# wwPDB EM Validation Summary Report

Oct 26, 2026 – 10:55 AM EDT

| | | |
|---|---|---|
| PDB ID | : | 9YWB / pdb_00009ywb |
| EMDB ID | : | EMD-73543 |
| Title | : | Hypomethylated nucleoplasmic pre-60S intermediate containing Nog2 at Rsa4-arrested 5S post-rotation state |
| Authors | : | Zhao, Y.; Li, H. |
| Deposited on | : | 2025-10-24 |
| Resolution | : | 2.85 Å(reported) |

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

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

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

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

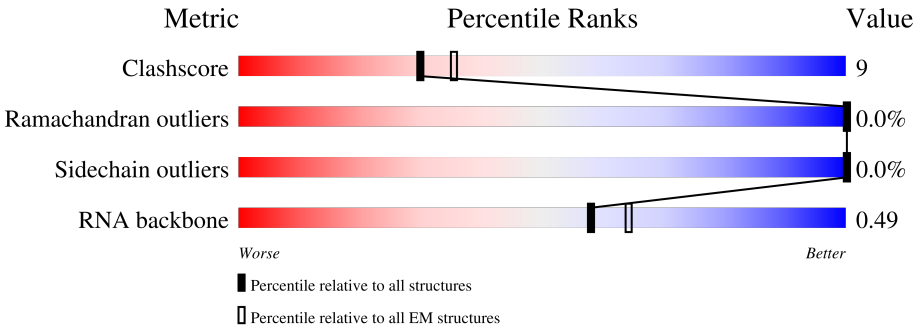
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev133 |
| Mogul | : | 2022.3.0, CSD as543be (2022) |
| MolProbity | : | 4-5-2 with Phenix2.2 |
| Buster-report | : | wwPDB partial adaption of 1.1.7 (2018) |
| Percentile statistics | : | 20250101.v01 (using entries in the PDB archive January 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 |

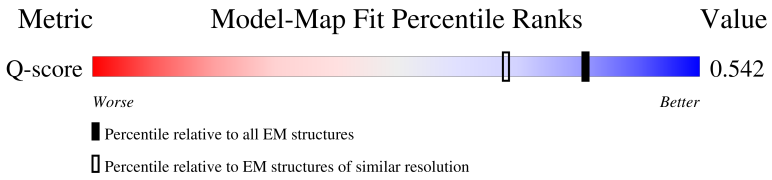
# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.85 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 | 11965 ( 2.35 - 3.35 ) |

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 | D | 297 | 27% 61% 25% 14% |
| 2 | J | 174 | 11% 66% 26% 7% |
| 3 | A | 254 | 75% 22% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 4 | a | 149 | 47% 16% 37% |
| 5 | B | 387 | 71% 29% |
| 6 | b | 647 | 29% 71% 29% |
| 7 | C | 362 | 80% 20% |
| 8 | c | 105 | 7% 70% 22% 8% |
| 9 | d | 113 | 6% 75% 19% 5% |
| 10 | E | 176 | 6% 72% 19% 9% |
| 11 | e | 130 | 77% 21% |
| 12 | F | 244 | 74% 17% 9% |
| 13 | f | 107 | 79% 21% |
| 14 | G | 256 | 62% 28% 10% |
| 15 | g | 121 | 6% 75% 17% 7% |
| 16 | I | 166 | 49% 55% 23% 21% |
| 17 | H | 191 | 70% 28% |
| 18 | h | 120 | 76% 23% |
| 19 | i | 100 | 81% 15% |
| 20 | j | 88 | 69% 27% |
| 21 | k | 78 | 8% 78% 21% |
| 22 | L | 199 | 7% 67% 27% 6% |
| 23 | l | 51 | 67% 31% |
| 24 | M | 138 | 75% 24% |
| 25 | p | 92 | 80% 18% |
| 26 | N | 204 | 66% 33% |
| 27 | u | 199 | 10% 54% 20% 25% |
| 28 | O | 199 | 93% 6% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 29 | P | 184 | 8% 78% 21% |
| 30 | Q | 186 | 5% 63% 11% 25% |
| 31 | R | 189 | 63% 19% 19% |
| 32 | r | 261 | 56% 26% 18% |
| 33 | S | 172 | 72% 27% |
| 34 | T | 160 | 21% 64% 26% 9% |
| 35 | U | 121 | 10% 61% 25% 14% |
| 36 | V | 137 | 77% 23% |
| 37 | W | 236 | 7% 75% 22% |
| 38 | X | 142 | 63% 22% 15% |
| 39 | Y | 127 | 65% 35% |
| 40 | y | 245 | 8% 65% 33% |
| 41 | Z | 136 | 73% 26% |
| 42 | z | 106 | 11% 42% 9% 48% |
| 43 | K | 165 | 31% 76% 13% 11% |
| 44 | 1 | 3396 | 6% 54% 29% 8% 8% |
| 45 | 3 | 158 | 60% 34% 5% |
| 46 | 5 | 120 | 17% 60% 31% 8% |
| 47 | x | 515 | 6% 55% 21% 24% |
| 48 | m | 486 | 15% 67% 26% 7% |
| 49 | 2 | 121 | 54% 37% 5% |
| 50 | t | 767 | 21% 36% 18% 46% |
| 51 | n | 334 | 10% 88% |
| 52 | 4 | 593 | 40% 62% 24% 14% |
| 53 | o | 175 | 16% 50% 13% 38% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 54 | s | 217 |   |
| 55 | q | 520 |   |
| 56 | Lr | 25 |   |

# 2 Entry composition (i)

There are 60 unique types of molecules in this entry. The entry contains 148851 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 1 | D | 255 | 2047 | 1303 | 354 | 388 | 2 | 0 | 0 |

- Molecule 2 is a protein called 60S ribosomal protein L11-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 2 | J | 161 | 1283 | 808 | 240 | 231 | 4 | 0 | 0 |

- Molecule 3 is a protein called 60S ribosomal protein L2-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 3 | A | 245 | 1863 | 1162 | 376 | 324 | 1 | 0 | 0 |

- Molecule 4 is a protein called 60S ribosomal protein L28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 4 | a | 94 | 742 | 484 | 131 | 126 | 1 | 0 | 0 |

- Molecule 5 is a protein called 60S ribosomal protein L3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 5 | B | 386 | 3081 | 1956 | 584 | 533 | 8 | 0 | 0 |

- Molecule 6 is a protein called Nucleolar GTP-binding protein 1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 6 | b | 647 | 5219 | 3269 | 940 | 984 | 26 | 0 | 0 |

- Molecule 7 is a protein called 60S ribosomal protein L4-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 7 | C | 361 | Total | C | N | O | S | 0 | 0 |
| | | | 2749 | 1730 | 522 | 494 | 3 | | |

- Molecule 8 is a protein called 60S ribosomal protein L30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 8 | c | 97 | Total | C | N | O | S | 0 | 0 |
| | | | 743 | 479 | 124 | 139 | 1 | | |

- Molecule 9 is a protein called 60S ribosomal protein L31-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 9 | d | 107 | Total | C | N | O | S | 0 | 0 |
| | | | 873 | 553 | 165 | 154 | 1 | | |

- Molecule 10 is a protein called 60S ribosomal protein L6-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 10 | E | 160 | Total | C | N | O | S | 0 | 0 |
| | | | 1274 | 820 | 230 | 223 | 1 | | |

- Molecule 11 is a protein called 60S ribosomal protein L32.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 11 | e | 127 | Total | C | N | O | S | 0 | 0 |
| | | | 1020 | 647 | 205 | 167 | 1 | | |

- Molecule 12 is a protein called 60S ribosomal protein L7-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 12 | F | 222 | Total | C | N | O | S | 0 | 0 |
| | | | 1784 | 1151 | 324 | 308 | 1 | | |

- Molecule 13 is a protein called 60S ribosomal protein L33-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 13 | f | 106 | Total | C | N | O | S | 0 | 0 |
| | | | 850 | 540 | 165 | 144 | 1 | | |

- Molecule 14 is a protein called Large ribosomal subunit protein eL8A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 14 | G | 230 | Total | C | N | O | S | 0 | 0 |
| | | | 1798 | 1149 | 323 | 323 | 3 | | |

- Molecule 15 is a protein called 60S ribosomal protein L34-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 15 | g | 112 | Total | C | N | O | S | 0 | 0 |
| | | | 881 | 546 | 179 | 152 | 4 | | |

- Molecule 16 is a protein called Bud site selection protein 20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 16 | I | 131 | Total | C | N | O | S | 0 | 0 |
| | | | 1056 | 660 | 195 | 198 | 3 | | |

- Molecule 17 is a protein called Large ribosomal subunit protein uL6A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 17 | H | 188 | Total | C | N | O | S | 0 | 0 |
| | | | 1493 | 948 | 271 | 270 | 4 | | |

- Molecule 18 is a protein called 60S ribosomal protein L35-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 18 | h | 119 | Total | C | N | O | S | 0 | 0 |
| | | | 969 | 615 | 186 | 167 | 1 | | |

- Molecule 19 is a protein called 60S ribosomal protein L36-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 19 | i | 96 | Total | C | N | O | S | 0 | 0 |
| | | | 743 | 465 | 148 | 128 | 2 | | |

- Molecule 20 is a protein called 60S ribosomal protein L37-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 20 | j | 85 | Total | C | N | O | S | 0 | 0 |
| | | | 670 | 408 | 146 | 111 | 5 | | |

- Molecule 21 is a protein called 60S ribosomal protein L38.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 21 | k | 77 | Total | C | N | O | 0 | 0 |
| | | | 612 | 391 | 115 | 106 | | |

- Molecule 22 is a protein called 60S ribosomal protein L13-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 22 | L | 187 | Total | C | N | O | 0 | 0 |
| | | | 1491 | 929 | 306 | 256 | | |

- Molecule 23 is a protein called 60S ribosomal protein L39.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 23 | l | 50 | Total | C | N | O | S | 0 | 0 |
| | | | 436 | 272 | 97 | 65 | 2 | | |

- Molecule 24 is a protein called 60S ribosomal protein L14-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 24 | M | 137 | Total | C | N | O | S | 0 | 0 |
| | | | 1059 | 678 | 200 | 179 | 2 | | |

- Molecule 25 is a protein called 60S ribosomal protein L43-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 25 | p | 91 | Total | C | N | O | S | 0 | 0 |
| | | | 694 | 429 | 138 | 121 | 6 | | |

- Molecule 26 is a protein called Large ribosomal subunit protein eL15A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 26 | N | 203 | Total | C | N | O | S | 0 | 0 |
| | | | 1720 | 1077 | 361 | 281 | 1 | | |

- Molecule 27 is a protein called Ribosome biogenesis protein RLP24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 27 | u | 149 | Total | C | N | O | S | 0 | 0 |
| | | | 1256 | 788 | 252 | 207 | 9 | | |

- Molecule 28 is a protein called Large ribosomal subunit protein uL13A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 28 | O | 197 | Total | C | N | O | S | 0 | 0 |
| | | | 1555 | 1003 | 289 | 262 | 1 | | |

- Molecule 29 is a protein called 60S ribosomal protein L17-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 29 | P | 183 | Total | C | N | O | 0 | 0 |
| | | | 1438 | 893 | 286 | 259 | | |

- Molecule 30 is a protein called 60S ribosomal protein L18-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 30 | Q | 139 | Total | C | N | O | S | 0 | 0 |
| | | | 1069 | 683 | 201 | 183 | 2 | | |

- Molecule 31 is a protein called 60S ribosomal protein L19-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 31 | R | 154 | Total | C | N | O | 0 | 0 |
| | | | 1241 | 772 | 262 | 207 | | |

- Molecule 32 is a protein called Ribosome biogenesis protein NSA2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 32 | r | 213 | Total | C | N | O | S | 0 | 0 |
| | | | 1719 | 1088 | 328 | 296 | 7 | | |

- Molecule 33 is a protein called Large ribosomal subunit protein eL20A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 33 | S | 170 | Total | C | N | O | S | 0 | 0 |
| | | | 1425 | 916 | 265 | 241 | 3 | | |

- Molecule 34 is a protein called 60S ribosomal protein L21-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 34 | T | 145 | Total | C | N | O | S | 0 | 0 |
| | | | 1161 | 734 | 223 | 200 | 4 | | |

- Molecule 35 is a protein called 60S ribosomal protein L22-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 35 | U | 104 | Total | C | N | O | 0 | 0 |
| | | | 826 | 535 | 136 | 155 | | |

- Molecule 36 is a protein called 60S ribosomal protein L23-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 36 | V | 136 | Total | C | N | O | S | 0 | 0 |
| | | | 1003 | 628 | 189 | 179 | 7 | | |

- Molecule 37 is a protein called Ribosome assembly factor MRT4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 37 | W | 227 | Total | C | N | O | S | 0 | 0 |
| | | | 1814 | 1149 | 310 | 350 | 5 | | |

- Molecule 38 is a protein called 60S ribosomal protein L25.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 38 | X | 120 | Total | C | N | O | S | 0 | 0 |
| | | | 959 | 617 | 168 | 172 | 2 | | |

- Molecule 39 is a protein called 60S ribosomal protein L26-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 39 | Y | 126 | Total | C | N | O | 0 | 0 |
| | | | 993 | 625 | 192 | 176 | | |

- Molecule 40 is a protein called Eukaryotic translation initiation factor 6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 40 | y | 242 | Total | C | N | O | S | 0 | 0 |
| | | | 1826 | 1131 | 317 | 372 | 6 | | |

- Molecule 41 is a protein called 60S ribosomal protein L27-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 41 | Z | 135 | Total | C | N | O | 0 | 0 |
| | | | 1092 | 710 | 202 | 180 | | |

- Molecule 42 is a protein called UPF0642 protein YBL028C.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 42 | z | 55 | Total | C | N | O | 0 | 0 |
| | | | 444 | 273 | 88 | 83 | | |

- Molecule 43 is a protein called 60S ribosomal protein L12.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 43 | K | 147 | Total | C | N | O | 0 | 0 |
| | | | 821 | 501 | 159 | 161 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 44 | 1 | 3116 | Total | C | N | O | P | 0 | 0 |
| | | | 66660 | 29773 | 12017 | 21754 | 3116 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 45 | 3 | 158 | Total | C | N | O | P | 0 | 0 |
| | | | 3353 | 1500 | 586 | 1109 | 158 | | |

- Molecule 46 is a protein called rRNA-processing protein CGR1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 46 | 5 | 110 | Total | C | N | O | S | 0 | 0 |
| | | | 934 | 579 | 191 | 161 | 3 | | |

- Molecule 47 is a protein called Ribosome assembly protein 4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 47 | x | 390 | Total | C | N | O | S | 0 | 0 |
| | | | 3051 | 1914 | 551 | 566 | 20 | | |

- Molecule 48 is a protein called Nucleolar GTP-binding protein 2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 48 | m | 453 | Total | C | N | O | S | 0 | 0 |
| | | | 3647 | 2309 | 656 | 672 | 10 | | |

- Molecule 49 is a RNA chain called 5S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 49 | 2 | 117 | Total | C | N | O | P | 0 | 0 |
| | | | 2494 | 1114 | 446 | 817 | 117 | | |

- Molecule 50 is a protein called Protein SDA1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 50 | t | 414 | Total | C | N | O | S | 0 | 0 |
| | | | 3289 | 2098 | 568 | 602 | 21 | | |

- Molecule 51 is a protein called Pre-rRNA-processing protein IPI1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 51 | n | 41 | Total | C | N | O | 0 | 0 |
| | | | 335 | 208 | 66 | 61 | | |

- Molecule 52 is a protein called Probable metalloprotease ARX1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 52 | 4 | 509 | Total | C | N | O | S | 0 | 0 |
| | | | 3945 | 2503 | 673 | 754 | 15 | | |

- Molecule 53 is a protein called Ribosome biogenesis protein ALB1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 53 | o | 109 | Total | C | N | O | 0 | 0 |
| | | | 872 | 543 | 171 | 158 | | |

- Molecule 54 is a protein called Large ribosomal subunit protein uL1A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 54 | s | 217 | Total | C | N | O | S | 0 | 0 |
| | | | 1718 | 1097 | 299 | 312 | 10 | | |

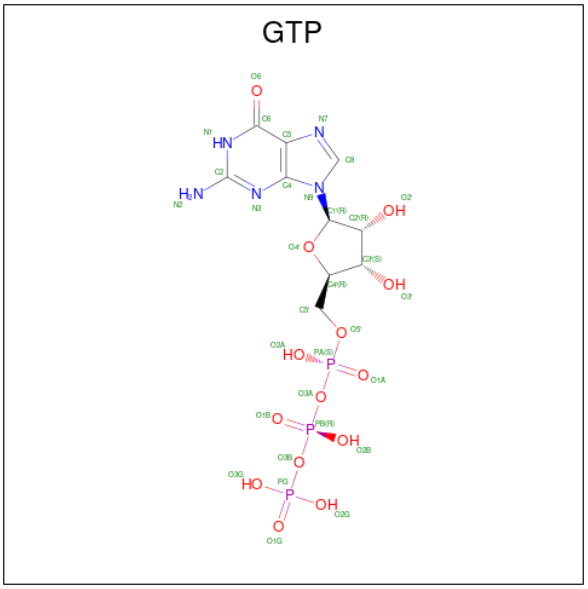
- Molecule 55 is a protein called Nuclear GTP-binding protein NUG1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 55 | q | 64 | Total | C | N | O | S | 0 | 0 |
| | | | 533 | 333 | 109 | 90 | 1 | | |

- Molecule 56 is a protein called Small ribosomal subunit protein eS32A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 56 | Lr | 20 | Total | C | N | O | S | 0 | 0 |
| | | | 191 | 118 | 51 | 21 | 1 | | |

- Molecule 57 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).




| Mol | Chain | Residues | Atoms | | | | | AltConf |
|---|---|---|---|---|---|---|---|---|
| 57 | m | 1 | Total | C | N | O | P | 0 |
| | | | 32 | 10 | 5 | 14 | 3 | |

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| 58 | m | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |

- Molecule 59 is POTASSIUM ION (CCD ID: K) (formula: K).

| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| 59 | m | 1 | Total | K | 0 |
| | | | 1 | 1 | |

- Molecule 60 is water.

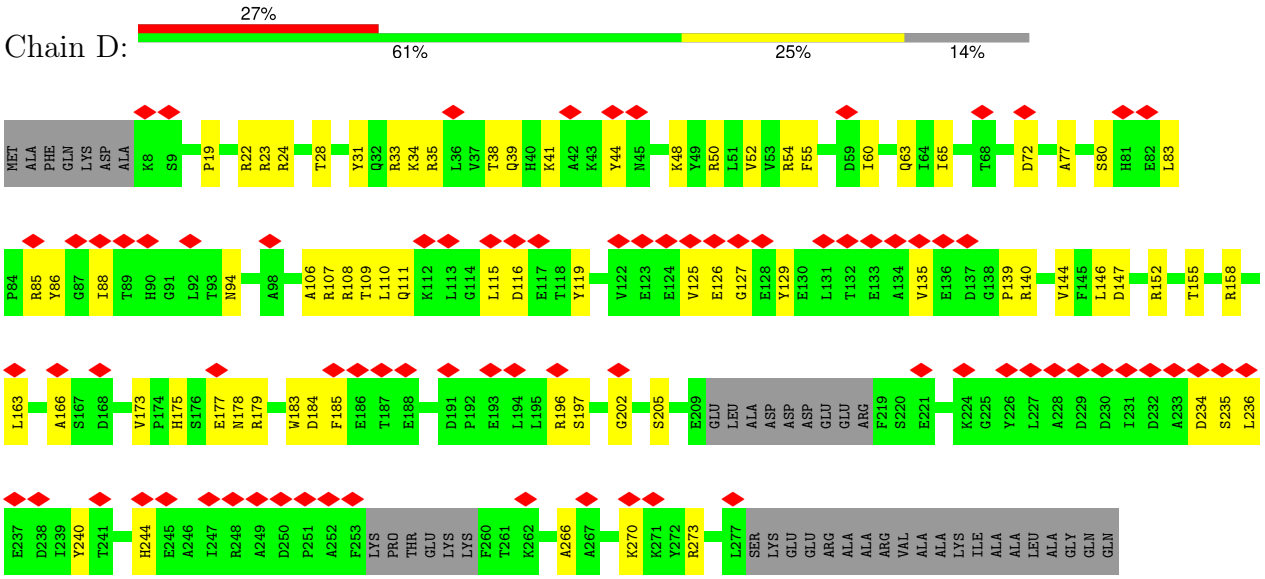
| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| 60 | m | 3 | Total | O | 0 |
| | | | 3 | 3 | |

# 3 Residue-property plots (i)

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

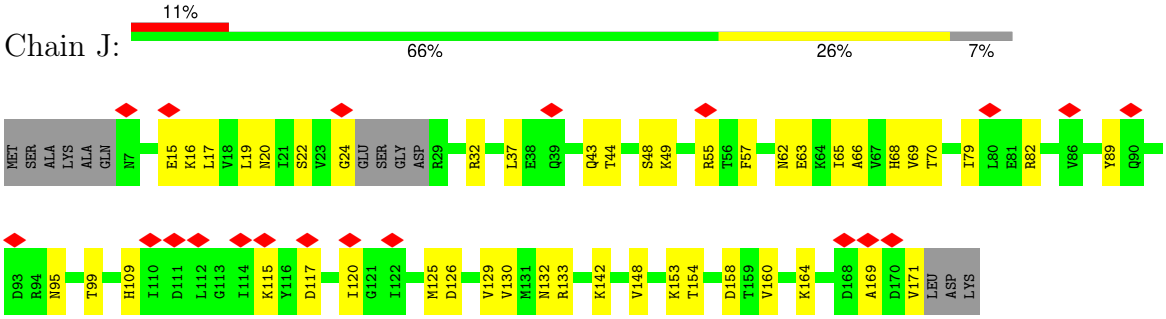
• Molecule 1: 60S ribosomal protein L5

Chain D:



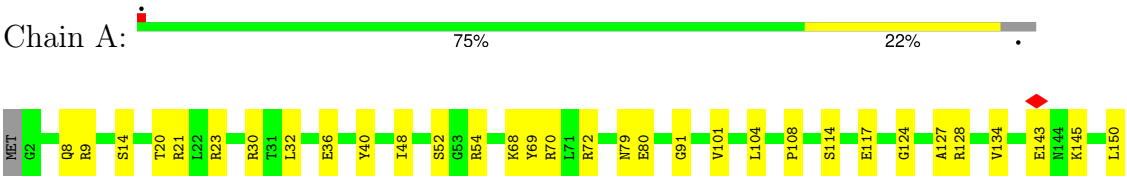

• Molecule 2: 60S ribosomal protein L11-A

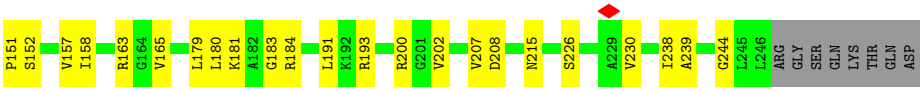
Chain J:




• Molecule 3: 60S ribosomal protein L2-A

Chain A:

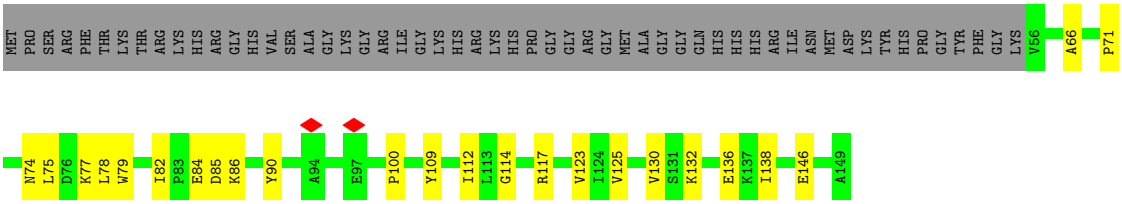





• Molecule 4: 60S ribosomal protein L28

Chain a:

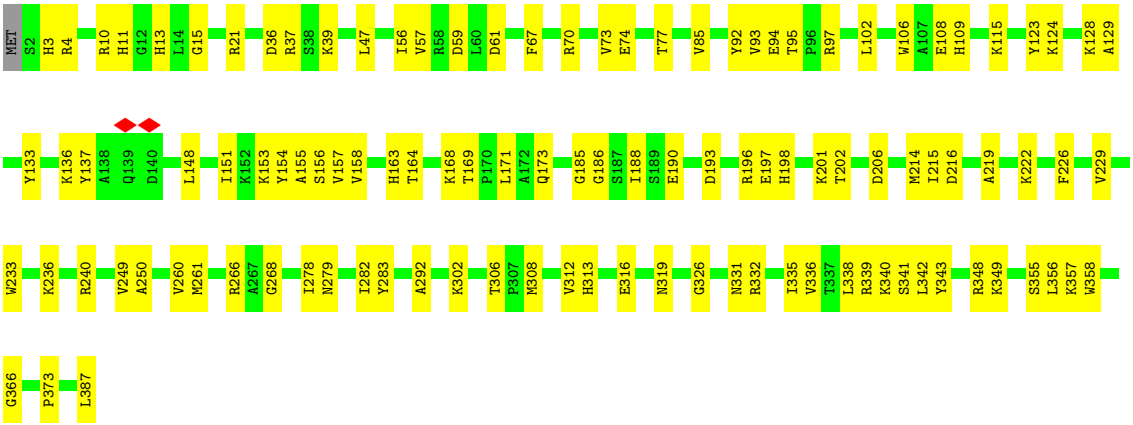



• Molecule 5: 60S ribosomal protein L3

Chain B:

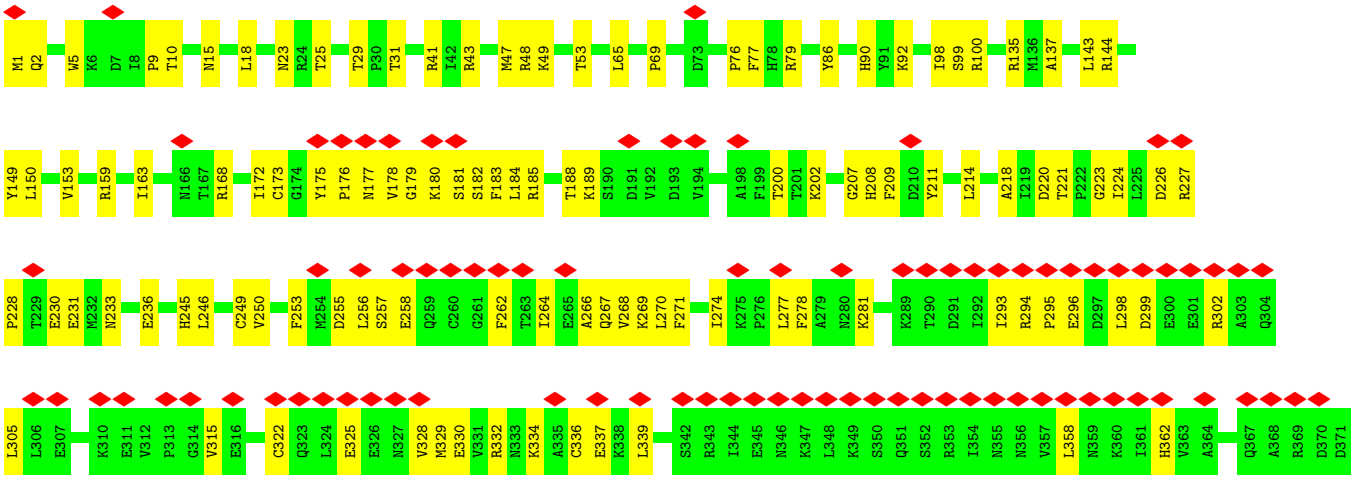


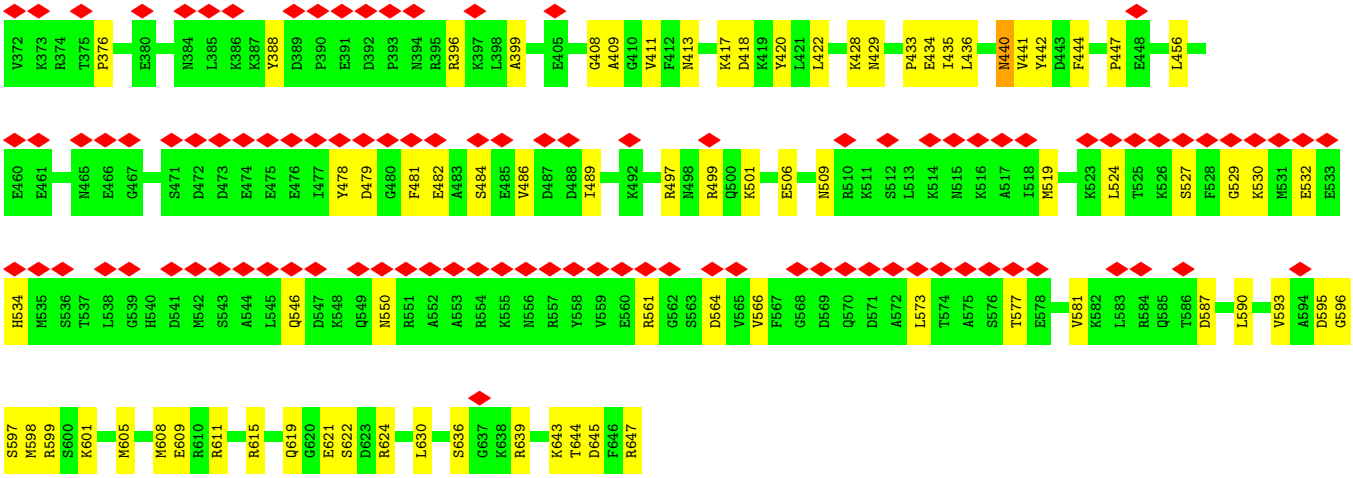




• Molecule 6: Nucleolar GTP-binding protein 1

Chain b:






• Molecule 7: 60S ribosomal protein L4-A

Chain C:



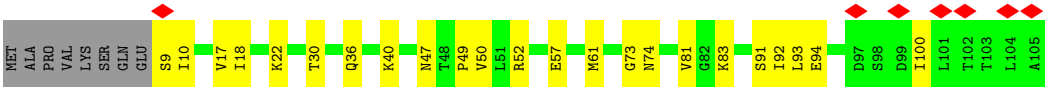




• Molecule 8: 60S ribosomal protein L30

Chain c:

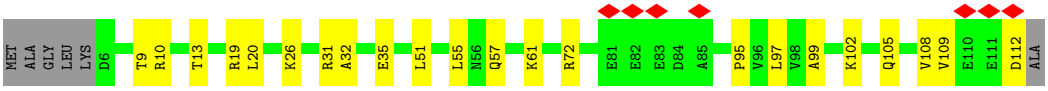



• Molecule 9: 60S ribosomal protein L31-A

Chain d:

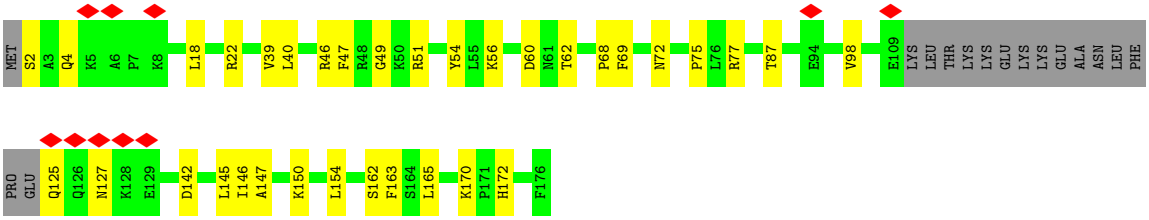



• Molecule 10: 60S ribosomal protein L6-A

Chain E:





• Molecule 11: 60S ribosomal protein L32

Chain e:

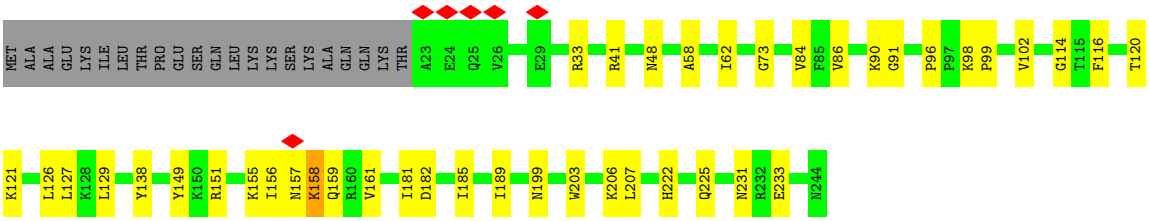





• Molecule 12: 60S ribosomal protein L7-A

Chain F:

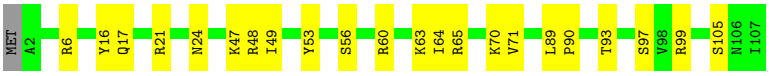


• Molecule 13: 60S ribosomal protein L33-A

Chain f:

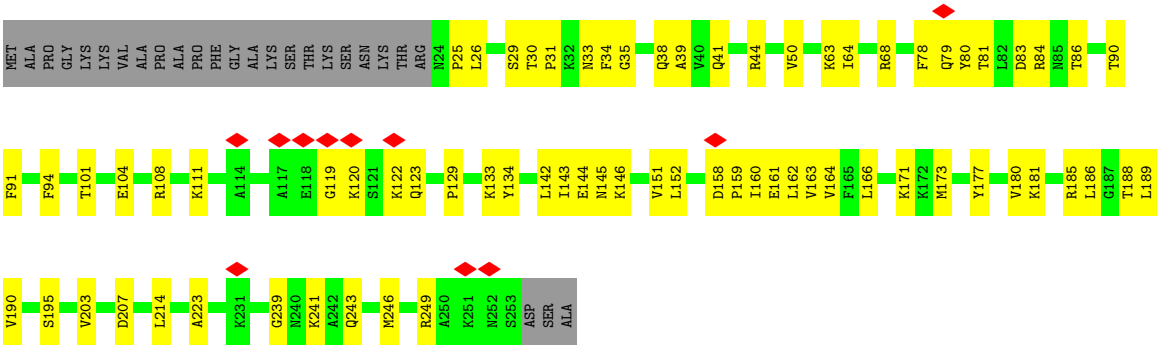


• Molecule 14: Large ribosomal subunit protein eL8A

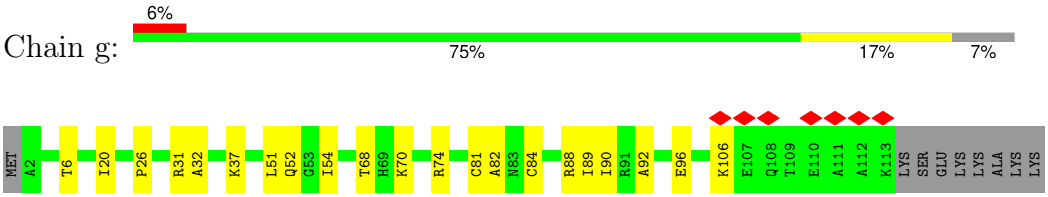
Chain G:



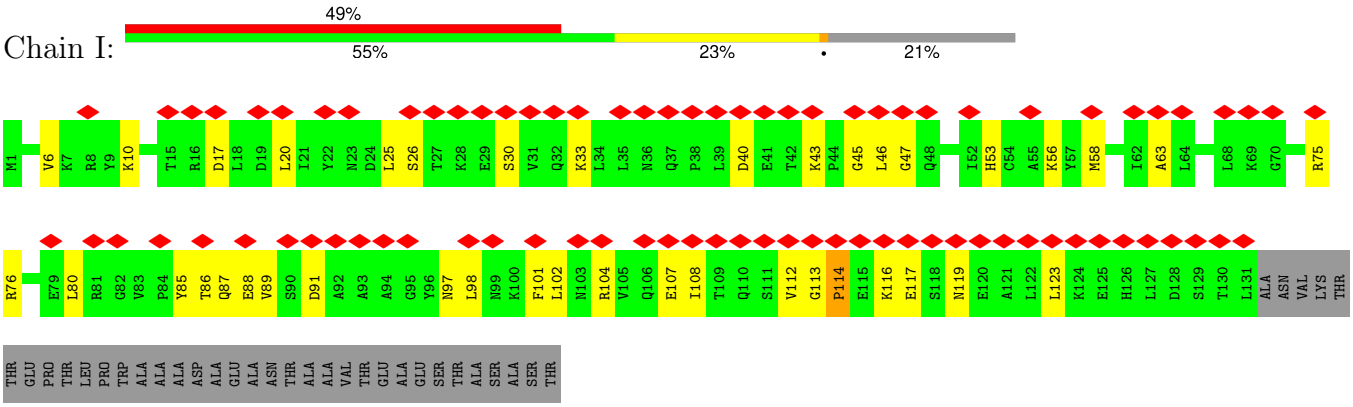
• Molecule 15: 60S ribosomal protein L34-A

Chain g:



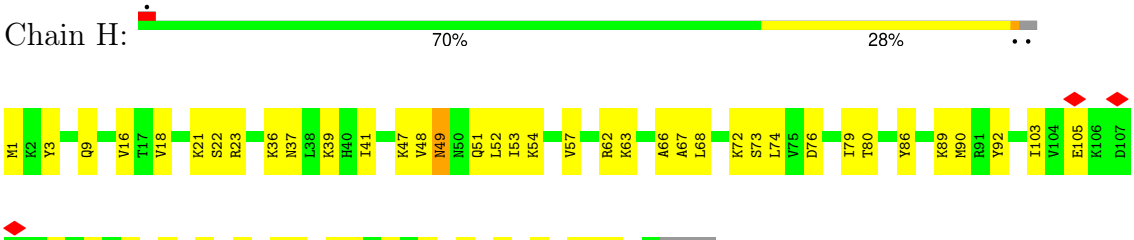

• Molecule 16: Bud site selection protein 20

Chain I:



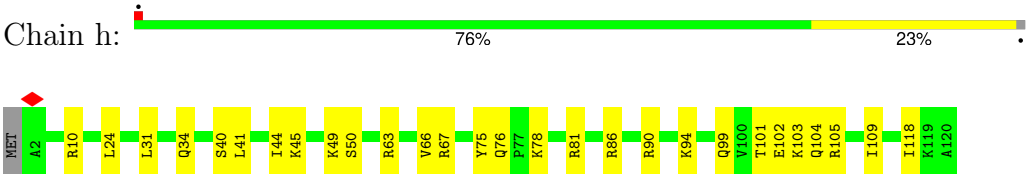

• Molecule 17: Large ribosomal subunit protein uL6A

Chain H:



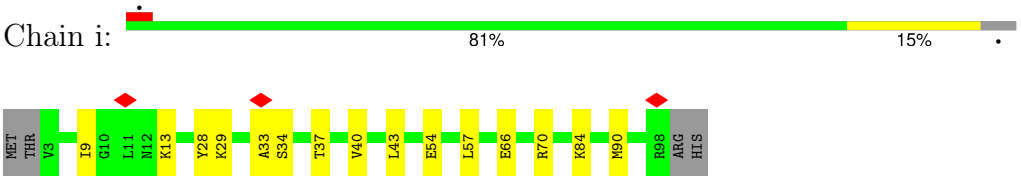

• Molecule 18: 60S ribosomal protein L35-A

Chain h:




• Molecule 19: 60S ribosomal protein L36-A

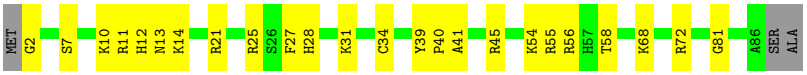
Chain i:



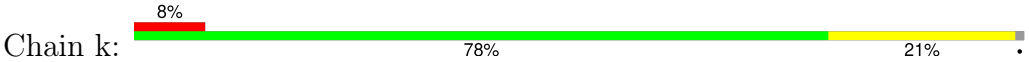

• Molecule 20: 60S ribosomal protein L37-A

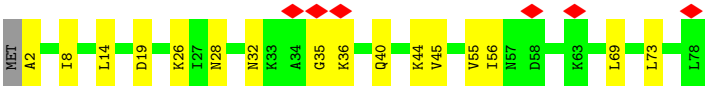
Chain j:





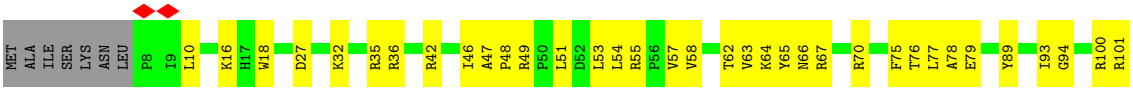

• Molecule 21: 60S ribosomal protein L38

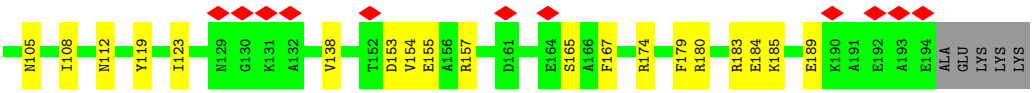



• Molecule 22: 60S ribosomal protein L13-A




• Molecule 23: 60S ribosomal protein L39

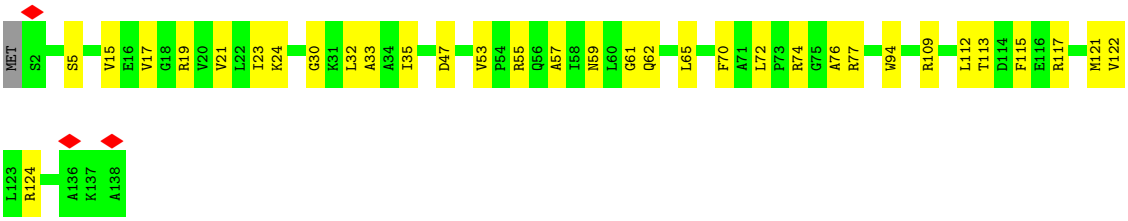




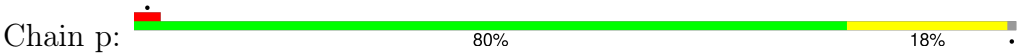


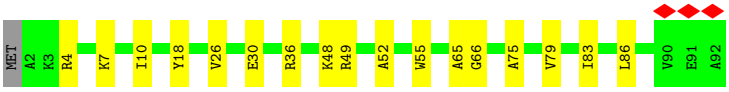
• Molecule 24: 60S ribosomal protein L14-A



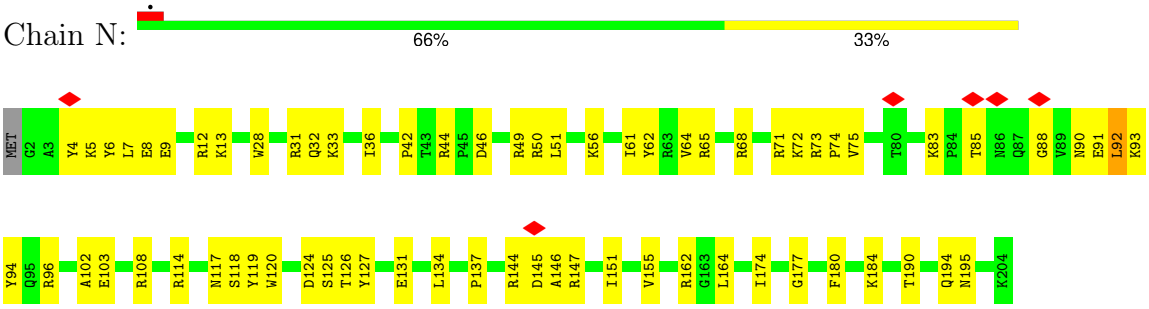

• Molecule 25: 60S ribosomal protein L43-A



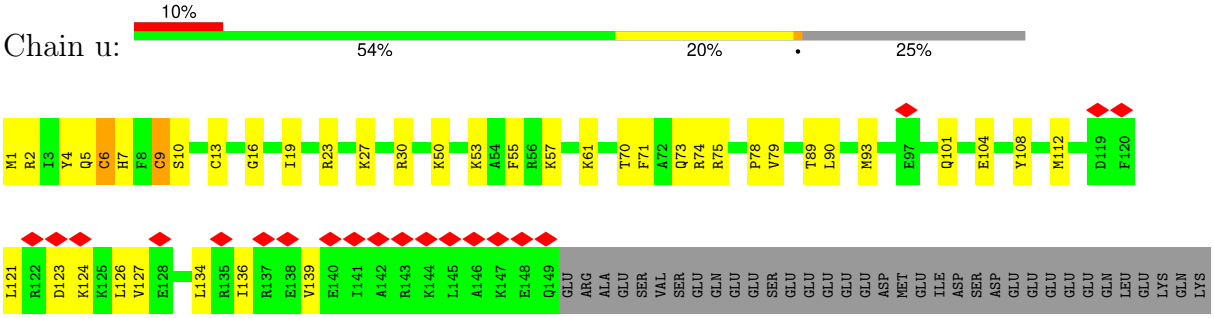

• Molecule 26: Large ribosomal subunit protein eL15A

Chain N:



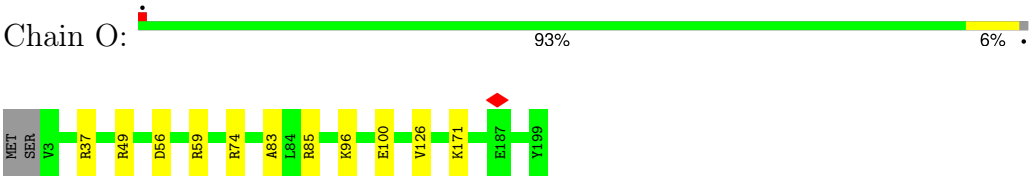

• Molecule 27: Ribosome biogenesis protein RLP24

Chain u:



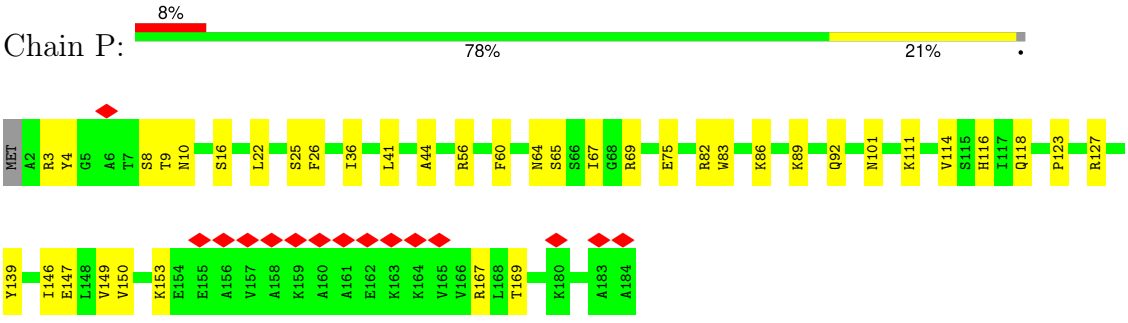

• Molecule 28: Large ribosomal subunit protein uL13A

Chain O:



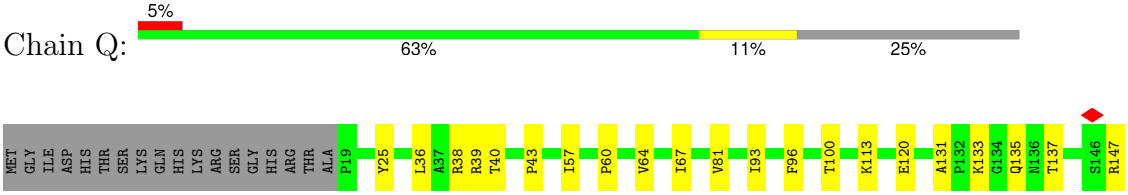

• Molecule 29: 60S ribosomal protein L17-A

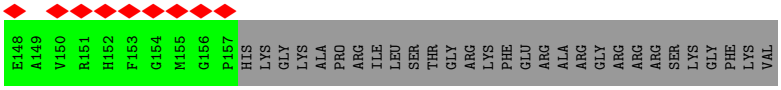
Chain P:




• Molecule 30: 60S ribosomal protein L18-A

Chain Q:

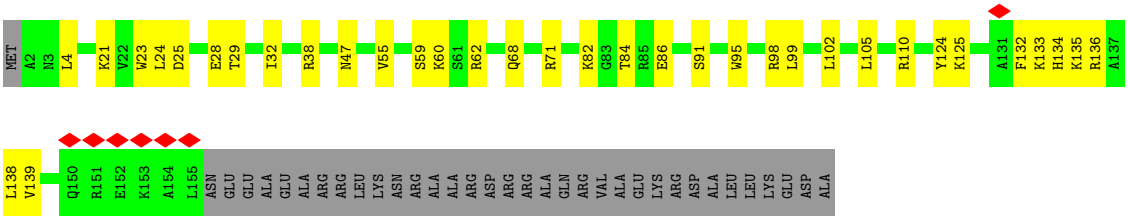




• Molecule 31: 60S ribosomal protein L19-A

Chain R:

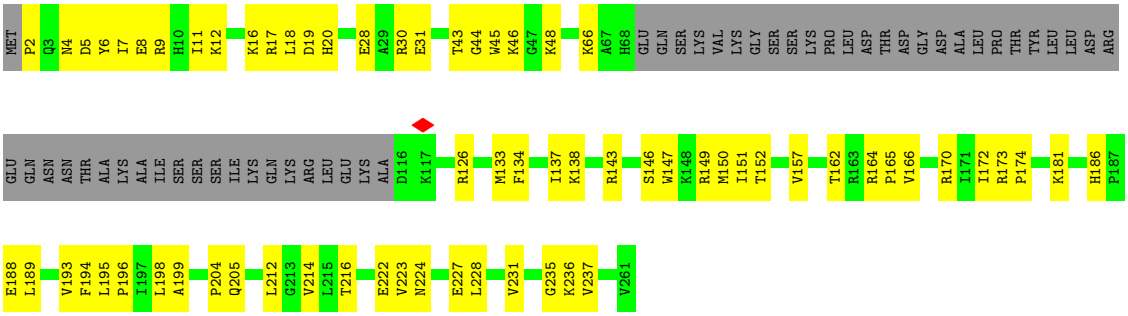


• Molecule 32: Ribosome biogenesis protein NSA2

Chain r:

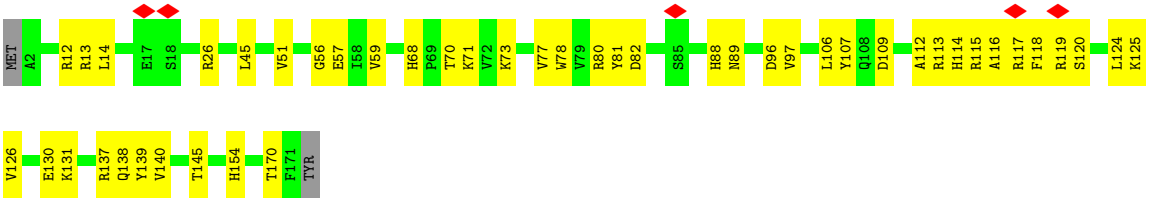


• Molecule 33: Large ribosomal subunit protein eL20A

Chain S:

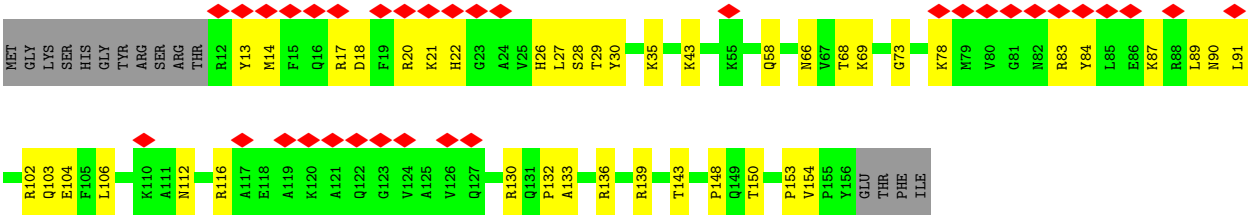


• Molecule 34: 60S ribosomal protein L21-A

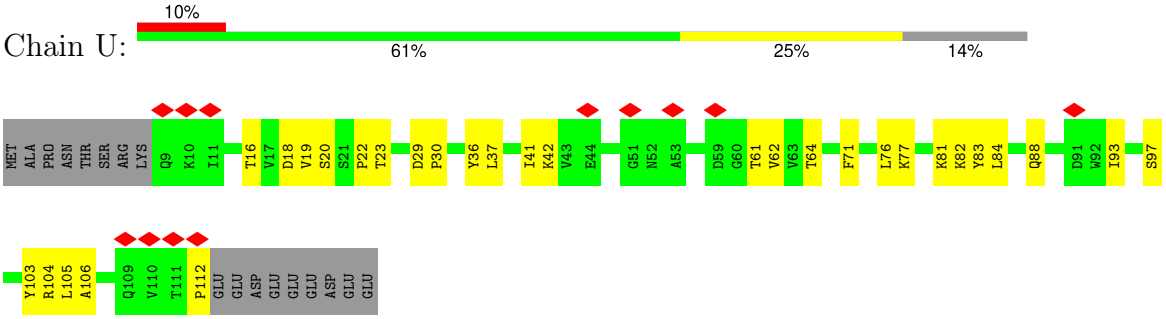
Chain T:



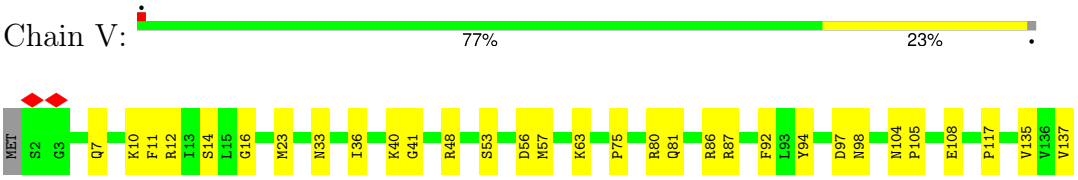
• Molecule 35: 60S ribosomal protein L22-A

Chain U:



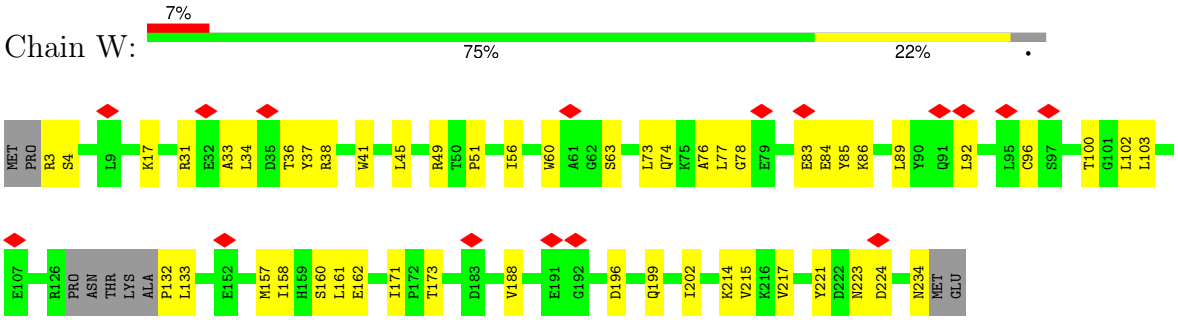

• Molecule 36: 60S ribosomal protein L23-A

Chain V:



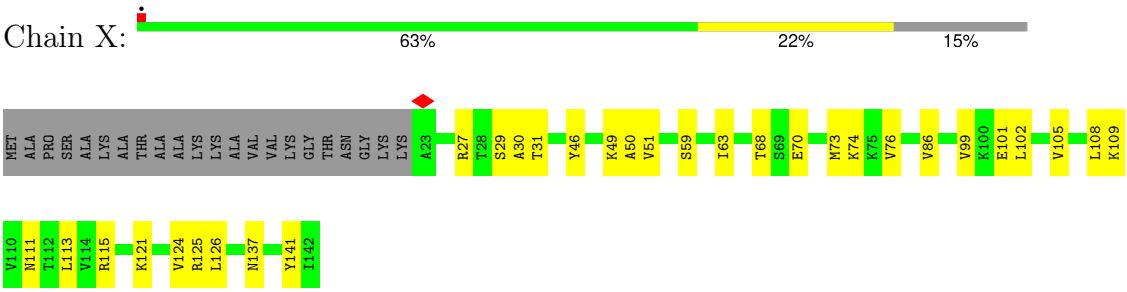

• Molecule 37: Ribosome assembly factor MRT4

Chain W:



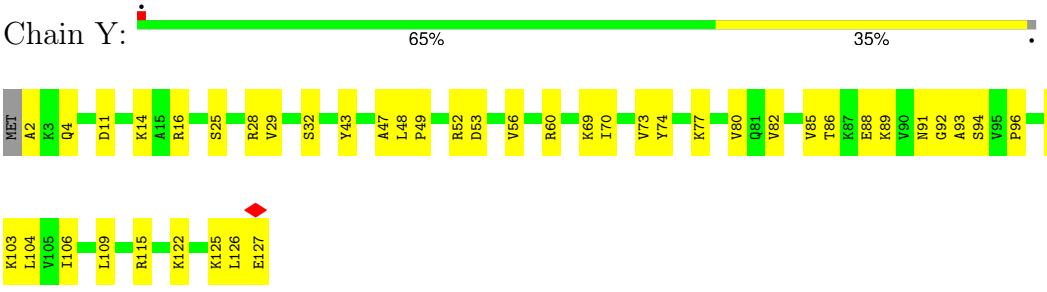

• Molecule 38: 60S ribosomal protein L25

Chain X:



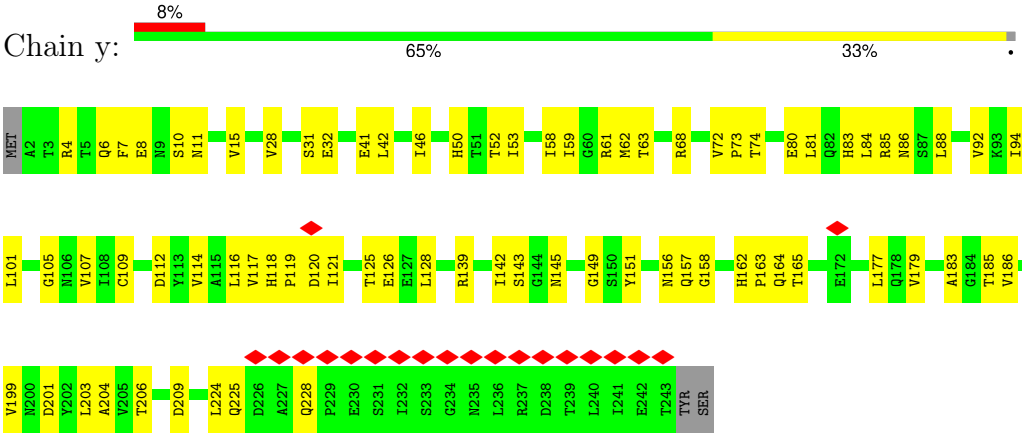

• Molecule 39: 60S ribosomal protein L26-A

Chain Y:



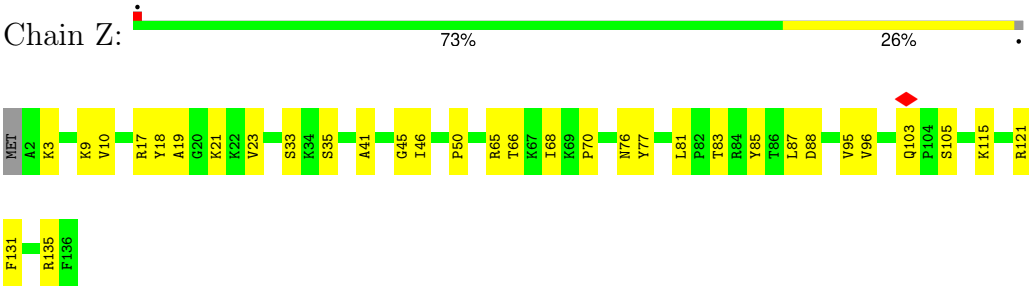
• Molecule 40: Eukaryotic translation initiation factor 6

Chain y:



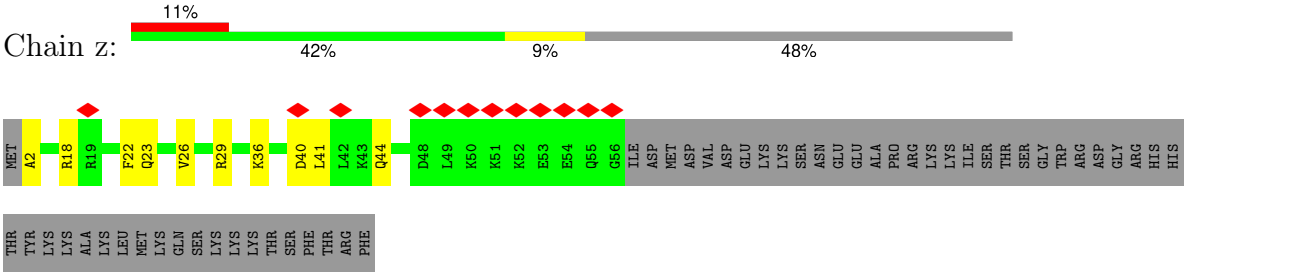

• Molecule 41: 60S ribosomal protein L27-A

Chain Z:



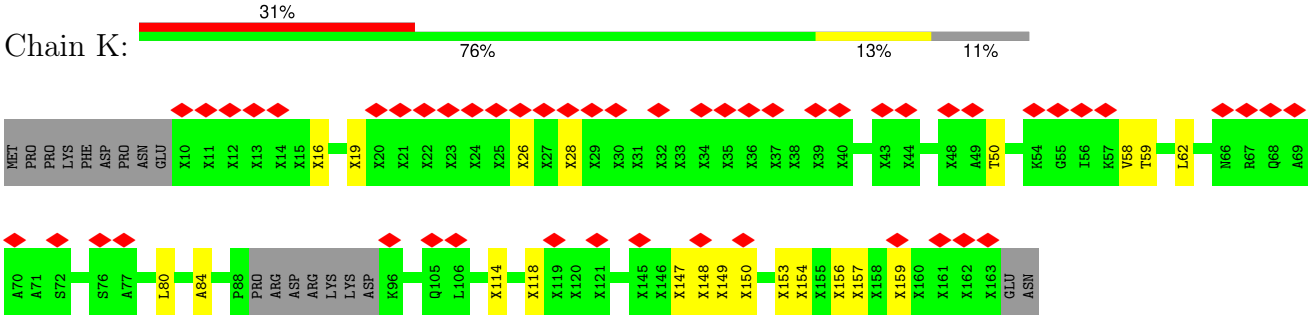

• Molecule 42: UPF0642 protein YBL028C

Chain z:




• Molecule 43: 60S ribosomal protein L12

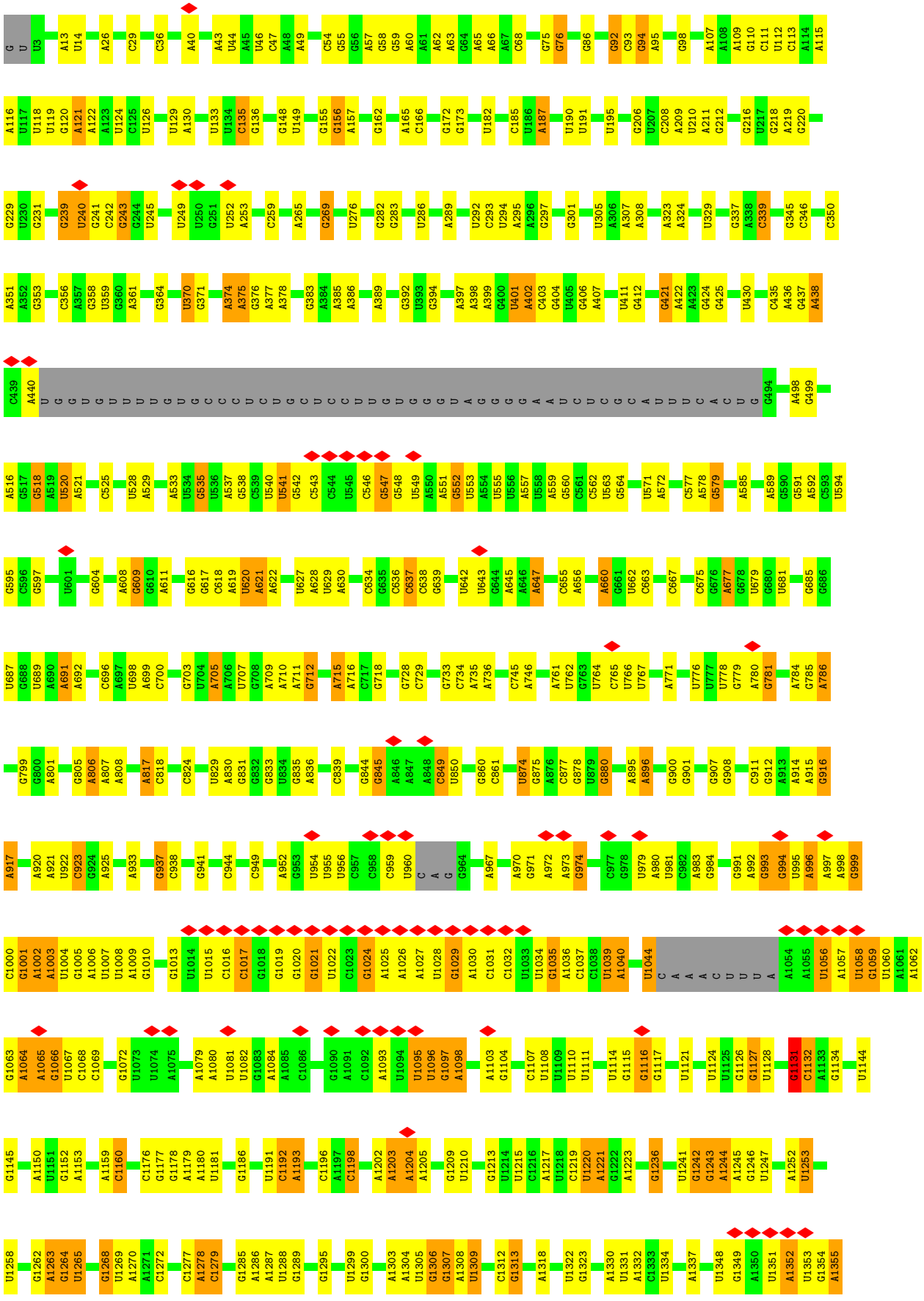
Chain K:

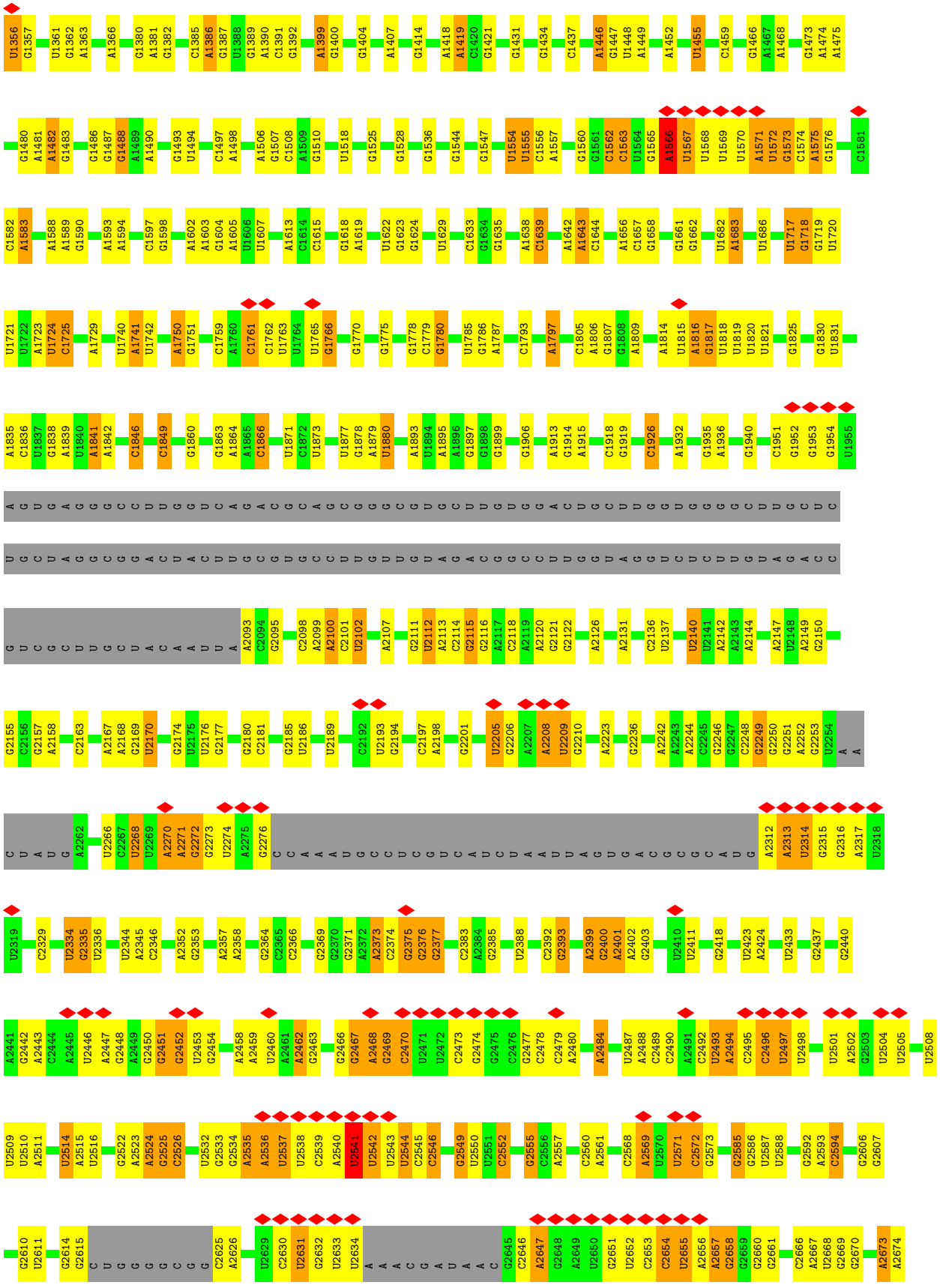


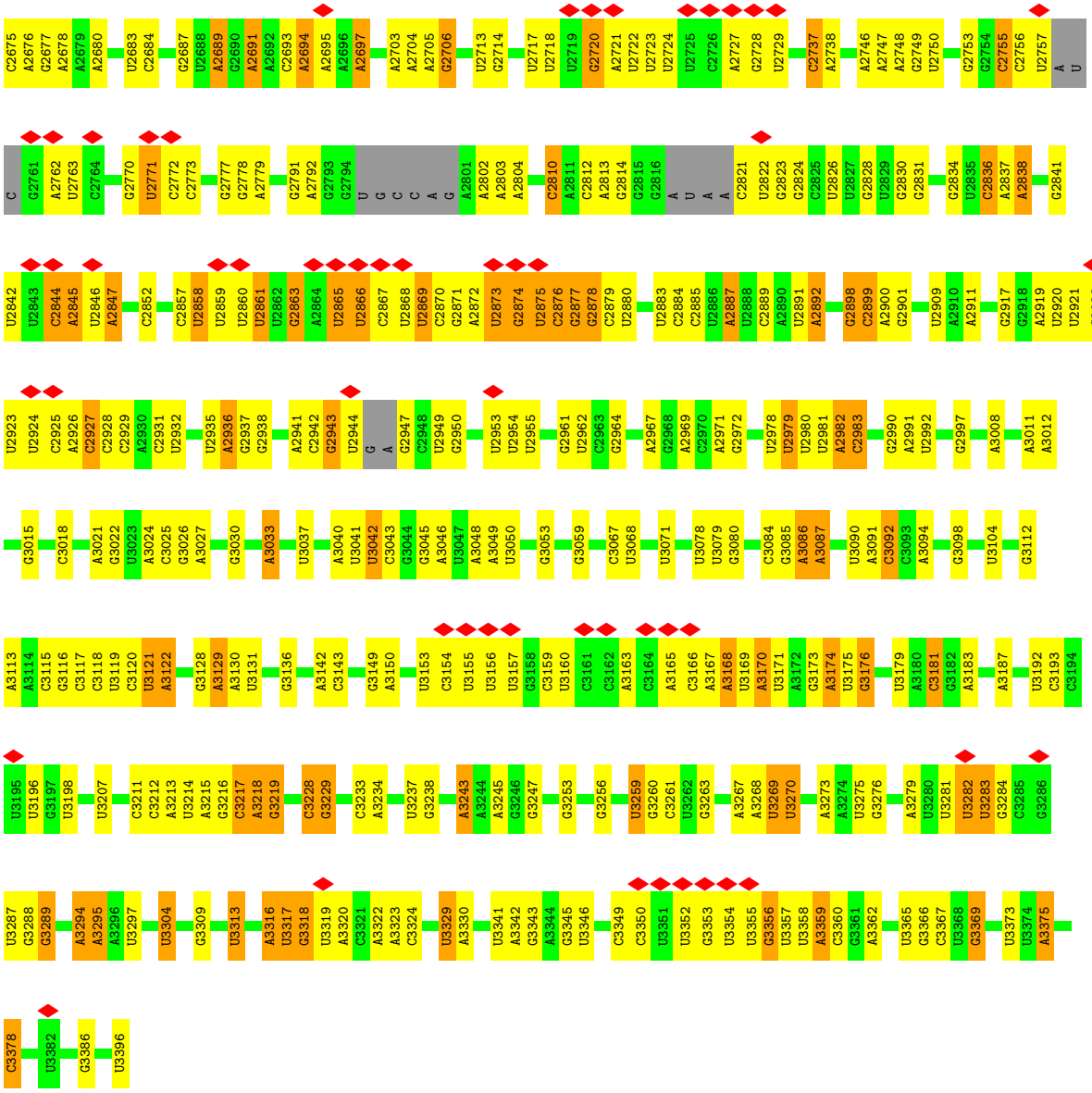

• Molecule 44: 25S ribosomal RNA

Chain 1:





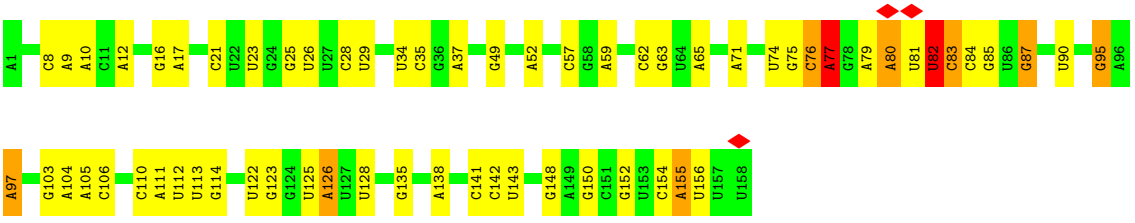




• Molecule 45: 5.8S rRNA

Chain 3:

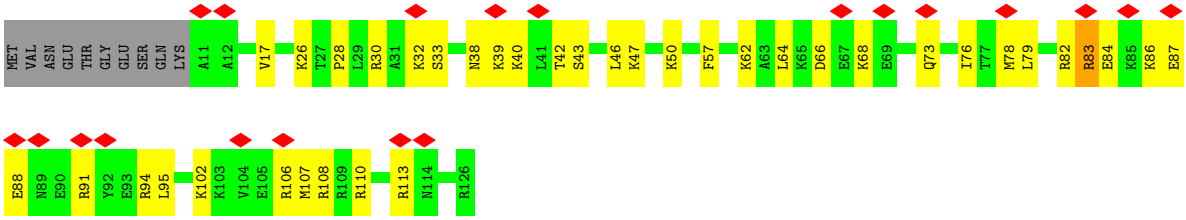


• Molecule 46: rRNA-processing protein CGR1

Chain 5:

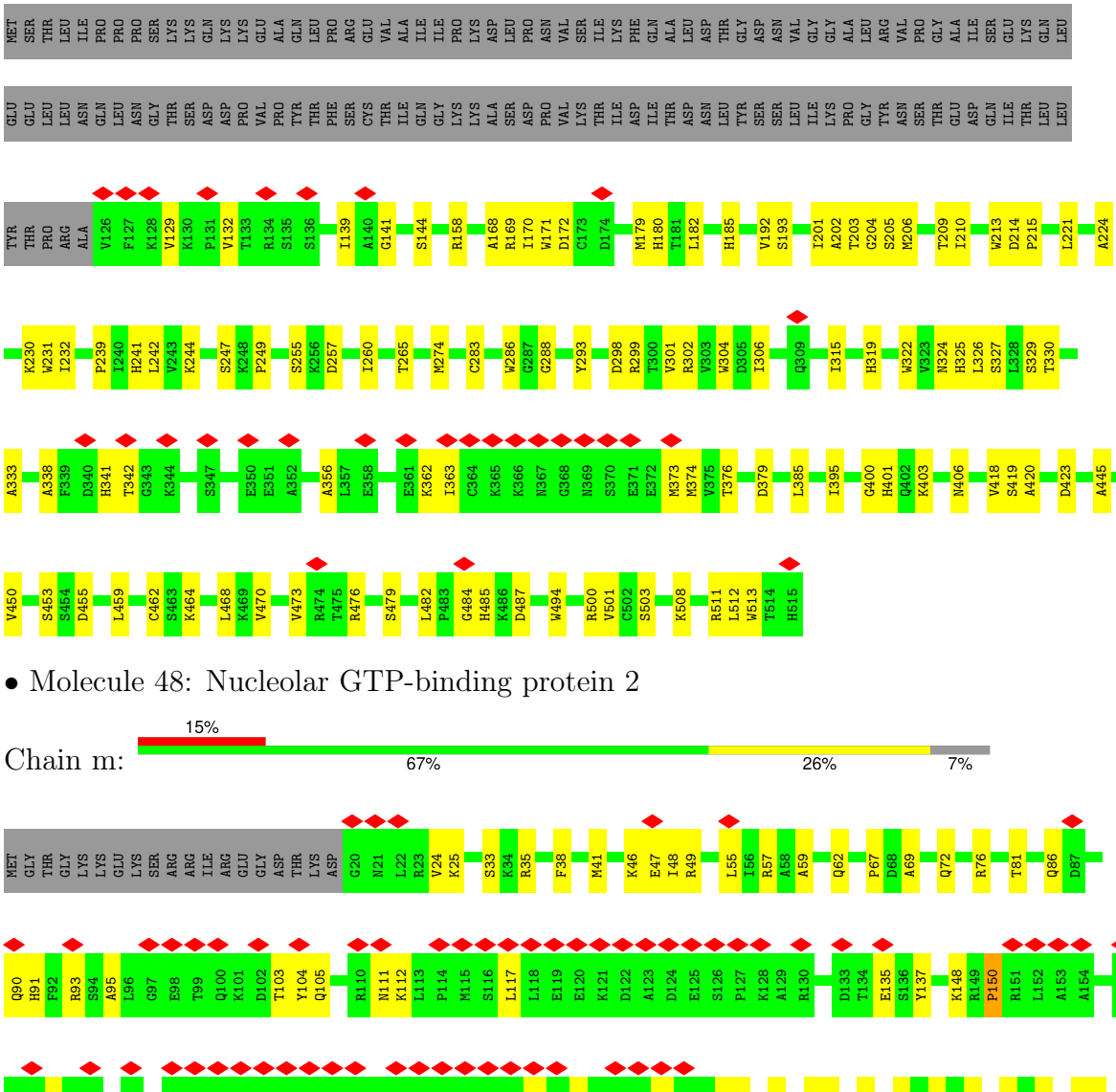





• Molecule 47: Ribosome assembly protein 4

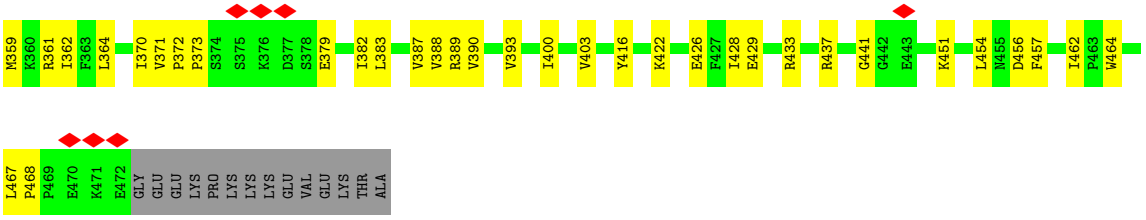
Chain x:




• Molecule 48: Nucleolar GTP-binding protein 2

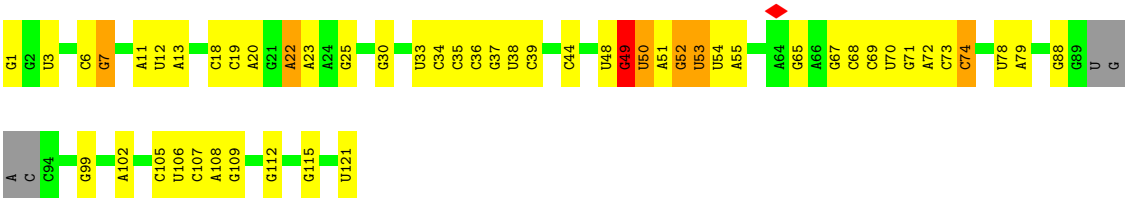
Chain m:




• Molecule 49: 5S rRNA

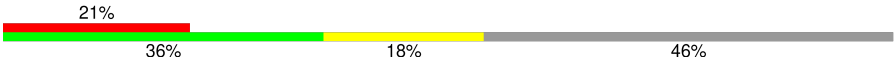
Chain 2:

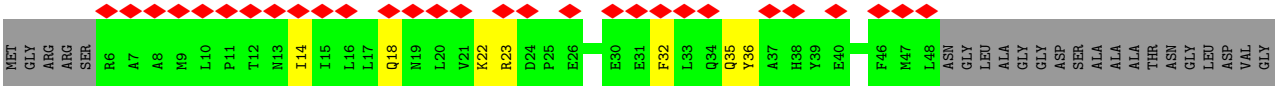


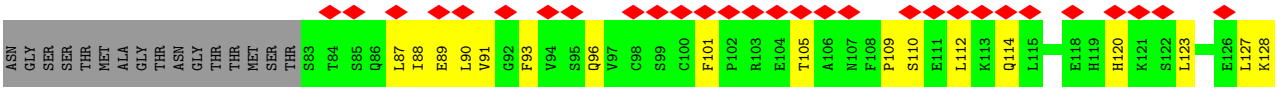



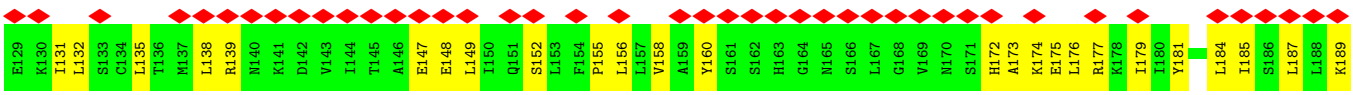

• Molecule 50: Protein SDA1

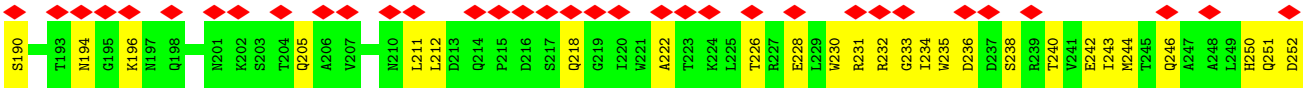
Chain t:

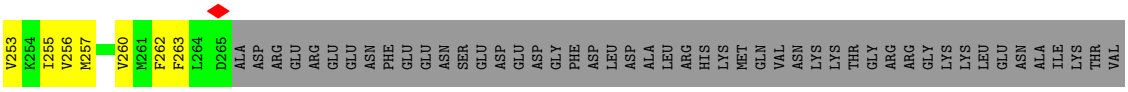


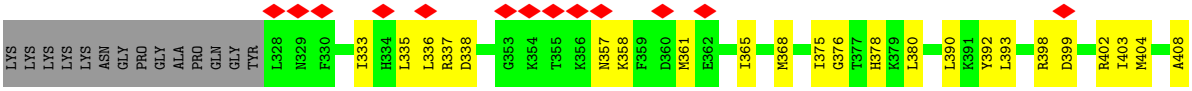



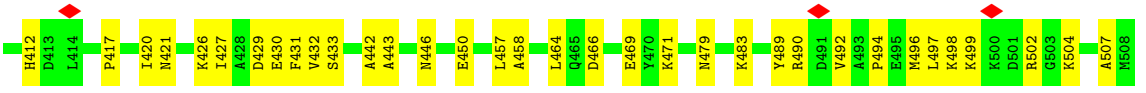



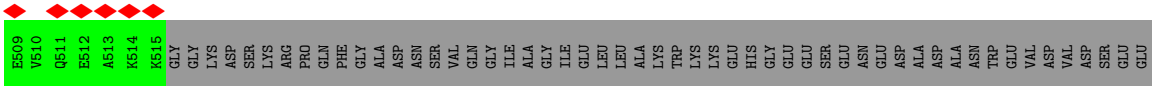



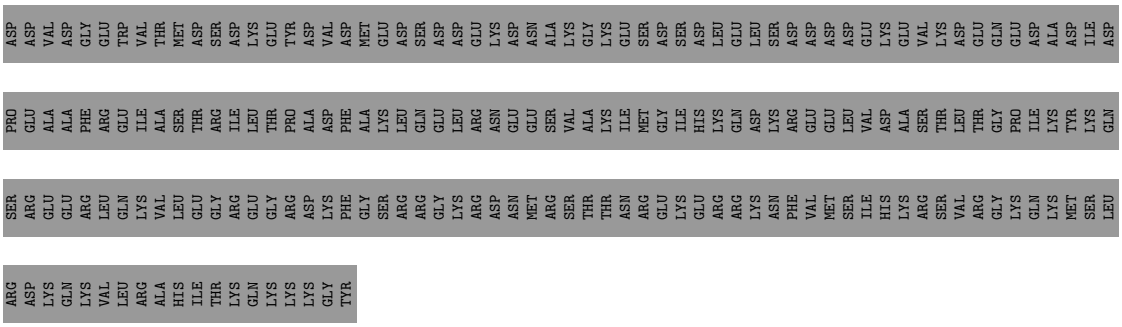



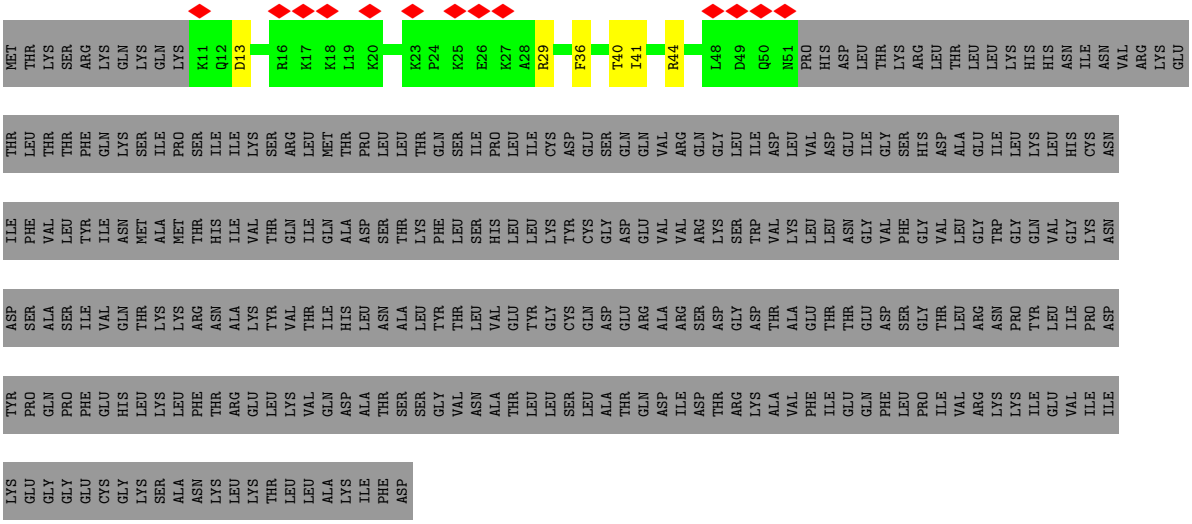






• Molecule 51: Pre-rRNA-processing protein IPI1

Chain n:

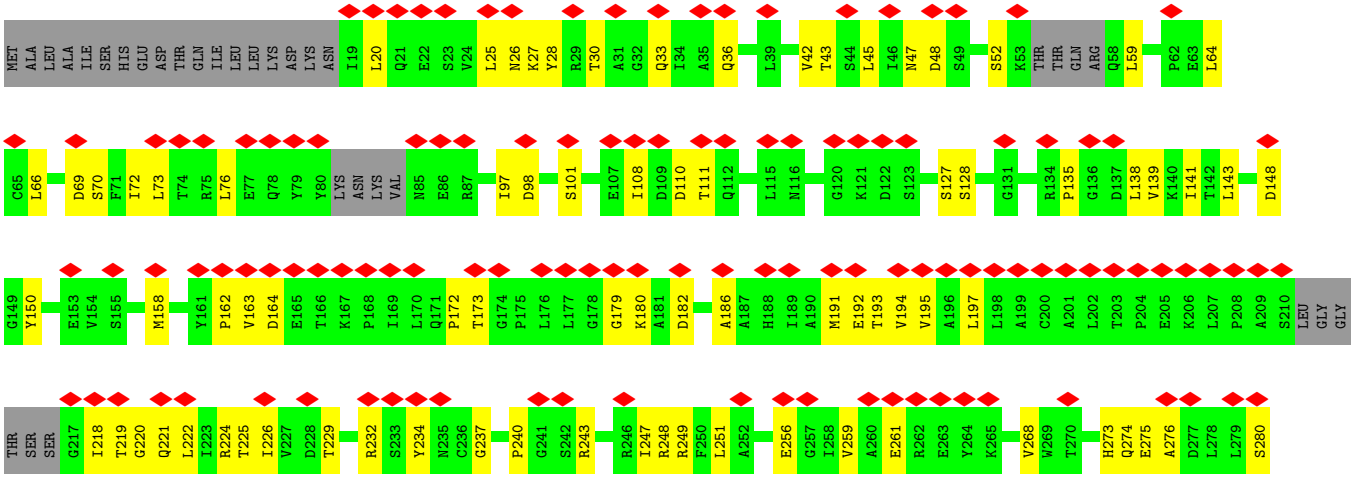


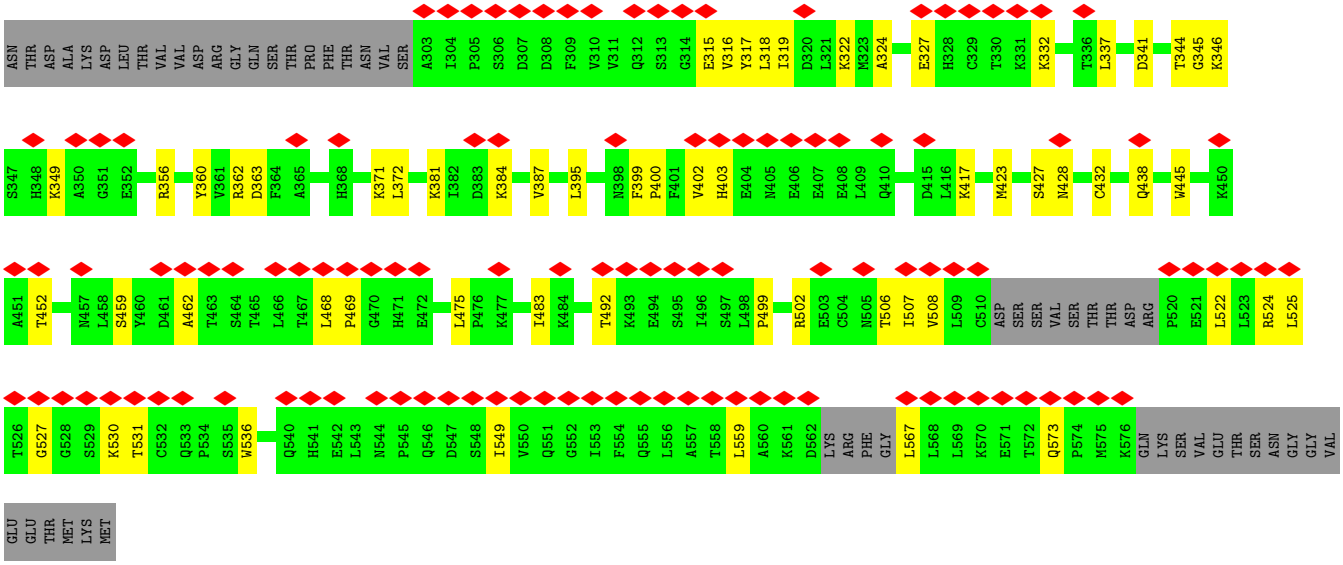




• Molecule 52: Probable metalloprotease ARX1

Chain 4:



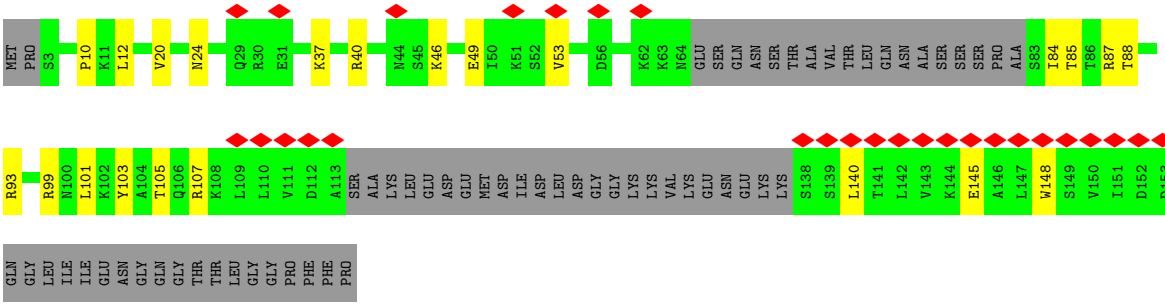





• Molecule 53: Ribosome biogenesis protein ALB1

Chain o:

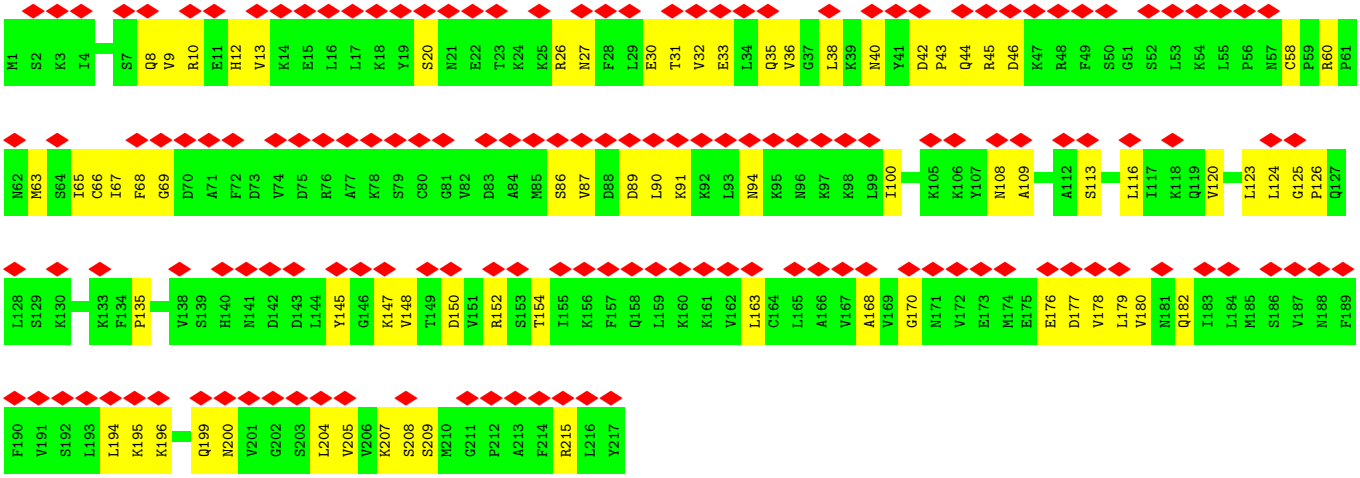


• Molecule 54: Large ribosomal subunit protein uL1A

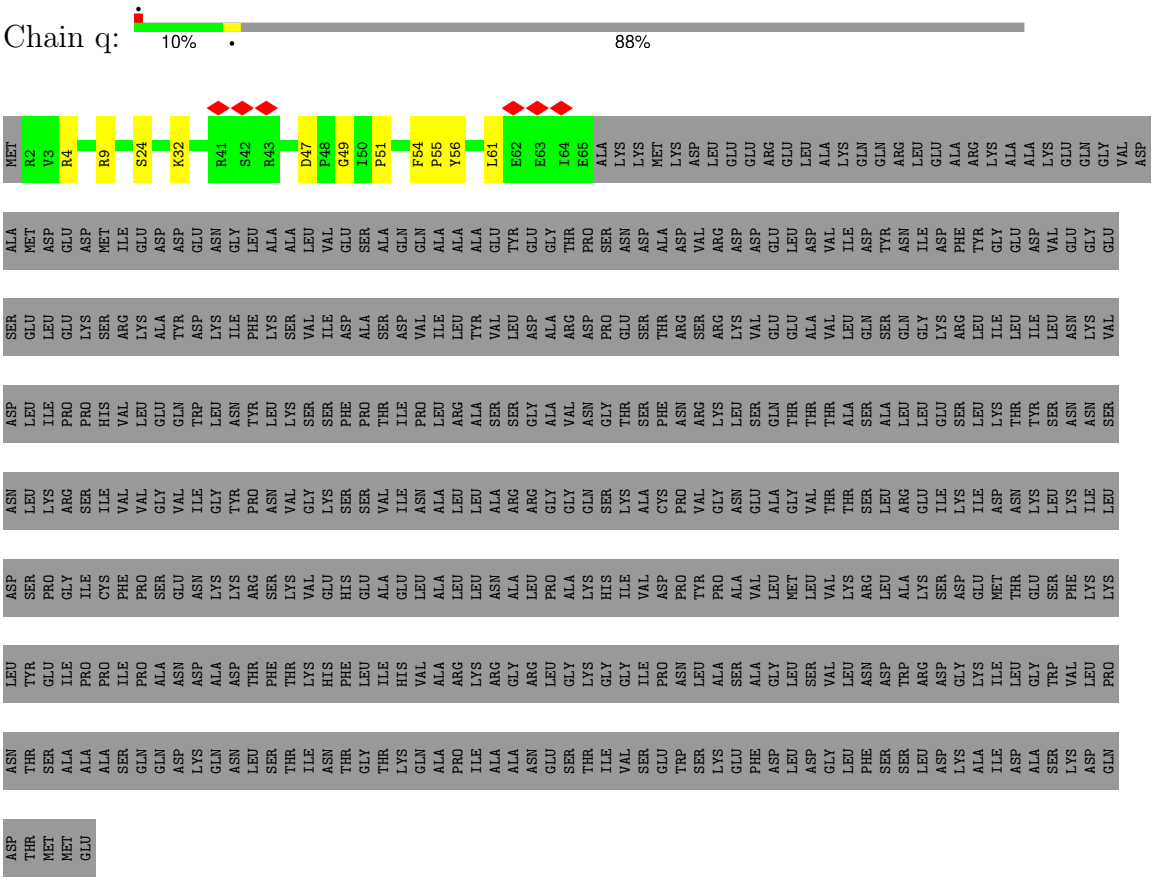
Chain s:



• Molecule 55: Nuclear GTP-binding protein NUG1

Chain q:




• Molecule 56: Small ribosomal subunit protein eS32A

Chain Lr:



# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 29051 | 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 ($e^-/Å^2$) | 50 | Depositor |
| Minimum defocus (nm) | 800 | Depositor |
| Maximum defocus (nm) | 3000 | Depositor |
| Magnification | 81000 | Depositor |
| Image detector | GATAN K3 BIOQUANTUM (6k x 4k) | Depositor |
| Maximum map value | 3.891 | Depositor |
| Minimum map value | -1.983 | Depositor |
| Average map value | 0.008 | Depositor |
| Map value standard deviation | 0.140 | Depositor |
| Recommended contour level | 0.4 | Depositor |
| Map size (Å) | 423.99997, 423.99997, 423.99997 | wwPDB |
| Map dimensions | 400, 400, 400 | 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: MG, K, GTP

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 | D | 0.09 | 0/2093 | 0.28 | 0/2827 |
| 2 | J | 0.11 | 0/1303 | 0.30 | 0/1747 |
| 3 | A | 0.16 | 0/1897 | 0.37 | 0/2550 |
| 4 | a | 0.16 | 0/758 | 0.31 | 0/1023 |
| 5 | B | 0.20 | 1/3152 (0.0%) | 0.38 | 0/4239 |
| 6 | b | 0.13 | 0/5305 | 0.35 | 0/7130 |
| 7 | C | 0.14 | 0/2801 | 0.34 | 0/3792 |
| 8 | c | 0.14 | 0/751 | 0.30 | 0/1008 |
| 9 | d | 0.13 | 0/887 | 0.29 | 0/1191 |
| 10 | E | 0.13 | 0/1295 | 0.33 | 0/1740 |
| 11 | e | 0.13 | 0/1041 | 0.29 | 0/1394 |
| 12 | F | 0.14 | 0/1821 | 0.36 | 0/2451 |
| 13 | f | 0.16 | 0/868 | 0.31 | 0/1168 |
| 14 | G | 0.16 | 0/1830 | 0.41 | 0/2469 |
| 15 | g | 0.15 | 0/891 | 0.32 | 0/1191 |
| 16 | I | 0.30 | 1/1072 (0.1%) | 0.55 | 3/1440 (0.2%) |
| 17 | H | 0.15 | 0/1514 | 0.32 | 0/2039 |
| 18 | h | 0.13 | 0/978 | 0.27 | 0/1301 |
| 19 | i | 0.14 | 0/749 | 0.38 | 1/995 (0.1%) |
| 20 | j | 0.14 | 0/685 | 0.29 | 0/908 |
| 21 | k | 0.14 | 0/618 | 0.35 | 0/826 |
| 22 | L | 0.14 | 0/1516 | 0.37 | 0/2037 |
| 23 | l | 0.14 | 0/443 | 0.29 | 0/588 |
| 24 | M | 0.14 | 0/1074 | 0.31 | 0/1446 |
| 25 | p | 0.14 | 0/701 | 0.34 | 0/934 |
| 26 | N | 0.16 | 0/1757 | 0.34 | 0/2354 |
| 27 | u | 0.16 | 0/1278 | 0.44 | 2/1699 (0.1%) |
| 28 | O | 0.14 | 0/1585 | 0.27 | 0/2128 |
| 29 | P | 0.14 | 0/1461 | 0.32 | 0/1964 |
| 30 | Q | 0.22 | 1/1086 (0.1%) | 0.30 | 0/1466 |
| 31 | R | 0.14 | 0/1258 | 0.34 | 0/1679 |
| 32 | r | 0.16 | 0/1750 | 0.42 | 0/2338 |

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | #\|Z\| >5 | RMSZ | #\|Z\| >5 |
| 33 | S | 0.15 | 0/1460 | 0.39 | 0/1962 |
| 34 | T | 0.10 | 0/1182 | 0.29 | 0/1586 |
| 35 | U | 0.13 | 0/843 | 0.37 | 0/1143 |
| 36 | V | 0.13 | 0/1018 | 0.33 | 0/1369 |
| 37 | W | 0.10 | 0/1843 | 0.28 | 0/2483 |
| 38 | X | 0.15 | 0/974 | 0.30 | 0/1314 |
| 39 | Y | 0.14 | 0/1004 | 0.30 | 0/1341 |
| 40 | y | 0.13 | 0/1848 | 0.34 | 0/2516 |
| 41 | Z | 0.15 | 0/1118 | 0.36 | 0/1497 |
| 42 | z | 0.08 | 0/445 | 0.20 | 0/585 |
| 43 | K | 0.11 | 0/363 | 0.35 | 0/494 |
| 44 | 1 | 0.26 | 0/74608 | 0.63 | 17/116301 (0.0%) |
| 45 | 3 | 0.28 | 0/3746 | 0.66 | 4/5832 (0.1%) |
| 46 | 5 | 0.15 | 0/941 | 0.40 | 0/1233 |
| 47 | x | 0.12 | 0/3130 | 0.31 | 0/4244 |
| 48 | m | 0.40 | 2/3722 (0.1%) | 0.63 | 4/5019 (0.1%) |
| 49 | 2 | 0.19 | 0/2787 | 0.61 | 1/4339 (0.0%) |
| 50 | t | 0.14 | 0/3341 | 0.42 | 0/4500 |
| 51 | n | 0.15 | 0/338 | 0.38 | 0/448 |
| 52 | 4 | 0.16 | 0/4015 | 0.43 | 0/5447 |
| 53 | o | 0.11 | 0/879 | 0.28 | 0/1171 |
| 54 | s | 0.14 | 0/1745 | 0.38 | 0/2342 |
| 55 | q | 0.13 | 0/540 | 0.33 | 0/710 |
| 56 | Lr | 0.11 | 0/192 | 0.26 | 0/246 |
| All | All | 0.22 | 5/158300 (0.0%) | 0.53 | 32/230184 (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 |
|---|---|---|---|
| 12 | F | 0 | 1 |
| 14 | G | 0 | 1 |
| 26 | N | 0 | 1 |
| All | All | 0 | 3 |

All (5) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 48 | m | 150 | PRO | CG-CD | -20.23 | 0.81 | 1.50 |
| 16 | I | 114 | PRO | CG-CD | -8.27 | 1.22 | 1.50 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 48 | m | 150 | PRO | CB-CG | 7.07 | 1.84 | 1.49 |
| 5 | B | 185 | GLY | C-N | -6.59 | 1.30 | 1.33 |
| 30 | Q | 60 | PRO | CA-C | 5.49 | 1.54 | 1.51 |

The worst 5 of 32 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 48 | m | 150 | PRO | N-CD-CG | -29.10 | 59.56 | 103.20 |
| 48 | m | 150 | PRO | CA-CB-CG | -21.58 | 63.50 | 104.50 |
| 16 | I | 114 | PRO | N-CD-CG | -11.55 | 85.88 | 103.20 |
| 48 | m | 150 | PRO | N-CA-CB | -10.57 | 93.90 | 103.31 |
| 16 | I | 114 | PRO | CA-CB-CG | -10.52 | 84.52 | 104.50 |

There are no chirality outliers.

All (3) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 12 | F | 158 | LYS | Peptide |
| 14 | G | 30 | THR | Peptide |
| 26 | N | 92 | LEU | Peptide |

## 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 | D | 2047 | 0 | 1988 | 55 | 0 |
| 2 | J | 1283 | 0 | 1315 | 34 | 0 |
| 3 | A | 1863 | 0 | 1930 | 44 | 0 |
| 4 | a | 742 | 0 | 785 | 17 | 0 |
| 5 | B | 3081 | 0 | 3165 | 89 | 0 |
| 6 | b | 5219 | 0 | 5266 | 167 | 0 |
| 7 | C | 2749 | 0 | 2863 | 64 | 0 |
| 8 | c | 743 | 0 | 797 | 16 | 0 |
| 9 | d | 873 | 0 | 914 | 17 | 0 |
| 10 | E | 1274 | 0 | 1361 | 24 | 0 |
| 11 | e | 1020 | 0 | 1090 | 21 | 0 |
| 12 | F | 1784 | 0 | 1862 | 32 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 13 | f | 850 | 0 | 880 | 18 | 0 |
| 14 | G | 1798 | 0 | 1894 | 52 | 0 |
| 15 | g | 881 | 0 | 945 | 21 | 0 |
| 16 | I | 1056 | 0 | 1084 | 30 | 0 |
| 17 | H | 1493 | 0 | 1566 | 45 | 0 |
| 18 | h | 969 | 0 | 1078 | 29 | 0 |
| 19 | i | 743 | 0 | 822 | 13 | 0 |
| 20 | j | 670 | 0 | 675 | 18 | 0 |
| 21 | k | 612 | 0 | 682 | 11 | 0 |
| 22 | L | 1491 | 0 | 1543 | 48 | 0 |
| 23 | l | 436 | 0 | 475 | 16 | 0 |
| 24 | M | 1059 | 0 | 1154 | 25 | 0 |
| 25 | p | 694 | 0 | 734 | 14 | 0 |
| 26 | N | 1720 | 0 | 1779 | 58 | 0 |
| 27 | u | 1256 | 0 | 1308 | 40 | 0 |
| 28 | O | 1555 | 0 | 1659 | 13 | 0 |
| 29 | P | 1438 | 0 | 1474 | 33 | 0 |
| 30 | Q | 1069 | 0 | 1149 | 15 | 0 |
| 31 | R | 1241 | 0 | 1330 | 30 | 0 |
| 32 | r | 1719 | 0 | 1820 | 59 | 0 |
| 33 | S | 1425 | 0 | 1466 | 50 | 0 |
| 34 | T | 1161 | 0 | 1212 | 38 | 0 |
| 35 | U | 826 | 0 | 843 | 23 | 0 |
| 36 | V | 1003 | 0 | 1048 | 23 | 0 |
| 37 | W | 1814 | 0 | 1833 | 33 | 0 |
| 38 | X | 959 | 0 | 1023 | 22 | 0 |
| 39 | Y | 993 | 0 | 1081 | 36 | 0 |
| 40 | y | 1826 | 0 | 1813 | 60 | 0 |
| 41 | Z | 1092 | 0 | 1155 | 26 | 0 |
| 42 | z | 444 | 0 | 478 | 10 | 0 |
| 43 | K | 821 | 0 | 438 | 12 | 0 |
| 44 | 1 | 66660 | 0 | 33500 | 757 | 0 |
| 45 | 3 | 3353 | 0 | 1695 | 45 | 0 |
| 46 | 5 | 934 | 0 | 1022 | 36 | 0 |
| 47 | x | 3051 | 0 | 3000 | 67 | 0 |
| 48 | m | 3647 | 0 | 3704 | 106 | 0 |
| 49 | 2 | 2494 | 0 | 1262 | 25 | 0 |
| 50 | t | 3289 | 0 | 3400 | 104 | 0 |
| 51 | n | 335 | 0 | 356 | 8 | 0 |
| 52 | 4 | 3945 | 0 | 4016 | 98 | 0 |
| 53 | o | 872 | 0 | 940 | 21 | 0 |
| 54 | s | 1718 | 0 | 1811 | 55 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 55 | q | 533 | 0 | 589 | 11 | 0 |
| 56 | Lr | 191 | 0 | 235 | 4 | 0 |
| 57 | m | 32 | 0 | 12 | 1 | 0 |
| 58 | m | 1 | 0 | 0 | 0 | 0 |
| 59 | m | 1 | 0 | 0 | 0 | 0 |
| 60 | m | 3 | 0 | 0 | 0 | 0 |
| All | All | 148851 | 0 | 115319 | 2272 | 0 |

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

The worst 5 of 2272 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) |
|---|---|---|---|
| 45:3:79:A:H3' | 45:3:80:A:H4' | 1.54 | 0.89 |
| 6:b:645:ASP:H | 44:1:2401:A:H61 | 1.20 | 0.88 |
| 14:G:68:ARG:NH1 | 44:1:2514:U:OP1 | 2.07 | 0.87 |
| 42:z:2:ALA:N | 44:1:2891:U:HO2' | 1.75 | 0.85 |
| 47:x:204:GLY:HA3 | 47:x:232:ILE:HD11 | 1.59 | 0.85 |

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 | D | 249/297 (84%) | 241 (97%) | 8 (3%) | 0 | 100 | 100 |
| 2 | J | 157/174 (90%) | 141 (90%) | 16 (10%) | 0 | 100 | 100 |
| 3 | A | 243/254 (96%) | 219 (90%) | 24 (10%) | 0 | 100 | 100 |
| 4 | a | 92/149 (62%) | 81 (88%) | 11 (12%) | 0 | 100 | 100 |
| 5 | B | 384/387 (99%) | 346 (90%) | 38 (10%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 6 | b | 645/647 (100%) | 588 (91%) | 57 (9%) | 0 | 100 | 100 |
| 7 | C | 359/362 (99%) | 330 (92%) | 29 (8%) | 0 | 100 | 100 |
| 8 | c | 95/105 (90%) | 94 (99%) | 1 (1%) | 0 | 100 | 100 |
| 9 | d | 105/113 (93%) | 102 (97%) | 3 (3%) | 0 | 100 | 100 |
| 10 | E | 156/176 (89%) | 145 (93%) | 11 (7%) | 0 | 100 | 100 |
| 11 | e | 125/130 (96%) | 120 (96%) | 5 (4%) | 0 | 100 | 100 |
| 12 | F | 220/244 (90%) | 205 (93%) | 15 (7%) | 0 | 100 | 100 |
| 13 | f | 104/107 (97%) | 99 (95%) | 5 (5%) | 0 | 100 | 100 |
| 14 | G | 228/256 (89%) | 210 (92%) | 18 (8%) | 0 | 100 | 100 |
| 15 | g | 110/121 (91%) | 106 (96%) | 4 (4%) | 0 | 100 | 100 |
| 16 | I | 129/166 (78%) | 120 (93%) | 9 (7%) | 0 | 100 | 100 |
| 17 | H | 186/191 (97%) | 171 (92%) | 15 (8%) | 0 | 100 | 100 |
| 18 | h | 117/120 (98%) | 113 (97%) | 4 (3%) | 0 | 100 | 100 |
| 19 | i | 94/100 (94%) | 88 (94%) | 6 (6%) | 0 | 100 | 100 |
| 20 | j | 83/88 (94%) | 82 (99%) | 1 (1%) | 0 | 100 | 100 |
| 21 | k | 75/78 (96%) | 68 (91%) | 7 (9%) | 0 | 100 | 100 |
| 22 | L | 185/199 (93%) | 171 (92%) | 14 (8%) | 0 | 100 | 100 |
| 23 | l | 48/51 (94%) | 46 (96%) | 2 (4%) | 0 | 100 | 100 |
| 24 | M | 135/138 (98%) | 127 (94%) | 8 (6%) | 0 | 100 | 100 |
| 25 | p | 89/92 (97%) | 84 (94%) | 5 (6%) | 0 | 100 | 100 |
| 26 | N | 201/204 (98%) | 192 (96%) | 9 (4%) | 0 | 100 | 100 |
| 27 | u | 147/199 (74%) | 136 (92%) | 11 (8%) | 0 | 100 | 100 |
| 28 | O | 195/199 (98%) | 191 (98%) | 4 (2%) | 0 | 100 | 100 |
| 29 | P | 181/184 (98%) | 169 (93%) | 12 (7%) | 0 | 100 | 100 |
| 30 | Q | 137/186 (74%) | 134 (98%) | 3 (2%) | 0 | 100 | 100 |
| 31 | R | 152/189 (80%) | 146 (96%) | 6 (4%) | 0 | 100 | 100 |
| 32 | r | 209/261 (80%) | 187 (90%) | 22 (10%) | 0 | 100 | 100 |
| 33 | S | 168/172 (98%) | 153 (91%) | 15 (9%) | 0 | 100 | 100 |
| 34 | T | 143/160 (89%) | 132 (92%) | 11 (8%) | 0 | 100 | 100 |
| 35 | U | 102/121 (84%) | 96 (94%) | 6 (6%) | 0 | 100 | 100 |
| 36 | V | 134/137 (98%) | 130 (97%) | 4 (3%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 37 | W | 223/236 (94%) | 215 (96%) | 8 (4%) | 0 | 100 | 100 |
| 38 | X | 118/142 (83%) | 112 (95%) | 6 (5%) | 0 | 100 | 100 |
| 39 | Y | 124/127 (98%) | 120 (97%) | 4 (3%) | 0 | 100 | 100 |
| 40 | y | 240/245 (98%) | 230 (96%) | 10 (4%) | 0 | 100 | 100 |
| 41 | Z | 133/136 (98%) | 122 (92%) | 11 (8%) | 0 | 100 | 100 |
| 42 | z | 53/106 (50%) | 53 (100%) | 0 | 0 | 100 | 100 |
| 43 | K | 53/165 (32%) | 50 (94%) | 3 (6%) | 0 | 100 | 100 |
| 46 | 5 | 106/120 (88%) | 97 (92%) | 8 (8%) | 1 (1%) | 14 | 28 |
| 47 | x | 388/515 (75%) | 368 (95%) | 20 (5%) | 0 | 100 | 100 |
| 48 | m | 451/486 (93%) | 429 (95%) | 22 (5%) | 0 | 100 | 100 |
| 50 | t | 408/767 (53%) | 371 (91%) | 37 (9%) | 0 | 100 | 100 |
| 51 | n | 39/334 (12%) | 31 (80%) | 8 (20%) | 0 | 100 | 100 |
| 52 | 4 | 495/593 (84%) | 455 (92%) | 40 (8%) | 0 | 100 | 100 |
| 53 | o | 103/175 (59%) | 103 (100%) | 0 | 0 | 100 | 100 |
| 54 | s | 215/217 (99%) | 203 (94%) | 12 (6%) | 0 | 100 | 100 |
| 55 | q | 62/520 (12%) | 62 (100%) | 0 | 0 | 100 | 100 |
| 56 | Lr | 18/25 (72%) | 18 (100%) | 0 | 0 | 100 | 100 |
| All | All | 9411/11666 (81%) | 8802 (94%) | 608 (6%) | 1 (0%) | 100 | 100 |

All (1) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 46 | 5 | 83 | ARG |

### 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 | D | 211/245 (86%) | 211 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 2 | J | 138/150 (92%) | 138 (100%) | 0 | 100 | 100 |
| 3 | A | 188/196 (96%) | 188 (100%) | 0 | 100 | 100 |
| 4 | a | 77/119 (65%) | 77 (100%) | 0 | 100 | 100 |
| 5 | B | 322/323 (100%) | 322 (100%) | 0 | 100 | 100 |
| 6 | b | 572/573 (100%) | 571 (100%) | 1 (0%) | 87 | 95 |
| 7 | C | 288/289 (100%) | 288 (100%) | 0 | 100 | 100 |
| 8 | c | 81/88 (92%) | 81 (100%) | 0 | 100 | 100 |
| 9 | d | 94/97 (97%) | 94 (100%) | 0 | 100 | 100 |
| 10 | E | 138/153 (90%) | 138 (100%) | 0 | 100 | 100 |
| 11 | e | 109/111 (98%) | 109 (100%) | 0 | 100 | 100 |
| 12 | F | 186/205 (91%) | 186 (100%) | 0 | 100 | 100 |
| 13 | f | 90/91 (99%) | 90 (100%) | 0 | 100 | 100 |
| 14 | G | 189/208 (91%) | 189 (100%) | 0 | 100 | 100 |
| 15 | g | 95/103 (92%) | 95 (100%) | 0 | 100 | 100 |
| 16 | I | 116/141 (82%) | 115 (99%) | 1 (1%) | 70 | 84 |
| 17 | H | 168/171 (98%) | 167 (99%) | 1 (1%) | 78 | 89 |
| 18 | h | 104/105 (99%) | 104 (100%) | 0 | 100 | 100 |
| 19 | i | 78/82 (95%) | 78 (100%) | 0 | 100 | 100 |
| 20 | j | 69/71 (97%) | 69 (100%) | 0 | 100 | 100 |
| 21 | k | 68/69 (99%) | 68 (100%) | 0 | 100 | 100 |
| 22 | L | 147/159 (92%) | 147 (100%) | 0 | 100 | 100 |
| 23 | l | 45/46 (98%) | 45 (100%) | 0 | 100 | 100 |
| 24 | M | 108/109 (99%) | 108 (100%) | 0 | 100 | 100 |
| 25 | p | 71/72 (99%) | 71 (100%) | 0 | 100 | 100 |
| 26 | N | 175/176 (99%) | 175 (100%) | 0 | 100 | 100 |
| 27 | u | 132/180 (73%) | 132 (100%) | 0 | 100 | 100 |
| 28 | O | 160/162 (99%) | 160 (100%) | 0 | 100 | 100 |
| 29 | P | 144/146 (99%) | 144 (100%) | 0 | 100 | 100 |
| 30 | Q | 113/151 (75%) | 113 (100%) | 0 | 100 | 100 |
| 31 | R | 127/154 (82%) | 127 (100%) | 0 | 100 | 100 |
| 32 | r | 187/229 (82%) | 187 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 33 | S | 154/156 (99%) | 154 (100%) | 0 | 100 | 100 |
| 34 | T | 124/137 (90%) | 124 (100%) | 0 | 100 | 100 |
| 35 | U | 91/107 (85%) | 91 (100%) | 0 | 100 | 100 |
| 36 | V | 104/105 (99%) | 104 (100%) | 0 | 100 | 100 |
| 37 | W | 201/213 (94%) | 201 (100%) | 0 | 100 | 100 |
| 38 | X | 104/118 (88%) | 104 (100%) | 0 | 100 | 100 |
| 39 | Y | 109/110 (99%) | 109 (100%) | 0 | 100 | 100 |
| 40 | y | 207/211 (98%) | 207 (100%) | 0 | 100 | 100 |
| 41 | Z | 115/116 (99%) | 115 (100%) | 0 | 100 | 100 |
| 42 | z | 48/95 (50%) | 48 (100%) | 0 | 100 | 100 |
| 43 | K | 31/65 (48%) | 31 (100%) | 0 | 100 | 100 |
| 46 | 5 | 97/106 (92%) | 97 (100%) | 0 | 100 | 100 |
| 47 | x | 340/451 (75%) | 340 (100%) | 0 | 100 | 100 |
| 48 | m | 400/428 (94%) | 399 (100%) | 1 (0%) | 86 | 93 |
| 50 | t | 367/665 (55%) | 367 (100%) | 0 | 100 | 100 |
| 51 | n | 38/302 (13%) | 38 (100%) | 0 | 100 | 100 |
| 52 | 4 | 445/520 (86%) | 445 (100%) | 0 | 100 | 100 |
| 53 | o | 99/153 (65%) | 99 (100%) | 0 | 100 | 100 |
| 54 | s | 198/198 (100%) | 198 (100%) | 0 | 100 | 100 |
| 55 | q | 58/445 (13%) | 58 (100%) | 0 | 100 | 100 |
| 56 | Lr | 19/23 (83%) | 19 (100%) | 0 | 100 | 100 |
| All | All | 8139/9898 (82%) | 8135 (100%) | 4 (0%) | 100 | 100 |

All (4) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 6 | b | 440 | ASN |
| 16 | I | 114 | PRO |
| 17 | H | 49 | ASN |
| 48 | m | 150 | PRO |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 78 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 47 | x | 307 | ASN |
| 52 | 4 | 555 | GLN |
| 48 | m | 86 | GLN |
| 50 | t | 357 | ASN |
| 54 | s | 182 | GLN |

### 5.3.3 RNA (i)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|---|---|---|---|---|
| 44 | 1 | 3104/3396 (91%) | 667 (21%) | 57 (1%) |
| 45 | 3 | 157/158 (99%) | 27 (17%) | 0 |
| 49 | 2 | 115/121 (95%) | 24 (20%) | 2 (1%) |
| All | All | 3376/3675 (91%) | 718 (21%) | 59 (1%) |

5 of 718 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 44 | 1 | 13 | A |
| 44 | 1 | 14 | U |
| 44 | 1 | 26 | A |
| 44 | 1 | 40 | A |
| 44 | 1 | 43 | A |

5 of 59 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 44 | 1 | 2101 | C |
| 44 | 1 | 3282 | U |
| 44 | 1 | 2452 | G |
| 44 | 1 | 3269 | U |
| 44 | 1 | 3078 | U |

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

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 | $\#\|Z\| > 2$ |
| 57 | GTP | m | 501 | 59,58 | 33,34,34 | 0.95 | 1 (3%) | 50,54,54 | 1.57 | 8 (16%) |

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 |
|---|---|---|---|---|---|---|---|
| 57 | GTP | m | 501 | 59,58 | - | 3/22/38/38 | 0/3/3/3 |

All (1) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 57 | m | 501 | GTP | C2-N3 | 2.03 | 1.38 | 1.33 |

The worst 5 of 8 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 57 | m | 501 | GTP | C5-C4-N3 | -4.80 | 120.75 | 128.39 |
| 57 | m | 501 | GTP | C2-N3-C4 | 4.58 | 120.18 | 112.30 |
| 57 | m | 501 | GTP | N9-C4-N3 | 3.10 | 132.15 | 125.95 |
| 57 | m | 501 | GTP | C2-N1-C6 | -2.84 | 119.97 | 125.11 |
| 57 | m | 501 | GTP | N9-C8-N7 | -2.73 | 108.33 | 113.40 |

There are no chirality outliers.

All (3) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 57 | m | 501 | GTP | C5'-O5'-PA-O1A |
| 57 | m | 501 | GTP | O4'-C4'-C5'-O5' |

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| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 57 | m | 501 | GTP | C3'-C4'-C5'-O5' |

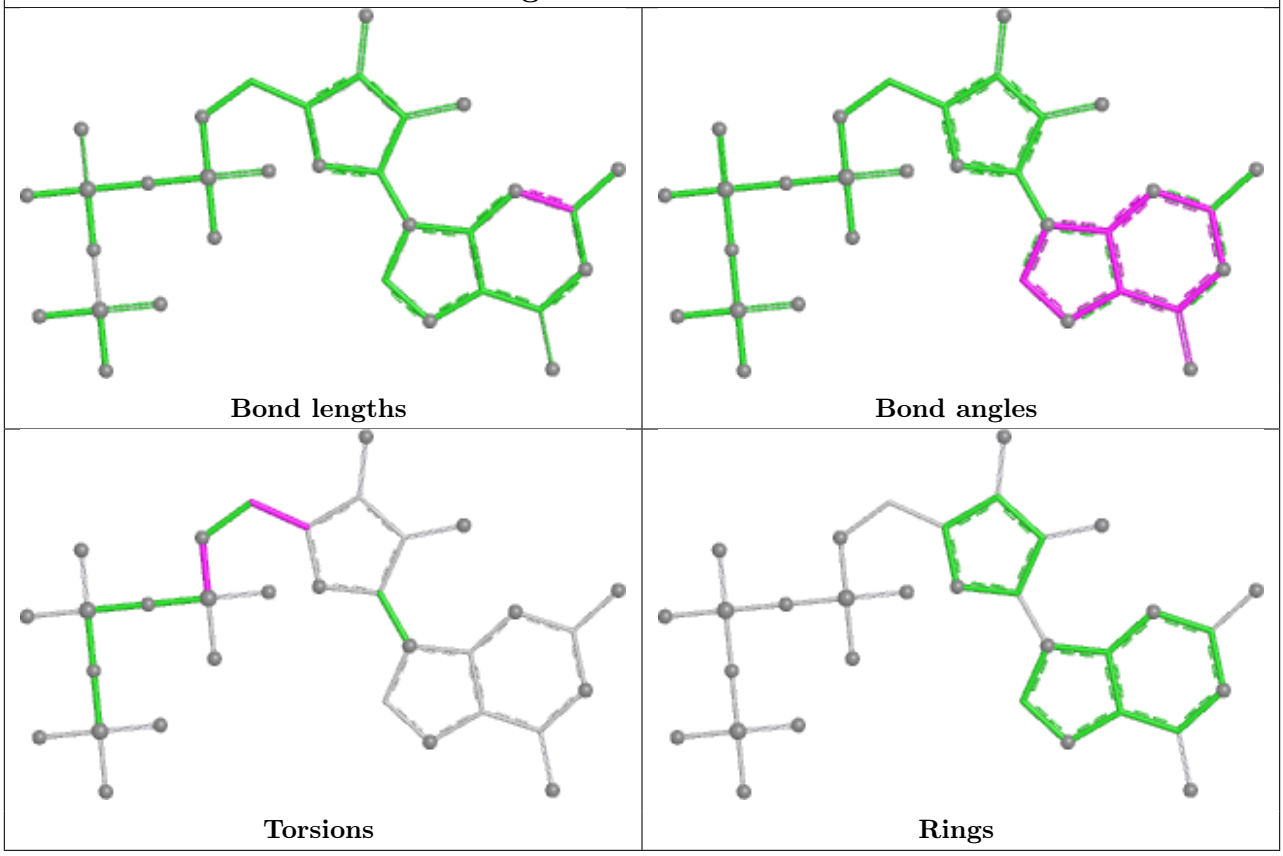
There are no ring outliers.

1 monomer is involved in 1 short contact:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|---|---|---|---|---|---|
| 57 | m | 501 | GTP | 1 | 0 |

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

**Ligand GTP m 501**



## 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 |
|---|---|---|
| 46 | 5 | 1 |

All chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|---|---|---|---|---|---|---|
| 1 | 5 | 114:ASN | C | 121:LYS | N | 3.15 |

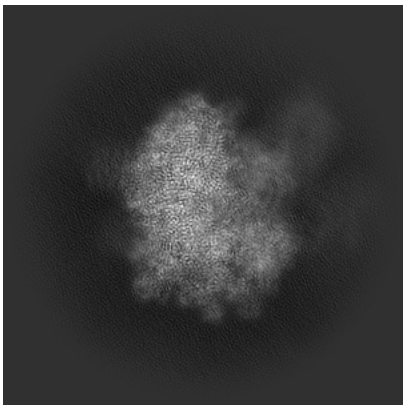
# 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-73543. These allow visual inspection of the internal detail of the map and identification of artifacts.

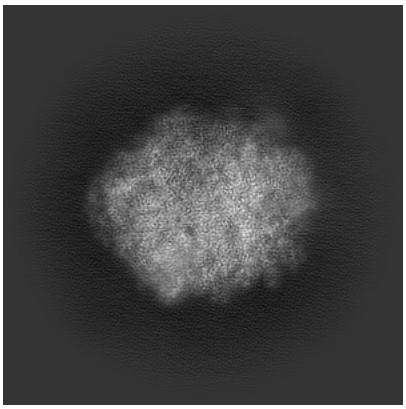
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

## 6.1 Orthogonal projections

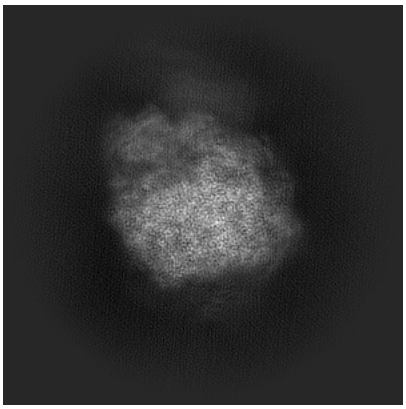
### 6.1.1 Primary map



X

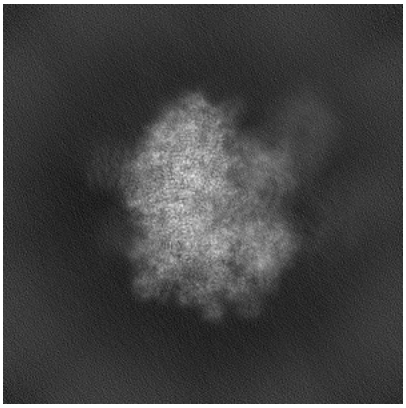


Y

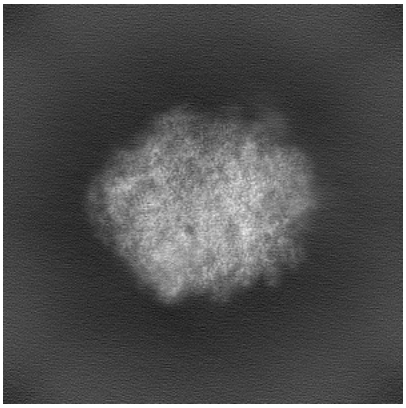


Z

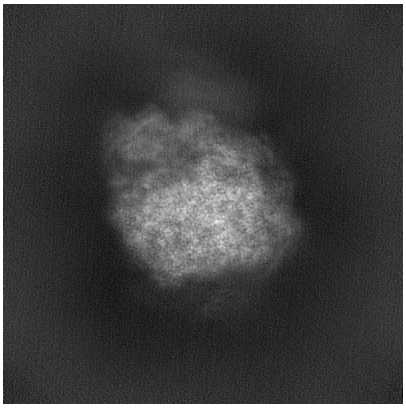
### 6.1.2 Raw map



X



Y

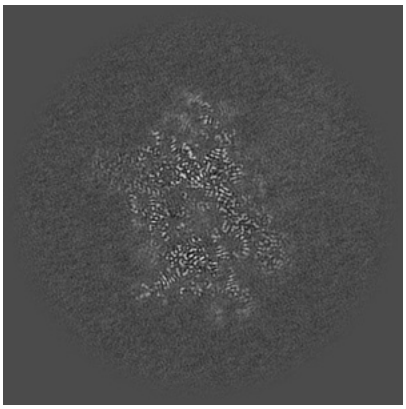


Z

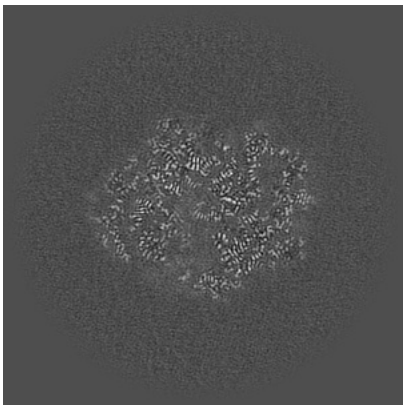
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices (i)

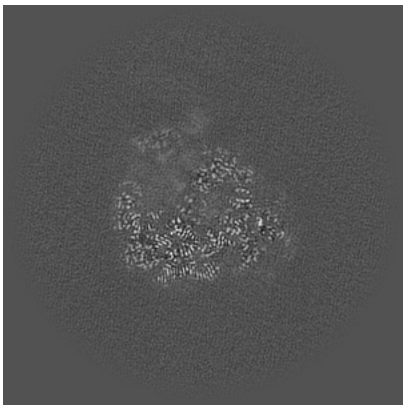
### 6.2.1 Primary map



X Index: 200

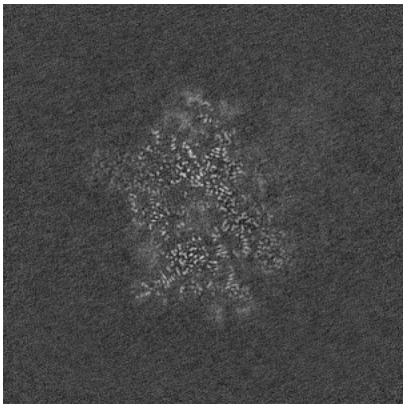


Y Index: 200

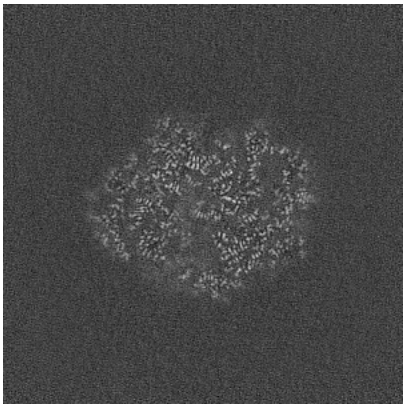


Z Index: 200

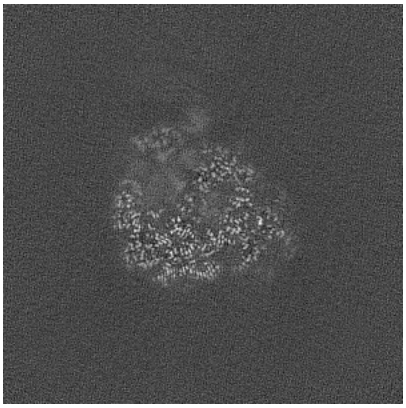
### 6.2.2 Raw map



X Index: 200



Y Index: 200

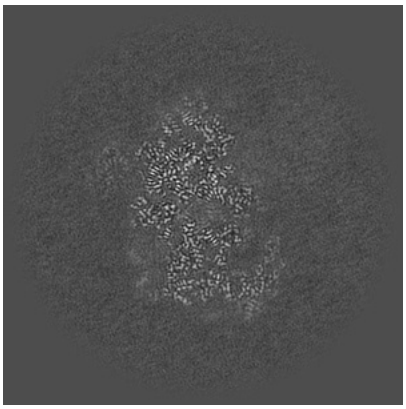


Z Index: 200

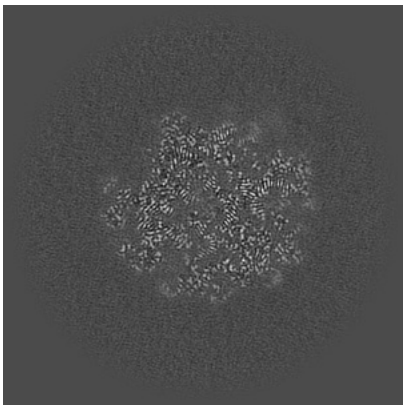
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices (i)

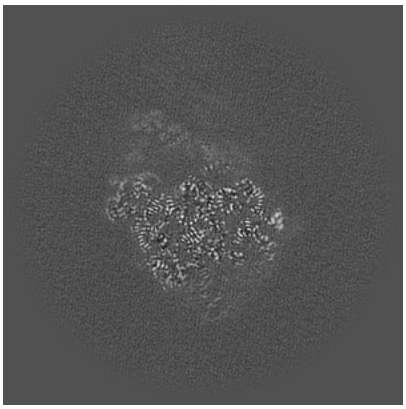
### 6.3.1 Primary map



X Index: 213

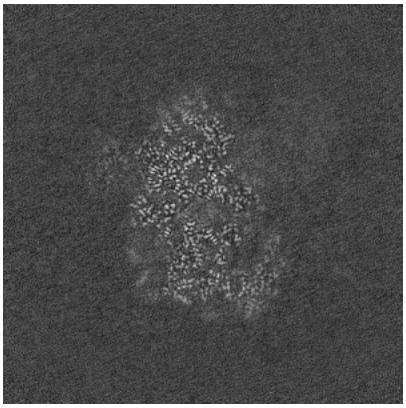


Y Index: 186

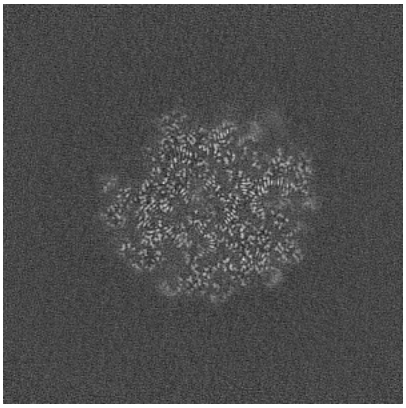


Z Index: 221

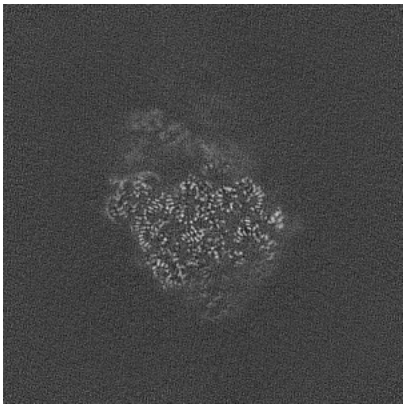
### 6.3.2 Raw map



X Index: 213



Y Index: 186

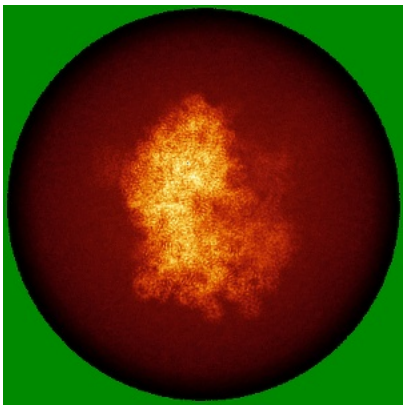


Z Index: 221

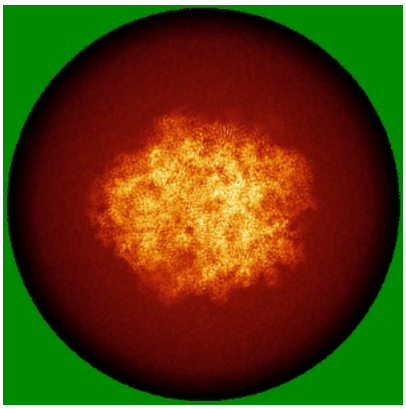
The images above show the largest variance slices of the map in three orthogonal directions.

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

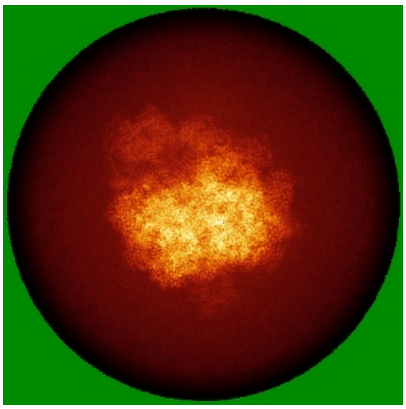
### 6.4.1 Primary map



X

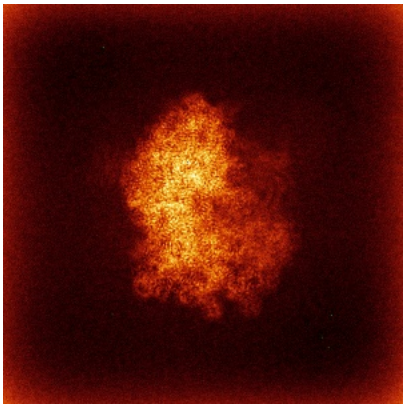


Y

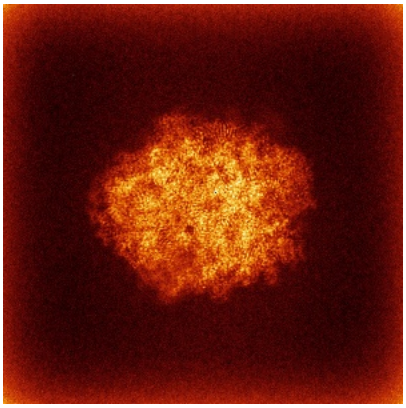


Z

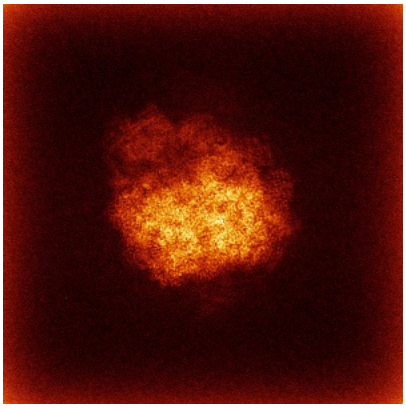
### 6.4.2 Raw map



X



Y

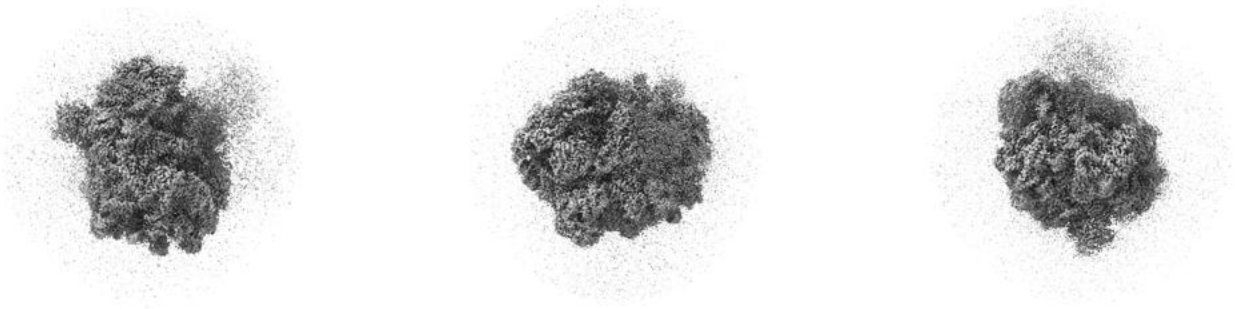


Z

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)

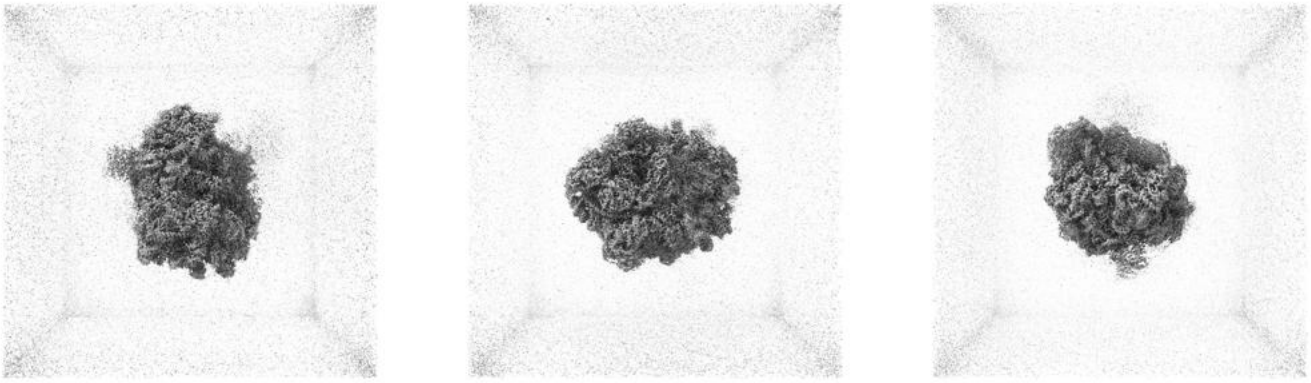
### 6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.4. 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.

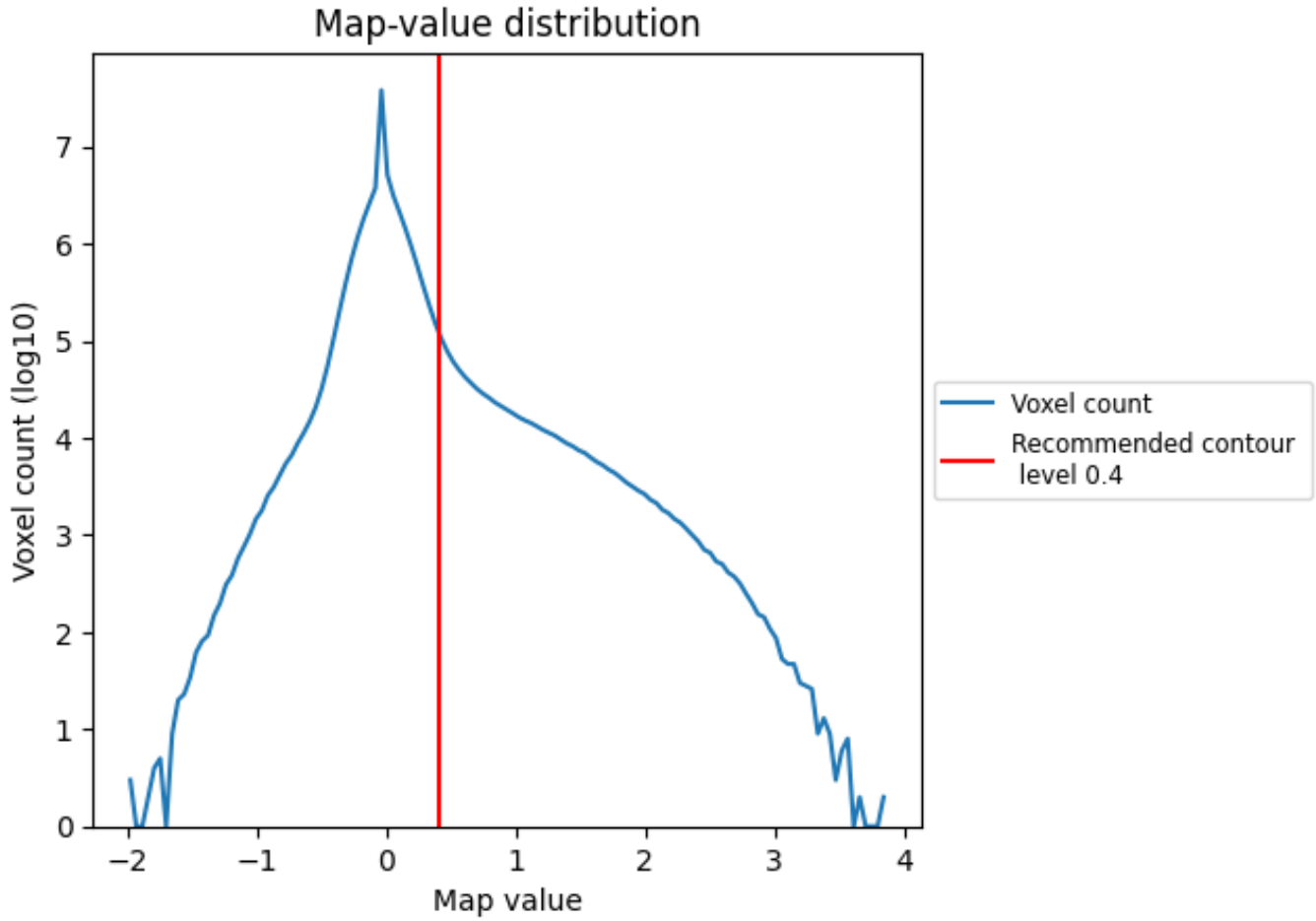
## 6.6 Mask visualisation (i)

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

# 7 Map analysis

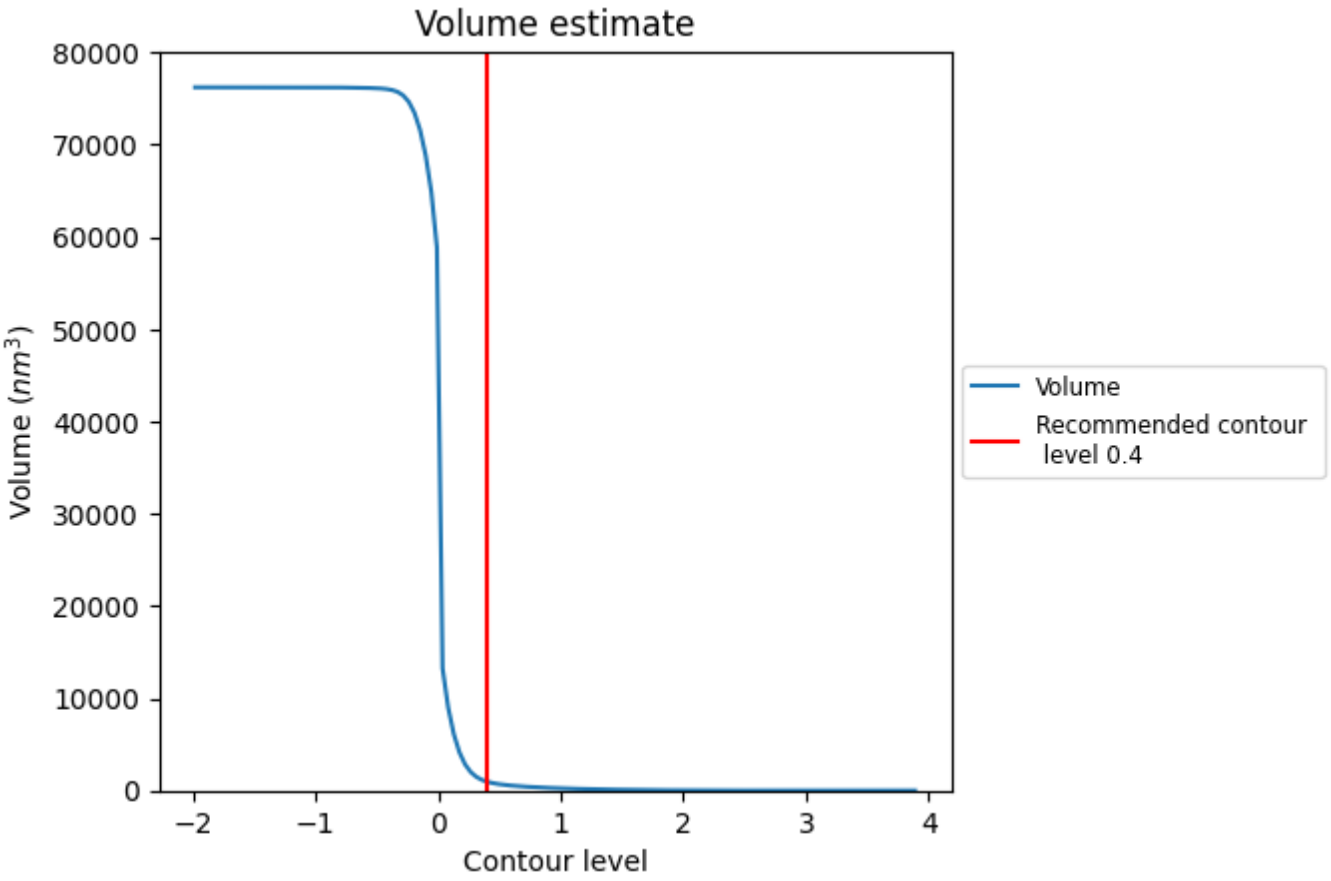
This section contains the results of statistical analysis of the map.

## 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.

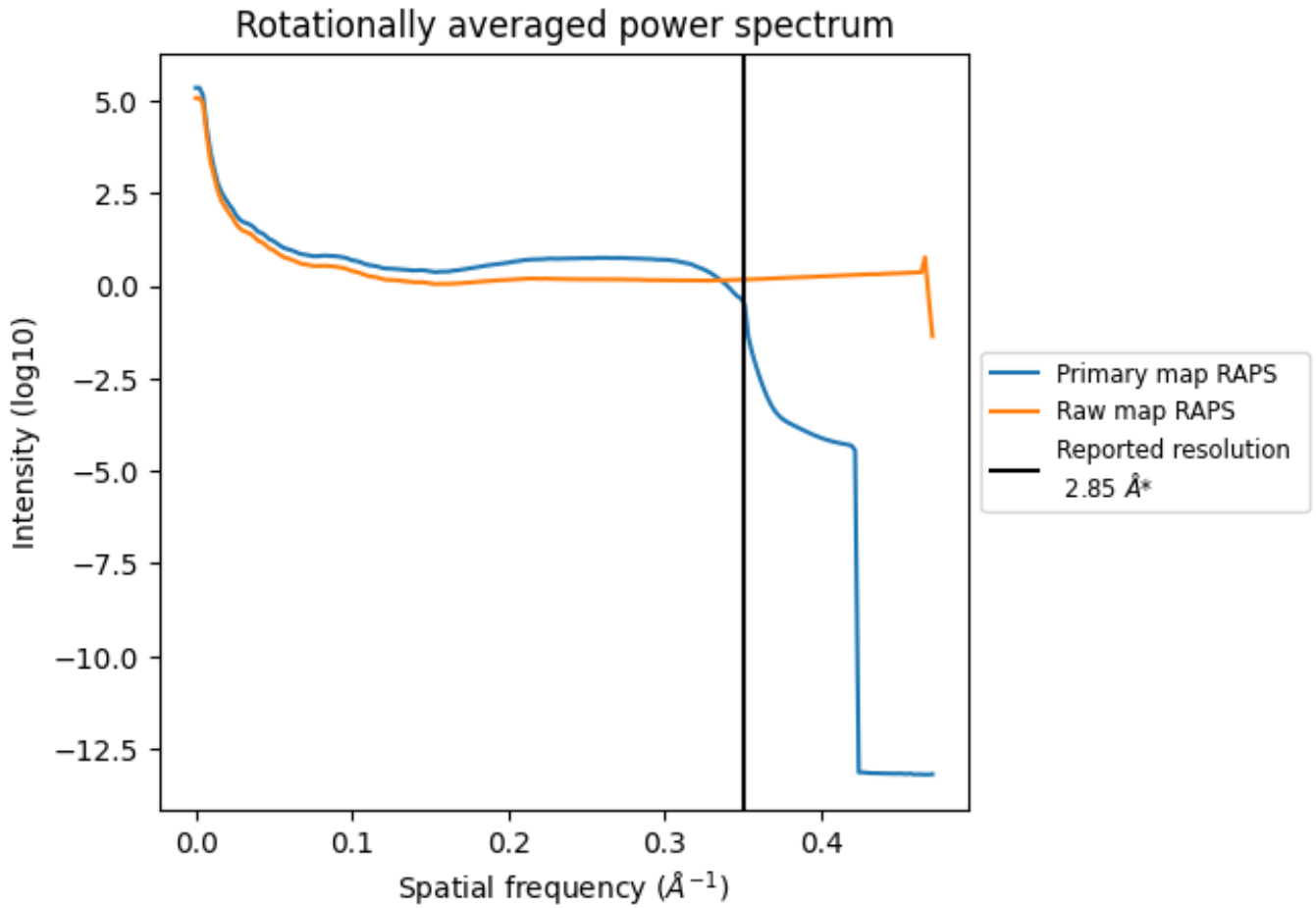
## 7.2 Volume estimate (i)




The volume at the recommended contour level is 961 $nm^3$; this corresponds to an approximate mass of 868 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)

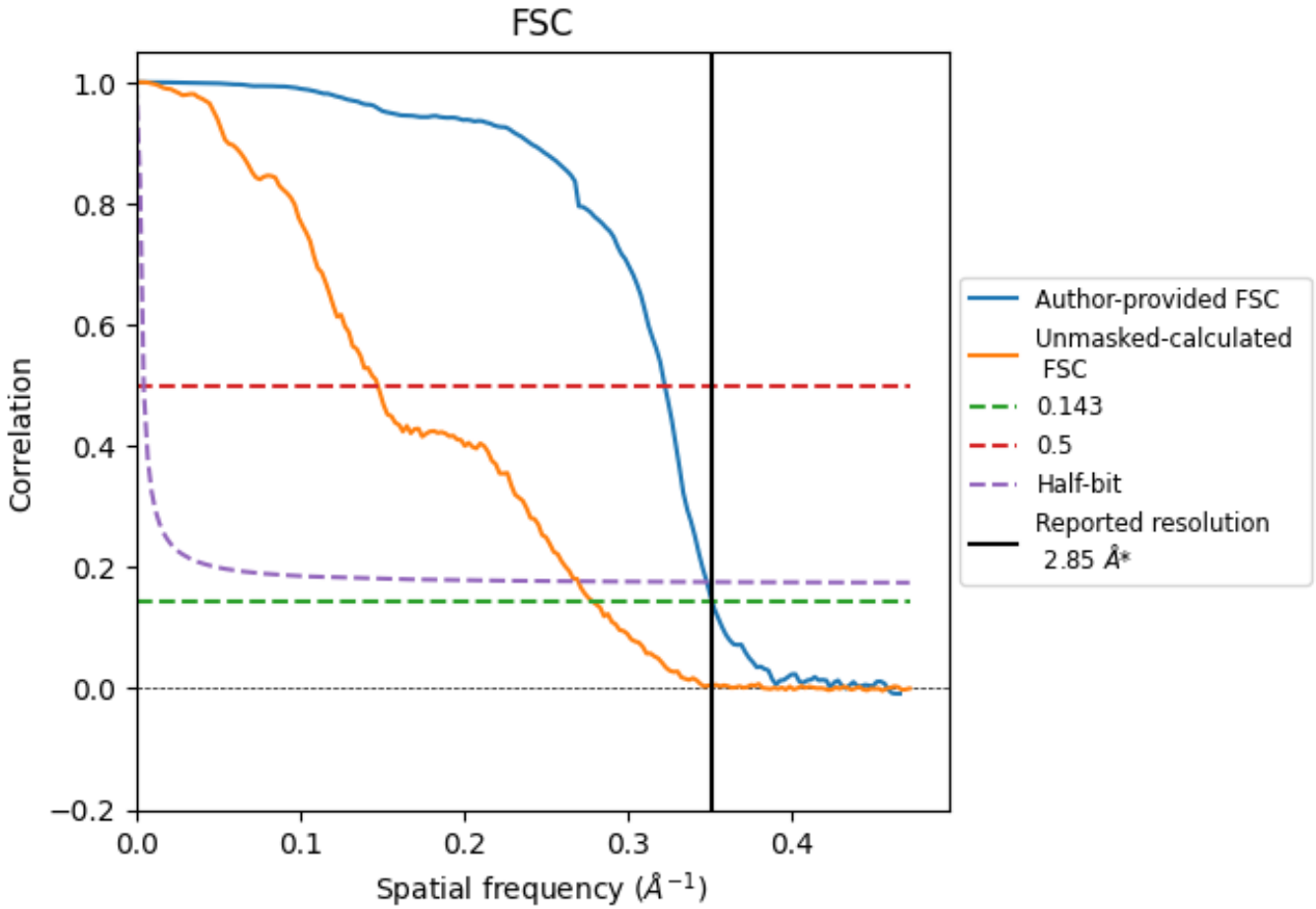



*Reported resolution corresponds to spatial frequency of 0.351 $Å^{-1}$

# 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 0.351 Å$^{-1}$

## 8.2 Resolution estimates (i)

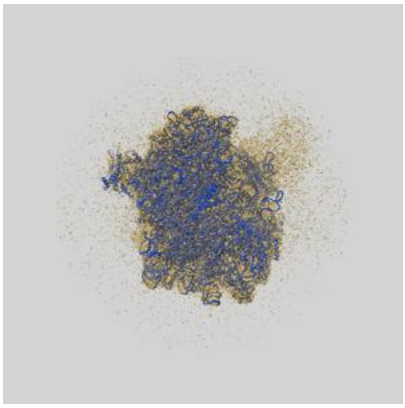
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---|---|---|---|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 2.85 | - | - |
| Author-provided FSC curve | 2.85 | 3.10 | 2.87 |
| Unmasked-calculated* | 3.59 | 6.79 | 3.71 |

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.59 differs from the reported value 2.85 by more than 10 %

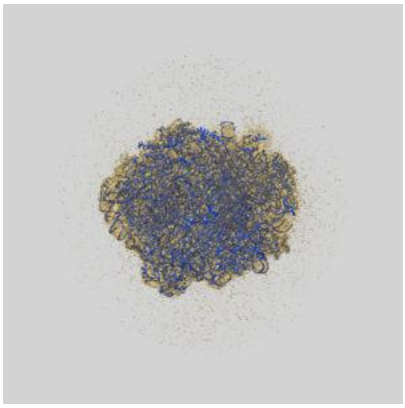
# 9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-73543 and PDB model 9YWB. Per-residue inclusion information can be found in section 3 on page 15.

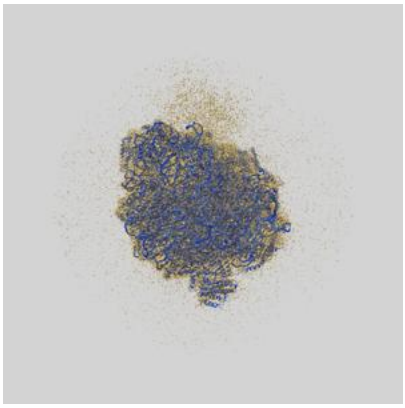
## 9.1 Map-model overlay



X



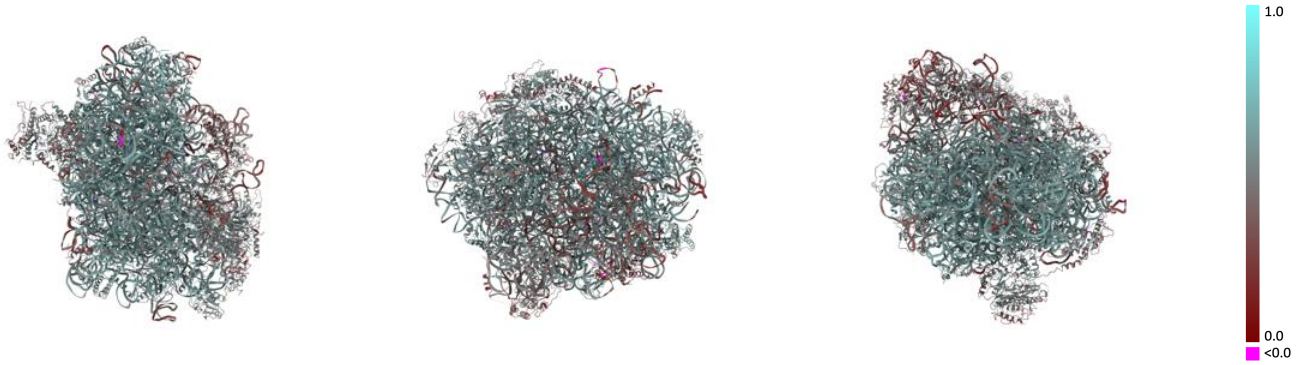
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.4 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.

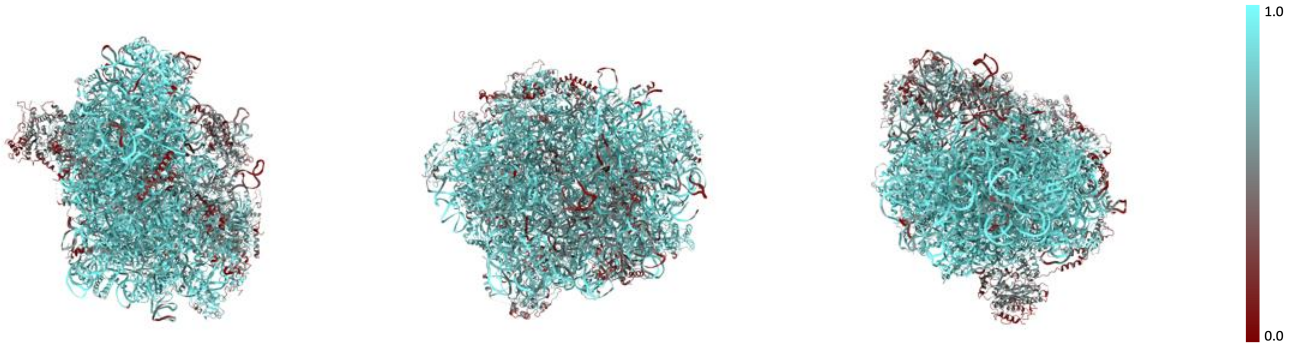
## 9.2 Q-score mapped to coordinate model (i)




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.

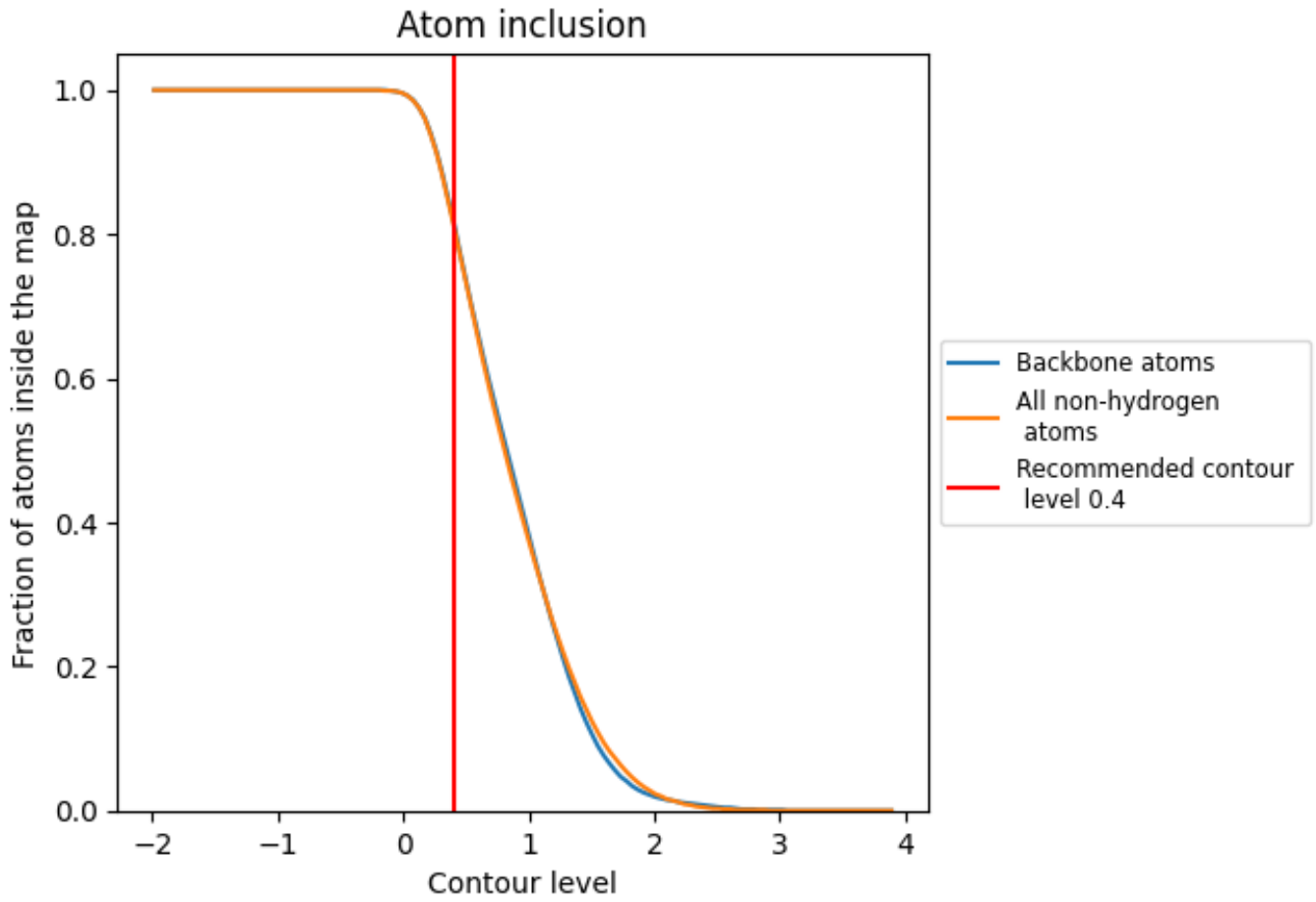
## 9.3 Atom inclusion mapped to coordinate model (i)




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 (0.4).

## 9.4 Atom inclusion (i)




At the recommended contour level, 82% of all backbone atoms, 82% 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 (0.4) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|---|---|---|
| All | 0.8150 | 0.5420 |
| 1 | 0.8830 | 0.5560 |
| 2 | 0.8670 | 0.5010 |
| 3 | 0.9530 | 0.6030 |
| 4 | 0.4170 | 0.4550 |
| 5 | 0.6090 | 0.4540 |
| A | 0.9300 | 0.6080 |
| B | 0.9230 | 0.5950 |
| C | 0.8810 | 0.5840 |
| D | 0.5440 | 0.4100 |
| E | 0.8210 | 0.5560 |
| F | 0.8780 | 0.5780 |
| G | 0.8250 | 0.5480 |
| H | 0.8800 | 0.5760 |
| I | 0.3370 | 0.4470 |
| J | 0.6670 | 0.4760 |
| K | 0.5630 | 0.4120 |
| L | 0.8540 | 0.5650 |
| Lr | 0.7870 | 0.5290 |
| M | 0.8930 | 0.5850 |
| N | 0.9150 | 0.6000 |
| O | 0.9450 | 0.6110 |
| P | 0.8550 | 0.5750 |
| Q | 0.8370 | 0.5700 |
| R | 0.8870 | 0.5810 |
| S | 0.8590 | 0.5530 |
| T | 0.5890 | 0.4370 |
| U | 0.7120 | 0.4700 |
| V | 0.9060 | 0.5900 |
| W | 0.7690 | 0.5260 |
| X | 0.9040 | 0.5870 |
| Y | 0.8790 | 0.5800 |
| Z | 0.8710 | 0.5610 |
| a | 0.8680 | 0.5800 |
| b | 0.6090 | 0.4810 |




*Continued on next page...*

*Continued from previous page...*

| Chain | Atom inclusion | Q-score |
|---|---|---|
| c | 0.7920 | 0.5420 |
| d | 0.8510 | 0.5780 |
| e | 0.8870 | 0.5880 |
| f | 0.9440 | 0.6110 |
| g | 0.8740 | 0.5790 |
| h | 0.9000 | 0.5910 |
| i | 0.8280 | 0.5580 |
| j | 0.9600 | 0.6190 |
| k | 0.7480 | 0.5220 |
| l | 0.9540 | 0.6180 |
| m | 0.7160 | 0.5130 |
| n | 0.4800 | 0.4520 |
| o | 0.6030 | 0.5090 |
| p | 0.8700 | 0.5840 |
| q | 0.7550 | 0.5540 |
| r | 0.8690 | 0.5740 |
| s | 0.3160 | 0.3040 |
| t | 0.4820 | 0.4200 |
| u | 0.7500 | 0.5310 |
| x | 0.7520 | 0.5250 |
| y | 0.7870 | 0.5430 |
| z | 0.6200 | 0.5070 |