# wwPDB EM Validation Summary Report (i)

Nov 7, 2026 – 10:03 am GMT

| | | |
|---|---|---|
| PDB ID | : | 9TCQ / pdb_00009tcq |
| EMDB ID | : | EMD-55796 |
| Title | : | Structural characterization of hibernating ribosomes in the Gram-negative pathogen Klebsiella quasipneumoniae with bS21 and E-site tRNA |
| Authors | : | Vasanthakrishnan, R.K.B.S.; Olivier, D.; Sophie, C.; Yann, L.C.; Sylvie, G.D.; Sassi, M.; Emmanuel, G.; Reynald, G. |
| Deposited on | : | 2025-11-21 |
| Resolution | : | 2.90 Å(reported) |
| Based on initial model | : | 8B0X |

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 (1)) were used in the production of this report:

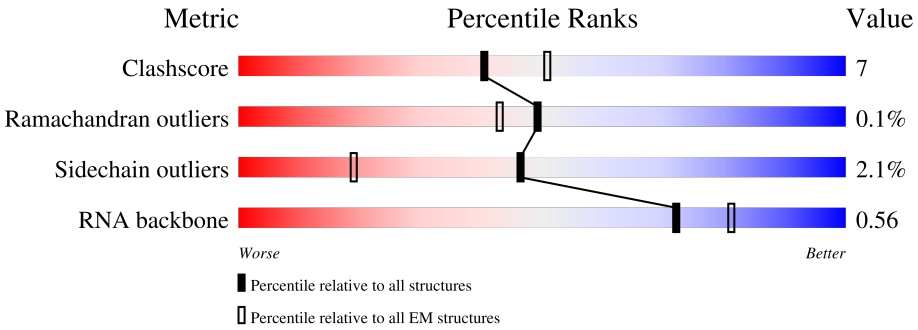
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev133 |
| Mogul | : | 1.8.4, CSD as541be (2020) |
| MolProbity | : | 4-5-2 with Phenix2.2 |
| Percentile statistics | : | 20250101.v01 (using entries in the PDB archive January 1st 2025) |
| EM percentile statistics | : | 202505.v01 (Using data in the EMDB archive up until May 2025) |
| MapQ | : | 1.9.13 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.51 |

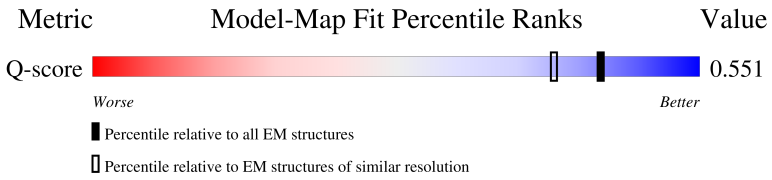
# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.90 Å.

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




| Metric | Whole archive (#Entries) | EM structures (#Entries) | Similar EM resolution (#Entries, resolution range(Å)) |
|---|---|---|---|
| Clashscore | 229148 | 23984 | - |
| Ramachandran outliers | 224038 | 23583 | - |
| Sidechain outliers | 223484 | 23102 | - |
| RNA backbone | 8273 | 3508 | - |
| Q-score | - | 25397 | 13054 ( 2.40 - 3.40 ) |

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 | 0 | 55 | 87% 75% 18% 7% |
| 2 | 1 | 46 | 54% 96% . |
| 3 | 2 | 65 | 75% 75% 23% . |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 4 | 3 | 38 | 97% 82% 18% |
| 5 | 4 | 70 | 100% 74% 26% |
| 6 | 5 | 234 | 62% 39% 23% 38% |
| 7 | A | 1550 | 84% 58% 37% |
| 8 | B | 241 | 93% 65% 27% 7% |
| 9 | C | 232 | 88% 72% 17% 11% |
| 10 | D | 206 | 100% 80% 19% |
| 11 | E | 167 | 86% 74% 19% 7% |
| 12 | F | 131 | 78% 55% 24% 21% |
| 13 | G | 156 | 98% 79% 18% |
| 14 | H | 130 | 97% 87% 12% |
| 15 | I | 130 | 97% 74% 22% |
| 16 | J | 103 | 95% 67% 26% 5% |
| 17 | K | 129 | 90% 66% 23% 9% |
| 18 | L | 124 | 97% 82% 15% |
| 19 | M | 118 | 98% 63% 34% |
| 20 | N | 101 | 99% 71% 28% |
| 21 | O | 89 | 96% 82% 17% |
| 22 | P | 82 | 94% 83% 16% |
| 23 | Q | 84 | 94% 74% 18% 6% |
| 24 | R | 75 | 83% 55% 28% 17% |
| 25 | S | 92 | 91% 61% 29% 9% |
| 26 | T | 87 | 98% 78% 21% |
| 27 | U | 71 | 99% 68% 30% |
| 28 | V | 77 | 100% 27% 53% 16% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 29 | X | 111 | 88% 73% 14% 12% |
| 30 | a | 2923 | 51% 62% 33% |
| 31 | b | 116 | 91% 72% 28% |
| 32 | c | 273 | 73% 90% 9% |
| 33 | d | 209 | 74% 84% 16% |
| 34 | e | 201 | 88% 86% 14% |
| 35 | f | 179 | 99% 73% 25% |
| 36 | g | 177 | 99% 78% 21% |
| 37 | h | 149 | 99% 70% 28% |
| 38 | i | 142 | 87% 78% 22% |
| 39 | j | 123 | 87% 80% 20% |
| 40 | k | 144 | 84% 85% 15% |
| 41 | l | 136 | 91% 81% 18% |
| 42 | m | 128 | 77% 83% 10% 7% |
| 43 | n | 117 | 99% 80% 18% |
| 44 | o | 115 | 89% 78% 21% |
| 45 | p | 118 | 66% 86% 14% |
| 46 | q | 103 | 91% 83% 16% |
| 47 | r | 110 | 87% 83% 17% |
| 48 | s | 100 | 84% 81% 12% 7% |
| 49 | t | 104 | 98% 88% 11% |
| 50 | u | 94 | 99% 79% 20% |
| 51 | v | 85 | 78% 80% 12% 8% |
| 52 | w | 78 | 85% 92% 6% |
| 53 | x | 63 | 97% 78% 19% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 54 | y | 59 |   |
| 55 | z | 57 |   |

# 2 Entry composition (i)

There are 58 unique types of molecules in this entry. The entry contains 146256 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein bL33.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 1 | 0 | 51 | 418 | 268 | 76 | 73 | 1 | 0 | 0 |

- Molecule 2 is a protein called Large ribosomal subunit protein bL34.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 2 | 1 | 46 | 377 | 228 | 90 | 57 | 2 | 0 | 0 |

- Molecule 3 is a protein called Large ribosomal subunit protein bL35.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 3 | 2 | 64 | 504 | 323 | 105 | 74 | 2 | 0 | 0 |

- Molecule 4 is a protein called Large ribosomal subunit protein bL36.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 4 | 3 | 38 | 302 | 185 | 65 | 48 | 4 | 0 | 0 |

- Molecule 5 is a protein called Large ribosomal subunit protein bL31.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 5 | 4 | 70 | 540 | 333 | 103 | 98 | 6 | 0 | 0 |

- Molecule 6 is a protein called Large ribosomal subunit protein uL1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 6 | 5 | 146 | 1105 | 688 | 204 | 211 | 2 | 0 | 0 |

- Molecule 7 is a RNA chain called 16S rRNA (1530-MER).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 7 | A | 1530 | Total | C | N | O | P | 0 | 0 |
| | | | 32847 | 14657 | 6028 | 10632 | 1530 | | |

- Molecule 8 is a protein called Small ribosomal subunit protein uS2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 8 | B | 224 | Total | C | N | O | S | 0 | 0 |
| | | | 1749 | 1106 | 315 | 320 | 8 | | |

- Molecule 9 is a protein called Small ribosomal subunit protein uS3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 9 | C | 206 | Total | C | N | O | S | 0 | 0 |
| | | | 1623 | 1028 | 305 | 287 | 3 | | |

- Molecule 10 is a protein called Small ribosomal subunit protein uS4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 10 | D | 205 | Total | C | N | O | S | 0 | 0 |
| | | | 1644 | 1025 | 316 | 298 | 5 | | |

- Molecule 11 is a protein called Small ribosomal subunit protein uS5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 11 | E | 156 | Total | C | N | O | S | 0 | 0 |
| | | | 1155 | 719 | 219 | 211 | 6 | | |

- Molecule 12 is a protein called Small ribosomal subunit protein bS6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 12 | F | 103 | Total | C | N | O | S | 0 | 0 |
| | | | 832 | 524 | 151 | 150 | 7 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| F | 62 | MET | LEU | variant | UNP A0A2N4W582 |

- Molecule 13 is a protein called Small ribosomal subunit protein uS7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 13 | G | 153 | Total | C | N | O | S | 0 | 0 |
| | | | 1204 | 751 | 231 | 218 | 4 | | |

- Molecule 14 is a protein called Small ribosomal subunit protein uS8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 14 | H | 129 | Total | C | N | O | S | 0 | 0 |
| | | | 977 | 616 | 171 | 184 | 6 | | |

- Molecule 15 is a protein called Small ribosomal subunit protein uS9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 15 | I | 126 | Total | C | N | O | S | 0 | 0 |
| | | | 1010 | 628 | 202 | 177 | 3 | | |

- Molecule 16 is a protein called Small ribosomal subunit protein uS10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 16 | J | 98 | Total | C | N | O | S | 0 | 0 |
| | | | 788 | 493 | 151 | 143 | 1 | | |

- Molecule 17 is a protein called Small ribosomal subunit protein uS11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 17 | K | 117 | Total | C | N | O | S | 0 | 0 |
| | | | 878 | 541 | 173 | 161 | 3 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| K | 119 | IAS | ASN | modified residue | UNP A0A1C1EGM1 |

- Molecule 18 is a protein called Small ribosomal subunit protein uS12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 18 | L | 123 | Total | C | N | O | S | 0 | 0 |
| | | | 958 | 592 | 196 | 165 | 5 | | |

- Molecule 19 is a protein called Small ribosomal subunit protein uS13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 19 | M | 116 | Total | C | N | O | S | 0 | 0 |
| | | | 907 | 564 | 181 | 158 | 4 | | |

- Molecule 20 is a protein called Small ribosomal subunit protein uS14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 20 | N | 100 | Total | C | N | O | S | 0 | 0 |
| | | | 805 | 500 | 164 | 138 | 3 | | |

- Molecule 21 is a protein called Small ribosomal subunit protein uS15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 21 | O | 88 | Total | C | N | O | S | 0 | 0 |
| | | | 710 | 438 | 144 | 127 | 1 | | |

- Molecule 22 is a protein called Small ribosomal subunit protein bS16.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 22 | P | 81 | Total | C | N | O | S | 0 | 0 |
| | | | 636 | 397 | 127 | 111 | 1 | | |

- Molecule 23 is a protein called Small ribosomal subunit protein uS17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 23 | Q | 79 | Total | C | N | O | S | 0 | 0 |
| | | | 639 | 402 | 121 | 112 | 4 | | |

- Molecule 24 is a protein called Small ribosomal subunit protein bS18.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 24 | R | 62 | Total | C | N | O | 0 | 0 |
| | | | 507 | 321 | 94 | 92 | | |

- Molecule 25 is a protein called Small ribosomal subunit protein uS19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 25 | S | 84 | Total | C | N | O | S | 0 | 0 |
| | | | 667 | 426 | 127 | 112 | 2 | | |

- Molecule 26 is a protein called Small ribosomal subunit protein bS20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 26 | T | 86 | Total | C | N | O | S | 0 | 0 |
| | | | 669 | 413 | 138 | 115 | 3 | | |

- Molecule 27 is a protein called Small ribosomal subunit protein bS21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 27 | U | 70 | Total | C | N | O | S | 0 | 0 |
| | | | 589 | 366 | 125 | 97 | 1 | | |

- Molecule 28 is a RNA chain called E-site RNA (77-MER).

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 28 | V | 77 | Total | C | N | O | P | S | 0 | 0 |
| | | | 1644 | 734 | 297 | 535 | 77 | 1 | | |

- Molecule 29 is a protein called Ribosomal subunit interface protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 29 | X | 98 | Total | C | N | O | S | 0 | 0 |
| | | | 778 | 484 | 149 | 142 | 3 | | |

- Molecule 30 is a RNA chain called RNA (2901-MER).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 30 | a | 2901 | Total | C | N | O | P | 0 | 0 |
| | | | 62284 | 27795 | 11452 | 20136 | 2901 | | |

- Molecule 31 is a RNA chain called 5S rRNA (119-MER).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 31 | b | 116 | Total | C | N | O | P | 0 | 0 |
| | | | 2483 | 1106 | 453 | 808 | 116 | | |

- Molecule 32 is a protein called Large ribosomal subunit protein uL2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 32 | c | 271 | Total | C | N | O | S | 0 | 0 |
| | | | 2080 | 1286 | 423 | 364 | 7 | | |

- Molecule 33 is a protein called Large ribosomal subunit protein uL3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 33 | d | 209 | Total | C | N | O | S | 0 | 0 |
| | | | 1567 | 981 | 289 | 294 | 3 | | |

- Molecule 34 is a protein called Large ribosomal subunit protein uL4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 34 | e | 201 | Total | C | N | O | S | 0 | 0 |
| | | | 1554 | 975 | 284 | 290 | 5 | | |

- Molecule 35 is a protein called Large ribosomal subunit protein uL5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 35 | f | 177 | Total | C | N | O | S | 0 | 0 |
| | | | 1410 | 899 | 249 | 256 | 6 | | |

- Molecule 36 is a protein called Large ribosomal subunit protein uL6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 36 | g | 176 | Total | C | N | O | S | 0 | 0 |
| | | | 1319 | 830 | 243 | 244 | 2 | | |

- Molecule 37 is a protein called Large ribosomal subunit protein bL9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 37 | h | 148 | Total | C | N | O | S | 0 | 0 |
| | | | 1099 | 693 | 197 | 208 | 1 | | |

- Molecule 38 is a protein called Large ribosomal subunit protein uL13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 38 | i | 142 | Total | C | N | O | S | 0 | 0 |
| | | | 1134 | 716 | 211 | 202 | 5 | | |

- Molecule 39 is a protein called Large ribosomal subunit protein uL14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 39 | j | 123 | Total | C | N | O | S | 0 | 0 |
| | | | 947 | 594 | 181 | 166 | 6 | | |

- Molecule 40 is a protein called Large ribosomal subunit protein uL15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 40 | k | 144 | Total | C | N | O | S | 0 | 0 |
| | | | 1063 | 658 | 211 | 191 | 3 | | |

- Molecule 41 is a protein called Large ribosomal subunit protein uL16.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 41 | l | 136 | Total | C | N | O | S | 0 | 0 |
| | | | 1074 | 685 | 204 | 179 | 6 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| l | 82 | MS6 | MET | modified residue | UNP A0A1C1EGZ5 |

- Molecule 42 is a protein called Large ribosomal subunit protein bL17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 42 | m | 119 | Total | C | N | O | S | 0 | 0 |
| | | | 950 | 588 | 195 | 162 | 5 | | |

- Molecule 43 is a protein called Large ribosomal subunit protein uL18.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 43 | n | 116 | Total | C | N | O | 0 | 0 |
| | | | 892 | 552 | 178 | 162 | | |

- Molecule 44 is a protein called Large ribosomal subunit protein bL19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 44 | o | 114 | Total | C | N | O | S | 0 | 0 |
| | | | 917 | 574 | 179 | 163 | 1 | | |

- Molecule 45 is a protein called Large ribosomal subunit protein bL20.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 45 | p | 117 | Total | C | N | O | 0 | 0 |
| | | | 947 | 604 | 192 | 151 | | |

- Molecule 46 is a protein called Large ribosomal subunit protein bL21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 46 | q | 103 | Total<br>816 | C<br>517 | N<br>153 | O<br>144 | S<br>2 | 0 | 0 |

- Molecule 47 is a protein called Large ribosomal subunit protein uL22.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 47 | r | 110 | Total<br>855 | C<br>530 | N<br>166 | O<br>156 | S<br>3 | 0 | 0 |

- Molecule 48 is a protein called Large ribosomal subunit protein uL23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 48 | s | 93 | Total<br>739 | C<br>467 | N<br>139 | O<br>131 | S<br>2 | 0 | 0 |

- Molecule 49 is a protein called Large ribosomal subunit protein uL24.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 49 | t | 102 | Total<br>779 | C<br>492 | N<br>146 | O<br>141 | 0 | 0 |

- Molecule 50 is a protein called Large ribosomal subunit protein bL25.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 50 | u | 94 | Total<br>749 | C<br>477 | N<br>136 | O<br>134 | S<br>2 | 0 | 0 |

- Molecule 51 is a protein called Large ribosomal subunit protein bL27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 51 | v | 78 | Total<br>592 | C<br>367 | N<br>118 | O<br>106 | S<br>1 | 0 | 0 |

- Molecule 52 is a protein called Large ribosomal subunit protein bL28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 52 | w | 77 | Total<br>625 | C<br>388 | N<br>129 | O<br>106 | S<br>2 | 0 | 0 |

- Molecule 53 is a protein called Large ribosomal subunit protein uL29.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 53 | x | 62 | Total<br>499 | C<br>308 | N<br>98 | O<br>92 | S<br>1 | 0 | 0 |

- Molecule 54 is a protein called Large ribosomal subunit protein uL30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 54 | y | 58 | Total<br>447 | C<br>279 | N<br>87 | O<br>79 | S<br>2 | 0 | 0 |

- Molecule 55 is a protein called Large ribosomal subunit protein bL32.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 55 | z | 56 | Total<br>443 | C<br>269 | N<br>94 | O<br>79 | S<br>1 | 0 | 0 |

- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| 56 | 3 | 1 | Total<br>1 | Zn<br>1 | 0 |
| 56 | 4 | 1 | Total<br>1 | Zn<br>1 | 0 |

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| 57 | A | 95 | Total<br>95 | Mg<br>95 | 0 |
| 57 | K | 1 | Total<br>1 | Mg<br>1 | 0 |
| 57 | a | 252 | Total<br>252 | Mg<br>252 | 0 |
| 57 | b | 5 | Total<br>5 | Mg<br>5 | 0 |
| 57 | c | 2 | Total<br>2 | Mg<br>2 | 0 |
| 57 | d | 1 | Total<br>1 | Mg<br>1 | 0 |
| 57 | m | 1 | Total<br>1 | Mg<br>1 | 0 |
| 57 | p | 1 | Total<br>1 | Mg<br>1 | 0 |

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| Mol | Chain | Residues | Atoms | AltConf |
|---|---|---|---|---|
| 57 | z | 1 | Total Mg<br>1 1 | 0 |

- Molecule 58 is POTASSIUM ION (CCD ID: K) (formula: K).

| Mol | Chain | Residues | Atoms | AltConf |
|---|---|---|---|---|
| 58 | A | 47 | Total K<br>47 47 | 0 |
| 58 | a | 116 | Total K<br>116 116 | 0 |
| 58 | b | 1 | Total K<br>1 1 | 0 |
| 58 | c | 3 | Total K<br>3 3 | 0 |
| 58 | e | 1 | Total K<br>1 1 | 0 |
| 58 | f | 1 | Total K<br>1 1 | 0 |

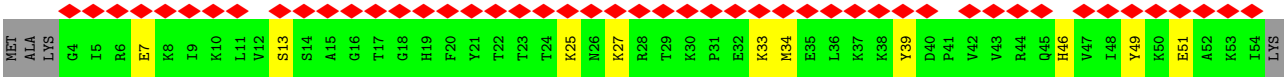
# 3 Residue-property plots (i)

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: Large ribosomal subunit protein bL33

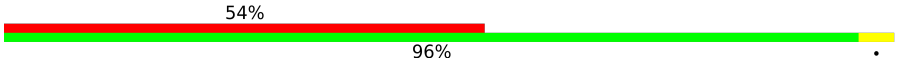
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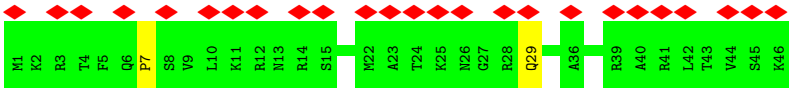



• Molecule 2: Large ribosomal subunit protein bL34

Chain 1:

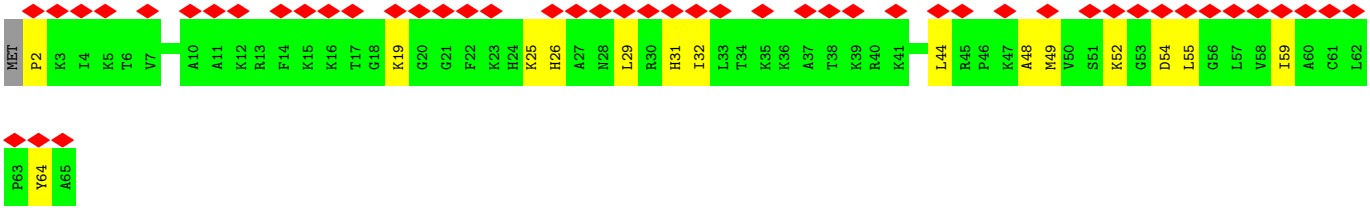



• Molecule 3: Large ribosomal subunit protein bL35

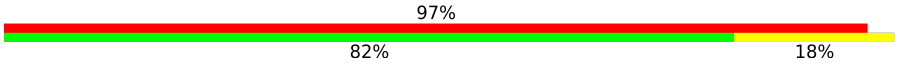
Chain 2:

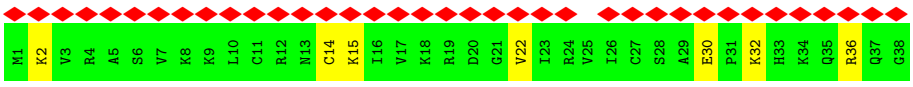



• Molecule 4: Large ribosomal subunit protein bL36

Chain 3:

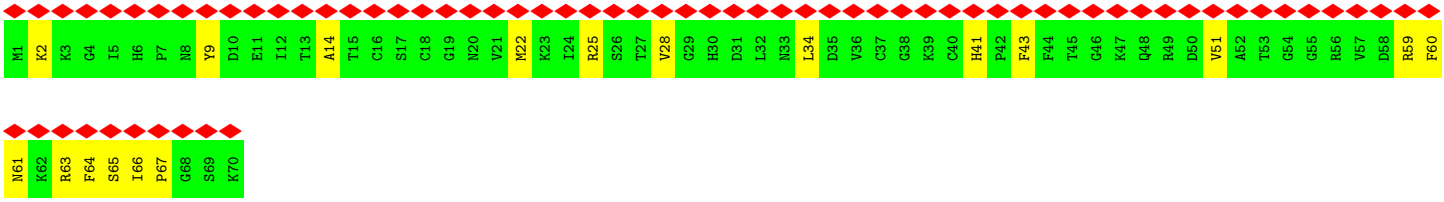



• Molecule 5: Large ribosomal subunit protein bL31

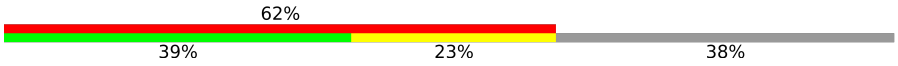
Chain 4:

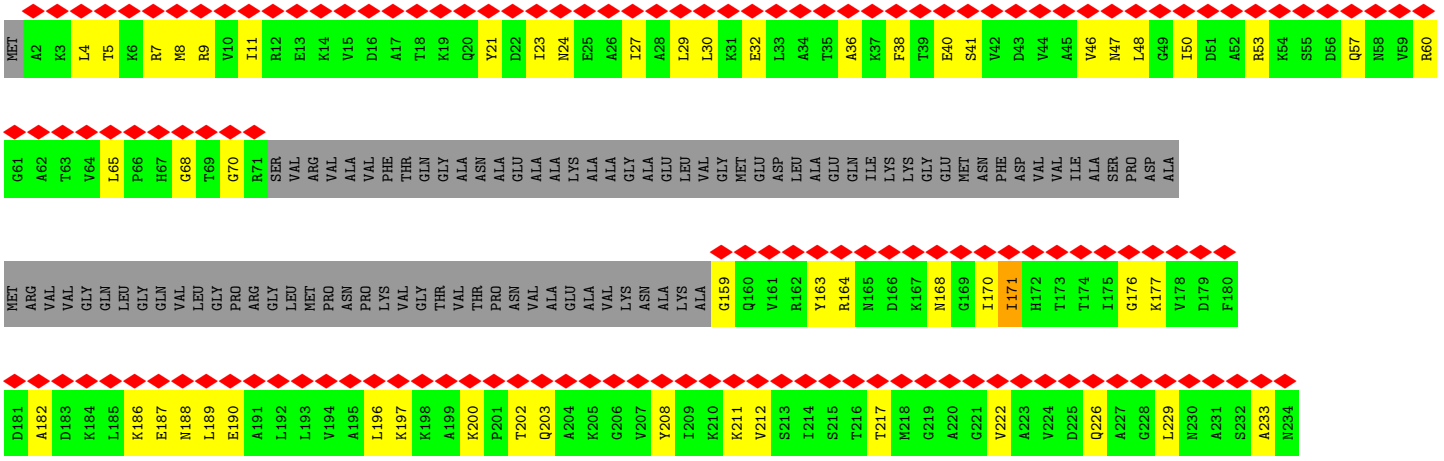





• Molecule 6: Large ribosomal subunit protein uL1

Chain 5:

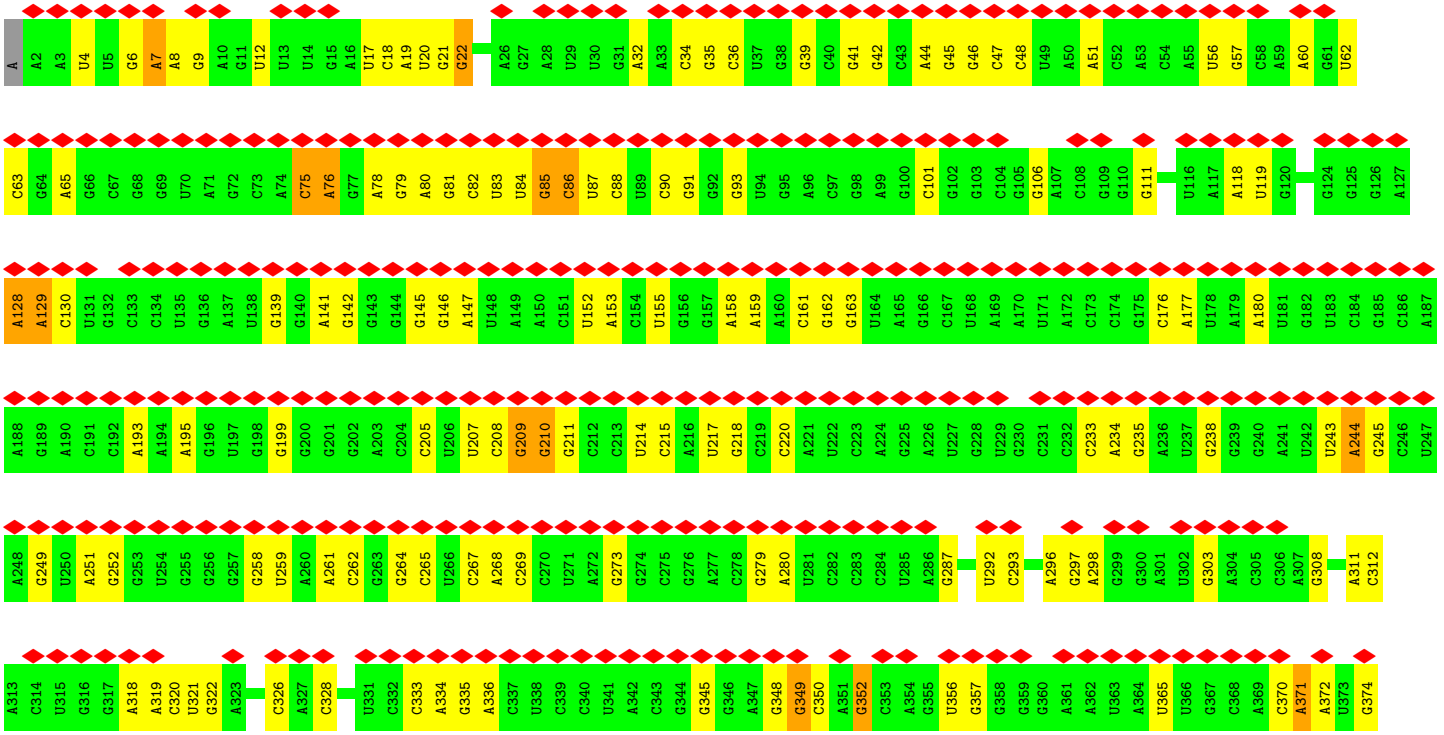


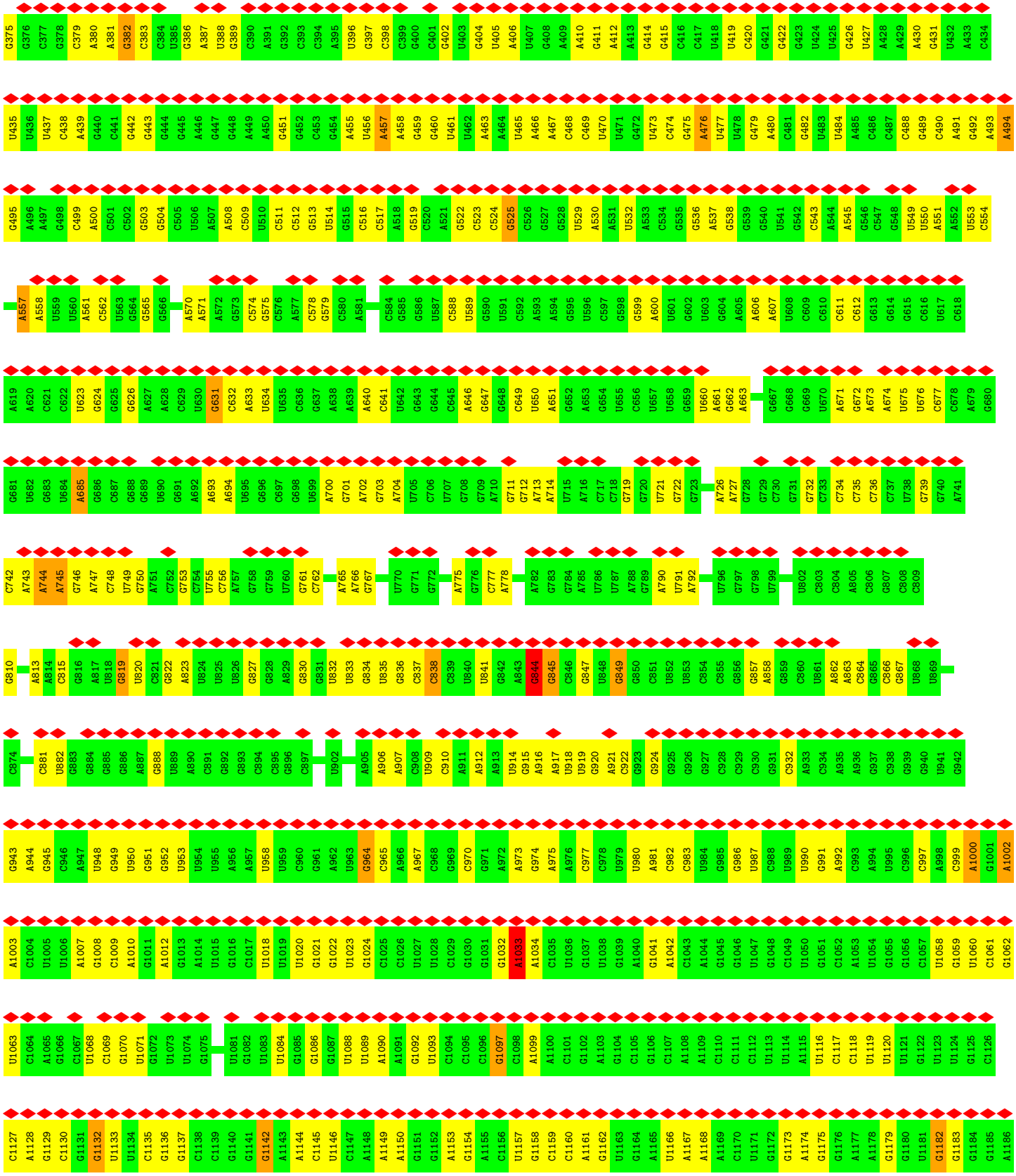



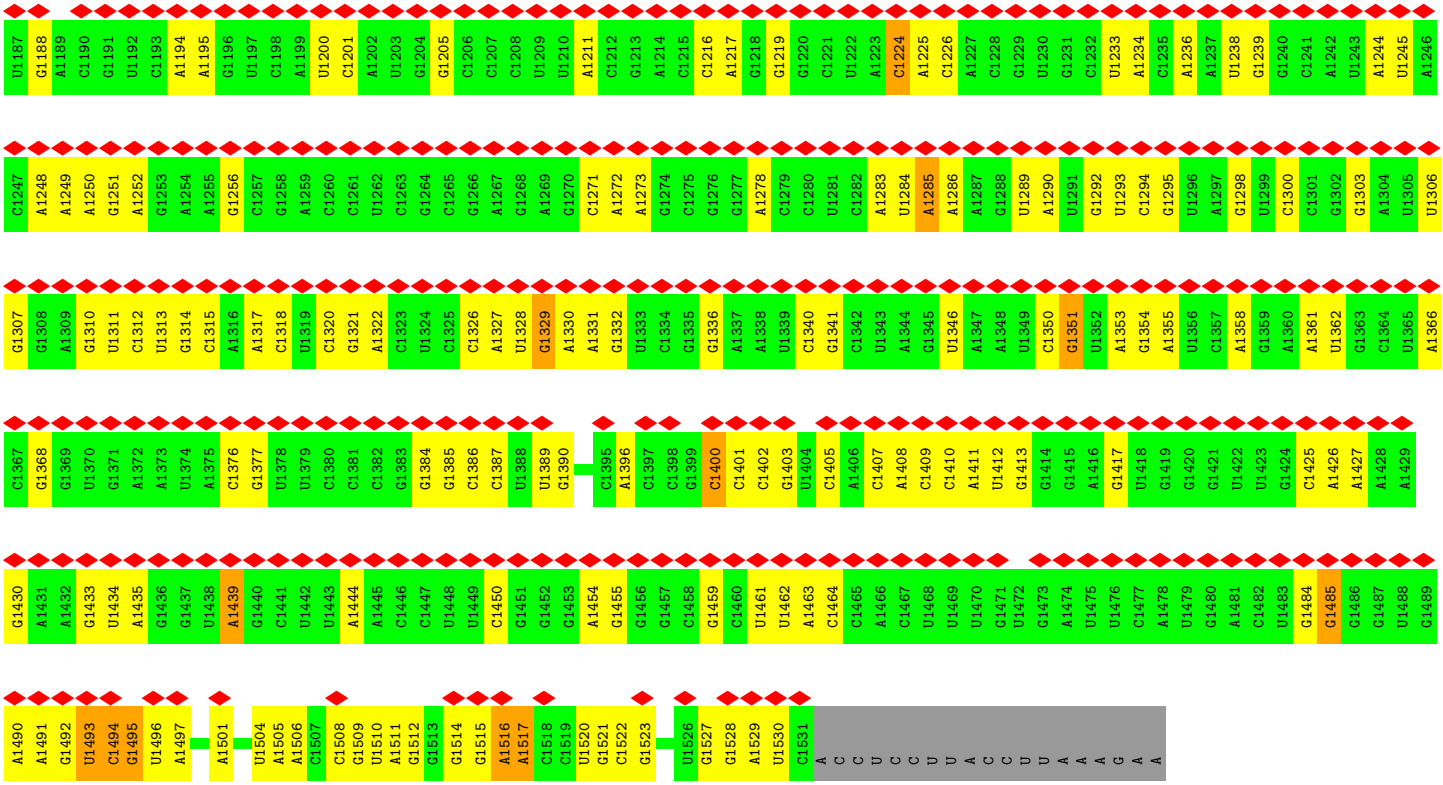

• Molecule 7: 16S rRNA (1530-MER)

Chain A:



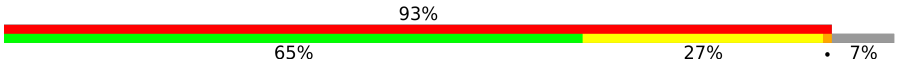



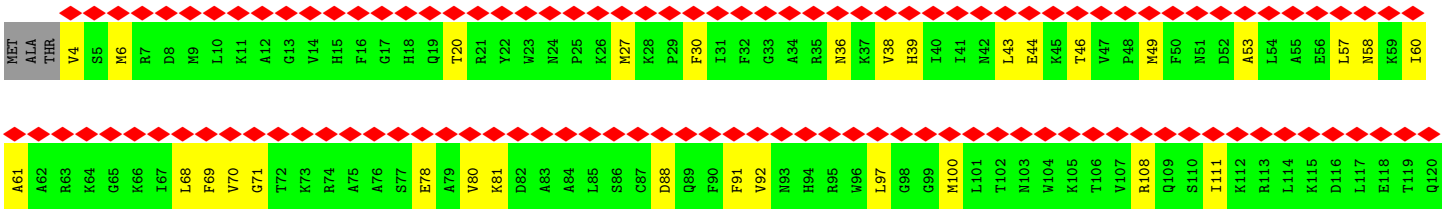

G375 G376 C377 G378 C379 A380 A381 G382 C383 C384 U385 G386 A387 U388 G389 C390 A391 G392 C393 C394 A395 U396 G397 C398 C399 G400 C401 G402 U403 G404 U405 A406 U407 G408 A409 A410 G411 A412 A413 G414 G415 C416 C417 U418 U419 C420 G421 G422 G423 U424 U425 G426 U427 A428 A429 A430 G431 U432 A433 C434
U435 U436 U437 C438 A439 G440 C441 G442 G443 G444 G445 A446 G447 G448 A449 A450 G451 C452 C453 G454 A455 U456 A457 A458 G459 G460 U461 U462 A463 A464 U465 A466 A467 C468 C469 U470 U471 G472 U473 C474 G475 A476 U477 U478 G479 A480 C481 G482 U483 U484 A485 C486 C487 C488 G489 C490 A491 G492 A493 A494
G495 A496 A497 G498 C499 A500 C501 C502 G503 G504 C505 U506 A507 A508 C509 U510 C511 C512 G513 U514 G515 C516 C517 A518 G519 C520 A521 G522 C523 C524 G525 C526 G527 G528 U529 A530 A531 U532 A533 C534 G535 G536 A537 G538 G539 G540 U541 G542 C543 A544 A545 G546 C547 G548 U549 U550 A551 A552 U553 C554
A557 A558 U559 U560 A561 C562 U563 G564 G565 G566 A570 A571 A572 G573 C574 G575 C576 A577 C578 G579 C580 A581 C584 G585 G586 U587 C588 U589 G590 U591 C592 A593 A594 G595 U596 C597 G598 G599 A600 U601 G602 U603 G604 A605 A606 A607 U608 C609 C610 C611 C612 G613 G614 G615 C616 U617 C618
A619 A620 C621 C622 U623 G624 G625 G626 A627 A628 C629 U630 G631 C632 A633 U634 U635 C636 G637 A638 A639 A640 C641 U642 G643 G644 C645 A646 G647 G648 C649 U650 A651 G652 A653 G654 U655 C656 U657 U658 G659 U660 A661 G662 A663 G667 G668 G669 U670 A671 G672 A673 A674 U675 U676 C677 C678 A679 G680
G681 U682 G683 U684 A685 G686 C687 G688 G689 U690 G691 A692 A693 A694 U695 G696 C697 G698 U699 A700 G701 A702 G703 A704 U705 C706 U707 G708 G709 A710 G711 G712 A713 A714 U715 A716 C717 C718 G719 G720 U721 G722 G723 A726 A727 G728 G729 C730 G731 G732 C733 C734 C735 C736 C737 U738 G739 G740 A741
C742 A743 A744 A745 G746 A747 C748 U749 G750 A751 C752 G753 C754 U755 C756 A757 G758 G759 U760 G761 C762 A765 A766 G767 U770 G771 G772 A775 G776 C777 A778 A782 G783 G784 A785 U786 U787 A788 G789 A790 U791 A792 U796 G797 G798 U799 U802 C803 C804 A805 C806 G807 C808 C809
G810 A813 A814 C815 G816 A817 U818 G819 U820 C821 G822 A823 U824 U825 U826 G827 G828 A829 G830 G831 U832 U833 G834 U835 G836 C837 C838 C839 U840 U841 G842 A843 G844 G845 C846 G847 U848 G849 G850 C851 U852 U853 C854 C855 C856 G857 A858 G859 C860 U861 A862 A863 C864 G865 C866 G867 U868 U869
C874 C881 U882 G883 G884 G885 G886 A887 G888 U889 A890 C891 G892 G893 C894 C895 G896 C897 U902 A905 A906 A907 C908 U909 C910 A911 A912 A913 U914 G915 A916 A917 U918 U919 G920 A921 C922 G923 G924 G925 G926 G927 C928 C929 C930 G931 C932 A933 C934 A935 A936 G937 C938 G939 G940 U941 G942
G943 A944 G945 C946 A947 U948 G949 U950 G951 G952 U953 U954 U955 A956 A957 U958 U959 C960 G961 A962 U963 G964 C965 A966 A967 C968 G969 C970 G971 A972 A973 G974 A975 A976 C977 G978 U979 U980 A981 C982 C983 U984 G985 G986 U987 C988 U989 U990 G991 A992 C993 A994 U995 C996 C997 A998 C999 A1000 G1001 A1002
A1003 C1004 U1005 U1006 A1007 G1008 C1009 A1010 G1011 A1012 G1013 A1014 U1015 G1016 C1017 U1018 U1019 U1020 G1021 G1022 U1023 G1024 C1025 C1026 U1027 U1028 C1029 G1030 G1031 G1032 A1033 A1034 C1035 U1036 G1037 U1038 G1039 A1040 G1041 A1042 C1043 A1044 G1045 G1046 U1047 G1048 C1049 U1050 G1051 C1052 A1053 U1054 G1055 G1056 C1057 U1058 G1059 U1060 C1061 G1062
U1063 C1064 A1065 G1066 C1067 U1068 C1069 G1070 U1071 G1072 U1073 U1074 G1075 U1081 G1082 U1083 U1084 G1085 G1086 G1087 U1088 U1089 A1090 A1091 G1092 U1093 C1094 C1095 C1096 G1097 C1098 A1099 A1100 C1101 G1102 A1103 G1104 C1105 G1106 C1107 A1108 A1109 C1110 C1111 C1112 U1113 U1114 A1115 U1116 C1117 C1118 U1119 U1120 U1121 G1122 U1123 U1124 G1125 C1126
C1127 A1128 G1129 C1130 G1131 G1132 U1133 U1134 C1135 G1136 G1137 C1138 C1139 G1140 G1141 G1142 A1143 A1144 C1145 U1146 C1147 A1148 A1149 A1150 G1151 G1152 A1153 G1154 A1155 C1156 U1157 G1158 C1159 C1160 A1161 G1162 U1163 G1164 A1165 U1166 A1167 A1168 A1169 C1170 U1171 G1172 G1173 A1174 G1175 G1176 A1177 A1178 G1179 G1180 U1181 G1182 G1183 G1184 G1185 A1186




• Molecule 8: Small ribosomal subunit protein uS2

Chain B:

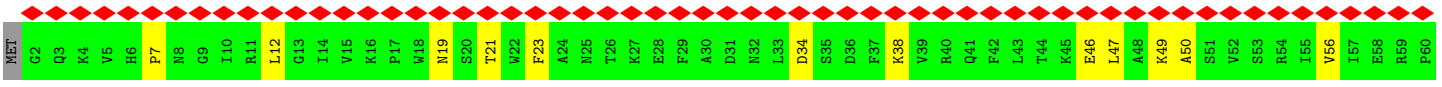


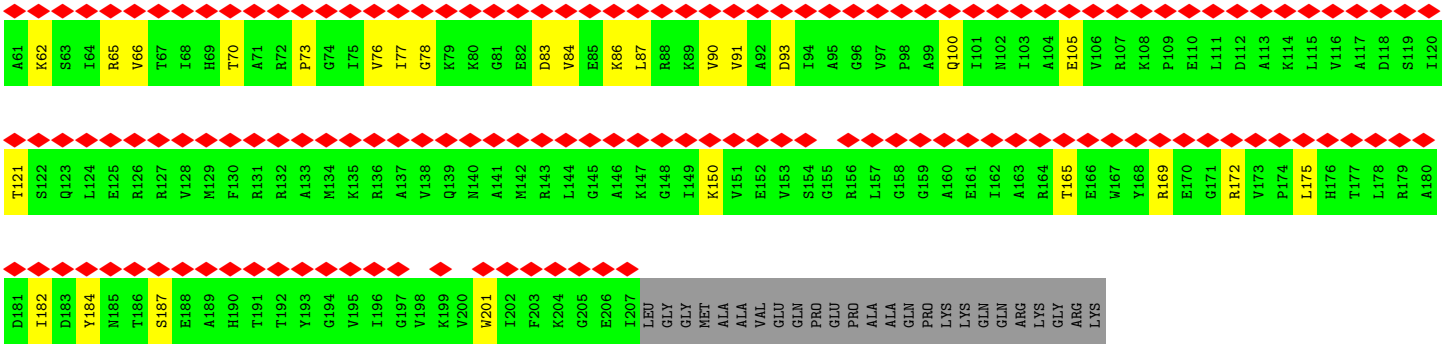




• Molecule 9: Small ribosomal subunit protein uS3

Chain C:






• Molecule 10: Small ribosomal subunit protein uS4

Chain D:



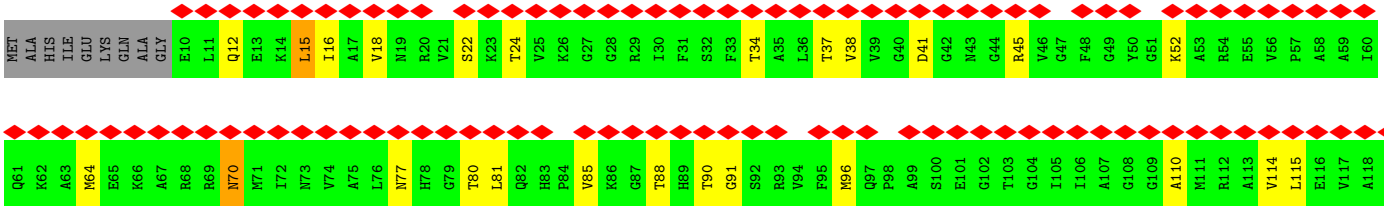




• Molecule 11: Small ribosomal subunit protein uS5

Chain E:

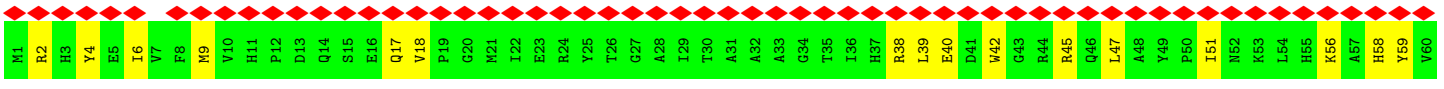


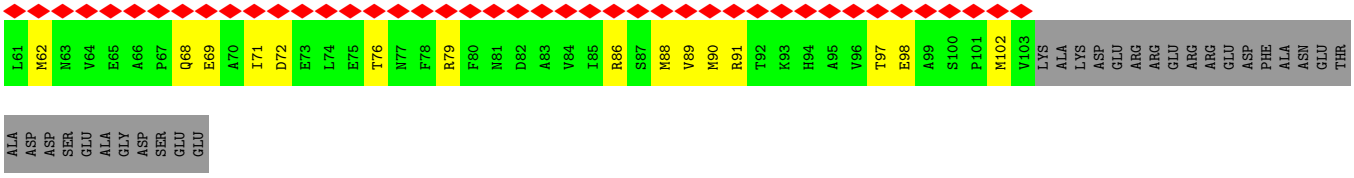




• Molecule 12: Small ribosomal subunit protein bS6

Chain F:

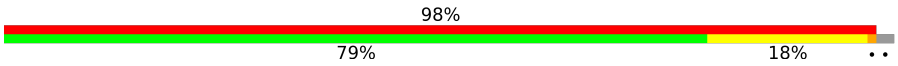


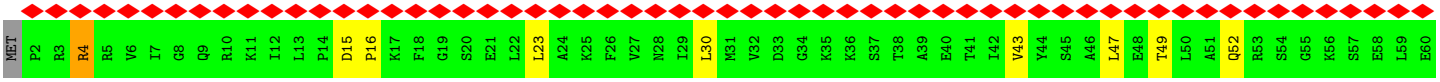



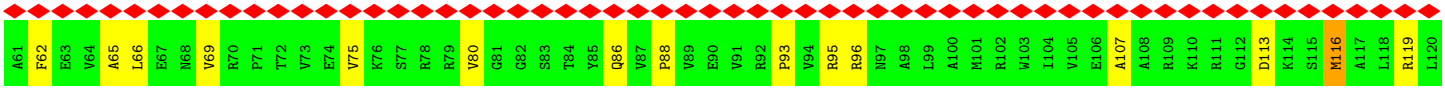


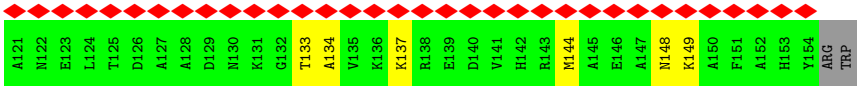

• Molecule 13: Small ribosomal subunit protein uS7

Chain G:



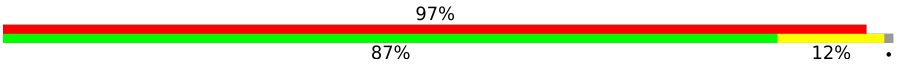



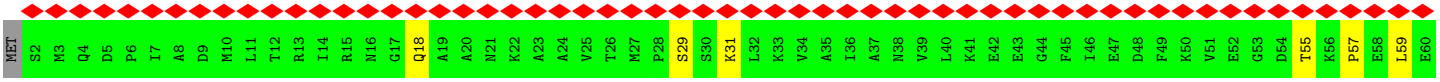



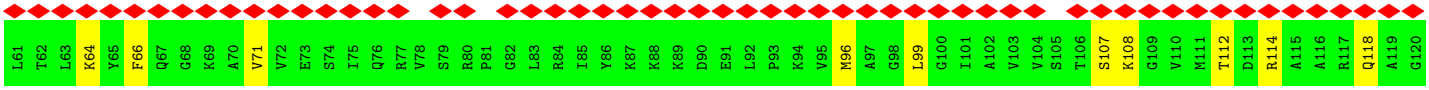



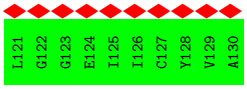

• Molecule 14: Small ribosomal subunit protein uS8

Chain H:



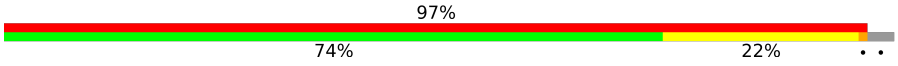



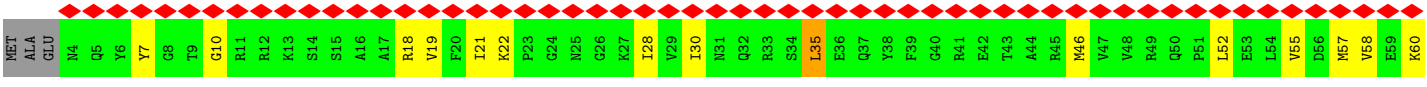



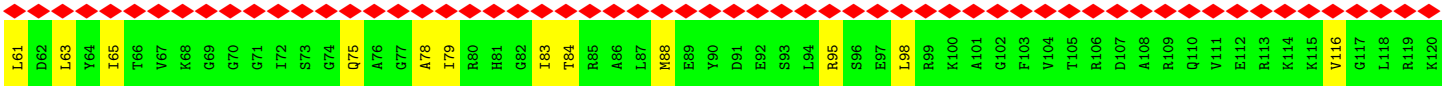



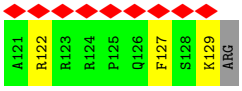

• Molecule 15: Small ribosomal subunit protein uS9

Chain I:



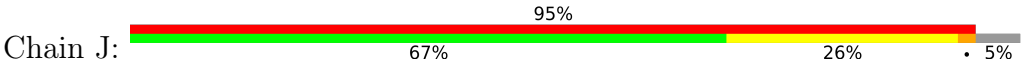



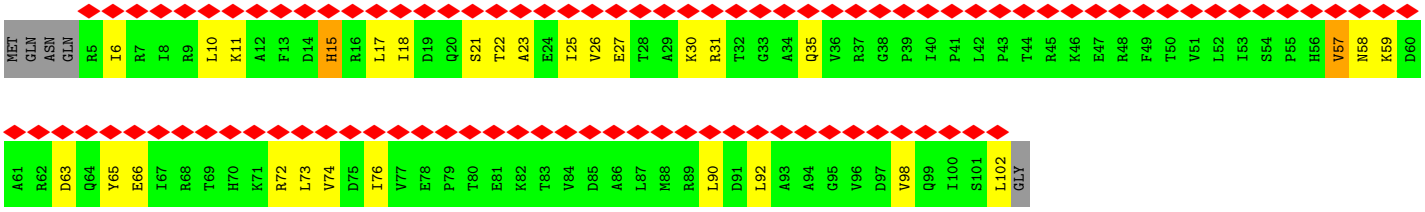



• Molecule 16: Small ribosomal subunit protein uS10

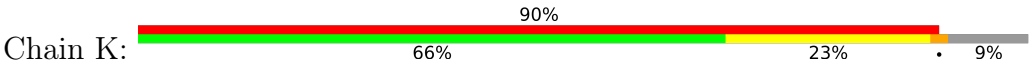
Chain J:




• Molecule 17: Small ribosomal subunit protein uS11

Chain K:

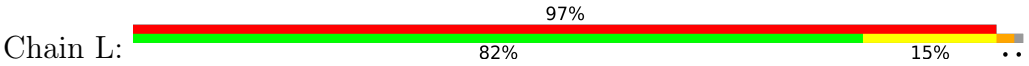


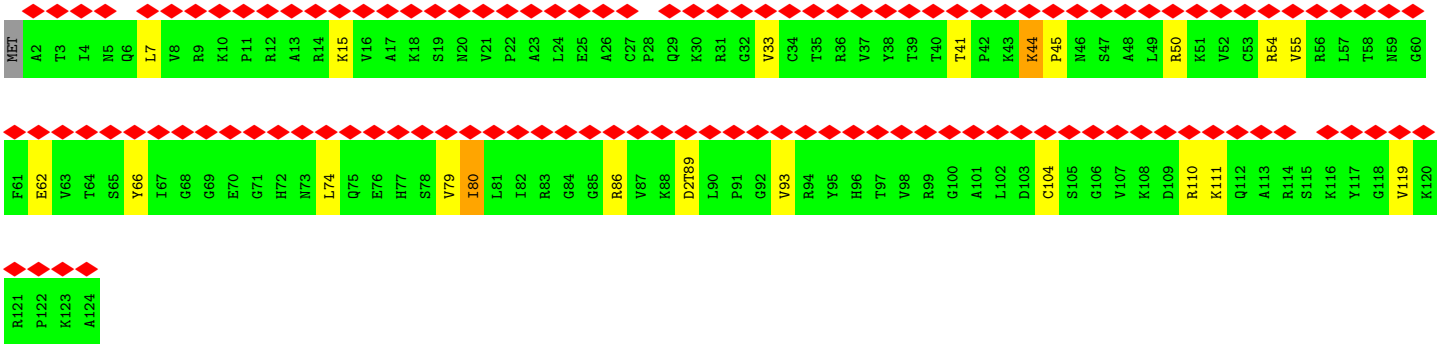




• Molecule 18: Small ribosomal subunit protein uS12

Chain L:

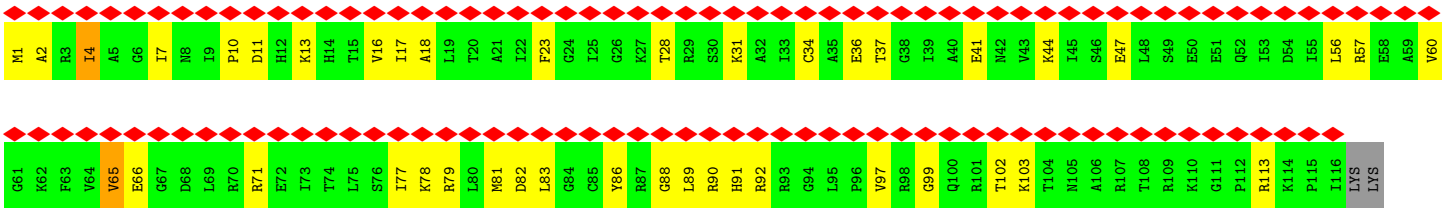



• Molecule 19: Small ribosomal subunit protein uS13

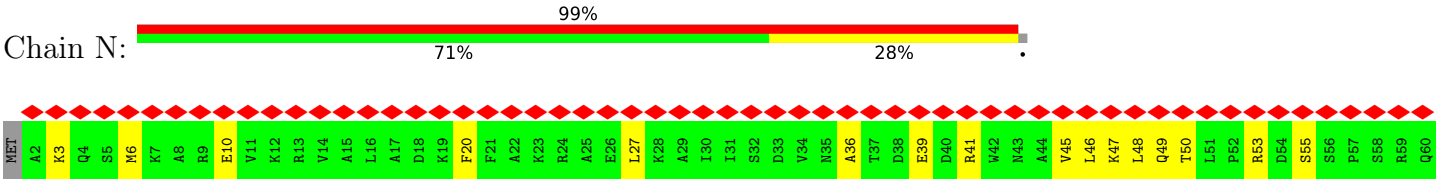
Chain M:



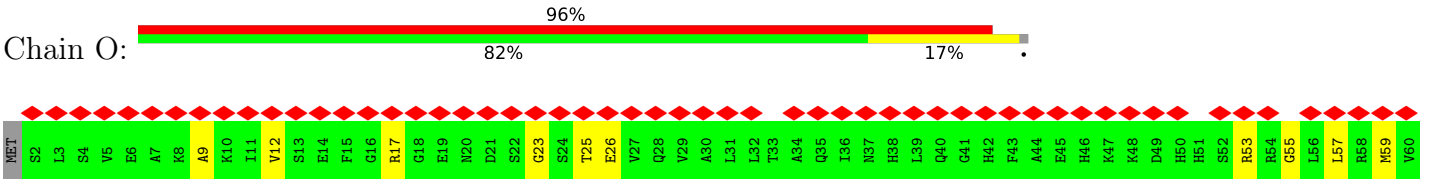
• Molecule 20: Small ribosomal subunit protein uS14

Chain N:



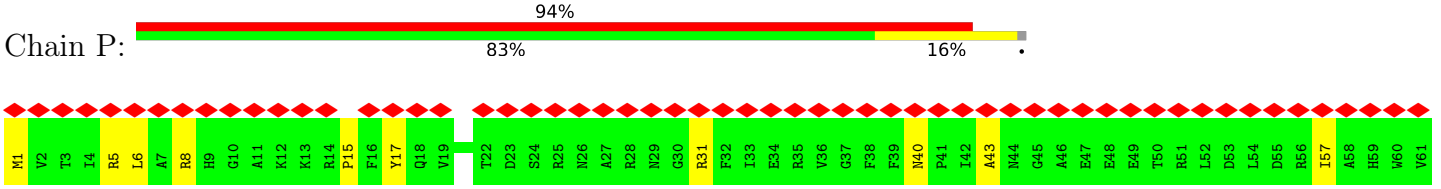

• Molecule 21: Small ribosomal subunit protein uS15

Chain O:



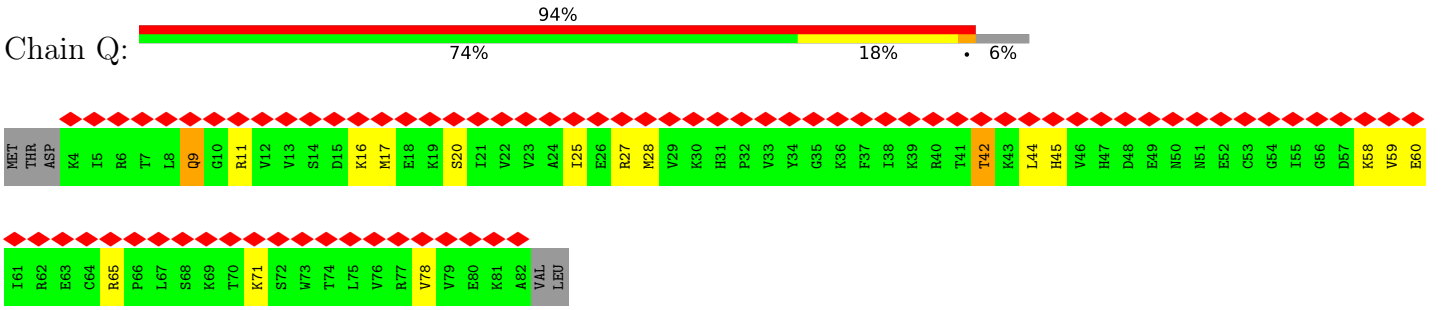

• Molecule 22: Small ribosomal subunit protein bS16

Chain P:



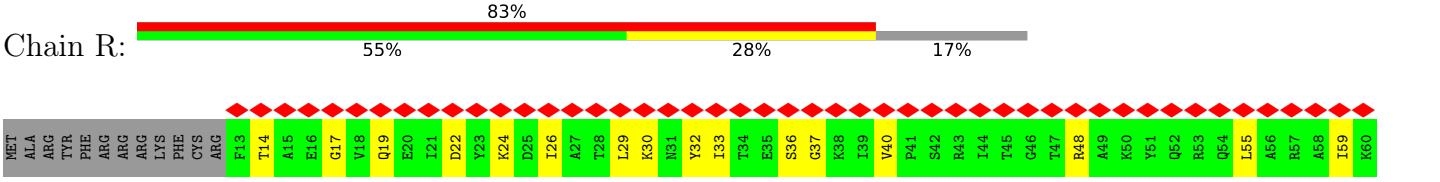

• Molecule 23: Small ribosomal subunit protein uS17

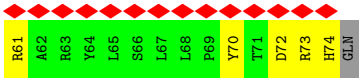
Chain Q:




• Molecule 24: Small ribosomal subunit protein bS18

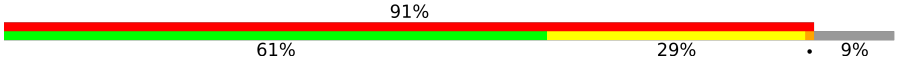
Chain R:

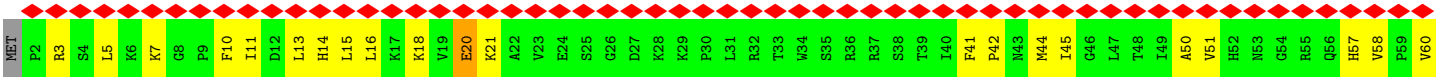


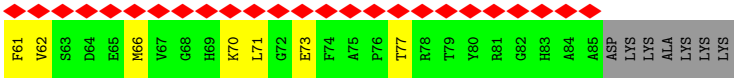



• Molecule 25: Small ribosomal subunit protein uS19

Chain S:

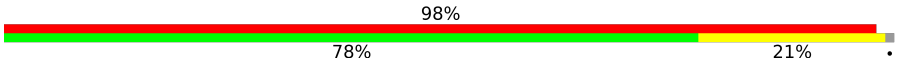


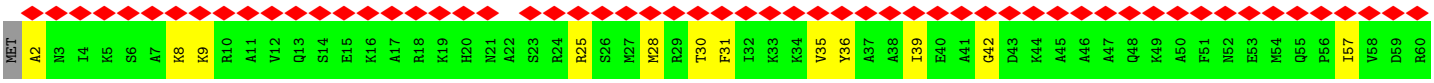



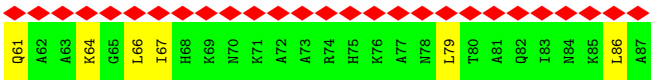




• Molecule 26: Small ribosomal subunit protein bS20

Chain T:

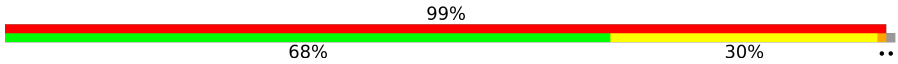



• Molecule 27: Small ribosomal subunit protein bS21

Chain U:



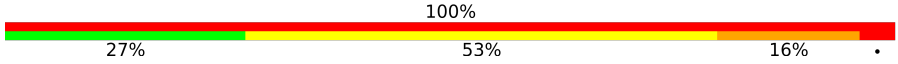


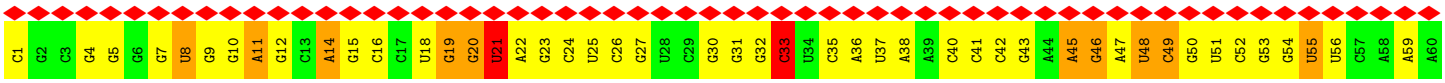


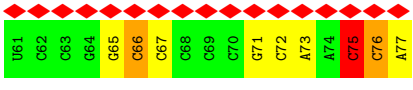



• Molecule 28: E-site RNA (77-MER)

Chain V:



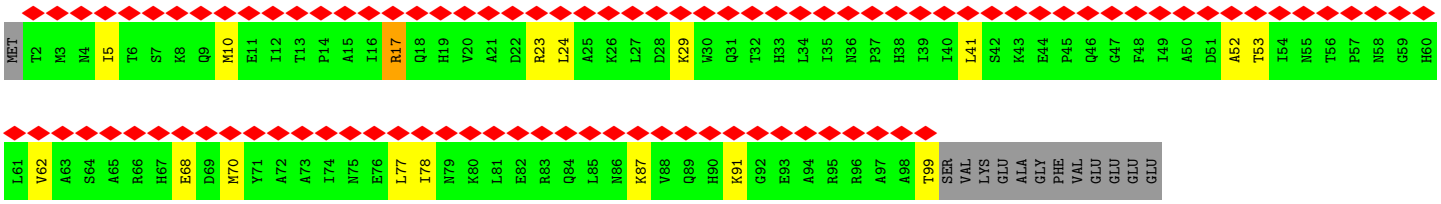




• Molecule 29: Ribosomal subunit interface protein

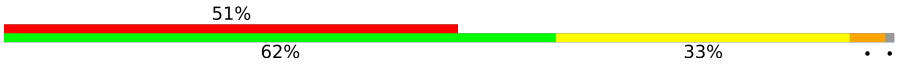
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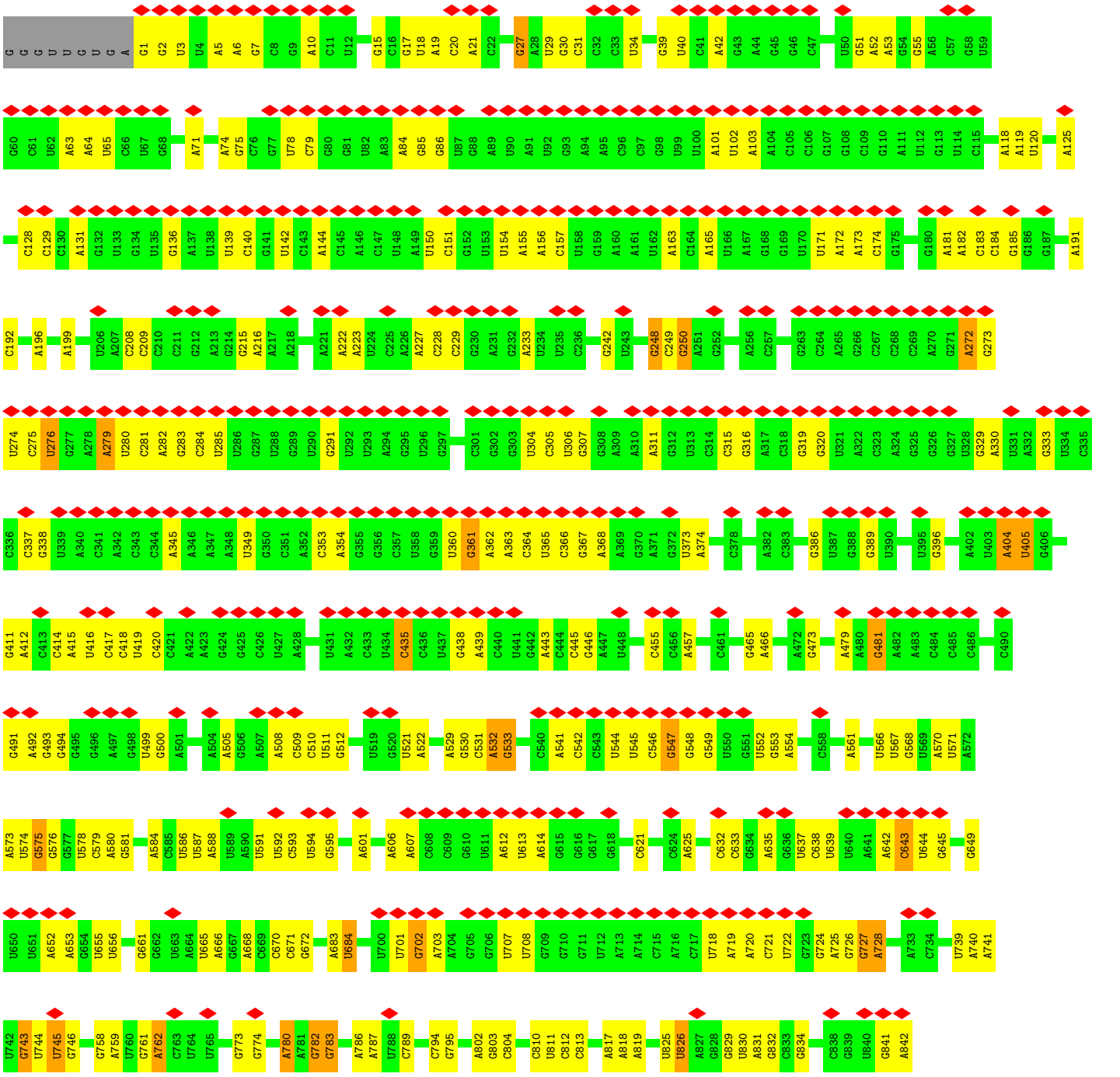


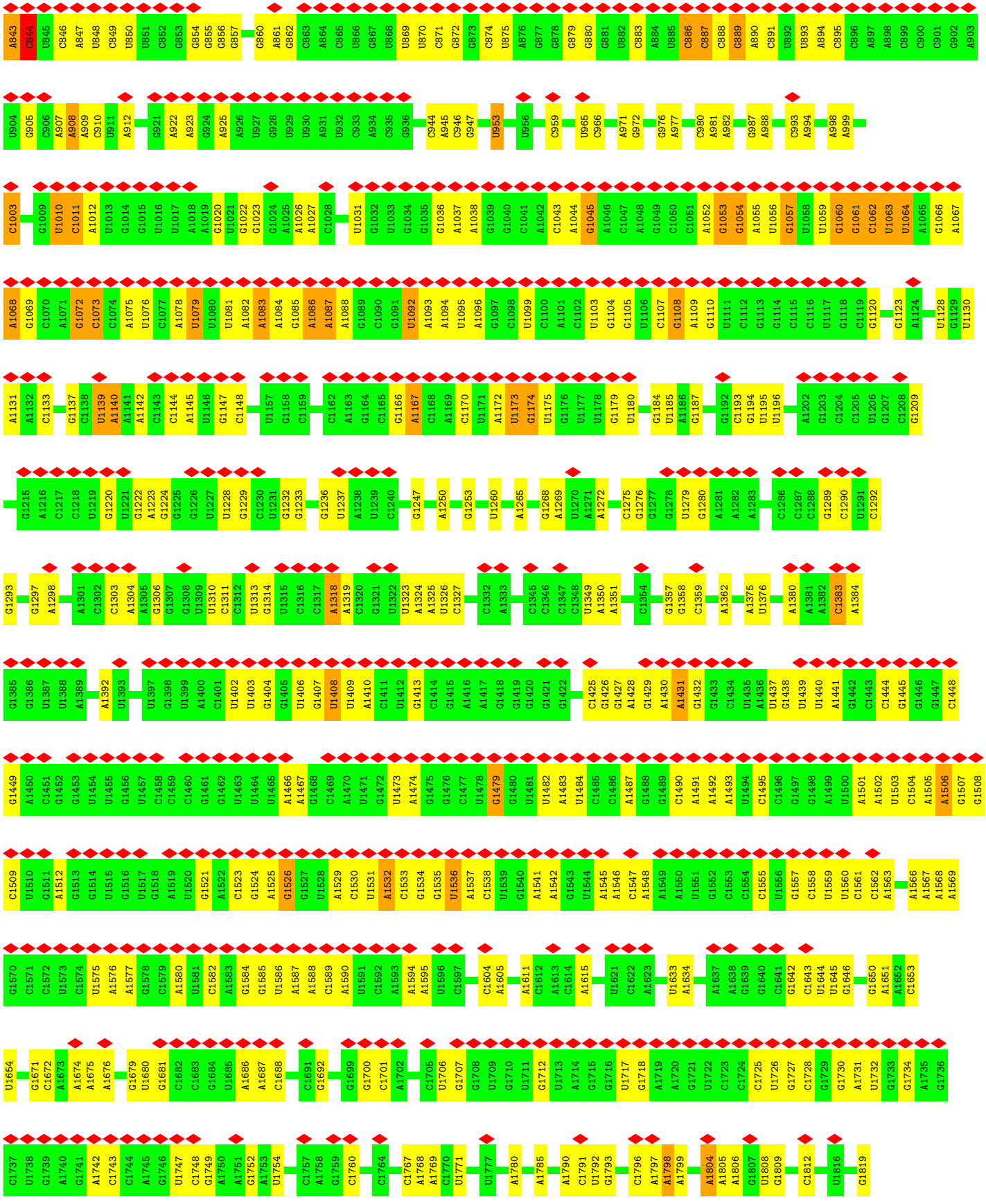


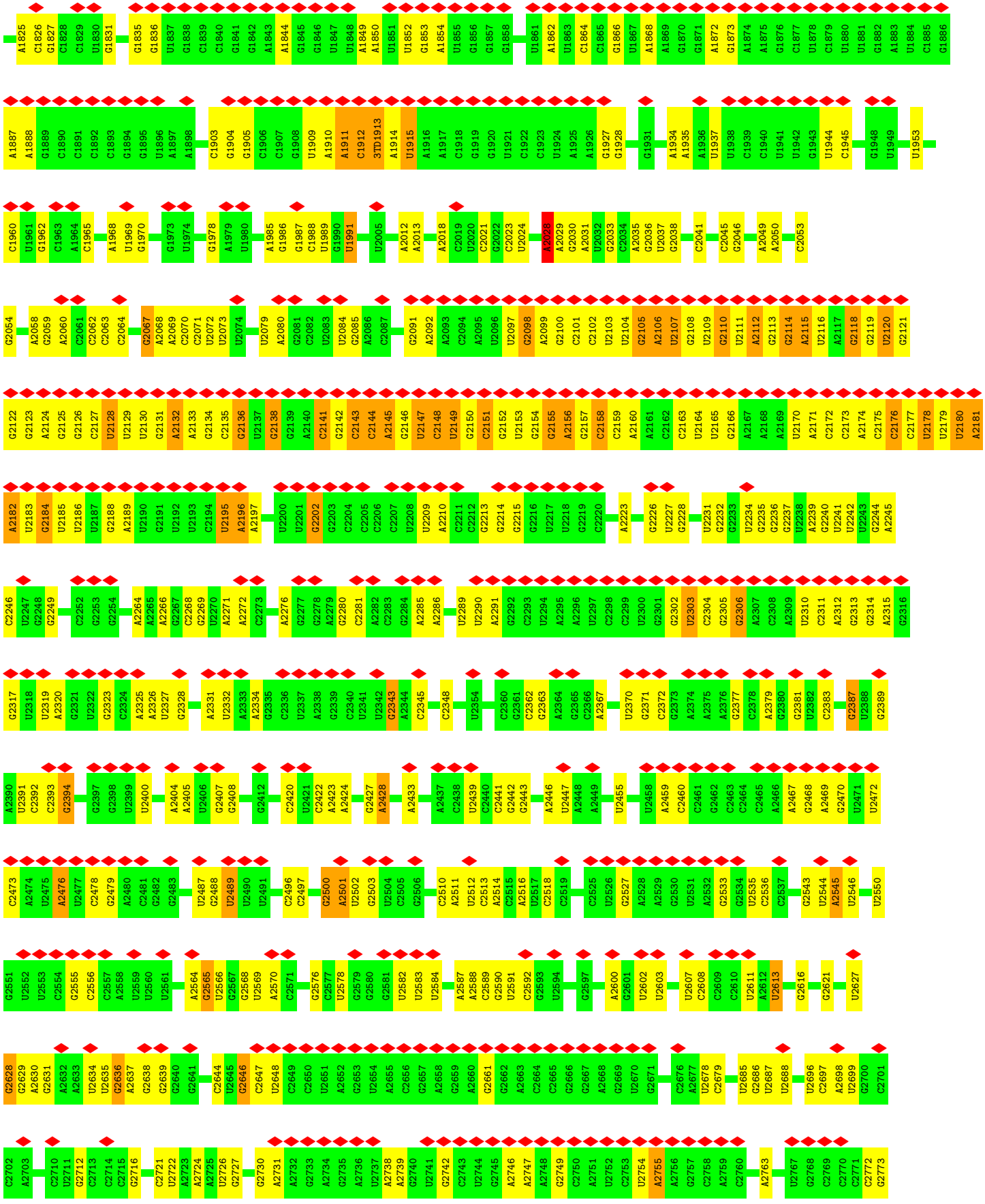

• Molecule 30: RNA (2901-MER)

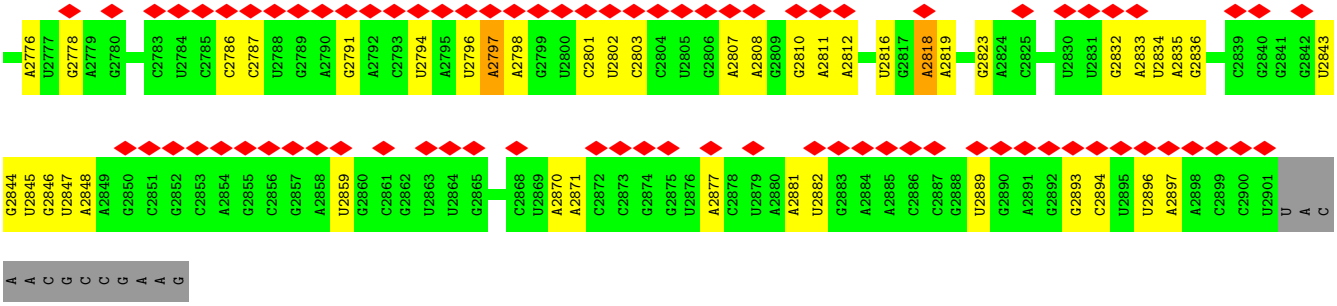
Chain a:



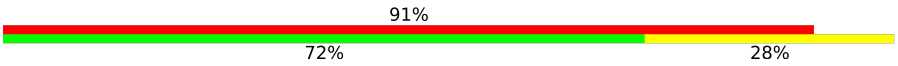


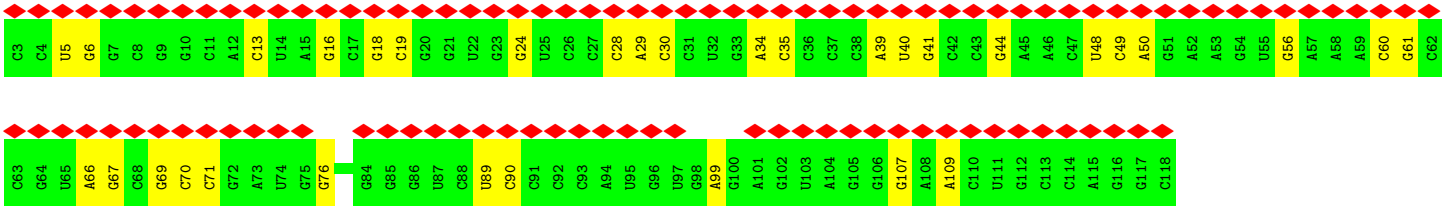

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G1931
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A1968 U1969 G1970
G1973 U1974
G1978 A1979 U1980
A1985 G1986 G1987 C1988 U1989 G1990 U1991
U2005
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C2053
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• Molecule 31: 5S rRNA (119-MER)

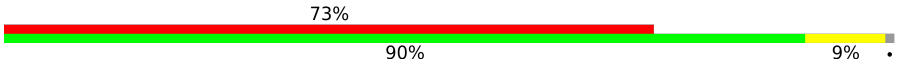
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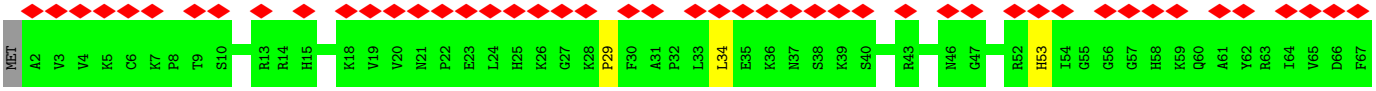


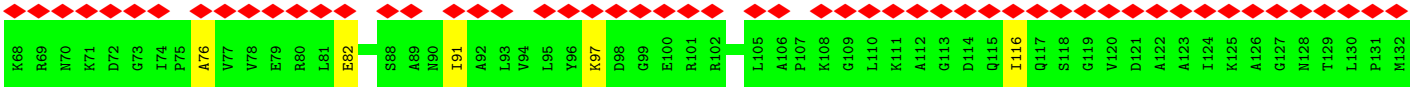



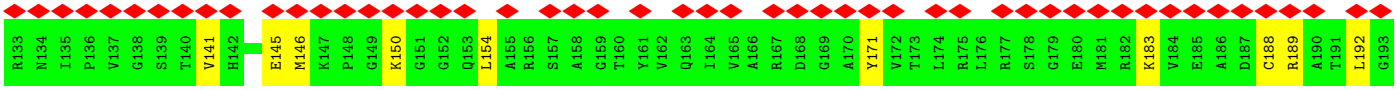

• Molecule 32: Large ribosomal subunit protein uL2

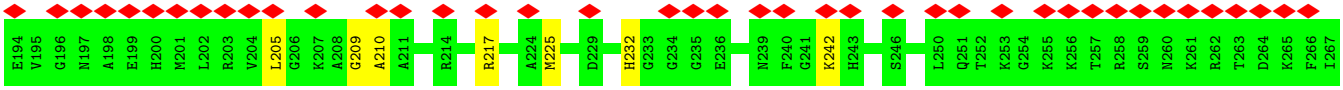
Chain c:

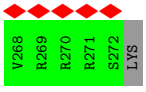


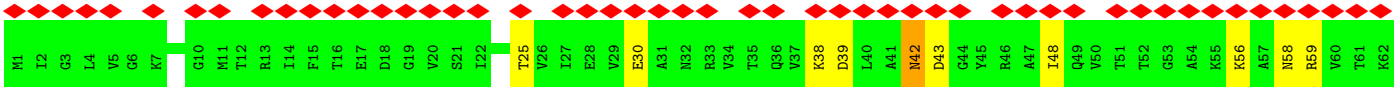



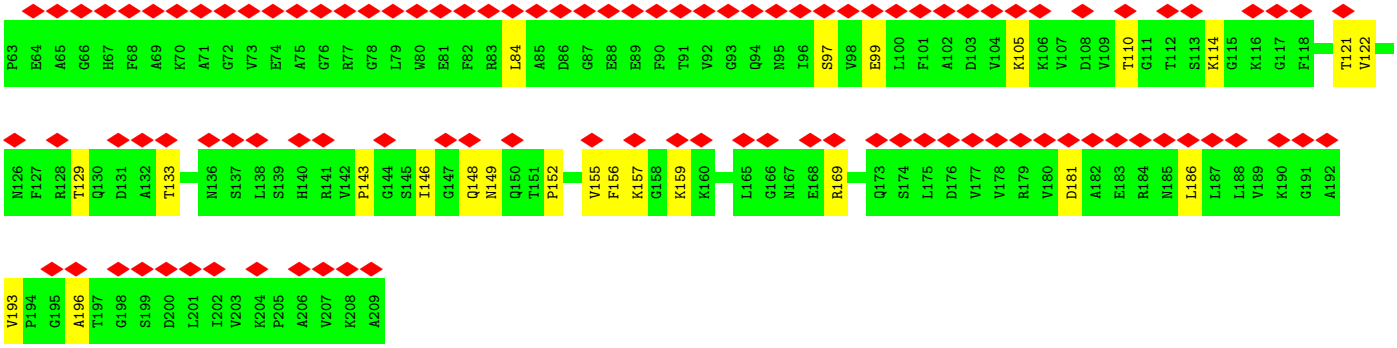




• Molecule 33: Large ribosomal subunit protein uL3

Chain d:



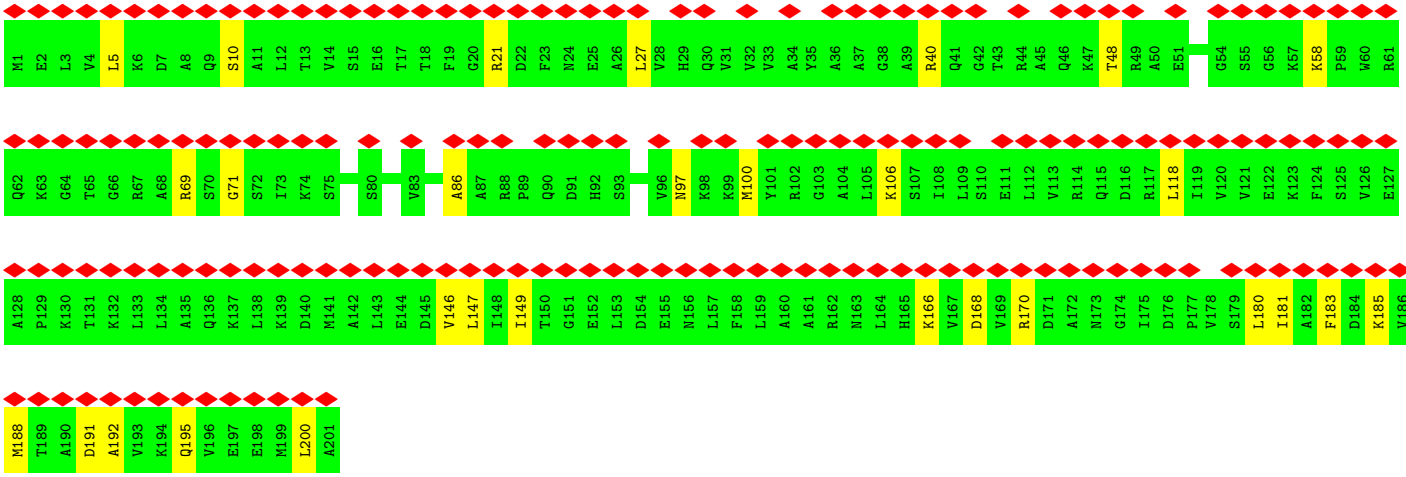






• Molecule 34: Large ribosomal subunit protein uL4

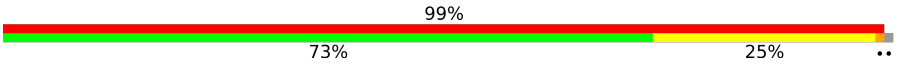
Chain e:

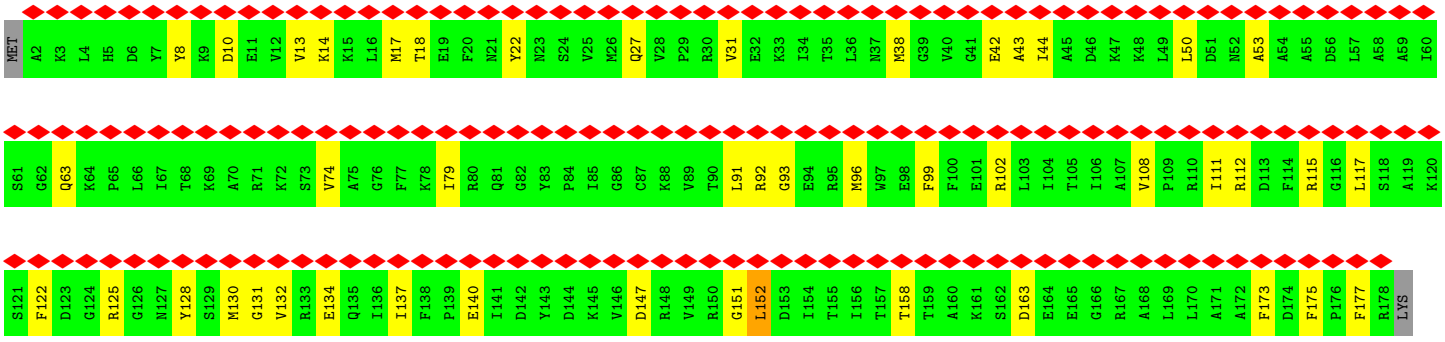



• Molecule 35: Large ribosomal subunit protein uL5

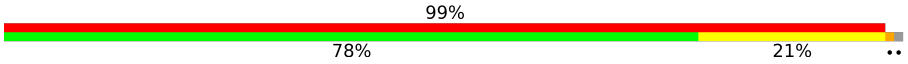
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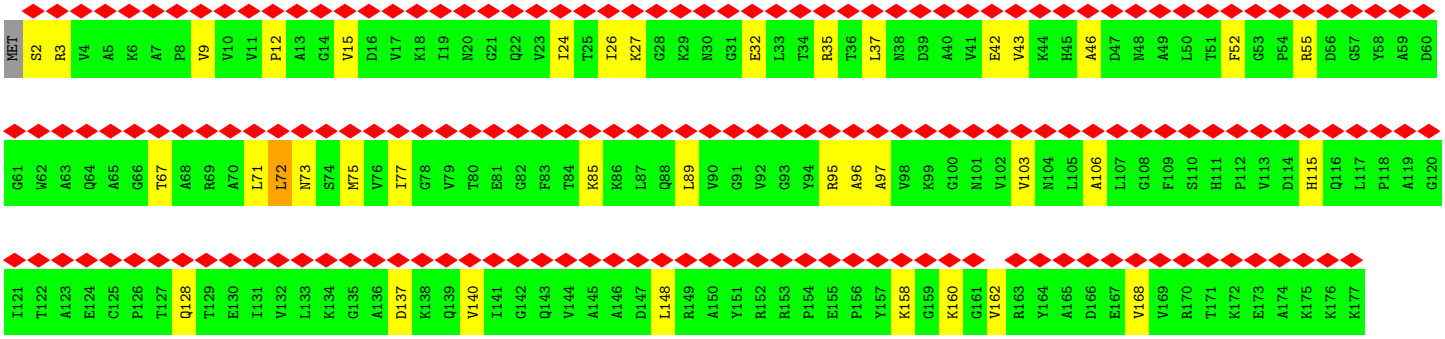



• Molecule 36: Large ribosomal subunit protein uL6

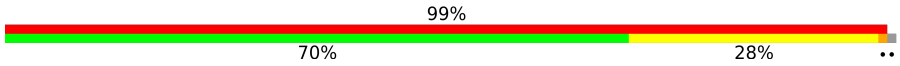
Chain g:

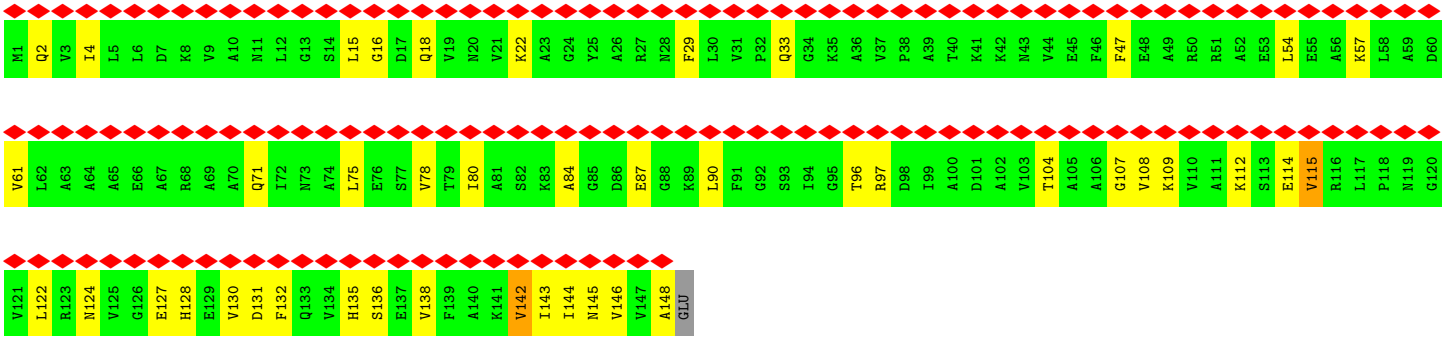





• Molecule 37: Large ribosomal subunit protein bL9

Chain h:

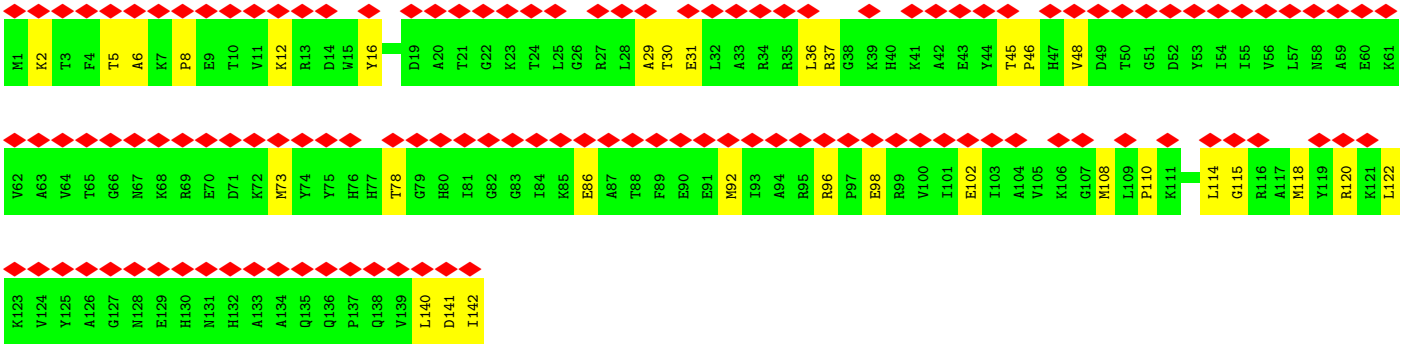



• Molecule 38: Large ribosomal subunit protein uL13

Chain i:

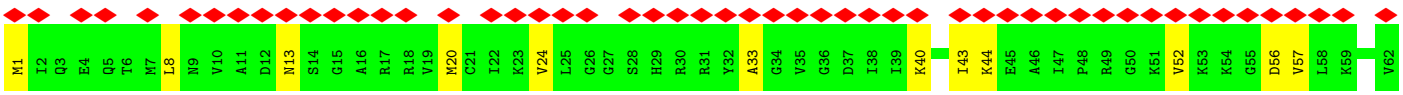


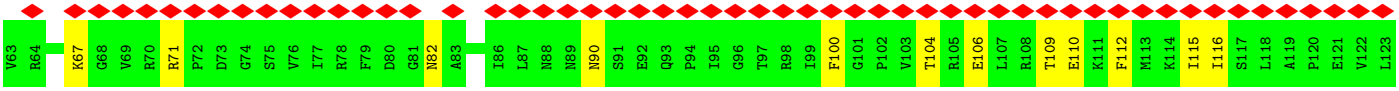




• Molecule 39: Large ribosomal subunit protein uL14

Chain j:



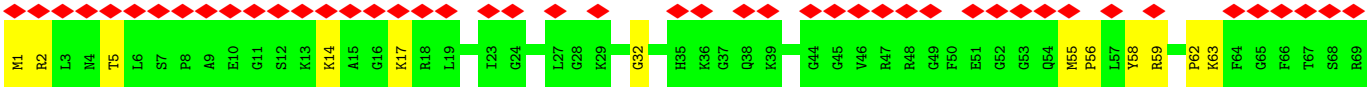



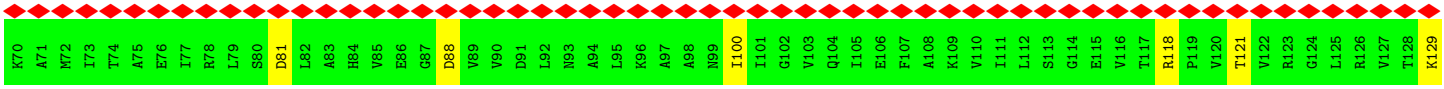


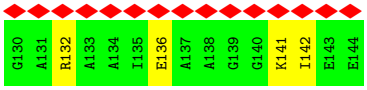

• Molecule 40: Large ribosomal subunit protein uL15

Chain k:



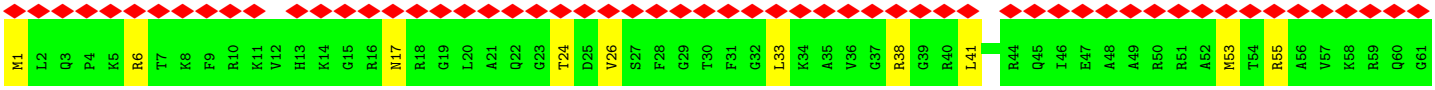



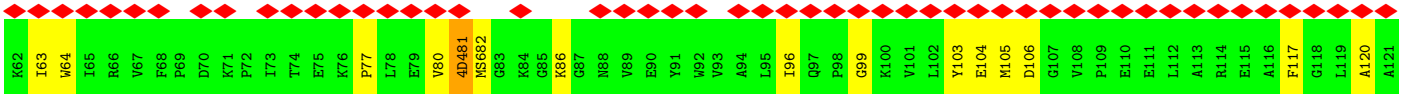



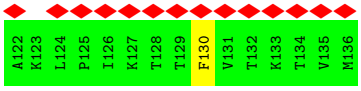

• Molecule 41: Large ribosomal subunit protein uL16

Chain l:



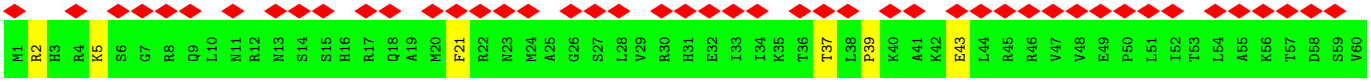



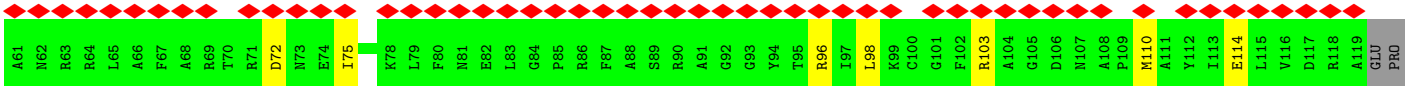



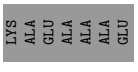

• Molecule 42: Large ribosomal subunit protein bL17

Chain m:



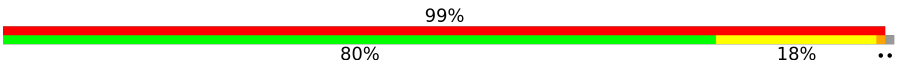



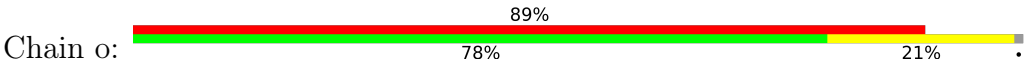

• Molecule 43: Large ribosomal subunit protein uL18

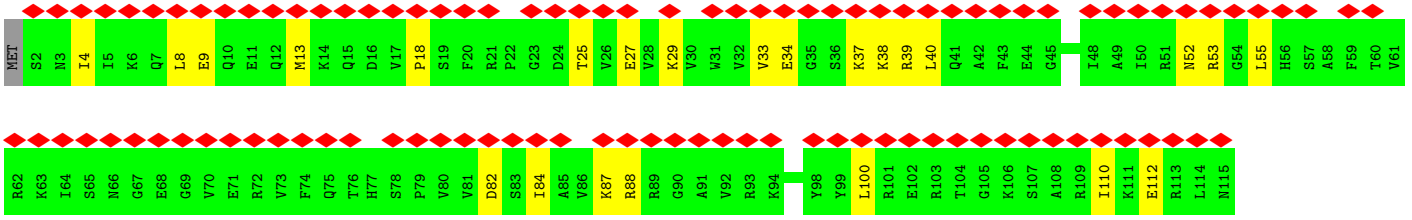
Chain n:



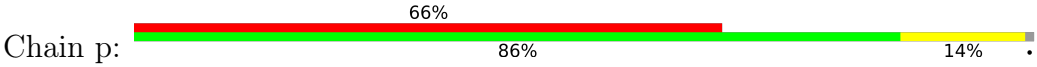


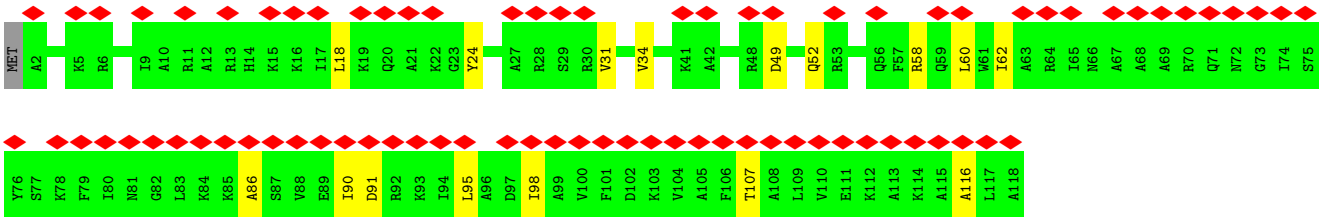

• Molecule 44: Large ribosomal subunit protein bL19



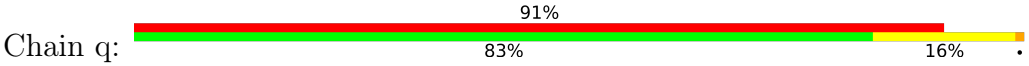



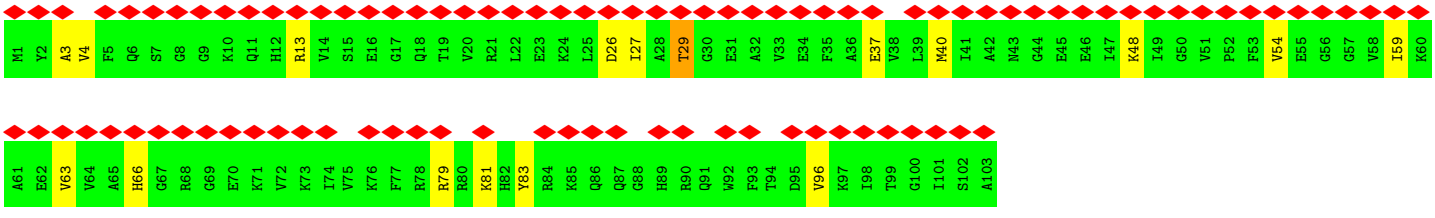

• Molecule 45: Large ribosomal subunit protein bL20



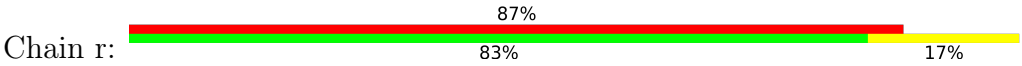



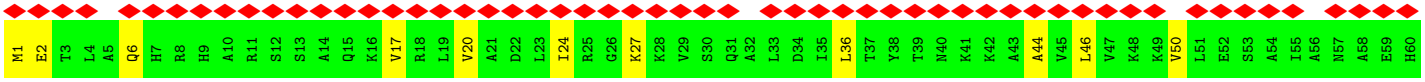

• Molecule 46: Large ribosomal subunit protein bL21

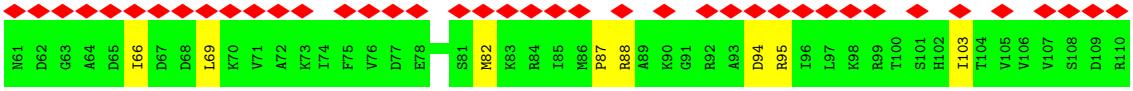



• Molecule 47: Large ribosomal subunit protein uL22



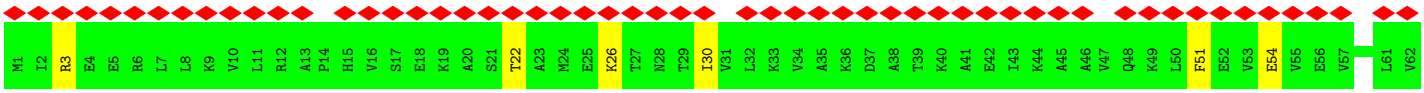



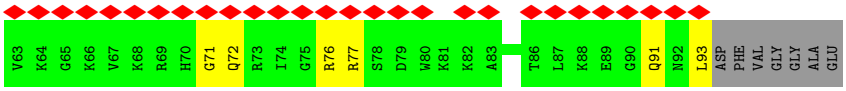



• Molecule 48: Large ribosomal subunit protein uL23

Chain s:

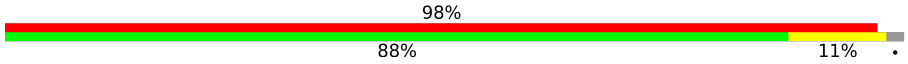


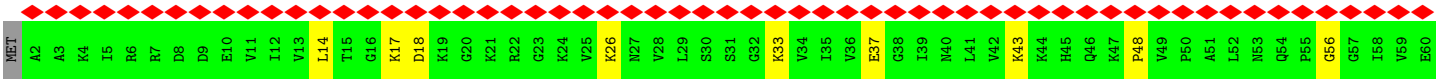



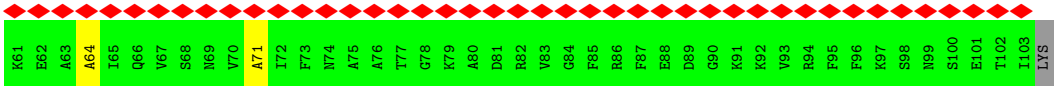




• Molecule 49: Large ribosomal subunit protein uL24

Chain t:

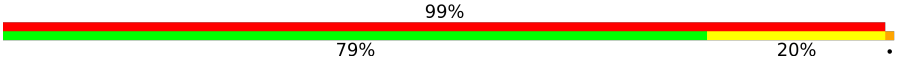


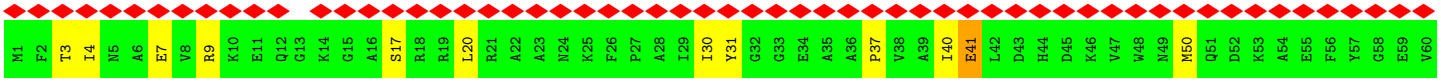



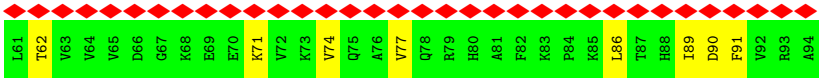




• Molecule 50: Large ribosomal subunit protein bL25

Chain u:



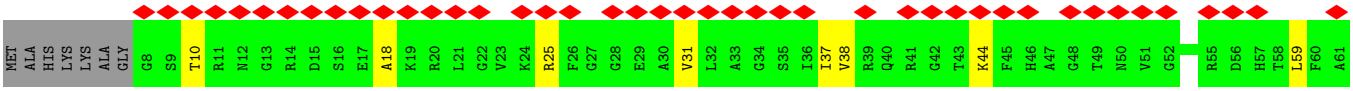



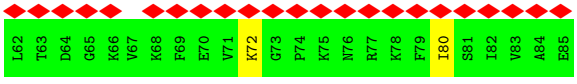




• Molecule 51: Large ribosomal subunit protein bL27

Chain v:

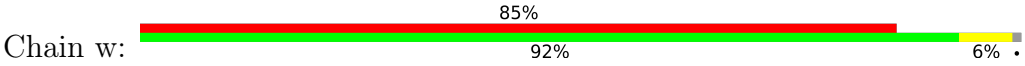


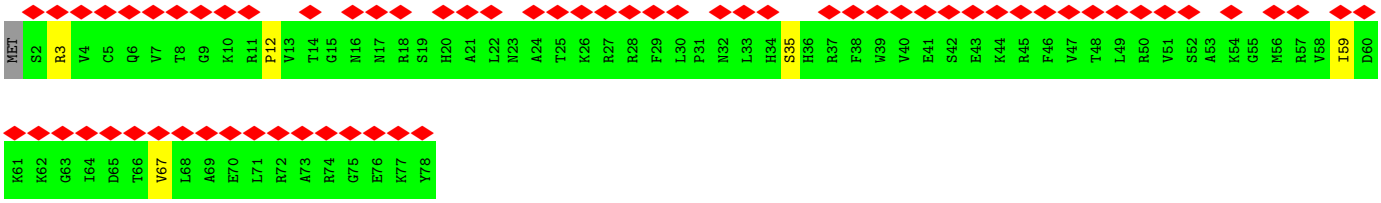




• Molecule 52: Large ribosomal subunit protein bL28

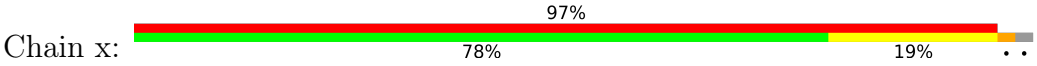
Chain w:

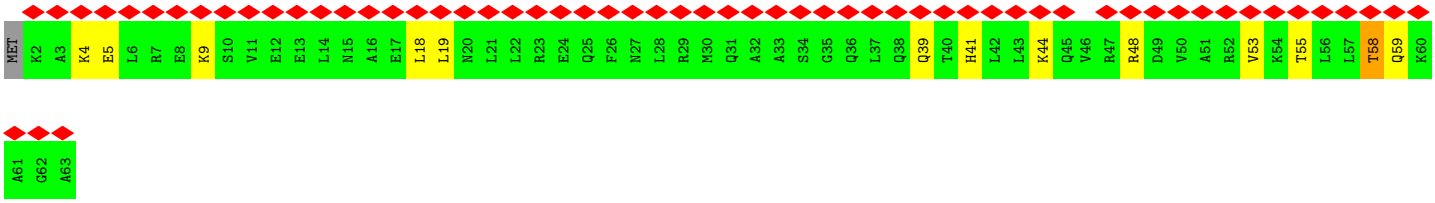



• Molecule 53: Large ribosomal subunit protein uL29

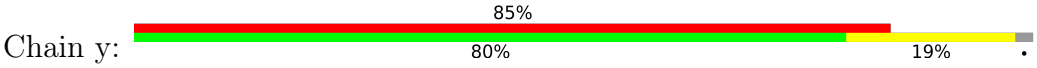
Chain x:

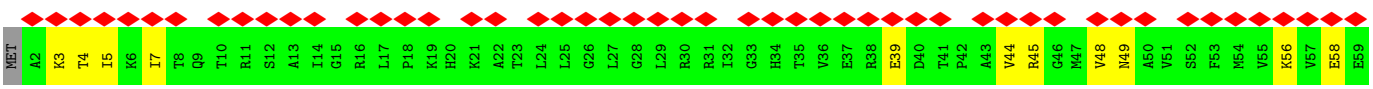



• Molecule 54: Large ribosomal subunit protein uL30

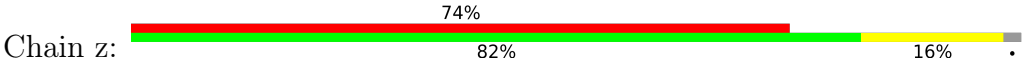
Chain y:

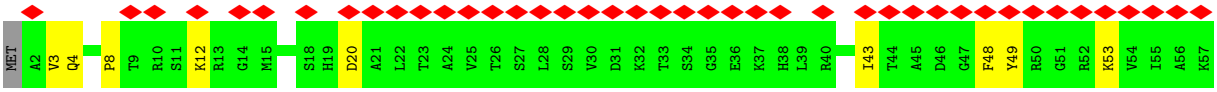



• Molecule 55: Large ribosomal subunit protein bL32

Chain z:



# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, C1 | Depositor |
| Number of particles used | 17191 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | TFS KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/Å^2$) | 35 | Depositor |
| Minimum defocus (nm) | 800 | Depositor |
| Maximum defocus (nm) | 2500 | Depositor |
| Magnification | 81000 | Depositor |
| Image detector | GATAN K3 (6k x 4k) | Depositor |
| Maximum map value | 1.397 | Depositor |
| Minimum map value | -0.605 | Depositor |
| Average map value | 0.001 | Depositor |
| Map value standard deviation | 0.054 | Depositor |
| Recommended contour level | 0.55 | Depositor |
| Map size (Å) | 542.72, 542.72, 542.72 | wwPDB |
| Map dimensions | 512, 512, 512 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.06, 1.06, 1.06 | 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: 5MU, OMC, 2MG, ZN, 6MZ, 1MG, MEQ, 4SU, 4OC, 2MA, IAS, MA6, K, MG, MS6, 3TD, OMG, G7M, D2T, 5MC, H2U, OMU, 4D4, UR3, PSU

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | #\|Z\| >5 | RMSZ | #\|Z\| >5 |
| 1 | 0 | 0.17 | 0/425 | 0.32 | 0/566 |
| 2 | 1 | 0.18 | 0/380 | 0.27 | 0/498 |
| 3 | 2 | 0.19 | 0/513 | 0.27 | 0/676 |
| 4 | 3 | 0.21 | 0/303 | 0.39 | 0/397 |
| 5 | 4 | 0.18 | 0/550 | 0.45 | 0/734 |
| 6 | 5 | 0.16 | 0/1112 | 0.38 | 0/1492 |
| 7 | A | 0.38 | 1/36501 (0.0%) | 0.72 | 4/56938 (0.0%) |
| 8 | B | 0.18 | 0/1780 | 0.46 | 0/2398 |
| 9 | C | 0.16 | 0/1650 | 0.34 | 0/2223 |
| 10 | D | 0.15 | 0/1665 | 0.30 | 0/2225 |
| 11 | E | 0.19 | 0/1168 | 0.37 | 0/1570 |
| 12 | F | 0.18 | 0/851 | 0.37 | 0/1152 |
| 13 | G | 0.15 | 0/1220 | 0.35 | 0/1638 |
| 14 | H | 0.18 | 0/987 | 0.33 | 0/1323 |
| 15 | I | 0.17 | 0/1022 | 0.39 | 0/1361 |
| 16 | J | 0.19 | 0/798 | 0.46 | 0/1078 |
| 17 | K | 0.17 | 0/885 | 0.34 | 0/1192 |
| 18 | L | 0.15 | 0/961 | 0.28 | 0/1287 |
| 19 | M | 0.17 | 0/916 | 0.42 | 0/1225 |
| 20 | N | 0.16 | 0/817 | 0.26 | 0/1088 |
| 21 | O | 0.17 | 0/718 | 0.31 | 0/955 |
| 22 | P | 0.18 | 0/646 | 0.34 | 0/870 |
| 23 | Q | 0.17 | 0/647 | 0.36 | 0/865 |
| 24 | R | 0.17 | 0/515 | 0.32 | 0/693 |
| 25 | S | 0.14 | 0/684 | 0.33 | 0/920 |
| 26 | T | 0.20 | 0/675 | 0.34 | 0/894 |
| 27 | U | 0.15 | 0/597 | 0.39 | 0/792 |
| 28 | V | 0.28 | 0/1724 | 0.80 | 1/2687 (0.0%) |
| 29 | X | 0.16 | 0/791 | 0.36 | 0/1069 |
| 30 | a | 0.43 | 0/69183 | 0.73 | 11/107924 (0.0%) |
| 31 | b | 0.38 | 0/2776 | 0.71 | 0/4328 |

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | #\|Z\| >5 | RMSZ | #\|Z\| >5 |
| 32 | c | 0.18 | 0/2118 | 0.29 | 0/2846 |
| 33 | d | 0.19 | 0/1577 | 0.30 | 0/2122 |
| 34 | e | 0.18 | 0/1573 | 0.28 | 0/2115 |
| 35 | f | 0.17 | 0/1434 | 0.40 | 0/1926 |
| 36 | g | 0.15 | 0/1339 | 0.36 | 1/1811 (0.1%) |
| 37 | h | 0.13 | 0/1110 | 0.36 | 0/1500 |
| 38 | i | 0.19 | 0/1157 | 0.35 | 0/1556 |
| 39 | j | 0.19 | 0/956 | 0.31 | 0/1281 |
| 40 | k | 0.17 | 0/1073 | 0.30 | 0/1427 |
| 41 | l | 0.20 | 0/1072 | 0.32 | 0/1434 |
| 42 | m | 0.19 | 0/963 | 0.35 | 0/1288 |
| 43 | n | 0.18 | 0/902 | 0.45 | 0/1209 |
| 44 | o | 0.18 | 0/929 | 0.31 | 0/1242 |
| 45 | p | 0.20 | 0/960 | 0.29 | 0/1278 |
| 46 | q | 0.19 | 0/829 | 0.40 | 0/1106 |
| 47 | r | 0.19 | 0/862 | 0.34 | 0/1154 |
| 48 | s | 0.18 | 0/745 | 0.35 | 0/996 |
| 49 | t | 0.15 | 0/787 | 0.28 | 0/1051 |
| 50 | u | 0.17 | 0/763 | 0.35 | 0/1024 |
| 51 | v | 0.19 | 0/599 | 0.31 | 0/795 |
| 52 | w | 0.19 | 0/635 | 0.31 | 0/848 |
| 53 | x | 0.15 | 0/500 | 0.31 | 0/665 |
| 54 | y | 0.19 | 0/451 | 0.31 | 0/603 |
| 55 | z | 0.18 | 0/449 | 0.29 | 0/597 |
| All | All | 0.36 | 1/157243 (0.0%) | 0.65 | 17/234932 (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 |
|---|---|---|---|
| 41 | l | 0 | 1 |

All (1) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 7 | A | 525 | G7M | O3'-P | 5.00 | 1.61 | 1.56 |

The worst 5 of 17 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 30 | a | 2098 | G | OP1-P-O3' | -10.94 | 75.19 | 108.00 |
| 30 | a | 2098 | G | OP2-P-O3' | -9.41 | 79.77 | 108.00 |
| 30 | a | 1310 | U | C2-N1-C1' | 7.02 | 126.12 | 117.70 |
| 30 | a | 1311 | C | C2-N1-C1' | 5.80 | 125.18 | 118.80 |
| 7 | A | 1033 | A | O4'-C1'-N9 | 5.71 | 112.77 | 108.20 |

There are no chirality outliers.

All (1) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 41 | l | 81 | 4D4 | Mainchain |

## 5.2 Too-close contacts (i)

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

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 1 | 0 | 418 | 0 | 449 | 5 | 0 |
| 2 | 1 | 377 | 0 | 418 | 1 | 0 |
| 3 | 2 | 504 | 0 | 572 | 10 | 0 |
| 4 | 3 | 302 | 0 | 340 | 4 | 0 |
| 5 | 4 | 540 | 0 | 537 | 12 | 0 |
| 6 | 5 | 1105 | 0 | 1165 | 34 | 0 |
| 7 | A | 32847 | 0 | 16541 | 375 | 0 |
| 8 | B | 1749 | 0 | 1774 | 39 | 0 |
| 9 | C | 1623 | 0 | 1696 | 22 | 0 |
| 10 | D | 1644 | 0 | 1706 | 27 | 0 |
| 11 | E | 1155 | 0 | 1206 | 21 | 0 |
| 12 | F | 832 | 0 | 821 | 22 | 0 |
| 13 | G | 1204 | 0 | 1254 | 20 | 0 |
| 14 | H | 977 | 0 | 1031 | 11 | 0 |
| 15 | I | 1010 | 0 | 1057 | 23 | 0 |
| 16 | J | 788 | 0 | 830 | 20 | 0 |
| 17 | K | 878 | 0 | 884 | 20 | 0 |
| 18 | L | 958 | 0 | 1019 | 12 | 0 |
| 19 | M | 907 | 0 | 977 | 34 | 0 |
| 20 | N | 805 | 0 | 846 | 24 | 0 |
| 21 | O | 710 | 0 | 735 | 8 | 0 |
| 22 | P | 636 | 0 | 649 | 8 | 0 |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 23 | Q | 639 | 0 | 684 | 11 | 0 |
| 24 | R | 507 | 0 | 525 | 16 | 0 |
| 25 | S | 667 | 0 | 691 | 19 | 0 |
| 26 | T | 669 | 0 | 717 | 12 | 0 |
| 27 | U | 589 | 0 | 629 | 19 | 0 |
| 28 | V | 1644 | 0 | 840 | 38 | 0 |
| 29 | X | 778 | 0 | 793 | 16 | 0 |
| 30 | a | 62284 | 0 | 31326 | 611 | 0 |
| 31 | b | 2483 | 0 | 1258 | 18 | 0 |
| 32 | c | 2080 | 0 | 2152 | 15 | 0 |
| 33 | d | 1567 | 0 | 1619 | 22 | 0 |
| 34 | e | 1554 | 0 | 1620 | 18 | 0 |
| 35 | f | 1410 | 0 | 1444 | 33 | 0 |
| 36 | g | 1319 | 0 | 1367 | 25 | 0 |
| 37 | h | 1099 | 0 | 1139 | 26 | 0 |
| 38 | i | 1134 | 0 | 1161 | 23 | 0 |
| 39 | j | 947 | 0 | 1025 | 14 | 0 |
| 40 | k | 1063 | 0 | 1130 | 15 | 0 |
| 41 | l | 1074 | 0 | 1138 | 15 | 0 |
| 42 | m | 950 | 0 | 994 | 7 | 0 |
| 43 | n | 892 | 0 | 923 | 12 | 0 |
| 44 | o | 917 | 0 | 962 | 17 | 0 |
| 45 | p | 947 | 0 | 1019 | 9 | 0 |
| 46 | q | 816 | 0 | 841 | 11 | 0 |
| 47 | r | 855 | 0 | 915 | 11 | 0 |
| 48 | s | 739 | 0 | 809 | 9 | 0 |
| 49 | t | 779 | 0 | 830 | 6 | 0 |
| 50 | u | 749 | 0 | 763 | 12 | 0 |
| 51 | v | 592 | 0 | 612 | 6 | 0 |
| 52 | w | 625 | 0 | 652 | 2 | 0 |
| 53 | x | 499 | 0 | 534 | 8 | 0 |
| 54 | y | 447 | 0 | 484 | 7 | 0 |
| 55 | z | 443 | 0 | 458 | 6 | 0 |
| 56 | 3 | 1 | 0 | 0 | 0 | 0 |
| 56 | 4 | 1 | 0 | 0 | 0 | 0 |
| 57 | A | 95 | 0 | 0 | 0 | 0 |
| 57 | K | 1 | 0 | 0 | 0 | 0 |
| 57 | a | 252 | 0 | 0 | 0 | 0 |
| 57 | b | 5 | 0 | 0 | 0 | 0 |
| 57 | c | 2 | 0 | 0 | 0 | 0 |
| 57 | d | 1 | 0 | 0 | 0 | 0 |
| 57 | m | 1 | 0 | 0 | 0 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 57 | p | 1 | 0 | 0 | 0 | 0 |
| 57 | z | 1 | 0 | 0 | 0 | 0 |
| 58 | A | 47 | 0 | 0 | 0 | 0 |
| 58 | a | 116 | 0 | 0 | 0 | 0 |
| 58 | b | 1 | 0 | 0 | 0 | 0 |
| 58 | c | 3 | 0 | 0 | 0 | 0 |
| 58 | e | 1 | 0 | 0 | 0 | 0 |
| 58 | f | 1 | 0 | 0 | 0 | 0 |
| All | All | 146256 | 0 | 98561 | 1714 | 0 |

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 1714 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 7:A:76:A:N6 | 7:A:91:G:H1 | 1.43 | 1.15 |
| 28:V:27:G:H1 | 28:V:45:A:N6 | 1.64 | 0.94 |
| 15:I:21:ILE:HD11 | 15:I:61:LEU:HG | 1.49 | 0.94 |
| 28:V:27:G:N1 | 28:V:45:A:N6 | 2.21 | 0.87 |
| 38:i:31:GLU:HG2 | 38:i:142:ILE:HD12 | 1.55 | 0.87 |

There are no symmetry-related clashes.

## 5.3 Torsion angles (i)

### 5.3.1 Protein backbone (i)

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

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 1 | 0 | 49/55 (89%) | 49 (100%) | 0 | 0 | 100 | 100 |
| 2 | 1 | 44/46 (96%) | 43 (98%) | 1 (2%) | 0 | 100 | 100 |
| 3 | 2 | 62/65 (95%) | 60 (97%) | 2 (3%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 4 | 3 | 36/38 (95%) | 33 (92%) | 3 (8%) | 0 | 100 | 100 |
| 5 | 4 | 68/70 (97%) | 58 (85%) | 10 (15%) | 0 | 100 | 100 |
| 6 | 5 | 142/234 (61%) | 127 (89%) | 15 (11%) | 0 | 100 | 100 |
| 8 | B | 222/241 (92%) | 205 (92%) | 17 (8%) | 0 | 100 | 100 |
| 9 | C | 204/232 (88%) | 197 (97%) | 7 (3%) | 0 | 100 | 100 |
| 10 | D | 203/206 (98%) | 201 (99%) | 2 (1%) | 0 | 100 | 100 |
| 11 | E | 154/167 (92%) | 149 (97%) | 5 (3%) | 0 | 100 | 100 |
| 12 | F | 101/131 (77%) | 100 (99%) | 1 (1%) | 0 | 100 | 100 |
| 13 | G | 151/156 (97%) | 145 (96%) | 6 (4%) | 0 | 100 | 100 |
| 14 | H | 127/130 (98%) | 122 (96%) | 5 (4%) | 0 | 100 | 100 |
| 15 | I | 124/130 (95%) | 119 (96%) | 5 (4%) | 0 | 100 | 100 |
| 16 | J | 96/103 (93%) | 88 (92%) | 7 (7%) | 1 (1%) | 12 | 39 |
| 17 | K | 113/129 (88%) | 108 (96%) | 5 (4%) | 0 | 100 | 100 |
| 18 | L | 120/124 (97%) | 112 (93%) | 8 (7%) | 0 | 100 | 100 |
| 19 | M | 114/118 (97%) | 109 (96%) | 5 (4%) | 0 | 100 | 100 |
| 20 | N | 98/101 (97%) | 96 (98%) | 2 (2%) | 0 | 100 | 100 |
| 21 | O | 86/89 (97%) | 85 (99%) | 1 (1%) | 0 | 100 | 100 |
| 22 | P | 79/82 (96%) | 77 (98%) | 2 (2%) | 0 | 100 | 100 |
| 23 | Q | 77/84 (92%) | 74 (96%) | 3 (4%) | 0 | 100 | 100 |
| 24 | R | 60/75 (80%) | 58 (97%) | 2 (3%) | 0 | 100 | 100 |
| 25 | S | 82/92 (89%) | 81 (99%) | 1 (1%) | 0 | 100 | 100 |
| 26 | T | 84/87 (97%) | 83 (99%) | 1 (1%) | 0 | 100 | 100 |
| 27 | U | 68/71 (96%) | 66 (97%) | 1 (2%) | 1 (2%) | 8 | 28 |
| 29 | X | 96/111 (86%) | 92 (96%) | 4 (4%) | 0 | 100 | 100 |
| 32 | c | 269/273 (98%) | 263 (98%) | 6 (2%) | 0 | 100 | 100 |
| 33 | d | 206/209 (99%) | 202 (98%) | 3 (2%) | 1 (0%) | 24 | 54 |
| 34 | e | 199/201 (99%) | 196 (98%) | 3 (2%) | 0 | 100 | 100 |
| 35 | f | 175/179 (98%) | 164 (94%) | 11 (6%) | 0 | 100 | 100 |
| 36 | g | 174/177 (98%) | 167 (96%) | 7 (4%) | 0 | 100 | 100 |
| 37 | h | 146/149 (98%) | 139 (95%) | 6 (4%) | 1 (1%) | 18 | 48 |
| 38 | i | 140/142 (99%) | 140 (100%) | 0 | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 39 | j | 121/123 (98%) | 119 (98%) | 2 (2%) | 0 | 100 | 100 |
| 40 | k | 142/144 (99%) | 139 (98%) | 3 (2%) | 0 | 100 | 100 |
| 41 | l | 132/136 (97%) | 130 (98%) | 2 (2%) | 0 | 100 | 100 |
| 42 | m | 117/128 (91%) | 114 (97%) | 3 (3%) | 0 | 100 | 100 |
| 43 | n | 114/117 (97%) | 108 (95%) | 6 (5%) | 0 | 100 | 100 |
| 44 | o | 112/115 (97%) | 110 (98%) | 2 (2%) | 0 | 100 | 100 |
| 45 | p | 115/118 (98%) | 113 (98%) | 2 (2%) | 0 | 100 | 100 |
| 46 | q | 101/103 (98%) | 98 (97%) | 3 (3%) | 0 | 100 | 100 |
| 47 | r | 108/110 (98%) | 105 (97%) | 3 (3%) | 0 | 100 | 100 |
| 48 | s | 91/100 (91%) | 89 (98%) | 2 (2%) | 0 | 100 | 100 |
| 49 | t | 100/104 (96%) | 92 (92%) | 8 (8%) | 0 | 100 | 100 |
| 50 | u | 92/94 (98%) | 88 (96%) | 4 (4%) | 0 | 100 | 100 |
| 51 | v | 76/85 (89%) | 75 (99%) | 1 (1%) | 0 | 100 | 100 |
| 52 | w | 75/78 (96%) | 75 (100%) | 0 | 0 | 100 | 100 |
| 53 | x | 60/63 (95%) | 60 (100%) | 0 | 0 | 100 | 100 |
| 54 | y | 56/59 (95%) | 55 (98%) | 1 (2%) | 0 | 100 | 100 |
| 55 | z | 54/57 (95%) | 54 (100%) | 0 | 0 | 100 | 100 |
| All | All | 5835/6231 (94%) | 5632 (96%) | 199 (3%) | 4 (0%) | 49 | 77 |

All (4) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 33 | d | 149 | ASN |
| 37 | h | 115 | VAL |
| 16 | J | 57 | VAL |
| 27 | U | 28 | VAL |

### 5.3.2 Protein sidechains (i)

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

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 1 | 0 | 46/49 (94%) | 45 (98%) | 1 (2%) | 45 | 77 |
| 2 | 1 | 38/38 (100%) | 37 (97%) | 1 (3%) | 40 | 73 |
| 3 | 2 | 51/52 (98%) | 49 (96%) | 2 (4%) | 28 | 63 |
| 4 | 3 | 34/34 (100%) | 33 (97%) | 1 (3%) | 37 | 71 |
| 5 | 4 | 60/60 (100%) | 58 (97%) | 2 (3%) | 33 | 67 |
| 6 | 5 | 116/180 (64%) | 113 (97%) | 3 (3%) | 40 | 73 |
| 8 | B | 185/198 (93%) | 180 (97%) | 5 (3%) | 39 | 73 |
| 9 | C | 170/189 (90%) | 165 (97%) | 5 (3%) | 37 | 71 |
| 10 | D | 171/172 (99%) | 169 (99%) | 2 (1%) | 63 | 86 |
| 11 | E | 119/126 (94%) | 113 (95%) | 6 (5%) | 22 | 53 |
| 12 | F | 88/111 (79%) | 85 (97%) | 3 (3%) | 32 | 66 |
| 13 | G | 126/129 (98%) | 123 (98%) | 3 (2%) | 43 | 75 |
| 14 | H | 104/105 (99%) | 102 (98%) | 2 (2%) | 50 | 79 |
| 15 | I | 104/107 (97%) | 102 (98%) | 2 (2%) | 50 | 79 |
| 16 | J | 87/91 (96%) | 83 (95%) | 4 (5%) | 24 | 57 |
| 17 | K | 89/98 (91%) | 84 (94%) | 5 (6%) | 19 | 50 |
| 18 | L | 102/103 (99%) | 99 (97%) | 3 (3%) | 37 | 71 |
| 19 | M | 96/98 (98%) | 92 (96%) | 4 (4%) | 26 | 60 |
| 20 | N | 83/84 (99%) | 81 (98%) | 2 (2%) | 43 | 75 |
| 21 | O | 75/76 (99%) | 74 (99%) | 1 (1%) | 61 | 86 |
| 22 | P | 63/63 (100%) | 62 (98%) | 1 (2%) | 55 | 83 |
| 23 | Q | 73/78 (94%) | 70 (96%) | 3 (4%) | 27 | 61 |
| 24 | R | 53/65 (82%) | 52 (98%) | 1 (2%) | 50 | 79 |
| 25 | S | 72/79 (91%) | 68 (94%) | 4 (6%) | 19 | 50 |
| 26 | T | 65/66 (98%) | 65 (100%) | 0 | 100 | 100 |
| 27 | U | 60/61 (98%) | 59 (98%) | 1 (2%) | 53 | 82 |
| 29 | X | 83/94 (88%) | 82 (99%) | 1 (1%) | 63 | 86 |
| 32 | c | 215/217 (99%) | 215 (100%) | 0 | 100 | 100 |
| 33 | d | 163/163 (100%) | 160 (98%) | 3 (2%) | 51 | 80 |
| 34 | e | 165/165 (100%) | 164 (99%) | 1 (1%) | 78 | 93 |
| 35 | f | 148/150 (99%) | 145 (98%) | 3 (2%) | 48 | 78 |
| 36 | g | 135/136 (99%) | 132 (98%) | 3 (2%) | 45 | 77 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 37 | h | 112/113 (99%) | 108 (96%) | 4 (4%) | 31 | 65 |
| 38 | i | 116/116 (100%) | 115 (99%) | 1 (1%) | 70 | 90 |
| 39 | j | 104/104 (100%) | 103 (99%) | 1 (1%) | 68 | 89 |
| 40 | k | 105/105 (100%) | 103 (98%) | 2 (2%) | 50 | 79 |
| 41 | l | 107/107 (100%) | 106 (99%) | 1 (1%) | 70 | 90 |
| 42 | m | 98/103 (95%) | 97 (99%) | 1 (1%) | 68 | 89 |
| 43 | n | 86/87 (99%) | 83 (96%) | 3 (4%) | 32 | 66 |
| 44 | o | 99/100 (99%) | 99 (100%) | 0 | 100 | 100 |
| 45 | p | 89/90 (99%) | 87 (98%) | 2 (2%) | 45 | 77 |
| 46 | q | 83/83 (100%) | 82 (99%) | 1 (1%) | 63 | 86 |
| 47 | r | 92/92 (100%) | 91 (99%) | 1 (1%) | 65 | 88 |
| 48 | s | 80/84 (95%) | 80 (100%) | 0 | 100 | 100 |
| 49 | t | 83/85 (98%) | 83 (100%) | 0 | 100 | 100 |
| 50 | u | 76/76 (100%) | 74 (97%) | 2 (3%) | 40 | 73 |
| 51 | v | 60/64 (94%) | 59 (98%) | 1 (2%) | 53 | 82 |
| 52 | w | 67/68 (98%) | 66 (98%) | 1 (2%) | 57 | 84 |
| 53 | x | 53/54 (98%) | 52 (98%) | 1 (2%) | 50 | 79 |
| 54 | y | 48/49 (98%) | 47 (98%) | 1 (2%) | 47 | 77 |
| 55 | z | 47/48 (98%) | 46 (98%) | 1 (2%) | 47 | 77 |
| All | All | 4844/5065 (96%) | 4742 (98%) | 102 (2%) | 46 | 77 |

5 of 102 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 22 | P | 1 | MET |
| 34 | e | 166 | LYS |
| 53 | x | 58 | THR |
| 23 | Q | 28 | MET |
| 25 | S | 66 | MET |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 39 | j | 88 | ASN |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 48 | s | 48 | GLN |
| 41 | l | 13 | HIS |
| 45 | p | 52 | GLN |
| 52 | w | 34 | HIS |

### 5.3.3 RNA (i)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|---|---|---|---|---|
| 28 | V | 76/77 (98%) | 24 (31%) | 2 (2%) |
| 30 | a | 2899/2923 (99%) | 437 (15%) | 0 |
| 31 | b | 115/116 (99%) | 12 (10%) | 0 |
| 7 | A | 1529/1550 (98%) | 216 (14%) | 2 (0%) |
| All | All | 4619/4666 (98%) | 689 (14%) | 4 (0%) |

5 of 689 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 7 | A | 4 | U |
| 7 | A | 7 | A |
| 7 | A | 8 | A |
| 7 | A | 9 | G |
| 7 | A | 22 | G |

All (4) RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 7 | A | 1033 | A |
| 7 | A | 1492 | G |
| 28 | V | 20 | G |
| 28 | V | 75 | C |

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

45 non-standard protein/DNA/RNA residues are 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 | $\#\|Z\|>2$ |
| 7 | 4OC | A | 1400 | 7 | 20,23,24 | 2.24 | 3 (15%) | 26,32,35 | 0.99 | 2 (7%) |
| 7 | 2MG | A | 964 | 7 | 23,26,27 | 2.57 | 4 (17%) | 32,38,41 | 2.07 | 10 (31%) |
| 18 | D2T | L | 89 | 18 | 7,9,10 | 1.22 | 1 (14%) | 6,11,13 | 1.56 | 1 (16%) |
| 30 | OMU | a | 2550 | 58,30,57 | 19,22,23 | 2.59 | 7 (36%) | 26,31,34 | 1.73 | 5 (19%) |
| 7 | 2MG | A | 1205 | 58,7 | 23,26,27 | 2.57 | 4 (17%) | 32,38,41 | 2.07 | 9 (28%) |
| 30 | 6MZ | a | 2028 | 30 | 22,25,26 | 2.39 | 3 (13%) | 30,36,39 | 2.36 | 10 (33%) |
| 30 | PSU | a | 2578 | 30 | 18,21,22 | 2.06 | 8 (44%) | 22,30,33 | 1.87 | 5 (22%) |
| 28 | OMC | V | 33 | 28 | 19,22,23 | 1.78 | 3 (15%) | 26,31,34 | 0.91 | 2 (7%) |
| 30 | PSU | a | 2455 | 30 | 18,21,22 | 2.00 | 7 (38%) | 22,30,33 | 1.89 | 4 (18%) |
| 28 | 4SU | V | 8 | 28 | 18,21,22 | 3.75 | 8 (44%) | 26,30,33 | 2.22 | 4 (15%) |
| 30 | PSU | a | 953 | 30 | 18,21,22 | 2.04 | 7 (38%) | 22,30,33 | 1.83 | 3 (13%) |
| 7 | 5MC | A | 965 | 7 | 18,22,23 | 1.91 | 5 (27%) | 26,32,35 | 1.30 | 2 (7%) |
| 30 | PSU | a | 744 | 30,57 | 18,21,22 | 1.99 | 7 (38%) | 22,30,33 | 1.79 | 3 (13%) |
| 30 | PSU | a | 1909 | 30 | 18,21,22 | 1.90 | 7 (38%) | 22,30,33 | 1.76 | 3 (13%) |
| 7 | G7M | A | 525 | 58,7 | 23,26,27 | 2.18 | 5 (21%) | 35,39,42 | 1.86 | 7 (20%) |
| 30 | 2MA | a | 2501 | 58,30,57 | 22,25,26 | 1.32 | 1 (4%) | 33,37,40 | 2.00 | 7 (21%) |
| 30 | 2MG | a | 2443 | 30 | 23,26,27 | 2.58 | 7 (30%) | 32,38,41 | 2.03 | 10 (31%) |
| 28 | H2U | V | 21 | 28 | 18,21,22 | 4.32 | 5 (27%) | 21,30,33 | 4.78 | 6 (28%) |
| 7 | MA6 | A | 1517 | 7 | 23,26,27 | 1.19 | 3 (13%) | 34,38,41 | 2.27 | 10 (29%) |
| 30 | 5MU | a | 1937 | 58,30 | 19,22,23 | 2.50 | 7 (36%) | 28,32,35 | 3.84 | 10 (35%) |
| 28 | 5MU | V | 55 | 28 | 19,22,23 | 2.36 | 7 (36%) | 28,32,35 | 3.69 | 10 (35%) |
| 28 | PSU | V | 56 | 28 | 18,21,22 | 1.93 | 7 (38%) | 22,30,33 | 1.82 | 3 (13%) |
| 30 | PSU | a | 2502 | 58,30 | 18,21,22 | 2.05 | 7 (38%) | 22,30,33 | 1.88 | 4 (18%) |
| 30 | 5MC | a | 1960 | 58,30 | 18,22,23 | 1.89 | 6 (33%) | 26,32,35 | 1.31 | 2 (7%) |
| 30 | PSU | a | 2603 | 30 | 18,21,22 | 2.01 | 7 (38%) | 22,30,33 | 1.80 | 3 (13%) |
| 30 | OMG | a | 2249 | 58,30 | 23,26,27 | 2.33 | 6 (26%) | 33,38,41 | 1.84 | 10 (30%) |
| 7 | UR3 | A | 1496 | 7 | 19,22,23 | 2.56 | 6 (31%) | 26,32,35 | 1.30 | 2 (7%) |
| 7 | MA6 | A | 1516 | 7 | 23,26,27 | 1.18 | 3 (13%) | 34,38,41 | 2.21 | 9 (26%) |
| 30 | 5MU | a | 745 | 30 | 19,22,23 | 2.48 | 7 (36%) | 28,32,35 | 3.85 | 11 (39%) |
| 30 | G7M | a | 2067 | 58,30 | 23,26,27 | 2.18 | 5 (21%) | 35,39,42 | 1.87 | 7 (20%) |
| 30 | 6MZ | a | 1615 | 30 | 22,25,26 | 2.40 | 3 (13%) | 30,36,39 | 2.27 | 10 (33%) |
| 30 | 2MG | a | 1831 | 30 | 23,26,27 | 2.57 | 4 (17%) | 32,38,41 | 2.06 | 10 (31%) |
| 30 | PSU | a | 1915 | 30 | 18,21,22 | 1.90 | 7 (38%) | 22,30,33 | 1.79 | 3 (13%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | $\#\|Z\|>2$ | Counts | RMSZ | $\#\|Z\|>2$ |
| 30 | 3TD | a | 1913 | - | 18,22,23 | 2.91 | 7 (38%) | 22,32,35 | 1.74 | 3 (13%) |
| 30 | H2U | a | 2447 | 30 | 18,21,22 | 4.16 | 5 (27%) | 21,30,33 | 5.22 | 6 (28%) |
| 30 | OMC | a | 2496 | 30,57 | 19,22,23 | 1.79 | 4 (21%) | 26,31,34 | 0.99 | 2 (7%) |
| 17 | IAS | K | 119 | 17 | 6,7,8 | 1.77 | 1 (16%) | 6,8,10 | 2.70 | 2 (33%) |
| 41 | MS6 | l | 82 | 41 | 5,7,8 | 0.53 | 0 | 2,7,9 | 1.79 | 1 (50%) |
| 7 | PSU | A | 514 | 57,7 | 18,21,22 | 1.97 | 7 (38%) | 22,30,33 | 1.78 | 4 (18%) |
| 30 | PSU | a | 2602 | 30 | 18,21,22 | 2.01 | 7 (38%) | 22,30,33 | 1.83 | 3 (13%) |
| 7 | 2MG | A | 1514 | 7 | 23,26,27 | 2.57 | 5 (21%) | 32,38,41 | 2.07 | 11 (34%) |
| 7 | 5MC | A | 1405 | 7 | 18,22,23 | 1.90 | 5 (27%) | 26,32,35 | 1.29 | 2 (7%) |
| 30 | 1MG | a | 743 | 30 | 22,26,27 | 2.51 | 5 (22%) | 33,39,42 | 2.04 | 7 (21%) |
| 33 | MEQ | d | 150 | 33 | 8,9,10 | 0.87 | 0 | 5,10,12 | 0.55 | 0 |
| 41 | 4D4 | l | 81 | 41 | 9,11,12 | 0.82 | 0 | 8,13,15 | 1.57 | 2 (25%) |

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 |
|---|---|---|---|---|---|---|---|
| 7 | 4OC | A | 1400 | 7 | - | 0/9/29/30 | 0/2/2/2 |
| 7 | 2MG | A | 964 | 7 | - | 0/9/27/28 | 0/3/3/3 |
| 18 | D2T | L | 89 | 18 | - | 4/7/12/14 | - |
| 30 | OMU | a | 2550 | 58,30,57 | - | 0/9/27/28 | 0/2/2/2 |
| 7 | 2MG | A | 1205 | 58,7 | - | 1/9/27/28 | 0/3/3/3 |
| 30 | 6MZ | a | 2028 | 30 | - | 2/9/27/28 | 0/3/3/3 |
| 30 | PSU | a | 2578 | 30 | - | 0/7/25/26 | 0/2/2/2 |
| 28 | OMC | V | 33 | 28 | - | 2/9/27/28 | 0/2/2/2 |
| 30 | PSU | a | 2455 | 30 | - | 0/7/25/26 | 0/2/2/2 |
| 28 | 4SU | V | 8 | 28 | - | 0/7/25/26 | 0/2/2/2 |
| 30 | PSU | a | 953 | 30 | - | 0/7/25/26 | 0/2/2/2 |
| 7 | 5MC | A | 965 | 7 | - | 0/7/25/26 | 0/2/2/2 |
| 30 | PSU | a | 744 | 30,57 | - | 1/7/25/26 | 0/2/2/2 |
| 30 | PSU | a | 1909 | 30 | - | 0/7/25/26 | 0/2/2/2 |
| 7 | G7M | A | 525 | 58,7 | - | 3/7/25/26 | 0/3/3/3 |
| 30 | 2MA | a | 2501 | 58,30,57 | - | 2/7/25/26 | 0/3/3/3 |
| 30 | 2MG | a | 2443 | 30 | - | 0/9/27/28 | 0/3/3/3 |
| 28 | H2U | V | 21 | 28 | - | 7/7/38/39 | 0/2/2/2 |
| 7 | MA6 | A | 1517 | 7 | - | 5/11/29/30 | 0/3/3/3 |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|---|---|---|---|---|---|---|---|
| 30 | 5MU | a | 1937 | 58,30 | - | 0/7/25/26 | 0/2/2/2 |
| 28 | 5MU | V | 55 | 28 | - | 0/7/25/26 | 0/2/2/2 |
| 28 | PSU | V | 56 | 28 | - | 0/7/25/26 | 0/2/2/2 |
| 30 | PSU | a | 2502 | 58,30 | - | 0/7/25/26 | 0/2/2/2 |
| 30 | 5MC | a | 1960 | 58,30 | - | 0/7/25/26 | 0/2/2/2 |
| 30 | PSU | a | 2603 | 30 | - | 0/7/25/26 | 0/2/2/2 |
| 30 | OMG | a | 2249 | 58,30 | - | 1/9/27/28 | 0/3/3/3 |
| 7 | UR3 | A | 1496 | 7 | - | 0/7/25/26 | 0/2/2/2 |
| 7 | MA6 | A | 1516 | 7 | - | 2/11/29/30 | 0/3/3/3 |
| 30 | 5MU | a | 745 | 30 | - | 0/7/25/26 | 0/2/2/2 |
| 30 | G7M | a | 2067 | 58,30 | - | 1/7/25/26 | 0/3/3/3 |
| 30 | 6MZ | a | 1615 | 30 | - | 0/9/27/28 | 0/3/3/3 |
| 30 | 2MG | a | 1831 | 30 | - | 4/9/27/28 | 0/3/3/3 |
| 30 | PSU | a | 1915 | 30 | - | 0/7/25/26 | 0/2/2/2 |
| 30 | 3TD | a | 1913 | - | - | 2/7/25/26 | 0/2/2/2 |
| 30 | H2U | a | 2447 | 30 | - | 2/7/38/39 | 0/2/2/2 |
| 30 | OMC | a | 2496 | 30,57 | - | 0/9/27/28 | 0/2/2/2 |
| 17 | IAS | K | 119 | 17 | - | 2/7/7/8 | - |
| 41 | MS6 | l | 82 | 41 | - | 1/4/6/8 | - |
| 7 | PSU | A | 514 | 57,7 | - | 0/7/25/26 | 0/2/2/2 |
| 30 | PSU | a | 2602 | 30 | - | 0/7/25/26 | 0/2/2/2 |
| 7 | 2MG | A | 1514 | 7 | - | 0/9/27/28 | 0/3/3/3 |
| 7 | 5MC | A | 1405 | 7 | - | 0/7/25/26 | 0/2/2/2 |
| 30 | 1MG | a | 743 | 30 | - | 0/7/25/26 | 0/3/3/3 |
| 33 | MEQ | d | 150 | 33 | - | 3/8/9/11 | - |
| 41 | 4D4 | l | 81 | 41 | - | 2/11/12/14 | - |

The worst 5 of 223 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 28 | V | 21 | H2U | O4-C4 | 10.25 | 1.44 | 1.23 |
| 30 | a | 1615 | 6MZ | C6-N6 | 10.14 | 1.45 | 1.34 |
| 30 | a | 2028 | 6MZ | C6-N6 | 10.03 | 1.45 | 1.34 |
| 30 | a | 2447 | H2U | O4-C4 | 10.03 | 1.43 | 1.23 |
| 7 | A | 964 | 2MG | O6-C6 | 9.16 | 1.41 | 1.23 |

The worst 5 of 240 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 30 | a | 2447 | H2U | C4-N3-C2 | -16.69 | 111.95 | 125.79 |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 28 | V | 21 | H2U | C4-N3-C2 | -13.26 | 114.79 | 125.79 |
| 28 | V | 21 | H2U | O2-C2-N1 | -11.05 | 109.24 | 123.11 |
| 30 | a | 2447 | H2U | O2-C2-N1 | -10.87 | 109.46 | 123.11 |
| 30 | a | 745 | 5MU | C5M-C5-C4 | 9.01 | 128.69 | 118.77 |

There are no chirality outliers.

5 of 47 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 18 | L | 89 | D2T | CA-CB-CG-OD1 |
| 18 | L | 89 | D2T | CA-CB-CG-OD2 |
| 18 | L | 89 | D2T | SB-CB-CG-OD2 |
| 28 | V | 21 | H2U | O4'-C4'-C5'-O5' |
| 28 | V | 21 | H2U | C3'-C4'-C5'-O5' |

There are no ring outliers.

12 monomers are involved in 18 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|---|---|---|---|---|---|
| 7 | A | 1400 | 4OC | 2 | 0 |
| 7 | A | 964 | 2MG | 3 | 0 |
| 30 | a | 2028 | 6MZ | 3 | 0 |
| 28 | V | 33 | OMC | 1 | 0 |
| 30 | a | 953 | PSU | 1 | 0 |
| 30 | a | 2501 | 2MA | 1 | 0 |
| 28 | V | 21 | H2U | 2 | 0 |
| 28 | V | 55 | 5MU | 1 | 0 |
| 7 | A | 1516 | MA6 | 1 | 0 |
| 30 | a | 1915 | PSU | 1 | 0 |
| 30 | a | 1913 | 3TD | 1 | 0 |
| 30 | a | 743 | 1MG | 1 | 0 |

## 5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry (i)

Of 530 ligands modelled in this entry, 530 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|---|---|---|
| 30 | a | 2 |

All chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|---|---|---|---|---|---|---|
| 1 | a | 1913:3TD | O3' | 1914:A | P | 5.28 |
| 1 | a | 1912:C | O3' | 1913:3TD | P | 3.05 |

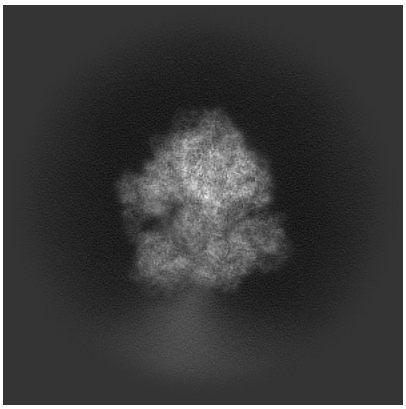
# 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-55796. These allow visual inspection of the internal detail of the map and identification of artifacts.

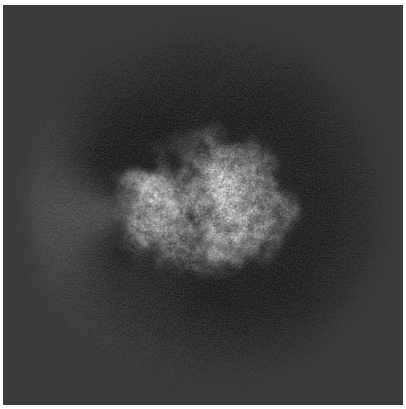
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

## 6.1 Orthogonal projections

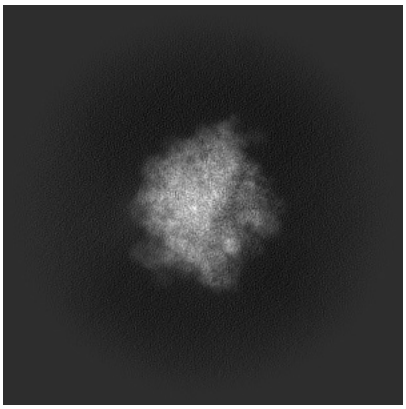
### 6.1.1 Primary map



X

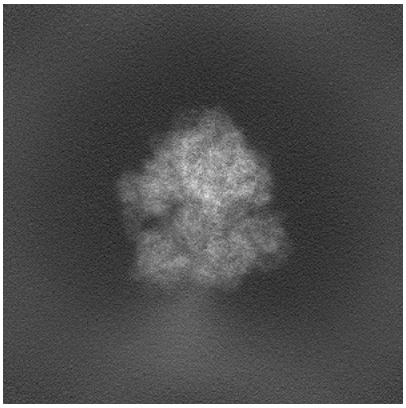


Y

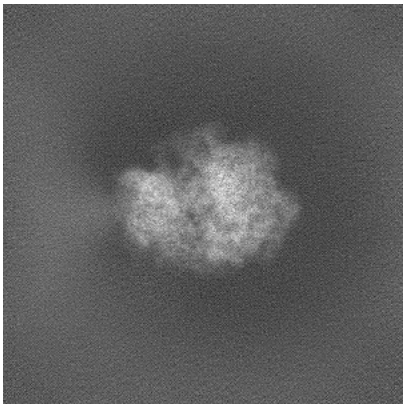


Z

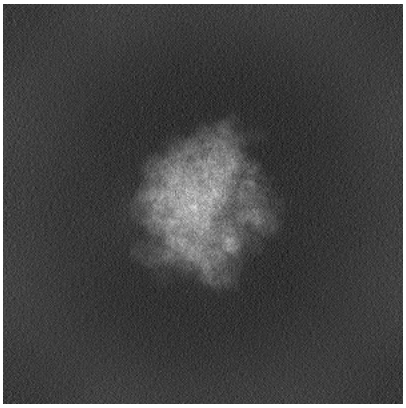
### 6.1.2 Raw map



X



Y

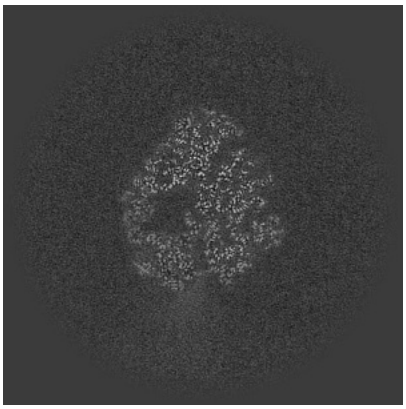


Z

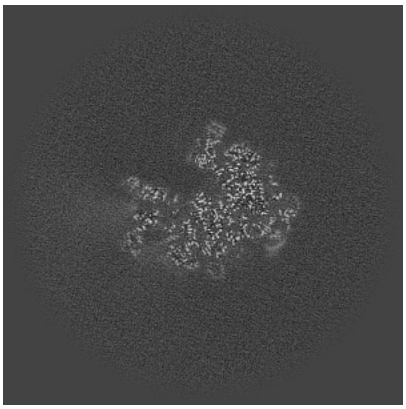
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices (i)

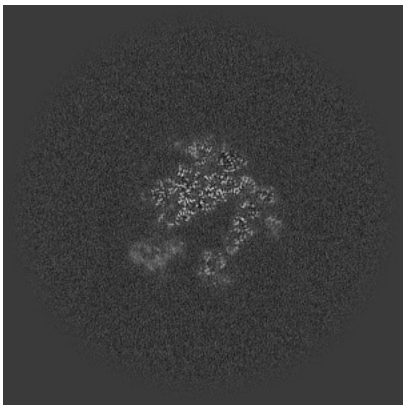
### 6.2.1 Primary map



X Index: 256

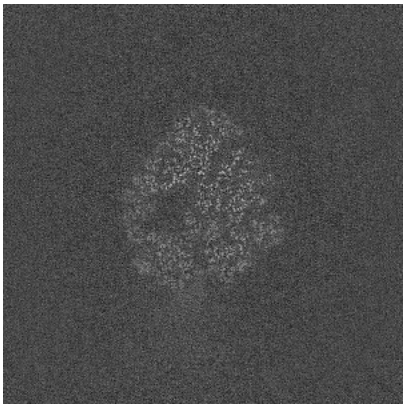


Y Index: 256

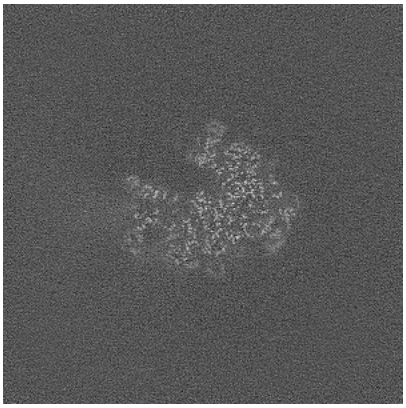


Z Index: 256

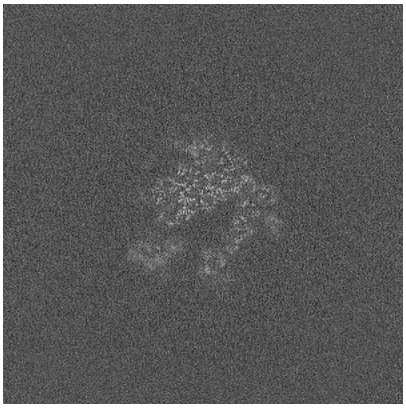
### 6.2.2 Raw map



X Index: 256



Y Index: 256

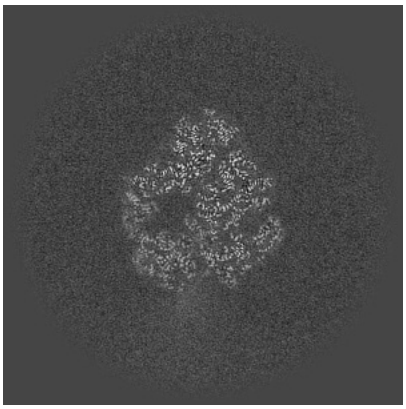


Z Index: 256

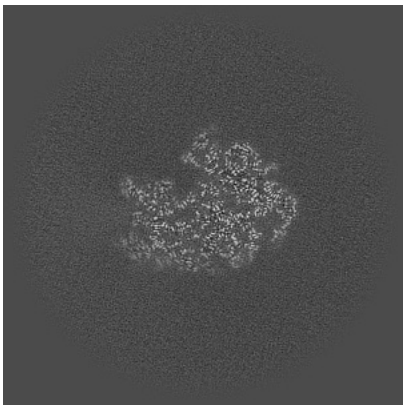
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices (i)

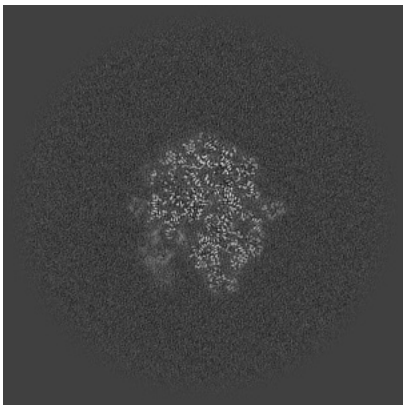
### 6.3.1 Primary map



X Index: 260

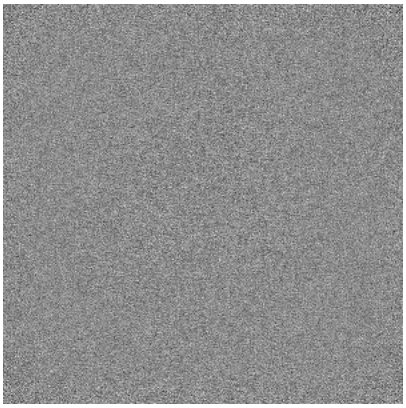


Y Index: 265

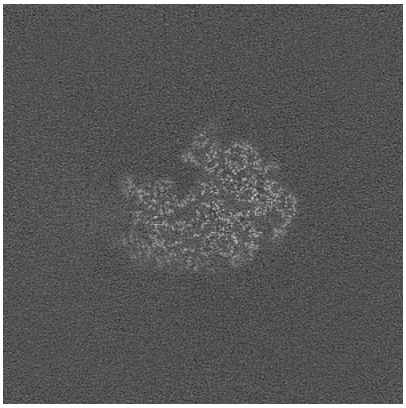


Z Index: 278

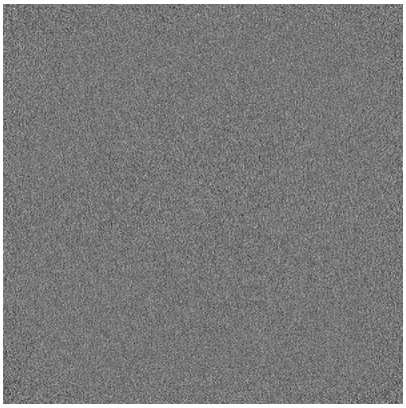
### 6.3.2 Raw map



X Index: 0



Y Index: 265

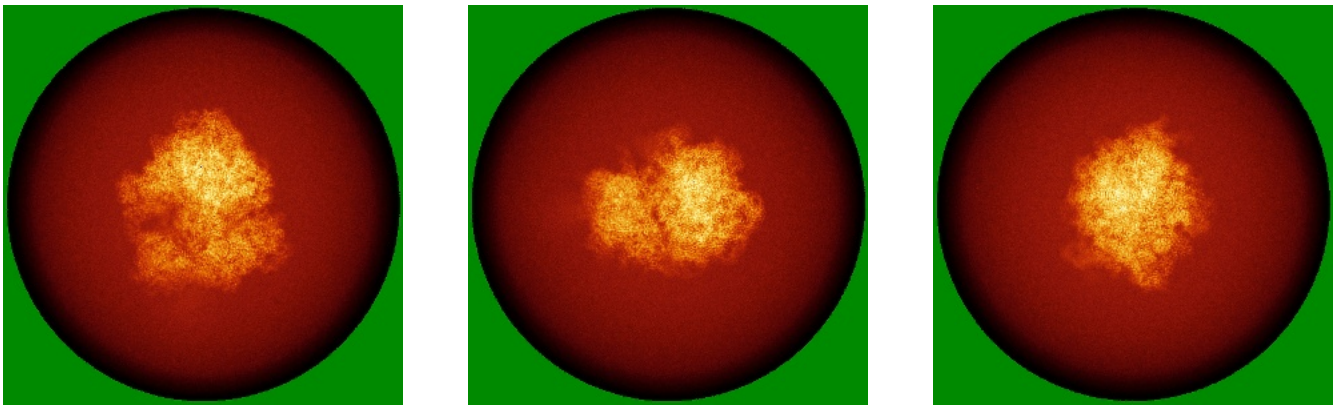


Z Index: 0

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

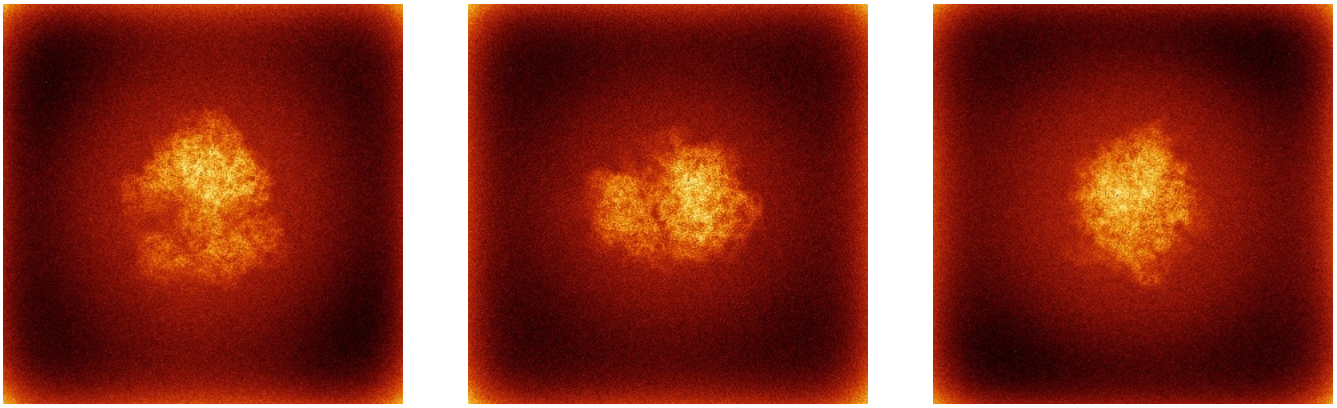
## 6.4 Orthogonal standard-deviation projections (False-color) (i)

### 6.4.1 Primary map



X Y Z

### 6.4.2 Raw map

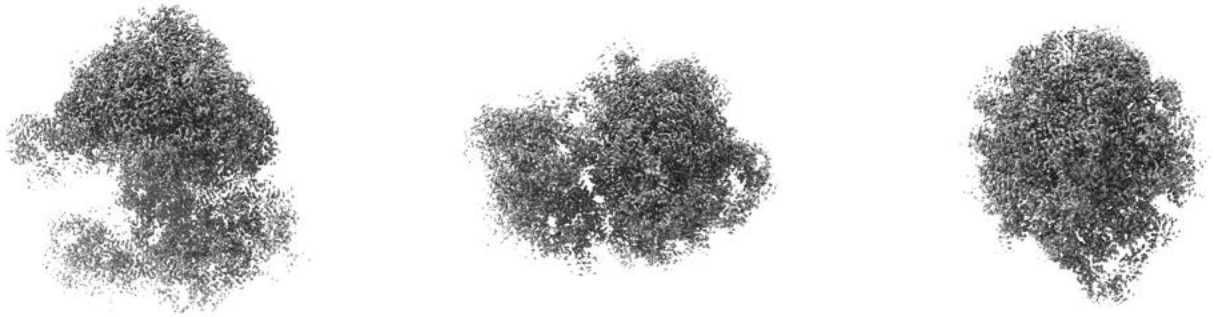


X Y Z

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

## 6.5 Orthogonal surface views (i)

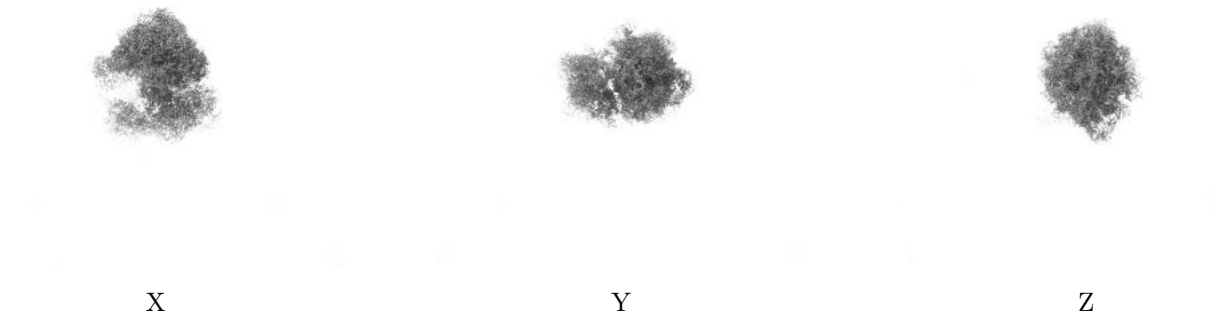
### 6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.55. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



X Y Z

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

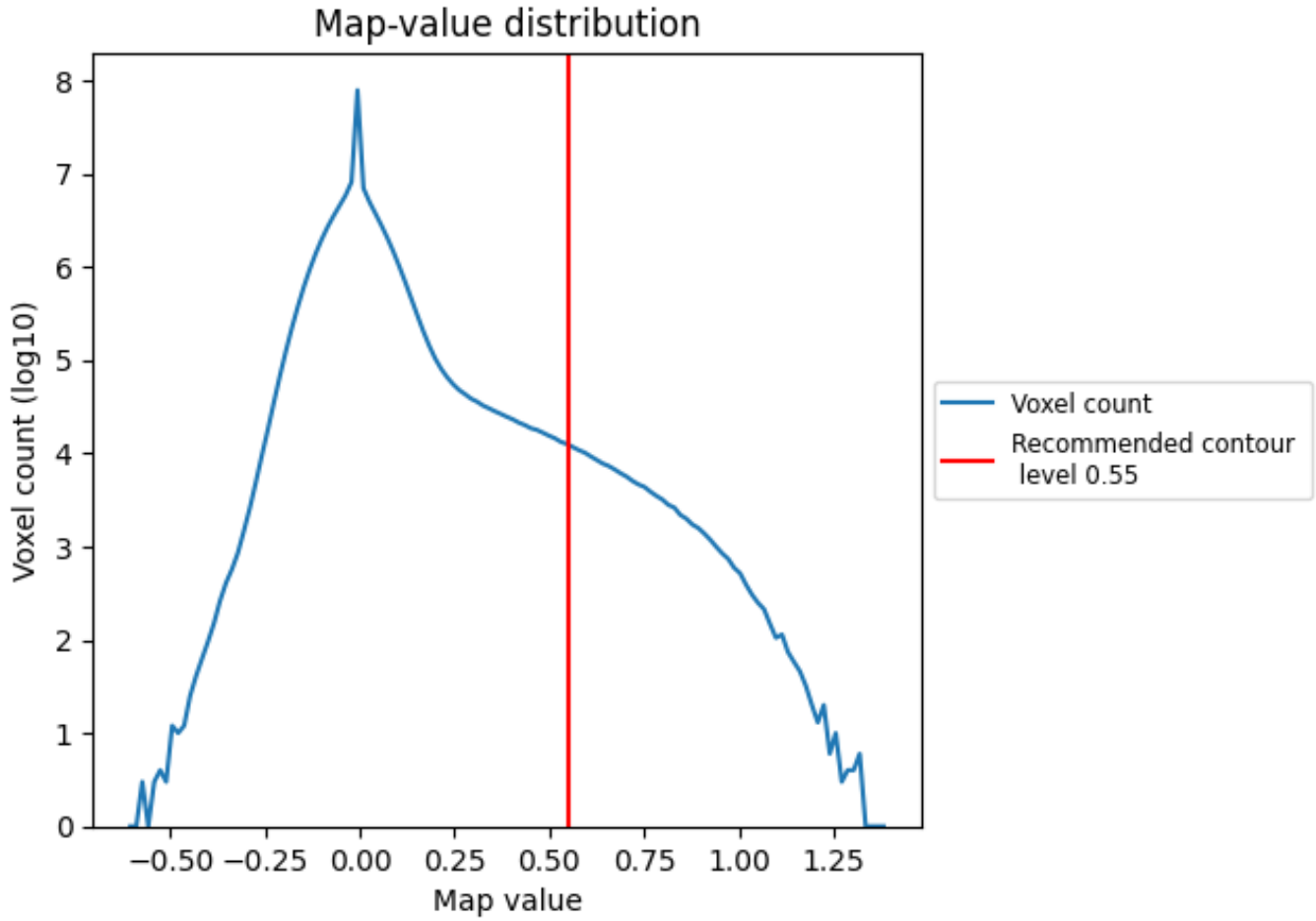
## 6.6 Mask visualisation (i)

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

# 7 Map analysis

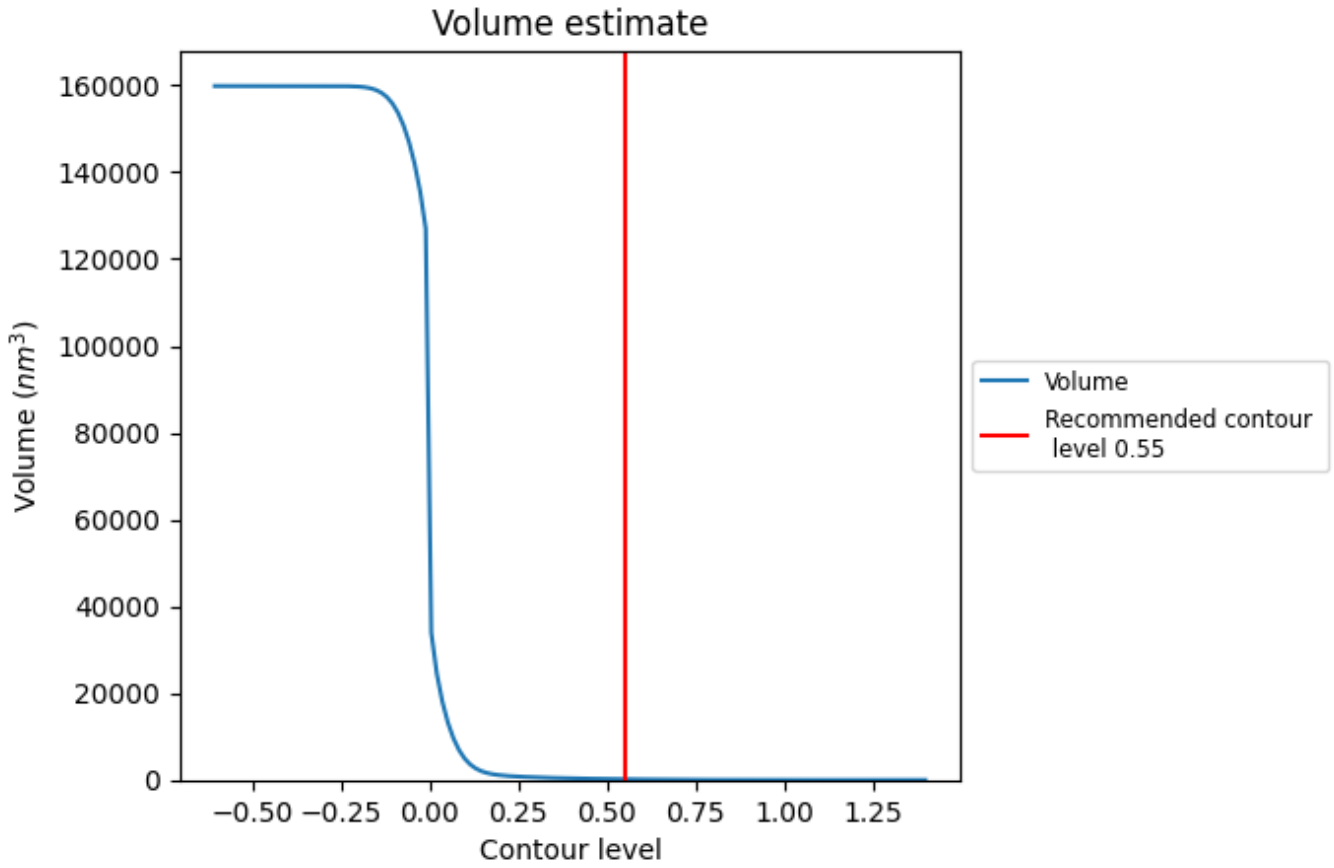
This section contains the results of statistical analysis of the map.

## 7.1 Map-value distribution




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.

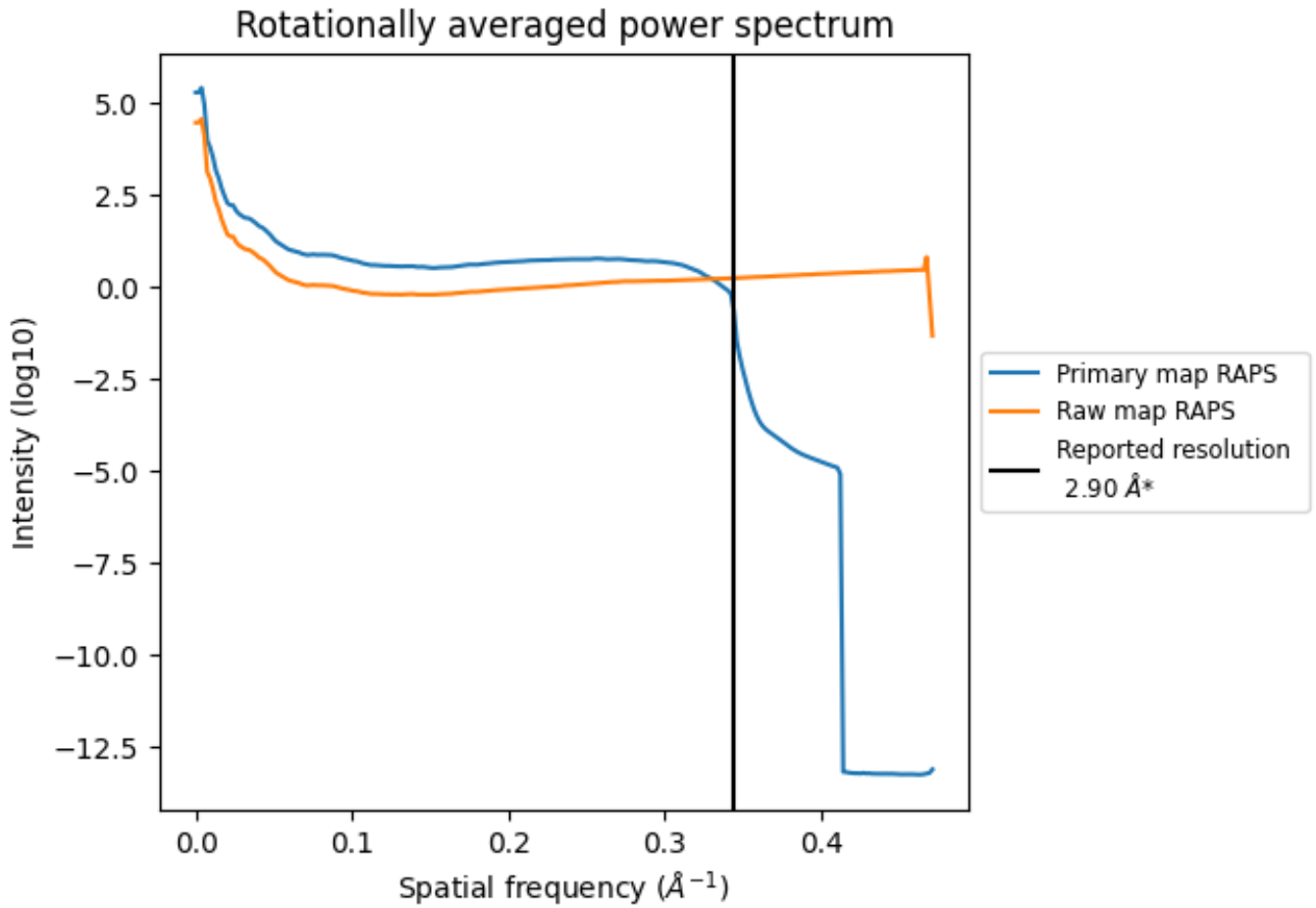
## 7.2 Volume estimate (i)




The volume at the recommended contour level is 165 $nm^3$; this corresponds to an approximate mass of 149 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)

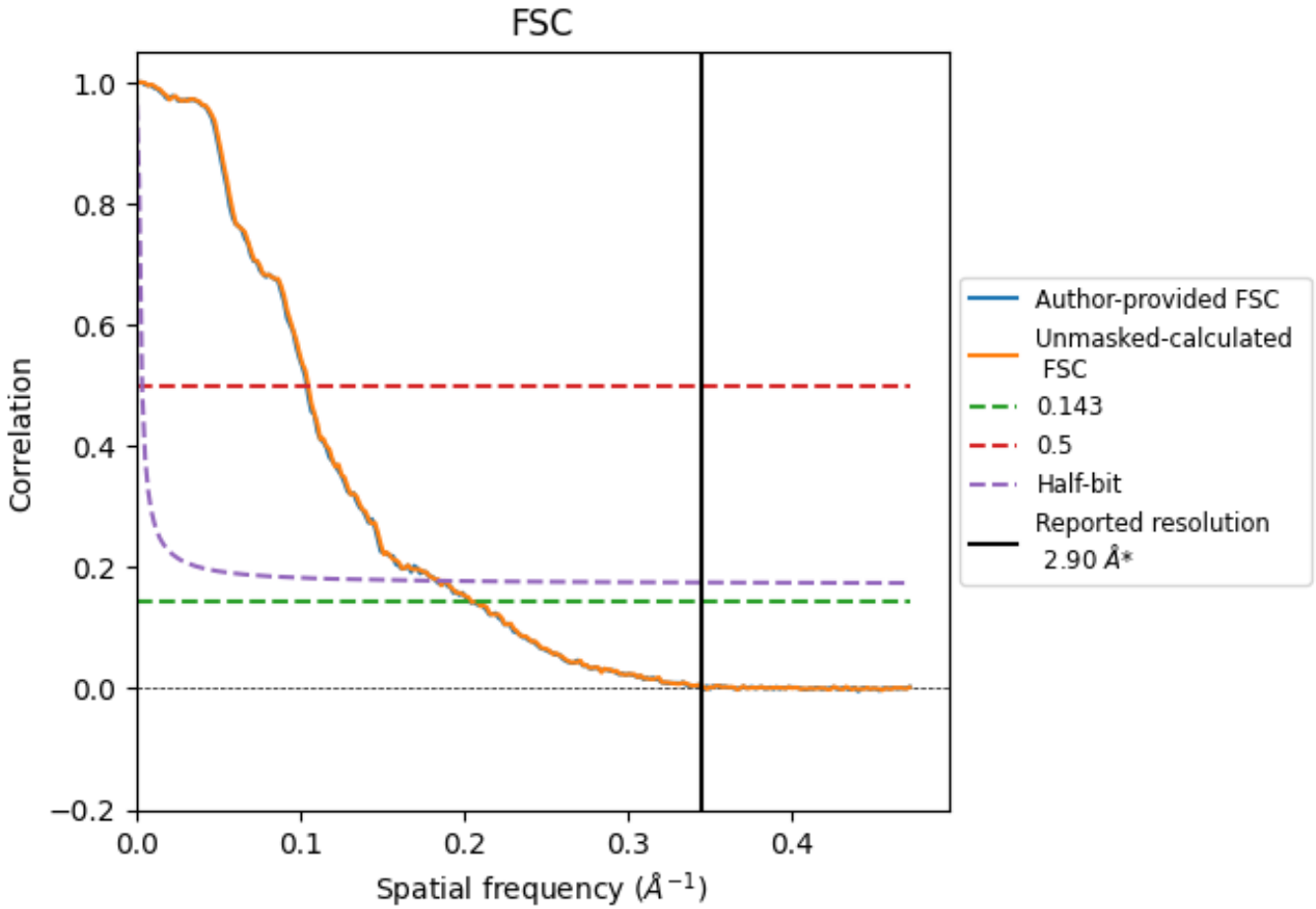



*Reported resolution corresponds to spatial frequency of 0.345 $Å^{-1}$

# 8 Fourier-Shell correlation

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

## 8.1 FSC




*Reported resolution corresponds to spatial frequency of 0.345 Å$^{-1}$

## 8.2 Resolution estimates (i)

| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---|---|---|---|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 2.90 | - | - |
| Author-provided FSC curve | 4.91 | 9.62 | 5.46 |
| Unmasked-calculated* | 4.89 | 9.52 | 5.41 |

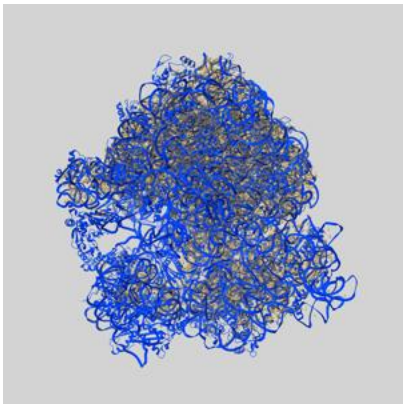
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.91 differs from the reported value 2.9 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.89 differs from the reported value 2.9 by more than 10 %

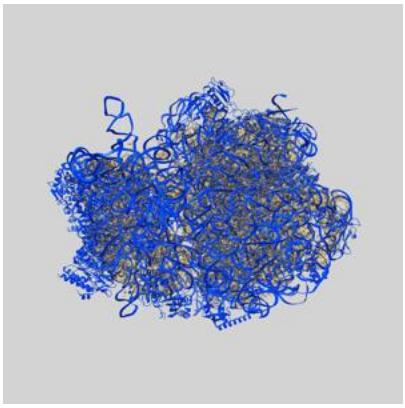
# 9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-55796 and PDB model 9TCQ. Per-residue inclusion information can be found in section 3 on page 16.

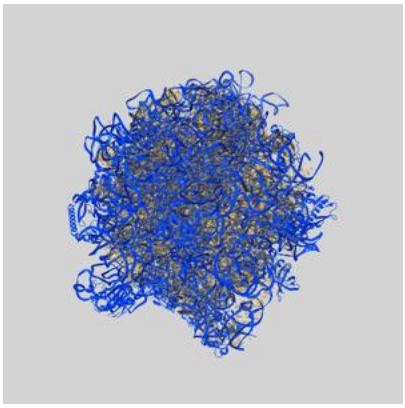
## 9.1 Map-model overlay



X



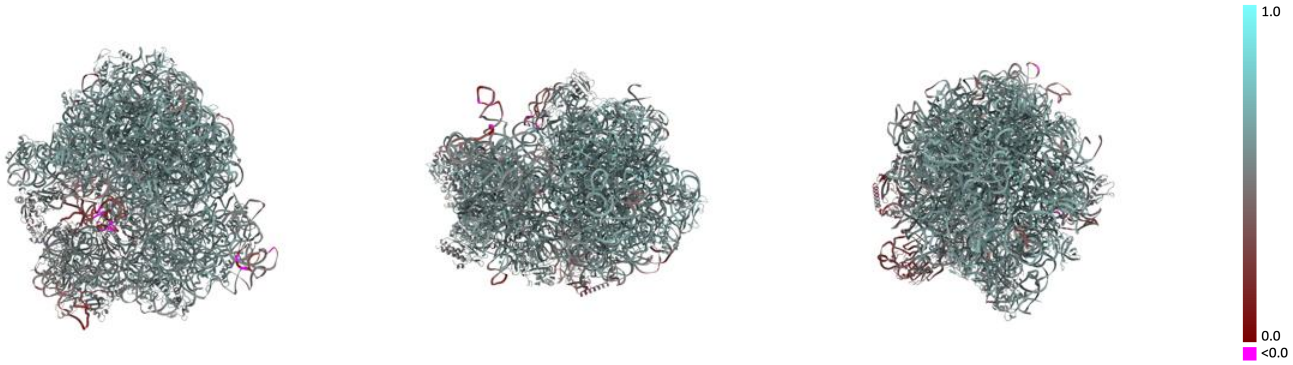
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.55 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.

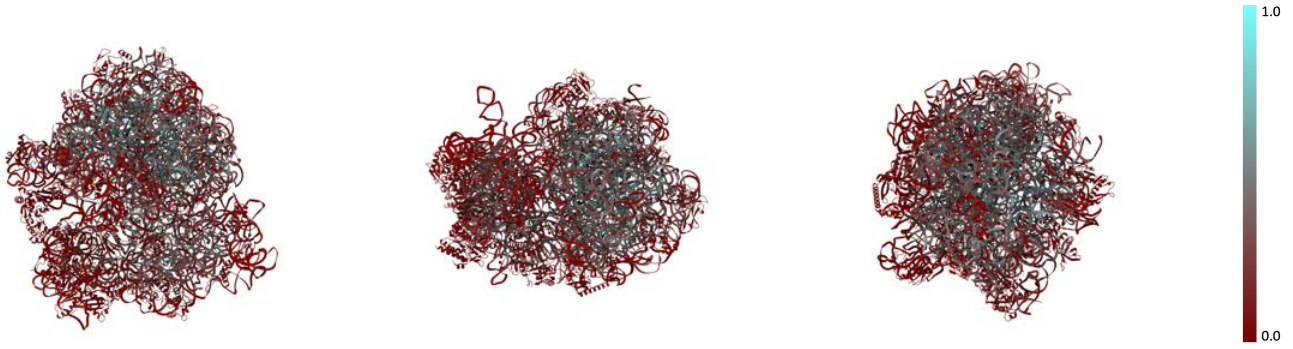
## 9.2 Q-score mapped to coordinate model (i)




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.

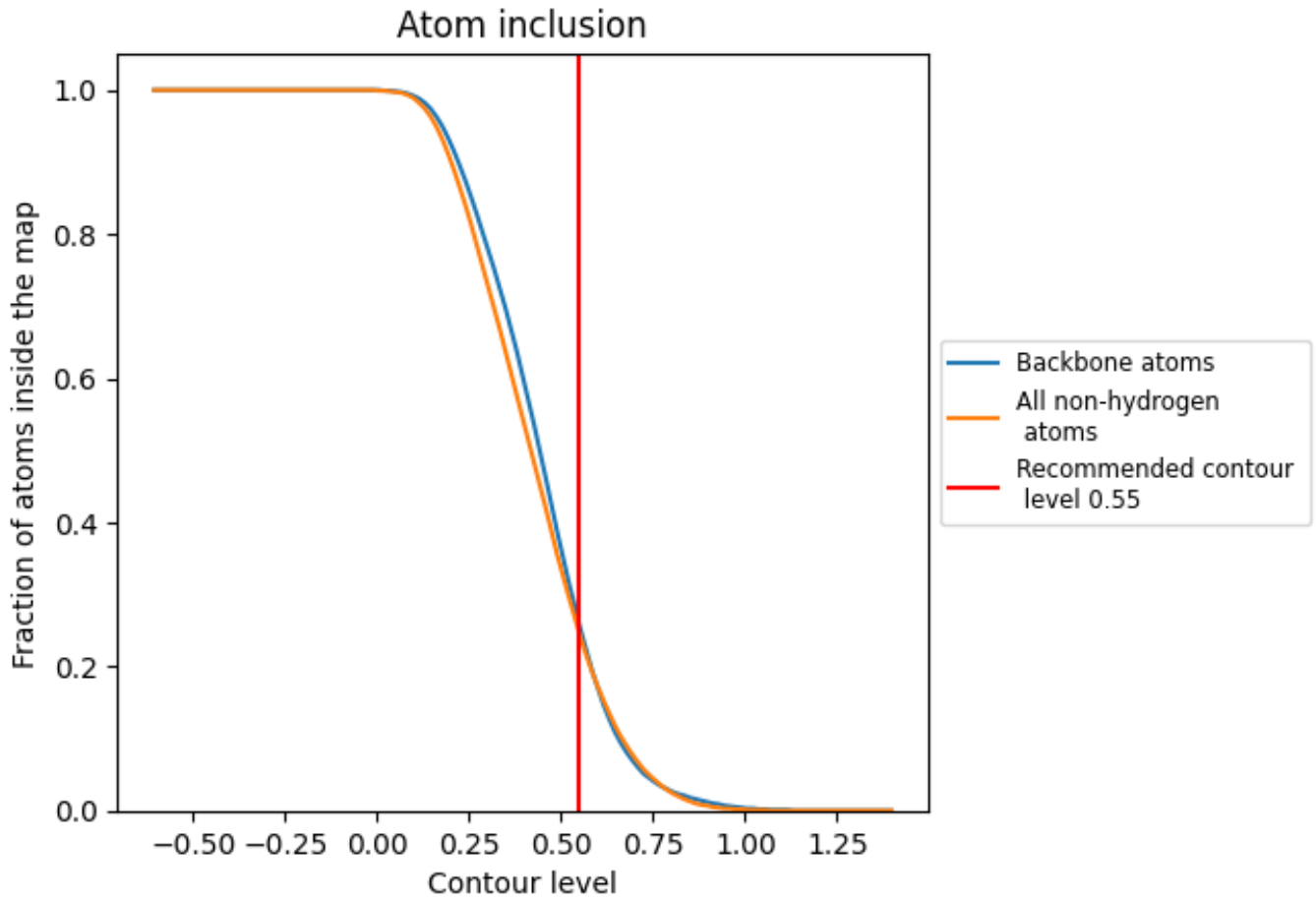
## 9.3 Atom inclusion mapped to coordinate model (i)




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 (0.55).

## 9.4 Atom inclusion (i)




At the recommended contour level, 26% of all backbone atoms, 24% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.55) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|---|---|---|
| All | 0.2450 | 0.5510 |
| 0 | 0.1470 | 0.5890 |
| 1 | 0.3890 | 0.6160 |
| 2 | 0.3340 | 0.6080 |
| 3 | 0.1770 | 0.5860 |
| 4 | 0.0000 | 0.4150 |
| 5 | 0.0000 | 0.3660 |
| A | 0.2100 | 0.5400 |
| B | 0.0120 | 0.5060 |
| C | 0.0350 | 0.5390 |
| D | 0.0430 | 0.5430 |
| E | 0.1340 | 0.5760 |
| F | 0.0420 | 0.5470 |
| G | 0.0100 | 0.5030 |
| H | 0.1060 | 0.5700 |
| I | 0.0150 | 0.5060 |
| J | 0.0130 | 0.4850 |
| K | 0.0510 | 0.5500 |
| L | 0.0970 | 0.5780 |
| M | 0.0030 | 0.4950 |
| N | 0.0150 | 0.5320 |
| O | 0.1050 | 0.5550 |
| P | 0.1320 | 0.5690 |
| Q | 0.0560 | 0.5590 |
| R | 0.1000 | 0.5300 |
| S | 0.0050 | 0.5140 |
| T | 0.0870 | 0.5440 |
| U | 0.0000 | 0.4410 |
| V | 0.0030 | 0.3380 |
| X | 0.0120 | 0.5200 |
| a | 0.3640 | 0.5640 |
| b | 0.1970 | 0.5520 |
| c | 0.2790 | 0.6070 |
| d | 0.2540 | 0.5970 |
| e | 0.1800 | 0.5760 |




*Continued on next page...*

*Continued from previous page...*

| Chain | Atom inclusion | Q-score |
|---|---|---|
| f | 0.0100 | 0.5090 |
| g | 0.0220 | 0.5190 |
| h | 0.0030 | 0.4200 |
| i | 0.2390 | 0.5930 |
| j | 0.1940 | 0.5990 |
| k | 0.2070 | 0.5920 |
| l | 0.1480 | 0.5920 |
| m | 0.3030 | 0.6030 |
| n | 0.0670 | 0.5620 |
| o | 0.2030 | 0.5850 |
| p | 0.3380 | 0.5980 |
| q | 0.1660 | 0.5950 |
| r | 0.2410 | 0.5910 |
| s | 0.1730 | 0.5730 |
| t | 0.0890 | 0.5630 |
| u | 0.0850 | 0.5730 |
| v | 0.2500 | 0.6080 |
| w | 0.2080 | 0.5840 |
| x | 0.1030 | 0.5580 |
| y | 0.2000 | 0.5860 |
| z | 0.2560 | 0.6010 |