | 0            |
| 54  | U1    | 1425   | 0        | 329      | 23      | 0            |
| 55  | U2    | 365    | 0        | 75       | 0       | 0            |
| 56  | U3    | 7035   | 0        | 1590     | 5       | 0            |
| 57  | U4    | 990    | 0        | 1054     | 13      | 0            |
| 58  | U5    | 2009   | 0        | 2130     | 16      | 0            |
| 59  | UA    | 1690   | 0        | 370      | 0       | 0            |
| 60  | UB    | 2775   | 0        | 620      | 1       | 0            |
| 61  | UC    | 3300   | 0        | 727      | 12      | 0            |
| All | All   | 173863 | 0        | 129519   | 2554    | 0            |

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

The worst 5 of 2554 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1            | Atom-2            | Interatomic distance (Å) | Clash overlap (Å) |
|-------------------|-------------------|--------------------------|-------------------|
| 12:AE:630:TYR:CE1 | 12:AE:637:ILE:CD1 | 1.86                     | 1.56              |
| 34:SA:283:U:N3    | 34:SA:283:U:C2    | 1.75                     | 1.54              |
| 34:SA:283:U:N1    | 34:SA:283:U:C6    | 1.70                     | 1.54              |
| 34:SA:283:U:N3    | 34:SA:283:U:C4    | 1.74                     | 1.53              |
| 34:SA:283:U:C2    | 34:SA:283:U:N1    | 1.74                     | 1.52              |

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

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

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

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

| Mol | Chain | Analysed        | Favoured   | Allowed  | Outliers | Percentiles |     |
|-----|-------|-----------------|------------|----------|----------|-------------|-----|
| 2   | 3B    | 237/327 (72%)   | 227 (96%)  | 10 (4%)  | 0        | 100         | 100 |
| 2   | 3C    | 237/327 (72%)   | 216 (91%)  | 21 (9%)  | 0        | 100         | 100 |
| 3   | 3D    | 366/504 (73%)   | 343 (94%)  | 23 (6%)  | 0        | 100         | 100 |
| 4   | 3E    | 378/511 (74%)   | 358 (95%)  | 20 (5%)  | 0        | 100         | 100 |
| 5   | 3F    | 353/573 (62%)   | 334 (95%)  | 19 (5%)  | 0        | 100         | 100 |
| 6   | 3G    | 120/126 (95%)   | 114 (95%)  | 6 (5%)   | 0        | 100         | 100 |
| 6   | 3H    | 120/126 (95%)   | 118 (98%)  | 2 (2%)   | 0        | 100         | 100 |
| 12  | AE    | 751/1769 (42%)  | 703 (94%)  | 48 (6%)  | 0        | 100         | 100 |
| 15  | B1    | 528/1183 (45%)  | 481 (91%)  | 47 (9%)  | 0        | 100         | 100 |
| 16  | BA    | 747/923 (81%)   | 669 (90%)  | 76 (10%) | 2 (0%)   | 36          | 72  |
| 17  | BB    | 770/943 (82%)   | 682 (89%)  | 86 (11%) | 2 (0%)   | 36          | 72  |
| 18  | BC    | 779/817 (95%)   | 678 (87%)  | 96 (12%) | 5 (1%)   | 21          | 59  |
| 19  | BD    | 317/594 (53%)   | 278 (88%)  | 39 (12%) | 0        | 100         | 100 |
| 20  | BE    | 741/939 (79%)   | 699 (94%)  | 42 (6%)  | 0        | 100         | 100 |
| 21  | CA    | 190/297 (64%)   | 180 (95%)  | 10 (5%)  | 0        | 100         | 100 |
| 22  | CB    | 1086/1237 (88%) | 1059 (98%) | 27 (2%)  | 0        | 100         | 100 |
| 23  | E1    | 213/252 (84%)   | 209 (98%)  | 4 (2%)   | 0        | 100         | 100 |
| 23  | E2    | 210/252 (83%)   | 204 (97%)  | 6 (3%)   | 0        | 100         | 100 |
| 24  | E3    | 256/483 (53%)   | 242 (94%)  | 12 (5%)  | 2 (1%)   | 16          | 54  |
| 26  | K1    | 173/316 (55%)   | 167 (96%)  | 6 (4%)   | 0        | 100         | 100 |
| 27  | MA    | 131/183 (72%)   | 128 (98%)  | 3 (2%)   | 0        | 100         | 100 |
| 28  | MB    | 182/290 (63%)   | 168 (92%)  | 14 (8%)  | 0        | 100         | 100 |

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| Mol | Chain | Analysed          | Favoured    | Allowed  | Outliers | Percentiles |     |
|-----|-------|-------------------|-------------|----------|----------|-------------|-----|
| 29  | MC    | 24/593 (4%)       | 24 (100%)   | 0        | 0        | 100         | 100 |
| 30  | P1    | 171/274 (62%)     | 161 (94%)   | 10 (6%)  | 0        | 100         | 100 |
| 31  | R1    | 353/367 (96%)     | 348 (99%)   | 5 (1%)   | 0        | 100         | 100 |
| 32  | R2    | 266/1729 (15%)    | 262 (98%)   | 4 (2%)   | 0        | 100         | 100 |
| 35  | SC    | 212/255 (83%)     | 170 (80%)   | 37 (18%) | 5 (2%)   | 4           | 27  |
| 36  | SF    | 235/261 (90%)     | 210 (89%)   | 24 (10%) | 1 (0%)   | 30          | 67  |
| 37  | SG    | 204/225 (91%)     | 181 (89%)   | 21 (10%) | 2 (1%)   | 12          | 49  |
| 38  | SH    | 170/236 (72%)     | 159 (94%)   | 11 (6%)  | 0        | 100         | 100 |
| 39  | SI    | 161/190 (85%)     | 142 (88%)   | 18 (11%) | 1 (1%)   | 21          | 59  |
| 40  | SJ    | 166/200 (83%)     | 146 (88%)   | 19 (11%) | 1 (1%)   | 21          | 59  |
| 41  | SK    | 173/197 (88%)     | 157 (91%)   | 15 (9%)  | 1 (1%)   | 21          | 59  |
| 42  | SM    | 139/156 (89%)     | 124 (89%)   | 13 (9%)  | 2 (1%)   | 9           | 40  |
| 43  | SN    | 122/143 (85%)     | 83 (68%)    | 35 (29%) | 4 (3%)   | 3           | 21  |
| 44  | SO    | 132/151 (87%)     | 129 (98%)   | 3 (2%)   | 0        | 100         | 100 |
| 45  | SP    | 107/137 (78%)     | 95 (89%)    | 12 (11%) | 0        | 100         | 100 |
| 46  | SR    | 123/143 (86%)     | 113 (92%)   | 8 (6%)   | 2 (2%)   | 7           | 38  |
| 47  | SX    | 127/130 (98%)     | 115 (91%)   | 12 (9%)  | 0        | 100         | 100 |
| 48  | SY    | 101/145 (70%)     | 82 (81%)    | 16 (16%) | 3 (3%)   | 3           | 23  |
| 49  | SZ    | 99/135 (73%)      | 88 (89%)    | 11 (11%) | 0        | 100         | 100 |
| 50  | Sc    | 77/82 (94%)       | 67 (87%)    | 10 (13%) | 0        | 100         | 100 |
| 51  | Sd    | 61/67 (91%)       | 57 (93%)    | 4 (7%)   | 0        | 100         | 100 |
| 52  | Sf    | 28/63 (44%)       | 28 (100%)   | 0        | 0        | 100         | 100 |
| 53  | Sg    | 49/152 (32%)      | 37 (76%)    | 12 (24%) | 0        | 100         | 100 |
| 57  | U4    | 124/189 (66%)     | 115 (93%)   | 8 (6%)   | 1 (1%)   | 16          | 54  |
| 58  | U5    | 246/274 (90%)     | 229 (93%)   | 17 (7%)  | 0        | 100         | 100 |
| All | All   | 12555/19466 (64%) | 11579 (92%) | 942 (8%) | 34 (0%)  | 37          | 72  |

5 of 34 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 18  | BC    | 298 | SER  |
| 24  | E3    | 306 | ALA  |
| 35  | SC    | 207 | LEU  |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 35  | SC    | 209 | ASN  |
| 37  | SG    | 50  | GLU  |

### 5.3.2 Protein sidechains ⓘ

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

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

| Mol | Chain | Analysed        | Rotameric   | Outliers | Percentiles |     |
|-----|-------|-----------------|-------------|----------|-------------|-----|
| 2   | 3B    | 202/240 (84%)   | 202 (100%)  | 0        | 100         | 100 |
| 2   | 3C    | 202/240 (84%)   | 202 (100%)  | 0        | 100         | 100 |
| 3   | 3D    | 317/435 (73%)   | 317 (100%)  | 0        | 100         | 100 |
| 4   | 3E    | 314/433 (72%)   | 314 (100%)  | 0        | 100         | 100 |
| 5   | 3F    | 317/503 (63%)   | 317 (100%)  | 0        | 100         | 100 |
| 6   | 3G    | 101/104 (97%)   | 101 (100%)  | 0        | 100         | 100 |
| 6   | 3H    | 101/104 (97%)   | 101 (100%)  | 0        | 100         | 100 |
| 12  | AE    | 698/744 (94%)   | 695 (100%)  | 3 (0%)   | 84          | 84  |
| 15  | B1    | 471/1039 (45%)  | 471 (100%)  | 0        | 100         | 100 |
| 16  | BA    | 663/812 (82%)   | 661 (100%)  | 2 (0%)   | 86          | 86  |
| 17  | BB    | 687/832 (83%)   | 685 (100%)  | 2 (0%)   | 86          | 86  |
| 18  | BC    | 687/719 (96%)   | 685 (100%)  | 2 (0%)   | 86          | 86  |
| 19  | BD    | 281/529 (53%)   | 281 (100%)  | 0        | 100         | 100 |
| 20  | BE    | 657/819 (80%)   | 657 (100%)  | 0        | 100         | 100 |
| 21  | CA    | 178/274 (65%)   | 178 (100%)  | 0        | 100         | 100 |
| 22  | CB    | 1000/1125 (89%) | 1000 (100%) | 0        | 100         | 100 |
| 23  | E1    | 191/222 (86%)   | 191 (100%)  | 0        | 100         | 100 |
| 23  | E2    | 193/222 (87%)   | 193 (100%)  | 0        | 100         | 100 |
| 24  | E3    | 232/424 (55%)   | 230 (99%)   | 2 (1%)   | 70          | 79  |
| 26  | K1    | 158/289 (55%)   | 157 (99%)   | 1 (1%)   | 78          | 83  |
| 27  | MA    | 123/172 (72%)   | 123 (100%)  | 0        | 100         | 100 |
| 28  | MB    | 164/258 (64%)   | 164 (100%)  | 0        | 100         | 100 |

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| Mol | Chain | Analysed          | Rotameric    | Outliers | Percentiles |     |
|-----|-------|-------------------|--------------|----------|-------------|-----|
| 29  | MC    | 24/148 (16%)      | 24 (100%)    | 0        | 100         | 100 |
| 30  | P1    | 151/238 (63%)     | 151 (100%)   | 0        | 100         | 100 |
| 31  | R1    | 302/312 (97%)     | 302 (100%)   | 0        | 100         | 100 |
| 32  | R2    | 235/1544 (15%)    | 234 (100%)   | 1 (0%)   | 84          | 84  |
| 35  | SC    | 191/224 (85%)     | 191 (100%)   | 0        | 100         | 100 |
| 36  | SF    | 203/222 (91%)     | 203 (100%)   | 0        | 100         | 100 |
| 37  | SG    | 173/191 (91%)     | 173 (100%)   | 0        | 100         | 100 |
| 38  | SH    | 141/201 (70%)     | 139 (99%)    | 2 (1%)   | 59          | 72  |
| 39  | SI    | 146/170 (86%)     | 146 (100%)   | 0        | 100         | 100 |
| 40  | SJ    | 138/161 (86%)     | 138 (100%)   | 0        | 100         | 100 |
| 41  | SK    | 149/166 (90%)     | 148 (99%)    | 1 (1%)   | 76          | 81  |
| 42  | SM    | 128/137 (93%)     | 127 (99%)    | 1 (1%)   | 73          | 80  |
| 43  | SN    | 88/119 (74%)      | 86 (98%)     | 2 (2%)   | 44          | 64  |
| 44  | SO    | 117/128 (91%)     | 117 (100%)   | 0        | 100         | 100 |
| 45  | SP    | 66/105 (63%)      | 66 (100%)    | 0        | 100         | 100 |
| 46  | SR    | 105/119 (88%)     | 105 (100%)   | 0        | 100         | 100 |
| 47  | SX    | 110/111 (99%)     | 110 (100%)   | 0        | 100         | 100 |
| 48  | SY    | 85/120 (71%)      | 85 (100%)    | 0        | 100         | 100 |
| 49  | SZ    | 85/113 (75%)      | 84 (99%)     | 1 (1%)   | 63          | 75  |
| 50  | Sc    | 68/71 (96%)       | 68 (100%)    | 0        | 100         | 100 |
| 51  | Sd    | 56/60 (93%)       | 56 (100%)    | 0        | 100         | 100 |
| 52  | Sf    | 27/54 (50%)       | 27 (100%)    | 0        | 100         | 100 |
| 53  | Sg    | 43/135 (32%)      | 43 (100%)    | 0        | 100         | 100 |
| 57  | U4    | 110/169 (65%)     | 110 (100%)   | 0        | 100         | 100 |
| 58  | U5    | 231/256 (90%)     | 231 (100%)   | 0        | 100         | 100 |
| All | All   | 11109/15813 (70%) | 11089 (100%) | 20 (0%)  | 85          | 87  |

5 of 20 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 38  | SH    | 188 | ARG  |
| 43  | SN    | 61  | VAL  |
| 49  | SZ    | 35  | VAL  |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 43  | SN    | 91  | VAL  |
| 17  | BB    | 271 | PHE  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 218 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 21  | CA    | 35  | HIS  |
| 24  | E3    | 226 | HIS  |
| 46  | SR    | 21  | HIS  |
| 22  | CB    | 253 | GLN  |
| 22  | CB    | 683 | ASN  |

### 5.3.3 RNA [i](#)

| Mol | Chain | Analysed        | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 1   | 3A    | 151/333 (45%)   | 31 (20%)          | 1 (0%)          |
| 34  | SA    | 1091/1812 (60%) | 268 (24%)         | 22 (2%)         |
| 7   | 5A    | 452/700 (64%)   | 102 (22%)         | 4 (0%)          |
| All | All   | 1694/2845 (59%) | 401 (23%)         | 27 (1%)         |

5 of 401 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 3A    | 9   | A    |
| 1   | 3A    | 14  | A    |
| 1   | 3A    | 15  | U    |
| 1   | 3A    | 22  | A    |
| 1   | 3A    | 24  | U    |

5 of 27 RNA pucker outliers are listed below:

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 34  | SA    | 503  | G    |
| 34  | SA    | 929  | A    |
| 34  | SA    | 1441 | C    |
| 34  | SA    | 913  | G    |
| 34  | SA    | 1083 | G    |

## 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 oligosaccharides 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](#)

There are no chain breaks in this entry.

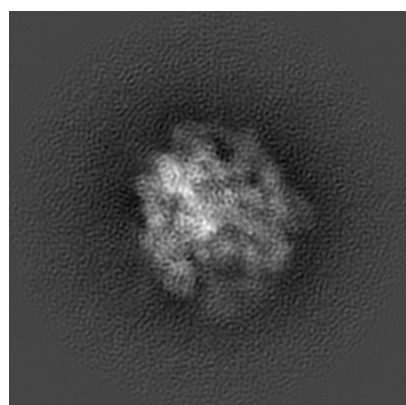
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6695. These allow visual inspection of the internal detail of the map and identification of artifacts.

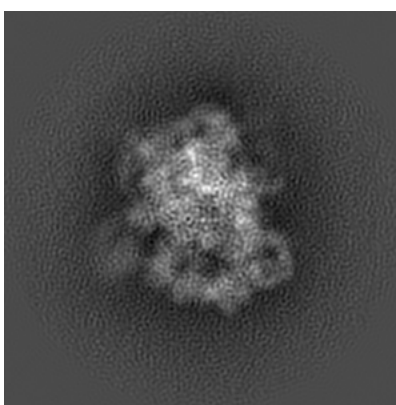
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

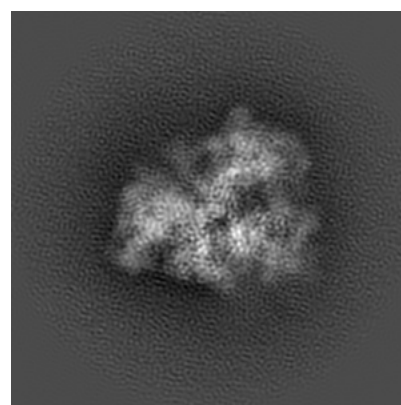
#### 6.1.1 Primary map



X



Y

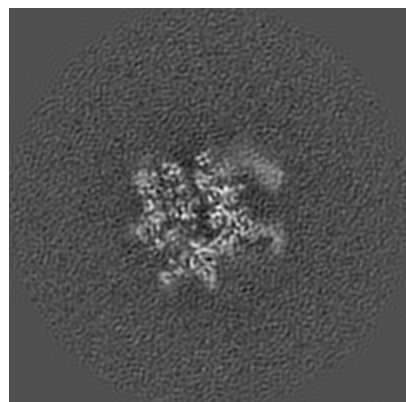


Z

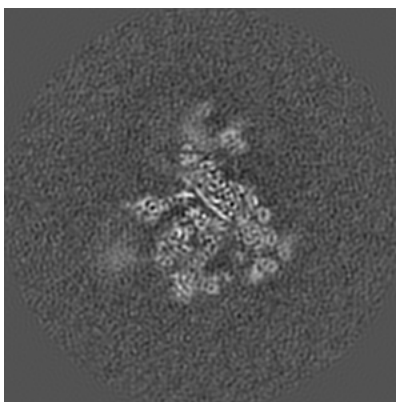
The images above show the map projected in three orthogonal directions.

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

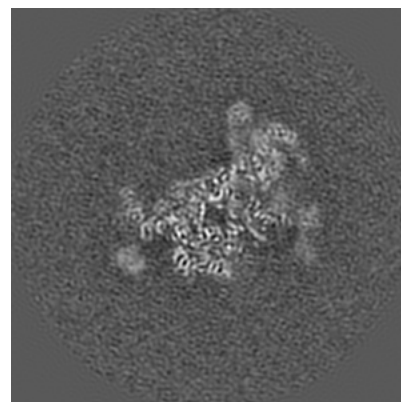
#### 6.2.1 Primary map



X Index: 200



Y Index: 200

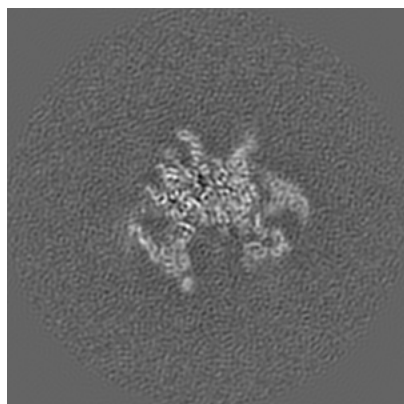


Z Index: 200

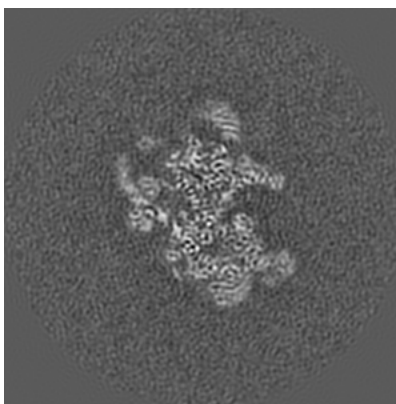
The images above show central slices of the map in three orthogonal directions.

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

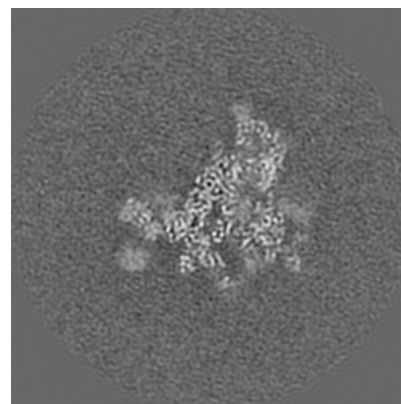
### 6.3.1 Primary map



X Index: 221



Y Index: 178

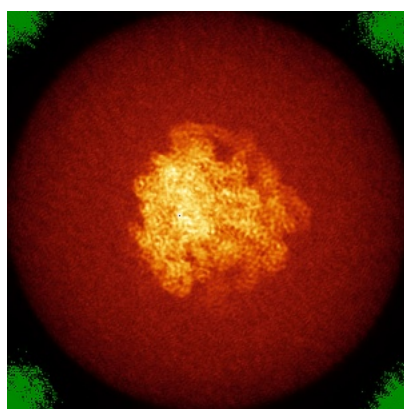


Z Index: 187

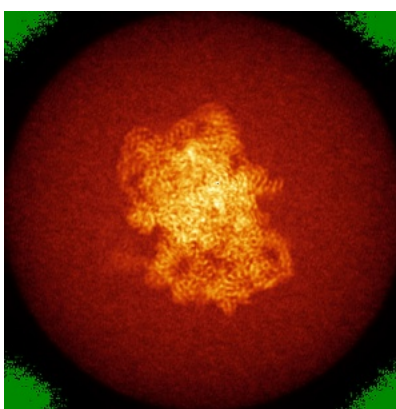
The images above show the largest variance slices of the map in three orthogonal directions.

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

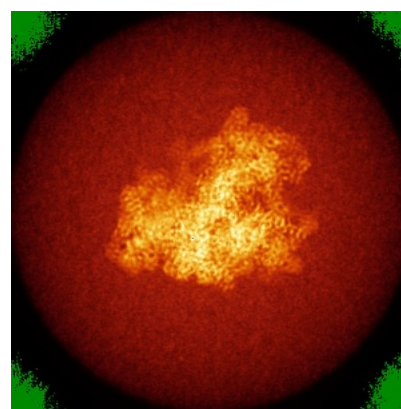
### 6.4.1 Primary map



X



Y

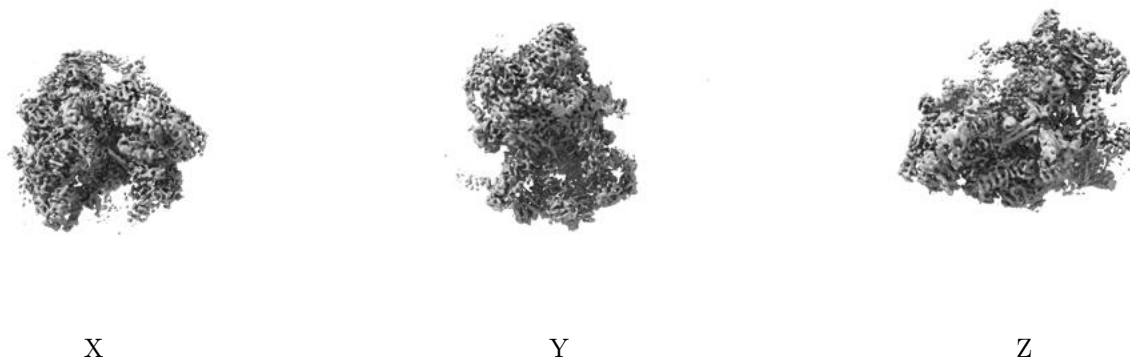


Z

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

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

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.09. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

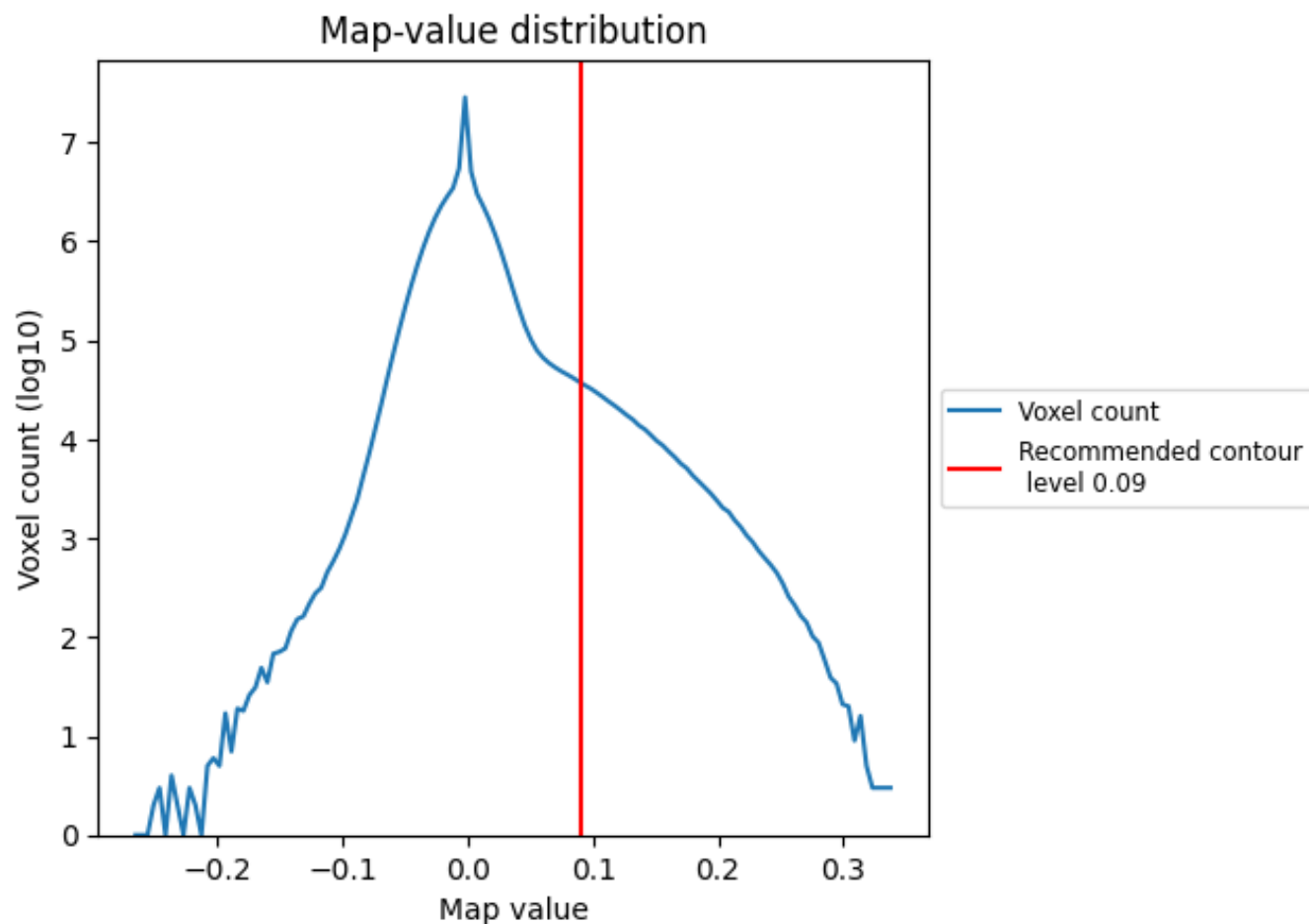
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

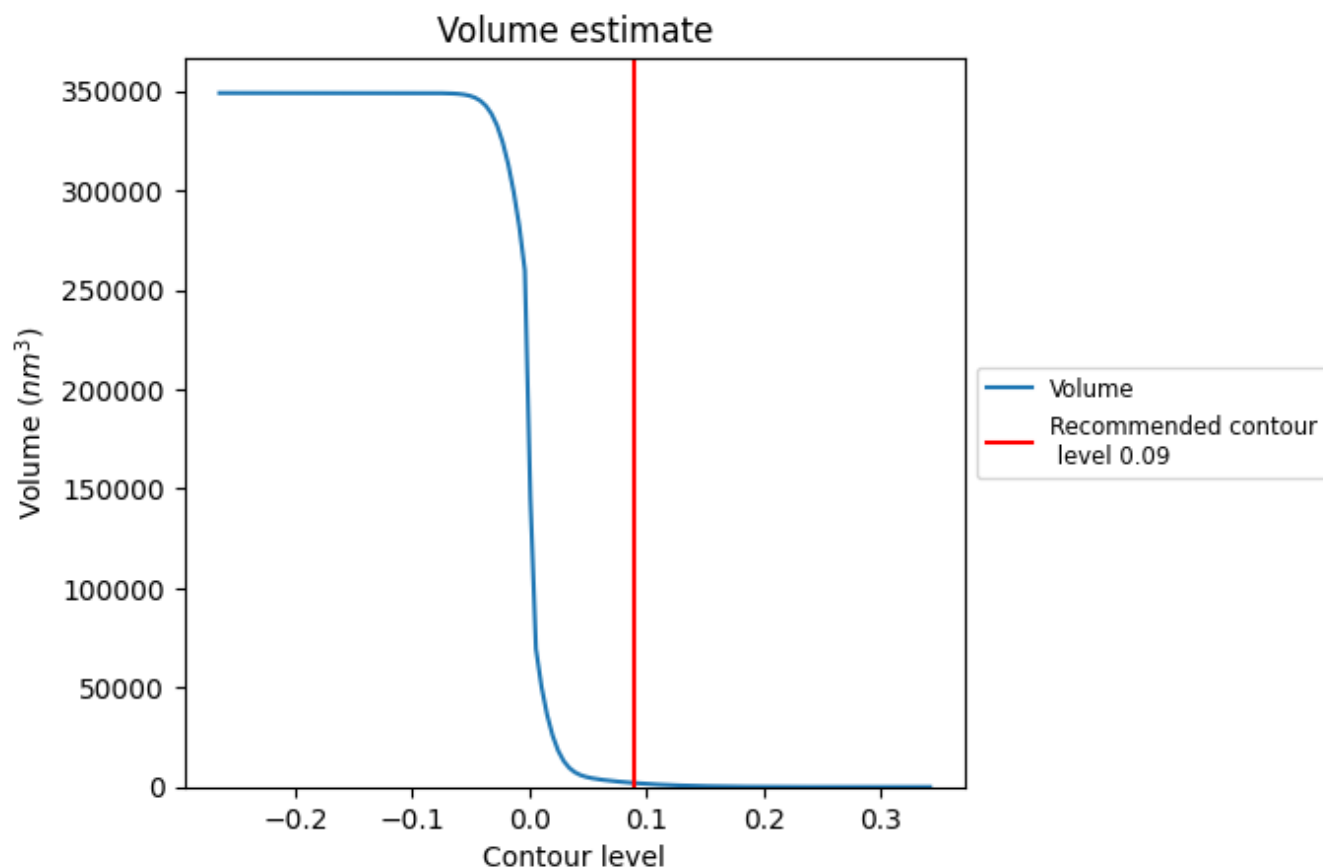
This section contains the results of statistical analysis of the map.

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



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

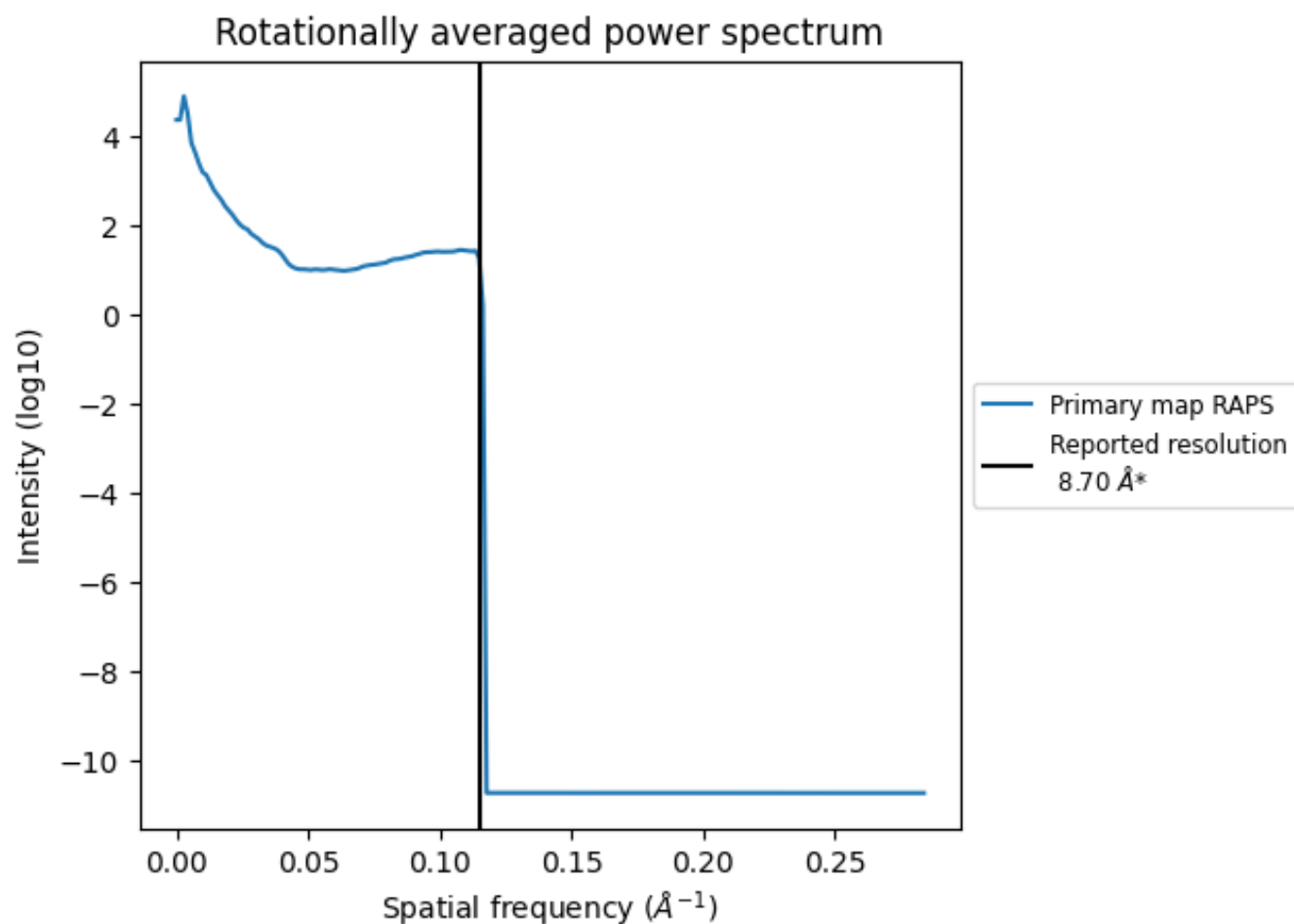
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1973  $\text{nm}^3$ ; this corresponds to an approximate mass of 1782 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 ⓘ

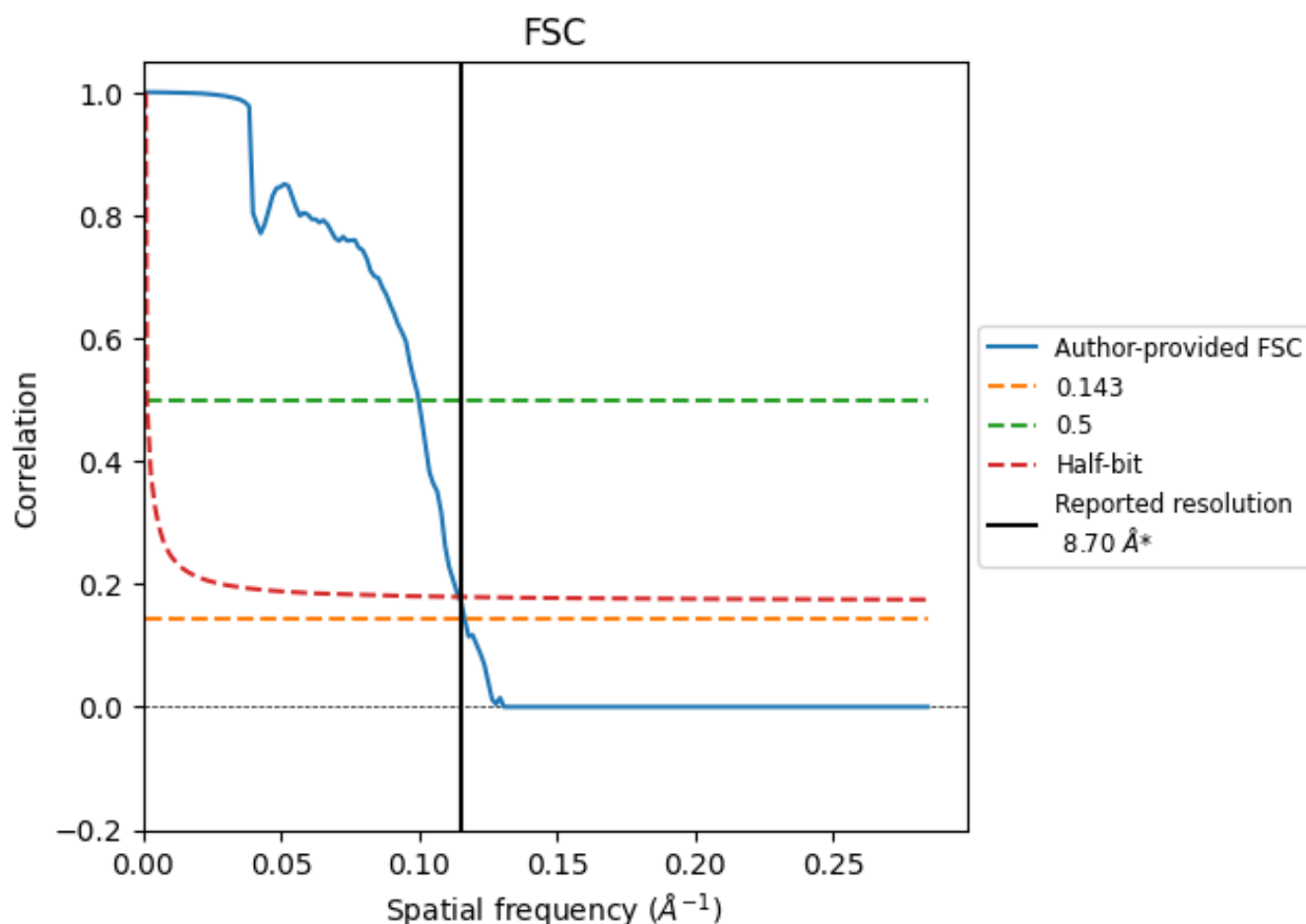


\*Reported resolution corresponds to spatial frequency of 0.115 Å<sup>-1</sup>

## 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 0.115 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

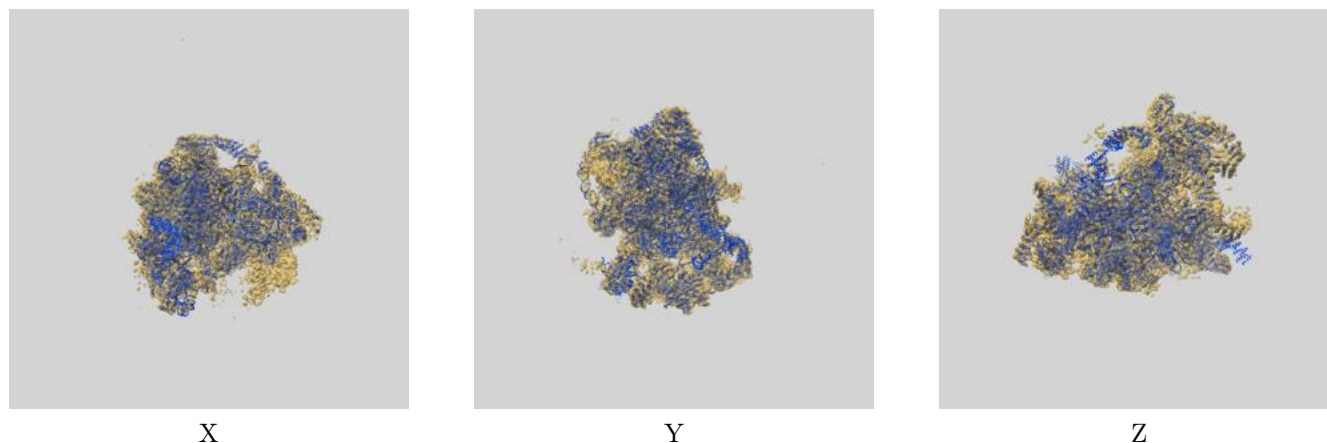
| Resolution estimate (Å)   | Estimation criterion (FSC cut-off) |       |          |
|---------------------------|------------------------------------|-------|----------|
|                           | 0.143                              | 0.5   | Half-bit |
| Reported by author        | 8.70                               | -     | -        |
| Author-provided FSC curve | 8.58                               | 10.02 | 8.74     |
| Unmasked-calculated*      | -                                  | -     | -        |

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

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

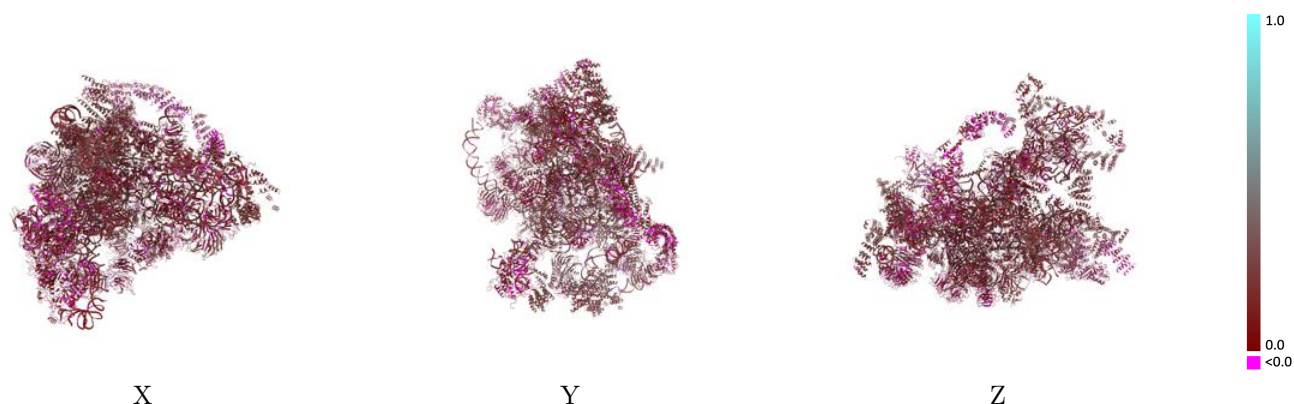
This section contains information regarding the fit between EMDB map EMD-6695 and PDB model 5WYJ. Per-residue inclusion information can be found in section [3](#) on page [15](#).

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



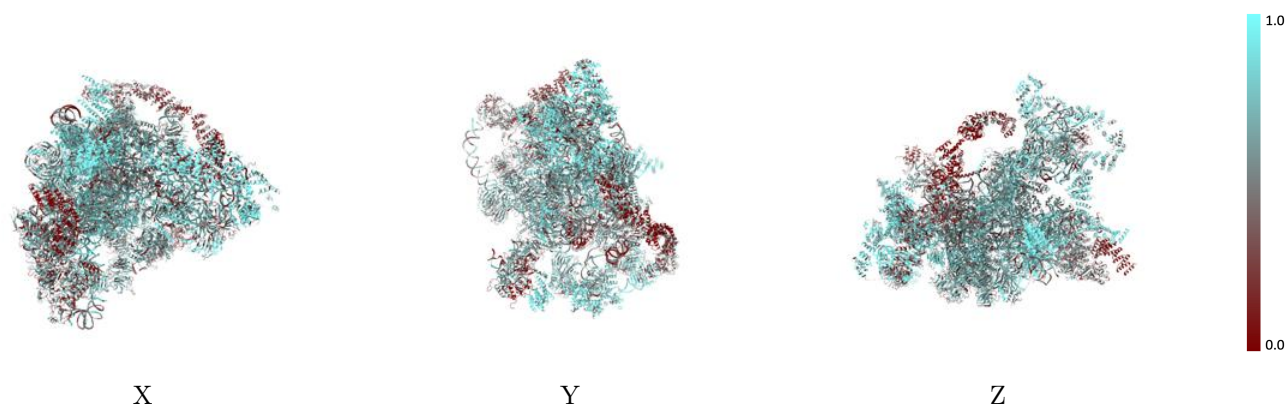
The images above show the 3D surface view of the map at the recommended contour level 0.09 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



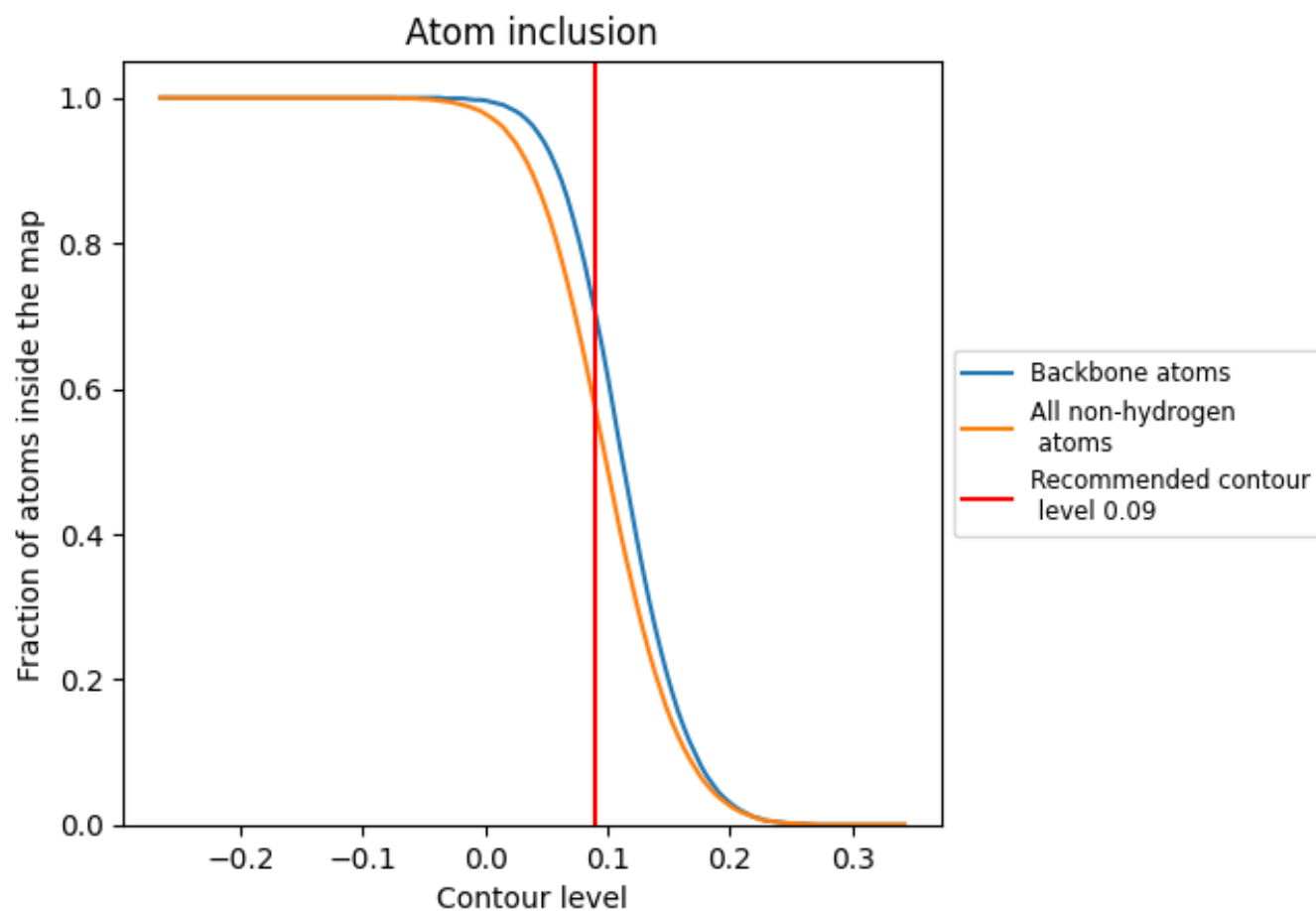
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.09).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 57% 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 (0.09) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion                                                                             | Q-score                                                                                    |
|-------|--------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| All   |  0.5720   |  0.1600   |
| 3A    |  0.7480   |  0.1830   |
| 3B    |  0.5460   |  0.1630   |
| 3C    |  0.3770   |  0.1290   |
| 3D    |  0.5850   |  0.1550   |
| 3E    |  0.5060   |  0.1500   |
| 3F    |  0.5810   |  0.1410   |
| 3G    |  0.5820   |  0.1580   |
| 3H    |  0.5550   |  0.1590   |
| 5A    |  0.4970   |  0.1750   |
| AA    |  0.7520   |  0.2230   |
| AB    |  0.6860   |  0.1990   |
| AC    |  0.5120   |  0.1480   |
| AD    |  0.7390   |  0.2190   |
| AE    |  0.3770  |  0.1220  |
| AF    |  0.8140 |  0.2410 |
| AG    |  0.6980 |  0.2000 |
| B1    |  0.5600 |  0.1420 |
| BA    |  0.5860 |  0.1550 |
| BB    |  0.5860 |  0.1320 |
| BC    |  0.4750 |  0.1160 |
| BD    |  0.5210 |  0.1110 |
| BE    |  0.5980 |  0.1430 |
| CA    |  0.3850 |  0.1130 |
| CB    |  0.4160 |  0.1210 |
| E1    |  0.4620 |  0.1290 |
| E2    |  0.4840 |  0.1330 |
| E3    |  0.4820 |  0.1220 |
| E4    |  0.6480 |  0.2180 |
| K1    |  0.4880 |  0.1450 |
| MA    |  0.6010 |  0.1550 |
| MB    |  0.5300 |  0.1350 |
| MC    |  0.7120 |  0.2100 |
| P1    |  0.5510 |  0.1530 |
| R1    |  0.5600 |  0.1470 |



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| Chain | Atom inclusion                                                                             | Q-score                                                                                    |
|-------|--------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| R2    |  0.0520   |  0.1040   |
| S1    |  0.7820   |  0.2440   |
| SA    |  0.7160   |  0.1710   |
| SC    |  0.4730   |  0.1580   |
| SF    |  0.5000   |  0.1300   |
| SG    |  0.5640   |  0.1610   |
| SH    |  0.3790   |  0.1150   |
| SI    |  0.4750   |  0.1500   |
| SJ    |  0.4860   |  0.1320   |
| SK    |  0.5270   |  0.1470   |
| SM    |  0.4040   |  0.1150   |
| SN    |  0.0690   |  0.0710   |
| SO    |  0.5170   |  0.1480   |
| SP    |  0.5060   |  0.1440   |
| SR    |  0.5840   |  0.1490   |
| SX    |  0.5150   |  0.1580   |
| SY    |  0.5010   |  0.1190   |
| SZ    |  0.5130  |  0.1450  |
| Sc    |  0.4320 |  0.1560 |
| Sd    |  0.5180 |  0.1400 |
| Sf    |  0.6430 |  0.1490 |
| Sg    |  0.0180 |  0.0120 |
| U1    |  0.8200 |  0.2560 |
| U2    |  0.9070 |  0.2620 |
| U3    |  0.7750 |  0.2360 |
| U4    |  0.5400 |  0.1660 |
| U5    |  0.1590 |  0.1000 |
| UA    |  0.9190 |  0.2650 |
| UB    |  0.8290 |  0.2540 |
| UC    |  0.8200 |  0.2700 |