



wwPDB EM Validation Summary Report ⓘ

Nov 2, 2022 – 09:23 PM EDT

PDB ID : 5TZS
EMDB ID : EMD-8473
Title : Architecture of the yeast small subunit processome
Authors : Chaker-Margot, M.; Barandun, J.; Hunziker, M.; Klinge, S.
Deposited on : 2016-11-22
Resolution : 5.10 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

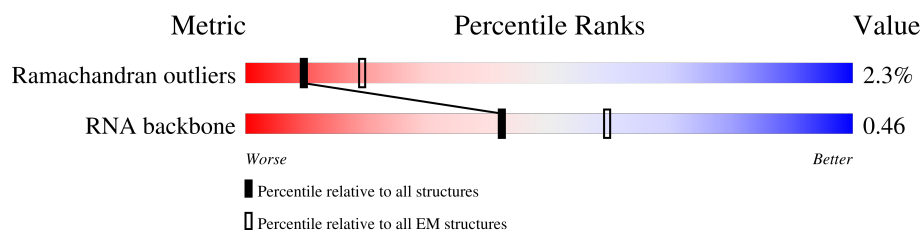
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 5.10 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 |
| 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 $\leq 5\%$. 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 | 0 | 364 | <div> <div>21%</div> <div>99%</div> <div>.</div> </div> |
| 2 | 1 | 1800 | <div> <div>12%</div> <div>14%</div> <div>12%</div> <div>71%</div> </div> |
| 3 | 2 | 126 | <div> <div>12%</div> <div>48%</div> <div>49%</div> <div>.</div> </div> |
| 4 | 3 | 236 | <div> <div>79%</div> <div>86%</div> <div>6%</div> <div>8%</div> </div> |
| 5 | 5 | 261 | <div> <div>48%</div> <div>86%</div> <div>7%</div> <div>8%</div> </div> |
| 6 | 6 | 225 | <div> <div>9%</div> <div>81%</div> <div>8%</div> <div>10%</div> </div> |
| 7 | 7 | 190 | <div> <div>95%</div> <div>88%</div> <div>9%</div> <div>.</div> </div> |
| 8 | 8 | 200 | <div> <div>63%</div> <div>84%</div> <div>.</div> <div>14%</div> </div> |
| 9 | 9 | 197 | <div> <div>21%</div> <div>86%</div> <div>8%</div> <div>6%</div> </div> |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 10 | A | 39 | 100% |
| 11 | B | 108 | 45% 100% |
| 12 | C | 143 | 80% 20% |
| 13 | D | 156 | 72% 94% 6% |
| 14 | E | 130 | 81% 97% .. |
| 15 | F | 135 | 21% 64% 33% |
| 16 | G | 67 | 9% 91% 7% |
| 17 | H | 544 | 44% 99% |
| 18 | I | 176 | 22% 94% 6% |
| 19 | J | 107 | 7% 98% |
| 19 | K | 107 | 16% 95% |
| 20 | M | 258 | 8% 99% |
| 21 | N | 545 | 20% 99% |
| 22 | O | 638 | 8% 98% |
| 23 | P | 306 | 7% 100% |
| 24 | Q | 710 | 19% 99% |
| 25 | R | 717 | 78% 100% |
| 26 | S | 250 | 14% 98% |
| 27 | T | 781 | 5% 96% |
| 28 | U | 284 | 13% 100% |
| 29 | V | 263 | 72% 100% |
| 30 | W | 104 | 9% 90% 10% |
| 31 | X | 640 | 72% 100% |
| 32 | Y | 641 | 93% 100% |
| 33 | Z | 151 | 5% 99% |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------------|
| 34 | a | 312 | 15% 98% . |
| 35 | b | 341 | 22% 100% |
| 36 | c | 221 | 7% 99% . |
| 37 | d | 216 | 24% 99% . |
| 38 | e | 126 | 7% 97% . |
| 38 | f | 126 | 8% 90% 10% |
| 39 | g | 573 | 11% 63% 36% . |
| 40 | h | 367 | 10% 97% . |
| 41 | i | 511 | 10% 92% 7% . |
| 42 | j | 252 | 21% 84% 16% |
| 42 | k | 252 | 15% 86% 13% . |
| 43 | l | 124 | 6% 100% |
| 44 | m | 156 | 14% 99% . |
| 45 | n | 160 | 14% 100% |
| 46 | o | 175 | 71% 99% . |
| 47 | p | 924 | 87% 96% . |
| 48 | q | 372 | 9% 100% |
| 49 | r | 145 | 6% 56% 43% . |
| 50 | s | 290 | 21% 97% . |
| 50 | t | 290 | . 89% 7% . |
| 50 | u | 290 | 9% 94% 6% |
| 51 | v | 580 | 15% 97% .. |
| 52 | y | 507 | 15% 93% 7% |
| 53 | z | 76 | 32% 100% |

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 98451 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 5' external transcribed spacer.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|----|------|-----|---------|-------|
| 1 | 0 | 364 | Total | C | N | O | P | 0 | 0 |
| | | | 4476 | 1871 | 43 | 2198 | 364 | | |

- Molecule 2 is a RNA chain called 18S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|-----|---------|-------|
| 2 | 1 | 515 | Total | C | N | O | P | 0 | 0 |
| | | | 10978 | 4908 | 1957 | 3598 | 515 | | |

- Molecule 3 is a RNA chain called U3 snoRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 3 | 2 | 126 | Total | C | N | O | P | 0 | 0 |
| | | | 2468 | 1095 | 388 | 859 | 126 | | |

- Molecule 4 is a protein called rpS6_ES6.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 4 | 3 | 216 | Total | C | N | O | 0 | 0 |
| | | | 1063 | 631 | 216 | 216 | | |

- Molecule 5 is a protein called rpS4_ES4.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 5 | 5 | 241 | Total | C | N | O | 0 | 0 |
| | | | 1185 | 703 | 241 | 241 | | |

- Molecule 6 is a protein called rpS5_US7.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 6 | 6 | 202 | Total | C | N | O | 0 | 0 |
| | | | 1000 | 596 | 202 | 202 | | |

- Molecule 7 is a protein called rpS7_eS7.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 7 | 7 | 186 | Total | C | N | O | 0 | 0 |
| | | | 923 | 551 | 186 | 186 | | |

- Molecule 8 is a protein called rpS8_eS8.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 8 | 8 | 173 | Total | C | N | O | 0 | 0 |
| | | | 849 | 503 | 173 | 173 | | |

- Molecule 9 is a protein called rpS9_uS4.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 9 | 9 | 185 | Total | C | N | O | 0 | 0 |
| | | | 915 | 545 | 185 | 185 | | |

- Molecule 10 is a DNA chain called 5' domain-associated.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---------|-------|
| 10 | A | 39 | Total | C | O | P | 0 | 0 |
| | | | 468 | 195 | 234 | 39 | | |

- Molecule 11 is a DNA chain called 3' domain-associated.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 11 | B | 108 | Total | C | O | P | 0 | 0 |
| | | | 1296 | 540 | 648 | 108 | | |

- Molecule 12 is a protein called rpS16_uS9.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 12 | C | 115 | Total | C | N | O | 0 | 0 |
| | | | 566 | 336 | 115 | 115 | | |

- Molecule 13 is a protein called rpS11_uS17.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 13 | D | 146 | Total | C | N | O | 0 | 0 |
| | | | 721 | 429 | 146 | 146 | | |

- Molecule 14 is a protein called rpS22_uS8.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 14 | E | 127 | Total | C | N | O | 0 | 0 |
| | | | 624 | 370 | 127 | 127 | | |

- Molecule 15 is a protein called rpS24_eS24.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 15 | F | 90 | Total | C | N | O | 0 | 0 |
| | | | 444 | 264 | 90 | 90 | | |

- Molecule 16 is a protein called rpS28_eS28.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 16 | G | 62 | Total | C | N | O | 0 | 0 |
| | | | 306 | 182 | 62 | 62 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| G | 17 | ALA | GLY | conflict | UNP Q3E7X9 |

- Molecule 17 is a protein called Utp4.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 17 | H | 544 | Total | C | N | O | 0 | 0 |
| | | | 2680 | 1592 | 544 | 544 | | |

- Molecule 18 is a protein called UtpA_CTD1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 18 | I | 176 | Total | C | N | O | 0 | 0 |
| | | | 880 | 528 | 176 | 176 | | |

- Molecule 19 is a protein called UtpA_CTD2.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 19 | J | 107 | Total | C | N | O | 0 | 0 |
| | | | 535 | 321 | 107 | 107 | | |
| 19 | K | 105 | Total | C | N | O | 0 | 0 |
| | | | 525 | 315 | 105 | 105 | | |

- Molecule 20 is a protein called Beta-propeller 2.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 20 | M | 258 | Total | C | N | O | 0 | 0 |
| | | | 1275 | 759 | 258 | 258 | | |

- Molecule 21 is a protein called Utp17.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 21 | N | 545 | Total | C | N | O | 0 | 0 |
| | | | 2678 | 1588 | 545 | 545 | | |

- Molecule 22 is a protein called Utp1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 22 | O | 638 | Total | C | N | O | 0 | 0 |
| | | | 3153 | 1877 | 638 | 638 | | |

- Molecule 23 is a protein called Utp6.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 23 | P | 306 | Total | C | N | O | 0 | 0 |
| | | | 1530 | 918 | 306 | 306 | | |

- Molecule 24 is a protein called Utp12.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 24 | Q | 710 | Total | C | N | O | 0 | 0 |
| | | | 3503 | 2083 | 710 | 710 | | |

- Molecule 25 is a protein called Utp13.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 25 | R | 717 | Total | C | N | O | 0 | 0 |
| | | | 3539 | 2105 | 717 | 717 | | |

- Molecule 26 is a protein called Utp18.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 26 | S | 250 | Total | C | N | O | 0 | 0 |
| | | | 1228 | 728 | 250 | 250 | | |

- Molecule 27 is a protein called Utp21.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 27 | T | 749 | Total | C | N | O | 0 | 0 |
| | | | 3691 | 2193 | 749 | 749 | | |

- Molecule 28 is a protein called Beta-propeller 5.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 28 | U | 284 | Total | C | N | O | 0 | 0 |
| | | | 1398 | 830 | 284 | 284 | | |

- Molecule 29 is a protein called Enp2.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 29 | V | 263 | Total | C | N | O | 0 | 0 |
| | | | 1298 | 772 | 263 | 263 | | |

- Molecule 30 is a protein called UtpA_CTD4.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 30 | W | 104 | Total | C | N | O | 0 | 0 |
| | | | 520 | 312 | 104 | 104 | | |

- Molecule 31 is a protein called Kre33.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 31 | X | 640 | Total | C | N | O | 0 | 0 |
| | | | 3155 | 1875 | 640 | 640 | | |

- Molecule 32 is a protein called Kre33.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 32 | Y | 641 | Total | C | N | O | 0 | 0 |
| | | | 3160 | 1878 | 641 | 641 | | |

- Molecule 33 is a protein called Imp3.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 33 | Z | 151 | Total | C | N | O | 0 | 0 |
| | | | 748 | 446 | 151 | 151 | | |

- Molecule 34 is a protein called Nop56.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 34 | a | 312 | Total | C | N | O | 0 | 0 |
| | | | 1544 | 920 | 312 | 312 | | |

- Molecule 35 is a protein called Nop58.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 35 | b | 341 | Total | C | N | O | 0 | 0 |
| | | | 1687 | 1005 | 341 | 341 | | |

- Molecule 36 is a protein called Nop1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 36 | c | 221 | Total | C | N | O | 0 | 0 |
| | | | 1088 | 646 | 221 | 221 | | |

- Molecule 37 is a protein called Nop1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 37 | d | 216 | Total | C | N | O | 0 | 0 |
| | | | 1064 | 632 | 216 | 216 | | |

- Molecule 38 is a protein called Snu13.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 38 | e | 122 | Total | C | N | O | 0 | 0 |
| | | | 606 | 362 | 122 | 122 | | |
| 38 | f | 114 | Total | C | N | O | 0 | 0 |
| | | | 566 | 338 | 114 | 114 | | |

- Molecule 39 is a protein called Ribosomal RNA-processing protein 9.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 39 | g | 365 | Total | C | N | O | 0 | 0 |
| | | | 1799 | 1069 | 365 | 365 | | |

- Molecule 40 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 40 | h | 355 | Total | C | N | O | 0 | 0 |
| | | | 1742 | 1032 | 355 | 355 | | |

- Molecule 41 is a protein called Bms1,Ribosome biogenesis protein BMS1,Bms1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 41 | i | 475 | Total | C | N | O | 0 | 0 |
| | | | 2347 | 1398 | 475 | 474 | | |

- Molecule 42 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 42 | j | 211 | Total | C | N | O | 0 | 0 |
| | | | 1047 | 625 | 211 | 211 | | |
| 42 | k | 218 | Total | C | N | O | 0 | 0 |
| | | | 1081 | 645 | 218 | 218 | | |

- Molecule 43 is a protein called Utp24.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 43 | l | 124 | Total | C | N | O | 0 | 0 |
| | | | 613 | 365 | 124 | 124 | | |

- Molecule 44 is a protein called Imp4.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 44 | m | 156 | Total | C | N | O | 0 | 0 |
| | | | 775 | 463 | 156 | 156 | | |

- Molecule 45 is a protein called Utp30.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 45 | n | 160 | Total | C | N | O | 0 | 0 |
| | | | 791 | 471 | 160 | 160 | | |

- Molecule 46 is a protein called Unassigned KH domain.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 46 | o | 173 | Total | C | N | O | 0 | 0 |
| | | | 858 | 512 | 173 | 173 | | |

- Molecule 47 is a protein called Utp20.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 47 | p | 924 | Total | C | N | O | 0 | 0 |
| | | | 4620 | 2772 | 924 | 924 | | |

- Molecule 48 is a protein called Repeat protein 2.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 48 | q | 372 | Total | C | N | O | 0 | 0 |
| | | | 1860 | 1116 | 372 | 372 | | |

- Molecule 49 is a protein called 40S ribosomal protein S23-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 49 | r | 82 | Total | C | N | O | 0 | 0 |
| | | | 402 | 238 | 82 | 82 | | |

- Molecule 50 is a protein called Beta-propeller 1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 50 | s | 290 | Total | C | N | O | 0 | 0 |
| | | | 1429 | 849 | 290 | 290 | | |
| 50 | t | 269 | Total | C | N | O | 0 | 0 |
| | | | 1076 | 538 | 269 | 269 | | |
| 50 | u | 274 | Total | C | N | O | 0 | 0 |
| | | | 1346 | 798 | 274 | 274 | | |

- Molecule 51 is a protein called Repeat protein 1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 51 | v | 577 | Total | C | N | O | 0 | 0 |
| | | | 2885 | 1731 | 577 | 577 | | |

- Molecule 52 is a protein called Unassigned protein helices.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 52 | y | 507 | Total | C | N | O | 0 | 0 |
| | | | 2535 | 1521 | 507 | 507 | | |

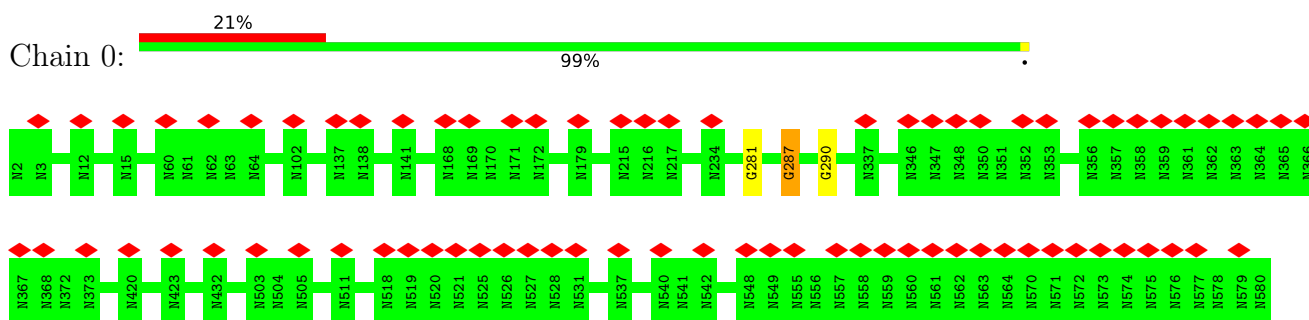
- Molecule 53 is a DNA chain called Unassigned RNA helices.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---------|-------|
| 53 | z | 76 | Total | C | O | P | 0 | 0 |
| | | | 912 | 380 | 456 | 76 | | |

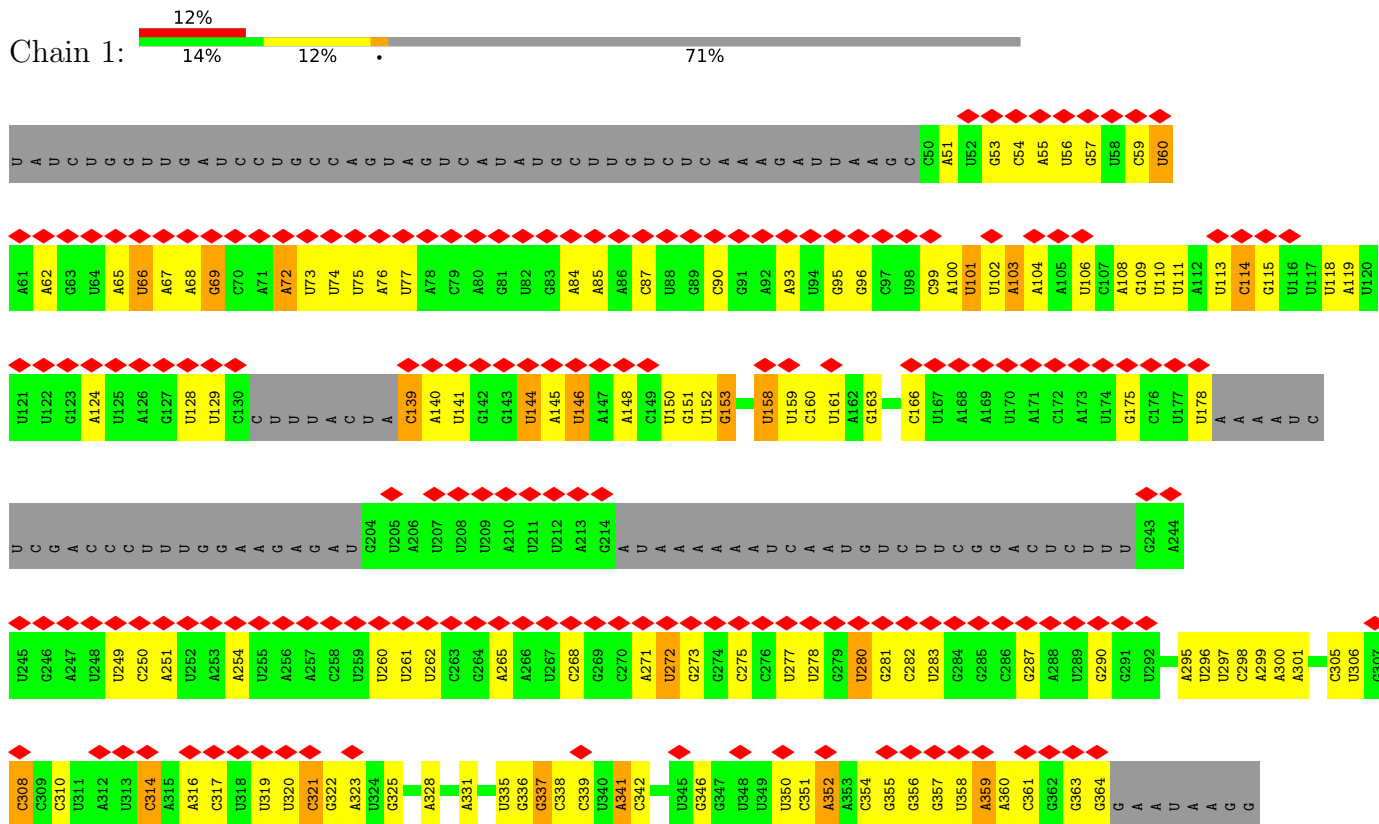
3 Residue-property plots

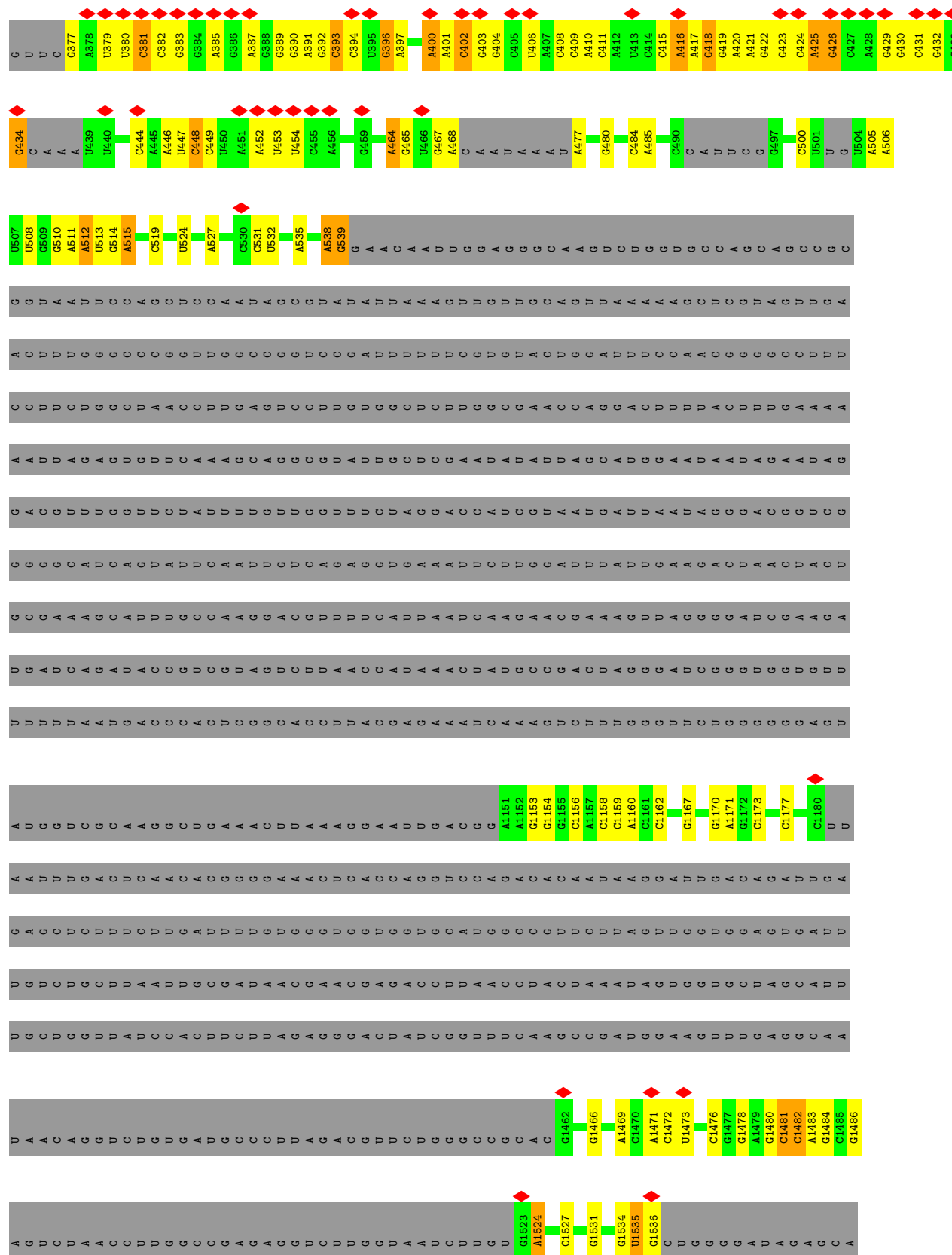
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 5' external transcribed spacer

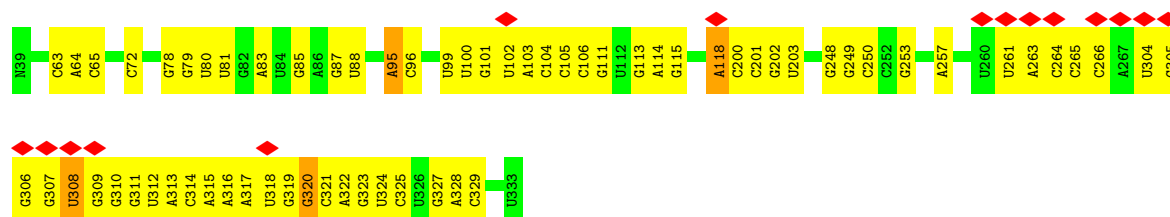


- Molecule 2: 18S ribosomal RNA

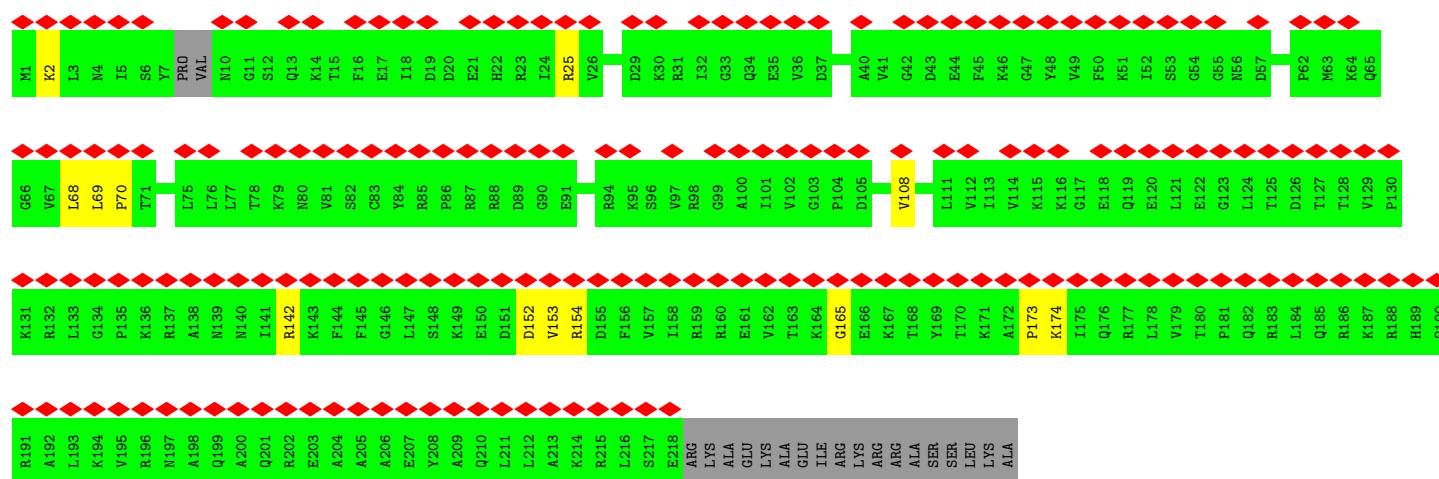
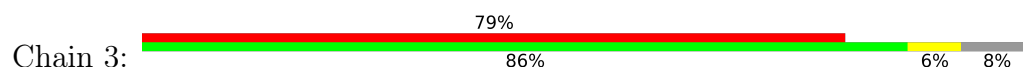




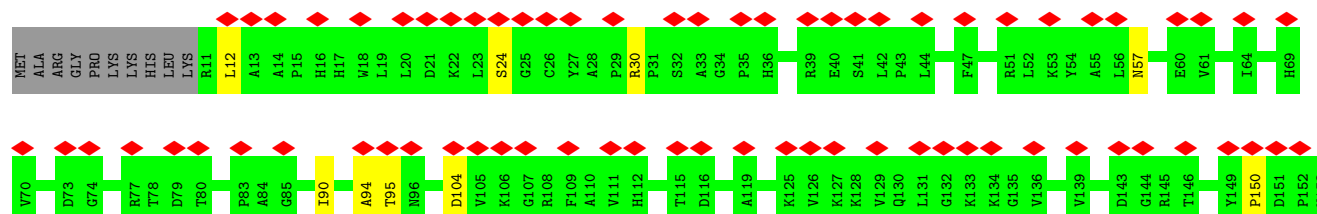
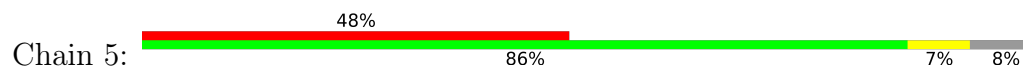
- Molecule 3: U3 snoRNA

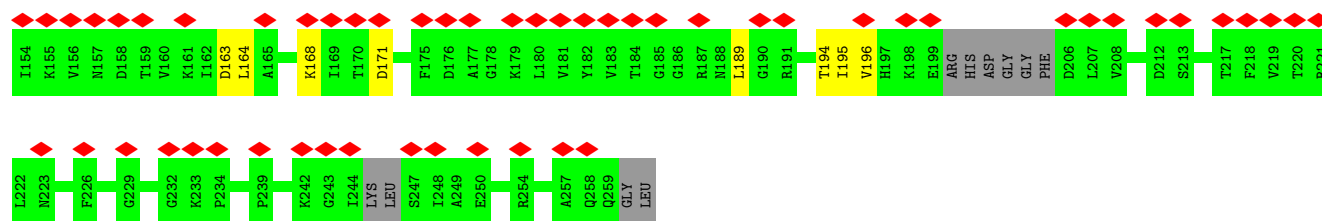


- Molecule 4: rpS6_ES6

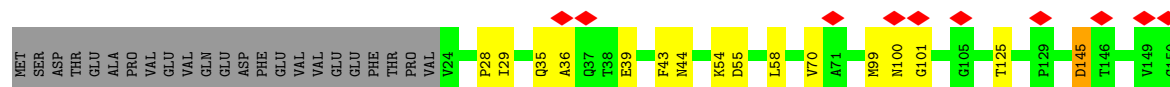
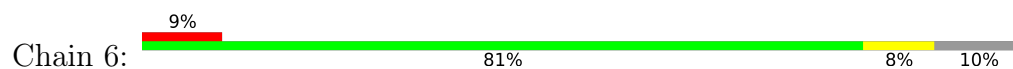


- Molecule 5: rpS4 ES4

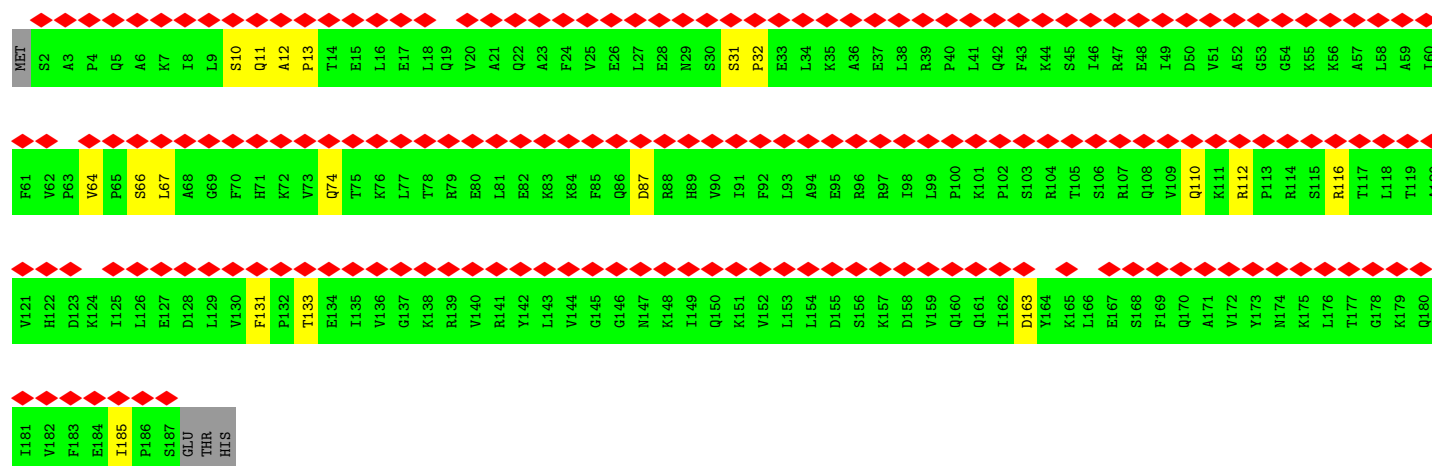
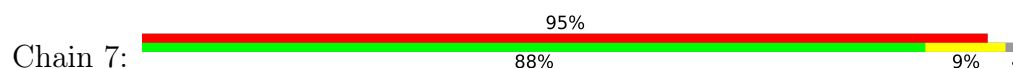




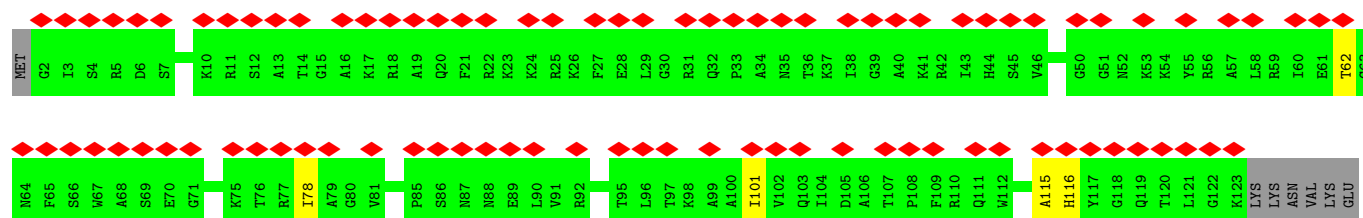
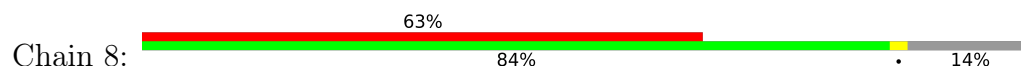
• Molecule 6: rpS5_US7

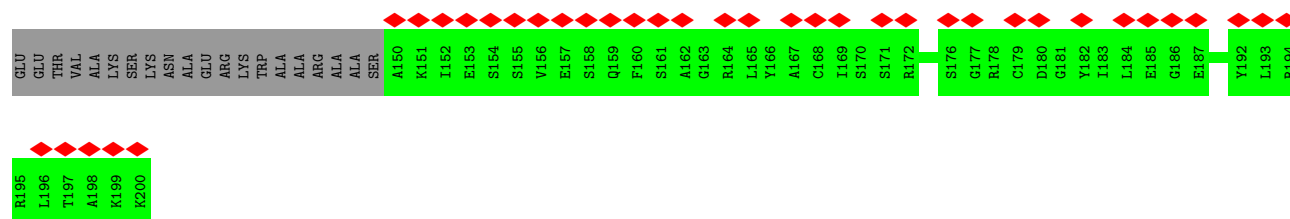


• Molecule 7: rpS7_eS7

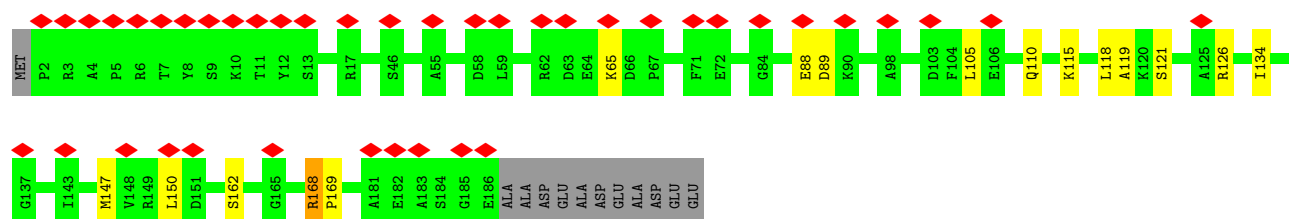
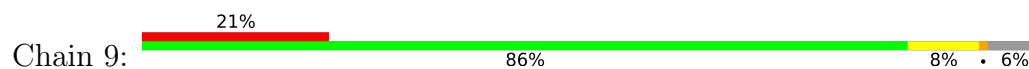


• Molecule 8: rpS8_eS8





- Molecule 9: rpS9_uS4

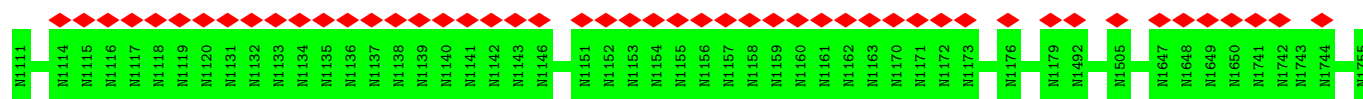


- Molecule 10: 5' domain-associated

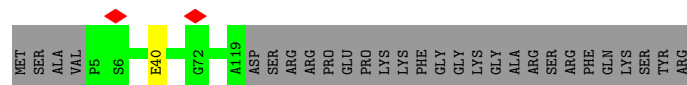
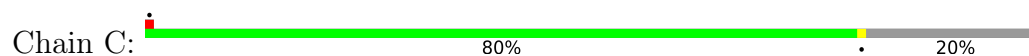


There are no outlier residues recorded for this chain.

- Molecule 11: 3' domain-associated

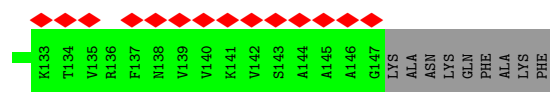


- Molecule 12: rpS16_uS9

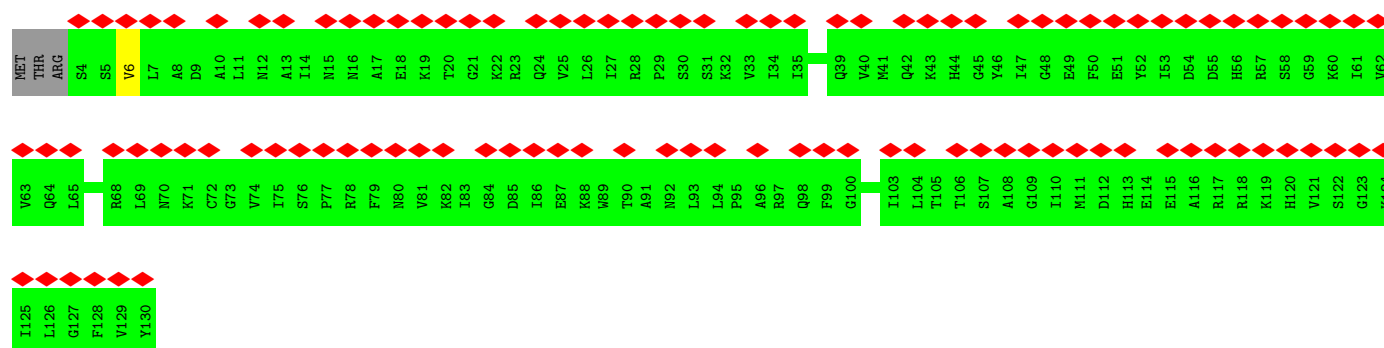
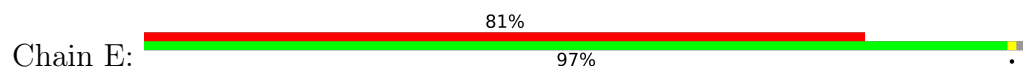


- Molecule 13: rpS11_uS17

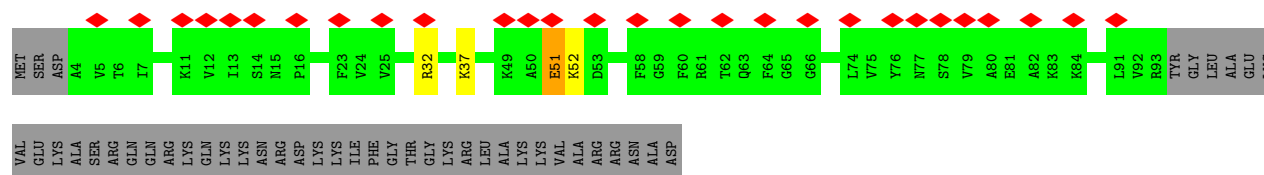




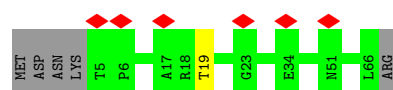
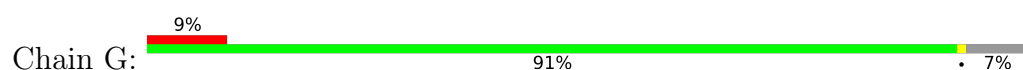
• Molecule 14: rpS22_uS8



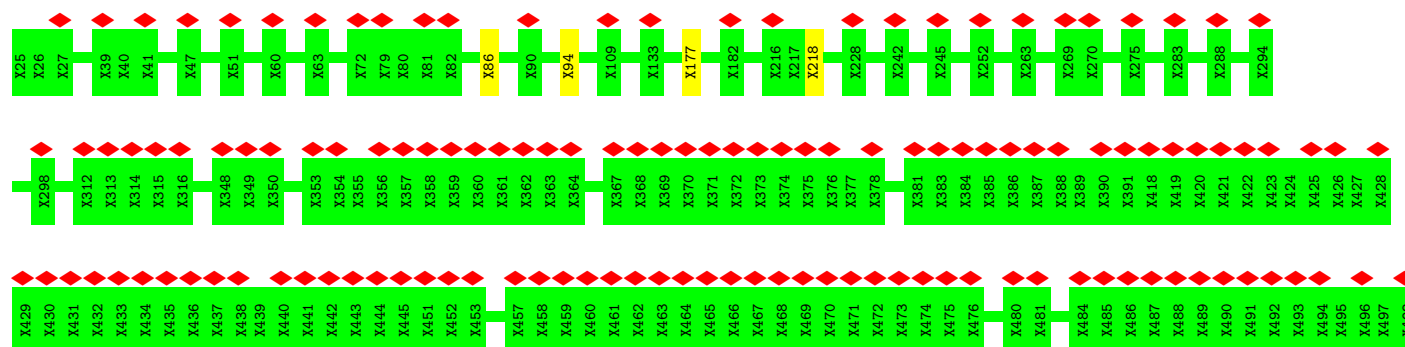
• Molecule 15: rpS24_eS24

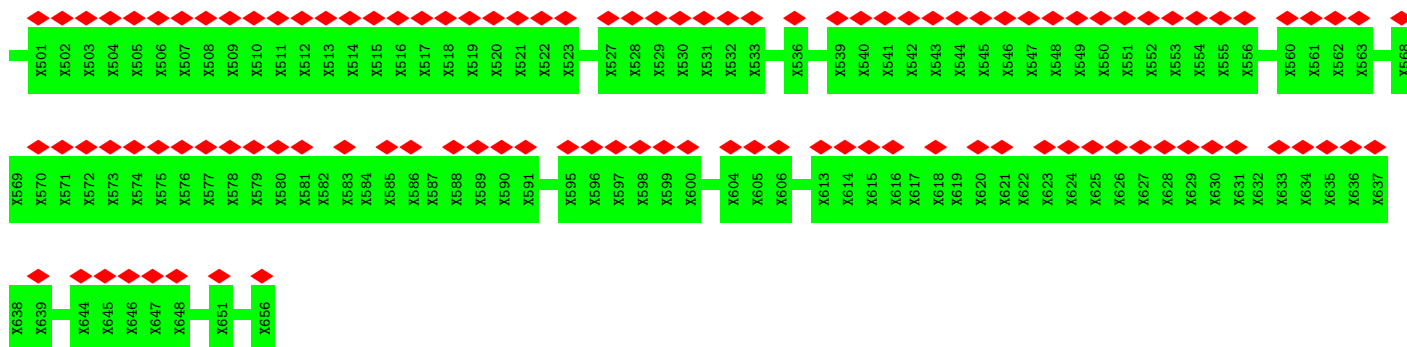


• Molecule 16: rpS28_eS28

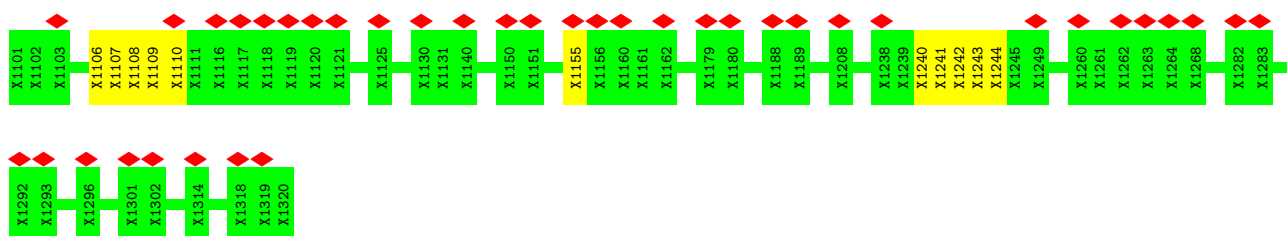


• Molecule 17: Utp4

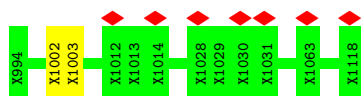




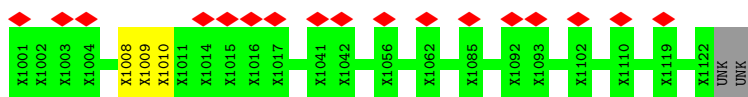
• Molecule 18: UtpA_CTD1



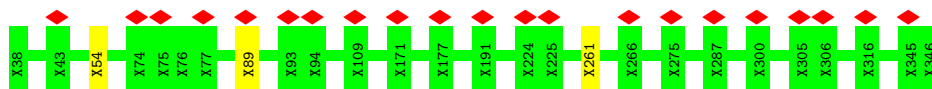
• Molecule 19: UtpA_CTD2



• Molecule 19: UtpA_CTD2

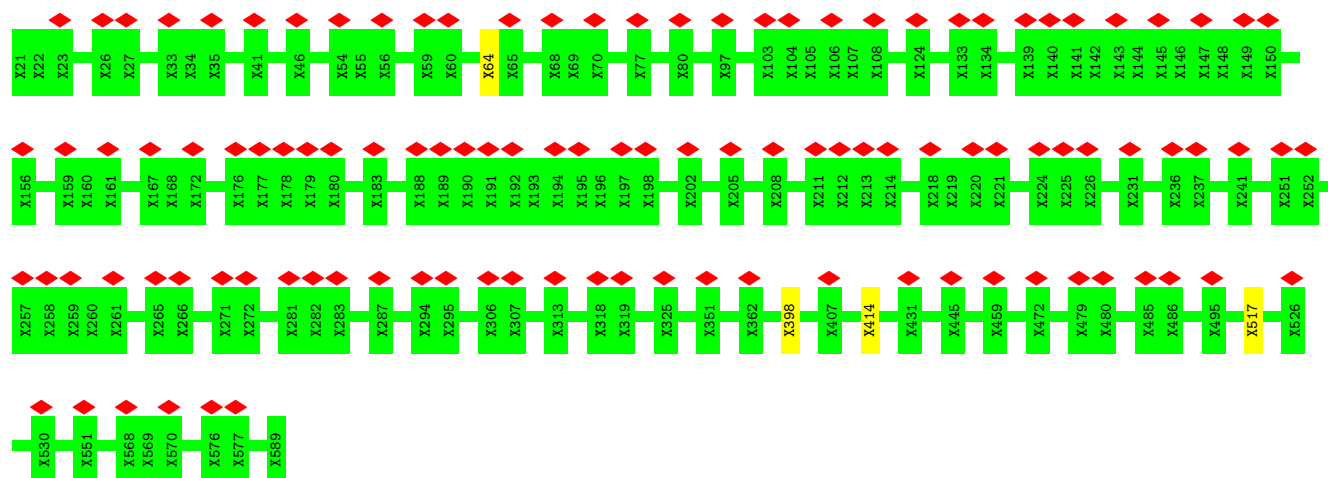


• Molecule 20: Beta-propeller 2

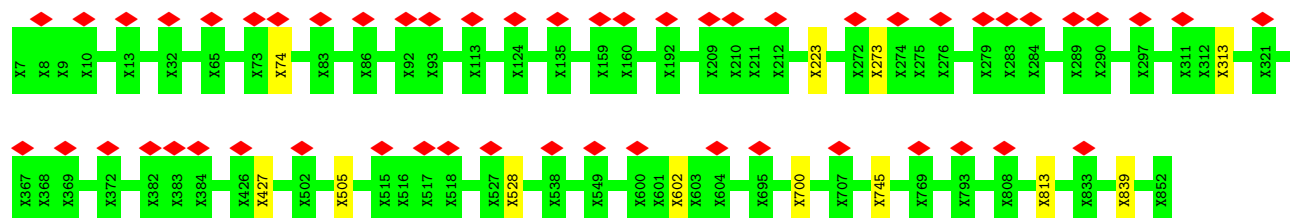


• Molecule 21: Utp17

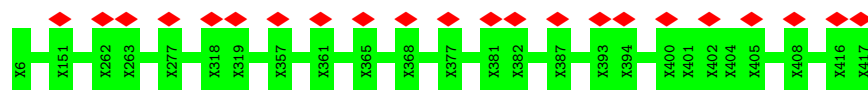




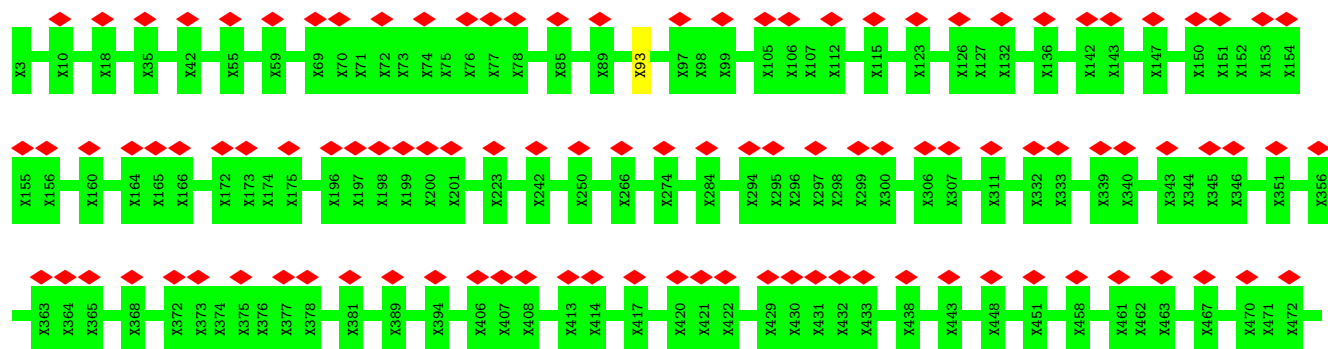
- Molecule 22: Utp1

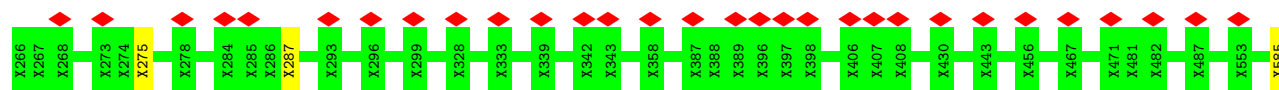


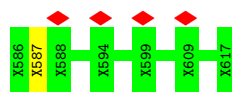
- Molecule 23: Utp6



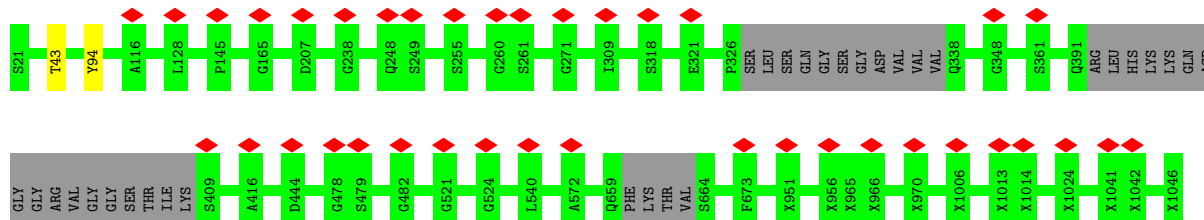
- Molecule 24: Utp12



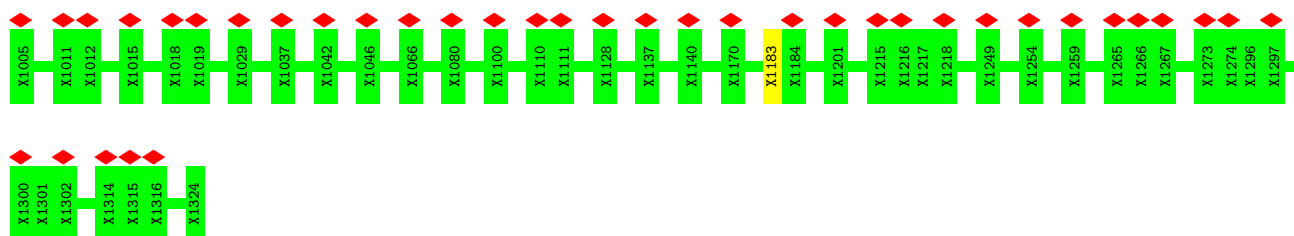




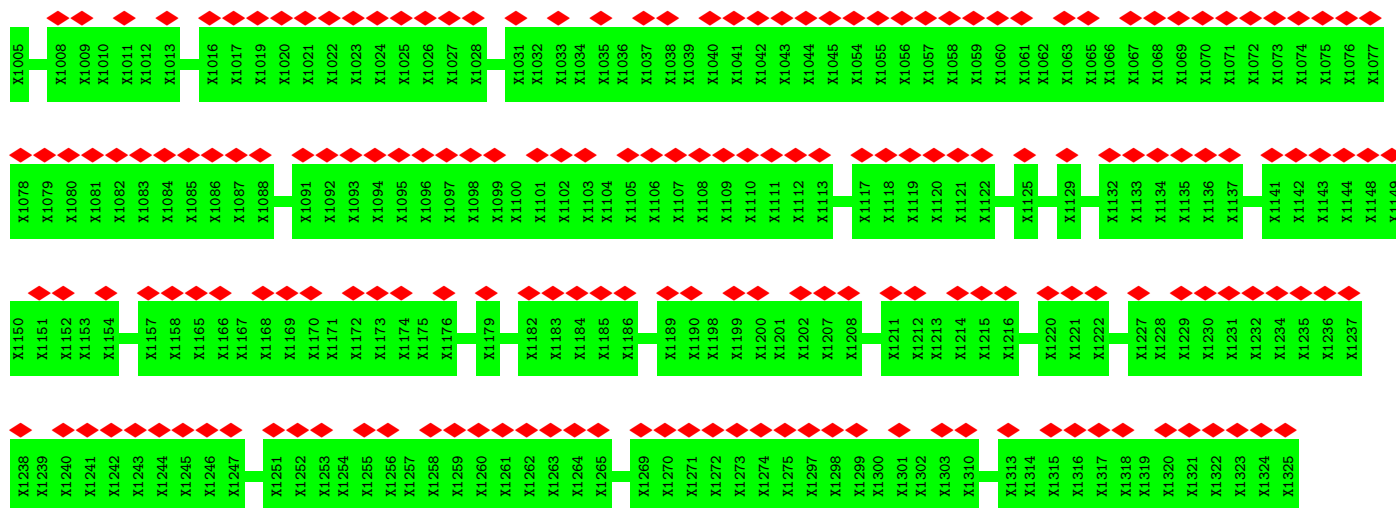
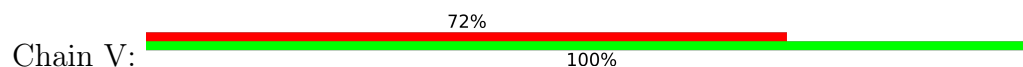
• Molecule 27: Utp21



• Molecule 28: Beta-propeller 5



• Molecule 29: Enp2

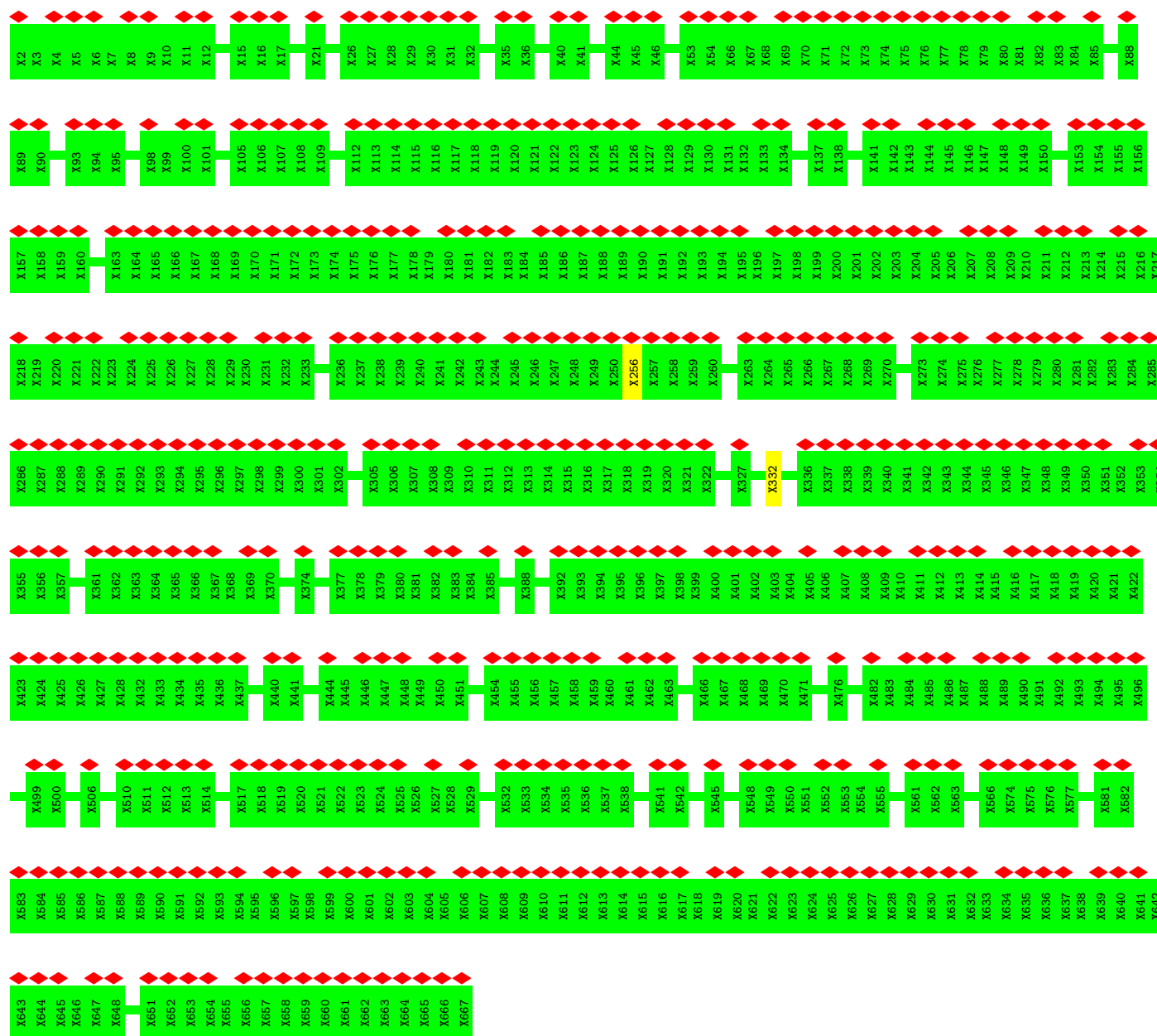
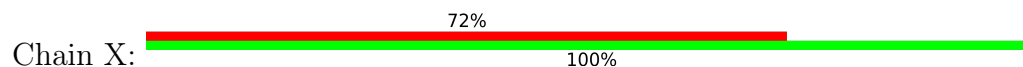


• Molecule 30: UtpA_CTD4

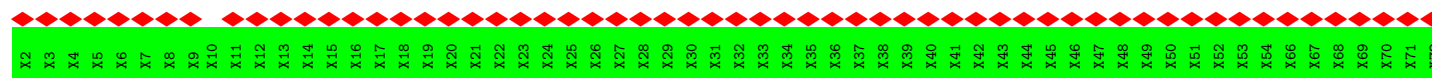


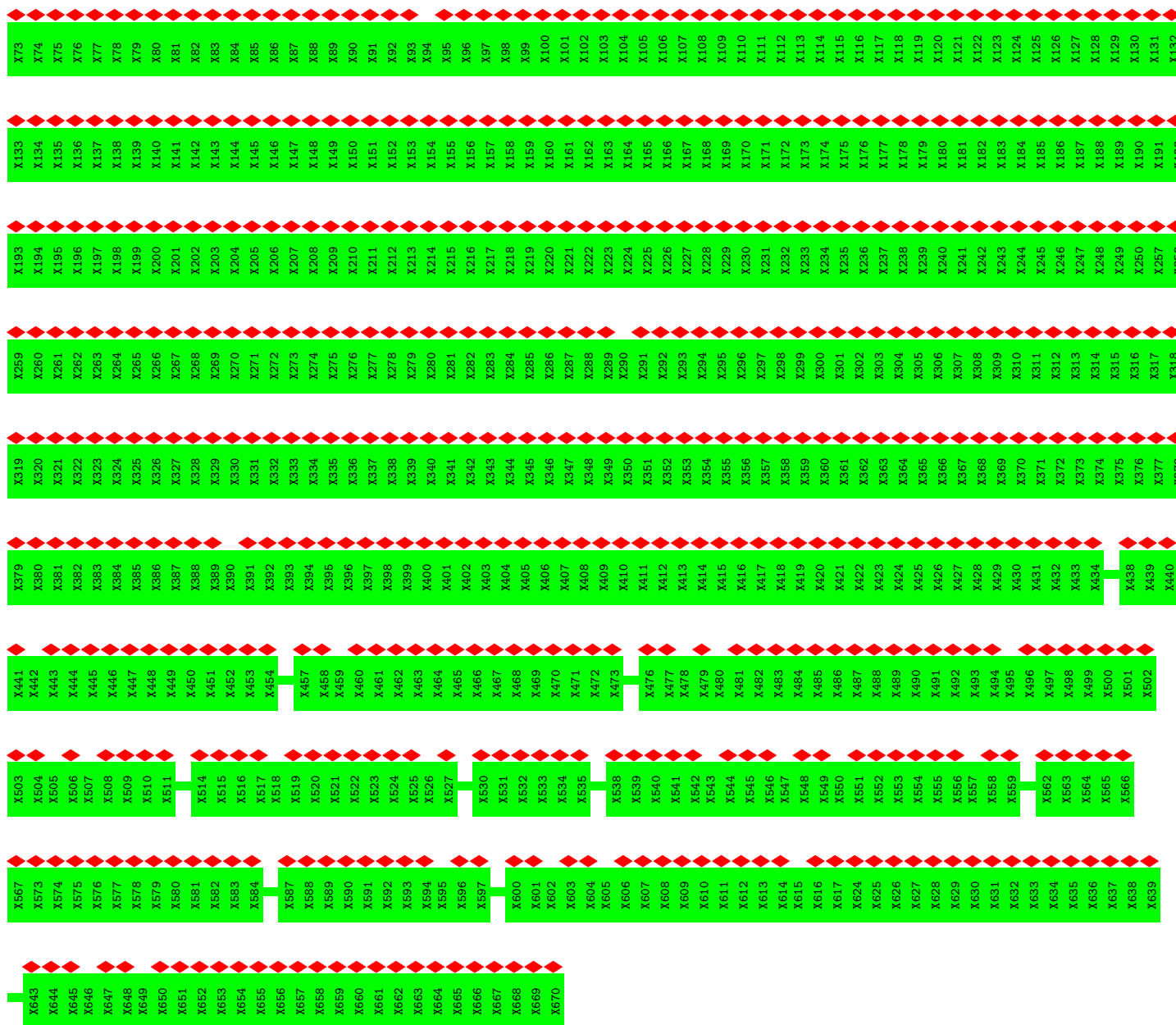


• Molecule 31: Kre33

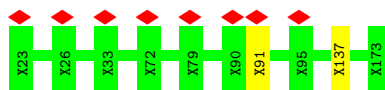


• Molecule 32: Kre33



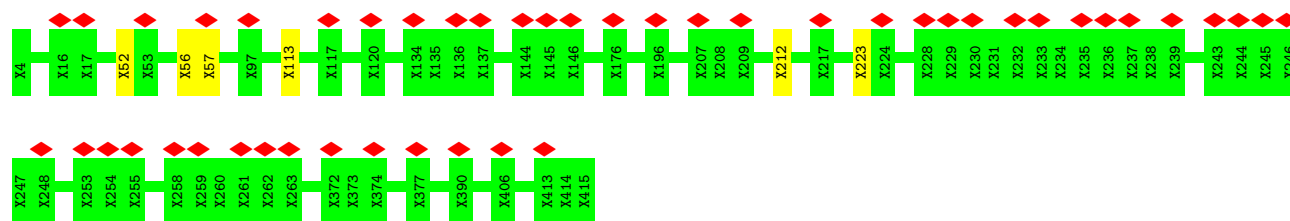


- Molecule 33: Imp3

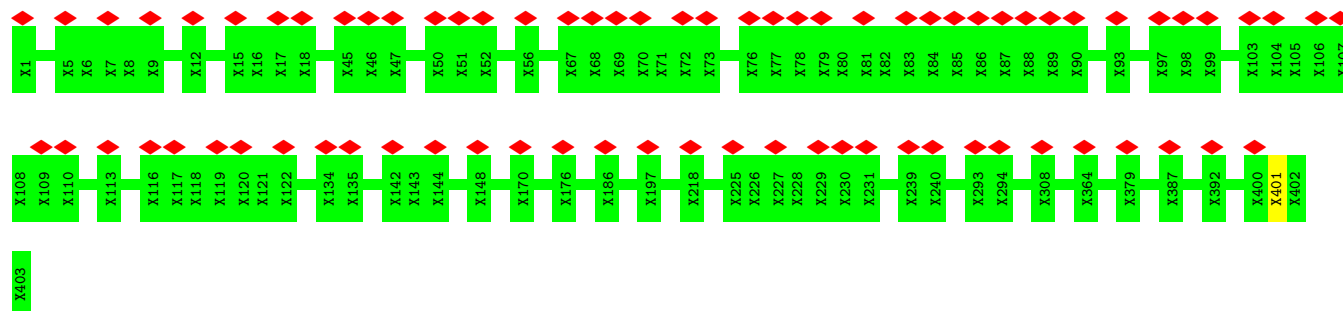


- Molecule 34: Nop56

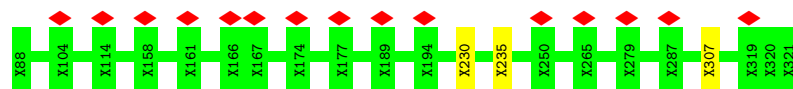




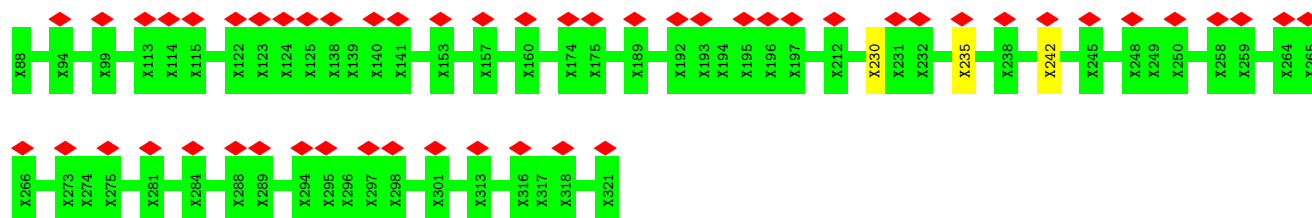
- Molecule 35: Nop58



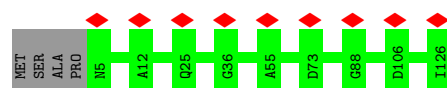
- Molecule 36: Nop1



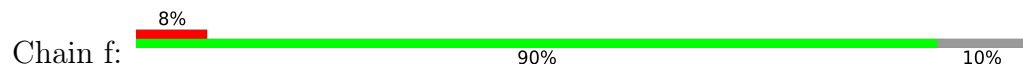
- Molecule 37: Nop1

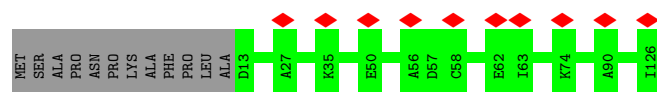


- Molecule 38: Snu13

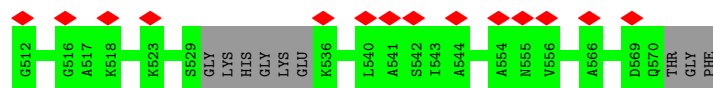
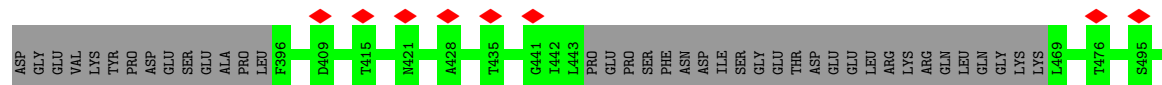
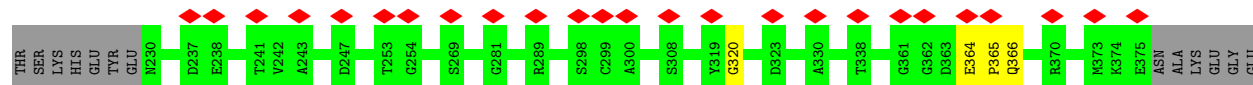
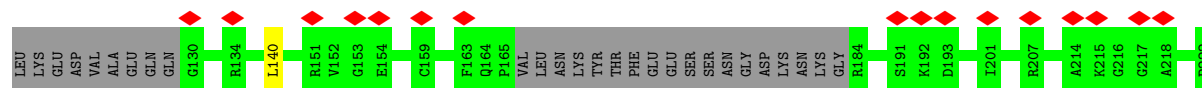
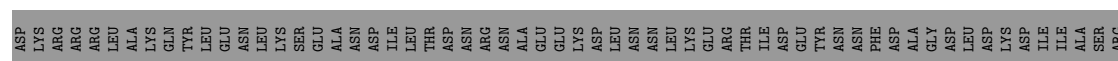


- Molecule 38: Snu13

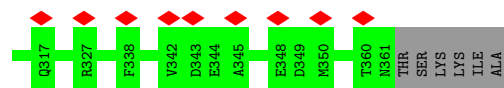
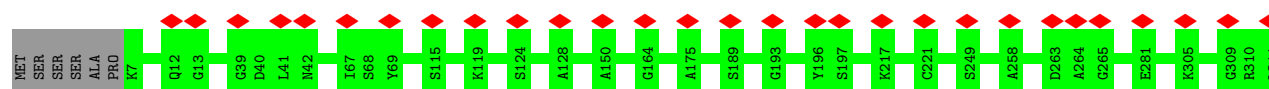




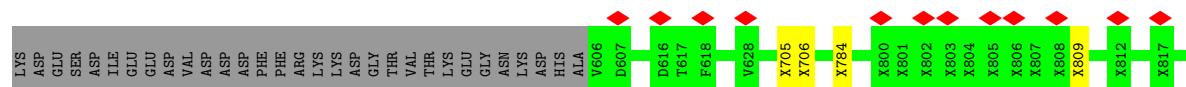
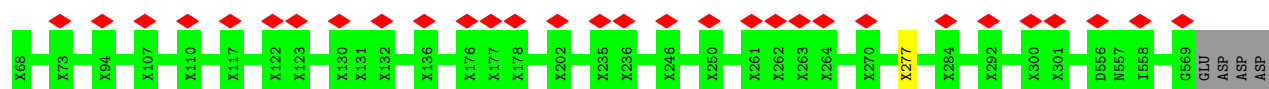
• Molecule 39: Ribosomal RNA-processing protein 9

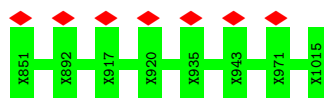


• Molecule 40: RNA 3'-terminal phosphate cyclase-like protein

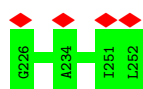
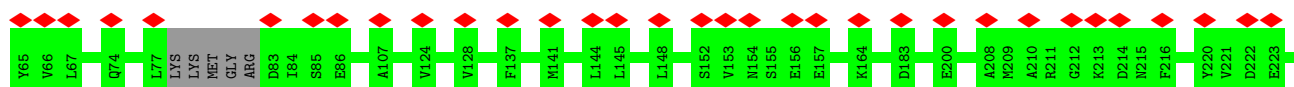
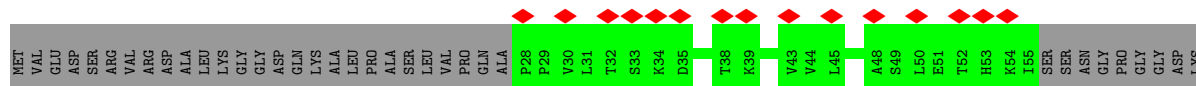
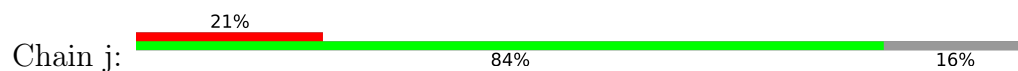


• Molecule 41: Bms1, Ribosome biogenesis protein BMS1, Bms1

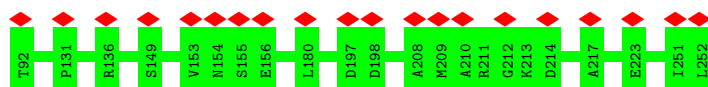
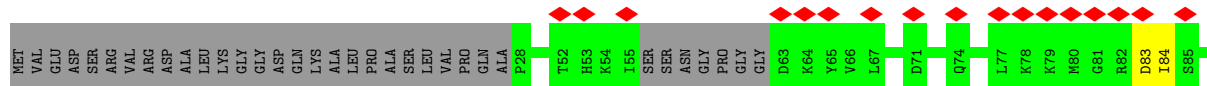
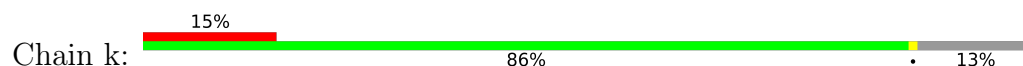




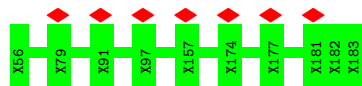
- Molecule 42: Ribosomal RNA small subunit methyltransferase NEP1



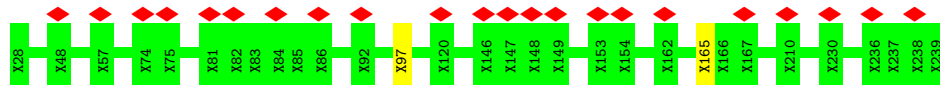
- Molecule 42: Ribosomal RNA small subunit methyltransferase NEP1



- Molecule 43: Utp24

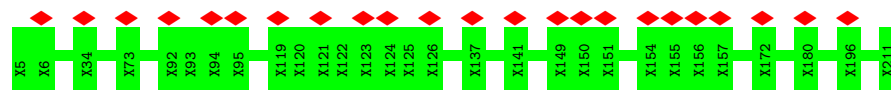


- Molecule 44: Imp4

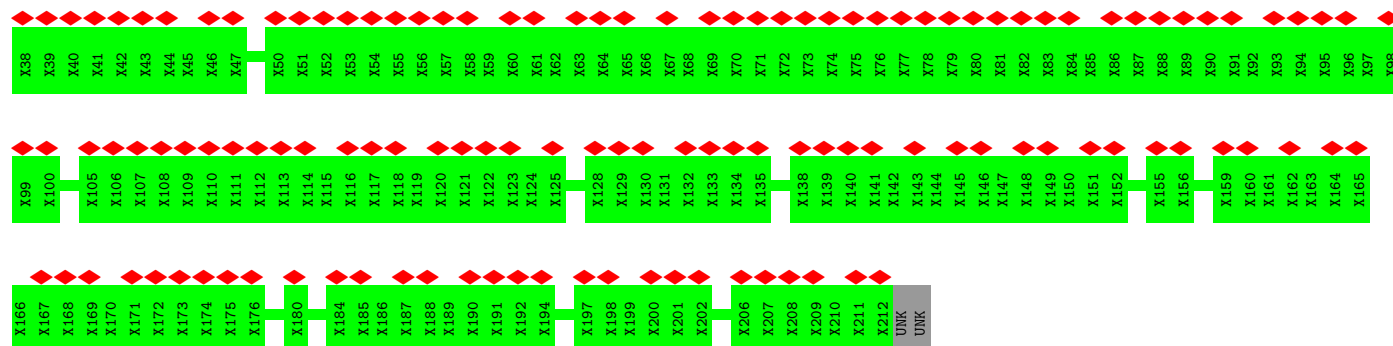


- Molecule 45: Utp30

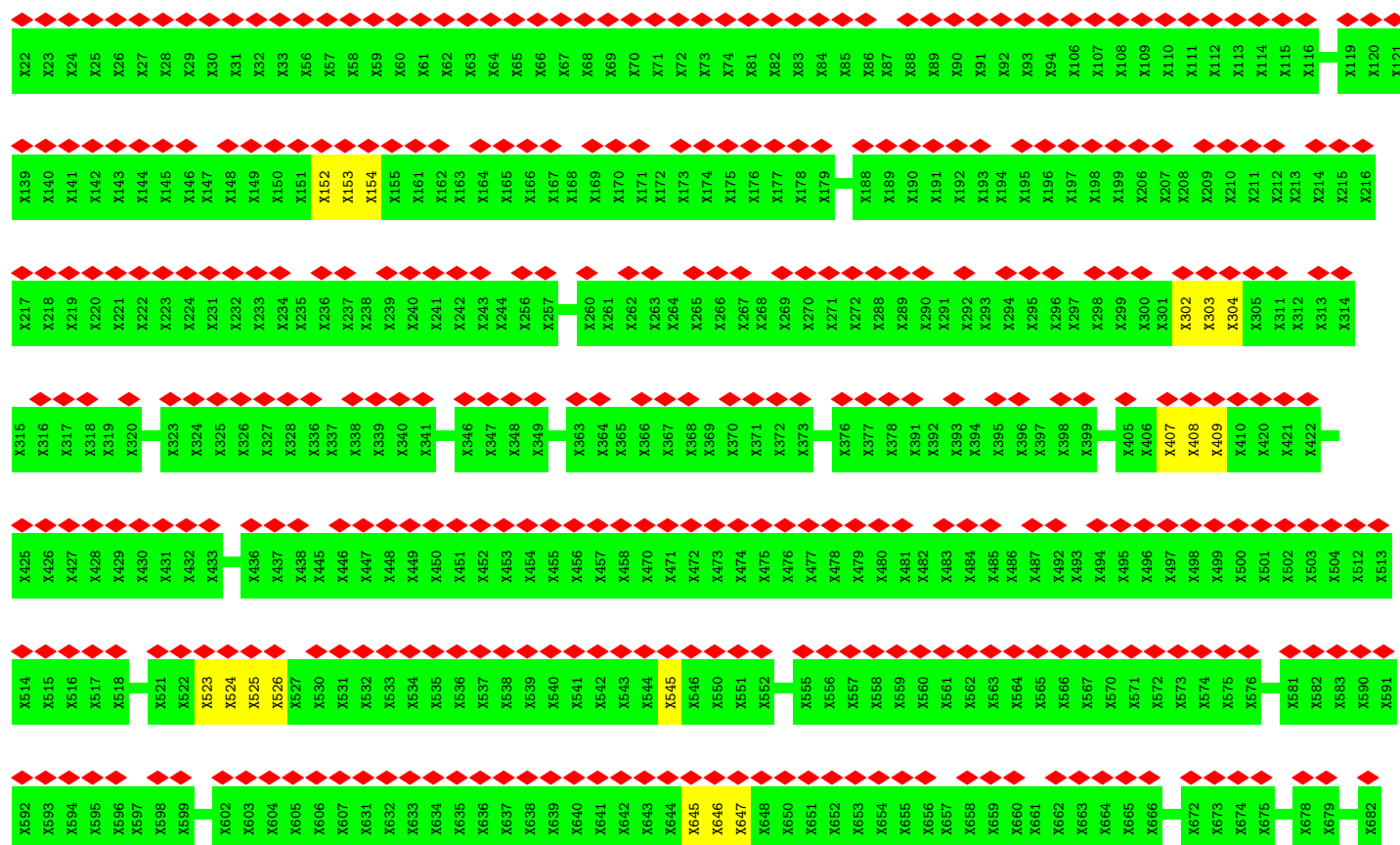
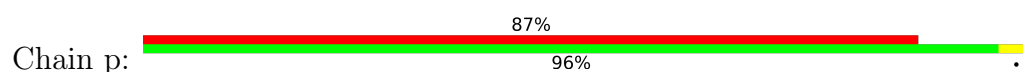


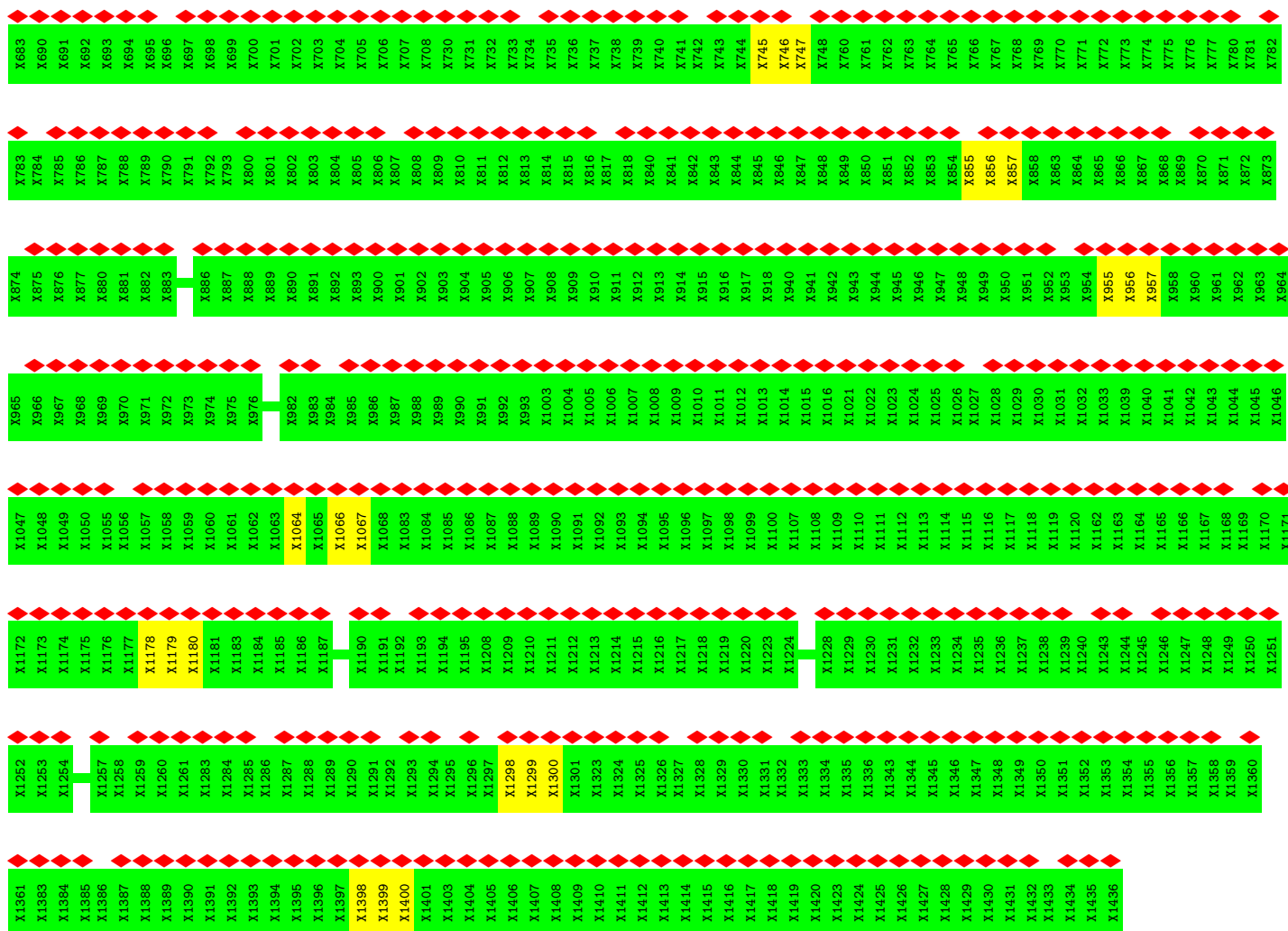


• Molecule 46: Unassigned KH domain

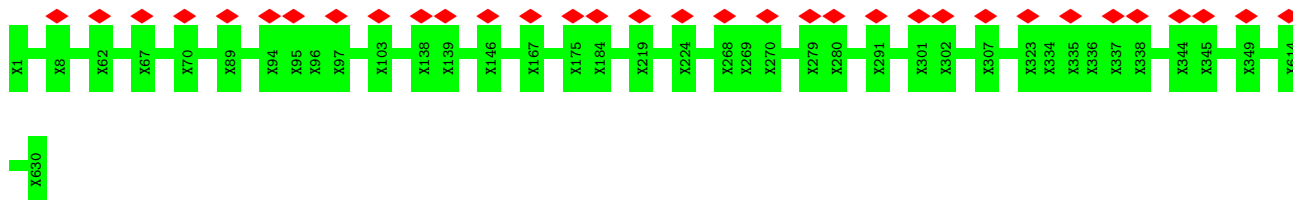


• Molecule 47: Utp20

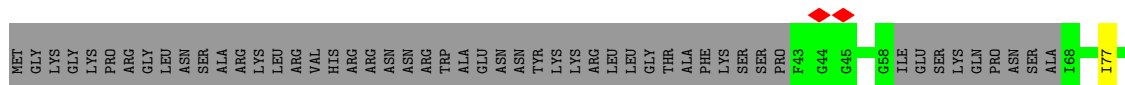




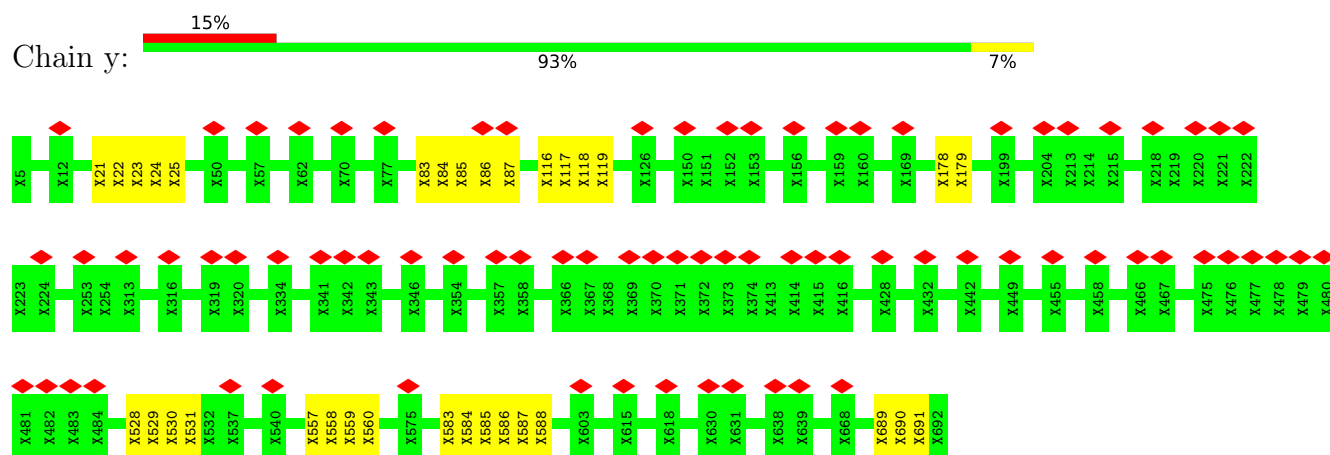
• Molecule 48: Repeat protein 2



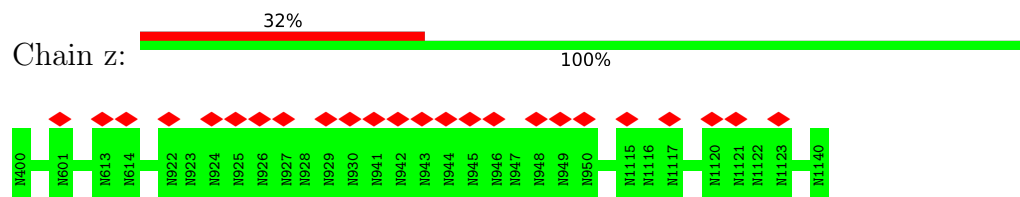
• Molecule 49: 40S ribosomal protein S23-A



- Molecule 52: Unassigned protein helices



- Molecule 53: Unassigned RNA helices



4 Experimental information

| Property | Value | Source |
|--------------------------------------|---|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, C1 | Depositor |
| Number of particles used | 33813 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 1.56 | Depositor |
| Minimum defocus (nm) | 600 | Depositor |
| Maximum defocus (nm) | 2600 | Depositor |
| Magnification | 22500 | Depositor |
| Image detector | GATAN K2 SUMMIT (4k x 4k) | Depositor |
| Maximum map value | 0.086 | Depositor |
| Minimum map value | -0.043 | Depositor |
| Average map value | 0.000 | Depositor |
| Map value standard deviation | 0.003 | Depositor |
| Recommended contour level | 0.018 | Depositor |
| Map size (Å) | 503.50003, 503.50003, 503.50003 | wwPDB |
| Map dimensions | 380, 380, 380 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.325, 1.325, 1.325 | 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 | 0 | 1.11 | 0/268 | 1.42 | 5/417 (1.2%) |
| 2 | 1 | 1.25 | 39/12260 (0.3%) | 1.71 | 368/19055 (1.9%) |
| 3 | 2 | 1.66 | 26/2443 (1.1%) | 1.69 | 73/3787 (1.9%) |
| 4 | 3 | 0.57 | 0/1061 | 0.81 | 1/1472 (0.1%) |
| 5 | 5 | 0.63 | 0/1182 | 0.92 | 0/1638 |
| 6 | 6 | 0.70 | 2/998 (0.2%) | 1.22 | 7/1388 (0.5%) |
| 7 | 7 | 0.51 | 0/922 | 0.85 | 0/1285 |
| 8 | 8 | 0.65 | 0/847 | 0.93 | 0/1173 |
| 9 | 9 | 0.56 | 0/914 | 0.82 | 0/1272 |
| 12 | C | 0.50 | 0/565 | 0.77 | 0/784 |
| 13 | D | 0.30 | 0/720 | 0.62 | 0/1001 |
| 14 | E | 0.34 | 0/623 | 0.63 | 0/864 |
| 15 | F | 0.38 | 0/443 | 0.73 | 0/615 |
| 16 | G | 0.46 | 0/305 | 0.80 | 0/423 |
| 27 | T | 0.51 | 0/3055 | 0.69 | 0/4243 |
| 38 | e | 0.25 | 0/605 | 0.56 | 0/843 |
| 38 | f | 0.26 | 0/565 | 0.57 | 0/787 |
| 39 | g | 0.41 | 0/1793 | 0.64 | 2/2485 (0.1%) |
| 40 | h | 0.40 | 0/1741 | 0.59 | 0/2416 |
| 41 | i | 0.32 | 0/265 | 0.50 | 0/367 |
| 42 | j | 0.36 | 0/1044 | 0.62 | 0/1452 |
| 42 | k | 0.39 | 0/1079 | 0.57 | 0/1502 |
| 49 | r | 0.37 | 0/399 | 0.58 | 0/549 |
| All | All | 0.95 | 67/34097 (0.2%) | 1.28 | 456/49818 (0.9%) |

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 | 2 | 0 | 1 |
| 6 | 6 | 0 | 3 |

Continued on next page...

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| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 9 | 9 | 0 | 3 |
| 12 | C | 0 | 1 |
| 15 | F | 0 | 2 |
| 16 | G | 0 | 1 |
| 17 | H | 0 | 4 |
| 18 | I | 0 | 11 |
| 19 | J | 0 | 2 |
| 19 | K | 0 | 3 |
| 20 | M | 0 | 3 |
| 21 | N | 0 | 4 |
| 22 | O | 0 | 12 |
| 24 | Q | 0 | 4 |
| 26 | S | 0 | 4 |
| 27 | T | 0 | 2 |
| 28 | U | 0 | 1 |
| 30 | W | 0 | 10 |
| 31 | X | 0 | 2 |
| 33 | Z | 0 | 2 |
| 34 | a | 0 | 6 |
| 35 | b | 0 | 1 |
| 36 | c | 0 | 3 |
| 37 | d | 0 | 3 |
| 39 | g | 0 | 2 |
| 41 | i | 0 | 5 |
| 44 | m | 0 | 2 |
| 47 | p | 0 | 38 |
| 50 | s | 0 | 9 |
| 50 | t | 0 | 11 |
| 50 | u | 0 | 1 |
| 51 | v | 0 | 13 |
| 52 | y | 0 | 33 |
| All | All | 0 | 202 |

The worst 5 of 67 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|--------|--------|-------------|----------|
| 3 | 2 | 308 | U | O3'-P | -63.84 | 0.84 | 1.61 |
| 2 | 1 | 1615 | C | O3'-P | -41.94 | 1.10 | 1.61 |
| 6 | 6 | 145 | ASP | C-N | -12.45 | 1.05 | 1.34 |
| 2 | 1 | 337 | G | C2-N2 | 10.63 | 1.45 | 1.34 |
| 3 | 2 | 118 | A | C1'-N9 | -10.57 | 1.32 | 1.46 |

The worst 5 of 456 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|------------|--------|-------------|----------|
| 2 | 1 | 1615 | C | OP2-P-O3' | -30.61 | 37.85 | 105.20 |
| 6 | 6 | 145 | ASP | O-C-N | -22.20 | 87.17 | 122.70 |
| 3 | 2 | 118 | A | O4'-C1'-N9 | -21.15 | 91.28 | 108.20 |
| 2 | 1 | 1615 | C | OP1-P-O3' | 17.13 | 142.90 | 105.20 |
| 2 | 1 | 1615 | C | O3'-P-O5' | -16.35 | 72.93 | 104.00 |

There are no chirality outliers.

5 of 202 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|-----------|
| 3 | 2 | 118 | A | Sidechain |
| 6 | 6 | 145 | ASP | Mainchain |
| 6 | 6 | 44 | ASN | Peptide |
| 6 | 6 | 99 | MET | Peptide |
| 9 | 9 | 88 | GLU | 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 | |
|-----|-------|---------------|-----------|----------|----------|-------------|----|
| 4 | 3 | 212/236 (90%) | 180 (85%) | 20 (9%) | 12 (6%) | 1 | 20 |
| 5 | 5 | 235/261 (90%) | 199 (85%) | 19 (8%) | 17 (7%) | 1 | 16 |
| 6 | 6 | 198/225 (88%) | 148 (75%) | 36 (18%) | 14 (7%) | 1 | 16 |
| 7 | 7 | 184/190 (97%) | 143 (78%) | 23 (12%) | 18 (10%) | 0 | 10 |
| 8 | 8 | 169/200 (84%) | 150 (89%) | 14 (8%) | 5 (3%) | 4 | 31 |
| 9 | 9 | 183/197 (93%) | 152 (83%) | 17 (9%) | 14 (8%) | 1 | 14 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-----------------|------------|----------|----------|-------------|-----|
| 12 | C | 113/143 (79%) | 107 (95%) | 6 (5%) | 0 | 100 | 100 |
| 13 | D | 144/156 (92%) | 125 (87%) | 19 (13%) | 0 | 100 | 100 |
| 14 | E | 125/130 (96%) | 113 (90%) | 11 (9%) | 1 (1%) | 19 | 60 |
| 15 | F | 88/135 (65%) | 72 (82%) | 13 (15%) | 3 (3%) | 3 | 29 |
| 16 | G | 60/67 (90%) | 53 (88%) | 7 (12%) | 0 | 100 | 100 |
| 27 | T | 613/781 (78%) | 565 (92%) | 48 (8%) | 0 | 100 | 100 |
| 38 | e | 120/126 (95%) | 118 (98%) | 2 (2%) | 0 | 100 | 100 |
| 38 | f | 112/126 (89%) | 110 (98%) | 2 (2%) | 0 | 100 | 100 |
| 39 | g | 353/573 (62%) | 337 (96%) | 15 (4%) | 1 (0%) | 41 | 76 |
| 40 | h | 353/367 (96%) | 340 (96%) | 13 (4%) | 0 | 100 | 100 |
| 41 | i | 50/511 (10%) | 48 (96%) | 2 (4%) | 0 | 100 | 100 |
| 42 | j | 205/252 (81%) | 190 (93%) | 15 (7%) | 0 | 100 | 100 |
| 42 | k | 214/252 (85%) | 201 (94%) | 11 (5%) | 2 (1%) | 17 | 56 |
| 49 | r | 76/145 (52%) | 66 (87%) | 9 (12%) | 1 (1%) | 12 | 48 |
| All | All | 3807/5073 (75%) | 3417 (90%) | 302 (8%) | 88 (2%) | 9 | 36 |

5 of 88 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 4 | 3 | 153 | VAL |
| 4 | 3 | 173 | PRO |
| 4 | 3 | 174 | LYS |
| 5 | 5 | 24 | SER |
| 5 | 5 | 95 | THR |

5.3.2 Protein sidechains ⓘ

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA ⓘ

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|----------------|-------------------|-----------------|
| 1 | 0 | 10/364 (2%) | 1 (10%) | 0 |
| 2 | 1 | 496/1800 (27%) | 119 (23%) | 22 (4%) |
| 3 | 2 | 95/126 (75%) | 20 (21%) | 3 (3%) |
| All | All | 601/2290 (26%) | 140 (23%) | 25 (4%) |

5 of 140 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | 0 | 287 | G |
| 2 | 1 | 57 | G |
| 2 | 1 | 60 | U |
| 2 | 1 | 67 | A |
| 2 | 1 | 68 | A |

5 of 25 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 2 | 1 | 512 | A |
| 2 | 1 | 1572 | G |
| 3 | 2 | 318 | U |
| 2 | 1 | 1535 | U |
| 2 | 1 | 1573 | 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 |
|-----|-------|------------------|
| 47 | p | 58 |

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| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 1 | 0 | 45 |
| 51 | v | 31 |
| 22 | O | 27 |
| 48 | q | 23 |
| 25 | R | 20 |
| 52 | y | 18 |
| 24 | Q | 18 |
| 41 | i | 16 |
| 17 | H | 16 |
| 23 | P | 15 |
| 26 | S | 13 |
| 21 | N | 11 |
| 18 | I | 11 |
| 29 | V | 11 |
| 20 | M | 11 |
| 45 | n | 10 |
| 11 | B | 9 |
| 3 | 2 | 8 |
| 2 | 1 | 8 |
| 53 | z | 7 |
| 34 | a | 7 |
| 44 | m | 7 |
| 31 | X | 7 |
| 32 | Y | 7 |
| 50 | t | 6 |
| 35 | b | 6 |
| 30 | W | 6 |
| 50 | s | 6 |
| 19 | K | 5 |
| 10 | A | 5 |
| 19 | J | 5 |
| 28 | U | 5 |
| 50 | u | 4 |
| 27 | T | 3 |
| 43 | l | 3 |
| 6 | 6 | 3 |
| 46 | o | 2 |
| 37 | d | 2 |
| 36 | c | 1 |

The worst 5 of 476 chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1 | y | 204:UNK | C | 213:UNK | N | 135.82 |
| 1 | y | 180:UNK | C | 185:UNK | N | 133.64 |
| 1 | y | 618:UNK | C | 625:UNK | N | 128.71 |
| 1 | z | 950:N | O3' | 1110:N | P | 127.24 |
| 1 | y | 144:UNK | C | 150:UNK | N | 117.41 |

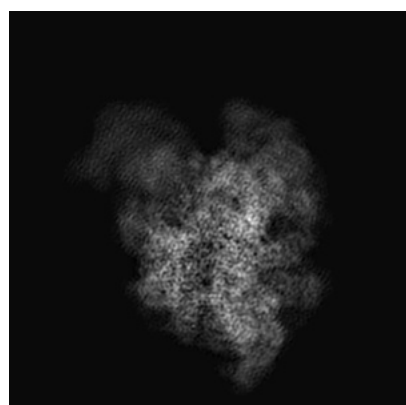
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8473. These allow visual inspection of the internal detail of the map and identification of artifacts.

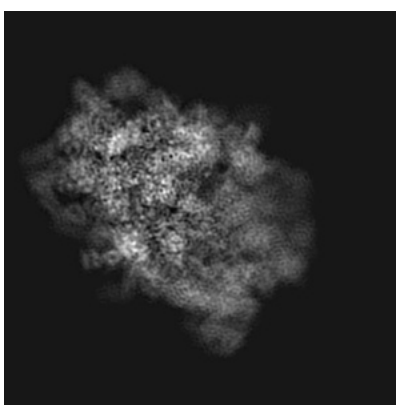
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

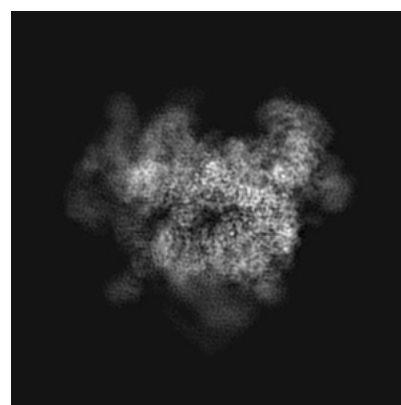
6.1.1 Primary map



X



Y

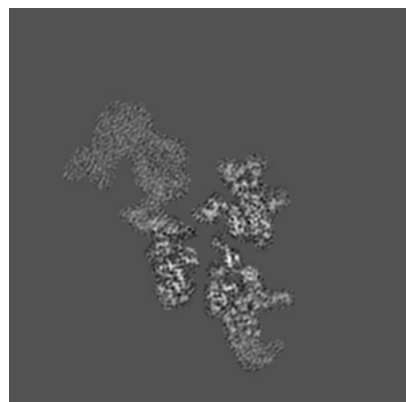


Z

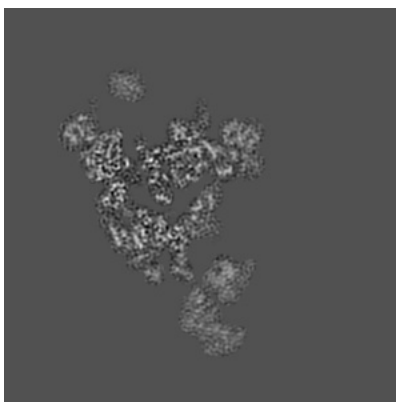
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

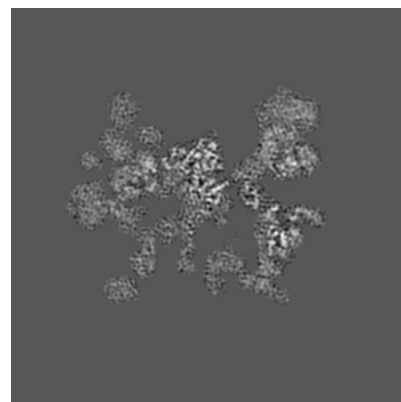
6.2.1 Primary map



X Index: 190



Y Index: 190

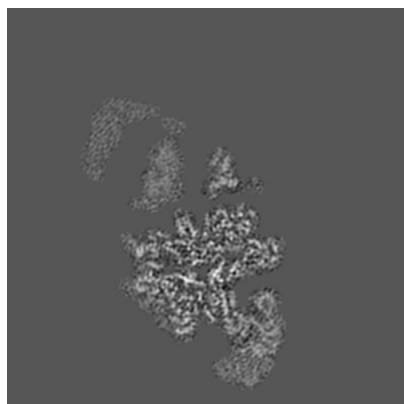


Z Index: 190

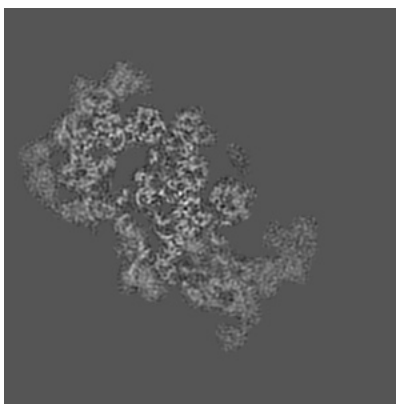
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

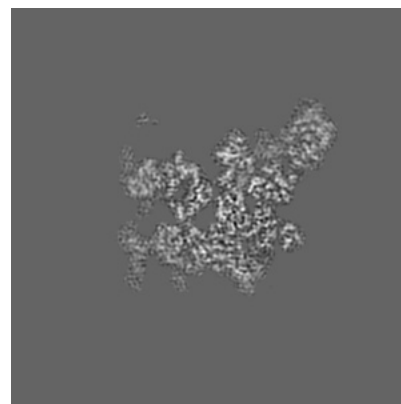
6.3.1 Primary map



X Index: 217



Y Index: 219



Z Index: 151

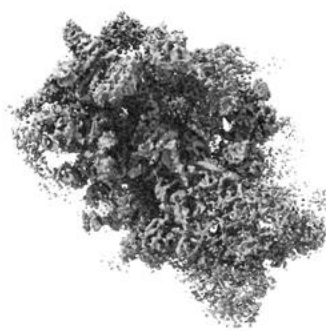
The images above show the largest variance slices of the map in three orthogonal directions.

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

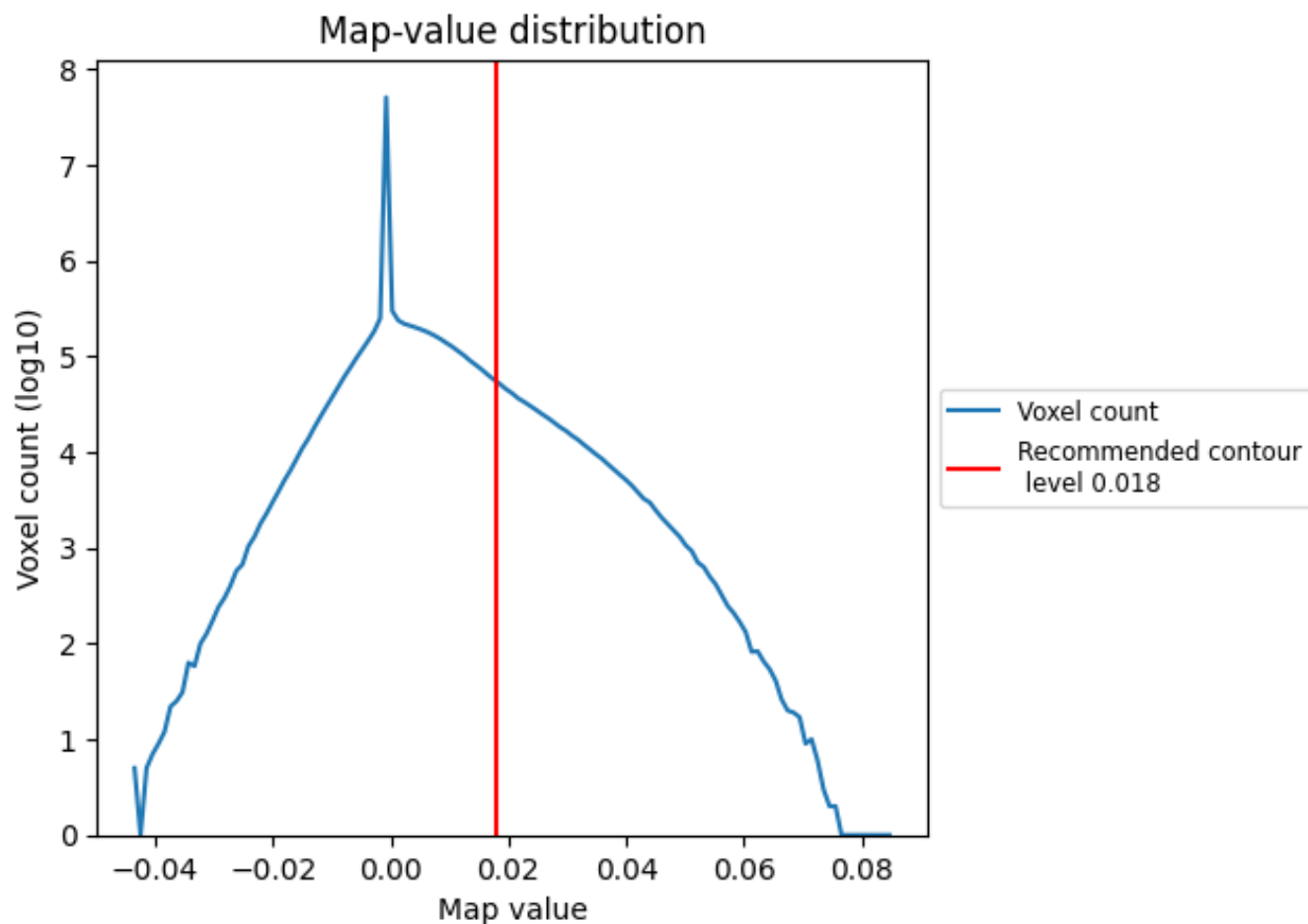
6.5 Mask visualisation

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

7 Map analysis [i](#)

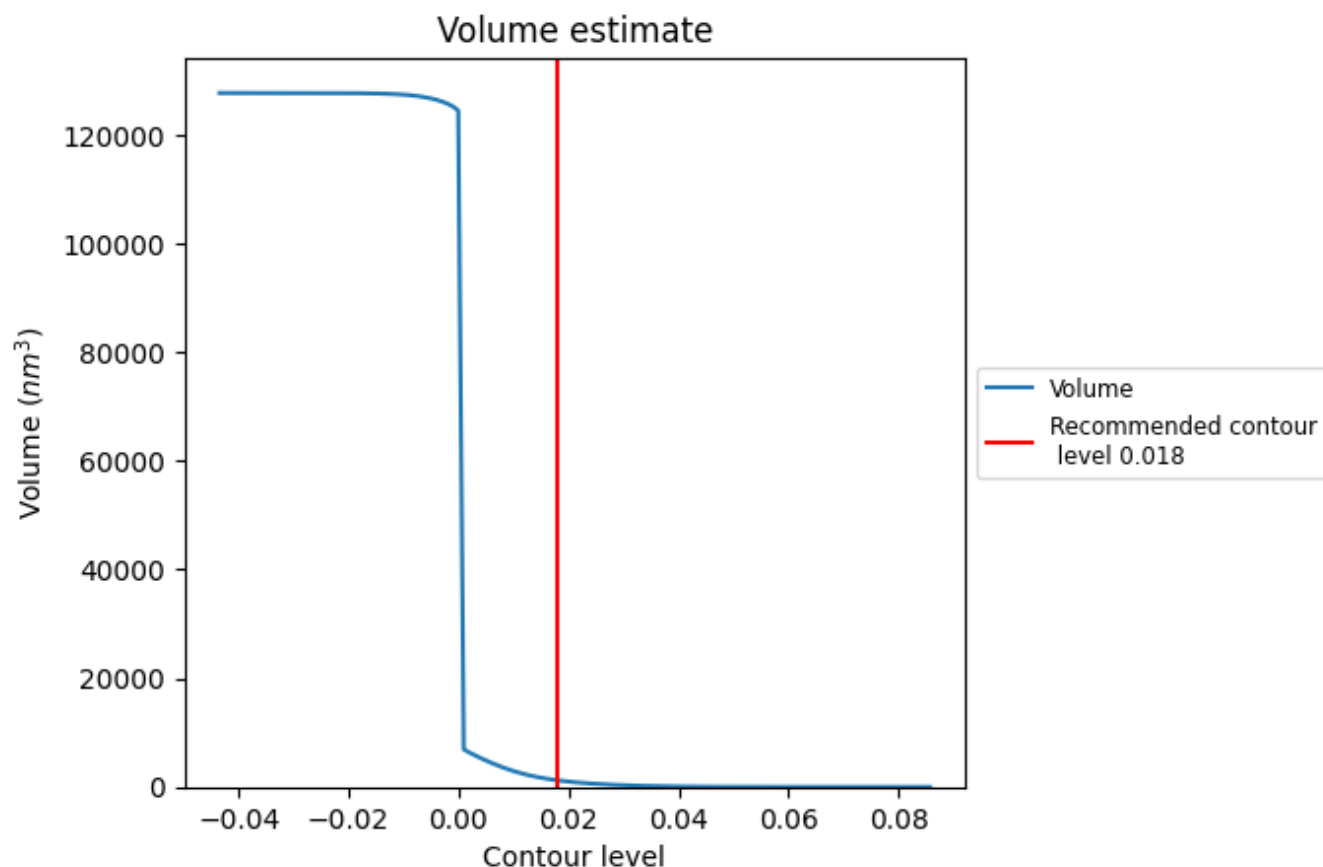
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

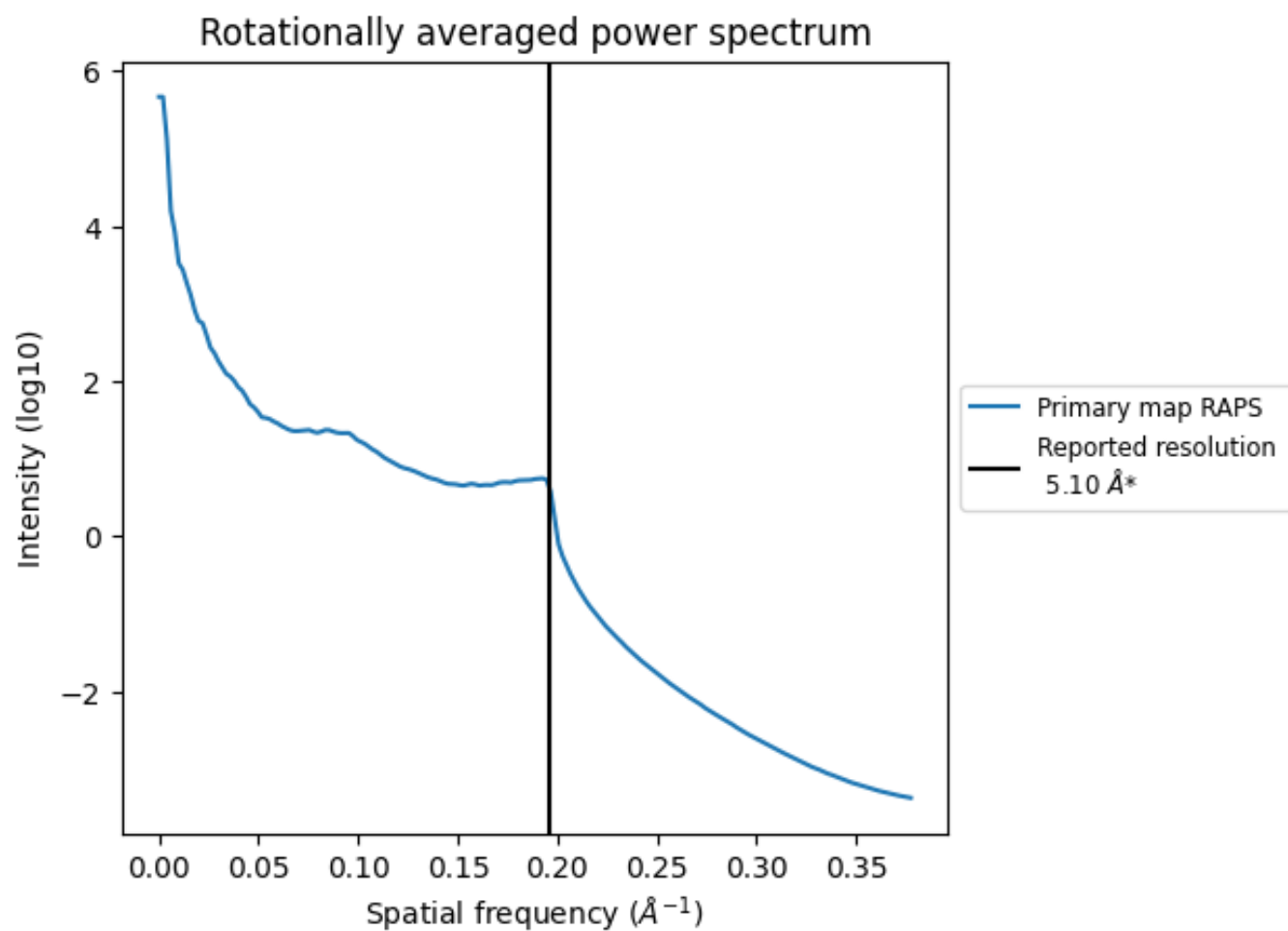
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1219 nm³; this corresponds to an approximate mass of 1101 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 ⓘ

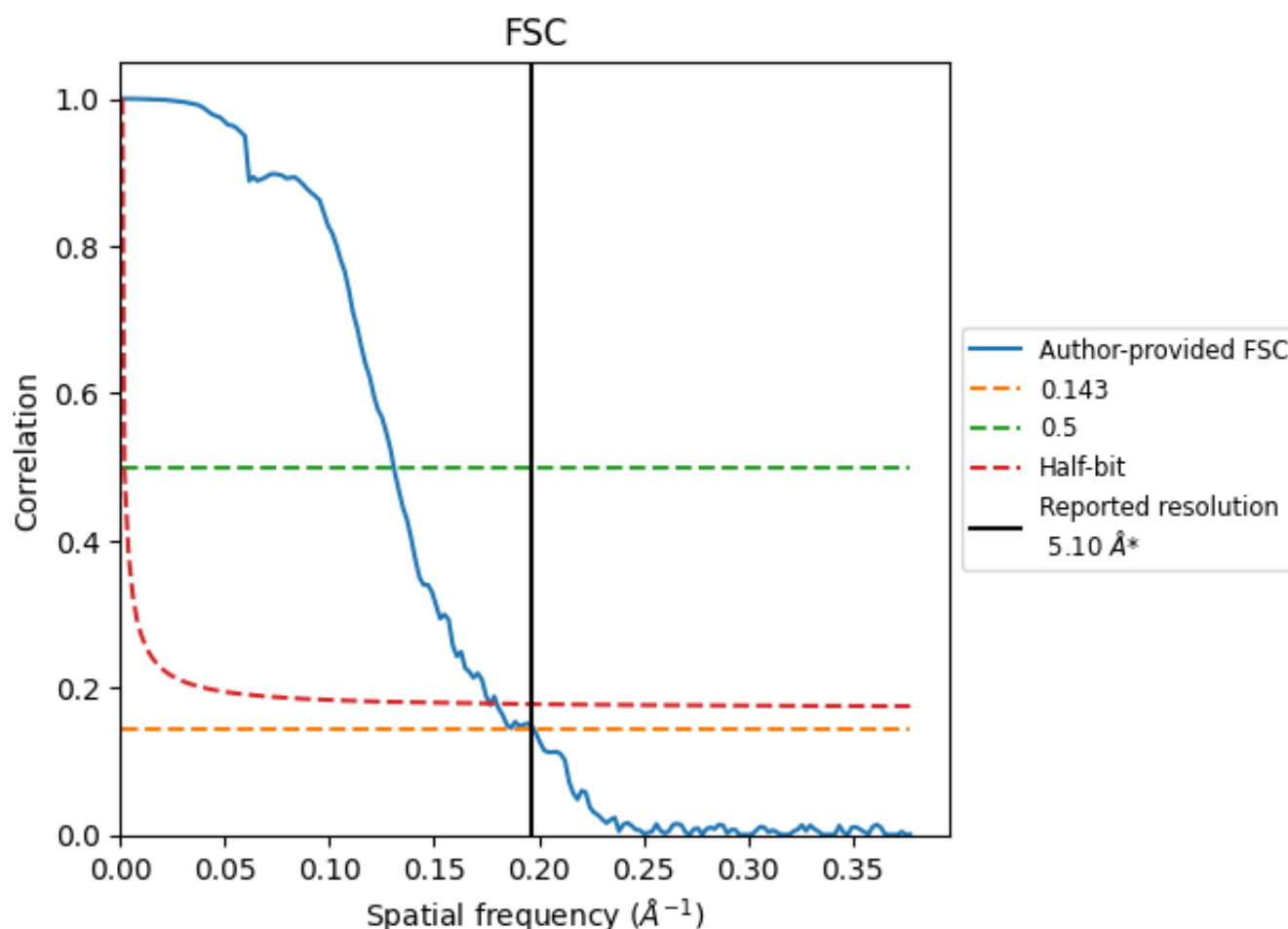


*Reported resolution corresponds to spatial frequency of 0.196 Å⁻¹

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 0.196 Å⁻¹

8.2 Resolution estimates [i](#)

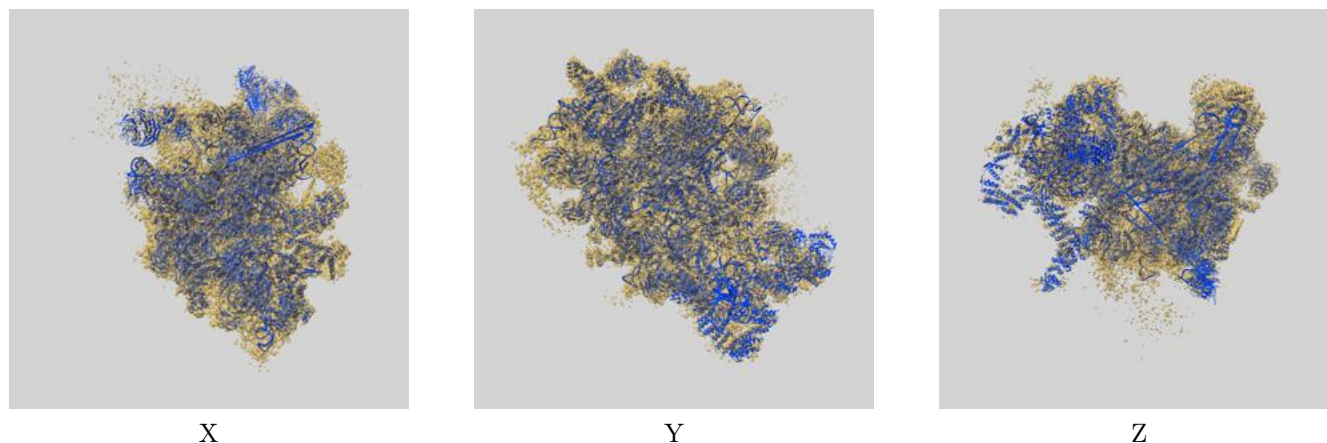
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---------------------------|------------------------------------|------|----------|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 5.10 | - | - |
| Author-provided FSC curve | 5.06 | 7.66 | 5.67 |
| Unmasked-calculated* | - | - | - |

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

9 Map-model fit [i](#)

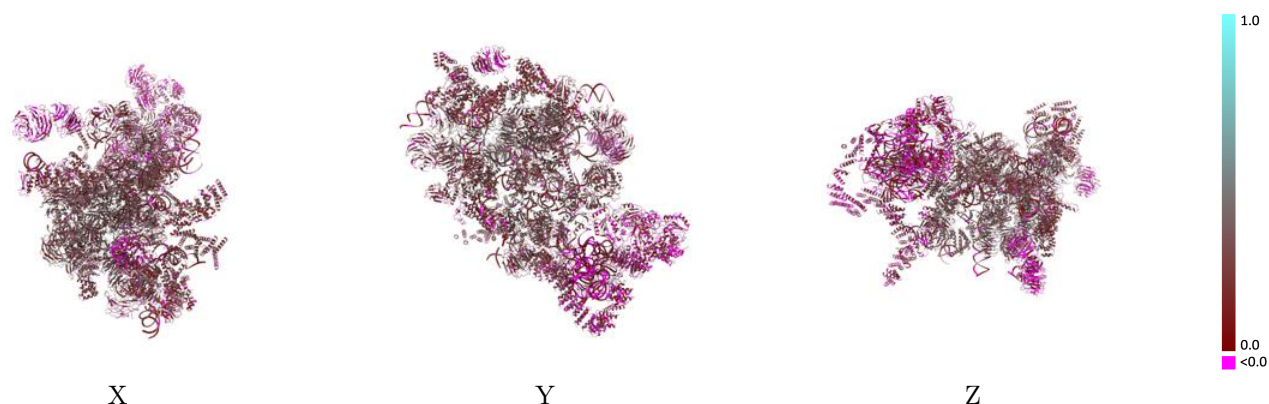
This section contains information regarding the fit between EMDB map EMD-8473 and PDB model 5TZS. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



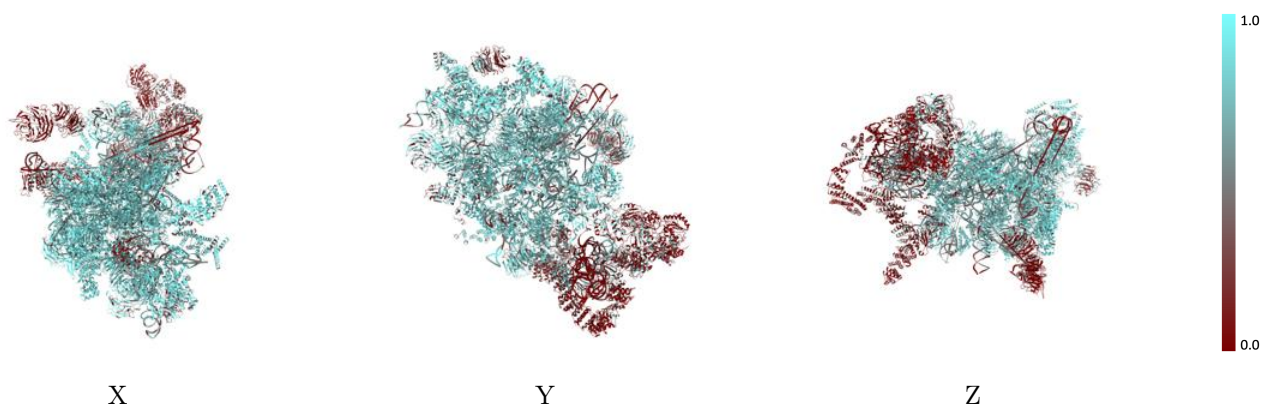
The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



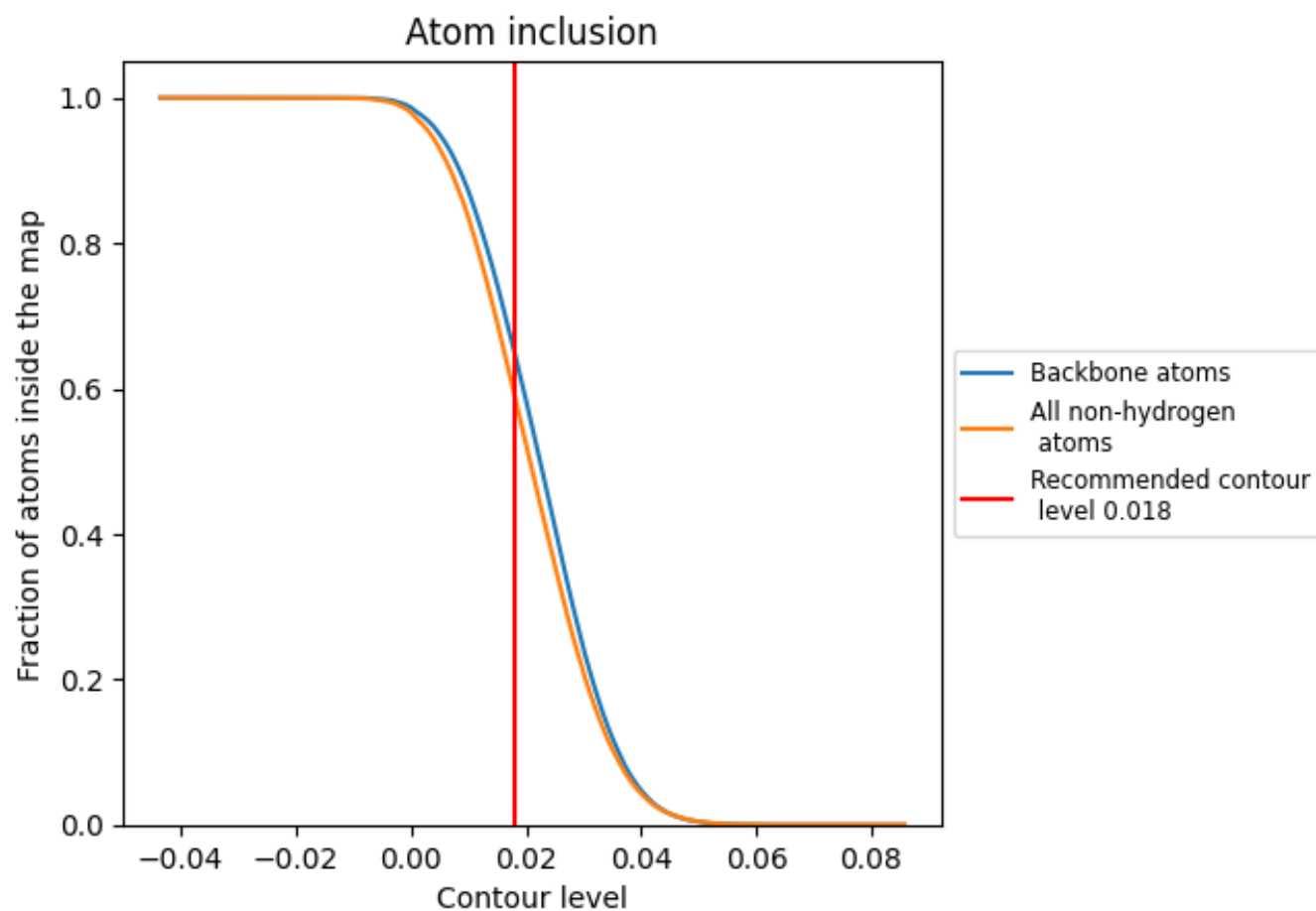
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.018).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 59% 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 (0.018) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| All |  0.5913 |  0.2220 |
| 0 |  0.6070 |  0.2240 |
| 1 |  0.4535 |  0.1320 |
| 2 |  0.7484 |  0.2460 |
| 3 |  0.1552 |  0.0920 |
| 5 |  0.4785 |  0.2120 |
| 6 |  0.7840 |  0.3030 |
| 7 |  0.0628 |  0.1230 |
| 8 |  0.2992 |  0.1450 |
| 9 |  0.6984 |  0.2580 |
| A |  0.7051 |  0.2770 |
| B |  0.4344 |  0.1860 |
| C |  0.8675 |  0.3440 |
| D |  0.2524 |  0.0990 |
| E |  0.2212 |  0.2220 |
| F |  0.6014 |  0.2400 |
| G |  0.8170 |  0.3800 |
| H |  0.5254 |  0.1500 |
| I |  0.7205 |  0.2200 |
| J |  0.8112 |  0.2700 |
| K |  0.7600 |  0.2390 |
| M |  0.8220 |  0.3410 |
| N |  0.7084 |  0.2560 |
| O |  0.8240 |  0.3370 |
| P |  0.8320 |  0.2500 |
| Q |  0.7259 |  0.2480 |
| R |  0.2292 |  0.0620 |
| S |  0.7891 |  0.3220 |
| T |  0.8464 |  0.3420 |
| U |  0.7639 |  0.2990 |
| V |  0.2935 |  0.1150 |
| W |  0.8269 |  0.2800 |
| X |  0.2849 |  0.1060 |
| Y |  0.0924 |  0.0530 |
| Z |  0.8275 |  0.3300 |



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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| a |  0.7591 |  0.2500 |
| b |  0.7178 |  0.2690 |
| c |  0.8281 |  0.3400 |
| d |  0.6758 |  0.3030 |
| e |  0.7921 |  0.3070 |
| f |  0.7827 |  0.2920 |
| g |  0.7399 |  0.2740 |
| h |  0.7830 |  0.3100 |
| i |  0.7836 |  0.3150 |
| j |  0.6714 |  0.2490 |
| k |  0.7151 |  0.2920 |
| l |  0.8548 |  0.3440 |
| m |  0.7832 |  0.3260 |
| n |  0.7661 |  0.2590 |
| o |  0.3089 |  0.1520 |
| p |  0.1710 |  0.1420 |
| q |  0.8022 |  0.2450 |
| r |  0.8010 |  0.3590 |
| s |  0.7180 |  0.2400 |
| t |  0.9126 |  0.3770 |
| u |  0.8105 |  0.3320 |
| v |  0.7584 |  0.2380 |
| y |  0.7499 |  0.2570 |
| z |  0.4704 |  0.2040 |