# wwPDB EM Validation Summary Report (i)

Nov 19, 2022 – 02:10 pm GMT

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|---|---|---|
| PDB ID | : | 5MC6 |
| EMDB ID | : | EMD-3461 |
| Title | : | Cryo-EM structure of a native ribosome-Ski2-Ski3-Ski8 complex from S. cerevisiae |
| Authors | : | Schmidt, C.; Kowalinski, E.; Shanmuganathan, V.; Defenouillere, Q.; Braunger, K.; Heuer, A.; Pech, M.; Namane, A.; Berninghausen, O.; Fromont-Racine, M.; Jacquier, A.; Conti, E.; Becker, T.; Beckmann, R. |
| Deposited on | : | 2016-11-09 |
| Resolution | : | 3.80 Å(reported) |

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

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

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

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

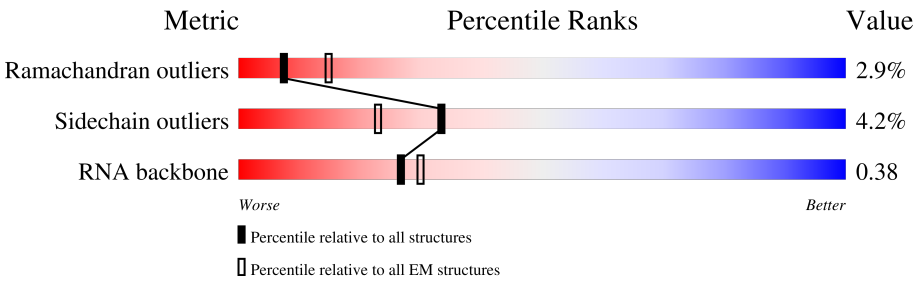
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev43 |
| Mogul | : | 1.8.4, CSD as541be (2020) |
| MolProbity | : | 4.02b-467 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| MapQ | : | 1.9.9 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.31.2 |

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.80 Å.

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




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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | 2 | 1800 | 12% 56% 41% • • |
| 2 | A | 240 | 27% 89% • 7% |
| 3 | B | 225 | 39% 83% 8% 8% |
| 4 | C | 105 | 27% 81% 10% 9% |
| 5 | D | 143 | 64% 75% 10% 15% |
| 6 | E | 142 | 41% 80% 7% 13% |
| 7 | F | 143 | 22% 92% 6% • • |
| 8 | G | 136 | 20% 61% 5% • 33% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 9 | H | 146 | 40% 89% 10% |
| 10 | I | 144 | 42% 85% 13% |
| 11 | J | 121 | 28% 83% 6% 12% |
| 12 | K | 108 | 29% 57% 7% 35% |
| 13 | L | 67 | 61% 91% 6% |
| 14 | M | 56 | 12% 89% 5% 5% |
| 15 | N | 152 | 24% 31% 66% |
| 16 | O | 319 | 38% 95% |
| 17 | P | 252 | 21% 76% 5% 18% |
| 18 | Q | 255 | 41% 76% 7% 16% |
| 19 | R | 254 | 15% 83% 13% |
| 20 | S | 261 | 44% 95% 5% |
| 21 | T | 236 | 43% 89% 6% |
| 22 | U | 190 | 61% 89% 7% |
| 23 | V | 200 | 37% 74% 16% 6% |
| 24 | W | 197 | 32% 87% 10% |
| 25 | X | 156 | 38% 93% 6% |
| 26 | Y | 151 | 34% 93% 6% |
| 27 | Z | 137 | 32% 85% 7% 7% |
| 28 | a | 87 | 30% 94% 5% |
| 29 | b | 130 | 23% 95% |
| 30 | c | 145 | 30% 96% |
| 31 | d | 135 | 42% 87% 9% |
| 32 | e | 119 | 35% 68% 13% 18% |
| 33 | f | 82 | 40% 93% 6% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 34 | g | 63 | 37% 92% 5% |
| 35 | l | 34 | 62% 38% 62% |
| 36 | m | 76 | 14% 55% 43% |
| 37 | n | 77 | 10% 60% 40% |
| 38 | h | 1287 | 76% 83% 13% |
| 39 | i | 1432 | 87% 92% 5% |
| 40 | j | 397 | 88% 95% |
| 40 | k | 397 | 70% 94% |
| 41 | AA | 256 | 24% 86% 5% 9% |
| 42 | AB | 137 | 28% 93% 7% |
| 43 | AC | 100 | 18% 90% 9% |
| 44 | AD | 191 | 25% 95% 5% |
| 45 | AE | 155 | 32% 60% 37% |
| 46 | AF | 88 | 8% 92% 7% |
| 47 | AG | 174 | 16% 90% 6% |
| 48 | AH | 142 | 8% 80% 6% 15% |
| 49 | AI | 78 | 28% 96% |
| 50 | AJ | 199 | 19% 90% 7% |
| 51 | AK | 127 | 8% 96% |
| 52 | AL | 51 | 10% 90% 8% |
| 53 | AM | 138 | 17% 92% 7% |
| 54 | AN | 136 | 25% 93% 6% |
| 55 | AO | 128 | 7% 37% 59% |
| 56 | AP | 106 | 13% 93% 6% |
| 57 | AQ | 204 | 10% 93% 6% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 58 | AR | 149 | 11% 90% 7% |
| 59 | AS | 25 | 56% 92% 8% |
| 60 | AT | 92 | 24% 96% |
| 61 | AU | 199 | 13% 95% |
| 62 | AV | 59 | 27% 97% |
| 63 | AW | 254 | 15% 96% |
| 64 | AX | 184 | 12% 93% 6% |
| 65 | AY | 105 | 29% 89% 8% |
| 66 | AZ | 210 | 91% 100% |
| 67 | BA | 387 | 15% 93% 7% |
| 68 | BB | 186 | 11% 95% 5% |
| 69 | BC | 113 | 19% 88% 8% |
| 70 | BD | 221 | 25% 89% 10% |
| 71 | BE | 362 | 12% 93% 7% |
| 72 | BF | 189 | 21% 95% |
| 73 | BG | 130 | 12% 94% |
| 74 | BH | 172 | 19% 95% 5% |
| 75 | BI | 297 | 19% 94% 5% |
| 76 | BJ | 160 | 19% 91% 8% |
| 77 | BK | 107 | 12% 94% 5% |
| 78 | BL | 121 | 18% 79% 17% |
| 79 | BM | 176 | 23% 83% 5% 11% |
| 80 | BN | 121 | 12% 89% 7% |
| 81 | BO | 244 | 9% 87% 9% |
| 82 | BP | 120 | 12% 96% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 83 | BQ | 3396 | 60% 32% 7% |
| 84 | BR | 121 | 69% 30% |
| 85 | BS | 158 | 66% 33% |
| 86 | BT | 157 | 92% 89% 8% |

# 2 Entry composition (i)

There are 86 unique types of molecules in this entry. The entry contains 229285 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 18S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 1 | 2 | 1767 | 37645 | 16830 | 6656 | 12392 | 1767 | 0 | 0 |

- Molecule 2 is a protein called 40S ribosomal protein S3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 2 | A | 223 | 1734 | 1101 | 313 | 314 | 6 | 0 | 0 |

- Molecule 3 is a protein called 40S ribosomal protein S5.

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

- Molecule 4 is a protein called 40S ribosomal protein S10-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 4 | C | 96 | 813 | 527 | 133 | 151 | 2 | 0 | 0 |

- Molecule 5 is a protein called 40S ribosomal protein S12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 5 | D | 121 | 877 | 552 | 153 | 170 | 2 | 0 | 0 |

- Molecule 6 is a protein called 40S ribosomal protein S15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 6 | E | 124 | 977 | 622 | 182 | 166 | 7 | 0 | 0 |

- Molecule 7 is a protein called 40S ribosomal protein S16-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 7 | F | 141 | 1105 | 708 | 203 | 194 | 0 | 0 |

- Molecule 8 is a protein called 40S ribosomal protein S17-B.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 8 | G | 91 | 746 | 467 | 144 | 133 | 2 | 0 | 0 |

- Molecule 9 is a protein called 40S ribosomal protein S18-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 9 | H | 145 | 1192 | 743 | 237 | 210 | 2 | 0 | 0 |

- Molecule 10 is a protein called 40S ribosomal protein S19-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 10 | I | 143 | 1112 | 694 | 208 | 208 | 2 | 0 | 0 |

- Molecule 11 is a protein called 40S ribosomal protein S20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 11 | J | 107 | 855 | 539 | 156 | 159 | 1 | 0 | 0 |

- Molecule 12 is a protein called 40S ribosomal protein S25-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 12 | K | 70 | 563 | 360 | 104 | 99 | 0 | 0 |

- Molecule 13 is a protein called 40S ribosomal protein S28-B.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 13 | L | 63 | 497 | 306 | 99 | 91 | 1 | 0 | 0 |

- Molecule 14 is a protein called 40S ribosomal protein S29-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 14 | M | 53 | 442 | 274 | 92 | 72 | 4 | 0 | 0 |

- Molecule 15 is a protein called Ubiquitin-40S ribosomal protein S31.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 15 | N | 51 | 397 | 249 | 73 | 71 | 4 | 0 | 0 |

- Molecule 16 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 16 | O | 318 | 2436 | 1541 | 418 | 469 | 8 | 0 | 0 |

- Molecule 17 is a protein called 40S ribosomal protein S0-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 17 | P | 206 | 1577 | 1014 | 278 | 283 | 2 | 0 | 0 |

- Molecule 18 is a protein called 40S ribosomal protein S1-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 18 | Q | 214 | 1709 | 1084 | 310 | 311 | 4 | 0 | 0 |

- Molecule 19 is a protein called 40S ribosomal protein S2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 19 | R | 220 | 1671 | 1072 | 297 | 300 | 2 | 0 | 0 |

- Molecule 20 is a protein called 40S ribosomal protein S4-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 20 | S | 260 | 2068 | 1316 | 389 | 360 | 3 | 0 | 0 |

- Molecule 21 is a protein called 40S ribosomal protein S6-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 21 | T | 226 | 1799 | 1129 | 346 | 321 | 3 | 0 | 0 |

- Molecule 22 is a protein called 40S ribosomal protein S7-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 22 | U | 184 | 1481 | 951 | 265 | 265 | 0 | 0 |

- Molecule 23 is a protein called 40S ribosomal protein S8-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 23 | V | 188 | 1489 | 925 | 298 | 264 | 2 | 0 | 0 |

- Molecule 24 is a protein called 40S ribosomal protein S9-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 24 | W | 178 | 1434 | 905 | 276 | 252 | 1 | 0 | 0 |

- Molecule 25 is a protein called 40S ribosomal protein S11-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 25 | X | 155 | 1213 | 774 | 230 | 206 | 3 | 0 | 0 |

- Molecule 26 is a protein called 40S ribosomal protein S13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 26 | Y | 150 | 1192 | 759 | 224 | 207 | 2 | 0 | 0 |

- Molecule 27 is a protein called 40S ribosomal protein S14-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 27 | Z | 127 | 891 | 545 | 182 | 163 | 1 | 0 | 0 |

- Molecule 28 is a protein called 40S ribosomal protein S21-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 28 | a | 87 | 684 | 420 | 125 | 137 | 2 | 0 | 0 |

- Molecule 29 is a protein called 40S ribosomal protein S22-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 29 | b | 129 | 1021 | 650 | 188 | 180 | 3 | 0 | 0 |

- Molecule 30 is a protein called 40S ribosomal protein S23-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 30 | c | 144 | 1121 | 708 | 220 | 191 | 2 | 0 | 0 |

- Molecule 31 is a protein called 40S ribosomal protein S24-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 31 | d | 132 | 1060 | 669 | 206 | 185 | 0 | 0 |

- Molecule 32 is a protein called 40S ribosomal protein S26-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 32 | e | 97 | 769 | 475 | 160 | 129 | 5 | 0 | 0 |

- Molecule 33 is a protein called 40S ribosomal protein S27-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 33 | f | 81 | 610 | 382 | 110 | 113 | 5 | 0 | 0 |

- Molecule 34 is a protein called 40S ribosomal protein S30-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 34 | g | 60 | 473 | 297 | 98 | 77 | 1 | 0 | 0 |

- Molecule 35 is a RNA chain called mRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 35 | l | 34 | 692 | 311 | 84 | 263 | 34 | 0 | 0 |

- Molecule 36 is a RNA chain called A-site tRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 36 | m | 76 | 1611 | 721 | 281 | 534 | 75 | 0 | 0 |

- Molecule 37 is a RNA chain called P-site tRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 37 | n | 77 | 1644 | 731 | 290 | 546 | 77 | 0 | 0 |

- Molecule 38 is a protein called Antiviral helicase SKI2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 38 | h | 1121 | 8814 | 5643 | 1504 | 1625 | 42 | 0 | 0 |

- Molecule 39 is a protein called Superkiller protein 3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 39 | i | 1365 | 9827 | 6302 | 1663 | 1825 | 37 | 0 | 0 |

- Molecule 40 is a protein called Antiviral protein SKI8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 40 | j | 392 | 2933 | 1861 | 500 | 558 | 14 | 0 | 0 |
| 40 | k | 388 | 2919 | 1851 | 502 | 552 | 14 | 0 | 0 |

- Molecule 41 is a protein called 60S ribosomal protein L8-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 41 | AA | 233 | 1804 | 1151 | 323 | 327 | 3 | 0 | 0 |

- Molecule 42 is a protein called 60S ribosomal protein L23-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 42 | AB | 136 | 1003 | 628 | 189 | 179 | 7 | 0 | 0 |

- Molecule 43 is a protein called 60S ribosomal protein L36-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 43 | AC | 99 | 771 | 481 | 156 | 132 | 2 | 0 | 0 |

- Molecule 44 is a protein called 60S ribosomal protein L9-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 44 | AD | 191 | 1518 | 963 | 274 | 277 | 4 | 0 | 0 |

- Molecule 45 is a protein called 60S ribosomal protein L24-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 45 | AE | 98 | 699 | 443 | 137 | 118 | 1 | 0 | 0 |

- Molecule 46 is a protein called 60S ribosomal protein L37-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 46 | AF | 87 | 681 | 414 | 148 | 114 | 5 | 0 | 0 |

- Molecule 47 is a protein called 60S ribosomal protein L11-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 47 | AG | 169 | 1353 | 847 | 253 | 249 | 4 | 0 | 0 |

- Molecule 48 is a protein called 60S ribosomal protein L25.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 48 | AH | 121 | 964 | 620 | 169 | 173 | 2 | 0 | 0 |

- Molecule 49 is a protein called 60S ribosomal protein L38.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 49 | AI | 77 | 612 | 391 | 115 | 106 | 0 | 0 |

- Molecule 50 is a protein called 60S ribosomal protein L13-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 50 | AJ | 193 | 1543 | 962 | 315 | 266 | 0 | 0 |

- Molecule 51 is a protein called 60S ribosomal protein L26-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 51 | AK | 126 | 993 | 625 | 192 | 176 | 0 | 0 |

- Molecule 52 is a protein called 60S ribosomal protein L39.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 52 | AL | 50 | 436 | 272 | 97 | 65 | 2 | 0 | 0 |

- Molecule 53 is a protein called 60S ribosomal protein L14-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 53 | AM | 136 | 1053 | 675 | 199 | 177 | 2 | 0 | 0 |

- Molecule 54 is a protein called 60S ribosomal protein L27-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 54 | AN | 135 | 1092 | 710 | 202 | 180 | 0 | 0 |

- Molecule 55 is a protein called Ubiquitin-60S ribosomal protein L40.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 55 | AO | 52 | 417 | 259 | 86 | 67 | 5 | 0 | 0 |

- Molecule 56 is a protein called 60S ribosomal protein L42-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 56 | AP | 105 | 847 | 534 | 170 | 138 | 5 | 0 | 0 |

- Molecule 57 is a protein called 60S ribosomal protein L15-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 57 | AQ | 203 | 1720 | 1077 | 361 | 281 | 1 | 0 | 0 |

- Molecule 58 is a protein called 60S ribosomal protein L28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 58 | AR | 148 | 1173 | 749 | 231 | 190 | 3 | 0 | 0 |

- Molecule 59 is a protein called 60S ribosomal protein L41-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 59 | AS | 25 | 233 | 142 | 63 | 27 | 1 | 0 | 0 |

- Molecule 60 is a protein called 60S ribosomal protein L43-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 60 | AT | 91 | 694 | 429 | 138 | 121 | 6 | 0 | 0 |

- Molecule 61 is a protein called 60S ribosomal protein L16-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 61 | AU | 197 | 1555 | 1003 | 289 | 262 | 1 | 0 | 0 |

- Molecule 62 is a protein called 60S ribosomal protein L29.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 62 | AV | 58 | 462 | 289 | 100 | 73 | 0 | 0 |

- Molecule 63 is a protein called 60S ribosomal protein L2-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 63 | AW | 252 | 1914 | 1191 | 388 | 334 | 1 | 0 | 0 |

- Molecule 64 is a protein called 60S ribosomal protein L17-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 64 | AX | 183 | 1420 | 882 | 281 | 257 | 0 | 0 |

- Molecule 65 is a protein called 60S ribosomal protein L30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 65 | AY | 97 | 742 | 479 | 124 | 138 | 1 | 0 | 0 |

- Molecule 66 is a protein called uL1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 66 | AZ | 210 | 1050 | 630 | 210 | 210 | 0 | 0 |

- Molecule 67 is a protein called 60S ribosomal protein L3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 67 | BA | 386 | 3075 | 1950 | 584 | 533 | 8 | 0 | 0 |

- Molecule 68 is a protein called 60S ribosomal protein L18-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 68 | BB | 185 | 1441 | 908 | 290 | 241 | 2 | 0 | 0 |

- Molecule 69 is a protein called 60S ribosomal protein L31-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 69 | BC | 109 | 876 | 556 | 167 | 152 | 1 | 0 | 0 |

- Molecule 70 is a protein called 60S ribosomal protein L10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 70 | BD | 220 | 1770 | 1121 | 335 | 307 | 7 | 0 | 0 |

- Molecule 71 is a protein called 60S ribosomal protein L4-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 71 | BE | 361 | 2748 | 1729 | 522 | 494 | 3 | 0 | 0 |

- Molecule 72 is a protein called 60S ribosomal protein L19-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 72 | BF | 188 | 1521 | 935 | 326 | 260 | 0 | 0 |

- Molecule 73 is a protein called 60S ribosomal protein L32.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 73 | BG | 127 | 1020 | 647 | 205 | 167 | 1 | 0 | 0 |

- Molecule 74 is a protein called 60S ribosomal protein L20-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 74 | BH | 172 | 1445 | 930 | 267 | 244 | 4 | 0 | 0 |

- Molecule 75 is a protein called 60S ribosomal protein L5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 75 | BI | 296 | 2375 | 1501 | 414 | 458 | 2 | 0 | 0 |

- Molecule 76 is a protein called 60S ribosomal protein L21-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 76 | BJ | 159 | 1276 | 805 | 246 | 221 | 4 | 0 | 0 |

- Molecule 77 is a protein called 60S ribosomal protein L33-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 77 | BK | 106 | 850 | 540 | 165 | 144 | 1 | 0 | 0 |

- Molecule 78 is a protein called 60S ribosomal protein L22-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 78 | BL | 100 | 796 | 516 | 131 | 149 | 0 | 0 |

- Molecule 79 is a protein called 60S ribosomal protein L6-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 79 | BM | 156 | 1239 | 800 | 222 | 216 | 1 | 0 | 0 |

- Molecule 80 is a protein called 60S ribosomal protein L34-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 80 | BN | 112 | 880 | 545 | 179 | 152 | 4 | 0 | 0 |

- Molecule 81 is a protein called 60S ribosomal protein L7-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 81 | BO | 222 | 1784 | 1151 | 324 | 308 | 1 | 0 | 0 |

- Molecule 82 is a protein called 60S ribosomal protein L35-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 82 | BP | 119 | 969 | 615 | 186 | 167 | 1 | 0 | 0 |

- Molecule 83 is a RNA chain called 25S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 83 | BQ | 3165 | 67695 | 30238 | 12201 | 22091 | 3165 | 0 | 0 |

- Molecule 84 is a RNA chain called 5S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 84 | BR | 121 | 2579 | 1152 | 461 | 845 | 121 | 0 | 0 |

- Molecule 85 is a RNA chain called 5.8S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 85 | BS | 158 | 3352 | 1500 | 586 | 1108 | 158 | 0 | 0 |

- Molecule 86 is a protein called Eukaryotic translation initiation factor 5A-1.

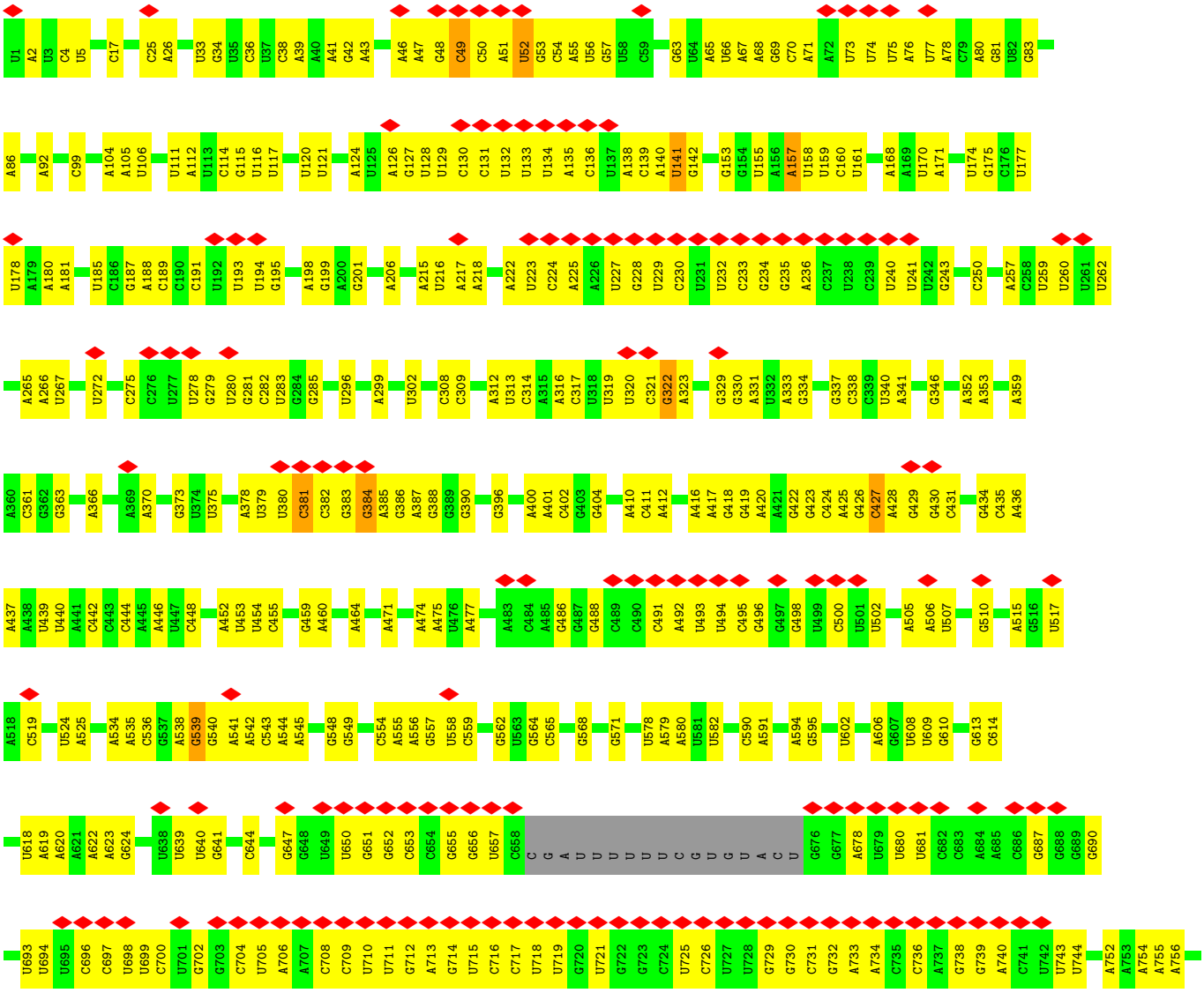
| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 86 | BT | 154 | 1143 | 709 | 195 | 230 | 9 | 0 | 0 |

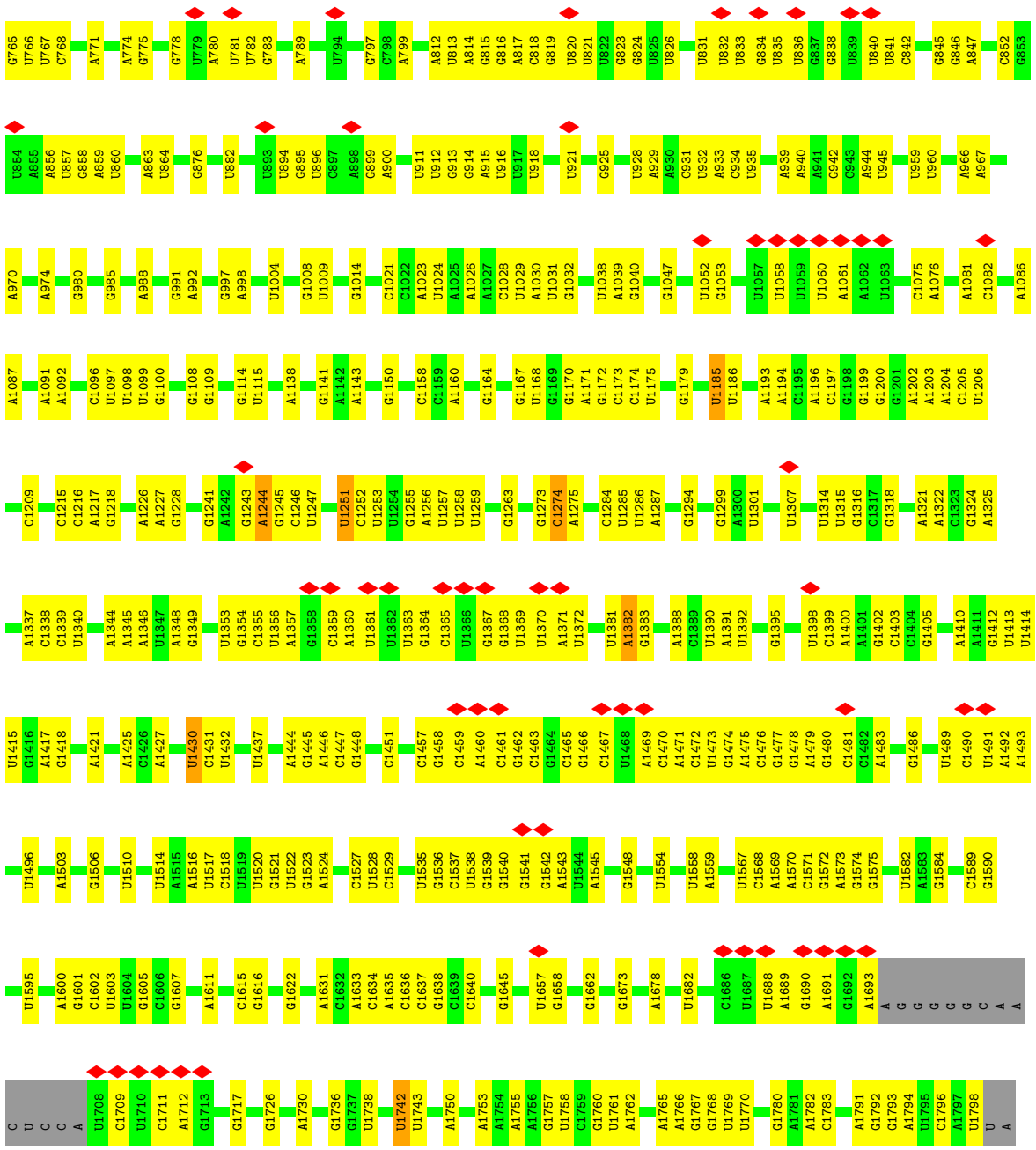
# 3 Residue-property plots (i)

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

- Molecule 1: 18S ribosomal RNA

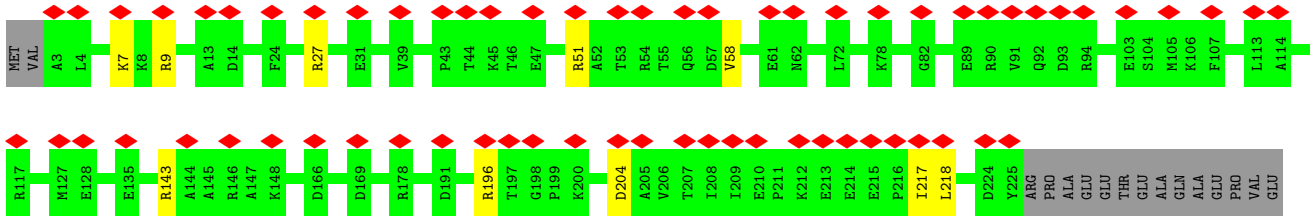
Chain 2:



• Molecule 2: 40S ribosomal protein S3

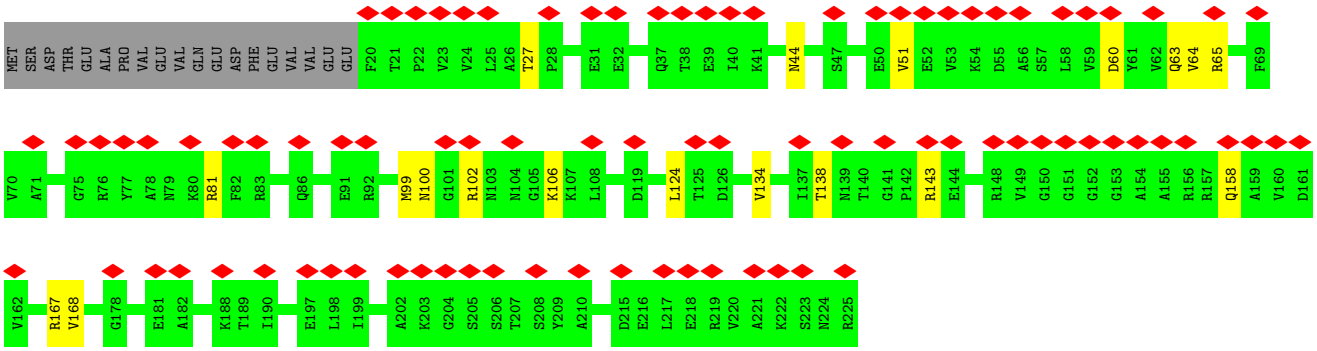
Chain A:



ALA

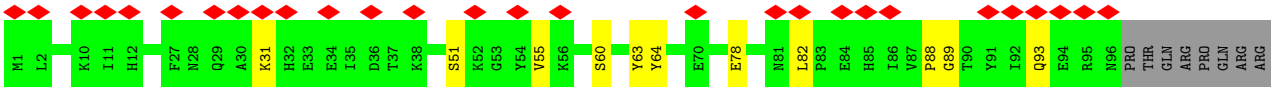
• Molecule 3: 40S ribosomal protein S5

Chain B:




• Molecule 4: 40S ribosomal protein S10-A

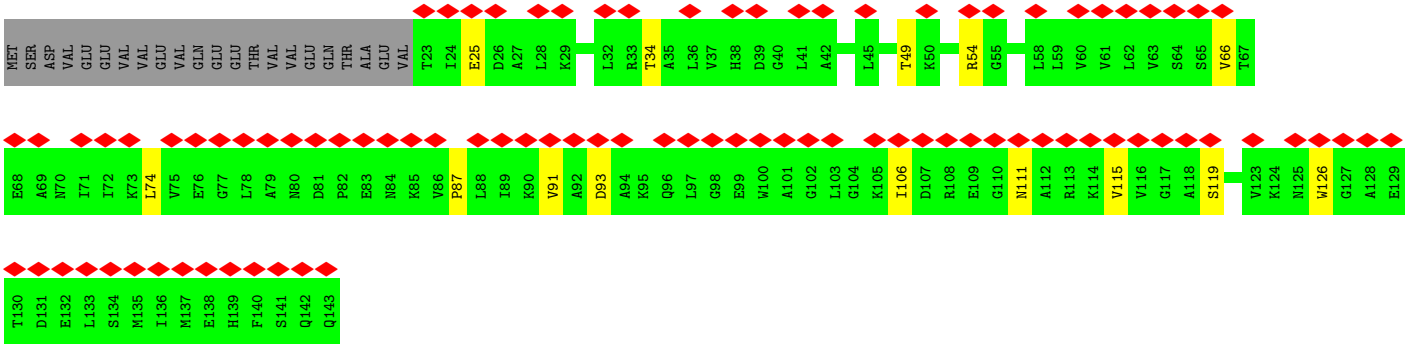
Chain C:




TYR

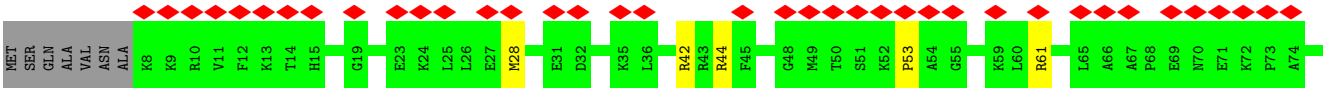
• Molecule 5: 40S ribosomal protein S12

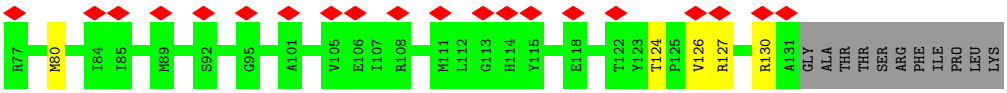
Chain D:




• Molecule 6: 40S ribosomal protein S15

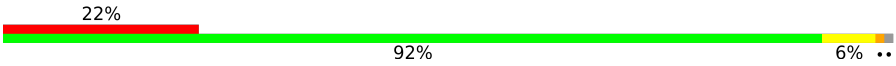
Chain E:

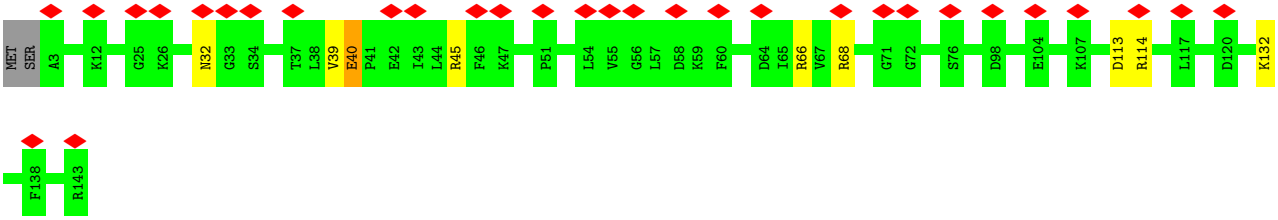





• Molecule 7: 40S ribosomal protein S16-A

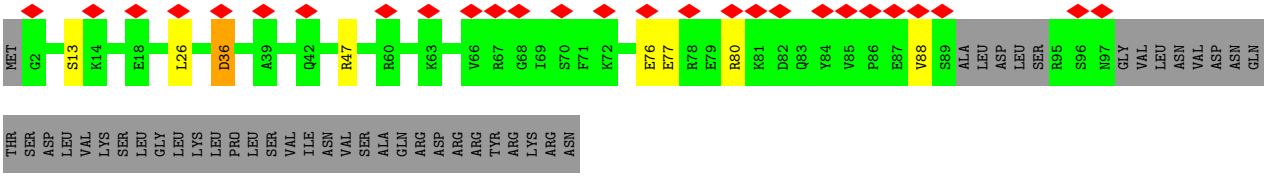
Chain F:



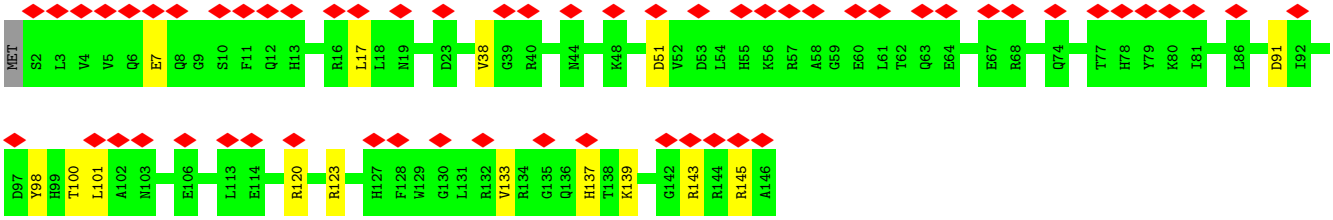

• Molecule 8: 40S ribosomal protein S17-B

Chain G:



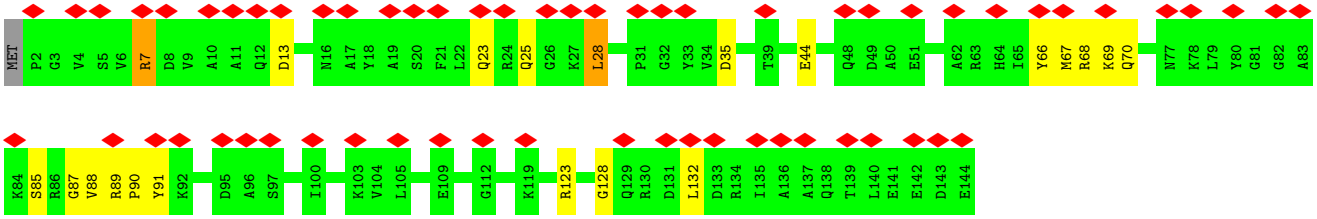

• Molecule 9: 40S ribosomal protein S18-A

Chain H:



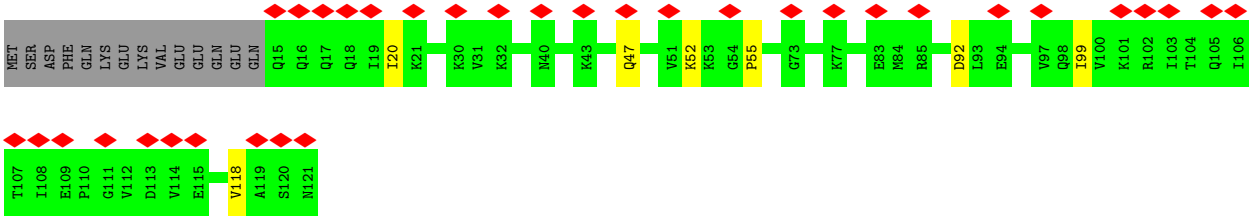

• Molecule 10: 40S ribosomal protein S19-A

Chain I:



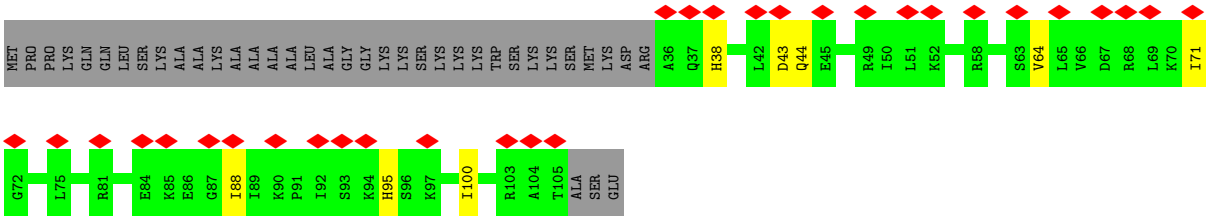

• Molecule 11: 40S ribosomal protein S20

Chain J:



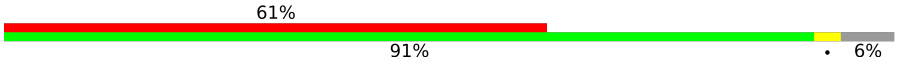

- Molecule 12: 40S ribosomal protein S25-A

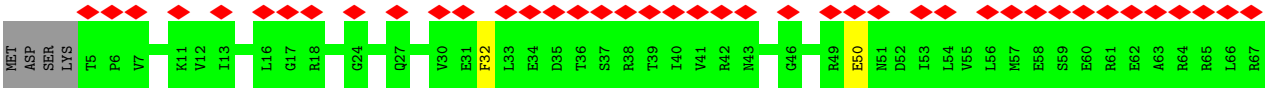
Chain K:




- Molecule 13: 40S ribosomal protein S28-B

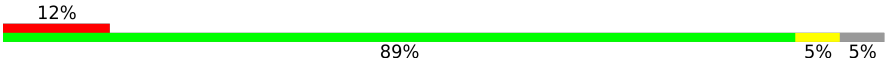
Chain L:

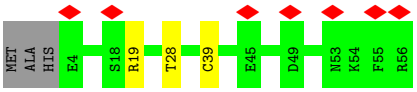



- Molecule 14: 40S ribosomal protein S29-A

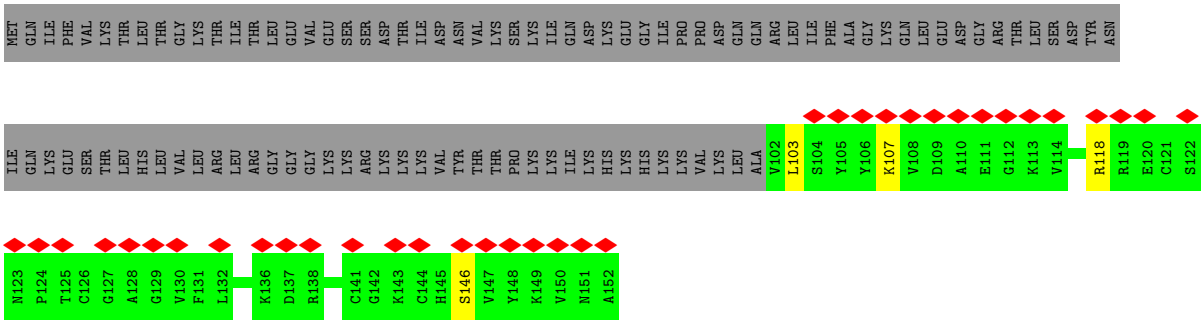
Chain M:



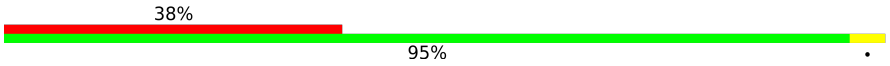

- Molecule 15: Ubiquitin-40S ribosomal protein S31

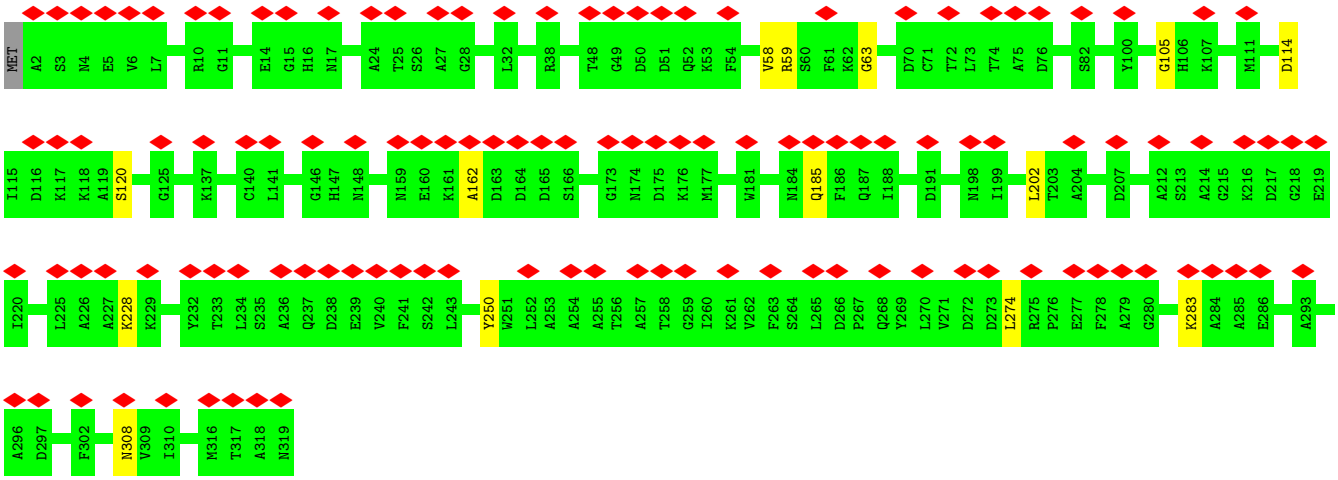
Chain N:




- Molecule 16: Guanine nucleotide-binding protein subunit beta-like protein

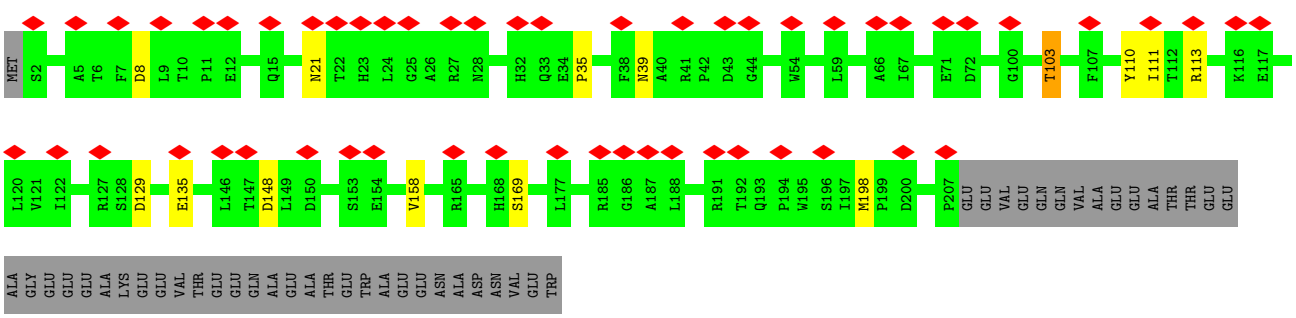
Chain O:





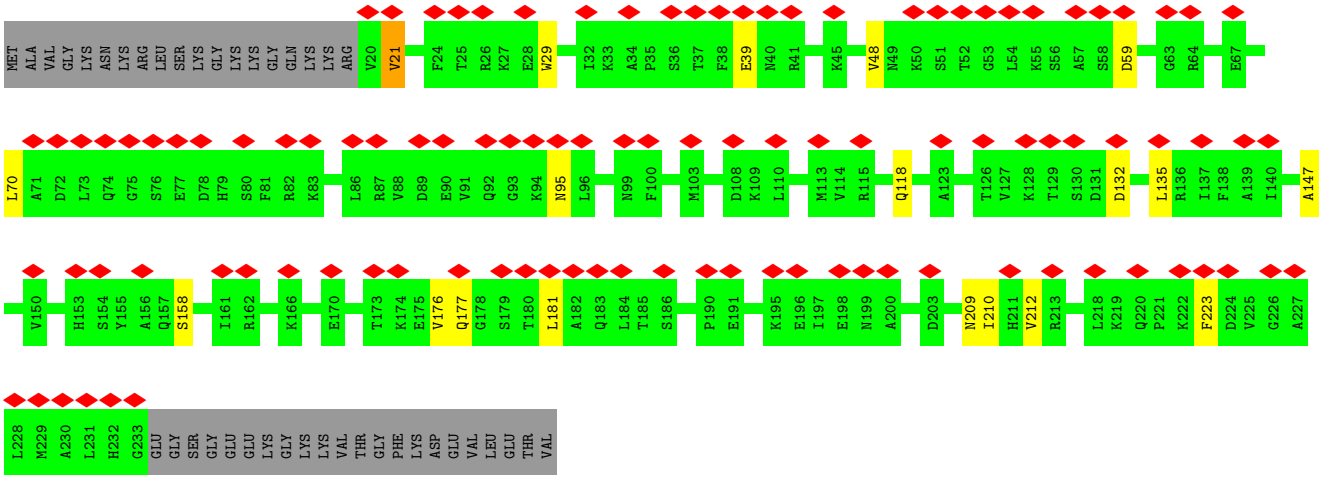

- Molecule 17: 40S ribosomal protein S0-A

Chain P:



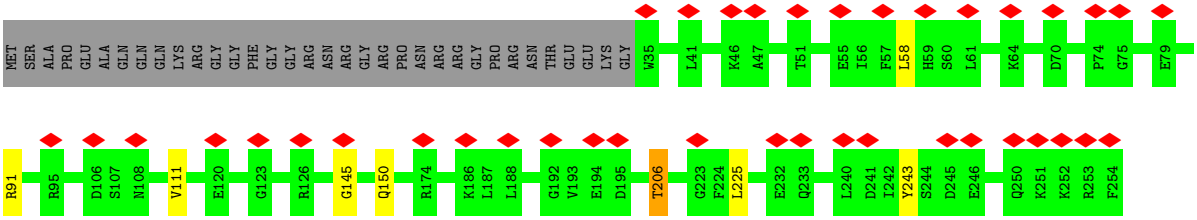

- Molecule 18: 40S ribosomal protein S1-A

Chain Q:



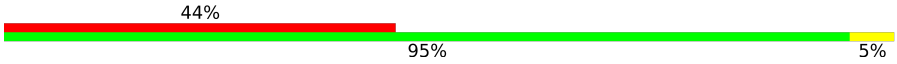

- Molecule 19: 40S ribosomal protein S2

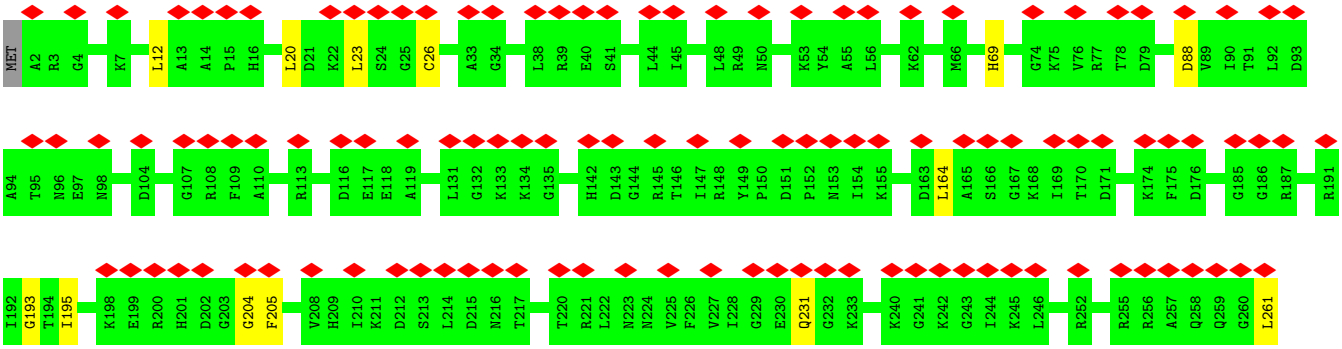
Chain R:




• Molecule 20: 40S ribosomal protein S4-A

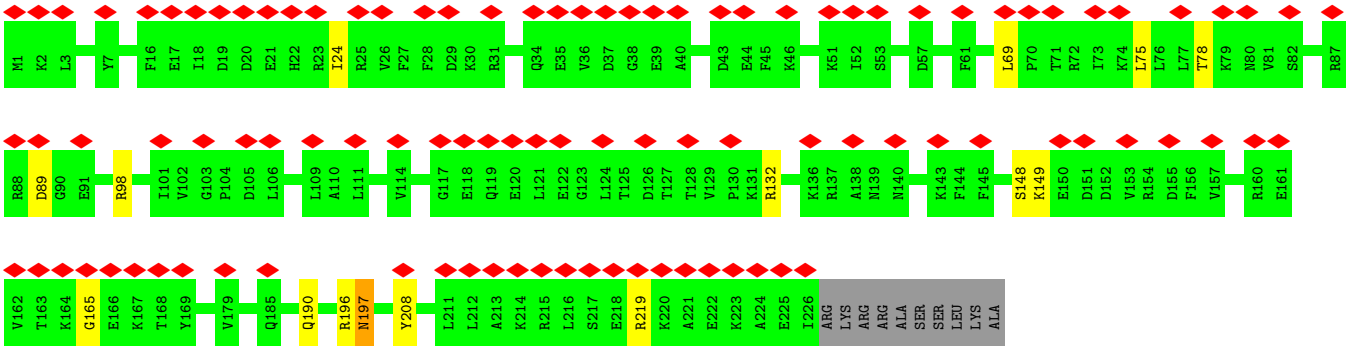
Chain S:



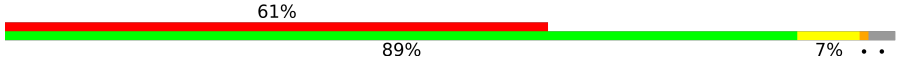

• Molecule 21: 40S ribosomal protein S6-A

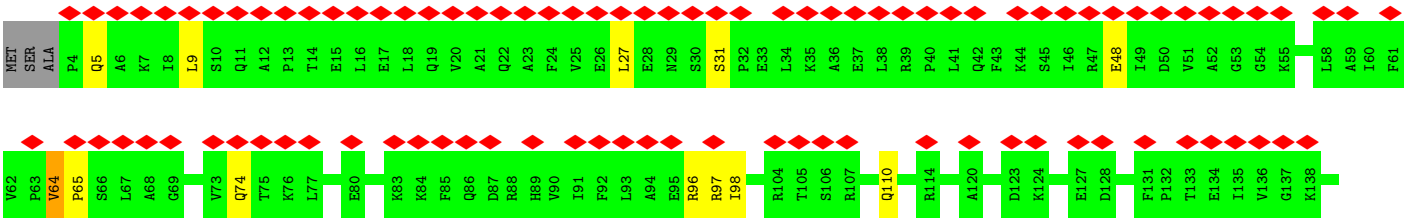
Chain T:

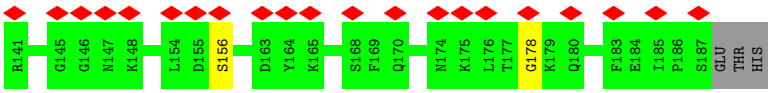



• Molecule 22: 40S ribosomal protein S7-A

Chain U:

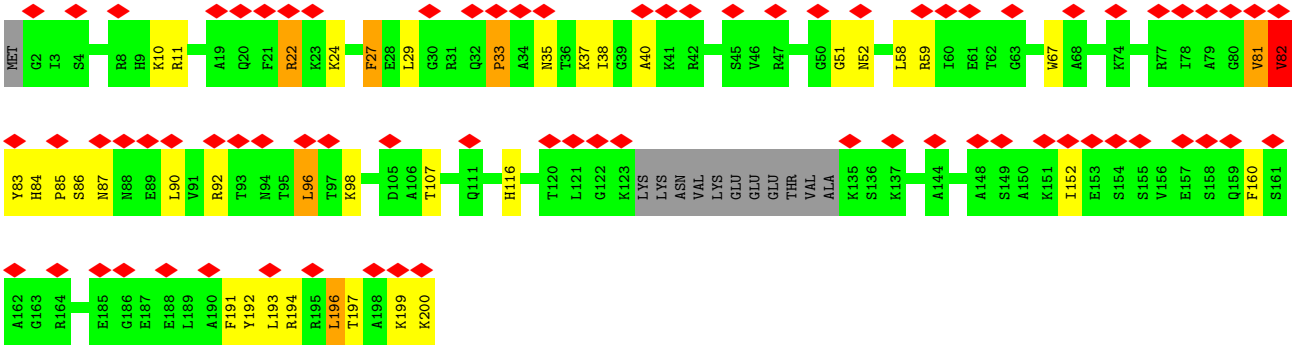




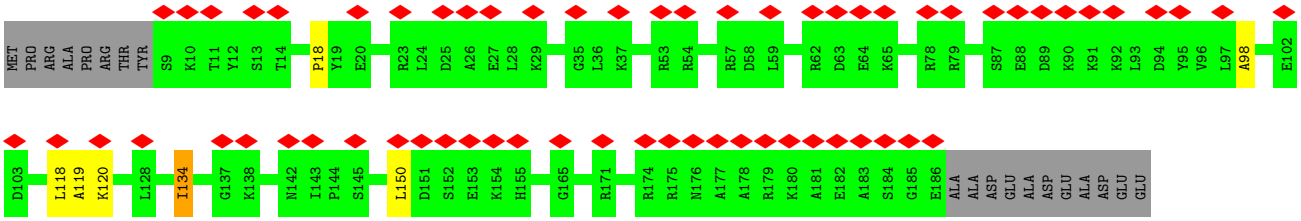

- Molecule 23: 40S ribosomal protein S8-A

Chain V:



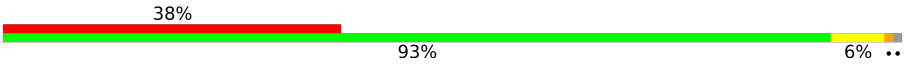

- Molecule 24: 40S ribosomal protein S9-A

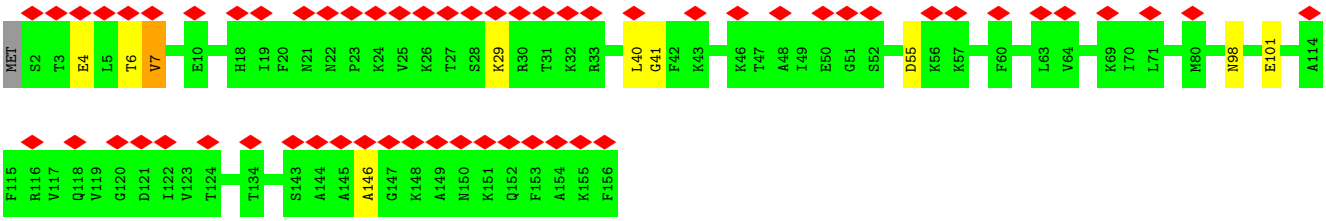
Chain W:




- Molecule 25: 40S ribosomal protein S11-A

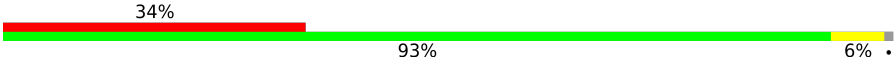
Chain X:

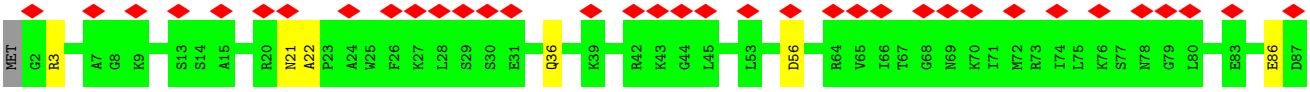


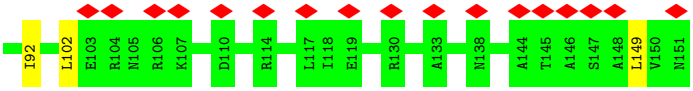




- Molecule 26: 40S ribosomal protein S13

Chain Y:

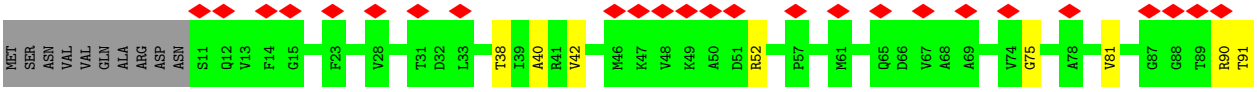


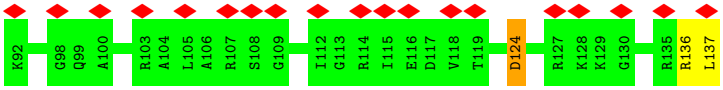






- Molecule 27: 40S ribosomal protein S14-A

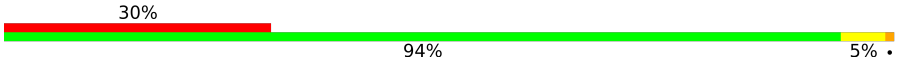
Chain Z:

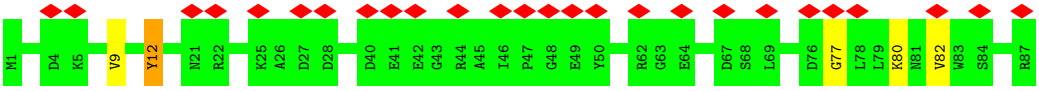



- Molecule 28: 40S ribosomal protein S21-A

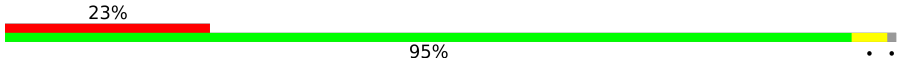
Chain a:

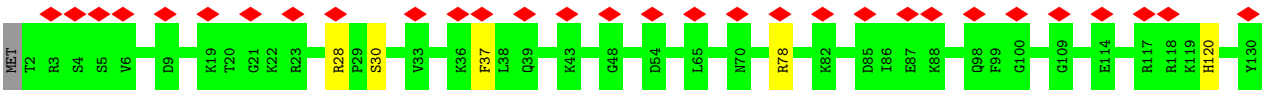



- Molecule 29: 40S ribosomal protein S22-A

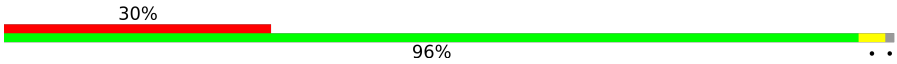
Chain b:

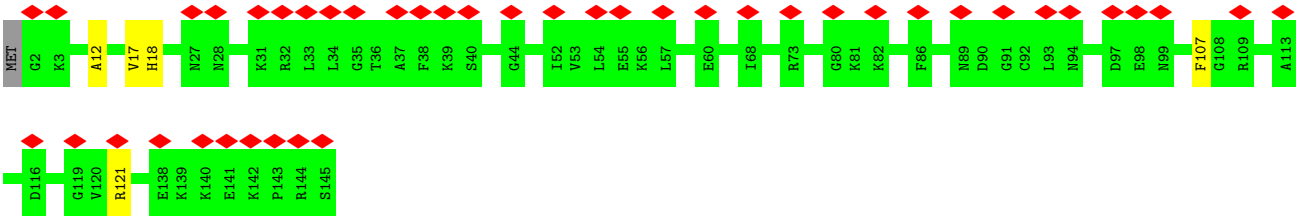



- Molecule 30: 40S ribosomal protein S23-A

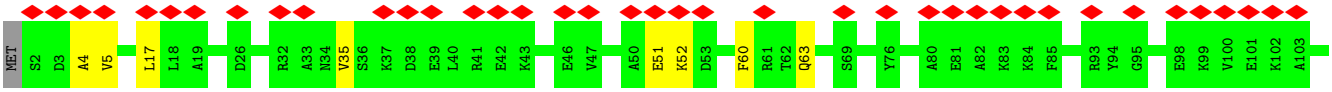
Chain c:

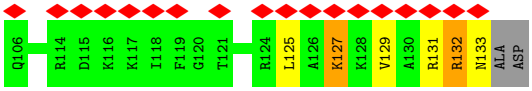



- Molecule 31: 40S ribosomal protein S24-A

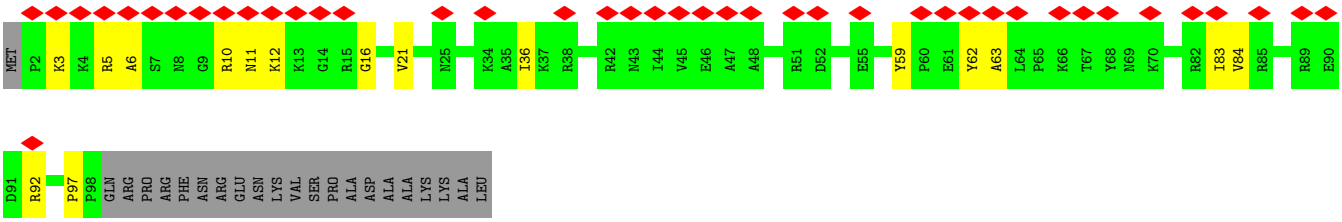
Chain d:





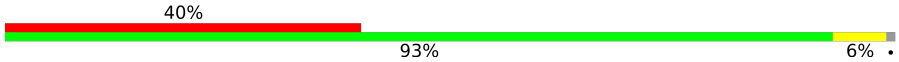

• Molecule 32: 40S ribosomal protein S26-A

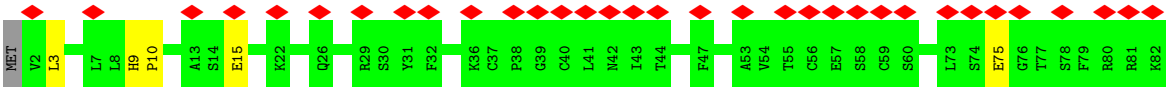
Chain e:




• Molecule 33: 40S ribosomal protein S27-A

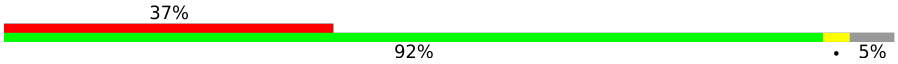
Chain f:

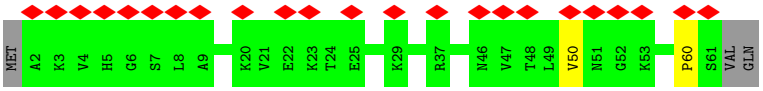



• Molecule 34: 40S ribosomal protein S30-A

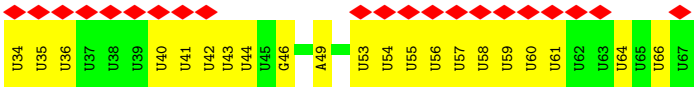
Chain g:



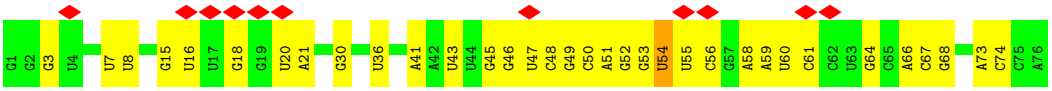

• Molecule 35: mRNA

Chain l:



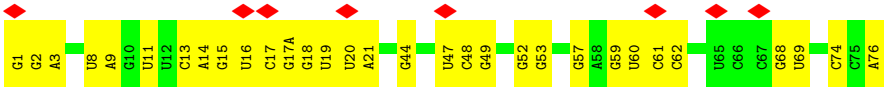

• Molecule 36: A-site tRNA

Chain m:



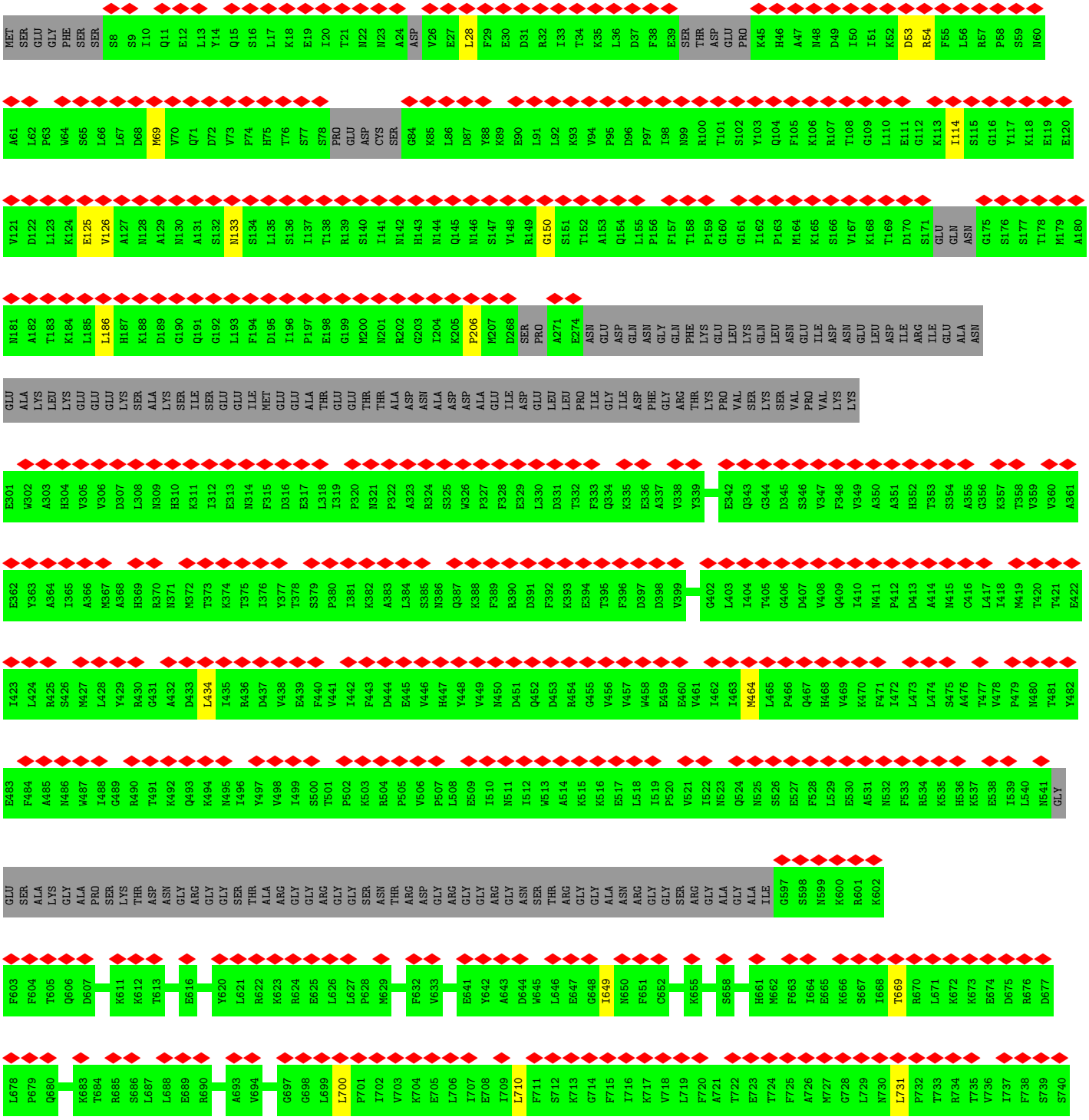

• Molecule 37: P-site tRNA

Chain n:




- Molecule 38: Antiviral helicase SKI2

Chain h:



I741 R742 K743 H744 D745 G746 N747 G748 L749 R750 E751 L752 G755 E756 M760 A761 G762 R763 A764 G765 R766 R767 G768 L769 D770 S771 T772 G773 T774 V775 I776 V777 M778 A779 Y780 N781 S782 P783 L784 S785 I786 A787 T788 F789 K790 E791 V792 T793 M794 G795 V796 P797 T798 R799 L800 Q801 S802 Q803

F804 R805 L806 T807 Y808 N809 M810 I811 L812 N813 L814 L815 R816 I817 E818 A819 L820 R821 V822 E823 E824 M825 I826 K827 Y828 S829 F830 S831 E832 K835 E836 T837 L838 Q839 P840 E841 H842 E843 K844 Q845 I846 K847 V848 L849 Q850 E851 E852 L853 Q854 T855 I856 E857 Y858 K859 S860 C861 E862 I863 C864

D865 N866 D867 I868 E869 K870 F871 L872 E873 L874 M875 L876 A877 Y878 K879 E880 A881 T882 V883 N884 L885 M886 Q887 E888 M889 V890 K891 S892 P893 S894 I895 L896 H897 I898 L899 K900 E901 G902 R903 L904 V905 A906 F907 R908 D909 P910 N911 D912 C913 L914 K915 L916 G917 F918 V919 F920 K921 V922 S923 L924

K925 D926 A927 V928 C929 V930 I931 M932 T933 F934 T935 K936 P937 Y938 K939 L940 P941 N942 G943 E944 P945 N946 H947 L948 I949 Y950 F951 P952 K953 A954 D955 G956 Y957 R958 R959 R960 P963 K964 F965 Q966 K967 T968 D969 F970 Y971 M972 E973 E974 V975 P976 V977 T978 A979 I980 E981 V982 I983 T984 K985

R986 K987 F988 A989 A990 P991 L992 G993 K994 V995 I996 K997 K998 D999 V1000 A1001 A1002 L1003 N1004 E1005 F1006 N1007 A1008 E1009 T1010 N1011 N1012 I1013 L1014 D1015 G1016 K1017 T1018 L1019 K1020 E1021 A1022 I1023 N1024 I1025 E1026 K1027 Q1028 G1029 L1030 K1031 I1032 H1033 Q1034 I1035 L1036 L1037 D1038 R1039 T1040 N1041 I1042 R1043 D1044 E1045

I1046 F1047 K1048 L1049 K1050 S1051 I1052 K1053 C1054 P1055 N1056 H1060 P1063 K1064 F1065 K1066 A1067 H1068 V1069 I1070 K1071 K1072 K1073 I1074 E1075 E1076 L1077 Y1078 H1079 L1080 M1081 S1082 D1083 Q1084 N1085 L1086 S1087 L1088 L1089 P1090 D1091 Y1092 E1093 K1094 R1095 L1096 A1097 V1098 L1099 K1100 D1101 T1102 E1103 F1104 I1105 D1106 Q1107 N1108

H1109 N1110 V1111 L1112 L1113 K1114 G1115 R1116 V1117 A1118 C1119 E1120 I1121 N1122 S1123 G1124 Y1125 E1126 L1127 V1128 L1129 T1130 E1131 L1132 I1133 L1134 D1135 N1136 F1137 L1138 G1139 S1140 F1141 E1142 P1143 E1144 E1145 I1146 V1147 A1148 L1149 L1150 S1151 V1152 F1153 V1154 Y1155 E1156 G1157 K1158 T1159 R1160 E1161 E1162 E1163 P1164 P1165 I1166 V1167 T1168

P1169 R1170 L1171 A1172 K1173 G1174 K1175 Q1176 R1177 I1178 E1179 E1180 I1181 Y1182 K1183 K1184 M1185 L1186 C1187 V1188 F1189 N1190 T1191 H1192 Q1193 I1194 P1195 L1196 T1197 Q1198 D1199 E1200 A1201 E1202 F1203 L1204 D1205 R1206 K1207 R1208 F1209 A1210 M1211 M1212 N1213 E1217 W1218 A1219 R1220 G1221 L1222 S1223 F1224 K1225 E1226 I1227 M1228 E1229 M1230

S1231 P1232 E1233 A1234 E1235 G1236 T1237 V1238 V1239 R1240 W1244 L1245 D1246 E1247 I1248 C1249 R1250 E1251 V1252 K1253 T1254 A1255 S1256 I1257 I1258 I1259 G1260 N1261 S1262 T1263 L1264 H1265 S1269 R1270 E1273 L1274 I1275 K1276 R1277 D1278 I1279 V1280 F1281 A1282 A1283 S1284 L1285 Y1286 L1287

- Molecule 39: Superkiller protein 3

Chain i: 87% 92% 5%

M1 S2 D3 I4 K5 Q6 L7 L8 K9 E10 A11 K12 Q13 E14 L15 T16 N17 R18 D19 Y20 E21 E22 T23 I24 E25 I26 S27 E28 K29 V30 L31 K32 L33 D34 P35 D36 N37 Y38 F39 A40 H41 I42 F43 L44 G45 K46 A47 L48 S49 S50 L51 P52 A53 S54 N55 N56 V57 S58 S59 N60

R61 N62 L63 E64 R65 A66 T67 N68 H69 Y70 V71 S72 A73 A74 K75 L76 V77 P78 D79 N80 L81 L82 A83 W84 K85 G86 L87 F88 L89 L90 F91 R92 T93 T94 E95 V96 V97 P98 D99 I100 L101 S102 Y103 D104 E105 Y106 F107 D108 L109 C110 G111 Q112 Y113 A114 D115 A116 L117 L118 K119 Q120

E121 GLN SER Q124 V125 E126 L127 I128 N129 D130 I131 K132 L133 L134 K135 K136 T137 H138 P139 D140 C141 Q142 K143 A144 F145 Y146 Q147 H148 L149 K150 P151 G152 S153 L154 M155 A156 E157 T158 I159 G160 R161 HIS LEU SER T165 P166 Q167 D168 A169 L170 L171 N172 L173 I174 K175 I176 L177 S178 N179 I180

E181 T182 T183 E184 I185 G186 K187 T188 L189 S190 Q191 N192 R193 L194 K195 L196 K197 A198 S199 D200 P201 D202 Y203 Q204 I205 K206 L207 N208 S209 F210 S211 W212 E213 I214 I215 K216 N217 S218 E219 I220 D221 Q222 L223 Y224 N225 Q226 L227 V228 N229 I230 L231 A232 D233 D234 Q235 K236 R237 S238 E239 I240

E241 N242 Q243 W244 L245 E246 Y247 R248 T249 K250 V251 L252 K253 S254 M255 P256 L257 D258 V259 K260 K261 D262 F263 F264 T265 K266 V267 K268 E269 M270 V271 E272 D273 M274 V275 L276 V277 N278 H279 Q280 S281 L282 L283 A284 W285 Q286 K287 Y288 F289 E290 W291 T292 D293 Y294 E295 D296 L297 D298 N299 M300

D301 A302 P303 L304 I305 I306 K307 Y308 F309 K310 K311 F312 P313 K314 D315 P316 L317 A318 M319 I320 L321 Y322 S323 W324 L325 S326 S327 K328 L329 S330 K331 Y332 D333 I334 K335 S336 L337 E338 S339 ALA ASN LYS PRO PRO GLU GLY HIS LYS LYS THR GLU LYS GLU THR ASP ILE LYS ASP VAL ASP

GLU THR ASN GLU ASP GLU VAL LYS ASP ARG VAL GLU ASP GLU VAL LYS ASP ARG VAL GLU ASP GLU VAL LYS ASP GLN ASP GLU GLU ALA LYS GLU ASP GLU GLU GLU ASP LEU D399 D400 I401 E402 I403 G404 L405 L406 E407 E408 E409 V410 V411 T412 V413 L414 T415 E416 N417 I418 V419 K420

C421 K422 N423 N424 I425 L426 A427 H428 R429 I430 L431 C432 Q433 Y434 Y435 L436 L437 T438 K439 E440 Y441 E442 A443 A444 L445 P446 Y447 I448 K449 N450 G451 I452 S453 L454 I455 A456 Y457 N458 I459 K460 D461 L462 G463 V464 H465 L466 P467 L468 T469 K470 R471 E472 F473 S474 L475 D476 L477 A478 T479 V480

Y481 T482 Y483 V484 D485 A486 P487 K488 D489 H490 N491 A492 A493 L494 K495 L496 Y497 D498 N499 I500 L501 S502 G503 D504 F505 S506 N507 I508 Q509 A510 K511 M512 G513 K514 G515 I516 I517 F518 I519 E520 R521 K522 N523 W524 K525 D526 A527 M528 T529 L530 L531 T532 Q533 V534 H535 E536 Q537 S538 P539 N540

N541 L542 E543 V544 L545 S546 E547 L548 S549 W550 S551 H554 M555 G556 Y557 M558 D559 E560 A561 L562 A563 G564 L565 D566 T567 V568 I569 K570 G571 I572 K573 G574 M575 D576 L577 R578 S579 I580 D581 F582 R583 A584 L585 N586 L587 W588 R589 K592 V593 Y594 I595 M596 K597 H598 A599 S600 ILE ASN

ASP A604 K605 Q606 E607 N608 V609 K610 C611 A612 F613 K614 L615 L616 I617 Q618 S619 I620 K621 I622 L623 D624 T625 F626 A627 P628 G629 F630 S631 T632 L633 G634 D635 I636 Y637 C638 H639 Y640 Y641 K642 D643 H644 L645 R646 A647 F648 K649 C650 Y651 F652 K653 A654 F655 D656 L657 D658 A659 G660 D661 Y662

T663 A664 A665 K666 Y667 I668 T669 E670 T671 Y672 A673 S674 K675 P676 N677 W678 Q679 A680 A681 S682 S683 I684 A685 S686 R687 L688 I689 K690 G691 E692 K693 A694 K695 A696 E697 L698 R699 S700 N701 N702 W703 P704 F705 R706 V707 V708 G709 I710 A711 H712 L713 E714 K715 Q716 E717 E718 S719 D720 S721 I722

E723 W724 F725 Q726 S727 A728 L729 R730 V731 D732 P733 N734 D735 V736 E737 V740 Q744 A745 Y746 H747 A748 C749 G750 R751 I752 E753 I756 K757 V758 F759 D760 K761 A762 I763 Q764 L765 R766 P767 S768 H769 T770 F771 A772 Q773 Y774 F775 K776 A777 I778 S779 L780 C781 D782 V783 G784 E785 Y786

L787 E788 S789 L790 D791 I792 L793 E794 K795 V796 C797 Q798 E799 A800 A801 T802 E803 E804 S805 F806 Q807 I808 G809 L810 V811 E812 V813 L814 N815 R816 C817 S818 L819 D820 L821 Y822 S823 Q824 G825 F826 L827 L828 K829 S830 V831 S832 I833 A834 K835 D836 T837 I838 E839 R840 I841 K842 I843 I844 I845 S846

E847 L848 K849 C850 E851 N852 Q853 Q854 V855 L859 S860 Q861 V862 L863 R864 L865 F866 I867 W868 I869 E870 S871 K872 V873 D874 T875 L876 P877 V878 E879 S880 L881 V882 S883 I884 F885 E886 N887 S888 Q889 F890 S891 G892 S893 E894 E895 I896 D897 S898 V899 D900 N901 I902 K903 I904 D905 T906 L907 L908

D909 S910 T911 T912 D913 D914 N915 V916 S917 I918 A919 C920 K921 F922 L923 I924 L925 A926 S927 K928 Y929 S930 V931 S932 D933 Q934 K935 F936 T937 D938 I939 A940 G941 T942 V943 R944 Y949 N950 I951 G952 I953 S954 E955 L956 T957 A958 F959 I960 T961 L962 K963 E964 P965 Q966 Y967 R968 D969 A970 A971

I972 F973 K976 K977 S978 I979 Q980 L981 Q982 S983 N984 T985 S986 E987 T988 W989 I990 G991 L992 G993 I994 A995 T996 M997 D998 I999 N1000 F1001 R1002 V1003 H1006 C1007 F1008 I1009 K1010 A1011 T1012 A1013 L1014 E1015 P1016 K1017 A1018 T1019 N1020 T1021 W1022 F1023 N1024 L1025 A1026 M1027 L1028 G1029 L1030 K1031 K1032 K1033

D1034 T1035 E1036 F1037 A1038 Q1039 Q1040 V1041 L1042 N1043 K1044 L1045 Q1046 S1047 L1048 A1049 P1050 Q1051 D1052 S1053 S1054 P1055 W1056 L1057 G1058 M1059 A1060 L1061 I1062 L1063 E1064 E1065 Q1066 G1067 D1068 I1069 I1070 G1071 S1072 S1073 K1074 L1075 F1076 A1077 H1078 S1079 F1080 I1081 L1082 S1083 N1084 G1085 R1086 S1087 K1088 A1089 A1090 Q1091 F1092 M1093

Y1094 A1095 K1096 N1097 V1098 L1099 E1100 N1101 H1102 I1103 N1104 N1105 G1106 D1107 D1108 E1109 R1110 D1111 I1112 E1113 T1114 V1115 E1116 K1117 L1118 T1119 T1120 A1121 S1122 I1123 A1124 L1125 E1126 Q1127 F1128 F1129 K1130 K1131 S1132 P1133 D1134 S1135 Q1136 F1137 A1138 L1139 Q1140 C1141 A1142 L1143 L1144 T1145 L1146 E1147 R1148 L1149 H1150 H1151 Y1152 E1153

N1154 A1155 N1156 E1157 L1158 A1159 N1160 R1161 L1162 I1163 G1164 I1165 L1166 E1167 K1168 K1169 F1170 E1171 K1172 T1173 Q1174 D1175 E1176 R1177 E1178 L1179 F1180 N1181 F1182 A1183 I1184 I1185 K1186 G1187 Q1188 F1189 A1190 R1191 I1192 H1193 L1194 G1195 L1196 G1197 N1198 F1199 E1200 L1201 S1202 I1203 E1204 D1207 I1212 I1213 S1214 E1215 S1216 S1217

D1218 E1219 K1220 S1221 M1222 K1223 T1224 K1225 I1226 H1229 I1230 C1231 L1232 G1233 L1234 S1235 Y1236 F1237 F1238 L1239 N1240 D1241 F1242 D1243 Q1244 T1245 L1246 N1247 Q1248 L1252 L1253 S1254 I1255 S1256 K1257 D1258 S1259 K1260 H1261 L1262 V1263 V1264 L1265 I1266 A1267 K1268 V1269 L1270 Y1271 D1272 V1273 G1274 E1275 S1276 D1277 T1278 K1279 E1280

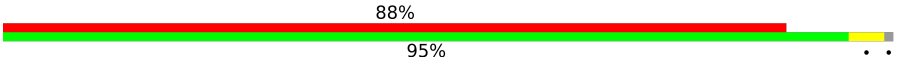
I1281 A1282 L1283 Q1284 E1285 L1286 T1287 E1288 Y1289 I1290 A1291 T1292 S1293 G1294 A1295 D1296 L1297 L1298 V1299 T1300 L1301 T1302 I1303 A1304 A1305 M1306 S1307 I1308 L1309 D1310 D1311 K1312 R1313 E1314 D1315 L1316 S1317 I1318 I1319 L1320 E1321 E1322 L1323 K1324 A1325 L1328 S1329 K1330 Q1331 I1332 I1333 D1334 K1335 H1336 K1337 D1338 A1339 P1340 Y1341

L1342 I1343 E1344 E1345 I1346 T1347 K1348 R1349 L1350 Y1351 R1352 N1353 D1354 T1355 G1356 K1357 Q1358 V1359 W1360 Q1361 R1362 S1363 A1364 Y1365 F1366 F1367 P1368 N1369 N1370 L1371 K1372 V1373 W1374 E1375 R1376 L1377 D1378 K1379 Q1382 R1383 R1384 I1385 A1386 S1387 N1388 G1389 Q1390 N1391 K1392 V1393 T1394 A1395 E1396 E1397 M1398 S1399 K1400 L1401 Y1402

C1403 E1404 S1405 K1406 R1409 S1410 I1411 Q1412 R1413 G1414 M1415 F1416 L1417 C1418 P1419 W1420 N1421 V1422 T1423 A1424 V1425 K1426 A1427 L1428 N1429 E1430 C1431 F1432

- Molecule 40: Antiviral protein SKI8

Chain j:



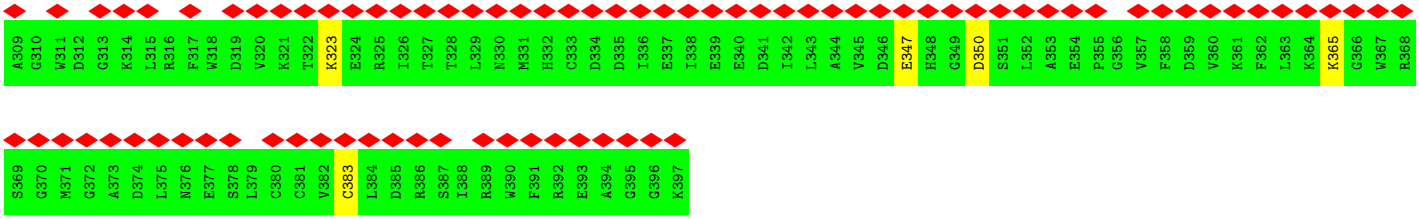

MET S2 K3 V4 F5 I6 A7 T8 A9 N10 A11 G12 K13 A14 H15 D16 A17 D18 I19 F20 S21 V22 S23 A24 C25 N26 S27 F28 C32 S33 G34 D35 L38 K39 V40 W41 D42 N43 K44 L45 L46 D47 N48 E49 N50 P51 K52 D53 K54 S55 Y56 S57 H58 F59 V60 H61 K62 S63

G64 L65 H66 H67 V68 D69 V70 L71 Q72 A73 I74 E75 R76 D77 A78 F79 E80 L81 C82 L83 V84 A85 T86 T87 S88 F89 S90 G91 D92 L93 L94 F95 Y96 R97 I98 T99 R100 E101 D102 E103 T104 K105 K106 V107 I108 F109 E110 K111 L112 D113 L114 L115 D116 S117 D118 M119 K120 K121 H122 S123

F124 W125 A126 L127 K128 W129 G130 A131 S132 N133 D134 R135 L136 L137 S138 H139 R140 L141 V142 A143 T144 D145 V146 K147 G148 T149 T150 Y151 I152 W153 K154 F155 H156 P157 F158 A159 D160 E161 SER ASN SER LEU T166 L167 N168 W169 S170 P171 T172 L173 E174 L175 Q176 G177 T178 V179 E180 S181 P182 M183

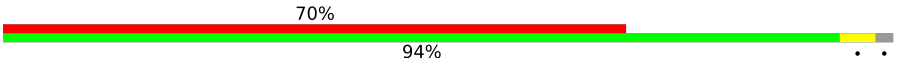
T184 P185 F188 A189 T190 S191 V192 D193 I194 S195 E196 R197 G198 L199 I200 A201 T202 N206 G207 T208 V209 Q210 I211 S212 E213 L214 S215 T216 L217 R218 P219 L220 Y221 N222 F223 E224 S225 Q226 H227 S228 M229 I230 N231 N232 S233 N234 S235 I236 R237 S238 V239 K240 F241 S242 P243 Q244 G245 S246

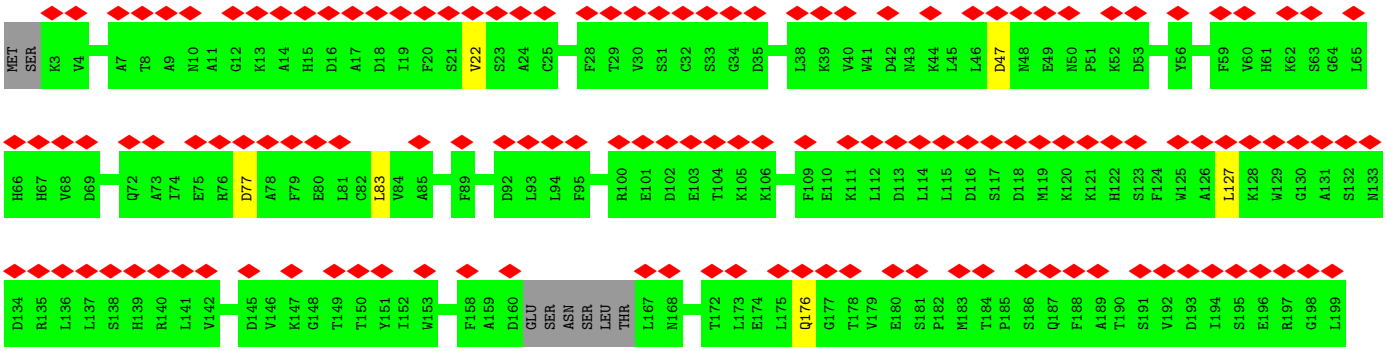
L247 L248 A249 I250 A251 H252 D253 S254 N255 S256 F257 G258 C259 I260 T261 L262 Y263 E264 T265 E266 F267 G268 E269 R270 I271 G272 S273 L274 S275 V276 P277 T278 H279 S280 S281 Q282 A283 S284 L285 G286 E287 F288 A289 S292 M295 S296 L297 S298 F299 N300 D301 S302 G303 E304 T305 L306 C307 S308




- Molecule 40: Antiviral protein SKI8

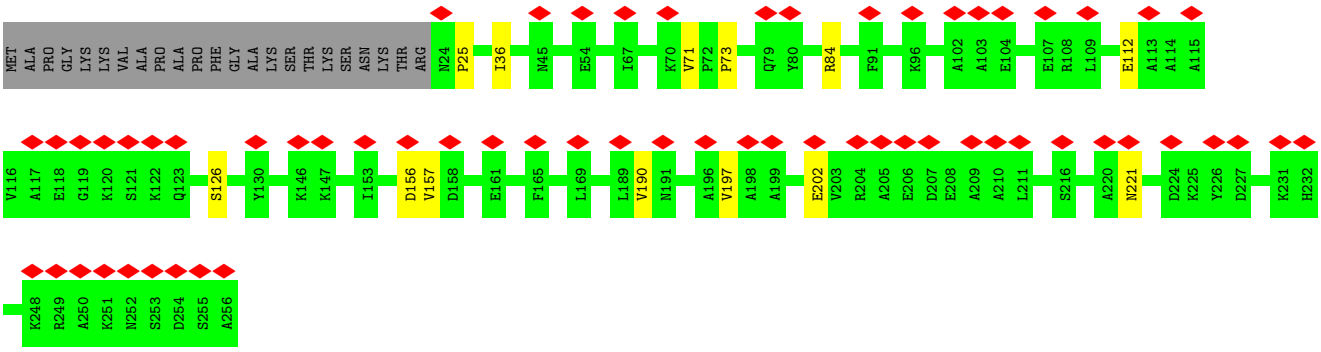
Chain k:



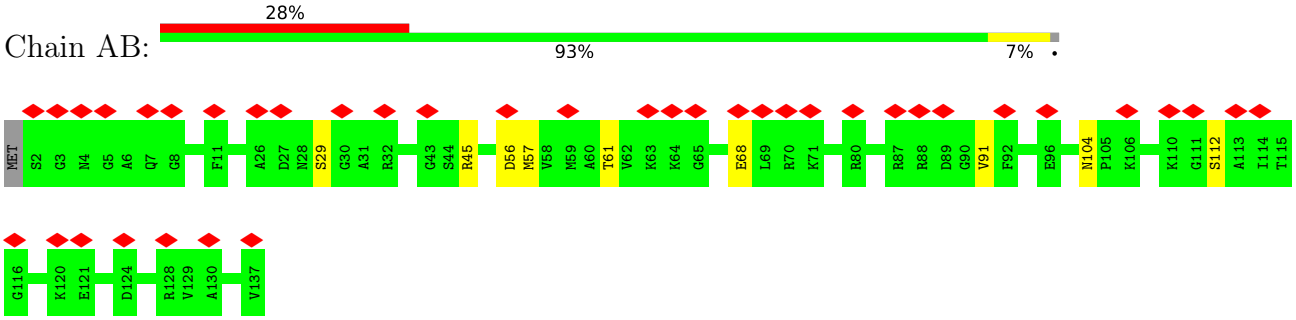

- Molecule 41: 60S ribosomal protein L8-A

Chain AA:



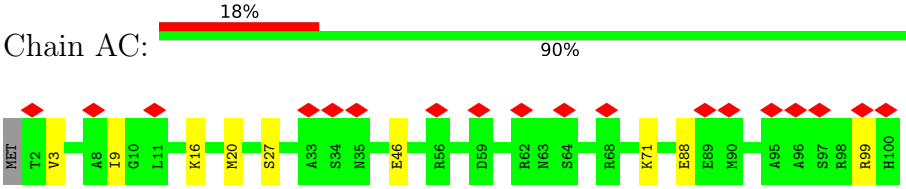

- Molecule 42: 60S ribosomal protein L23-A

Chain AB:



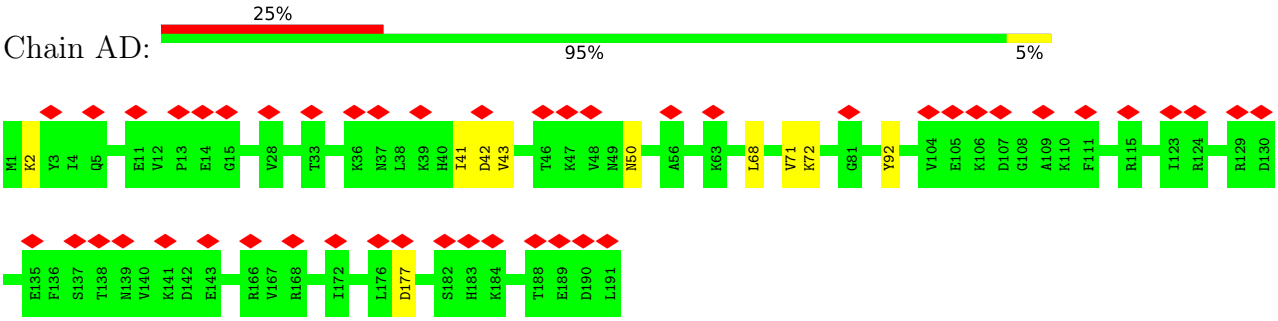

- Molecule 43: 60S ribosomal protein L36-A

Chain AC:



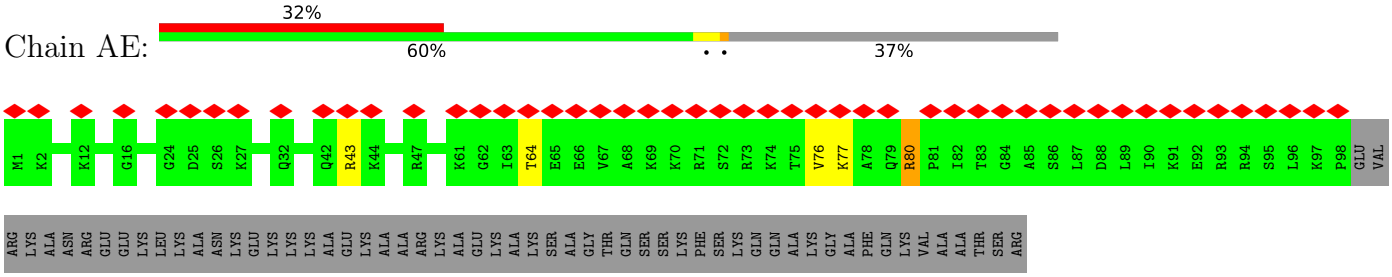

- Molecule 44: 60S ribosomal protein L9-A

Chain AD:



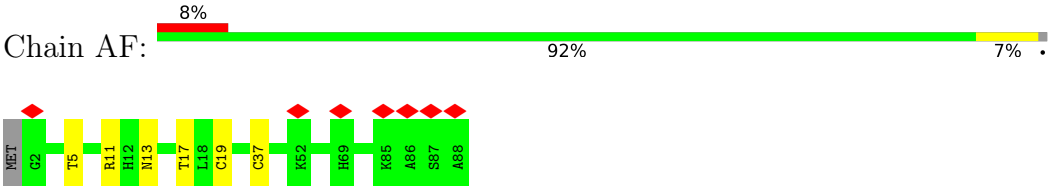

- Molecule 45: 60S ribosomal protein L24-A

Chain AE:



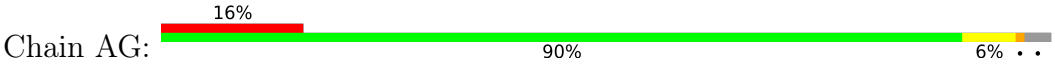

- Molecule 46: 60S ribosomal protein L37-A

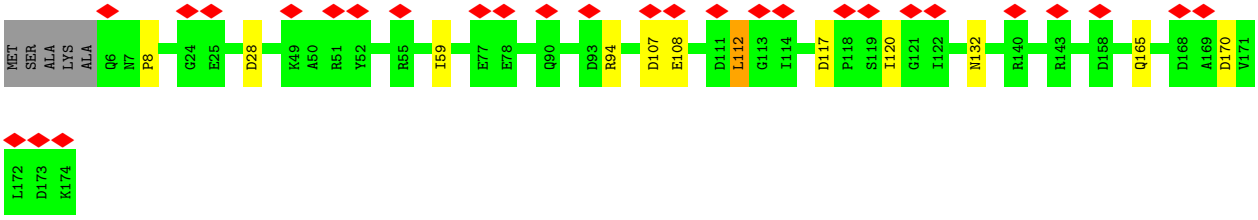
Chain AF:




- Molecule 47: 60S ribosomal protein L11-A

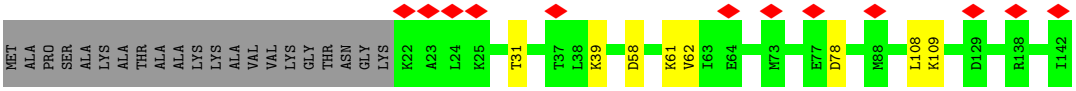
Chain AG:





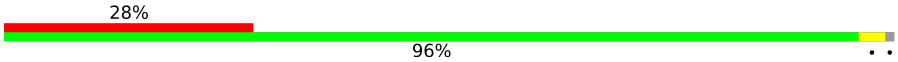

- Molecule 48: 60S ribosomal protein L25

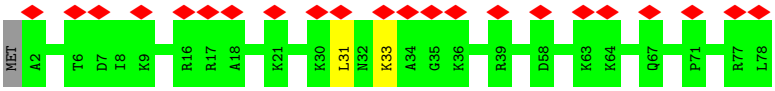
Chain AH:




- Molecule 49: 60S ribosomal protein L38

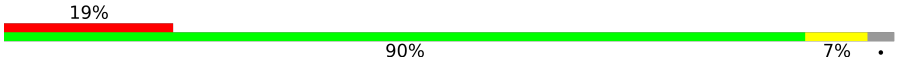
Chain AI:

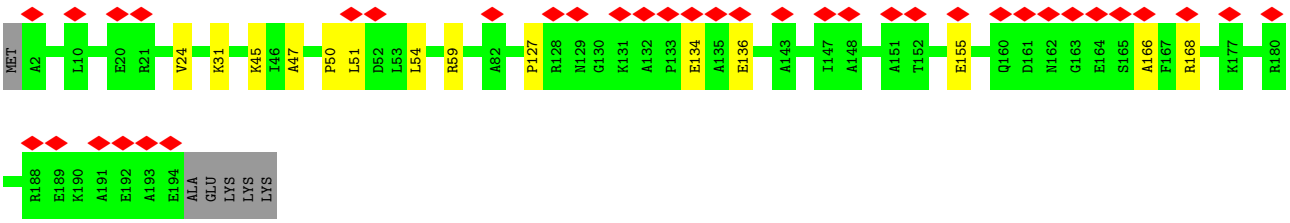



- Molecule 50: 60S ribosomal protein L13-A

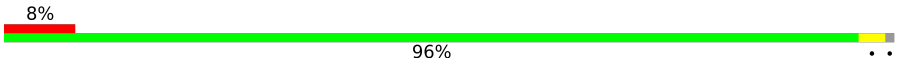
Chain AJ:

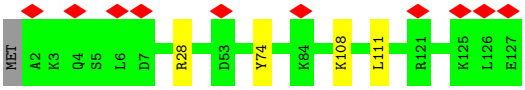



- Molecule 51: 60S ribosomal protein L26-A

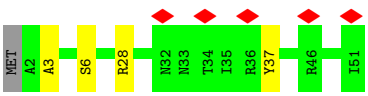
Chain AK:



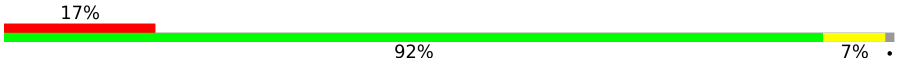

- Molecule 52: 60S ribosomal protein L39

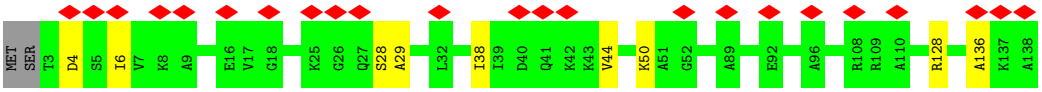
Chain AL:




- Molecule 53: 60S ribosomal protein L14-A

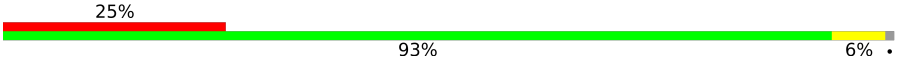
Chain AM:

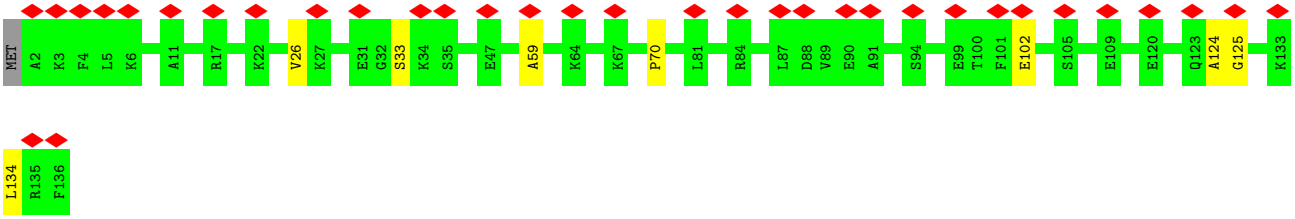



• Molecule 54: 60S ribosomal protein L27-A

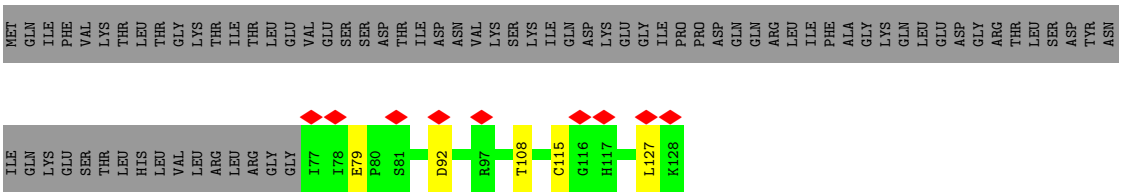
Chain AN:



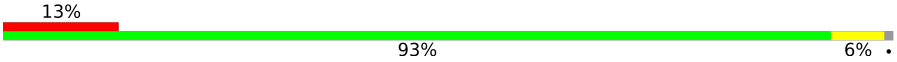

• Molecule 55: Ubiquitin-60S ribosomal protein L40

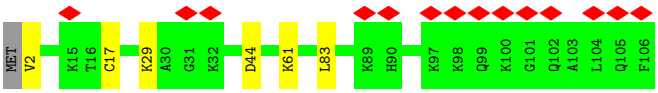
Chain AO:




• Molecule 56: 60S ribosomal protein L42-A

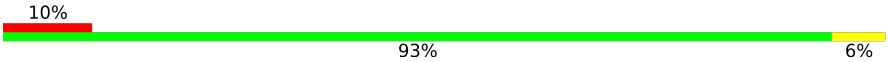
Chain AP:

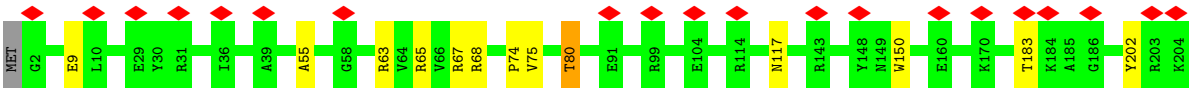



• Molecule 57: 60S ribosomal protein L15-A

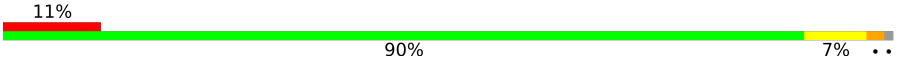
Chain AQ:

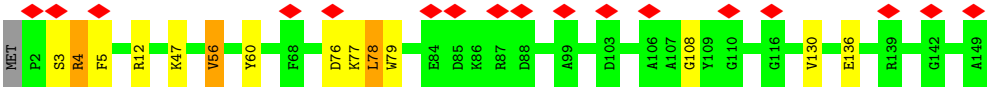



• Molecule 58: 60S ribosomal protein L28

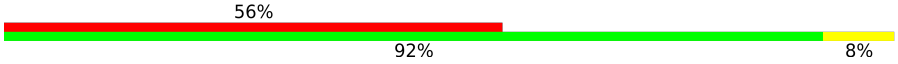
Chain AR:

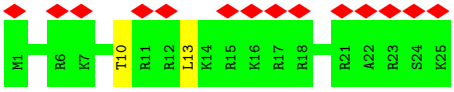


• Molecule 59: 60S ribosomal protein L41-A

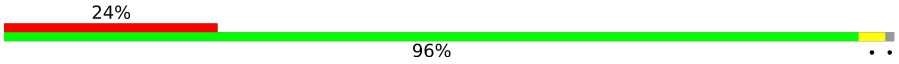
Chain AS:

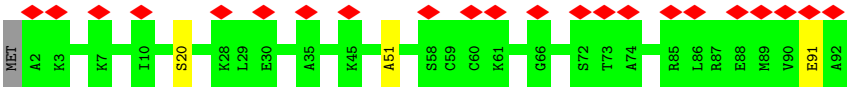



• Molecule 60: 60S ribosomal protein L43-A

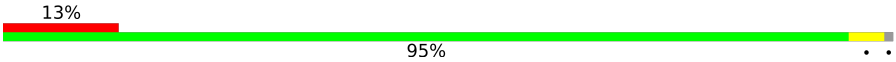
Chain AT:

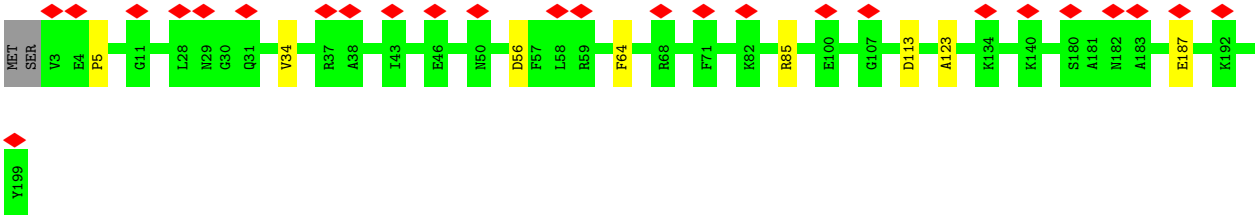



• Molecule 61: 60S ribosomal protein L16-A

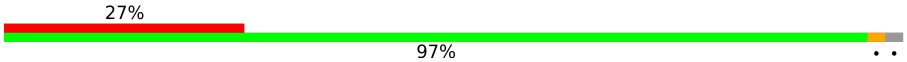
Chain AU:

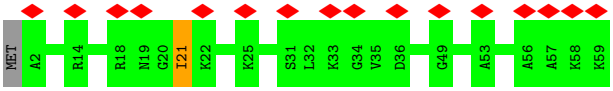



• Molecule 62: 60S ribosomal protein L29

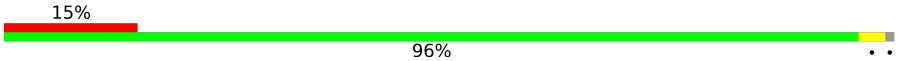
Chain AV:

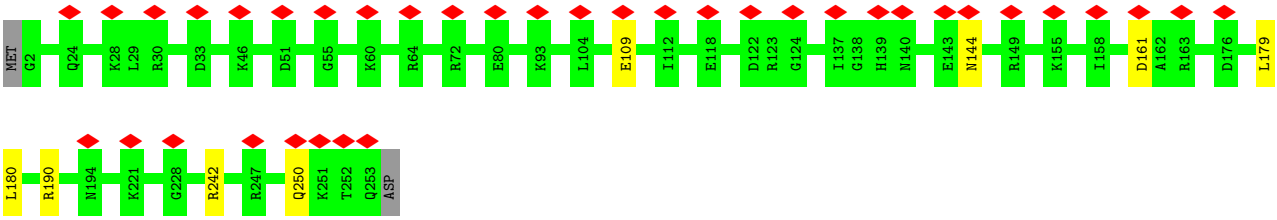



• Molecule 63: 60S ribosomal protein L2-A

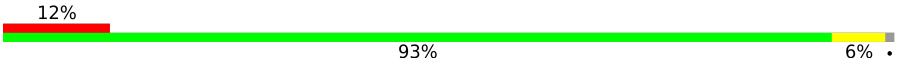
Chain AW:

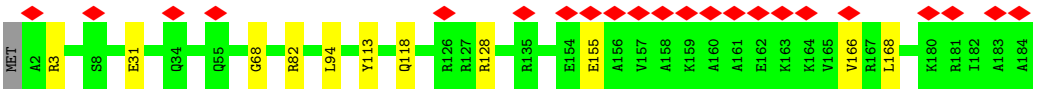



• Molecule 64: 60S ribosomal protein L17-A

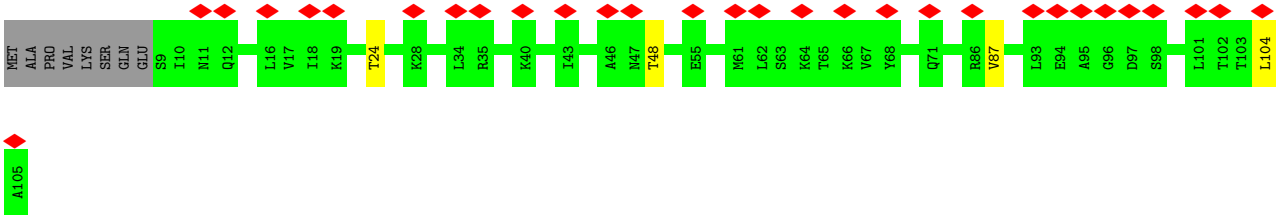
Chain AX:





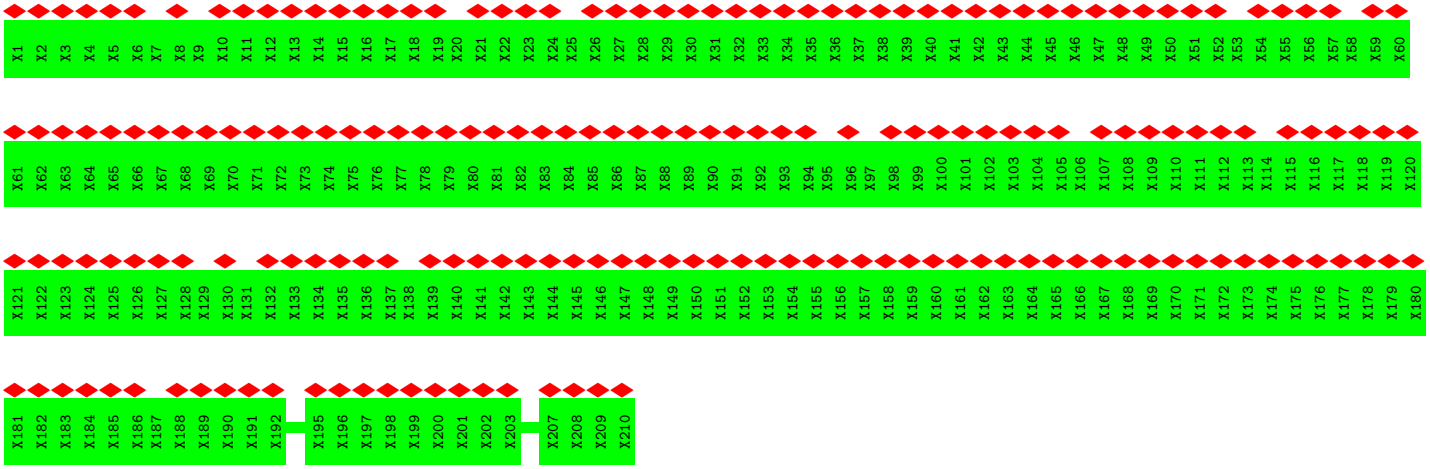

• Molecule 65: 60S ribosomal protein L30

Chain AY:



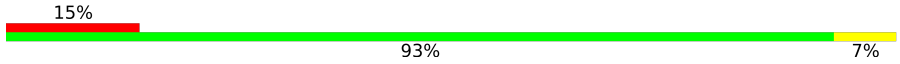

• Molecule 66: uL1

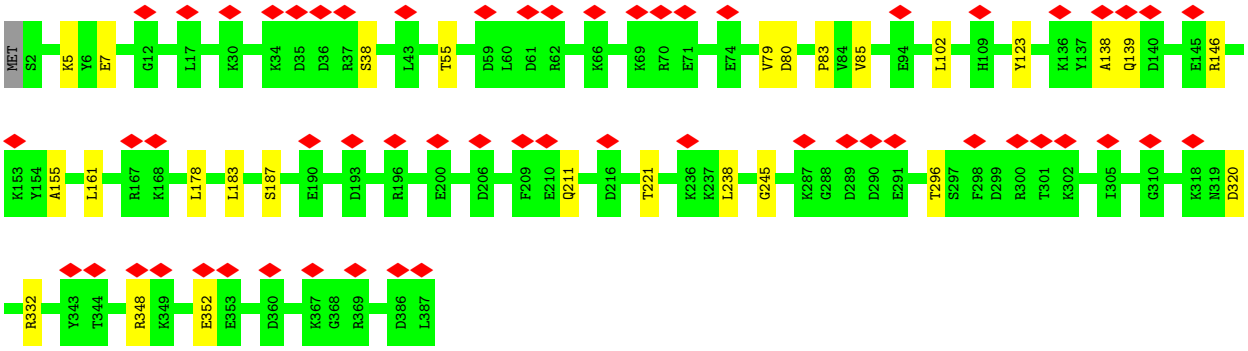
Chain AZ:




• Molecule 67: 60S ribosomal protein L3

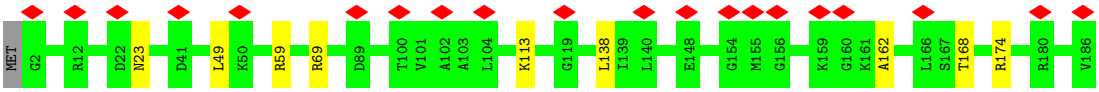
Chain BA:



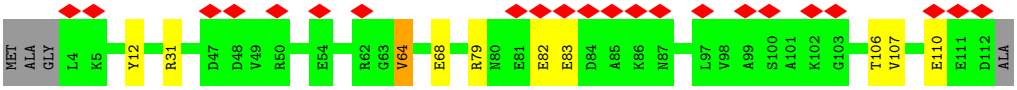

• Molecule 68: 60S ribosomal protein L18-A

Chain BB: 11% 95% 5%



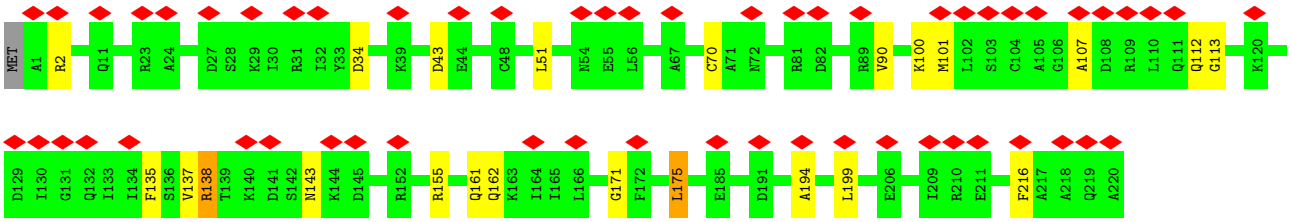

• Molecule 69: 60S ribosomal protein L31-A

Chain BC: 19% 88% 8%



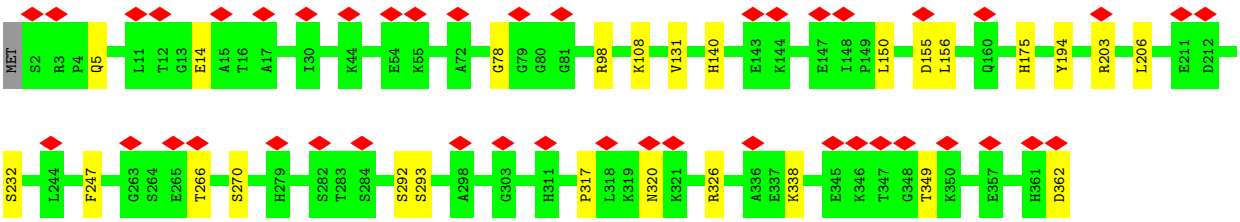

• Molecule 70: 60S ribosomal protein L10

Chain BD: 25% 89% 10%



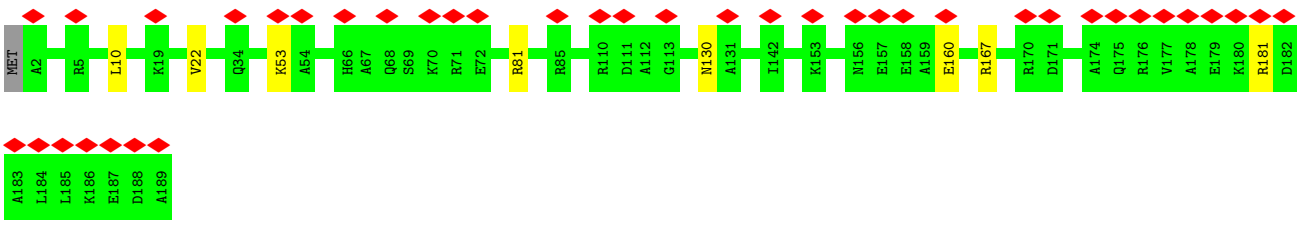

• Molecule 71: 60S ribosomal protein L4-A

Chain BE: 12% 93% 7%



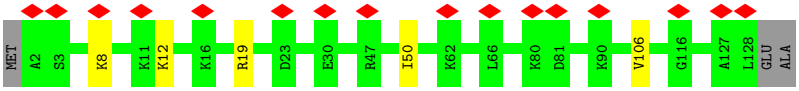

• Molecule 72: 60S ribosomal protein L19-A

Chain BF: 21% 95%



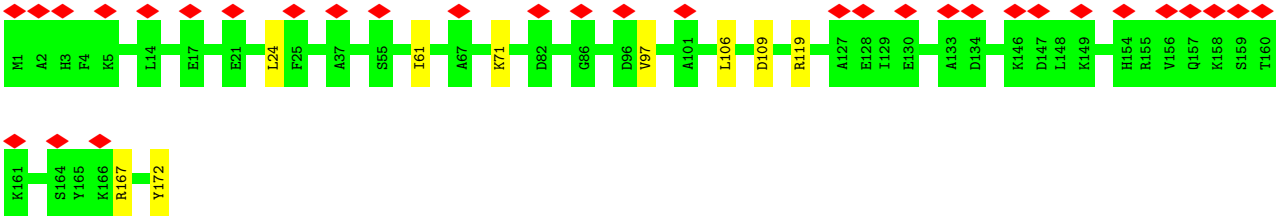

• Molecule 73: 60S ribosomal protein L32

Chain BG: 12% 94%



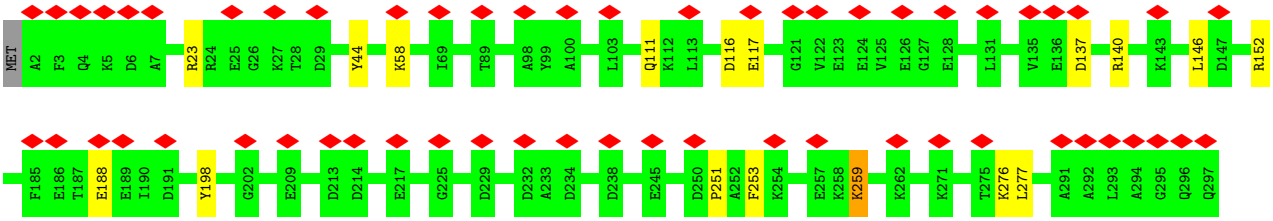

• Molecule 74: 60S ribosomal protein L20-A

Chain BH: 19% 95% 5%



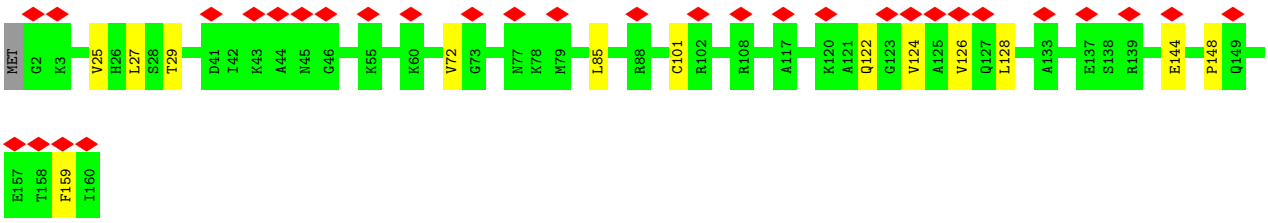

• Molecule 75: 60S ribosomal protein L5

Chain BI: 19% 94% 5%



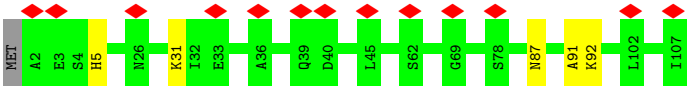

• Molecule 76: 60S ribosomal protein L21-A

Chain BJ: 19% 91% 8%



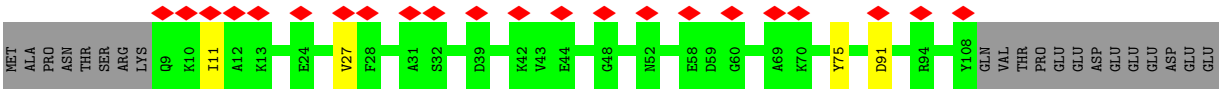

• Molecule 77: 60S ribosomal protein L33-A

Chain BK: 12% 94% 5%



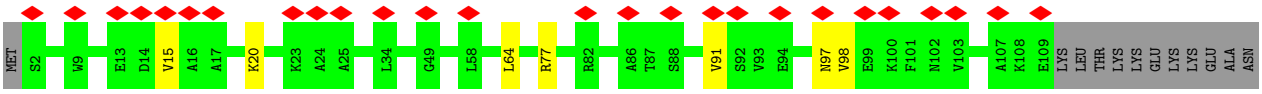

• Molecule 78: 60S ribosomal protein L22-A

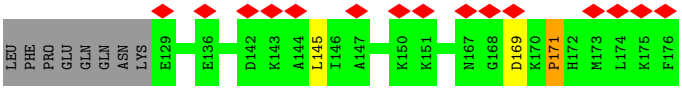
Chain BL: 18% 79% 17%




• Molecule 79: 60S ribosomal protein L6-A

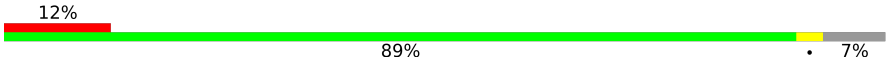
Chain BM:

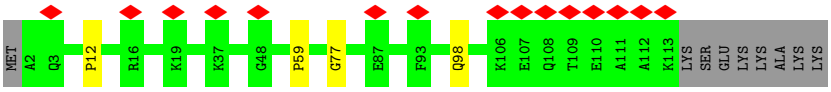



• Molecule 80: 60S ribosomal protein L34-A

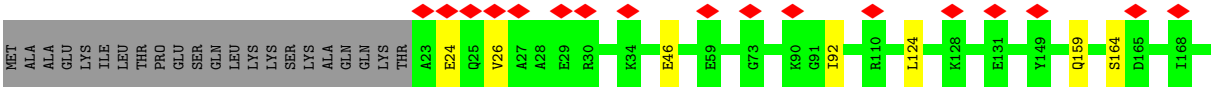
Chain BN:



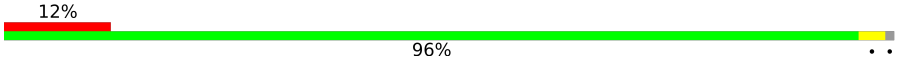

• Molecule 81: 60S ribosomal protein L7-A

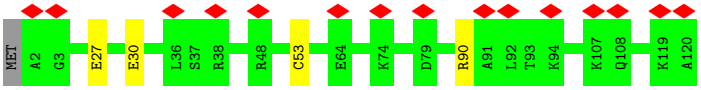
Chain BO:



• Molecule 82: 60S ribosomal protein L35-A

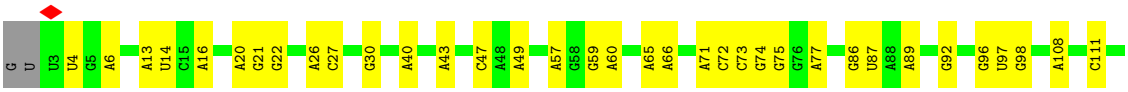
Chain BP:

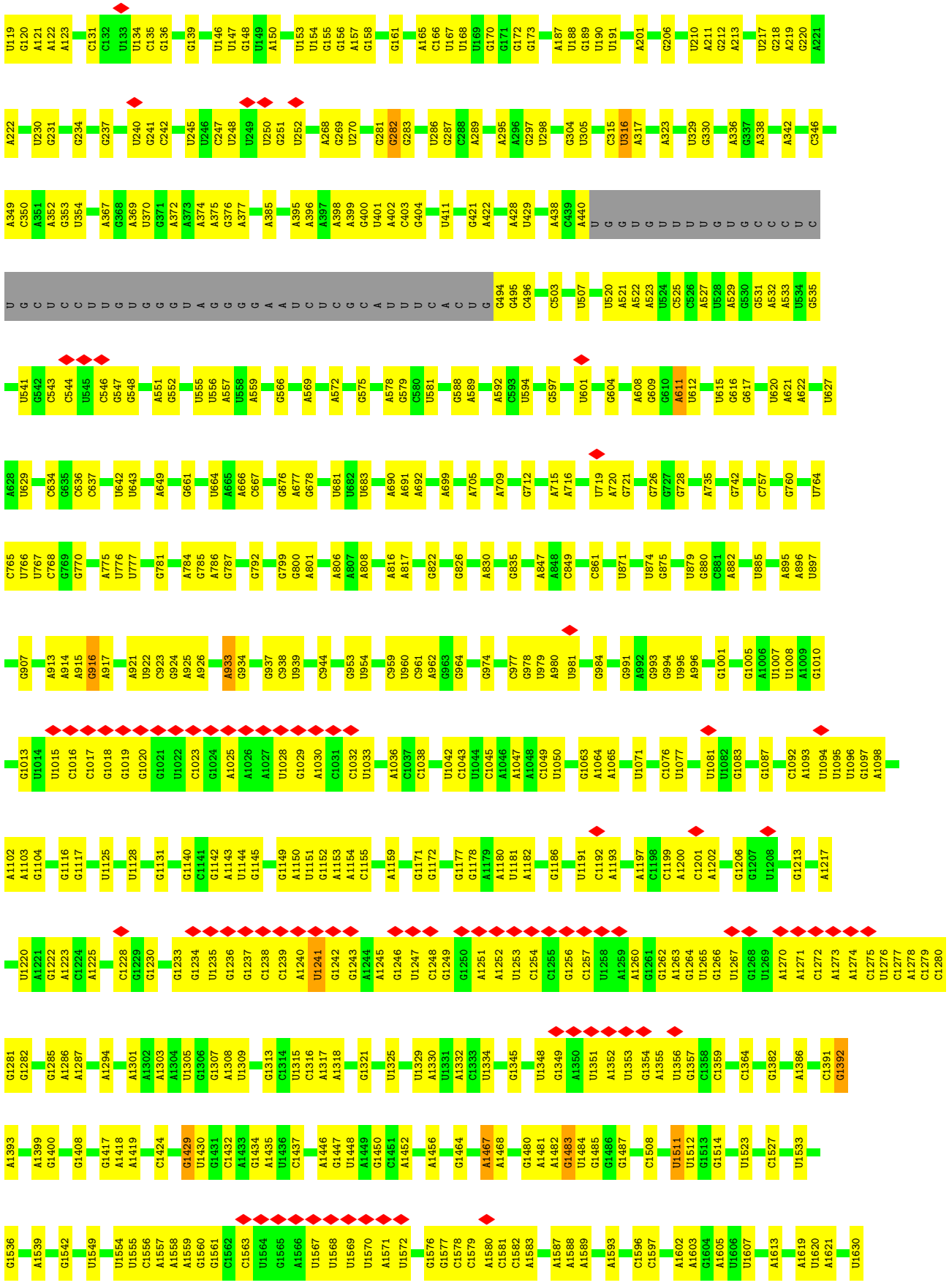


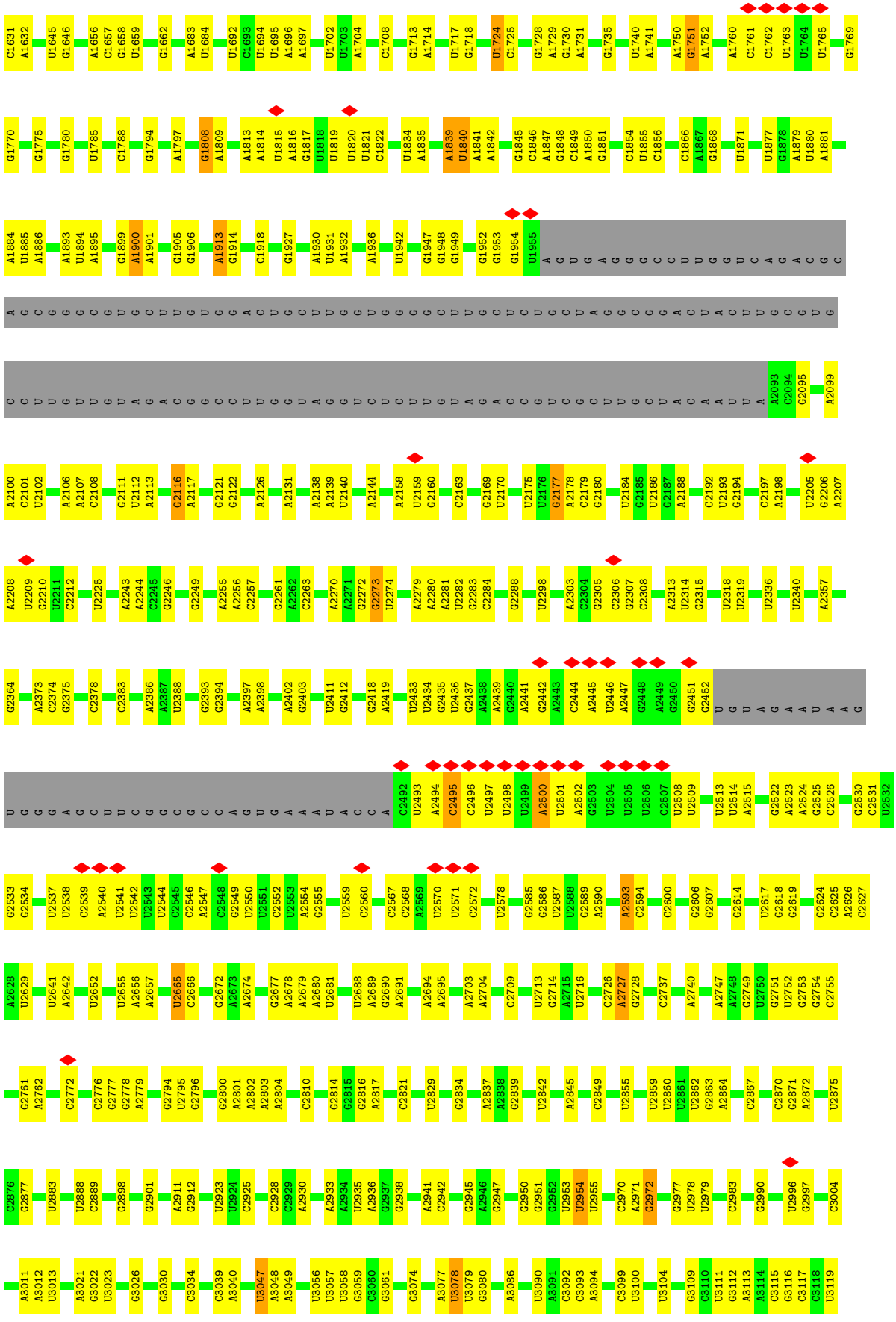




• Molecule 83: 25S ribosomal RNA

Chain BQ:




U119 G120 A121 A122 A123 C131 C132 U133 U134 C135 G136 G139 U146 U147 G148 U149 A150 U153 U154 G155 G156 A157 G158 G161 A165 C166 U167 U168 U169 G170 G171 G172 G173 A187 U188 G189 U190 U191 A201 G206 U210 A211 G212 A213 U217 G218 A219 G220 A221
A222 U230 G231 G234 G237 U240 G241 C242 U245 U246 C247 U248 U249 U250 G251 U252 A268 G269 U270 G281 G282 G283 U286 G287 C288 A289 A295 A296 G297 U298 G304 U305 C315 U316 A317 A323 U329 G330 A336 G337 A338 A342 C346
A349 C350 A351 A352 G353 U354 A367 G368 A369 U370 G371 A372 A373 A374 A375 G376 A377 A385 A395 A396 A397 A398 A399 G400 U401 A402 C403 G404 U411 G421 A422 A428 U429 A438 C439 A440 U G G U U G U U U U G U C C C U U C
U G C U C C U U G U G G G U A G G G G A A U C U C A U U C A C U G G494 G495 C496 C503 U507 U520 A521 A522 A523 U524 C525 C526 A527 U528 A529 G530 G531 A532 A533 U534 G535
U541 G542 C543 C544 U545 C546 G547 G548 A551 G552 U555 U556 A557 U558 A559 G566 A569 A572 G575 A578 G579 C580 U581 G588 A589 A592 C593 U594 G597 U601 G604 A608 G609 G610 A611 U612 U615 C616 G617 U620 A621 A622 U627
A628 U629 C634 G635 C636 C637 U642 U643 A649 G661 U664 A665 A666 C667 G676 A677 G678 U681 U682 U683 A690 A691 A692 A699 A705 A709 G712 A715 A716 U719 A720 G721 G726 G727 G728 A735 G742 C757 G760 U764
C765 U766 U767 C768 G769 G770 A775 U776 U777 G781 A784 G785 A786 G787 G792 G799 G800 A801 A806 A807 A808 A816 A817 G822 G826 A830 G835 A847 A848 C849 C861 U871 U874 G875 U879 G880 C881 A882 U885 A895 A896 U897
G907 A913 A914 A915 G916 A917 A921 U922 C923 G924 A925 A926 A933 G934 G937 C938 U939 C944 G953 U954 C959 U960 C961 A962 G963 G964 G974 C977 G978 U979 A980 U981 G984 G991 A992 G993 G994 U995 A996 G1001 G1005 A1006 U1007 U1008 A1009 G1010
G1013 U1014 U1015 C1016 C1017 G1018 G1019 G1020 G1021 U1022 C1023 G1024 A1025 A1026 A1027 U1028 G1029 A1030 C1031 C1032 U1033 A1036 C1037 C1038 U1042 C1043 U1044 C1045 A1046 A1047 A1048 C1049 U1050 G1063 A1064 A1065 U1071 C1076 U1077 U1081 U1082 G1083 G1087 C1092 A1093 U1094 U1095 U1096 G1097 A1098
A1102 A1103 G1104 G1116 G1117 U1125 U1128 G1131 G1140 C1141 G1142 A1143 U1144 G1145 G1149 A1150 U1151 G1152 A1153 A1154 C1155 A1159 G1171 G1172 G1177 G1178 A1179 A1180 U1181 A1182 G1186 U1191 C1192 A1193 A1197 C1198 C1199 A1200 C1201 A1202 G1206 G1207 U1208 G1213 A1217
U1220 A1221 G1222 A1223 C1224 A1225 C1228 G1229 G1230 G1233 G1234 U1235 G1236 G1237 C1238 C1239 A1240 U1241 G1242 G1243 A1244 A1245 G1246 U1247 C1248 G1249 G1250 A1251 A1252 U1253 C1254 C1255 G1256 C1257 U1258 A1259 A1260 G1261 G1262 A1263 G1264 U1265 G1266 U1267 G1268 U1269 A1270 A1271 C1272 A1273 A1274 C1275 U1276 C1277 A1278 C1279 C1280
G1281 G1282 G1285 A1286 A1287 A1294 A1301 A1302 A1303 A1304 U1305 G1306 G1307 A1308 U1309 G1313 C1314 U1315 C1316 A1317 A1318 G1321 U1325 U1329 A1330 U1331 A1332 C1333 U1334 G1345 U1348 G1349 A1350 U1351 A1352 U1353 G1354 A1355 U1356 G1357 C1358 C1359 C1364 G1382 A1386 C1391 G1392
A1393 A1399 G1400 G1408 G1417 A1418 A1419 C1424 G1429 U1430 G1431 C1432 A1433 G1434 A1435 U1436 C1437 A1446 G1447 U1448 A1449 G1450 C1451 A1452 A1456 G1464 A1467 A1468 G1480 A1481 A1482 G1483 U1484 G1485 G1486 G1487 C1508 U1511 U1512 G1513 G1514 U1523 C1527 U1533
G1536 A1539 G1542 U1549 U1554 U1555 C1556 A1557 A1558 A1559 G1560 G1561 C1562 C1563 U1564 G1565 A1566 U1567 U1568 U1569 U1570 A1571 U1572 G1576 G1577 C1578 C1579 A1580 C1581 C1582 A1583 A1587 A1588 A1589 A1593 C1596 C1597 A1602 A1603 G1604 A1605 U1606 U1607 A1613 A1619 U1620 A1621 U1630


C1631 A1632 U1645 G1646 A1656 C1657 G1658 U1659 G1662 A1683 U1684 U1692 C1693 U1694 U1695 A1696 A1697 U1702 U1703 A1704 C1708 G1713 A1714 U1717 G1718 U1724 C1725 G1728 A1729 G1730 A1731 G1735 U1740 A1741 A1750 G1751 A1752 A1760 C1761 C1762 U1763 U1764 U1765 G1769
G1770 G1775 G1780 U1785 C1788 G1794 A1797 G1808 A1809 A1813 A1814 U1815 A1816 G1817 U1818 U1819 U1820 U1821 C1822 U1834 A1835 A1839 U1840 A1841 A1842 G1845 C1846 A1847 G1848 C1849 A1850 G1851 C1854 U1855 C1856 C1866 A1867 G1868 U1871 U1877 G1878 A1879 U1880 A1881
A1884 U1885 A1886 A1893 U1894 A1895 G1899 A1900 A1901 G1905 G1906 A1913 G1914 C1918 G1927 A1930 U1931 A1932 A1936 U1942 G1947 G1948 G1949 G1952 G1953 G1954 U1955 A G U G A G G C U C A G A C A C G C
A C C G G G U U G U A G A C G G C C U U G G C U U G G U G G G G U U G G C U C U A G C U G U U G A G C C A A C U U G C
C C U U G U U G U A G A C G G C C U U G G C U A G G U C U G U U C U U G U A G C C G G C U U C A A U U U A A2093 C2094 G2095 A2099
A2100 C2101 U2102 A2106 A2107 C2108 G2111 U2112 A2113 G2116 A2117 G2121 G2122 A2126 A2131 A2138 A2139 U2140 A2144 A2158 U2159 G2160 C2163 G2169 U2170 U2175 U2176 G2177 A2178 C2179 G2180 U2184 G2185 U2186 G2187 A2188 C2192 U2193 G2194 C2197 A2198 U2205 G2206 A2207
A2208 U2209 G2210 U2211 C2212 U2225 A2243 A2244 C2245 G2246 G2249 A2255 A2256 C2257 G2261 A2262 C2263 A2270 A2271 C2272 G2273 U2274 A2279 A2280 A2281 U2282 G2283 C2284 G2288 U2298 A2303 C2304 G2305 C2306 G2307 C2308 A2313 U2314 G2315 U2318 U2319 U2336 U2340 A2357
G2364 A2373 C2374 G2375 C2378 C2383 A2386 A2387 U2388 G2393 G2394 A2397 A2398 A2402 G2403 U2411 G2412 G2418 A2419 U2433 U2434 G2435 U2436 G2437 A2438 A2439 G2440 A2441 G2442 A2443 C2444 A2445 U2446 A2447 G2448 A2449 G2450 G2451 G2452 U G U A G A A U A G
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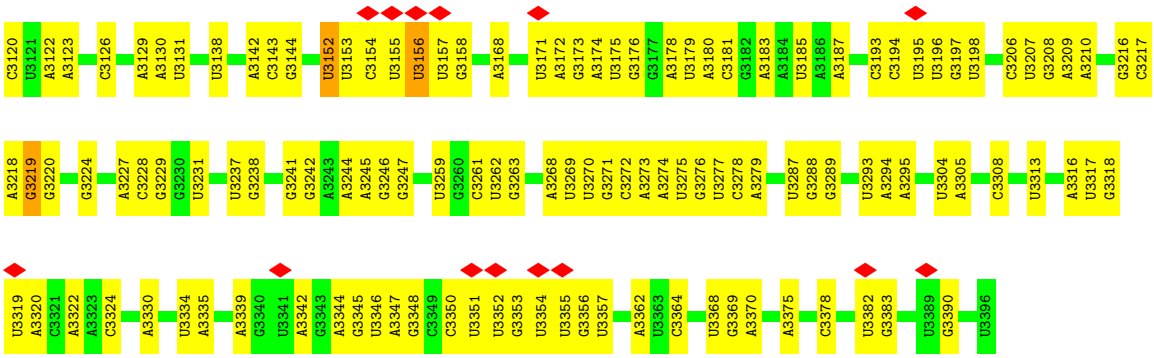
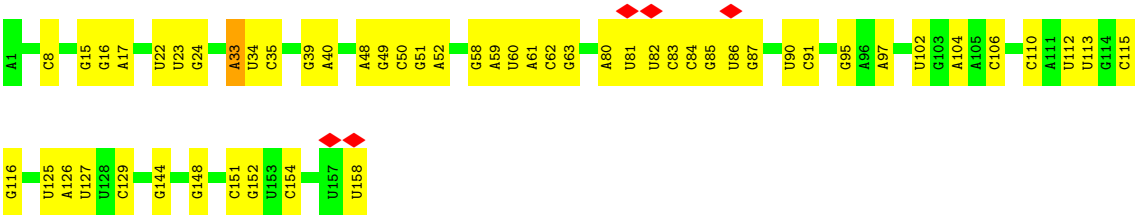



- Molecule 84: 5S ribosomal RNA

Chain BR:

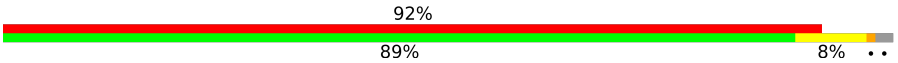
- Molecule 85: 5.8S ribosomal RNA

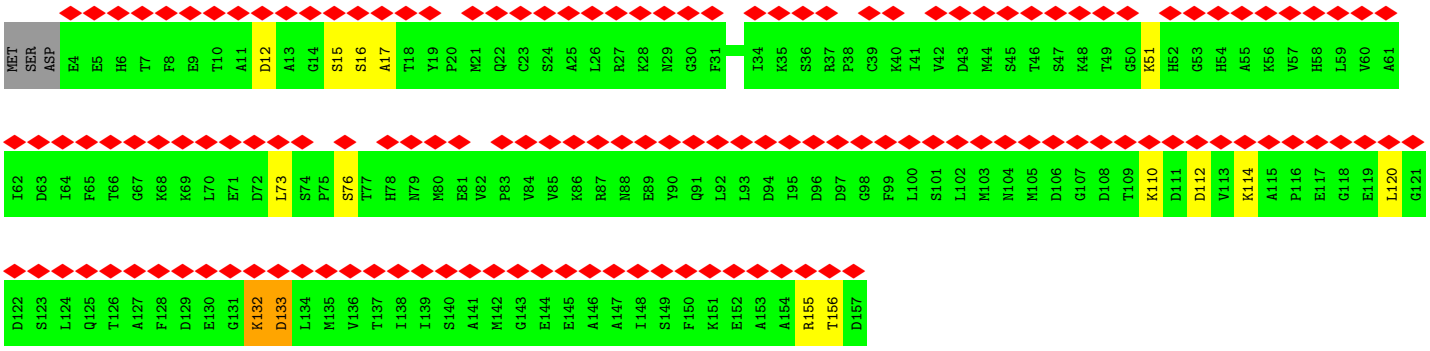
Chain BS:




- Molecule 86: Eukaryotic translation initiation factor 5A-1

Chain BT:



# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, C1 | Depositor |
| Number of particles used | 31503 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | NONE | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/Å^2$) | 2.8 | Depositor |
| Minimum defocus (nm) | Not provided | |
| Maximum defocus (nm) | Not provided | |
| Magnification | Not provided | |
| Image detector | FEI FALCON II (4k x 4k) | Depositor |
| Maximum map value | 0.152 | Depositor |
| Minimum map value | -0.075 | Depositor |
| Average map value | -0.001 | Depositor |
| Map value standard deviation | 0.010 | Depositor |
| Recommended contour level | 0.04 | Depositor |
| Map size (Å) | 520.32, 520.32, 520.32 | wwPDB |
| Map dimensions | 480, 480, 480 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.084, 1.084, 1.084 | Depositor |

# 5 Model quality (i)

## 5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 5CT

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 | 2 | 0.33 | 2/42103 (0.0%) | 0.73 | 20/65603 (0.0%) |
| 2 | A | 0.37 | 0/1759 | 0.62 | 0/2368 |
| 3 | B | 0.39 | 0/1629 | 0.67 | 0/2202 |
| 4 | C | 0.39 | 0/833 | 0.59 | 0/1126 |
| 5 | D | 0.40 | 0/885 | 0.61 | 0/1202 |
| 6 | E | 0.40 | 0/998 | 0.64 | 0/1341 |
| 7 | F | 0.40 | 0/1125 | 0.69 | 1/1510 (0.1%) |
| 8 | G | 0.49 | 2/754 (0.3%) | 0.74 | 1/1005 (0.1%) |
| 9 | H | 0.41 | 0/1211 | 0.75 | 0/1628 |
| 10 | I | 0.42 | 0/1130 | 0.68 | 0/1517 |
| 11 | J | 0.36 | 0/865 | 0.62 | 0/1169 |
| 12 | K | 0.40 | 0/571 | 0.65 | 0/768 |
| 13 | L | 0.37 | 0/499 | 0.69 | 0/670 |
| 14 | M | 0.38 | 0/452 | 0.63 | 0/600 |
| 15 | N | 0.39 | 0/404 | 0.61 | 0/542 |
| 16 | O | 0.35 | 0/2489 | 0.52 | 0/3389 |
| 17 | P | 0.39 | 0/1617 | 0.62 | 0/2215 |
| 18 | Q | 0.40 | 0/1735 | 0.62 | 0/2335 |
| 19 | R | 0.35 | 0/1702 | 0.57 | 0/2310 |
| 20 | S | 0.39 | 0/2109 | 0.61 | 0/2839 |
| 21 | T | 0.38 | 0/1823 | 0.62 | 0/2439 |
| 22 | U | 0.40 | 0/1506 | 0.57 | 0/2028 |
| 23 | V | 0.46 | 0/1514 | 0.78 | 1/2021 (0.0%) |
| 24 | W | 0.40 | 0/1456 | 0.65 | 0/1949 |
| 25 | X | 0.42 | 2/1239 (0.2%) | 0.56 | 0/1673 |
| 26 | Y | 0.39 | 0/1215 | 0.66 | 0/1638 |
| 27 | Z | 0.41 | 0/901 | 0.71 | 0/1217 |
| 28 | a | 0.38 | 0/693 | 0.64 | 0/935 |
| 29 | b | 0.35 | 0/1038 | 0.65 | 1/1395 (0.1%) |
| 30 | c | 0.36 | 0/1139 | 0.61 | 0/1518 |
| 31 | d | 0.41 | 0/1074 | 0.70 | 2/1431 (0.1%) |
| 32 | e | 0.61 | 0/782 | 0.80 | 0/1047 |

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | #\|Z\| >5 | RMSZ | #\|Z\| >5 |
| 33 | f | 0.37 | 0/620 | 0.57 | 0/838 |
| 34 | g | 0.39 | 0/481 | 0.60 | 0/640 |
| 35 | l | 0.47 | 1/764 (0.1%) | 0.79 | 0/1179 |
| 36 | m | 0.26 | 0/1799 | 0.72 | 1/2801 (0.0%) |
| 37 | n | 0.36 | 1/1835 (0.1%) | 0.71 | 0/2858 |
| 38 | h | 0.40 | 2/8985 (0.0%) | 0.56 | 1/12155 (0.0%) |
| 39 | i | 0.38 | 0/10027 | 0.54 | 0/13707 |
| 40 | j | 0.37 | 0/3001 | 0.52 | 0/4083 |
| 40 | k | 0.37 | 0/2988 | 0.54 | 0/4060 |
| 41 | AA | 0.42 | 0/1836 | 0.63 | 0/2481 |
| 42 | AB | 0.39 | 0/1018 | 0.66 | 0/1369 |
| 43 | AC | 0.43 | 0/778 | 0.73 | 0/1034 |
| 44 | AD | 0.41 | 0/1539 | 0.66 | 0/2073 |
| 45 | AE | 0.42 | 0/712 | 0.66 | 1/958 (0.1%) |
| 46 | AF | 0.45 | 0/696 | 0.74 | 0/923 |
| 47 | AG | 0.43 | 0/1374 | 0.71 | 0/1842 |
| 48 | AH | 0.38 | 0/979 | 0.64 | 0/1321 |
| 49 | AI | 0.40 | 0/618 | 0.61 | 0/826 |
| 50 | AJ | 0.45 | 0/1568 | 0.74 | 0/2106 |
| 51 | AK | 0.39 | 0/1004 | 0.67 | 0/1341 |
| 52 | AL | 0.44 | 0/443 | 0.74 | 0/588 |
| 53 | AM | 0.40 | 0/1068 | 0.70 | 0/1438 |
| 54 | AN | 0.41 | 0/1118 | 0.65 | 0/1497 |
| 55 | AO | 0.42 | 0/423 | 0.69 | 0/562 |
| 56 | AP | 0.41 | 0/860 | 0.66 | 0/1136 |
| 57 | AQ | 0.44 | 0/1757 | 0.77 | 1/2354 (0.0%) |
| 58 | AR | 0.42 | 0/1204 | 0.73 | 1/1612 (0.1%) |
| 59 | AS | 0.50 | 0/234 | 0.86 | 0/300 |
| 60 | AT | 0.39 | 0/701 | 0.72 | 0/934 |
| 61 | AU | 0.41 | 0/1585 | 0.66 | 0/2128 |
| 62 | AV | 0.39 | 0/473 | 0.66 | 0/629 |
| 63 | AW | 0.39 | 0/1948 | 0.75 | 0/2617 |
| 64 | AX | 0.42 | 0/1443 | 0.73 | 0/1944 |
| 65 | AY | 0.41 | 0/750 | 0.63 | 0/1008 |
| 67 | BA | 0.41 | 0/3146 | 0.69 | 0/4228 |
| 68 | BB | 0.40 | 0/1465 | 0.73 | 0/1965 |
| 69 | BC | 0.39 | 0/890 | 0.67 | 0/1196 |
| 70 | BD | 0.43 | 0/1807 | 0.71 | 0/2425 |
| 71 | BE | 0.41 | 0/2800 | 0.68 | 0/3790 |
| 72 | BF | 0.43 | 0/1538 | 0.71 | 0/2050 |
| 73 | BG | 0.39 | 0/1041 | 0.64 | 0/1394 |
| 74 | BH | 0.41 | 0/1481 | 0.67 | 0/1990 |
| 75 | BI | 0.42 | 0/2425 | 0.66 | 0/3271 |

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | #\|Z\| >5 | RMSZ | #\|Z\| >5 |
| 76 | BJ | 0.40 | 0/1300 | 0.68 | 0/1743 |
| 77 | BK | 0.41 | 0/868 | 0.69 | 0/1168 |
| 78 | BL | 0.44 | 0/812 | 0.60 | 0/1099 |
| 79 | BM | 0.40 | 0/1260 | 0.65 | 0/1694 |
| 80 | BN | 0.41 | 0/890 | 0.71 | 0/1189 |
| 81 | BO | 0.42 | 0/1821 | 0.67 | 0/2451 |
| 82 | BP | 0.39 | 0/978 | 0.69 | 0/1301 |
| 83 | BQ | 0.34 | 4/75774 (0.0%) | 0.75 | 37/118137 (0.0%) |
| 84 | BR | 0.31 | 0/2883 | 0.73 | 1/4491 (0.0%) |
| 85 | BS | 0.32 | 0/3745 | 0.73 | 1/5829 (0.0%) |
| 86 | BT | 0.32 | 0/1142 | 0.61 | 0/1537 |
| All | All | 0.37 | 14/243945 (0.0%) | 0.70 | 70/355920 (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 |
|---|---|---|---|
| 9 | H | 0 | 1 |
| 10 | I | 0 | 2 |
| 21 | T | 0 | 2 |
| 22 | U | 0 | 1 |
| 23 | V | 0 | 3 |
| 32 | e | 0 | 2 |
| 57 | AQ | 0 | 1 |
| 58 | AR | 0 | 2 |
| 63 | AW | 0 | 1 |
| 69 | BC | 0 | 1 |
| 70 | BD | 0 | 1 |
| 86 | BT | 0 | 1 |
| All | All | 0 | 18 |

The worst 5 of 14 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 1 | 2 | 52 | U | O3'-P | 23.25 | 1.89 | 1.61 |
| 83 | BQ | 683 | U | N1-C2 | 10.32 | 1.47 | 1.38 |
| 37 | n | 1 | G | OP3-P | -10.19 | 1.49 | 1.61 |
| 35 | l | 34 | U | OP3-P | -10.13 | 1.49 | 1.61 |
| 83 | BQ | 683 | U | C4-C5 | 8.78 | 1.51 | 1.43 |

The worst 5 of 70 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 1 | 2 | 52 | U | P-O3'-C3' | -14.01 | 102.89 | 119.70 |
| 1 | 2 | 52 | U | C5'-C4'-O4' | -13.02 | 93.47 | 109.10 |
| 83 | BQ | 2972 | G | N9-C1'-C2' | -11.36 | 99.23 | 114.00 |
| 1 | 2 | 428 | A | N9-C1'-C2' | -10.27 | 100.66 | 114.00 |
| 83 | BQ | 933 | A | C2'-C3'-O3' | 9.73 | 130.90 | 109.50 |

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 9 | H | 143 | ARG | Peptide |
| 10 | I | 88 | VAL | Peptide |
| 10 | I | 89 | ARG | Peptide |
| 21 | T | 196 | ARG | Peptide |
| 21 | T | 197 | ASN | 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 |
|---|---|---|---|---|---|---|
| 2 | A | 221/240 (92%) | 194 (88%) | 24 (11%) | 3 (1%) | 11 46 |
| 3 | B | 204/225 (91%) | 172 (84%) | 24 (12%) | 8 (4%) | 3 28 |
| 4 | C | 94/105 (90%) | 72 (77%) | 16 (17%) | 6 (6%) | 1 20 |
| 5 | D | 119/143 (83%) | 92 (77%) | 17 (14%) | 10 (8%) | 1 13 |
| 6 | E | 122/142 (86%) | 101 (83%) | 18 (15%) | 3 (2%) | 5 36 |
| 7 | F | 139/143 (97%) | 119 (86%) | 15 (11%) | 5 (4%) | 3 30 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 8 | G | 87/136 (64%) | 73 (84%) | 11 (13%) | 3 (3%) | 3 | 31 |
| 9 | H | 143/146 (98%) | 123 (86%) | 17 (12%) | 3 (2%) | 7 | 40 |
| 10 | I | 141/144 (98%) | 112 (79%) | 21 (15%) | 8 (6%) | 1 | 21 |
| 11 | J | 105/121 (87%) | 94 (90%) | 10 (10%) | 1 (1%) | 15 | 52 |
| 12 | K | 68/108 (63%) | 54 (79%) | 9 (13%) | 5 (7%) | 1 | 16 |
| 13 | L | 61/67 (91%) | 57 (93%) | 4 (7%) | 0 | 100 | 100 |
| 14 | M | 51/56 (91%) | 41 (80%) | 10 (20%) | 0 | 100 | 100 |
| 15 | N | 49/152 (32%) | 40 (82%) | 6 (12%) | 3 (6%) | 1 | 20 |
| 16 | O | 316/319 (99%) | 274 (87%) | 37 (12%) | 5 (2%) | 9 | 44 |
| 17 | P | 204/252 (81%) | 176 (86%) | 20 (10%) | 8 (4%) | 3 | 28 |
| 18 | Q | 212/255 (83%) | 170 (80%) | 31 (15%) | 11 (5%) | 2 | 23 |
| 19 | R | 218/254 (86%) | 184 (84%) | 30 (14%) | 4 (2%) | 8 | 42 |
| 20 | S | 258/261 (99%) | 213 (83%) | 36 (14%) | 9 (4%) | 3 | 31 |
| 21 | T | 224/236 (95%) | 188 (84%) | 29 (13%) | 7 (3%) | 4 | 33 |
| 22 | U | 182/190 (96%) | 142 (78%) | 31 (17%) | 9 (5%) | 2 | 24 |
| 23 | V | 184/200 (92%) | 128 (70%) | 30 (16%) | 26 (14%) | 0 | 4 |
| 24 | W | 176/197 (89%) | 149 (85%) | 21 (12%) | 6 (3%) | 3 | 31 |
| 25 | X | 153/156 (98%) | 129 (84%) | 17 (11%) | 7 (5%) | 2 | 24 |
| 26 | Y | 148/151 (98%) | 134 (90%) | 11 (7%) | 3 (2%) | 7 | 41 |
| 27 | Z | 125/137 (91%) | 103 (82%) | 17 (14%) | 5 (4%) | 3 | 28 |
| 28 | a | 85/87 (98%) | 67 (79%) | 14 (16%) | 4 (5%) | 2 | 24 |
| 29 | b | 127/130 (98%) | 116 (91%) | 8 (6%) | 3 (2%) | 6 | 37 |
| 30 | c | 142/145 (98%) | 120 (84%) | 21 (15%) | 1 (1%) | 22 | 60 |
| 31 | d | 130/135 (96%) | 109 (84%) | 14 (11%) | 7 (5%) | 2 | 22 |
| 32 | e | 95/119 (80%) | 70 (74%) | 17 (18%) | 8 (8%) | 1 | 13 |
| 33 | f | 79/82 (96%) | 61 (77%) | 14 (18%) | 4 (5%) | 2 | 23 |
| 34 | g | 58/63 (92%) | 48 (83%) | 8 (14%) | 2 (3%) | 3 | 31 |
| 38 | h | 1107/1287 (86%) | 965 (87%) | 124 (11%) | 18 (2%) | 9 | 44 |
| 39 | i | 1355/1432 (95%) | 1158 (86%) | 172 (13%) | 25 (2%) | 8 | 42 |
| 40 | j | 388/397 (98%) | 335 (86%) | 46 (12%) | 7 (2%) | 8 | 42 |
| 40 | k | 382/397 (96%) | 333 (87%) | 40 (10%) | 9 (2%) | 6 | 37 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 41 | AA | 231/256 (90%) | 194 (84%) | 32 (14%) | 5 (2%) | 6 | 39 |
| 42 | AB | 134/137 (98%) | 117 (87%) | 14 (10%) | 3 (2%) | 6 | 39 |
| 43 | AC | 97/100 (97%) | 80 (82%) | 13 (13%) | 4 (4%) | 3 | 27 |
| 44 | AD | 189/191 (99%) | 166 (88%) | 19 (10%) | 4 (2%) | 7 | 40 |
| 45 | AE | 96/155 (62%) | 73 (76%) | 18 (19%) | 5 (5%) | 2 | 23 |
| 46 | AF | 85/88 (97%) | 70 (82%) | 14 (16%) | 1 (1%) | 13 | 50 |
| 47 | AG | 167/174 (96%) | 143 (86%) | 18 (11%) | 6 (4%) | 3 | 30 |
| 48 | AH | 119/142 (84%) | 103 (87%) | 14 (12%) | 2 (2%) | 9 | 43 |
| 49 | AI | 75/78 (96%) | 66 (88%) | 8 (11%) | 1 (1%) | 12 | 48 |
| 50 | AJ | 191/199 (96%) | 158 (83%) | 27 (14%) | 6 (3%) | 4 | 33 |
| 51 | AK | 124/127 (98%) | 115 (93%) | 9 (7%) | 0 | 100 | 100 |
| 52 | AL | 48/51 (94%) | 42 (88%) | 5 (10%) | 1 (2%) | 7 | 40 |
| 53 | AM | 134/138 (97%) | 119 (89%) | 12 (9%) | 3 (2%) | 6 | 39 |
| 54 | AN | 133/136 (98%) | 118 (89%) | 10 (8%) | 5 (4%) | 3 | 29 |
| 55 | AO | 50/128 (39%) | 45 (90%) | 3 (6%) | 2 (4%) | 3 | 28 |
| 56 | AP | 103/106 (97%) | 86 (84%) | 16 (16%) | 1 (1%) | 15 | 52 |
| 57 | AQ | 201/204 (98%) | 175 (87%) | 21 (10%) | 5 (2%) | 5 | 36 |
| 58 | AR | 146/149 (98%) | 118 (81%) | 21 (14%) | 7 (5%) | 2 | 24 |
| 59 | AS | 23/25 (92%) | 23 (100%) | 0 | 0 | 100 | 100 |
| 60 | AT | 89/92 (97%) | 81 (91%) | 7 (8%) | 1 (1%) | 14 | 51 |
| 61 | AU | 195/199 (98%) | 177 (91%) | 15 (8%) | 3 (2%) | 10 | 46 |
| 62 | AV | 56/59 (95%) | 50 (89%) | 5 (9%) | 1 (2%) | 8 | 42 |
| 63 | AW | 250/254 (98%) | 218 (87%) | 31 (12%) | 1 (0%) | 34 | 70 |
| 64 | AX | 181/184 (98%) | 158 (87%) | 19 (10%) | 4 (2%) | 6 | 39 |
| 65 | AY | 95/105 (90%) | 86 (90%) | 8 (8%) | 1 (1%) | 14 | 51 |
| 67 | BA | 384/387 (99%) | 332 (86%) | 41 (11%) | 11 (3%) | 4 | 34 |
| 68 | BB | 183/186 (98%) | 163 (89%) | 17 (9%) | 3 (2%) | 9 | 44 |
| 69 | BC | 107/113 (95%) | 94 (88%) | 11 (10%) | 2 (2%) | 8 | 42 |
| 70 | BD | 218/221 (99%) | 185 (85%) | 24 (11%) | 9 (4%) | 3 | 27 |
| 71 | BE | 359/362 (99%) | 306 (85%) | 38 (11%) | 15 (4%) | 3 | 26 |
| 72 | BF | 186/189 (98%) | 167 (90%) | 16 (9%) | 3 (2%) | 9 | 44 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 73 | BG | 125/130 (96%) | 110 (88%) | 13 (10%) | 2 (2%) | 9 | 44 |
| 74 | BH | 170/172 (99%) | 151 (89%) | 16 (9%) | 3 (2%) | 8 | 42 |
| 75 | BI | 294/297 (99%) | 263 (90%) | 22 (8%) | 9 (3%) | 4 | 33 |
| 76 | BJ | 157/160 (98%) | 133 (85%) | 18 (12%) | 6 (4%) | 3 | 29 |
| 77 | BK | 104/107 (97%) | 93 (89%) | 9 (9%) | 2 (2%) | 8 | 42 |
| 78 | BL | 98/121 (81%) | 79 (81%) | 16 (16%) | 3 (3%) | 4 | 33 |
| 79 | BM | 152/176 (86%) | 137 (90%) | 11 (7%) | 4 (3%) | 5 | 36 |
| 80 | BN | 110/121 (91%) | 104 (94%) | 3 (3%) | 3 (3%) | 5 | 35 |
| 81 | BO | 220/244 (90%) | 199 (90%) | 16 (7%) | 5 (2%) | 6 | 38 |
| 82 | BP | 117/120 (98%) | 106 (91%) | 10 (8%) | 1 (1%) | 17 | 54 |
| 86 | BT | 151/157 (96%) | 127 (84%) | 14 (9%) | 10 (7%) | 1 | 19 |
| All | All | 14299/15550 (92%) | 12246 (86%) | 1644 (12%) | 409 (3%) | 7 | 34 |

5 of 409 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | A | 196 | ARG |
| 3 | B | 100 | ASN |
| 5 | D | 115 | VAL |
| 5 | D | 126 | TRP |
| 7 | F | 32 | ASN |

### 5.3.2 Protein sidechains (i)

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

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 2 | A | 182/195 (93%) | 175 (96%) | 7 (4%) | 33 | 61 |
| 3 | B | 173/191 (91%) | 162 (94%) | 11 (6%) | 17 | 48 |
| 4 | C | 88/98 (90%) | 83 (94%) | 5 (6%) | 20 | 52 |
| 5 | D | 89/119 (75%) | 85 (96%) | 4 (4%) | 27 | 57 |
| 6 | E | 101/118 (86%) | 94 (93%) | 7 (7%) | 15 | 46 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 7 | F | 117/119 (98%) | 113 (97%) | 4 (3%) | 37 | 64 |
| 8 | G | 80/124 (64%) | 75 (94%) | 5 (6%) | 18 | 49 |
| 9 | H | 128/129 (99%) | 117 (91%) | 11 (9%) | 10 | 40 |
| 10 | I | 115/116 (99%) | 102 (89%) | 13 (11%) | 6 | 28 |
| 11 | J | 100/114 (88%) | 94 (94%) | 6 (6%) | 19 | 50 |
| 12 | K | 61/89 (68%) | 58 (95%) | 3 (5%) | 25 | 55 |
| 13 | L | 56/60 (93%) | 54 (96%) | 2 (4%) | 35 | 63 |
| 14 | M | 47/49 (96%) | 44 (94%) | 3 (6%) | 17 | 48 |
| 15 | N | 43/135 (32%) | 42 (98%) | 1 (2%) | 50 | 72 |
| 16 | O | 259/262 (99%) | 250 (96%) | 9 (4%) | 36 | 64 |
| 17 | P | 164/210 (78%) | 157 (96%) | 7 (4%) | 29 | 58 |
| 18 | Q | 191/224 (85%) | 182 (95%) | 9 (5%) | 26 | 56 |
| 19 | R | 180/205 (88%) | 175 (97%) | 5 (3%) | 43 | 68 |
| 20 | S | 221/222 (100%) | 217 (98%) | 4 (2%) | 59 | 77 |
| 21 | T | 188/201 (94%) | 181 (96%) | 7 (4%) | 34 | 62 |
| 22 | U | 165/170 (97%) | 160 (97%) | 5 (3%) | 41 | 66 |
| 23 | V | 150/161 (93%) | 133 (89%) | 17 (11%) | 6 | 28 |
| 24 | W | 152/166 (92%) | 150 (99%) | 2 (1%) | 69 | 82 |
| 25 | X | 129/137 (94%) | 126 (98%) | 3 (2%) | 50 | 72 |
| 26 | Y | 127/128 (99%) | 121 (95%) | 6 (5%) | 26 | 56 |
| 27 | Z | 81/105 (77%) | 74 (91%) | 7 (9%) | 10 | 40 |
| 28 | a | 74/74 (100%) | 72 (97%) | 2 (3%) | 44 | 69 |
| 29 | b | 110/111 (99%) | 109 (99%) | 1 (1%) | 78 | 88 |
| 30 | c | 119/120 (99%) | 115 (97%) | 4 (3%) | 37 | 64 |
| 31 | d | 111/113 (98%) | 103 (93%) | 8 (7%) | 14 | 45 |
| 32 | e | 83/101 (82%) | 77 (93%) | 6 (7%) | 14 | 45 |
| 33 | f | 70/71 (99%) | 69 (99%) | 1 (1%) | 67 | 81 |
| 34 | g | 50/54 (93%) | 50 (100%) | 0 | 100 | 100 |
| 38 | h | 936/1139 (82%) | 901 (96%) | 35 (4%) | 34 | 62 |
| 39 | i | 849/1279 (66%) | 823 (97%) | 26 (3%) | 40 | 65 |
| 40 | j | 296/347 (85%) | 288 (97%) | 8 (3%) | 44 | 69 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 40 | k | 295/347 (85%) | 290 (98%) | 5 (2%) | 60 | 78 |
| 41 | AA | 187/208 (90%) | 179 (96%) | 8 (4%) | 29 | 58 |
| 42 | AB | 104/105 (99%) | 98 (94%) | 6 (6%) | 20 | 51 |
| 43 | AC | 81/82 (99%) | 76 (94%) | 5 (6%) | 18 | 49 |
| 44 | AD | 171/171 (100%) | 165 (96%) | 6 (4%) | 36 | 64 |
| 45 | AE | 57/129 (44%) | 57 (100%) | 0 | 100 | 100 |
| 46 | AF | 70/71 (99%) | 65 (93%) | 5 (7%) | 14 | 45 |
| 47 | AG | 147/150 (98%) | 140 (95%) | 7 (5%) | 25 | 56 |
| 48 | AH | 104/118 (88%) | 98 (94%) | 6 (6%) | 20 | 51 |
| 49 | AI | 68/69 (99%) | 67 (98%) | 1 (2%) | 65 | 81 |
| 50 | AJ | 154/159 (97%) | 146 (95%) | 8 (5%) | 23 | 54 |
| 51 | AK | 109/110 (99%) | 105 (96%) | 4 (4%) | 34 | 62 |
| 52 | AL | 45/46 (98%) | 42 (93%) | 3 (7%) | 16 | 47 |
| 53 | AM | 107/109 (98%) | 101 (94%) | 6 (6%) | 21 | 52 |
| 54 | AN | 115/116 (99%) | 112 (97%) | 3 (3%) | 46 | 69 |
| 55 | AO | 47/116 (40%) | 44 (94%) | 3 (6%) | 17 | 48 |
| 56 | AP | 90/91 (99%) | 85 (94%) | 5 (6%) | 21 | 52 |
| 57 | AQ | 175/176 (99%) | 168 (96%) | 7 (4%) | 31 | 59 |
| 58 | AR | 118/119 (99%) | 111 (94%) | 7 (6%) | 19 | 51 |
| 59 | AS | 23/23 (100%) | 21 (91%) | 2 (9%) | 10 | 38 |
| 60 | AT | 71/72 (99%) | 69 (97%) | 2 (3%) | 43 | 68 |
| 61 | AU | 160/162 (99%) | 155 (97%) | 5 (3%) | 40 | 65 |
| 62 | AV | 46/47 (98%) | 45 (98%) | 1 (2%) | 52 | 72 |
| 63 | AW | 193/196 (98%) | 187 (97%) | 6 (3%) | 40 | 65 |
| 64 | AX | 140/146 (96%) | 133 (95%) | 7 (5%) | 24 | 55 |
| 65 | AY | 81/88 (92%) | 78 (96%) | 3 (4%) | 34 | 62 |
| 67 | BA | 320/323 (99%) | 304 (95%) | 16 (5%) | 24 | 55 |
| 68 | BB | 150/151 (99%) | 144 (96%) | 6 (4%) | 31 | 59 |
| 69 | BC | 92/97 (95%) | 84 (91%) | 8 (9%) | 10 | 38 |
| 70 | BD | 184/187 (98%) | 169 (92%) | 15 (8%) | 11 | 40 |
| 71 | BE | 288/289 (100%) | 277 (96%) | 11 (4%) | 33 | 61 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 72 | BF | 153/154 (99%) | 148 (97%) | 5 (3%) | 38 | 65 |
| 73 | BG | 109/111 (98%) | 106 (97%) | 3 (3%) | 43 | 68 |
| 74 | BH | 156/156 (100%) | 150 (96%) | 6 (4%) | 33 | 61 |
| 75 | BI | 244/245 (100%) | 235 (96%) | 9 (4%) | 34 | 62 |
| 76 | BJ | 136/137 (99%) | 129 (95%) | 7 (5%) | 24 | 54 |
| 77 | BK | 90/91 (99%) | 87 (97%) | 3 (3%) | 38 | 65 |
| 78 | BL | 87/107 (81%) | 86 (99%) | 1 (1%) | 73 | 85 |
| 79 | BM | 134/153 (88%) | 127 (95%) | 7 (5%) | 23 | 54 |
| 80 | BN | 95/103 (92%) | 94 (99%) | 1 (1%) | 73 | 85 |
| 81 | BO | 186/205 (91%) | 181 (97%) | 5 (3%) | 44 | 69 |
| 82 | BP | 104/105 (99%) | 101 (97%) | 3 (3%) | 42 | 67 |
| 86 | BT | 118/132 (89%) | 113 (96%) | 5 (4%) | 30 | 58 |
| All | All | 11689/13228 (88%) | 11203 (96%) | 486 (4%) | 33 | 58 |

5 of 486 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 39 | i | 505 | PHE |
| 74 | BH | 119 | ARG |
| 46 | AF | 17 | THR |
| 73 | BG | 106 | VAL |
| 81 | BO | 24 | GLU |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 56 | AP | 27 | GLN |
| 65 | AY | 71 | GLN |
| 58 | AR | 65 | GLN |
| 63 | AW | 209 | HIS |
| 71 | BE | 59 | GLN |

### 5.3.3 RNA (i)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|---|---|---|---|---|
| 1 | 2 | 1764/1800 (98%) | 729 (41%) | 100 (5%) |

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| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|---|---|---|---|---|
| 35 | l | 33/34 (97%) | 20 (60%) | 0 |
| 36 | m | 75/76 (98%) | 34 (45%) | 0 |
| 37 | n | 76/77 (98%) | 30 (39%) | 0 |
| 83 | BQ | 3162/3396 (93%) | 1066 (33%) | 177 (5%) |
| 84 | BR | 120/121 (99%) | 35 (29%) | 7 (5%) |
| 85 | BS | 157/158 (99%) | 50 (31%) | 10 (6%) |
| All | All | 5387/5662 (95%) | 1964 (36%) | 294 (5%) |

5 of 1964 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | 2 | 2 | A |
| 1 | 2 | 4 | C |
| 1 | 2 | 5 | U |
| 1 | 2 | 17 | C |
| 1 | 2 | 25 | C |

5 of 294 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 83 | BQ | 2625 | C |
| 85 | BS | 33 | A |
| 83 | BQ | 2754 | G |
| 83 | BQ | 3172 | A |
| 1 | 2 | 1761 | U |

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | $\#\|Z\| > 2$ | Counts | RMSZ | $\#\|Z\| > 2$ |
| 86 | 5CT | BT | 51 | 86 | 13,14,15 | 0.34 | 0 | 9,15,17 | 1.20 | 2 (22%) |

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|---|---|---|---|---|---|---|---|
| 86 | 5CT | BT | 51 | 86 | - | 5/13/14/16 | - |

There are no bond length outliers.

All (2) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 86 | BT | 51 | 5CT | C1-NZ-CE | -2.30 | 108.27 | 113.42 |
| 86 | BT | 51 | 5CT | C4-C3-C2 | -2.03 | 109.19 | 113.47 |

There are no chirality outliers.

All (5) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 86 | BT | 51 | 5CT | O-C-CA-CB |
| 86 | BT | 51 | 5CT | C2-C3-C4-N1 |
| 86 | BT | 51 | 5CT | CG-CD-CE-NZ |
| 86 | BT | 51 | 5CT | C2-C1-NZ-CE |
| 86 | BT | 51 | 5CT | CD-CE-NZ-C1 |

There are no ring outliers.

No monomer is involved in short contacts.

## 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 |
|---|---|---|
| 1 | 2 | 1 |

All chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|---|---|---|---|---|---|---|
| 1 | 2 | 52:U | O3' | 53:G | P | 1.89 |

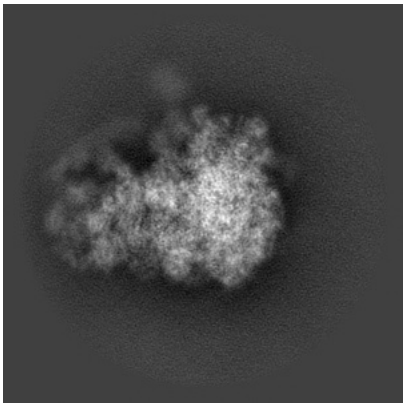
# 6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-3461. These allow visual inspection of the internal detail of the map and identification of artifacts.

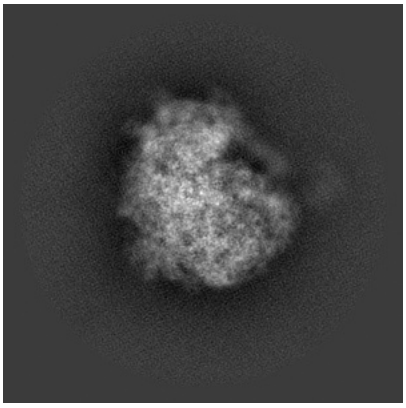
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

## 6.1 Orthogonal projections (i)

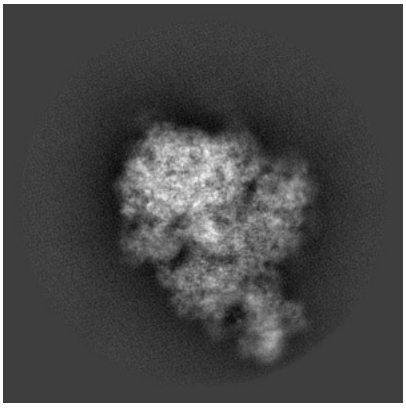
### 6.1.1 Primary map



X



Y

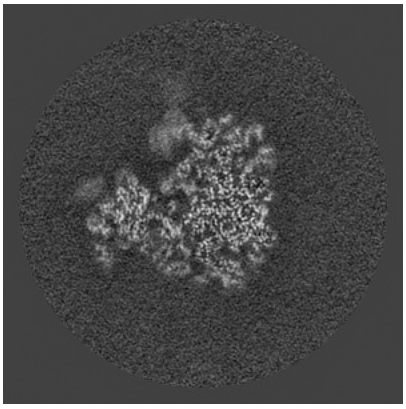


Z

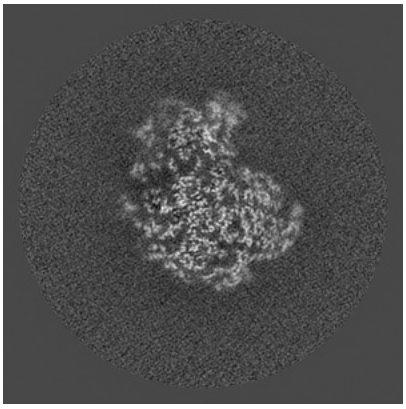
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices (i)

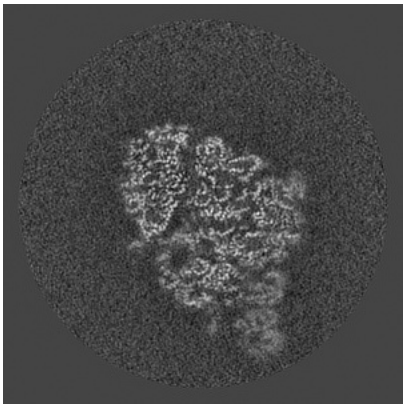
### 6.2.1 Primary map



X Index: 240



Y Index: 240

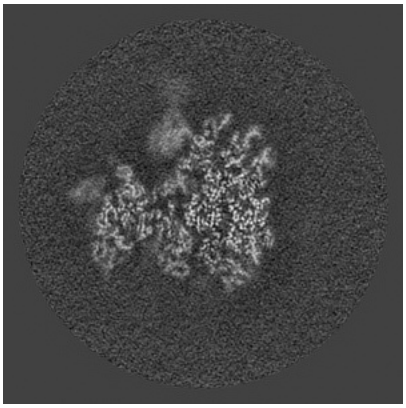


Z Index: 240

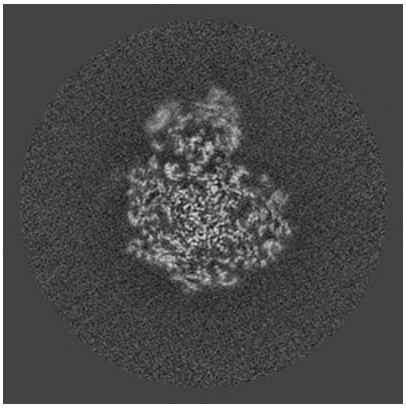
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices (i)

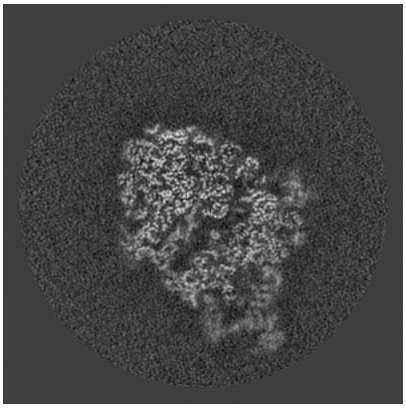
### 6.3.1 Primary map



X Index: 245



Y Index: 253



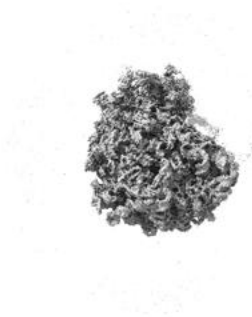
Z Index: 247

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

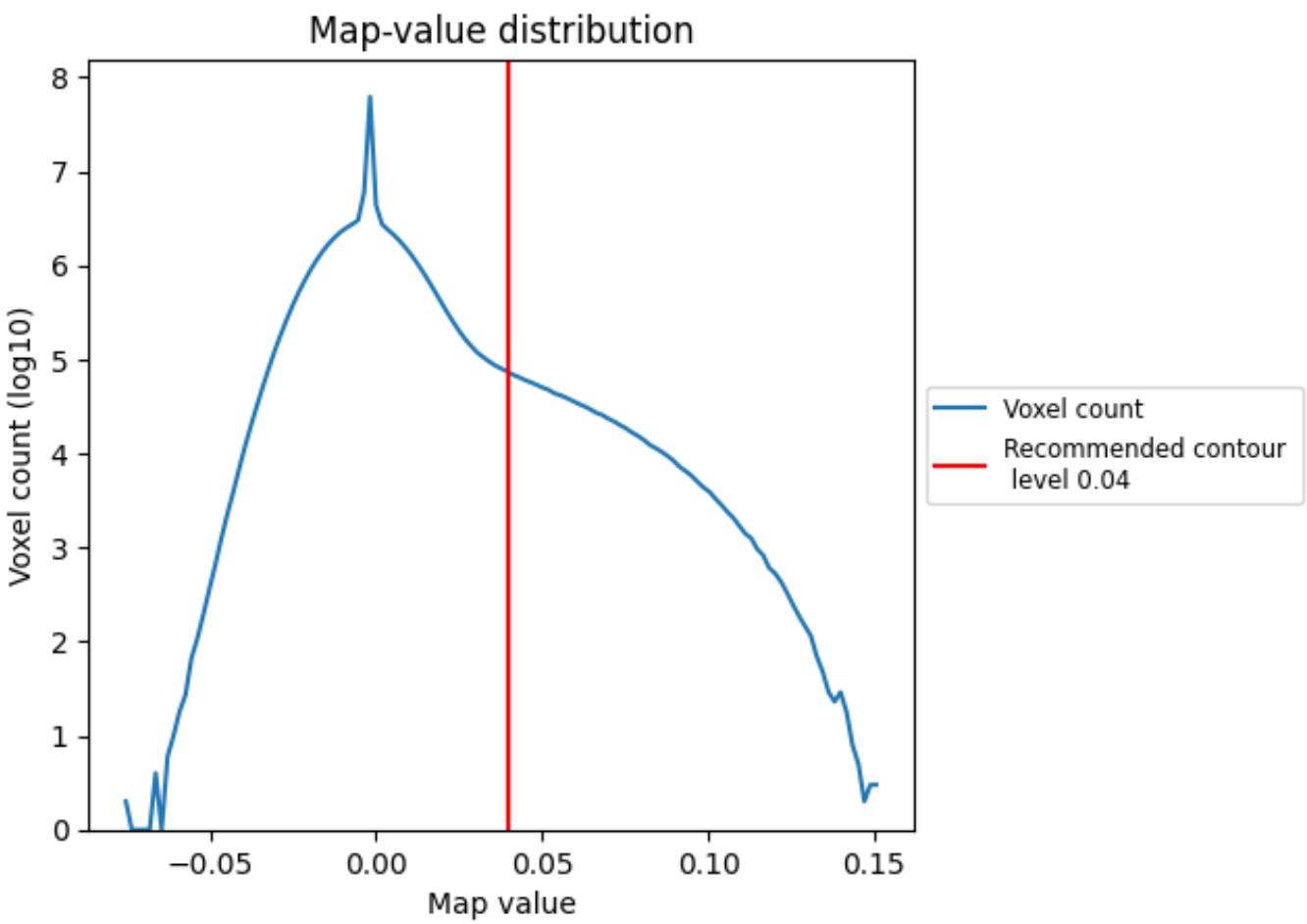
## 6.5 Mask visualisation (i)

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

# 7 Map analysis (i)

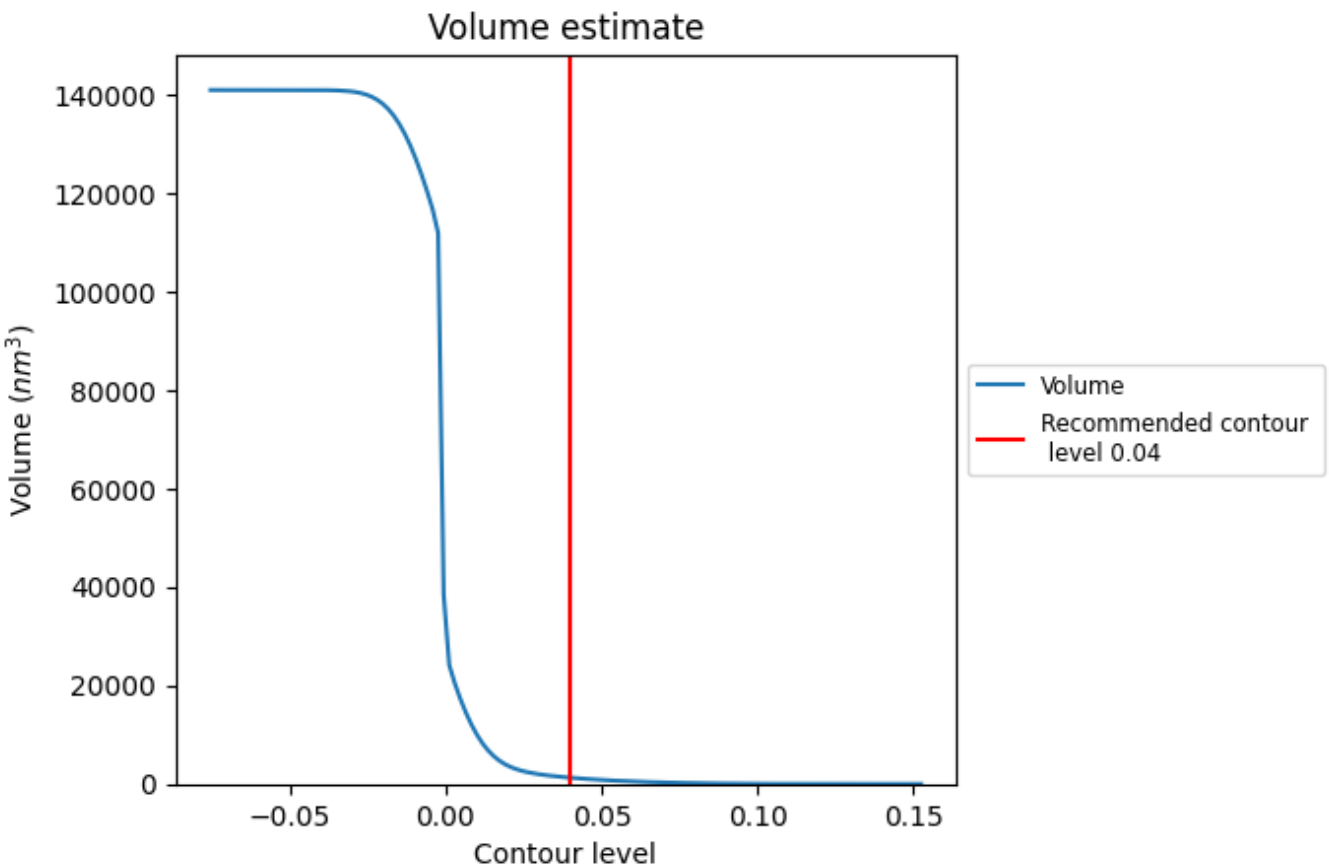
This section contains the results of statistical analysis of the map.

## 7.1 Map-value distribution (i)




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

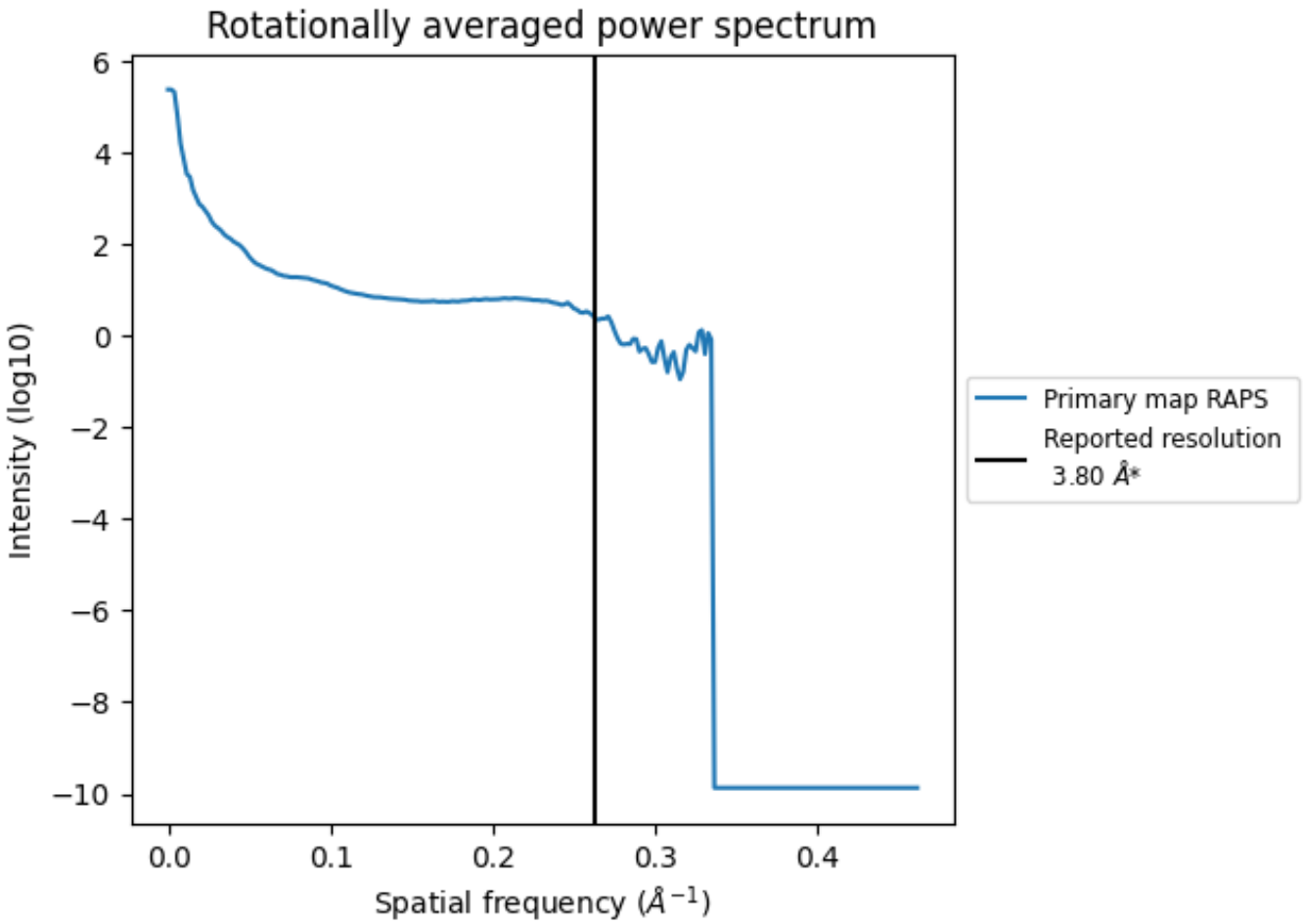
## 7.2 Volume estimate (i)




The volume at the recommended contour level is 1270 $nm^3$; this corresponds to an approximate mass of 1147 kDa.

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

## 7.3 Rotationally averaged power spectrum (i)




*Reported resolution corresponds to spatial frequency of 0.263 Å$^{-1}$

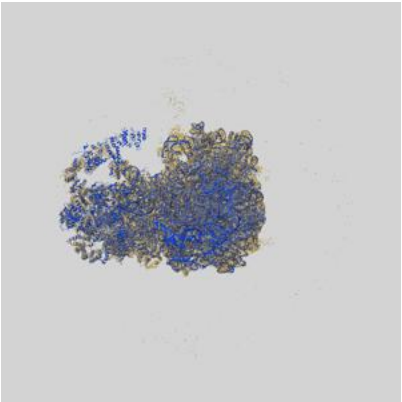
# 8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

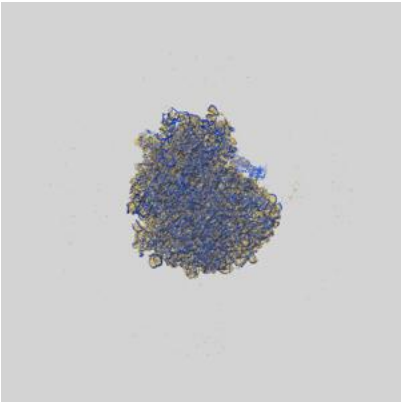
# 9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-3461 and PDB model 5MC6. Per-residue inclusion information can be found in section 3 on page 20.

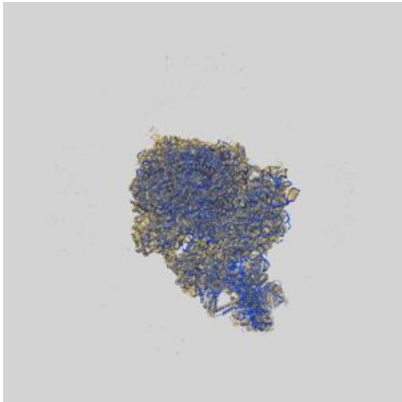
## 9.1 Map-model overlay (i)



X



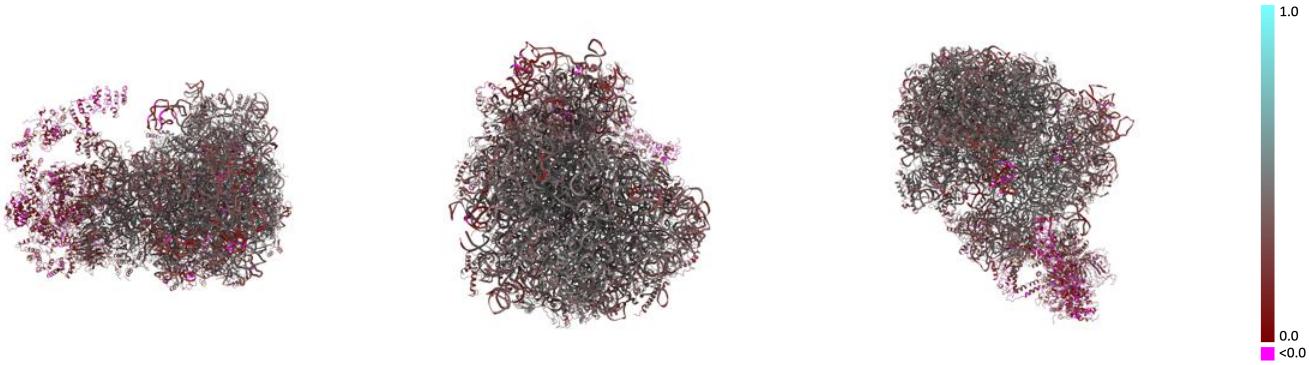
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04 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.

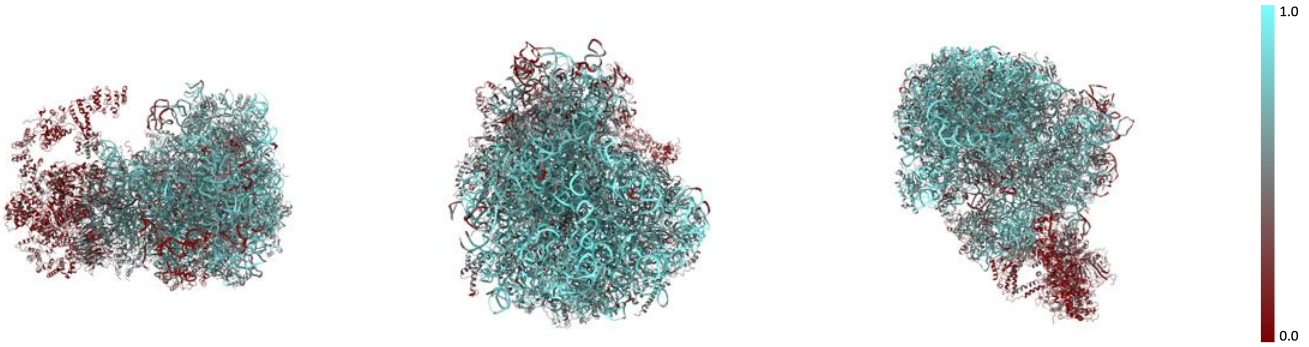
## 9.2 Q-score mapped to coordinate model (i)




X Y Z

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.

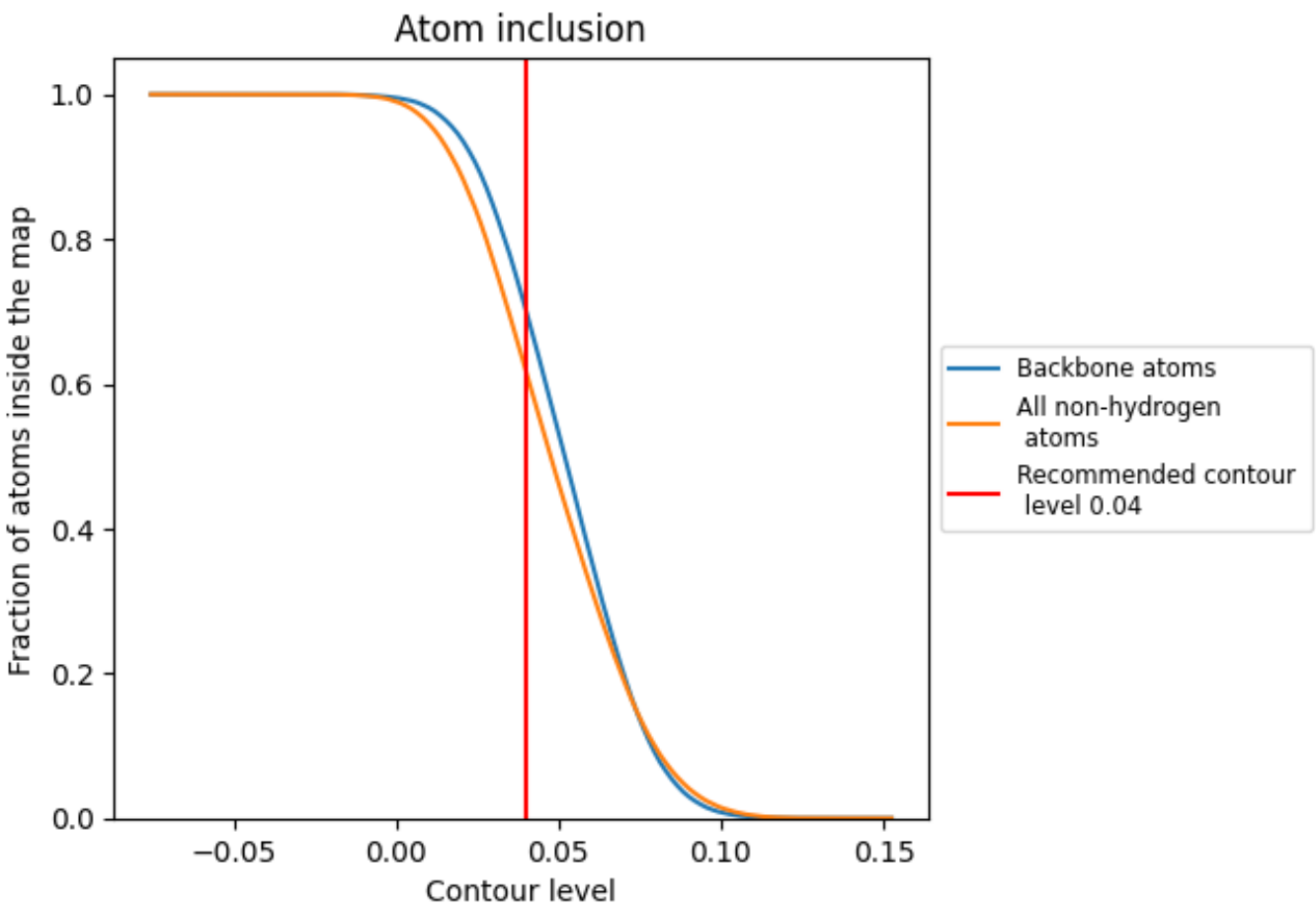
## 9.3 Atom inclusion mapped to coordinate model (i)




X Y Z

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 (0.04).

## 9.4 Atom inclusion (i)




At the recommended contour level, 70% of all backbone atoms, 62% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.04) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|---|---|---|
| All | 0.6174 | 0.3620 |
| 2 | 0.7276 | 0.3590 |
| A | 0.4944 | 0.3910 |
| AA | 0.5147 | 0.3680 |
| AB | 0.5169 | 0.4220 |
| AC | 0.5584 | 0.3700 |
| AD | 0.5208 | 0.3780 |
| AE | 0.4085 | 0.3450 |
| AF | 0.6687 | 0.4610 |
| AG | 0.5802 | 0.3740 |
| AH | 0.6242 | 0.4290 |
| AI | 0.5159 | 0.3720 |
| AJ | 0.5992 | 0.3970 |
| AK | 0.6429 | 0.4260 |
| AL | 0.6241 | 0.4640 |
| AM | 0.5595 | 0.3630 |
| AN | 0.5397 | 0.3760 |
| AO | 0.5856 | 0.4030 |
| AP | 0.5882 | 0.4350 |
| AQ | 0.6359 | 0.4330 |
| AR | 0.6322 | 0.4220 |
| AS | 0.4009 | 0.3980 |
| AT | 0.5590 | 0.4280 |
| AU | 0.5951 | 0.4140 |
| AV | 0.5686 | 0.3950 |
| AW | 0.5982 | 0.4500 |
| AX | 0.6265 | 0.4410 |
| AY | 0.5164 | 0.3840 |
| AZ | 0.1600 | 0.3360 |
| B | 0.4322 | 0.3190 |
| BA | 0.6074 | 0.4230 |
| BB | 0.6194 | 0.4260 |
| BC | 0.5776 | 0.4330 |
| BD | 0.5236 | 0.3950 |
| BE | 0.6266 | 0.4240 |

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| Chain | Atom inclusion | Q-score |
|---|---|---|
| BF | 0.5682 | 0.3980 |
| BG | 0.6016 | 0.4350 |
| BH | 0.5735 | 0.4020 |
| BI | 0.5982 | 0.3630 |
| BJ | 0.5685 | 0.4280 |
| BK | 0.6127 | 0.4340 |
| BL | 0.5358 | 0.3630 |
| BM | 0.5598 | 0.3760 |
| BN | 0.5852 | 0.4230 |
| BO | 0.6062 | 0.3950 |
| BP | 0.6193 | 0.3980 |
| BQ | 0.8208 | 0.4040 |
| BR | 0.8841 | 0.4050 |
| BS | 0.8616 | 0.4220 |
| BT | 0.1121 | 0.2900 |
| C | 0.4711 | 0.3480 |
| D | 0.2722 | 0.2450 |
| E | 0.4299 | 0.2960 |
| F | 0.5134 | 0.3470 |
| G | 0.4917 | 0.3700 |
| H | 0.4705 | 0.3120 |
| I | 0.4422 | 0.2390 |
| J | 0.4857 | 0.3610 |
| K | 0.4516 | 0.2770 |
| L | 0.3312 | 0.3320 |
| M | 0.6288 | 0.4270 |
| N | 0.2972 | 0.1920 |
| O | 0.4575 | 0.3280 |
| P | 0.5107 | 0.3600 |
| Q | 0.4163 | 0.3170 |
| R | 0.5481 | 0.4150 |
| S | 0.4374 | 0.3460 |
| T | 0.4164 | 0.3090 |
| U | 0.3127 | 0.2740 |
| V | 0.4666 | 0.2950 |
| W | 0.5198 | 0.3250 |
| X | 0.4484 | 0.3800 |
| Y | 0.4978 | 0.3600 |
| Z | 0.4838 | 0.3360 |
| a | 0.5000 | 0.3860 |
| b | 0.5381 | 0.4090 |
| c | 0.4945 | 0.4090 |

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| Chain | Atom inclusion | Q-score |
|---|---|---|
| d | 0.4222 | 0.2950 |
| e | 0.4357 | 0.3140 |
| f | 0.4359 | 0.3540 |
| g | 0.4420 | 0.3550 |
| h | 0.1761 | 0.2120 |
| i | 0.1487 | 0.1490 |
| j | 0.1567 | 0.1890 |
| k | 0.2925 | 0.2970 |
| l | 0.3367 | 0.3130 |
| m | 0.6034 | 0.3260 |
| n | 0.6442 | 0.3490 |