# wwPDB EM Validation Summary Report (i)

Jun 2, 2024 – 07:57 AM EDT

| | | |
|---|---|---|
| PDB ID | : | 7UQZ |
| EMDB ID | : | EMD-26703 |
| Title | : | Nucleoplasmic pre-60S intermediate of the Nog2 containing pre-rotation state from a SPB1 D52A strain |
| Authors | : | Sekulski, K.; Cruz, V.E.; Weirich, C.S.; Erzberger, J.P. |
| Deposited on | : | 2022-04-20 |
| Resolution | : | 2.44 Å(reported) |
| Based on initial model | : | 3JCT |

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

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

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

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

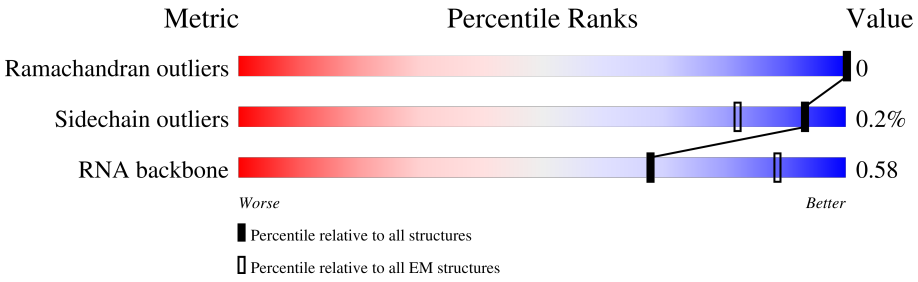
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev92 |
| Mogul | : | 1.8.5 (274361), CSD as541be (2020) |
| MolProbity | : | 4.02b-467 |
| buster-report | : | 1.1.7 (2018) |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| MapQ | : | 1.9.13 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.36.2 |

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.44 Å.

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




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

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

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | A | 254 | 6% 84% 16% |
| 2 | 1 | 3396 | 14% 72% 15% 12% |
| 3 | 2 | 158 | 5% 81% 19% |
| 4 | 3 | 121 | 73% 79% 20% |
| 5 | 5 | 114 | 64% 64% 36% |
| 6 | 6 | 74 | 62% 54% 23% 22% |
| 7 | 8 | 165 | 85% 96% |
| 8 | 9 | 175 | 22% 67% 33% |

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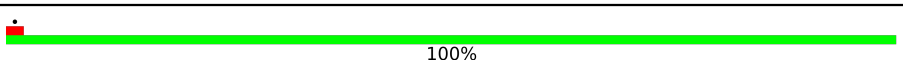
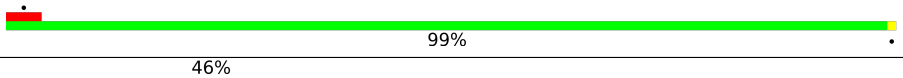
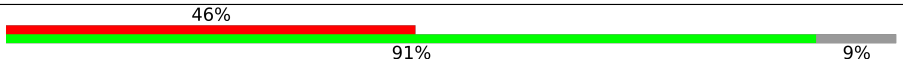
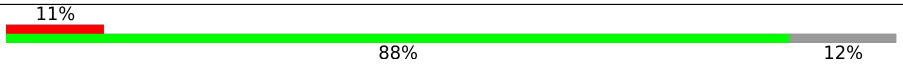
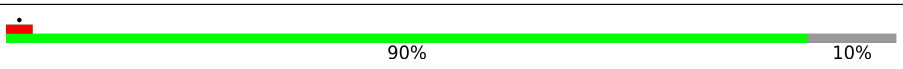
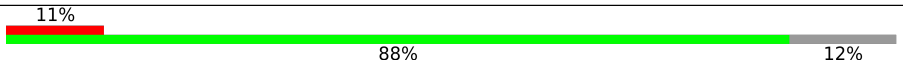
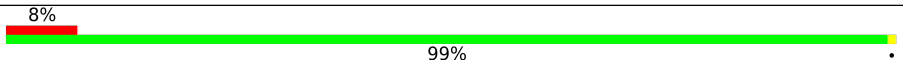
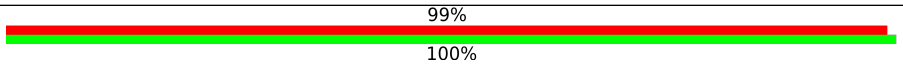
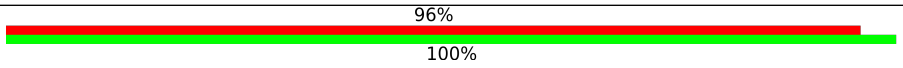
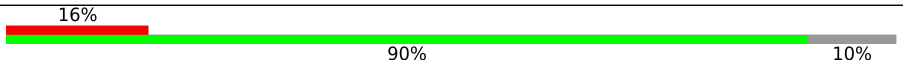
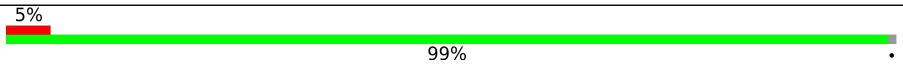
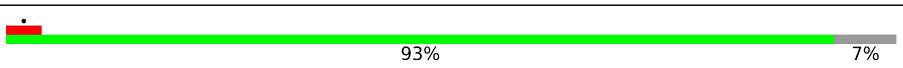
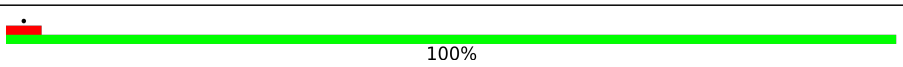
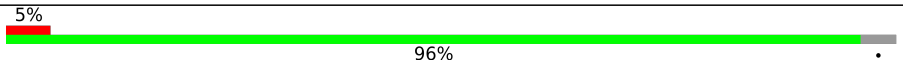
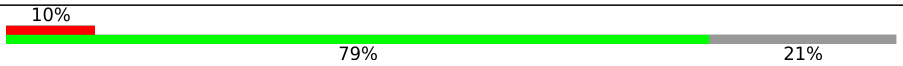
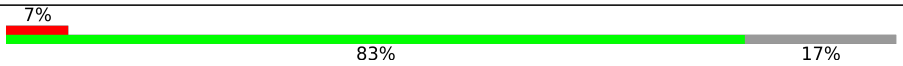
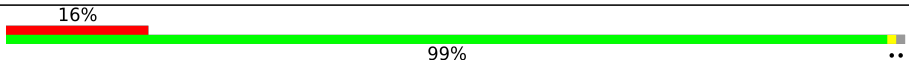
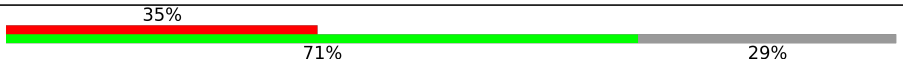
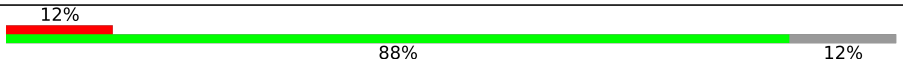
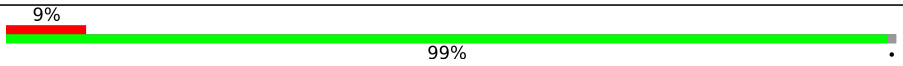
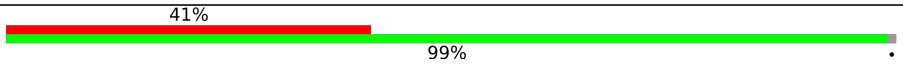
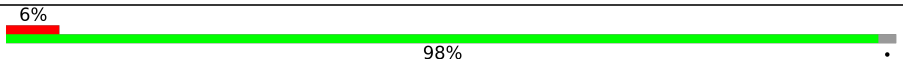
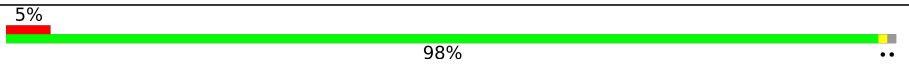
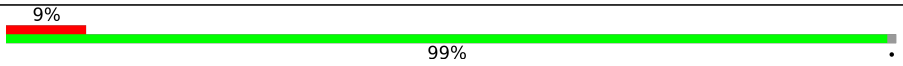
| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 9 | B | 386 |   |
| 10 | C | 362 |   |
| 11 | D | 297 |   |
| 12 | E | 176 |   |
| 13 | F | 244 |   |
| 14 | G | 256 |   |
| 15 | H | 191 |   |
| 16 | I | 131 |   |
| 17 | J | 171 |   |
| 18 | K | 339 | |
| 19 | L | 199 |   |
| 20 | M | 138 |   |
| 21 | N | 203 |   |
| 22 | O | 197 |   |
| 23 | P | 183 |   |
| 24 | Q | 186 |   |
| 25 | R | 189 |   |
| 26 | S | 172 |   |
| 27 | T | 160 |   |
| 28 | U | 121 |   |
| 29 | V | 137 |   |
| 30 | W | 236 |   |
| 31 | X | 142 |   |
| 32 | Y | 127 |   |
| 33 | Z | 136 |   |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 34 | a | 149 | 12% 62% 38% |
| 35 | b | 647 | 20% 99% |
| 36 | c | 105 | 20% 92% 8% |
| 37 | d | 113 | 10% 95% 5% |
| 38 | e | 130 | 5% 98% |
| 39 | f | 107 | 99% |
| 40 | g | 120 | 9% 93% 7% |
| 41 | h | 120 | 99% |
| 42 | i | 99 | 25% 100% |
| 43 | j | 87 | 97% |
| 44 | k | 78 | 26% 99% |
| 45 | l | 50 | 100% |
| 46 | m | 472 | 21% 99% |
| 47 | n | 605 | 32% 61% 39% |
| 48 | o | 220 | 42% 60% 40% |
| 49 | p | 92 | 7% 98% |
| 50 | q | 455 | 26% 34% 66% |
| 51 | r | 261 | 7% 88% 12% |
| 52 | s | 520 | 7% 14% 86% |
| 53 | t | 321 | 73% 89% 11% |
| 54 | u | 199 | 5% 75% 25% |
| 55 | v | 344 | 45% 85% 15% |
| 56 | w | 202 | 46% 96% |
| 57 | x | 515 | 37% 98% |
| 58 | y | 244 | 9% 100% |

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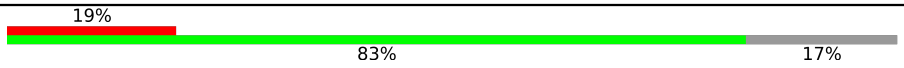
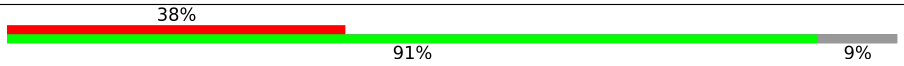
| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 59 | z | 105 |   |
| 60 | 4 | 592 |   |

# 2 Entry composition (i)

There are 66 unique types of molecules in this entry. The entry contains 157839 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 L2-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 1 | A | 213 | 1634 | 1023 | 326 | 284 | 1 | 0 | 0 |

- Molecule 2 is a RNA chain called 25S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 2 | 1 | 2986 | 63938 | 28571 | 11549 | 20832 | 2986 | 0 | 0 |

- Molecule 3 is a RNA chain called 5.8S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 3 | 2 | 158 | 3353 | 1500 | 586 | 1109 | 158 | 0 | 0 |

- Molecule 4 is a RNA chain called 5S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 4 | 3 | 121 | 2579 | 1152 | 461 | 845 | 121 | 0 | 0 |

- Molecule 5 is a protein called rRNA-processing protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 5 | 5 | 73 | 645 | 395 | 133 | 114 | 3 | 0 | 0 |

- Molecule 6 is a RNA chain called ITS2 rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 6 | 6 | 58 | 1227 | 550 | 210 | 409 | 58 | 0 | 0 |

- Molecule 7 is a protein called 60S ribosomal protein L12-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 7 | 8 | 158 | Total | C | N | O | S | 0 | 0 |
| | | | 1196 | 750 | 216 | 228 | 2 | | |

- Molecule 8 is a protein called Ribosome biogenesis protein ALB1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 8 | 9 | 118 | Total | C | N | O | 0 | 0 |
| | | | 937 | 590 | 181 | 166 | | |

- Molecule 9 is a protein called 60S ribosomal protein L3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 9 | B | 386 | Total | C | N | O | S | 0 | 0 |
| | | | 3081 | 1956 | 584 | 533 | 8 | | |

- Molecule 10 is a protein called 60S ribosomal protein L4-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 10 | C | 361 | Total | C | N | O | S | 0 | 0 |
| | | | 2749 | 1730 | 522 | 494 | 3 | | |

- Molecule 11 is a protein called 60S ribosomal protein L5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 11 | D | 270 | Total | C | N | O | S | 0 | 0 |
| | | | 2180 | 1379 | 382 | 417 | 2 | | |

- Molecule 12 is a protein called 60S ribosomal protein L6-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 12 | E | 155 | Total | C | N | O | S | 0 | 0 |
| | | | 1230 | 795 | 221 | 213 | 1 | | |

- Molecule 13 is a protein called 60S ribosomal protein L7-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 13 | F | 219 | Total | C | N | O | S | 0 | 0 |
| | | | 1761 | 1138 | 320 | 302 | 1 | | |

- Molecule 14 is a protein called 60S ribosomal protein L8-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 14 | G | 224 | Total | C | N | O | S | 0 | 0 |
| | | | 1753 | 1122 | 314 | 314 | 3 | | |

- Molecule 15 is a protein called 60S ribosomal protein L9-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 15 | H | 191 | Total | C | N | O | S | 0 | 0 |
| | | | 1518 | 963 | 274 | 277 | 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 |
| | | | 1059 | 662 | 195 | 198 | 4 | | |

- Molecule 17 is a protein called 60S ribosomal protein L11-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 17 | J | 171 | Total | C | N | O | S | 0 | 0 |
| | | | 1368 | 856 | 256 | 252 | 4 | | |

- Molecule 18 is a protein called Proteasome-interacting protein CIC1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 18 | K | 268 | Total | C | N | O | S | 0 | 0 |
| | | | 2155 | 1387 | 355 | 409 | 4 | | |

- Molecule 19 is a protein called 60S ribosomal protein L13-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 19 | L | 180 | Total | C | N | O | 0 | 0 |
| | | | 1438 | 892 | 296 | 250 | | |

- Molecule 20 is a protein called 60S ribosomal protein L14-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 20 | M | 137 | Total | C | N | O | S | 0 | 0 |
| | | | 1059 | 678 | 200 | 179 | 2 | | |

- Molecule 21 is a protein called 60S ribosomal protein L15-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 21 | N | 189 | Total | C | N | O | S | 0 | 0 |
| | | | 1620 | 1016 | 342 | 261 | 1 | | |

- Molecule 22 is a protein called 60S ribosomal protein L16-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 22 | O | 197 | Total | C | N | O | S | 0 | 0 |
| | | | 1555 | 1003 | 289 | 262 | 1 | | |

- Molecule 23 is a protein called 60S ribosomal protein L17-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 23 | P | 175 | Total | C | N | O | 0 | 0 |
| | | | 1388 | 862 | 277 | 249 | | |

- Molecule 24 is a protein called 60S ribosomal protein L18-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 24 | Q | 147 | Total | C | N | O | S | 0 | 0 |
| | | | 1136 | 718 | 219 | 198 | 1 | | |

- Molecule 25 is a protein called 60S ribosomal protein L19-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 25 | R | 156 | Total | C | N | O | 0 | 0 |
| | | | 1258 | 781 | 265 | 212 | | |

- Molecule 26 is a protein called 60S ribosomal protein L20-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 26 | S | 171 | Total | C | N | O | S | 0 | 0 |
| | | | 1437 | 925 | 266 | 243 | 3 | | |

- Molecule 27 is a protein called 60S ribosomal protein L21-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 27 | T | 114 | Total | C | N | O | S | 0 | 0 |
| | | | 905 | 568 | 175 | 159 | 3 | | |

- Molecule 28 is a protein called 60S ribosomal protein L22-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 28 | U | 106 | Total<br>844 | C<br>545 | N<br>138 | O<br>161 | 0 | 0 |

- Molecule 29 is a protein called 60S ribosomal protein L23-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 29 | V | 136 | Total<br>1003 | C<br>628 | N<br>189 | O<br>179 | S<br>7 | 0 | 0 |

- Molecule 30 is a protein called Ribosome assembly factor MRT4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 30 | W | 234 | Total<br>1888 | C<br>1194 | N<br>323 | O<br>365 | S<br>6 | 0 | 0 |

- Molecule 31 is a protein called 60S ribosomal protein L25.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 31 | X | 139 | Total<br>1088 | C<br>697 | N<br>194 | O<br>195 | S<br>2 | 0 | 0 |

- Molecule 32 is a protein called 60S ribosomal protein L26-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 32 | Y | 126 | Total<br>993 | C<br>625 | N<br>192 | O<br>176 | 0 | 0 |

- Molecule 33 is a protein called 60S ribosomal protein L27-A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 33 | Z | 135 | Total<br>1092 | C<br>710 | N<br>202 | O<br>180 | 0 | 0 |

- Molecule 34 is a protein called 60S ribosomal protein L28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 34 | a | 92 | Total<br>731 | C<br>477 | N<br>129 | O<br>124 | S<br>1 | 0 | 0 |

- Molecule 35 is a protein called Nucleolar GTP-binding protein 1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 35 | b | 642 | Total | C | N | O | S | 0 | 0 |
| | | | 5185 | 3251 | 938 | 970 | 26 | | |

- Molecule 36 is a protein called 60S ribosomal protein L30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 36 | c | 97 | Total | C | N | O | S | 0 | 0 |
| | | | 743 | 479 | 124 | 139 | 1 | | |

- Molecule 37 is a protein called 60S ribosomal protein L31-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 37 | d | 107 | Total | C | N | O | S | 0 | 0 |
| | | | 873 | 553 | 165 | 154 | 1 | | |

- Molecule 38 is a protein called 60S ribosomal protein L32.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 38 | e | 127 | Total | C | N | O | S | 0 | 0 |
| | | | 1020 | 647 | 205 | 167 | 1 | | |

- Molecule 39 is a protein called 60S ribosomal protein L33-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 39 | f | 106 | Total | C | N | O | S | 0 | 0 |
| | | | 850 | 540 | 165 | 144 | 1 | | |

- Molecule 40 is a protein called 60S ribosomal protein L34-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 40 | g | 112 | Total | C | N | O | S | 0 | 0 |
| | | | 881 | 546 | 179 | 152 | 4 | | |

- Molecule 41 is a protein called 60S ribosomal protein L35-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 41 | h | 119 | Total | C | N | O | S | 0 | 0 |
| | | | 969 | 615 | 186 | 167 | 1 | | |

- Molecule 42 is a protein called 60S ribosomal protein L36-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 42 | i | 99 | Total<br>771 | C<br>481 | N<br>156 | O<br>132 | S<br>2 | 0 | 0 |

- Molecule 43 is a protein called 60S ribosomal protein L37-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 43 | j | 84 | Total<br>665 | C<br>405 | N<br>145 | O<br>110 | S<br>5 | 0 | 0 |

- Molecule 44 is a protein called 60S ribosomal protein L38.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 44 | k | 77 | Total<br>612 | C<br>391 | N<br>115 | O<br>106 | 0 | 0 |

- Molecule 45 is a protein called 60S ribosomal protein L39.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 45 | l | 50 | Total<br>436 | C<br>272 | N<br>97 | O<br>65 | S<br>2 | 0 | 0 |

- Molecule 46 is a protein called Nucleolar GTP-binding protein 2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 46 | m | 466 | Total<br>3754 | C<br>2372 | N<br>681 | O<br>691 | S<br>10 | 0 | 0 |

- Molecule 47 is a protein called Pescadillo homolog.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 47 | n | 369 | Total<br>3014 | C<br>1954 | N<br>521 | O<br>530 | S<br>9 | 0 | 0 |

- Molecule 48 is a protein called Ribosome biogenesis protein 15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 48 | o | 133 | Total<br>1107 | C<br>716 | N<br>198 | O<br>189 | S<br>4 | 0 | 0 |

- Molecule 49 is a protein called 60S ribosomal protein L43-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 49 | p | 91 | Total | C | N | O | S | 0 | 0 |
| | | | 694 | 429 | 138 | 121 | 6 | | |

- Molecule 50 is a protein called Ribosome biogenesis protein NOP53.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 50 | q | 156 | Total | C | N | O | S | 0 | 0 |
| | | | 1298 | 821 | 233 | 243 | 1 | | |

- Molecule 51 is a protein called Ribosome biogenesis protein NSA2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 51 | r | 230 | Total | C | N | O | S | 0 | 0 |
| | | | 1860 | 1177 | 352 | 324 | 7 | | |

- Molecule 52 is a protein called Nuclear GTP-binding protein NUG1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 52 | s | 72 | Total | C | N | O | S | 0 | 0 |
| | | | 602 | 377 | 118 | 104 | 3 | | |

- Molecule 53 is a protein called Ribosome biogenesis protein RLP7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 53 | t | 287 | Total | C | N | O | S | 0 | 0 |
| | | | 2306 | 1459 | 427 | 417 | 3 | | |

- Molecule 54 is a protein called Ribosome biogenesis protein RLP24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 54 | u | 150 | Total | C | N | O | S | 0 | 0 |
| | | | 1265 | 793 | 253 | 210 | 9 | | |

- Molecule 55 is a protein called Ribosome production factor 2 homolog.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 55 | v | 293 | Total | C | N | O | S | 0 | 0 |
| | | | 2366 | 1512 | 415 | 422 | 17 | | |

- Molecule 56 is a protein called Ribosome biogenesis regulatory protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 56 | w | 194 | Total | C | N | O | S | 0 | 0 |
| | | | 1541 | 965 | 277 | 294 | 5 | | |

- Molecule 57 is a protein called RSA4 isoform 1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 57 | x | 504 | Total | C | N | O | S | 0 | 0 |
| | | | 3927 | 2468 | 695 | 743 | 21 | | |

- Molecule 58 is a protein called Eukaryotic translation initiation factor 6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 58 | y | 244 | Total | C | N | O | S | 0 | 0 |
| | | | 1849 | 1146 | 319 | 377 | 7 | | |

- Molecule 59 is a protein called UPF0642 protein YBL028C.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 59 | z | 87 | Total | C | N | O | S | 0 | 0 |
| | | | 714 | 444 | 142 | 127 | 1 | | |

- Molecule 60 is a protein called Probable metalloprotease ARX1.

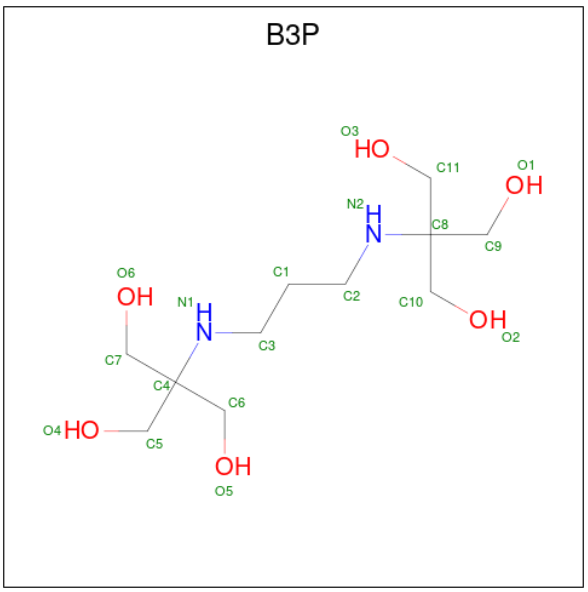
| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 60 | 4 | 538 | Total | C | N | O | S | 0 | 0 |
| | | | 4166 | 2633 | 718 | 800 | 15 | | |

- Molecule 61 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| 61 | 1 | 77 | Total | Mg | 0 |
| | | | 77 | 77 | |
| 61 | R | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 61 | V | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 61 | b | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 61 | m | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |

- Molecule 62 is 2-[3-(2-HYDROXY-1,1-DIHYDROXYMETHYL-ETHYLAMINO)-PROPYL AMINO]-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: B3P) (formula:

$C_{11}H_{26}N_2O_6$).

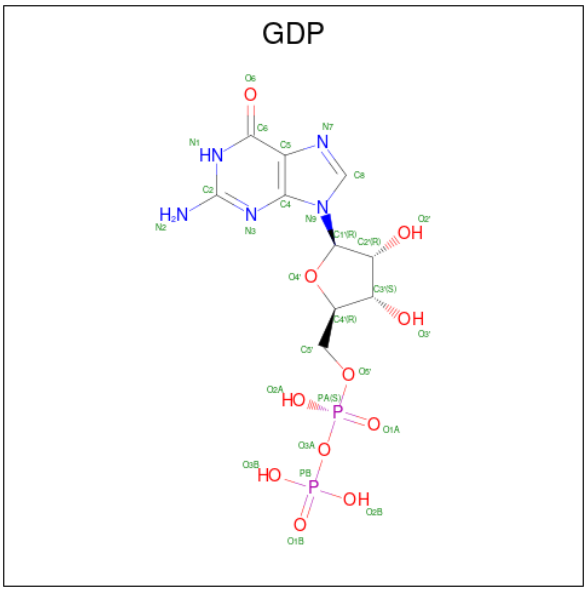



| Mol | Chain | Residues | Atoms | AltConf |
|---|---|---|---|---|
| 62 | 1 | 1 | Total C N O<br>19 11 2 6 | 0 |
| 62 | 1 | 1 | Total C N O<br>19 11 2 6 | 0 |
| 62 | 1 | 1 | Total C N O<br>19 11 2 6 | 0 |

- Molecule 63 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | AltConf |
|---|---|---|---|---|
| 63 | I | 1 | Total Zn<br>1 1 | 0 |
| 63 | g | 1 | Total Zn<br>1 1 | 0 |
| 63 | j | 1 | Total Zn<br>1 1 | 0 |
| 63 | p | 1 | Total Zn<br>1 1 | 0 |
| 63 | u | 1 | Total Zn<br>1 1 | 0 |

- Molecule 64 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$) (labeled as "Ligand of Interest" by depositor).




| Mol | Chain | Residues | Atoms | | | | | AltConf |
|---|---|---|---|---|---|---|---|---|
| 64 | b | 1 | Total | C | N | O | P | 0 |
| | | | 28 | 10 | 5 | 11 | 2 | |
| 64 | m | 1 | Total | C | N | O | P | 0 |
| | | | 28 | 10 | 5 | 11 | 2 | |

- Molecule 65 is POTASSIUM ION (three-letter code: K) (formula: K) (labeled as "Ligand of Interest" by depositor).

| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| 65 | m | 1 | Total | K | 0 |
| | | | 1 | 1 | |

- Molecule 66 is water.

| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| 66 | A | 2 | Total | O | 0 |
| | | | 2 | 2 | |
| 66 | 1 | 330 | Total | O | 0 |
| | | | 330 | 330 | |
| 66 | 2 | 7 | Total | O | 0 |
| | | | 7 | 7 | |
| 66 | B | 1 | Total | O | 0 |
| | | | 1 | 1 | |
| 66 | C | 5 | Total | O | 0 |
| | | | 5 | 5 | |
| 66 | E | 2 | Total | O | 0 |
| | | | 2 | 2 | |

*Continued on next page...*

*Continued from previous page...*

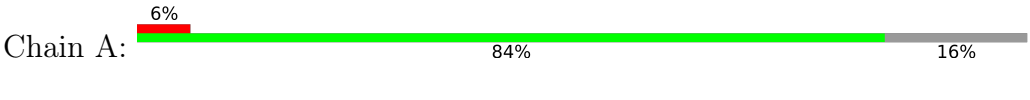
| Mol | Chain | Residues | Atoms | AltConf |
|---|---|---|---|---|
| 66 | F | 3 | Total O<br>3 3 | 0 |
| 66 | N | 3 | Total O<br>3 3 | 0 |
| 66 | O | 1 | Total O<br>1 1 | 0 |
| 66 | R | 1 | Total O<br>1 1 | 0 |
| 66 | V | 3 | Total O<br>3 3 | 0 |
| 66 | X | 1 | Total O<br>1 1 | 0 |
| 66 | b | 3 | Total O<br>3 3 | 0 |
| 66 | d | 1 | Total O<br>1 1 | 0 |
| 66 | j | 6 | Total O<br>6 6 | 0 |
| 66 | m | 4 | Total O<br>4 4 | 0 |

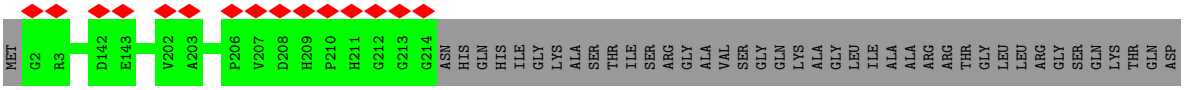
# 3 Residue-property plots (i)

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: 60S ribosomal protein L2-A

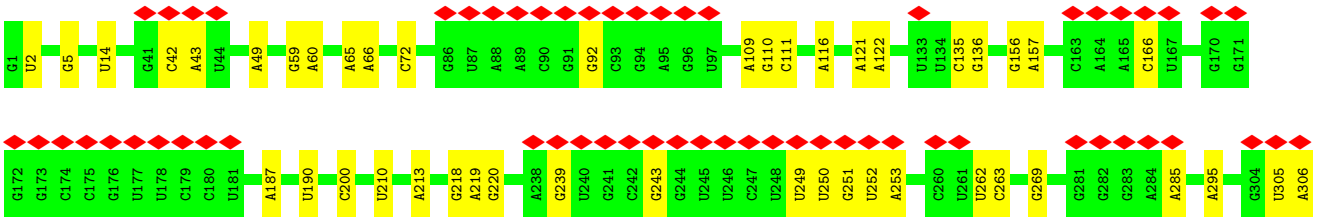
Chain A:



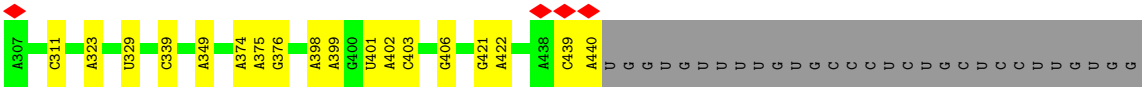

• Molecule 2: 25S rRNA

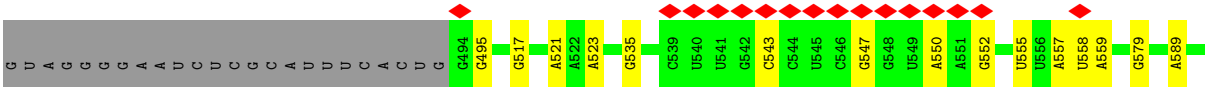
Chain 1:

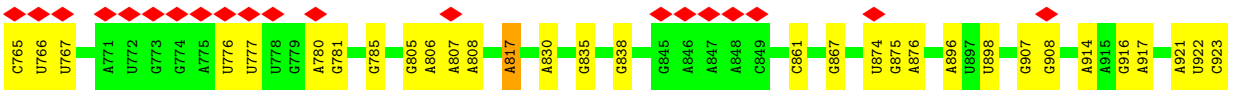


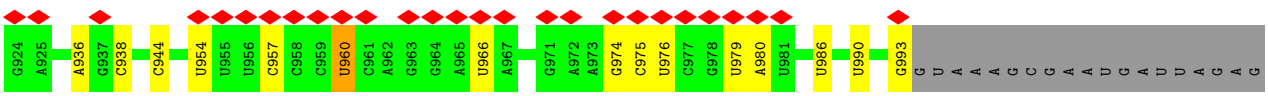


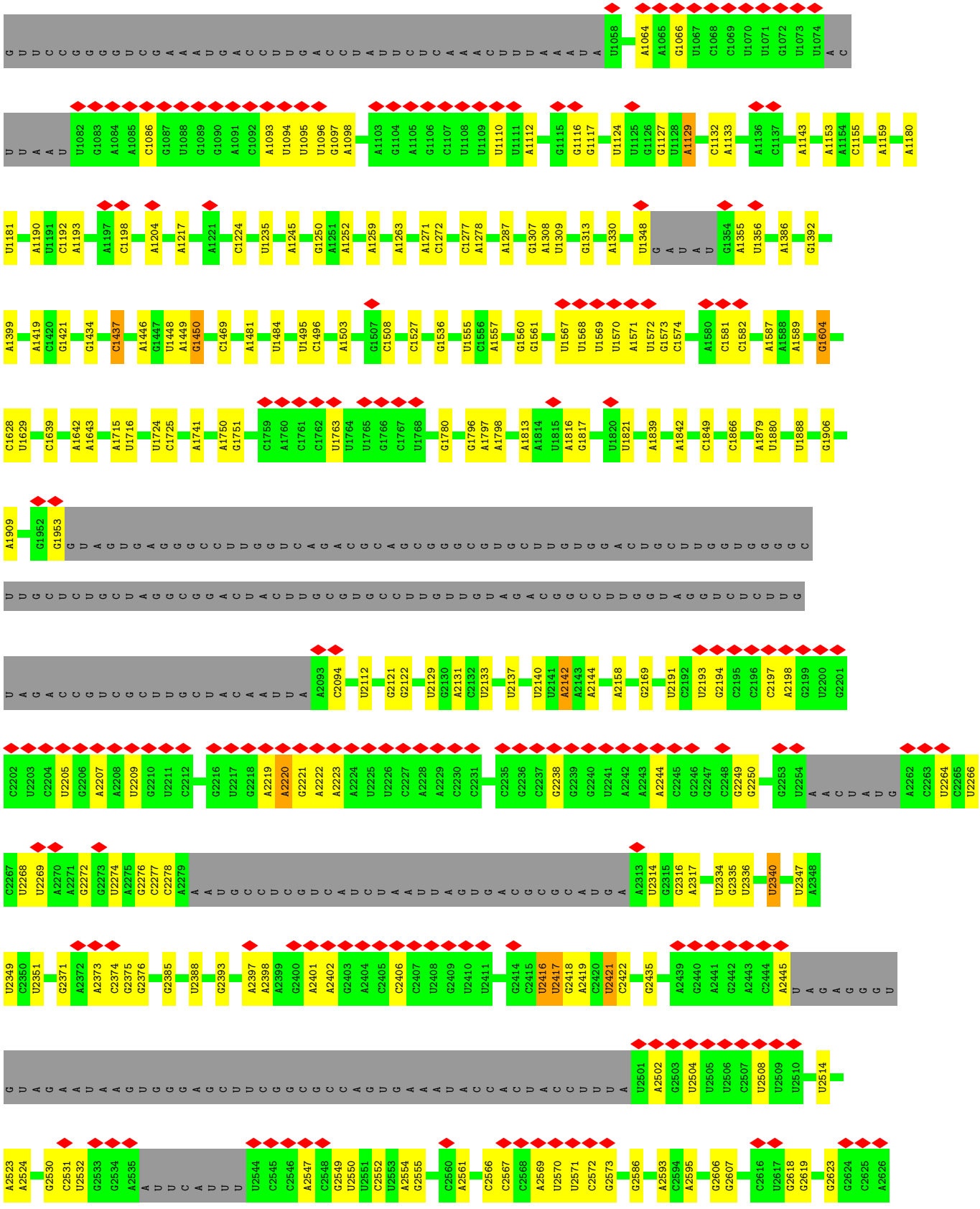


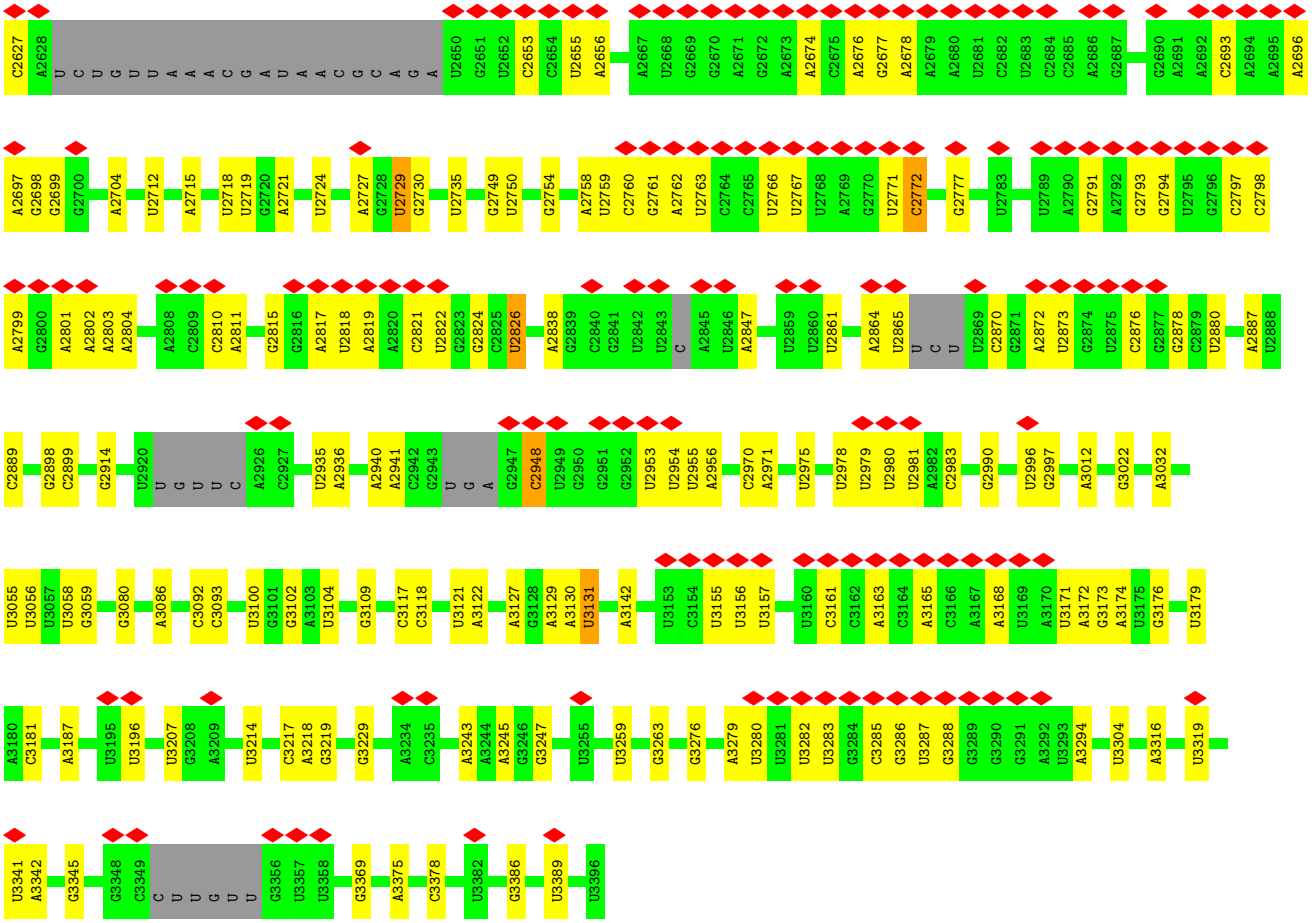






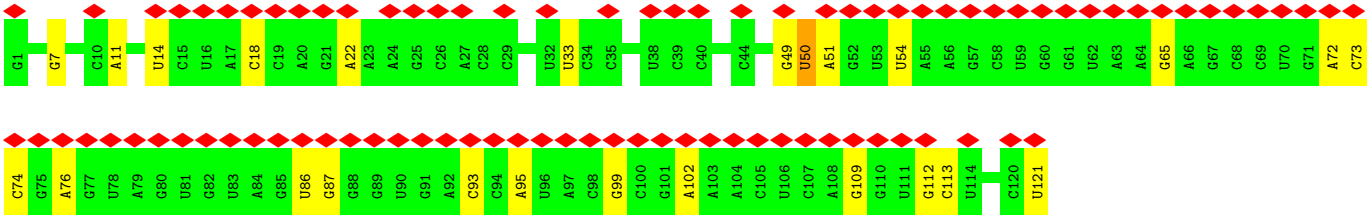


• Molecule 3: 5.8S rRNA

Chain 2:

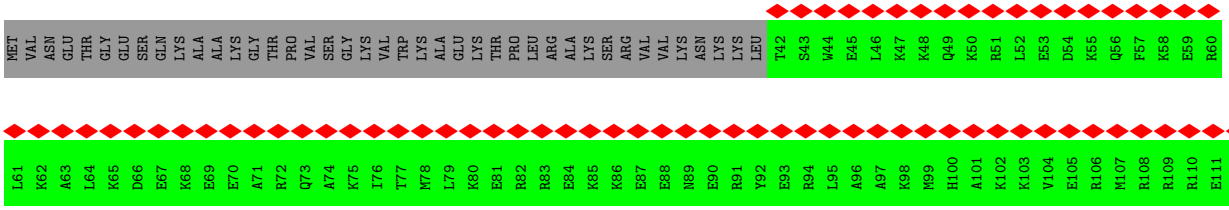
• Molecule 4: 5S rRNA

Chain 3:



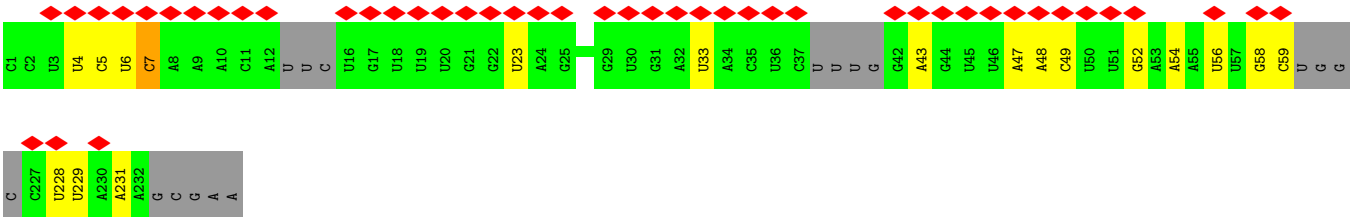
• Molecule 5: rRNA-processing protein

Chain 5:



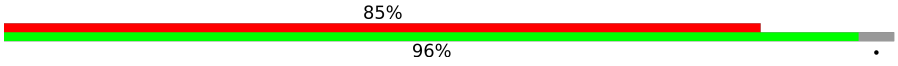

• Molecule 6: ITS2 rRNA

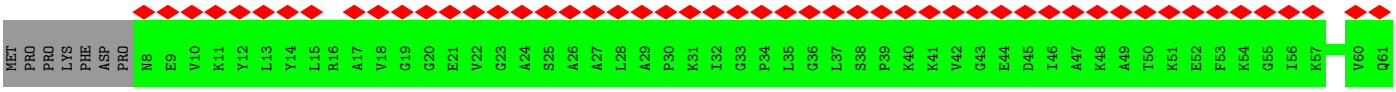
Chain 6:

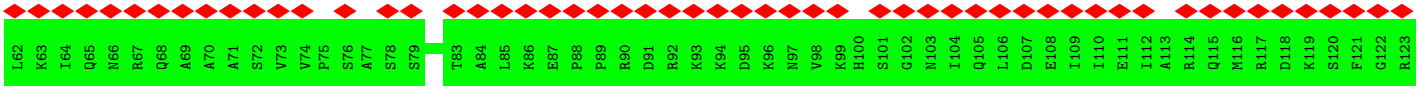


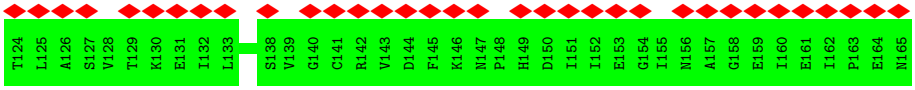

• Molecule 7: 60S ribosomal protein L12-A

Chain 8:



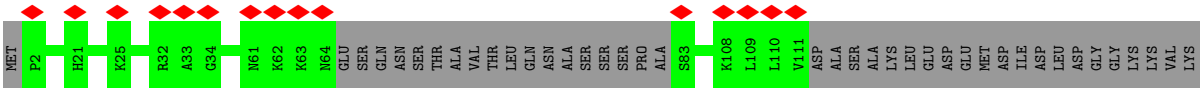



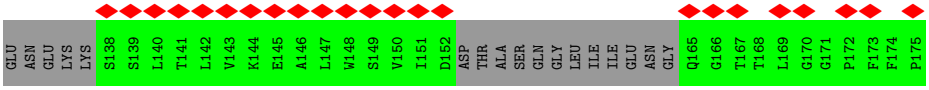




• Molecule 8: Ribosome biogenesis protein ALB1

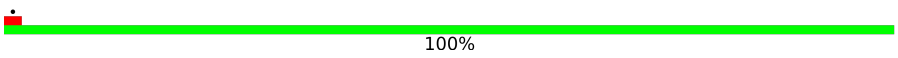
Chain 9:

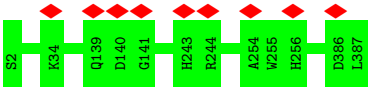



• Molecule 9: 60S ribosomal protein L3

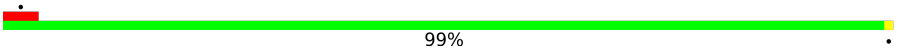
Chain B:

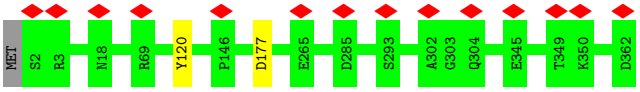





• Molecule 10: 60S ribosomal protein L4-A

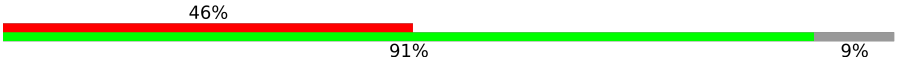
Chain C:

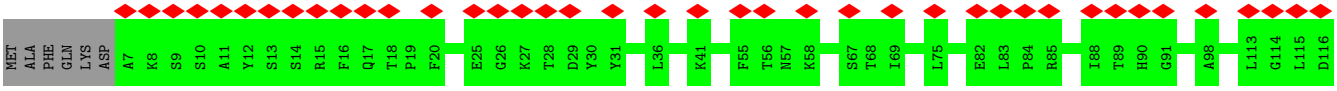


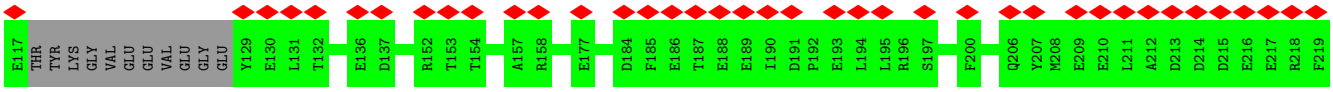



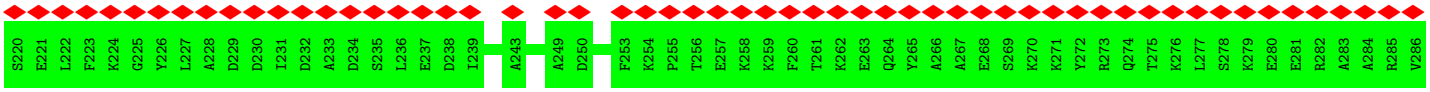

• Molecule 11: 60S ribosomal protein L5

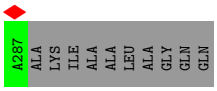
Chain D:



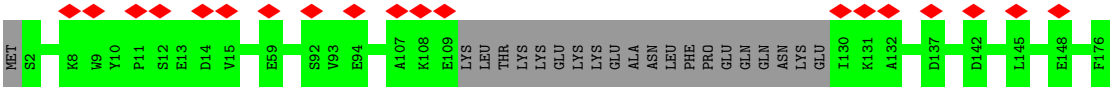



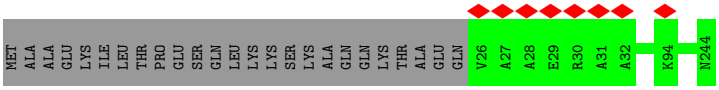

• Molecule 12: 60S ribosomal protein L6-A

Chain E:



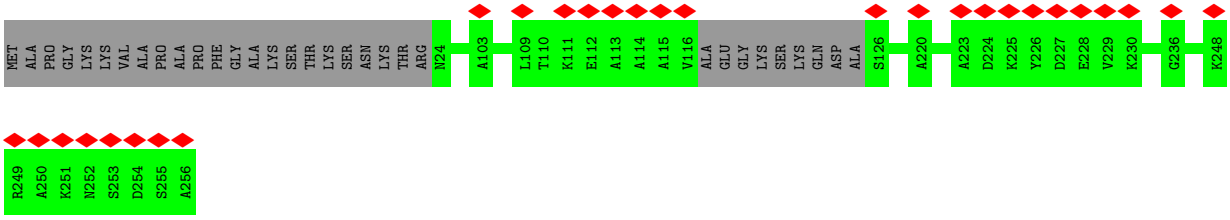

• Molecule 13: 60S ribosomal protein L7-A

Chain F:



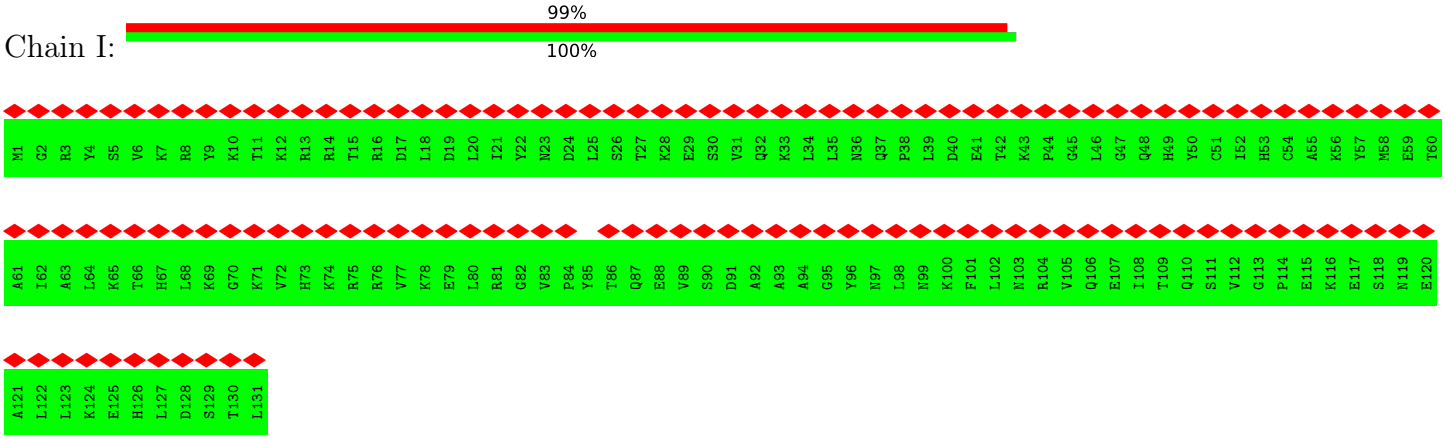

• Molecule 14: 60S ribosomal protein L8-A

Chain G:

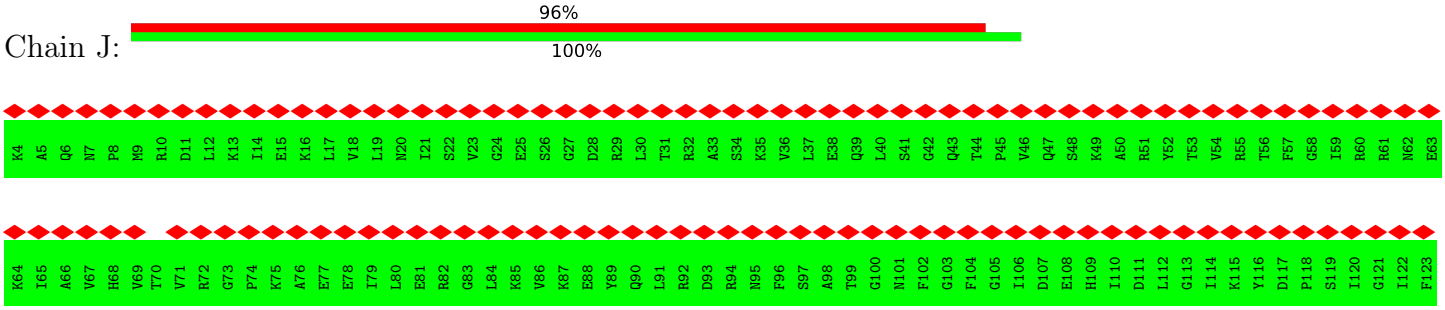



• Molecule 15: 60S ribosomal protein L9-A

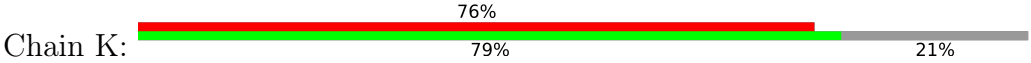
• Molecule 16: Bud site selection protein 20

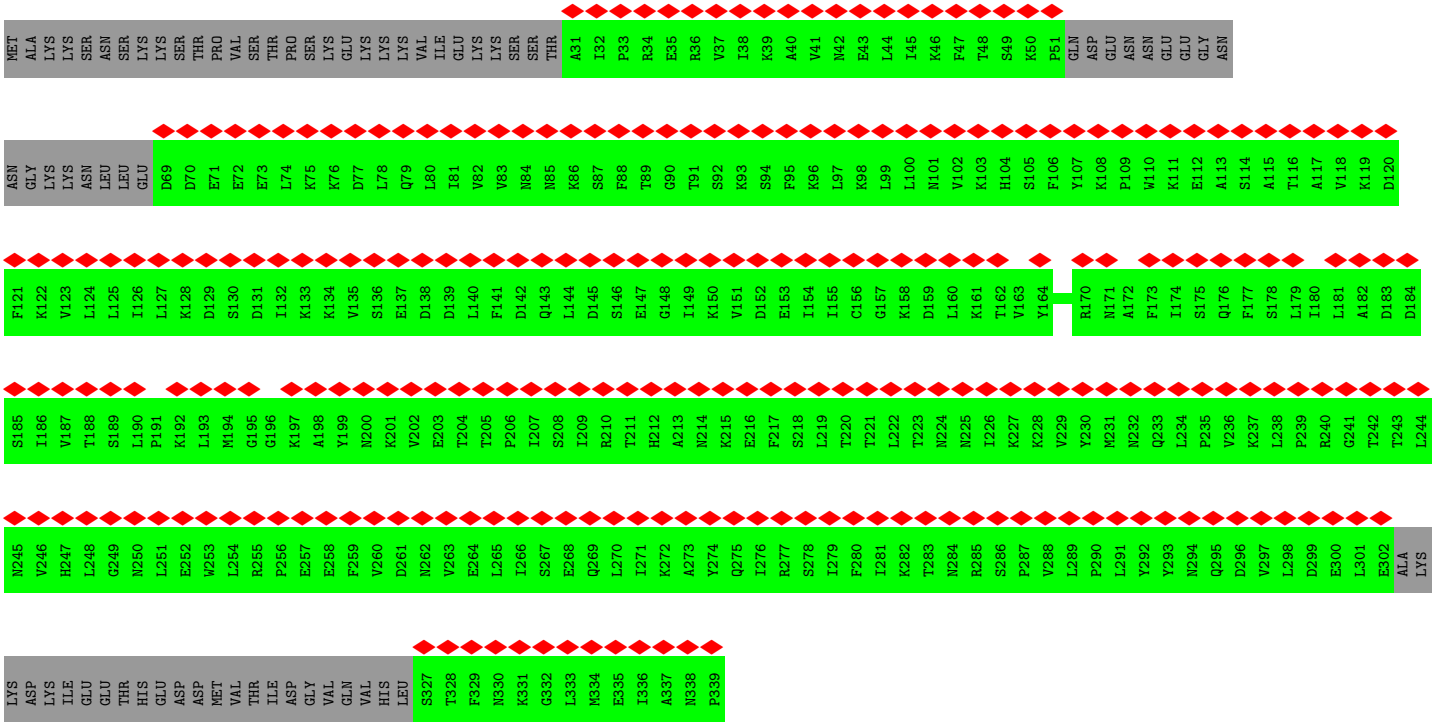



• Molecule 17: 60S ribosomal protein L11-A

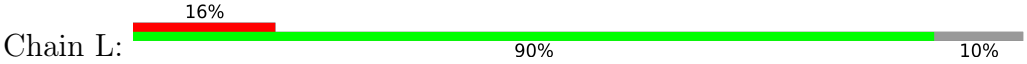


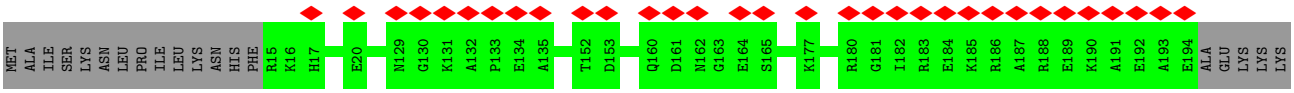

• Molecule 18: Proteasome-interacting protein CIC1



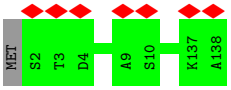



• Molecule 19: 60S ribosomal protein L13-A

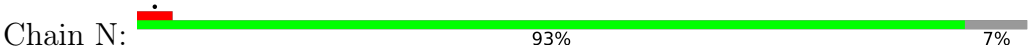


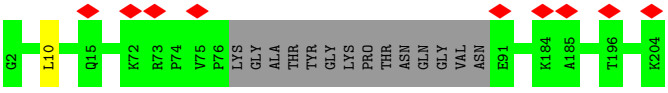




• Molecule 20: 60S ribosomal protein L14-A

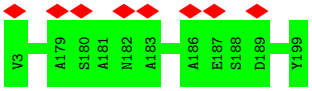



• Molecule 21: 60S ribosomal protein L15-A



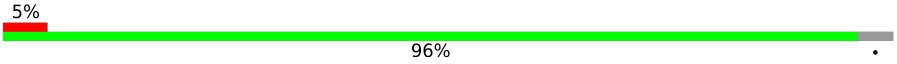



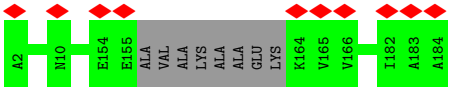

• Molecule 22: 60S ribosomal protein L16-A




• Molecule 23: 60S ribosomal protein L17-A

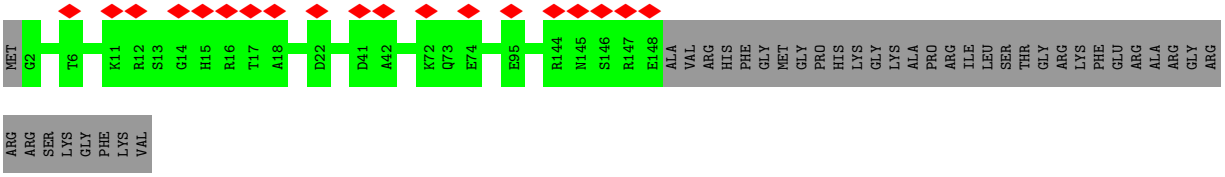
Chain P:



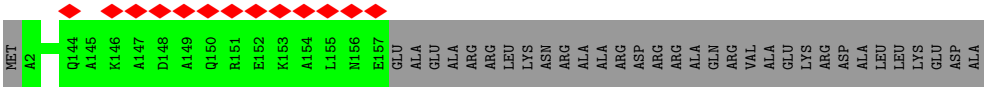

• Molecule 24: 60S ribosomal protein L18-A

Chain Q:



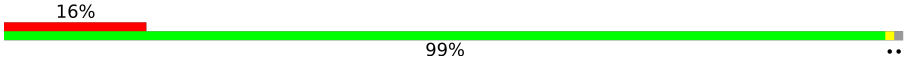

• Molecule 25: 60S ribosomal protein L19-A

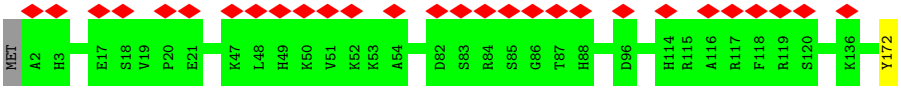
Chain R:




• Molecule 26: 60S ribosomal protein L20-A

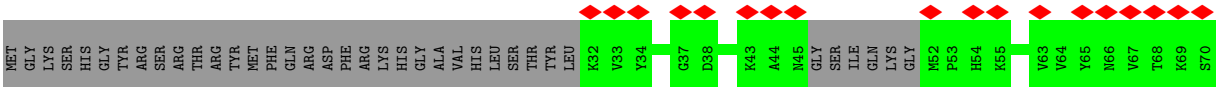
Chain S:

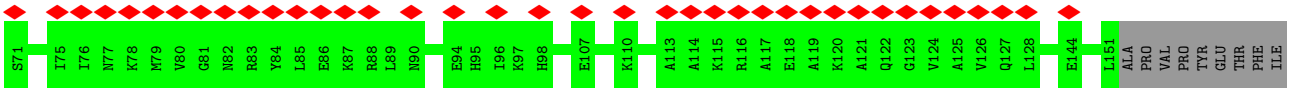



• Molecule 27: 60S ribosomal protein L21-A

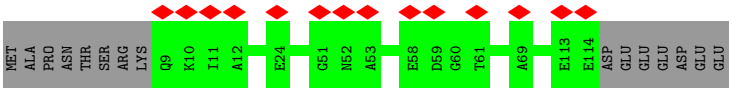
Chain T:



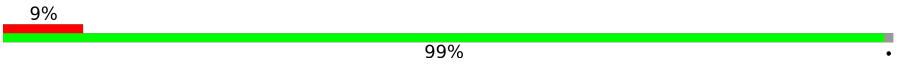

• Molecule 28: 60S ribosomal protein L22-A

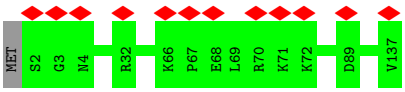
Chain U:




• Molecule 29: 60S ribosomal protein L23-A

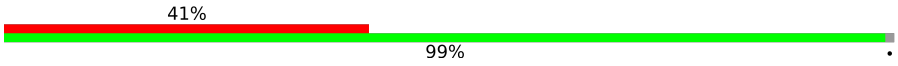
Chain V:

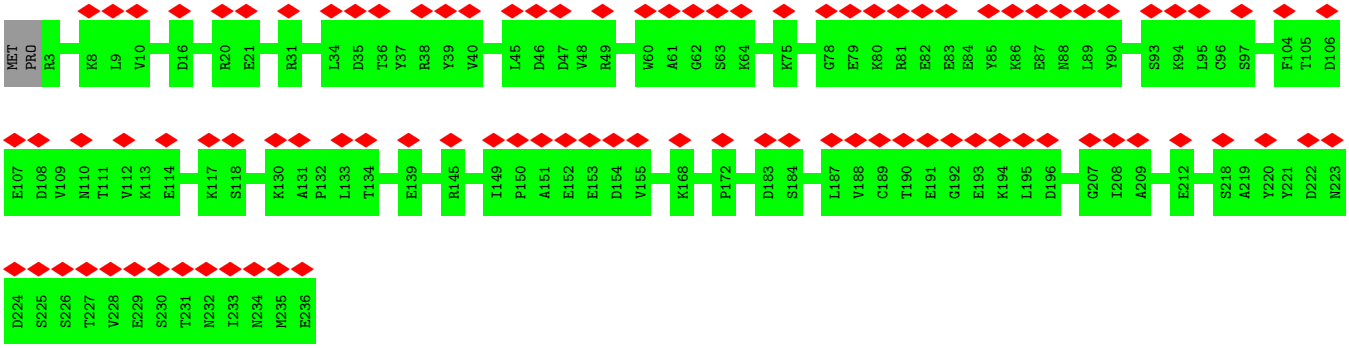



• Molecule 30: Ribosome assembly factor MRT4

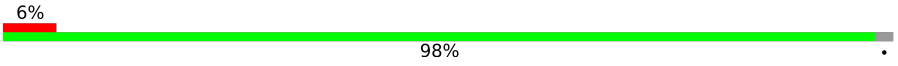
Chain W:

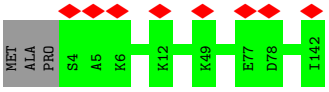



• Molecule 31: 60S ribosomal protein L25

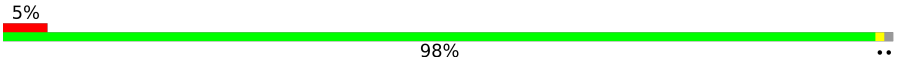
Chain X:

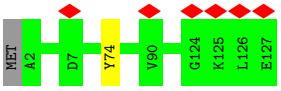



• Molecule 32: 60S ribosomal protein L26-A

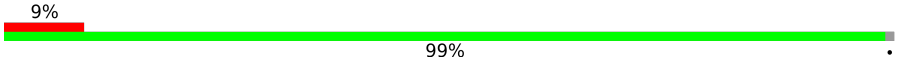
Chain Y:

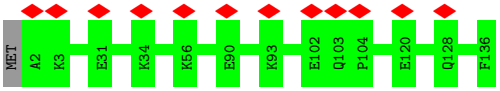



• Molecule 33: 60S ribosomal protein L27-A

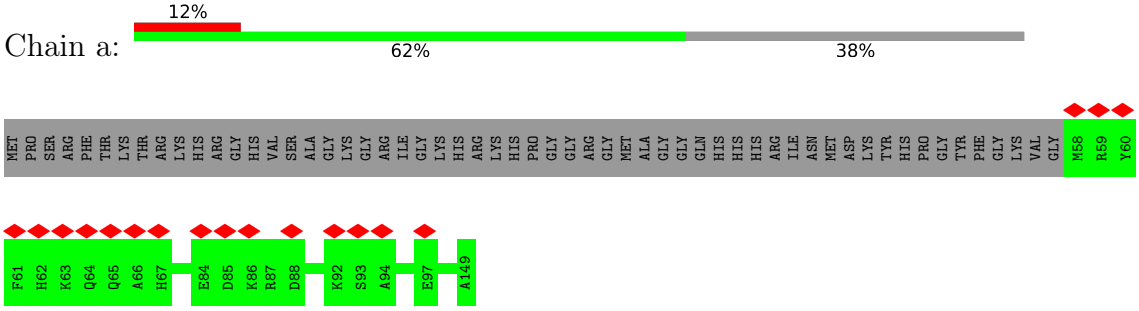
Chain Z:



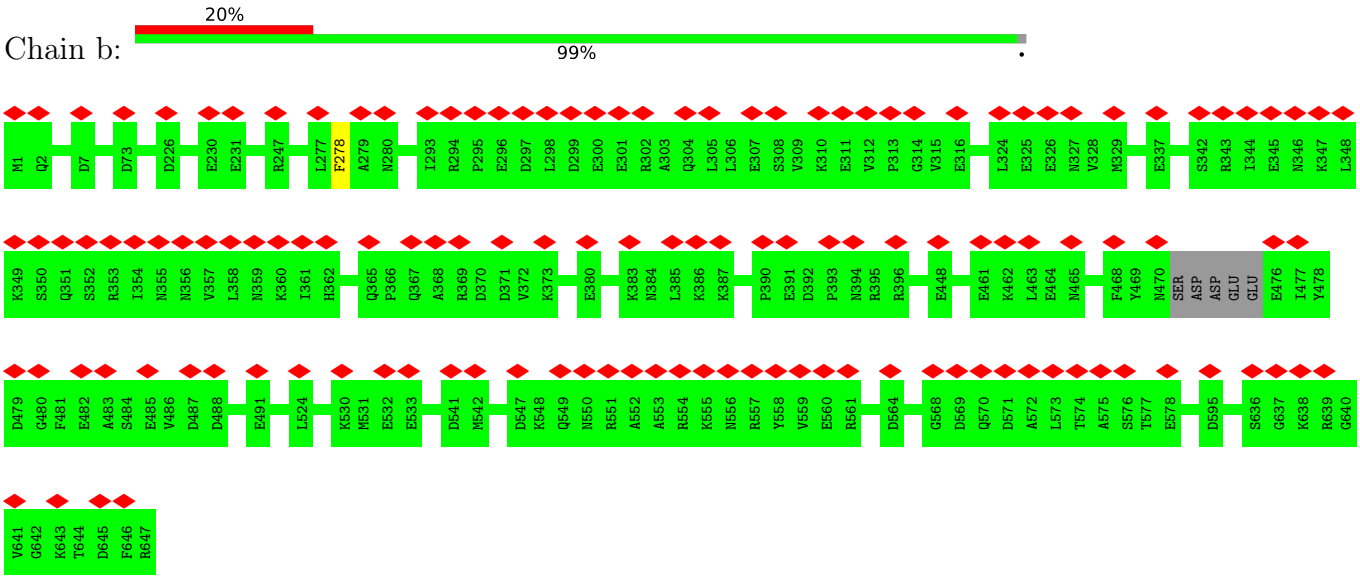
• Molecule 34: 60S ribosomal protein L28

Chain a:



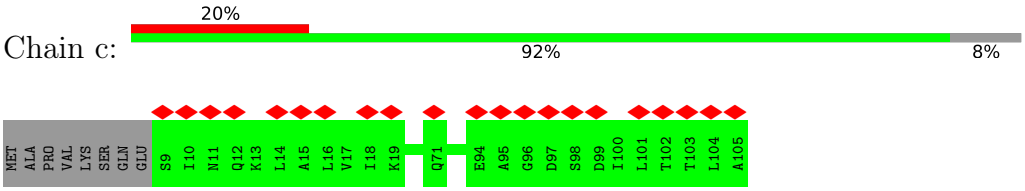

• Molecule 35: Nucleolar GTP-binding protein 1

Chain b:



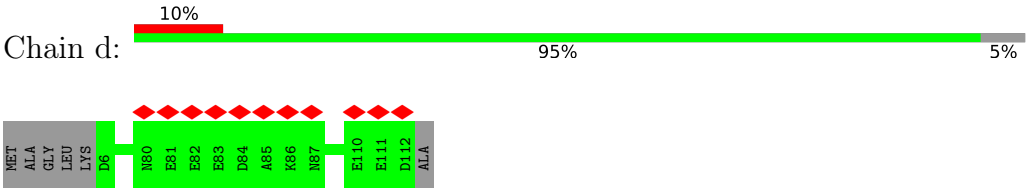

• Molecule 36: 60S ribosomal protein L30

Chain c:



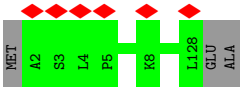

• Molecule 37: 60S ribosomal protein L31-A

Chain d:



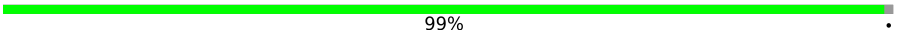

• Molecule 38: 60S ribosomal protein L32

Chain e:



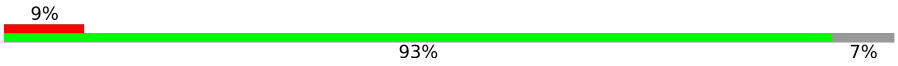

• Molecule 39: 60S ribosomal protein L33-A

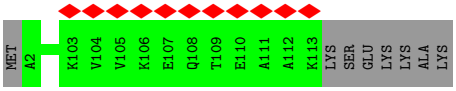
Chain f:



• Molecule 40: 60S ribosomal protein L34-A

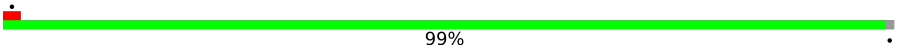
Chain g:

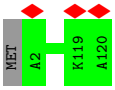



• Molecule 41: 60S ribosomal protein L35-A

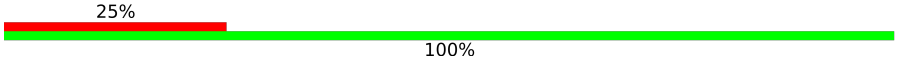
Chain h:

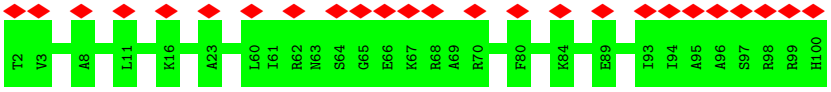



• Molecule 42: 60S ribosomal protein L36-A

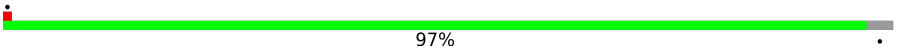
Chain i:

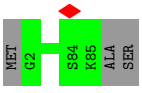



• Molecule 43: 60S ribosomal protein L37-A

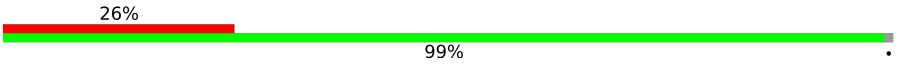
Chain j:

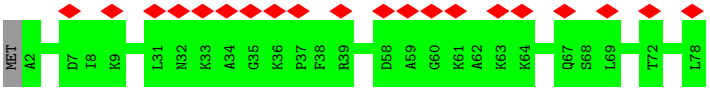



• Molecule 44: 60S ribosomal protein L38

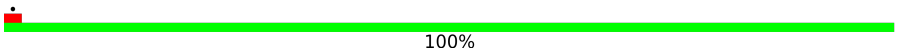
Chain k:



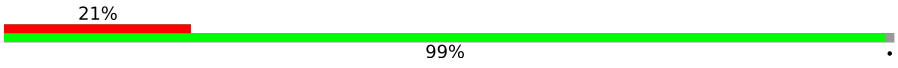

• Molecule 45: 60S ribosomal protein L39

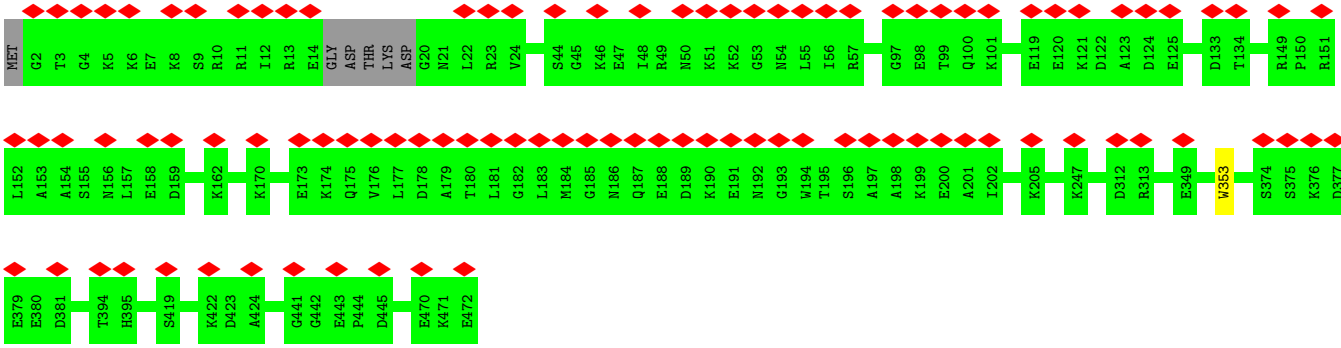
Chain l:



• Molecule 46: Nucleolar GTP-binding protein 2

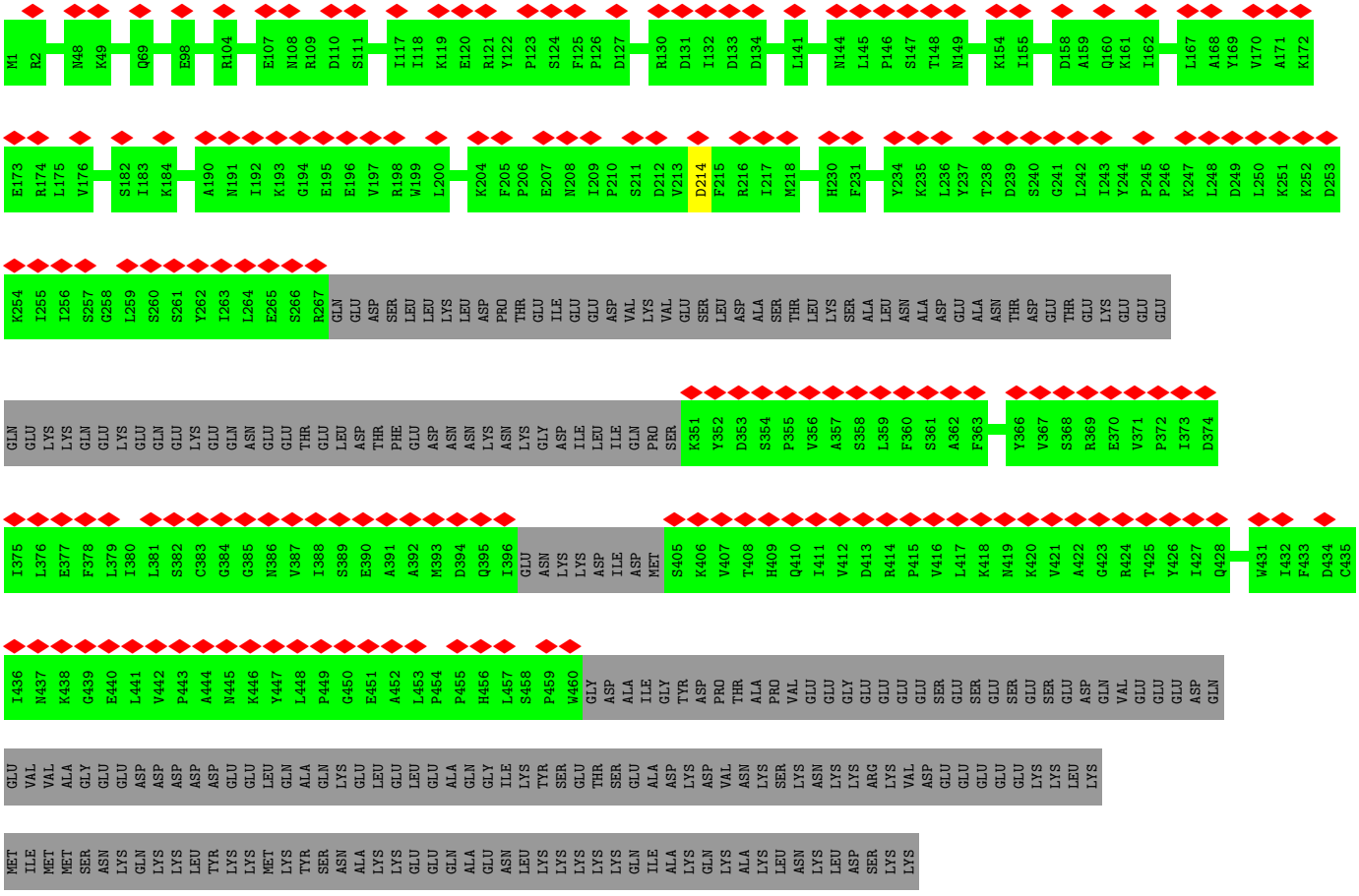
Chain m:



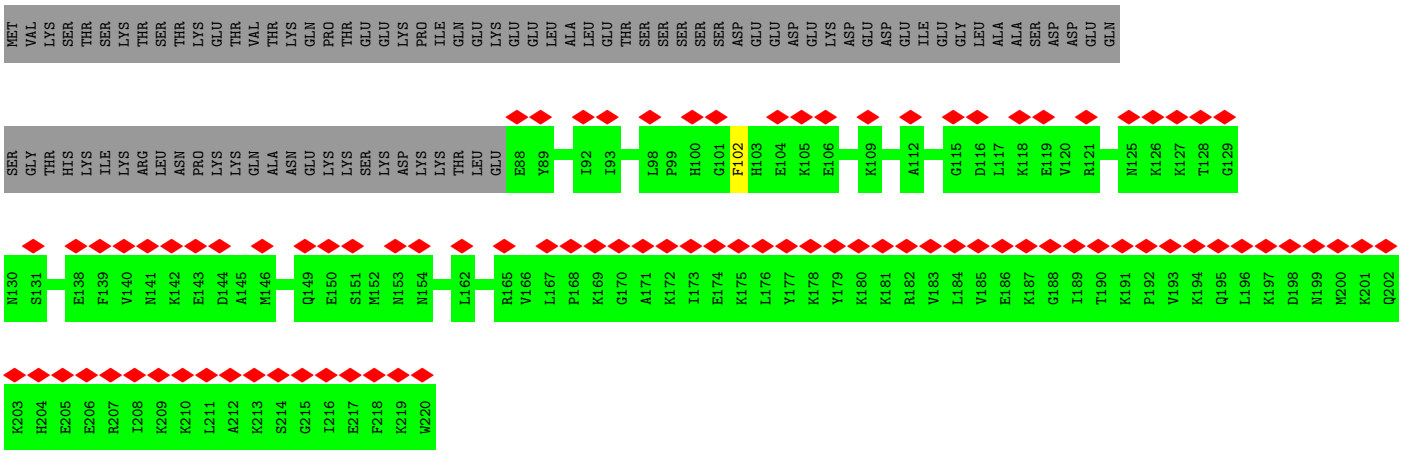

• Molecule 47: Pescadillo homolog

Chain n:



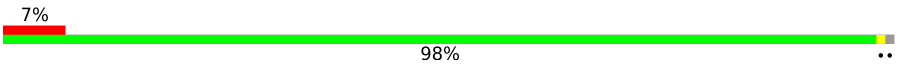
• Molecule 48: Ribosome biogenesis protein 15

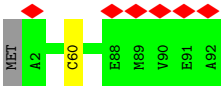
Chain o:




• Molecule 49: 60S ribosomal protein L43-A

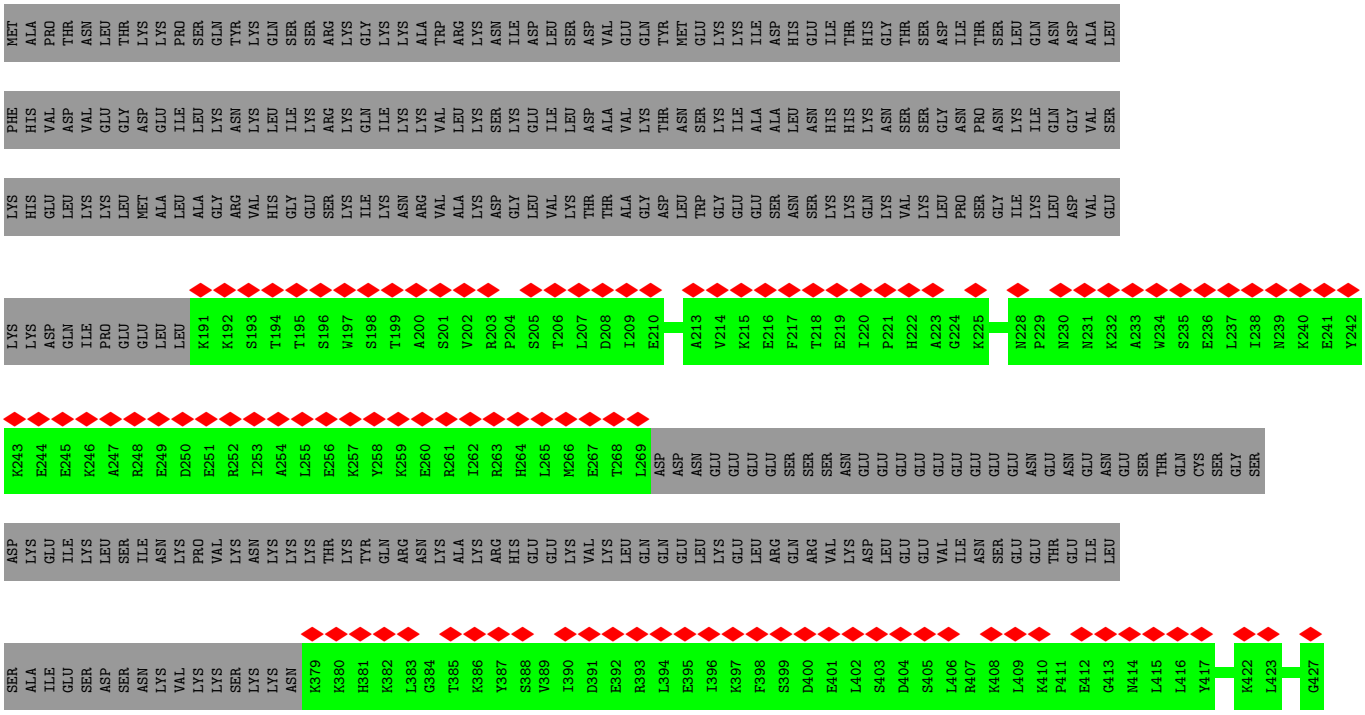
Chain p:

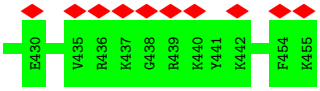



• Molecule 50: Ribosome biogenesis protein NOP53

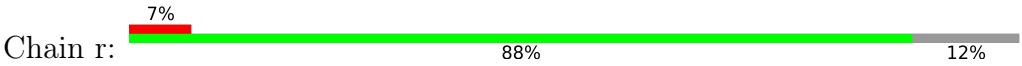
Chain q:

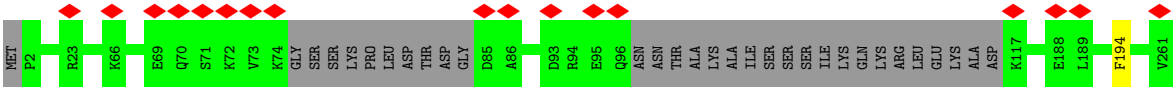





• Molecule 51: Ribosome biogenesis protein NSA2

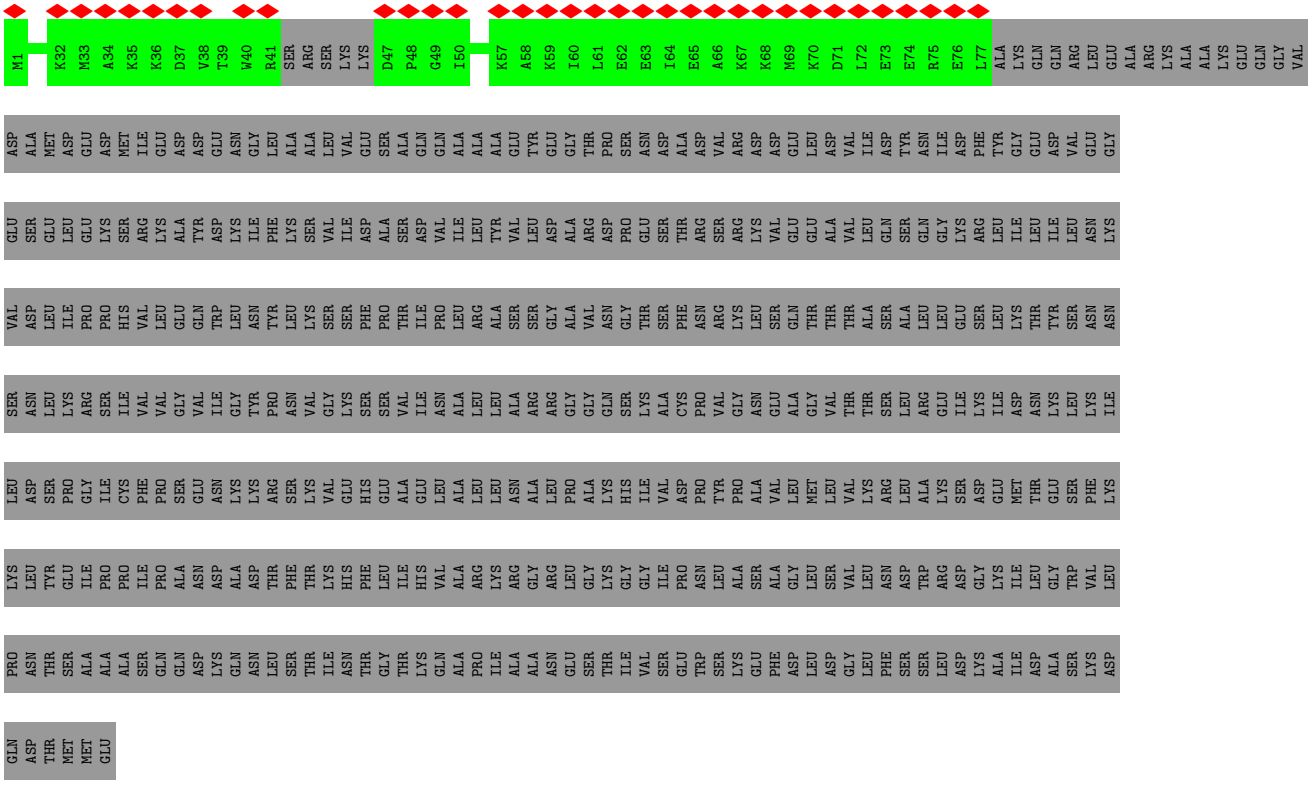
Chain r:



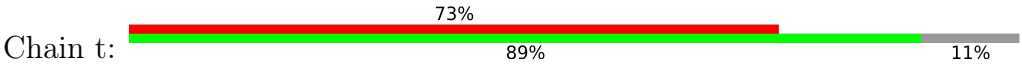

• Molecule 52: Nuclear GTP-binding protein NUG1

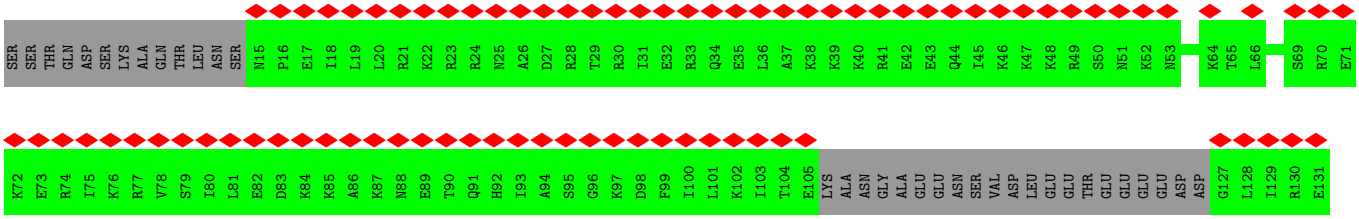
Chain s:

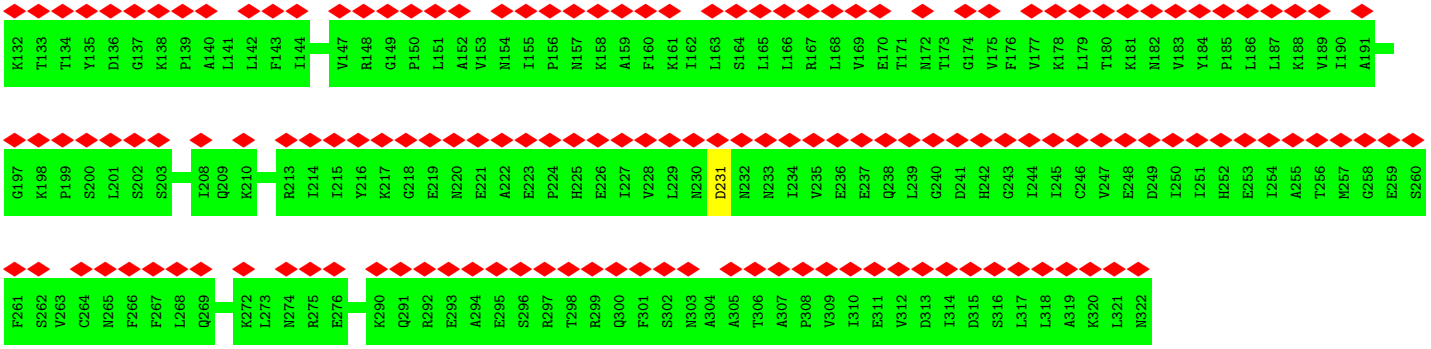



• Molecule 53: Ribosome biogenesis protein RLP7

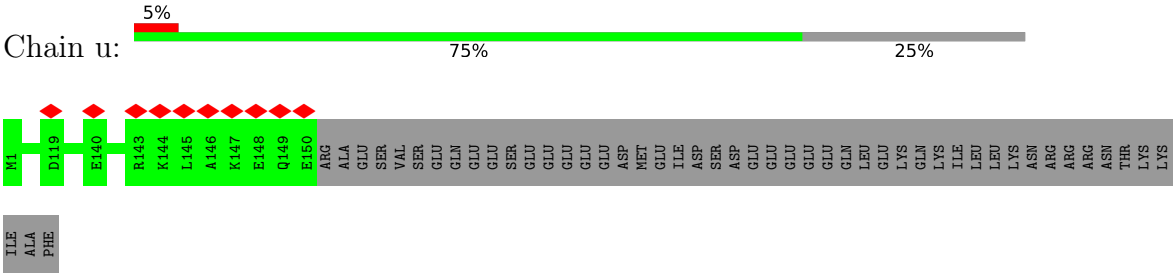
Chain t:



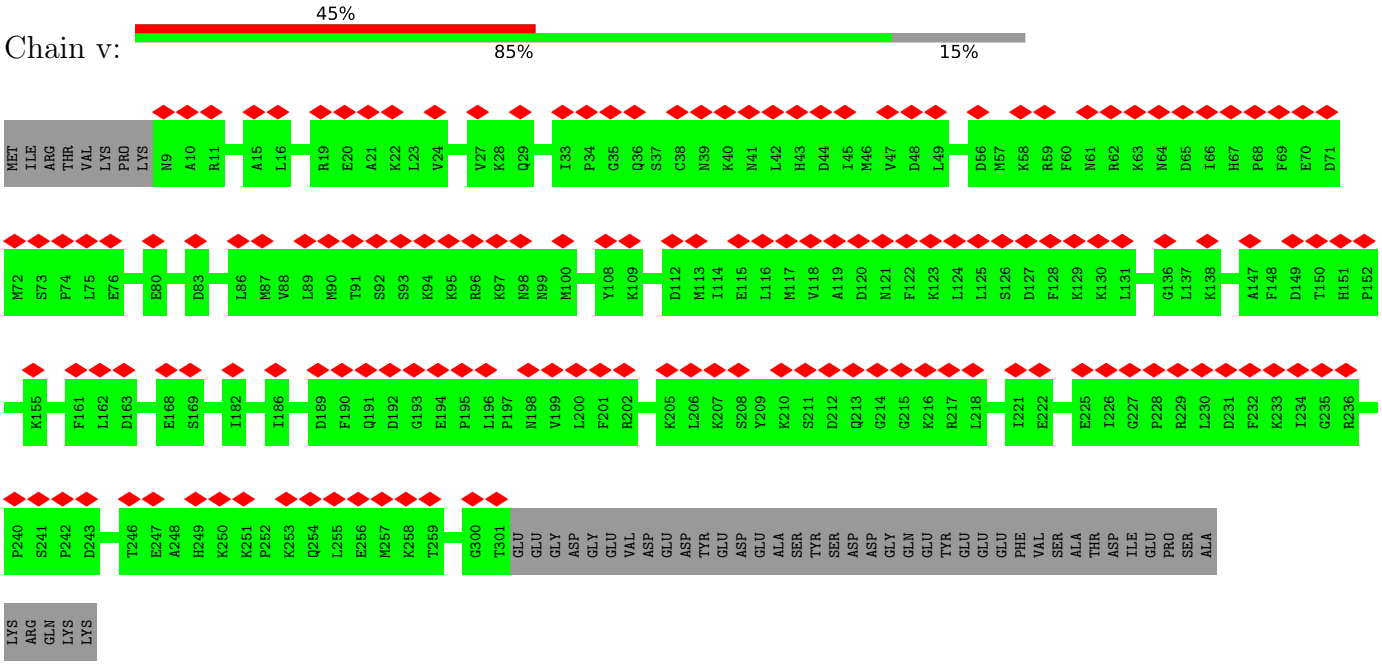





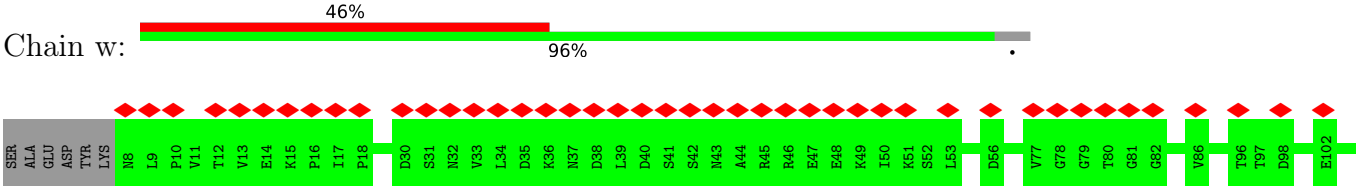

• Molecule 54: Ribosome biogenesis protein RLP24

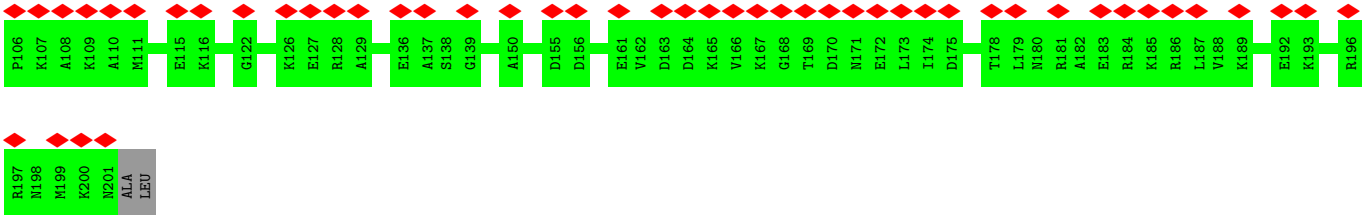



• Molecule 55: Ribosome production factor 2 homolog

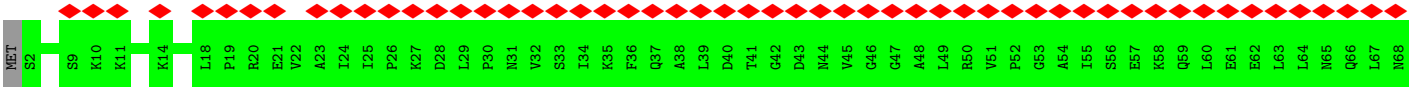


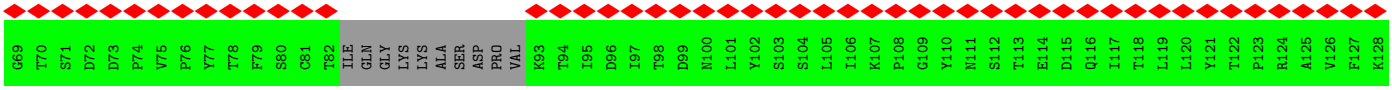

• Molecule 56: Ribosome biogenesis regulatory protein

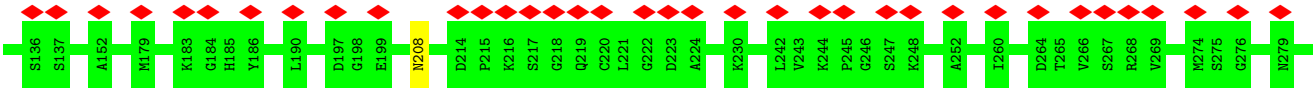


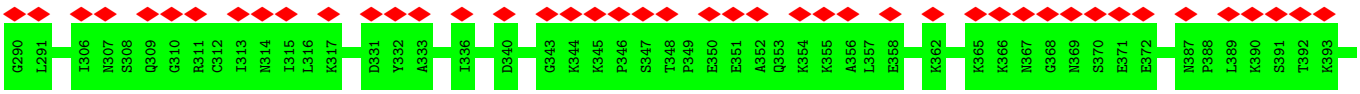


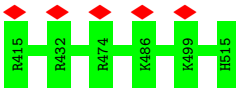

• Molecule 57: RSA4 isoform 1



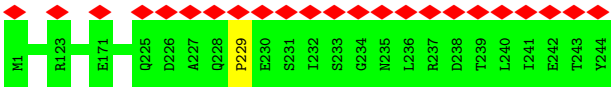



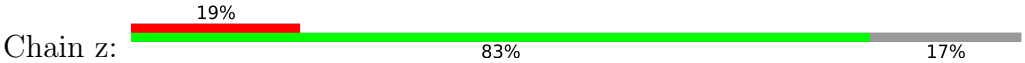



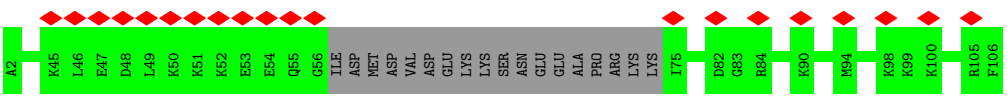




• Molecule 58: Eukaryotic translation initiation factor 6

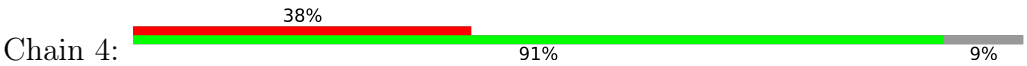


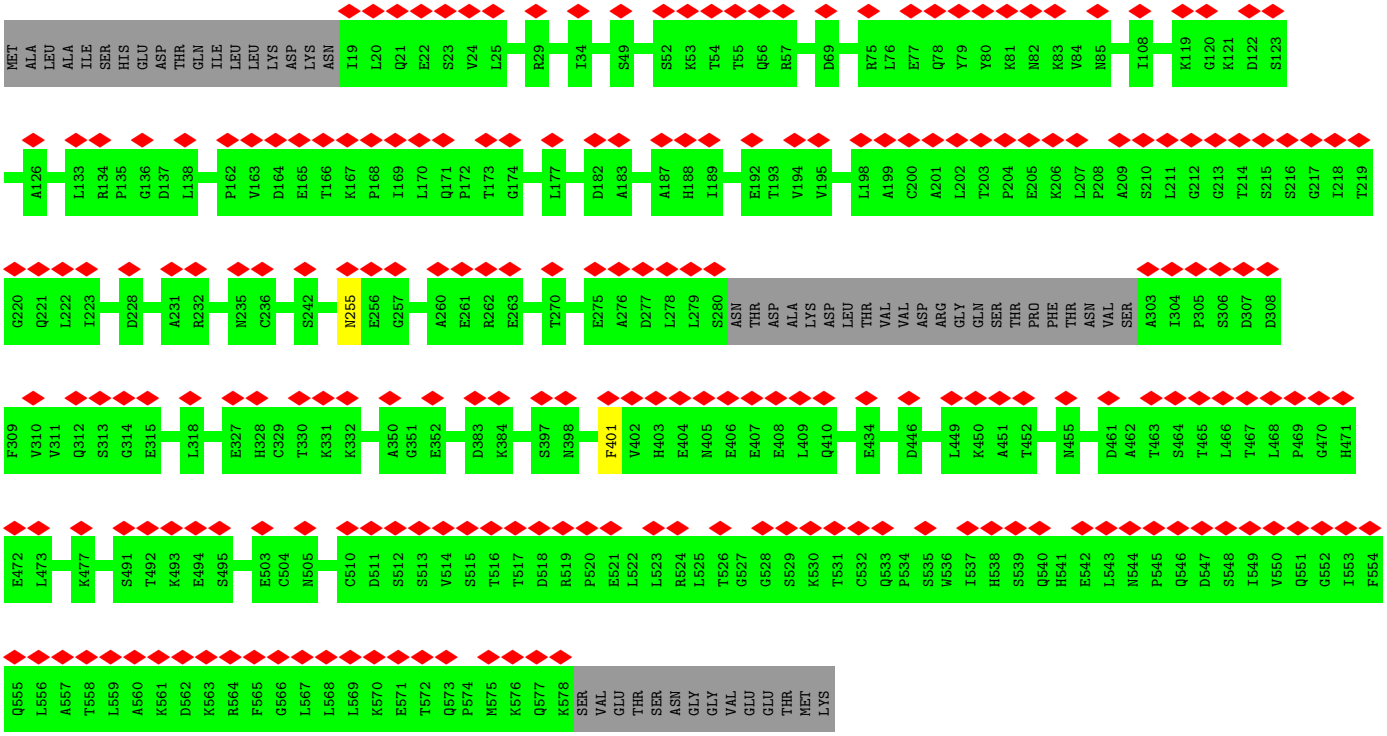

• Molecule 59: UPF0642 protein YBL028C




• Molecule 60: Probable metalloprotease ARX1




MET ALA LEU ALA ILE SER HIS GLU ASP THR GLN ILE LEU LEU LYS ASP LYS ASN I19 L20 Q21 E22 S23 V24 L25 R29 I34 S49 S52 K53 T54 T55 Q56 R57 D69 R75 L76 E77 Q78 Y79 Y80 K81 N82 K83 V84 N85 I108 K119 G120 K121 D122 S123
A126 L133 R134 P135 G136 D137 L138 P162 V163 D164 E165 T166 K167 P168 I169 L170 Q171 P172 T173 G174 L177 D182 A183 A187 H188 I189 E192 T193 V194 V195 L198 A199 C200 A201 L202 T203 P204 E205 K206 L207 P208 A209 S210 L211 G212 G213 T214 S215 S216 G217 I218 T219
G220 Q221 L222 I223 D228 A231 R232 N235 C236 S242 N255 E256 G257 A260 E261 R262 E263 T270 E275 A276 D277 L278 L279 S280 ASN THR ASP ALA LYS ASP LEU THR VAL VAL ASP ARG GLY GLN SER THR PRO PHE THR ASN VAL SER A303 I304 P305 S306 D307 D308
F309 V310 V311 Q312 S313 G314 E315 L318 E327 H328 C329 T330 K331 K332 A350 G351 E352 D383 K384 S397 N398 F401 V402 H403 E404 N405 E406 E407 E408 L409 Q410 E434 D446 L449 K450 A451 T452 N455 D461 A462 T463 S464 T465 L466 T467 L468 P469 G470 H471
E472 L473 K477 S491 T492 K493 E494 S495 E503 C504 N505 C510 D511 S512 S513 V514 S515 T516 T517 D518 R519 P520 E521 L522 L523 R524 L525 T526 G527 G528 S529 K530 T531 C532 Q533 P534 S535 W536 I537 H538 S539 Q540 H541 E542 L543 N544 P545 Q546 D547 S548 I549 V550 Q551 G552 I553 F554
Q555 L556 A557 T558 L559 A560 K561 D562 K563 R564 F565 G566 L567 L568 L569 K570 E571 T572 Q573 P574 M575 K576 Q577 K578 SER VAL GLU THR SER ASN GLY GLY VAL GLU GLU THR MET LYS

# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, C1 | Depositor |
| Number of particles used | 534641 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | NONE | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/Å^2$) | 1.4 | Depositor |
| Minimum defocus (nm) | 900 | Depositor |
| Maximum defocus (nm) | 2200 | Depositor |
| Magnification | 81000 | Depositor |
| Image detector | GATAN K3 (6k x 4k) | Depositor |
| Maximum map value | 0.272 | Depositor |
| Minimum map value | -0.123 | Depositor |
| Average map value | 0.000 | Depositor |
| Map value standard deviation | 0.009 | Depositor |
| Recommended contour level | 0.032 | Depositor |
| Map size (Å) | 432.00003, 432.00003, 432.00003 | wwPDB |
| Map dimensions | 400, 400, 400 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.08, 1.08, 1.08 | 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: OMG, 1MA, K, OMC, MG, B3P, ZN, 5MC, OMU, A2M, PSU, GDP

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 | A | 0.25 | 0/1666 | 0.56 | 0/2241 |
| 2 | 1 | 0.26 | 0/70311 | 0.82 | 19/109609 (0.0%) |
| 3 | 2 | 0.27 | 0/3724 | 0.79 | 1/5798 (0.0%) |
| 4 | 3 | 0.18 | 0/2861 | 0.77 | 0/4457 |
| 5 | 5 | 0.24 | 0/649 | 0.50 | 0/848 |
| 6 | 6 | 0.22 | 0/1367 | 0.87 | 1/2118 (0.0%) |
| 7 | 8 | 0.25 | 0/1210 | 0.47 | 0/1627 |
| 8 | 9 | 0.24 | 0/948 | 0.46 | 0/1264 |
| 9 | B | 0.25 | 0/3152 | 0.54 | 0/4239 |
| 10 | C | 0.25 | 0/2801 | 0.50 | 0/3792 |
| 11 | D | 0.24 | 0/2227 | 0.49 | 0/3004 |
| 12 | E | 0.25 | 0/1251 | 0.49 | 0/1682 |
| 13 | F | 0.25 | 0/1798 | 0.49 | 0/2420 |
| 14 | G | 0.25 | 0/1784 | 0.46 | 0/2408 |
| 15 | H | 0.25 | 0/1539 | 0.51 | 0/2073 |
| 16 | I | 0.23 | 0/1075 | 0.47 | 0/1443 |
| 17 | J | 0.24 | 0/1389 | 0.52 | 0/1860 |
| 18 | K | 0.24 | 0/2190 | 0.46 | 0/2955 |
| 19 | L | 0.24 | 0/1460 | 0.55 | 0/1960 |
| 20 | M | 0.24 | 0/1074 | 0.50 | 0/1446 |
| 21 | N | 0.24 | 0/1654 | 0.58 | 0/2213 |
| 22 | O | 0.26 | 0/1585 | 0.49 | 0/2128 |
| 23 | P | 0.24 | 0/1410 | 0.55 | 0/1893 |
| 24 | Q | 0.24 | 0/1153 | 0.53 | 0/1555 |
| 25 | R | 0.24 | 0/1275 | 0.52 | 0/1702 |
| 26 | S | 0.25 | 0/1473 | 0.50 | 0/1980 |
| 27 | T | 0.25 | 0/916 | 0.49 | 0/1226 |
| 28 | U | 0.26 | 0/861 | 0.48 | 0/1167 |
| 29 | V | 0.27 | 0/1018 | 0.53 | 0/1369 |
| 30 | W | 0.24 | 0/1920 | 0.48 | 0/2586 |
| 31 | X | 0.25 | 0/1103 | 0.49 | 0/1484 |
| 32 | Y | 0.24 | 0/1004 | 0.53 | 0/1341 |

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | #\|Z\| >5 | RMSZ | #\|Z\| >5 |
| 33 | Z | 0.25 | 0/1118 | 0.46 | 0/1497 |
| 34 | a | 0.24 | 0/747 | 0.46 | 0/1008 |
| 35 | b | 0.25 | 0/5270 | 0.49 | 0/7080 |
| 36 | c | 0.25 | 0/751 | 0.44 | 0/1008 |
| 37 | d | 0.24 | 0/887 | 0.53 | 0/1191 |
| 38 | e | 0.23 | 0/1041 | 0.51 | 0/1394 |
| 39 | f | 0.26 | 0/868 | 0.55 | 0/1168 |
| 40 | g | 0.24 | 0/891 | 0.55 | 0/1191 |
| 41 | h | 0.25 | 0/978 | 0.49 | 0/1301 |
| 42 | i | 0.24 | 0/778 | 0.53 | 0/1034 |
| 43 | j | 0.25 | 0/680 | 0.57 | 0/901 |
| 44 | k | 0.25 | 0/618 | 0.52 | 0/826 |
| 45 | l | 0.23 | 0/443 | 0.58 | 0/588 |
| 46 | m | 0.25 | 0/3828 | 0.49 | 0/5154 |
| 47 | n | 0.25 | 0/3085 | 0.47 | 0/4166 |
| 48 | o | 0.24 | 0/1129 | 0.47 | 0/1502 |
| 49 | p | 0.25 | 0/701 | 0.56 | 0/934 |
| 50 | q | 0.24 | 0/1321 | 0.48 | 0/1766 |
| 51 | r | 0.25 | 0/1892 | 0.51 | 0/2528 |
| 52 | s | 0.24 | 0/608 | 0.49 | 0/798 |
| 53 | t | 0.25 | 0/2333 | 0.50 | 0/3128 |
| 54 | u | 0.26 | 0/1287 | 0.53 | 0/1711 |
| 55 | v | 0.25 | 0/2410 | 0.48 | 0/3220 |
| 56 | w | 0.23 | 0/1565 | 0.46 | 0/2108 |
| 57 | x | 0.24 | 0/4022 | 0.50 | 0/5460 |
| 58 | y | 0.39 | 1/1872 (0.1%) | 0.53 | 0/2548 |
| 59 | z | 0.24 | 0/721 | 0.46 | 0/948 |
| 60 | 4 | 0.24 | 0/4242 | 0.46 | 0/5758 |
| All | All | 0.25 | 1/165934 (0.0%) | 0.68 | 21/239804 (0.0%) |

All (1) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 58 | y | 229 | PRO | N-CD | 13.17 | 1.66 | 1.47 |

The worst 5 of 21 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 2 | 1 | 1495 | U | C2-N1-C1' | 7.61 | 126.84 | 117.70 |
| 2 | 1 | 1496 | C | C2-N1-C1' | 7.31 | 126.84 | 118.80 |
| 2 | 1 | 406 | G | O4'-C1'-N9 | 7.26 | 114.01 | 108.20 |
| 2 | 1 | 1495 | U | C6-N1-C1' | -7.26 | 111.04 | 121.20 |

*Continued on next page...*

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| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 2 | 1 | 922 | U | C2-N1-C1' | 6.71 | 125.75 | 117.70 |

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 5.3 Torsion angles (i)

### 5.3.1 Protein backbone (i)

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

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 1 | A | 211/254 (83%) | 200 (95%) | 11 (5%) | 0 | 100 | 100 |
| 5 | 5 | 71/114 (62%) | 71 (100%) | 0 | 0 | 100 | 100 |
| 7 | 8 | 156/165 (94%) | 153 (98%) | 3 (2%) | 0 | 100 | 100 |
| 8 | 9 | 110/175 (63%) | 109 (99%) | 1 (1%) | 0 | 100 | 100 |
| 9 | B | 384/386 (100%) | 379 (99%) | 5 (1%) | 0 | 100 | 100 |
| 10 | C | 359/362 (99%) | 348 (97%) | 11 (3%) | 0 | 100 | 100 |
| 11 | D | 266/297 (90%) | 259 (97%) | 7 (3%) | 0 | 100 | 100 |
| 12 | E | 151/176 (86%) | 144 (95%) | 7 (5%) | 0 | 100 | 100 |
| 13 | F | 217/244 (89%) | 213 (98%) | 4 (2%) | 0 | 100 | 100 |
| 14 | G | 220/256 (86%) | 217 (99%) | 3 (1%) | 0 | 100 | 100 |
| 15 | H | 189/191 (99%) | 183 (97%) | 6 (3%) | 0 | 100 | 100 |
| 16 | I | 129/131 (98%) | 124 (96%) | 5 (4%) | 0 | 100 | 100 |
| 17 | J | 169/171 (99%) | 166 (98%) | 3 (2%) | 0 | 100 | 100 |
| 18 | K | 262/339 (77%) | 259 (99%) | 3 (1%) | 0 | 100 | 100 |
| 19 | L | 178/199 (89%) | 175 (98%) | 3 (2%) | 0 | 100 | 100 |

*Continued on next page...*

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 20 | M | 135/138 (98%) | 132 (98%) | 3 (2%) | 0 | 100 | 100 |
| 21 | N | 185/203 (91%) | 178 (96%) | 7 (4%) | 0 | 100 | 100 |
| 22 | O | 195/197 (99%) | 193 (99%) | 2 (1%) | 0 | 100 | 100 |
| 23 | P | 171/183 (93%) | 164 (96%) | 7 (4%) | 0 | 100 | 100 |
| 24 | Q | 145/186 (78%) | 143 (99%) | 2 (1%) | 0 | 100 | 100 |
| 25 | R | 154/189 (82%) | 152 (99%) | 2 (1%) | 0 | 100 | 100 |
| 26 | S | 169/172 (98%) | 164 (97%) | 5 (3%) | 0 | 100 | 100 |
| 27 | T | 110/160 (69%) | 107 (97%) | 3 (3%) | 0 | 100 | 100 |
| 28 | U | 104/121 (86%) | 100 (96%) | 4 (4%) | 0 | 100 | 100 |
| 29 | V | 134/137 (98%) | 132 (98%) | 2 (2%) | 0 | 100 | 100 |
| 30 | W | 232/236 (98%) | 229 (99%) | 3 (1%) | 0 | 100 | 100 |
| 31 | X | 137/142 (96%) | 135 (98%) | 2 (2%) | 0 | 100 | 100 |
| 32 | Y | 124/127 (98%) | 119 (96%) | 5 (4%) | 0 | 100 | 100 |
| 33 | Z | 133/136 (98%) | 129 (97%) | 4 (3%) | 0 | 100 | 100 |
| 34 | a | 90/149 (60%) | 87 (97%) | 3 (3%) | 0 | 100 | 100 |
| 35 | b | 638/647 (99%) | 619 (97%) | 19 (3%) | 0 | 100 | 100 |
| 36 | c | 95/105 (90%) | 95 (100%) | 0 | 0 | 100 | 100 |
| 37 | d | 105/113 (93%) | 104 (99%) | 1 (1%) | 0 | 100 | 100 |
| 38 | e | 125/130 (96%) | 123 (98%) | 2 (2%) | 0 | 100 | 100 |
| 39 | f | 104/107 (97%) | 100 (96%) | 4 (4%) | 0 | 100 | 100 |
| 40 | g | 110/120 (92%) | 109 (99%) | 1 (1%) | 0 | 100 | 100 |
| 41 | h | 117/120 (98%) | 113 (97%) | 4 (3%) | 0 | 100 | 100 |
| 42 | i | 97/99 (98%) | 94 (97%) | 3 (3%) | 0 | 100 | 100 |
| 43 | j | 82/87 (94%) | 80 (98%) | 2 (2%) | 0 | 100 | 100 |
| 44 | k | 75/78 (96%) | 75 (100%) | 0 | 0 | 100 | 100 |
| 45 | l | 48/50 (96%) | 47 (98%) | 1 (2%) | 0 | 100 | 100 |
| 46 | m | 462/472 (98%) | 456 (99%) | 6 (1%) | 0 | 100 | 100 |
| 47 | n | 363/605 (60%) | 352 (97%) | 11 (3%) | 0 | 100 | 100 |
| 48 | o | 131/220 (60%) | 127 (97%) | 4 (3%) | 0 | 100 | 100 |
| 49 | p | 89/92 (97%) | 85 (96%) | 4 (4%) | 0 | 100 | 100 |
| 50 | q | 152/455 (33%) | 145 (95%) | 7 (5%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 51 | r | 224/261 (86%) | 219 (98%) | 5 (2%) | 0 | 100 | 100 |
| 52 | s | 68/520 (13%) | 65 (96%) | 3 (4%) | 0 | 100 | 100 |
| 53 | t | 283/321 (88%) | 279 (99%) | 4 (1%) | 0 | 100 | 100 |
| 54 | u | 148/199 (74%) | 147 (99%) | 1 (1%) | 0 | 100 | 100 |
| 55 | v | 291/344 (85%) | 284 (98%) | 7 (2%) | 0 | 100 | 100 |
| 56 | w | 192/202 (95%) | 188 (98%) | 4 (2%) | 0 | 100 | 100 |
| 57 | x | 500/515 (97%) | 489 (98%) | 11 (2%) | 0 | 100 | 100 |
| 58 | y | 242/244 (99%) | 230 (95%) | 12 (5%) | 0 | 100 | 100 |
| 59 | z | 83/105 (79%) | 83 (100%) | 0 | 0 | 100 | 100 |
| 60 | 4 | 534/592 (90%) | 526 (98%) | 8 (2%) | 0 | 100 | 100 |
| All | All | 10648/12739 (84%) | 10398 (98%) | 250 (2%) | 0 | 100 | 100 |

There are no Ramachandran outliers to report.

### 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 | A | 166/196 (85%) | 166 (100%) | 0 | 100 | 100 |
| 5 | 5 | 67/101 (66%) | 67 (100%) | 0 | 100 | 100 |
| 7 | 8 | 129/136 (95%) | 129 (100%) | 0 | 100 | 100 |
| 8 | 9 | 106/153 (69%) | 106 (100%) | 0 | 100 | 100 |
| 9 | B | 322/322 (100%) | 322 (100%) | 0 | 100 | 100 |
| 10 | C | 288/289 (100%) | 286 (99%) | 2 (1%) | 84 | 90 |
| 11 | D | 226/245 (92%) | 226 (100%) | 0 | 100 | 100 |
| 12 | E | 133/153 (87%) | 133 (100%) | 0 | 100 | 100 |
| 13 | F | 184/205 (90%) | 184 (100%) | 0 | 100 | 100 |
| 14 | G | 185/208 (89%) | 185 (100%) | 0 | 100 | 100 |
| 15 | H | 171/171 (100%) | 170 (99%) | 1 (1%) | 86 | 91 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 16 | I | 117/117 (100%) | 117 (100%) | 0 | 100 | 100 |
| 17 | J | 148/148 (100%) | 148 (100%) | 0 | 100 | 100 |
| 18 | K | 247/313 (79%) | 247 (100%) | 0 | 100 | 100 |
| 19 | L | 142/159 (89%) | 142 (100%) | 0 | 100 | 100 |
| 20 | M | 108/109 (99%) | 108 (100%) | 0 | 100 | 100 |
| 21 | N | 165/175 (94%) | 164 (99%) | 1 (1%) | 86 | 91 |
| 22 | O | 160/160 (100%) | 160 (100%) | 0 | 100 | 100 |
| 23 | P | 141/145 (97%) | 141 (100%) | 0 | 100 | 100 |
| 24 | Q | 121/151 (80%) | 121 (100%) | 0 | 100 | 100 |
| 25 | R | 129/154 (84%) | 129 (100%) | 0 | 100 | 100 |
| 26 | S | 155/156 (99%) | 154 (99%) | 1 (1%) | 86 | 91 |
| 27 | T | 98/137 (72%) | 98 (100%) | 0 | 100 | 100 |
| 28 | U | 93/107 (87%) | 93 (100%) | 0 | 100 | 100 |
| 29 | V | 104/105 (99%) | 104 (100%) | 0 | 100 | 100 |
| 30 | W | 211/213 (99%) | 211 (100%) | 0 | 100 | 100 |
| 31 | X | 116/118 (98%) | 116 (100%) | 0 | 100 | 100 |
| 32 | Y | 109/110 (99%) | 108 (99%) | 1 (1%) | 78 | 87 |
| 33 | Z | 115/116 (99%) | 115 (100%) | 0 | 100 | 100 |
| 34 | a | 76/119 (64%) | 76 (100%) | 0 | 100 | 100 |
| 35 | b | 568/573 (99%) | 567 (100%) | 1 (0%) | 93 | 96 |
| 36 | c | 81/88 (92%) | 81 (100%) | 0 | 100 | 100 |
| 37 | d | 94/97 (97%) | 94 (100%) | 0 | 100 | 100 |
| 38 | e | 109/111 (98%) | 109 (100%) | 0 | 100 | 100 |
| 39 | f | 90/91 (99%) | 90 (100%) | 0 | 100 | 100 |
| 40 | g | 95/102 (93%) | 95 (100%) | 0 | 100 | 100 |
| 41 | h | 104/105 (99%) | 104 (100%) | 0 | 100 | 100 |
| 42 | i | 81/81 (100%) | 81 (100%) | 0 | 100 | 100 |
| 43 | j | 69/71 (97%) | 69 (100%) | 0 | 100 | 100 |
| 44 | k | 68/69 (99%) | 68 (100%) | 0 | 100 | 100 |
| 45 | l | 45/45 (100%) | 45 (100%) | 0 | 100 | 100 |
| 46 | m | 411/416 (99%) | 410 (100%) | 1 (0%) | 93 | 96 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles |
|---|---|---|---|---|---|
| 47 | n | 332/548 (61%) | 331 (100%) | 1 (0%) | 92 95 |
| 48 | o | 118/199 (59%) | 117 (99%) | 1 (1%) | 81 88 |
| 49 | p | 71/72 (99%) | 70 (99%) | 1 (1%) | 67 78 |
| 50 | q | 145/420 (34%) | 145 (100%) | 0 | 100 100 |
| 51 | r | 203/229 (89%) | 202 (100%) | 1 (0%) | 88 93 |
| 52 | s | 65/445 (15%) | 65 (100%) | 0 | 100 100 |
| 53 | t | 256/286 (90%) | 255 (100%) | 1 (0%) | 91 94 |
| 54 | u | 133/180 (74%) | 133 (100%) | 0 | 100 100 |
| 55 | v | 264/309 (85%) | 264 (100%) | 0 | 100 100 |
| 56 | w | 172/178 (97%) | 172 (100%) | 0 | 100 100 |
| 57 | x | 442/451 (98%) | 441 (100%) | 1 (0%) | 93 96 |
| 58 | y | 210/210 (100%) | 210 (100%) | 0 | 100 100 |
| 59 | z | 77/94 (82%) | 77 (100%) | 0 | 100 100 |
| 60 | 4 | 471/519 (91%) | 469 (100%) | 2 (0%) | 91 94 |
| All | All | 9306/10980 (85%) | 9290 (100%) | 16 (0%) | 93 96 |

5 of 16 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 60 | 4 | 255 | ASN |
| 57 | x | 208 | ASN |
| 47 | n | 214 | ASP |
| 53 | t | 231 | ASP |
| 46 | m | 353 | TRP |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 11 | D | 45 | ASN |

### 5.3.3 RNA (i)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|---|---|---|---|---|
| 2 | 1 | 2970/3396 (87%) | 493 (16%) | 4 (0%) |
| 3 | 2 | 157/158 (99%) | 28 (17%) | 0 |

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| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|---|---|---|---|---|
| 4 | 3 | 120/121 (99%) | 25 (20%) | 0 |
| 6 | 6 | 54/74 (72%) | 18 (33%) | 0 |
| All | All | 3301/3749 (88%) | 564 (17%) | 4 (0%) |

5 of 564 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | 1 | 2 | U |
| 2 | 1 | 5 | G |
| 2 | 1 | 14 | U |
| 2 | 1 | 42 | C |
| 2 | 1 | 43 | A |

All (4) RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | 1 | 374 | A |
| 2 | 1 | 1355 | A |
| 2 | 1 | 1568 | U |
| 2 | 1 | 3121 | U |

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

55 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 | $\#\|Z\| > 2$ |
| 2 | PSU | 1 | 1124 | 2 | 18,21,22 | 1.19 | 2 (11%) | 22,30,33 | 1.46 | 4 (18%) |
| 2 | PSU | 1 | 2340 | 2 | 18,21,22 | 1.11 | 1 (5%) | 22,30,33 | 1.47 | 4 (18%) |
| 2 | OMG | 1 | 1450 | 2 | 18,26,27 | 1.37 | 3 (16%) | 19,38,41 | 1.36 | 2 (10%) |
| 2 | A2M | 1 | 649 | 2 | 18,25,26 | 1.51 | 1 (5%) | 18,36,39 | 0.93 | 1 (5%) |
| 2 | PSU | 1 | 966 | 2 | 18,21,22 | 1.19 | 3 (16%) | 22,30,33 | 1.42 | 4 (18%) |
| 2 | A2M | 1 | 1133 | 2 | 18,25,26 | 1.51 | 1 (5%) | 18,36,39 | 0.93 | 0 |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | $\#\|Z\|>2$ | Counts | RMSZ | $\#\|Z\|>2$ |
| 2 | PSU | 1 | 2735 | 2 | 18,21,22 | 1.14 | 1 (5%) | 22,30,33 | 1.51 | 4 (18%) |
| 2 | OMG | 1 | 2815 | 2 | 18,26,27 | 1.38 | 2 (11%) | 19,38,41 | 1.48 | 2 (10%) |
| 2 | OMU | 1 | 2347 | 2 | 19,22,23 | 0.83 | 1 (5%) | 26,31,34 | 0.81 | 1 (3%) |
| 2 | 1MA | 1 | 2142 | 2 | 16,25,26 | 0.97 | 2 (12%) | 18,37,40 | 1.08 | 2 (11%) |
| 2 | PSU | 1 | 2129 | 2 | 18,21,22 | 1.14 | 2 (11%) | 22,30,33 | 1.43 | 4 (18%) |
| 2 | PSU | 1 | 2351 | 2 | 18,21,22 | 1.12 | 1 (5%) | 22,30,33 | 1.48 | 4 (18%) |
| 2 | PSU | 1 | 2416 | 2 | 18,21,22 | 1.13 | 1 (5%) | 22,30,33 | 1.47 | 5 (22%) |
| 2 | PSU | 1 | 2191 | 2 | 18,21,22 | 1.13 | 1 (5%) | 22,30,33 | 1.44 | 5 (22%) |
| 2 | A2M | 1 | 1449 | 61,2 | 18,25,26 | 1.45 | 1 (5%) | 18,36,39 | 1.00 | 1 (5%) |
| 2 | OMU | 1 | 2421 | 2 | 19,22,23 | 0.81 | 1 (5%) | 26,31,34 | 0.87 | 2 (7%) |
| 2 | OMC | 1 | 663 | 2 | 19,22,23 | 0.55 | 0 | 26,31,34 | 0.70 | 0 |
| 3 | PSU | 2 | 73 | 3 | 18,21,22 | 1.09 | 1 (5%) | 22,30,33 | 1.44 | 4 (18%) |
| 2 | PSU | 1 | 1110 | 2 | 18,21,22 | 1.16 | 1 (5%) | 22,30,33 | 1.46 | 4 (18%) |
| 2 | OMC | 1 | 650 | 2 | 19,22,23 | 0.54 | 0 | 26,31,34 | 0.64 | 0 |
| 2 | OMG | 1 | 908 | 2 | 18,26,27 | 1.39 | 3 (16%) | 19,38,41 | 1.49 | 2 (10%) |
| 2 | 5MC | 1 | 2870 | 2 | 18,22,23 | 0.93 | 2 (11%) | 26,32,35 | 1.19 | 2 (7%) |
| 2 | PSU | 1 | 2865 | 2 | 18,21,22 | 1.20 | 3 (16%) | 22,30,33 | 1.43 | 4 (18%) |
| 2 | PSU | 1 | 2826 | 61,2 | 18,21,22 | 1.12 | 1 (5%) | 22,30,33 | 1.52 | 4 (18%) |
| 2 | OMU | 1 | 1888 | 2 | 19,22,23 | 1.16 | 1 (5%) | 26,31,34 | 1.32 | 4 (15%) |
| 2 | OMC | 1 | 2959 | 2 | 19,22,23 | 0.59 | 0 | 26,31,34 | 0.76 | 0 |
| 2 | A2M | 1 | 2220 | 2 | 18,25,26 | 1.52 | 1 (5%) | 18,36,39 | 1.11 | 2 (11%) |
| 2 | OMG | 1 | 867 | 2 | 18,26,27 | 1.32 | 3 (16%) | 19,38,41 | 1.49 | 2 (10%) |
| 2 | A2M | 1 | 876 | 2 | 18,25,26 | 1.50 | 1 (5%) | 18,36,39 | 0.95 | 0 |
| 2 | PSU | 1 | 2264 | 2 | 18,21,22 | 1.19 | 3 (16%) | 22,30,33 | 1.44 | 4 (18%) |
| 2 | PSU | 1 | 986 | 2 | 18,21,22 | 1.10 | 2 (11%) | 22,30,33 | 1.38 | 4 (18%) |
| 2 | PSU | 1 | 2880 | 2 | 18,21,22 | 1.14 | 1 (5%) | 22,30,33 | 1.44 | 4 (18%) |
| 2 | PSU | 1 | 776 | 2 | 18,21,22 | 1.22 | 2 (11%) | 22,30,33 | 1.47 | 5 (22%) |
| 2 | PSU | 1 | 2133 | 2 | 18,21,22 | 1.05 | 1 (5%) | 22,30,33 | 1.53 | 4 (18%) |
| 2 | PSU | 1 | 2349 | 61,2 | 18,21,22 | 1.10 | 1 (5%) | 22,30,33 | 1.39 | 5 (22%) |
| 2 | A2M | 1 | 807 | 2 | 18,25,26 | 1.45 | 1 (5%) | 18,36,39 | 1.08 | 1 (5%) |
| 2 | OMC | 1 | 1437 | 61,2 | 19,22,23 | 0.58 | 0 | 26,31,34 | 1.07 | 2 (7%) |
| 2 | OMU | 1 | 2729 | 2 | 19,22,23 | 0.77 | 1 (5%) | 26,31,34 | 0.89 | 2 (7%) |
| 2 | OMG | 1 | 2791 | 2 | 18,26,27 | 1.42 | 2 (11%) | 19,38,41 | 1.49 | 2 (10%) |
| 2 | OMC | 1 | 2337 | 2 | 19,22,23 | 0.52 | 0 | 26,31,34 | 0.67 | 0 |
| 2 | OMU | 1 | 2724 | 2 | 19,22,23 | 0.80 | 1 (5%) | 26,31,34 | 0.85 | 1 (3%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | $\#\|Z\|>2$ | Counts | RMSZ | $\#\|Z\|>2$ |
| 4 | PSU | 3 | 50 | 4 | 18,21,22 | 1.19 | 2 (11%) | 22,30,33 | 1.49 | 4 (18%) |
| 2 | OMU | 1 | 898 | 2 | 19,22,23 | 0.78 | 1 (5%) | 26,31,34 | 0.88 | 2 (7%) |
| 2 | PSU | 1 | 990 | 2 | 18,21,22 | 1.15 | 2 (11%) | 22,30,33 | 1.47 | 4 (18%) |
| 2 | PSU | 1 | 2266 | 2 | 18,21,22 | 1.18 | 2 (11%) | 22,30,33 | 1.44 | 5 (22%) |
| 2 | OMG | 1 | 805 | 2 | 18,26,27 | 1.34 | 3 (16%) | 19,38,41 | 1.47 | 2 (10%) |
| 2 | PSU | 1 | 2314 | 2 | 18,21,22 | 1.16 | 1 (5%) | 22,30,33 | 1.47 | 4 (18%) |
| 2 | OMG | 1 | 2793 | 2 | 18,26,27 | 1.39 | 3 (16%) | 19,38,41 | 1.46 | 2 (10%) |
| 2 | OMC | 1 | 2948 | 2 | 19,22,23 | 0.56 | 0 | 26,31,34 | 0.83 | 1 (3%) |
| 2 | PSU | 1 | 2975 | 2 | 18,21,22 | 1.12 | 1 (5%) | 22,30,33 | 1.52 | 4 (18%) |
| 2 | OMU | 1 | 2417 | 2 | 19,22,23 | 0.79 | 1 (5%) | 26,31,34 | 0.93 | 2 (7%) |
| 2 | 5MC | 1 | 2278 | 2 | 18,22,23 | 0.96 | 2 (11%) | 26,32,35 | 1.12 | 3 (11%) |
| 2 | PSU | 1 | 960 | 2 | 18,21,22 | 1.13 | 1 (5%) | 22,30,33 | 1.41 | 5 (22%) |
| 2 | A2M | 1 | 817 | 61,2 | 18,25,26 | 1.41 | 1 (5%) | 18,36,39 | 1.09 | 1 (5%) |
| 2 | OMC | 1 | 2197 | 2 | 19,22,23 | 0.46 | 0 | 26,31,34 | 0.67 | 0 |

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 |
|---|---|---|---|---|---|---|---|
| 2 | PSU | 1 | 1124 | 2 | - | 0/7/25/26 | 0/2/2/2 |
| 2 | PSU | 1 | 2340 | 2 | - | 3/7/25/26 | 0/2/2/2 |
| 2 | OMG | 1 | 1450 | 2 | - | 3/5/27/28 | 0/3/3/3 |
| 2 | A2M | 1 | 649 | 2 | - | 3/5/27/28 | 0/3/3/3 |
| 2 | PSU | 1 | 966 | 2 | - | 0/7/25/26 | 0/2/2/2 |
| 2 | A2M | 1 | 1133 | 2 | - | 0/5/27/28 | 0/3/3/3 |
| 2 | PSU | 1 | 2735 | 2 | - | 0/7/25/26 | 0/2/2/2 |
| 2 | OMG | 1 | 2815 | 2 | - | 0/5/27/28 | 0/3/3/3 |
| 2 | OMU | 1 | 2347 | 2 | - | 2/9/27/28 | 0/2/2/2 |
| 2 | 1MA | 1 | 2142 | 2 | - | 2/3/25/26 | 0/3/3/3 |
| 2 | PSU | 1 | 2129 | 2 | - | 0/7/25/26 | 0/2/2/2 |
| 2 | PSU | 1 | 2351 | 2 | - | 0/7/25/26 | 0/2/2/2 |
| 2 | PSU | 1 | 2416 | 2 | - | 3/7/25/26 | 0/2/2/2 |
| 2 | PSU | 1 | 2191 | 2 | - | 0/7/25/26 | 0/2/2/2 |
| 2 | A2M | 1 | 1449 | 61,2 | - | 0/5/27/28 | 0/3/3/3 |
| 2 | OMU | 1 | 2421 | 2 | - | 2/9/27/28 | 0/2/2/2 |
| 2 | OMC | 1 | 663 | 2 | - | 0/9/27/28 | 0/2/2/2 |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|---|---|---|---|---|---|---|---|
| 3 | PSU | 2 | 73 | 3 | - | 0/7/25/26 | 0/2/2/2 |
| 2 | PSU | 1 | 1110 | 2 | - | 0/7/25/26 | 0/2/2/2 |
| 2 | OMC | 1 | 650 | 2 | - | 0/9/27/28 | 0/2/2/2 |
| 2 | OMG | 1 | 908 | 2 | - | 1/5/27/28 | 0/3/3/3 |
| 2 | 5MC | 1 | 2870 | 2 | - | 0/7/25/26 | 0/2/2/2 |
| 2 | PSU | 1 | 2865 | 2 | - | 2/7/25/26 | 0/2/2/2 |
| 2 | PSU | 1 | 2826 | 61,2 | - | 2/7/25/26 | 0/2/2/2 |
| 2 | OMU | 1 | 1888 | 2 | - | 2/9/27/28 | 0/2/2/2 |
| 2 | OMC | 1 | 2959 | 2 | - | 0/9/27/28 | 0/2/2/2 |
| 2 | A2M | 1 | 2220 | 2 | - | 3/5/27/28 | 0/3/3/3 |
| 2 | OMG | 1 | 867 | 2 | - | 0/5/27/28 | 0/3/3/3 |
| 2 | A2M | 1 | 876 | 2 | - | 0/5/27/28 | 0/3/3/3 |
| 2 | PSU | 1 | 2264 | 2 | - | 0/7/25/26 | 0/2/2/2 |
| 2 | PSU | 1 | 986 | 2 | - | 0/7/25/26 | 0/2/2/2 |
| 2 | PSU | 1 | 2880 | 2 | - | 0/7/25/26 | 0/2/2/2 |
| 2 | PSU | 1 | 776 | 2 | - | 3/7/25/26 | 0/2/2/2 |
| 2 | PSU | 1 | 2133 | 2 | - | 0/7/25/26 | 0/2/2/2 |
| 2 | PSU | 1 | 2349 | 61,2 | - | 0/7/25/26 | 0/2/2/2 |
| 2 | A2M | 1 | 807 | 2 | - | 0/5/27/28 | 0/3/3/3 |
| 2 | OMC | 1 | 1437 | 61,2 | - | 3/9/27/28 | 0/2/2/2 |
| 2 | OMU | 1 | 2729 | 2 | - | 2/9/27/28 | 0/2/2/2 |
| 2 | OMG | 1 | 2791 | 2 | - | 0/5/27/28 | 0/3/3/3 |
| 2 | OMC | 1 | 2337 | 2 | - | 0/9/27/28 | 0/2/2/2 |
| 2 | OMU | 1 | 2724 | 2 | - | 0/9/27/28 | 0/2/2/2 |
| 4 | PSU | 3 | 50 | 4 | - | 2/7/25/26 | 0/2/2/2 |
| 2 | OMU | 1 | 898 | 2 | - | 0/9/27/28 | 0/2/2/2 |
| 2 | PSU | 1 | 990 | 2 | - | 0/7/25/26 | 0/2/2/2 |
| 2 | PSU | 1 | 2266 | 2 | - | 0/7/25/26 | 0/2/2/2 |
| 2 | OMG | 1 | 805 | 2 | - | 0/5/27/28 | 0/3/3/3 |
| 2 | PSU | 1 | 2314 | 2 | - | 0/7/25/26 | 0/2/2/2 |
| 2 | OMG | 1 | 2793 | 2 | - | 0/5/27/28 | 0/3/3/3 |
| 2 | OMC | 1 | 2948 | 2 | - | 2/9/27/28 | 0/2/2/2 |
| 2 | PSU | 1 | 2975 | 2 | - | 0/7/25/26 | 0/2/2/2 |
| 2 | OMU | 1 | 2417 | 2 | - | 2/9/27/28 | 0/2/2/2 |
| 2 | 5MC | 1 | 2278 | 2 | - | 0/7/25/26 | 0/2/2/2 |
| 2 | PSU | 1 | 960 | 2 | - | 2/7/25/26 | 0/2/2/2 |
| 2 | A2M | 1 | 817 | 61,2 | - | 2/5/27/28 | 0/3/3/3 |
| 2 | OMC | 1 | 2197 | 2 | - | 2/9/27/28 | 0/2/2/2 |

The worst 5 of 76 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 2 | 1 | 2220 | A2M | O5'-C5' | -4.80 | 1.33 | 1.44 |
| 2 | 1 | 876 | A2M | O5'-C5' | -4.69 | 1.33 | 1.44 |
| 2 | 1 | 1449 | A2M | O5'-C5' | -4.62 | 1.33 | 1.44 |
| 2 | 1 | 1133 | A2M | O5'-C5' | -4.55 | 1.33 | 1.44 |
| 2 | 1 | 2791 | OMG | C6-N1 | 4.53 | 1.44 | 1.37 |

The worst 5 of 146 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 2 | 1 | 2826 | PSU | C6-C5-C4 | 4.31 | 121.21 | 118.20 |
| 2 | 1 | 2865 | PSU | C6-C5-C4 | 4.31 | 121.21 | 118.20 |
| 2 | 1 | 2735 | PSU | C6-C5-C4 | 4.27 | 121.19 | 118.20 |
| 2 | 1 | 2975 | PSU | C6-C5-C4 | 4.26 | 121.17 | 118.20 |
| 4 | 3 | 50 | PSU | C6-C5-C4 | 4.23 | 121.16 | 118.20 |

There are no chirality outliers.

5 of 48 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 2 | 1 | 649 | A2M | C3'-C4'-C5'-O5' |
| 2 | 1 | 960 | PSU | C3'-C4'-C5'-O5' |
| 2 | 1 | 960 | PSU | O4'-C4'-C5'-O5' |
| 2 | 1 | 1450 | OMG | O4'-C4'-C5'-O5' |
| 2 | 1 | 1888 | OMU | O4'-C1'-N1-C2 |

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry (i)

Of 92 ligands modelled in this entry, 87 are monoatomic - leaving 5 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 | $\#\|Z\| > 2$ |
| 64 | GDP | m | 501 | 61,65 | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.26 | 4 (13%) |
| 62 | B3P | 1 | 3479 | - | 18,18,18 | 1.48 | 2 (11%) | 21,23,23 | 1.99 | 6 (28%) |
| 62 | B3P | 1 | 3478 | 61 | 18,18,18 | 1.50 | 2 (11%) | 21,23,23 | 1.95 | 6 (28%) |
| 64 | GDP | b | 801 | 61 | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.26 | 4 (13%) |
| 62 | B3P | 1 | 3480 | - | 18,18,18 | 1.52 | 2 (11%) | 21,23,23 | 1.99 | 6 (28%) |

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 |
|---|---|---|---|---|---|---|---|
| 64 | GDP | m | 501 | 61,65 | - | 3/12/32/32 | 0/3/3/3 |
| 62 | B3P | 1 | 3479 | - | - | 10/28/28/28 | - |
| 62 | B3P | 1 | 3478 | 61 | - | 7/28/28/28 | - |
| 64 | GDP | b | 801 | 61 | - | 5/12/32/32 | 0/3/3/3 |
| 62 | B3P | 1 | 3480 | - | - | 6/28/28/28 | - |

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

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 62 | 1 | 3480 | B3P | C6-C4 | 5.08 | 1.59 | 1.53 |
| 62 | 1 | 3478 | B3P | C6-C4 | 5.03 | 1.59 | 1.53 |
| 62 | 1 | 3479 | B3P | C6-C4 | 4.68 | 1.59 | 1.53 |
| 62 | 1 | 3479 | B3P | C7-C4 | 2.79 | 1.56 | 1.53 |
| 62 | 1 | 3480 | B3P | C7-C4 | 2.58 | 1.56 | 1.53 |

The worst 5 of 26 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 62 | 1 | 3480 | B3P | O5-C6-C4 | 5.04 | 121.83 | 111.63 |
| 62 | 1 | 3478 | B3P | O5-C6-C4 | 4.99 | 121.75 | 111.63 |
| 62 | 1 | 3479 | B3P | O5-C6-C4 | 4.93 | 121.62 | 111.63 |
| 62 | 1 | 3479 | B3P | C2-N2-C8 | -4.32 | 109.95 | 116.08 |
| 62 | 1 | 3480 | B3P | C2-N2-C8 | -3.93 | 110.50 | 116.08 |

There are no chirality outliers.

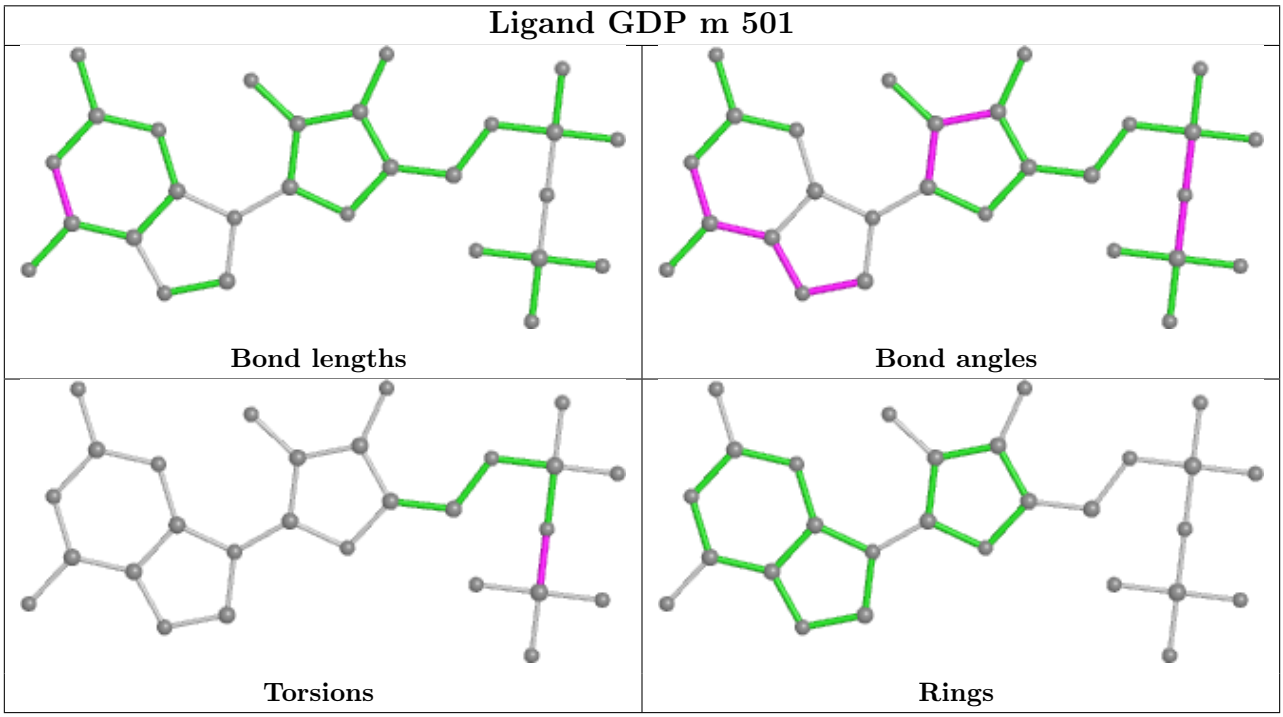
5 of 31 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 62 | 1 | 3478 | B3P | N1-C4-C6-O5 |
| 62 | 1 | 3478 | B3P | C5-C4-C6-O5 |
| 62 | 1 | 3478 | B3P | C7-C4-C6-O5 |
| 62 | 1 | 3478 | B3P | O3-C11-C8-N2 |
| 62 | 1 | 3478 | B3P | O3-C11-C8-C10 |

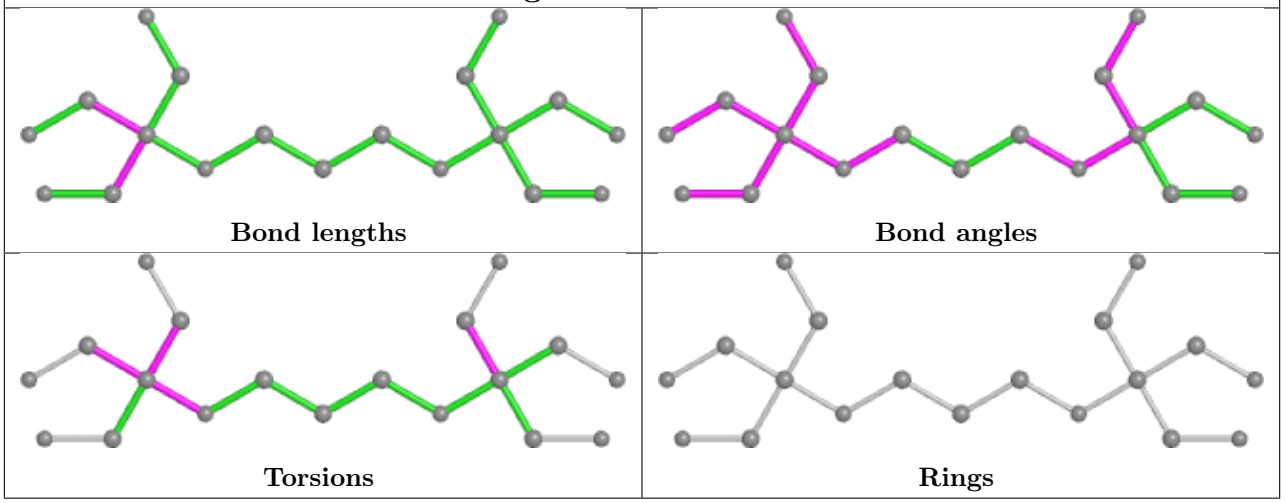
There are no ring outliers.

No monomer is involved in short contacts.

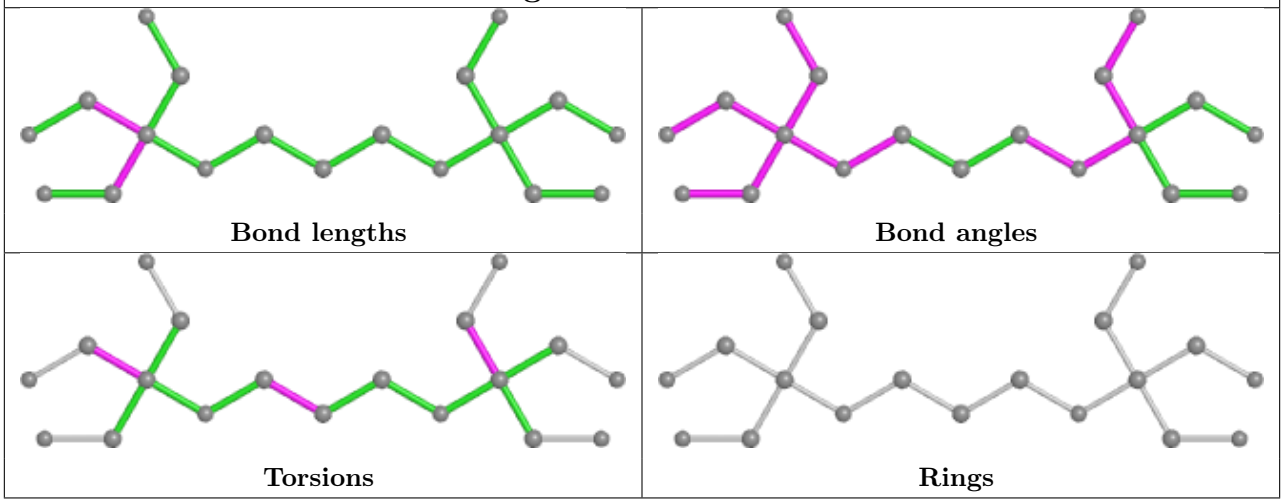
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



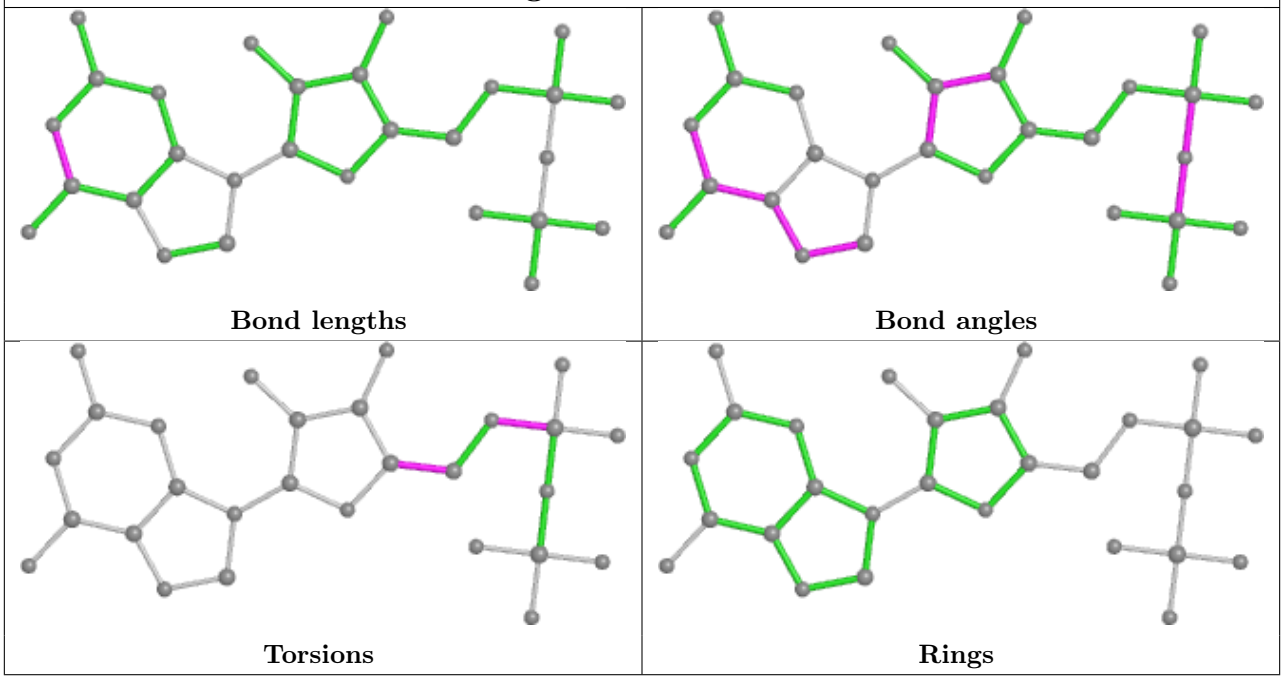
## Ligand B3P 1 3479



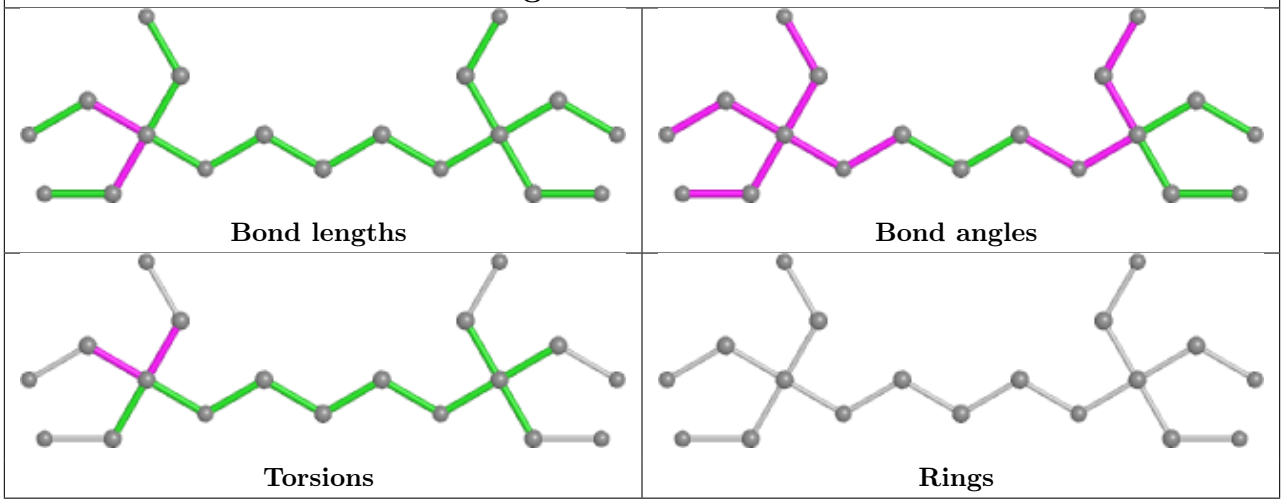

## Ligand B3P 1 3478




## Ligand GDP b 801



**Ligand B3P 1 3480**




## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

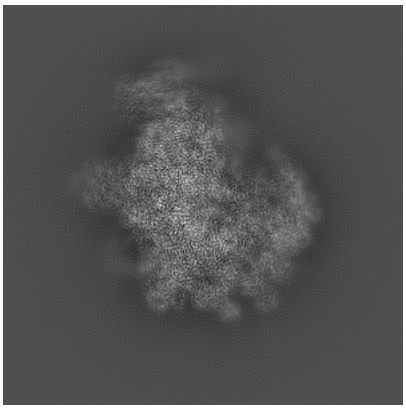
# 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-26703. These allow visual inspection of the internal detail of the map and identification of artifacts.

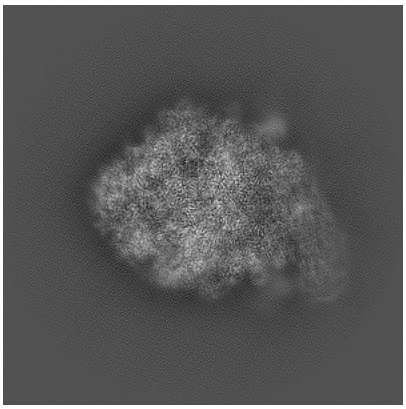
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

## 6.1 Orthogonal projections

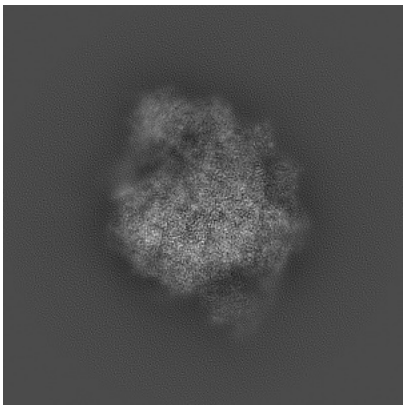
### 6.1.1 Primary map



X

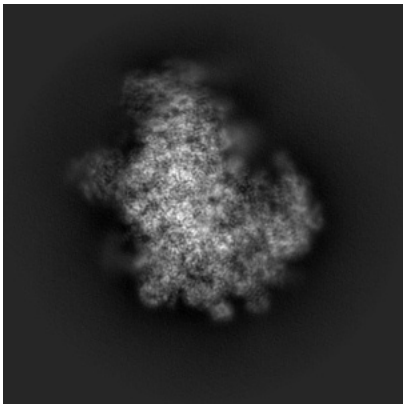


Y

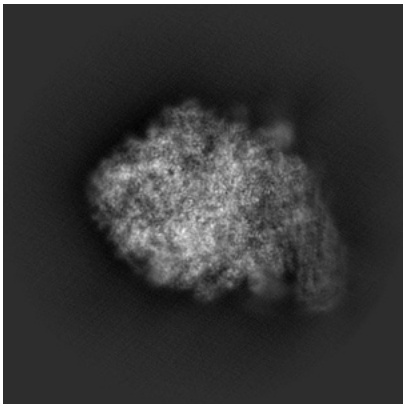


Z

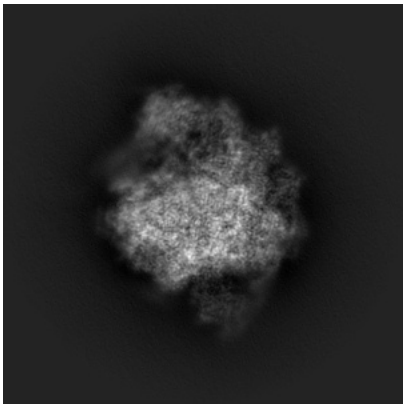
### 6.1.2 Raw map



X



Y

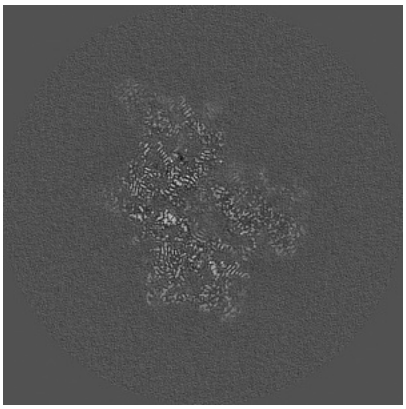


Z

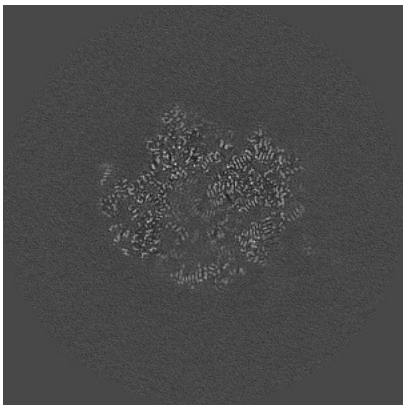
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices (i)

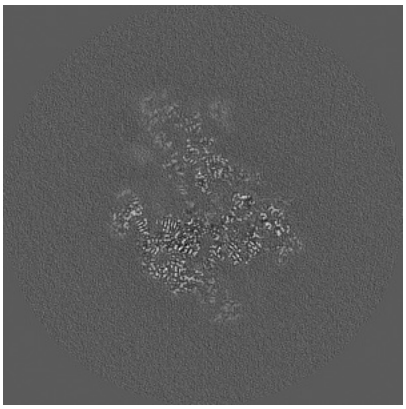
### 6.2.1 Primary map



X Index: 200

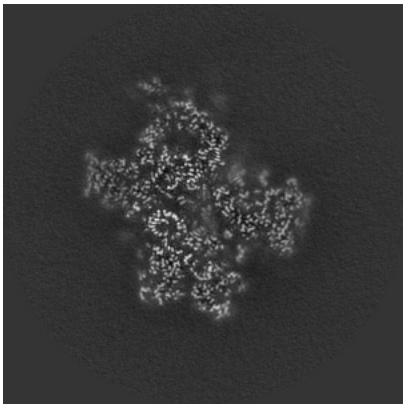


Y Index: 200

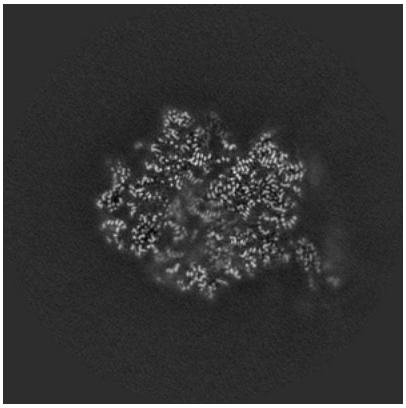


Z Index: 200

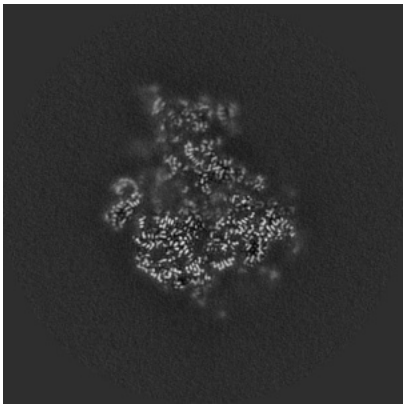
### 6.2.2 Raw map



X Index: 200



Y Index: 200

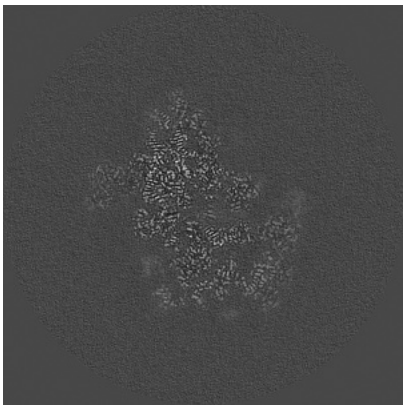


Z Index: 200

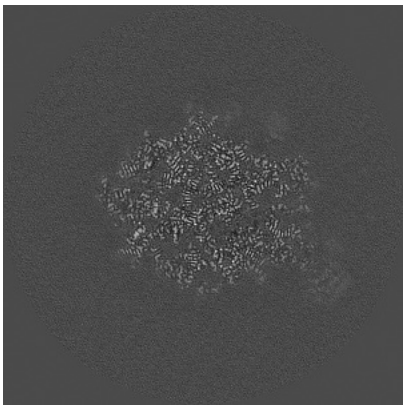
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices (i)

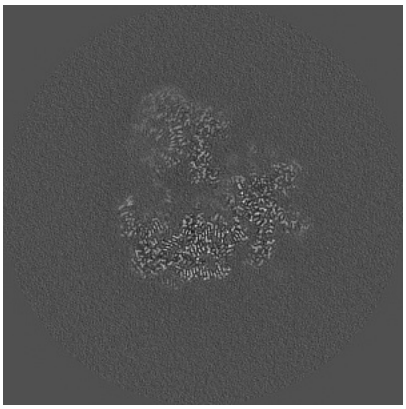
### 6.3.1 Primary map



X Index: 222

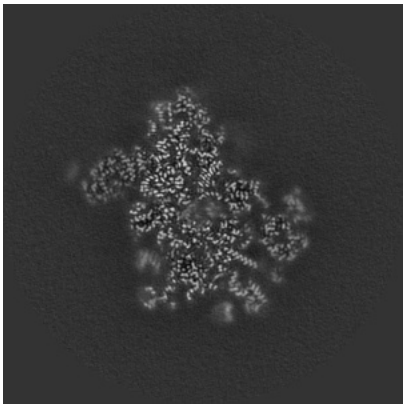


Y Index: 172

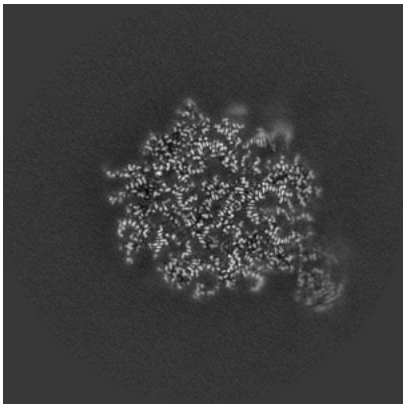


Z Index: 186

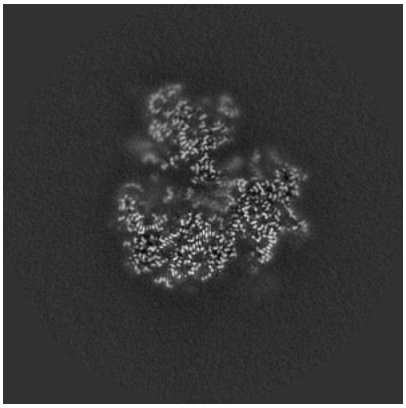
### 6.3.2 Raw map



X Index: 217



Y Index: 179

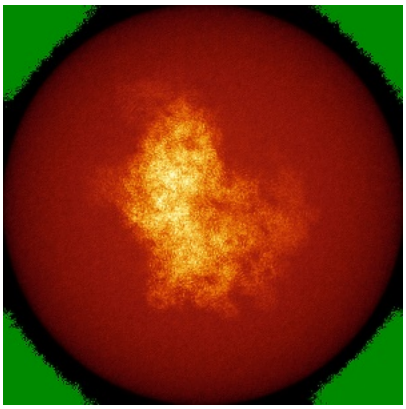


Z Index: 187

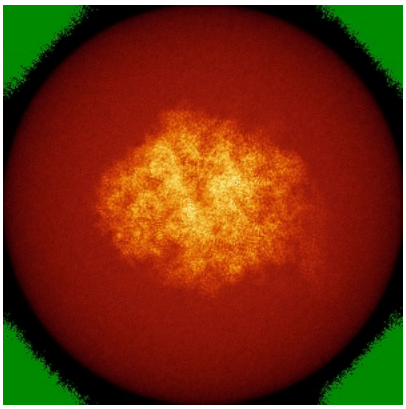
The images above show the largest variance slices of the map in three orthogonal directions.

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

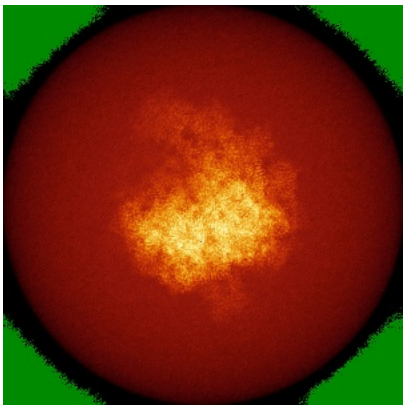
### 6.4.1 Primary map



X

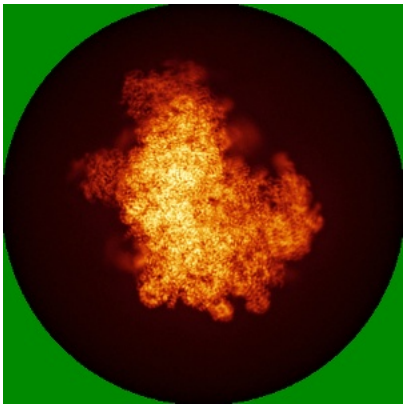


Y

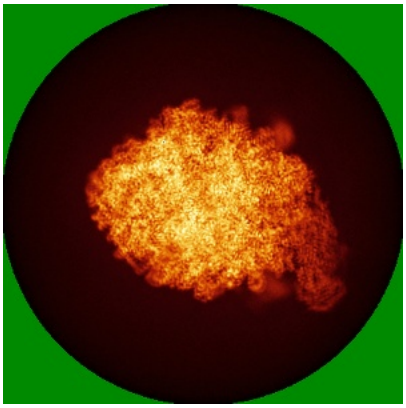


Z

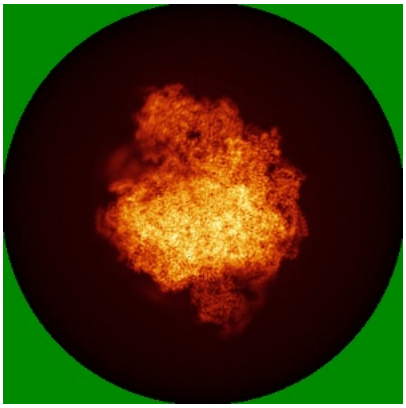
### 6.4.2 Raw map



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.

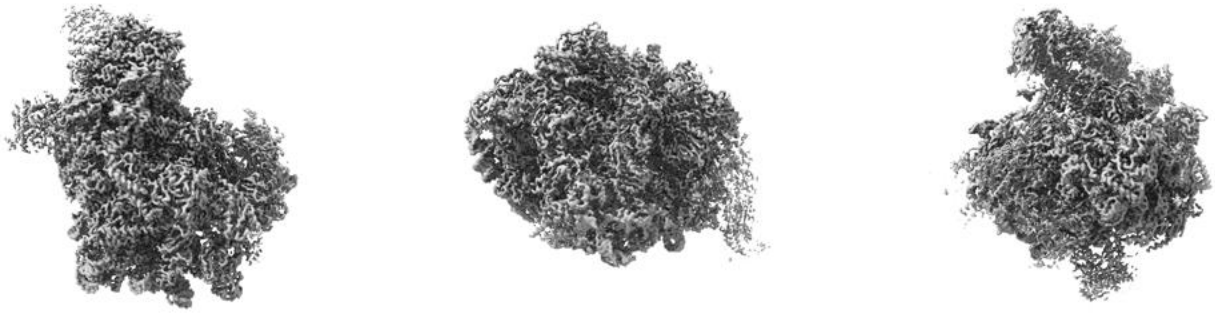
## 6.5 Orthogonal surface views (i)

### 6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.032. 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.

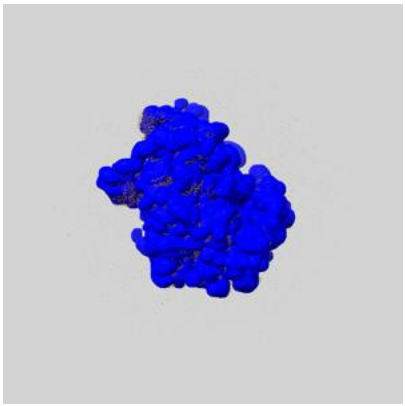
## 6.6 Mask visualisation

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

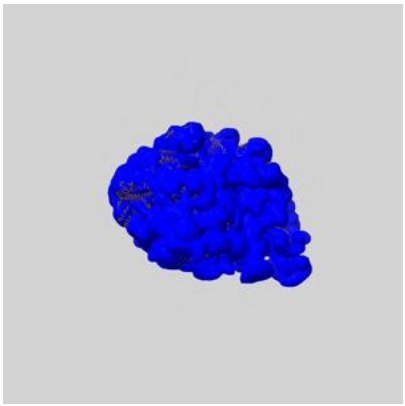
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

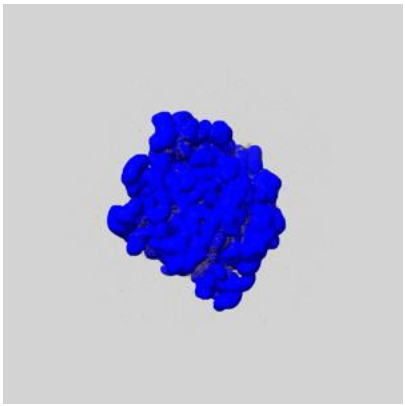
### 6.6.1 emd_26703_msk_1.map



X



Y

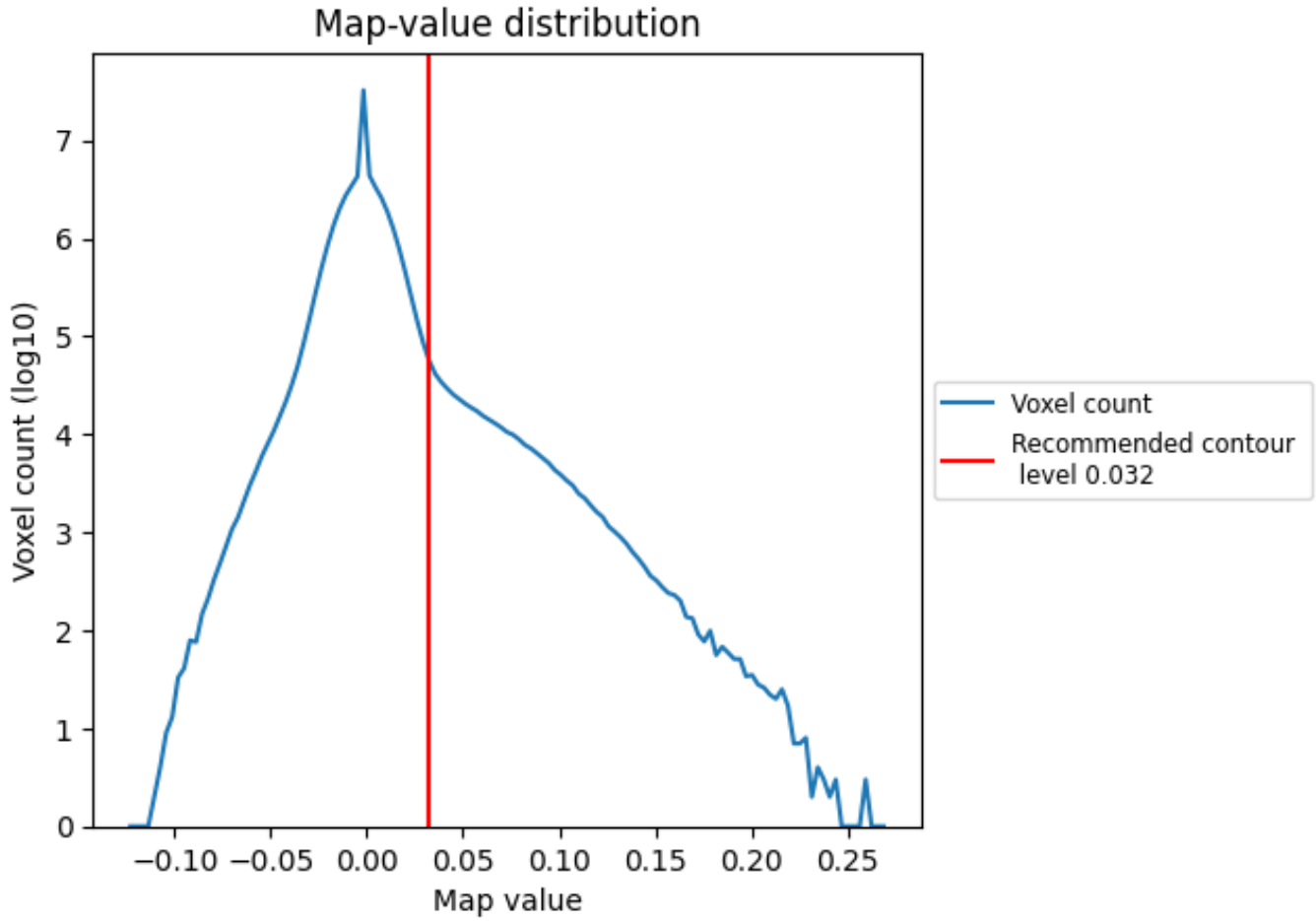


Z

# 7 Map analysis

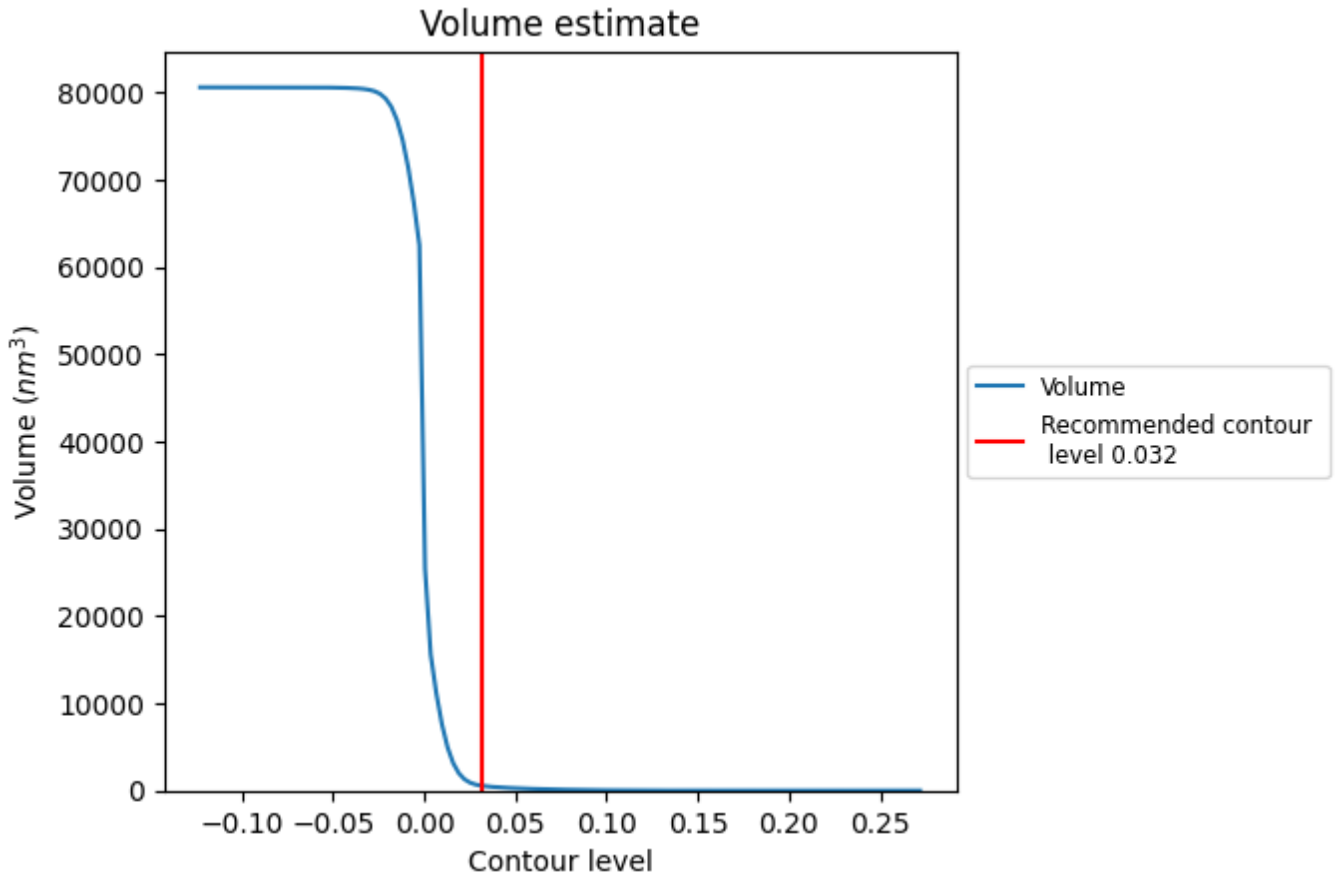
This section contains the results of statistical analysis of the map.

## 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.

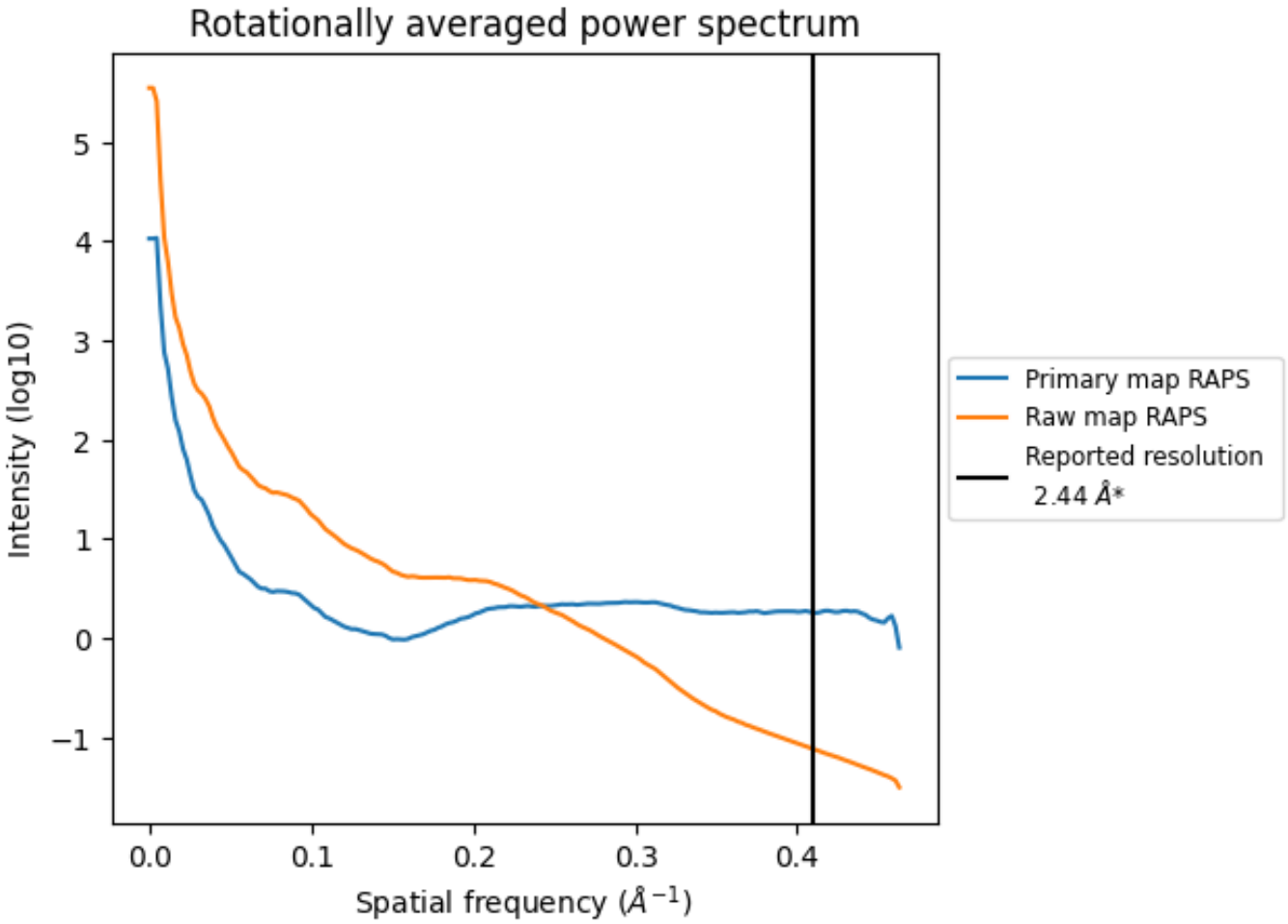
## 7.2 Volume estimate (i)




The volume at the recommended contour level is 540 $nm^3$; this corresponds to an approximate mass of 488 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)

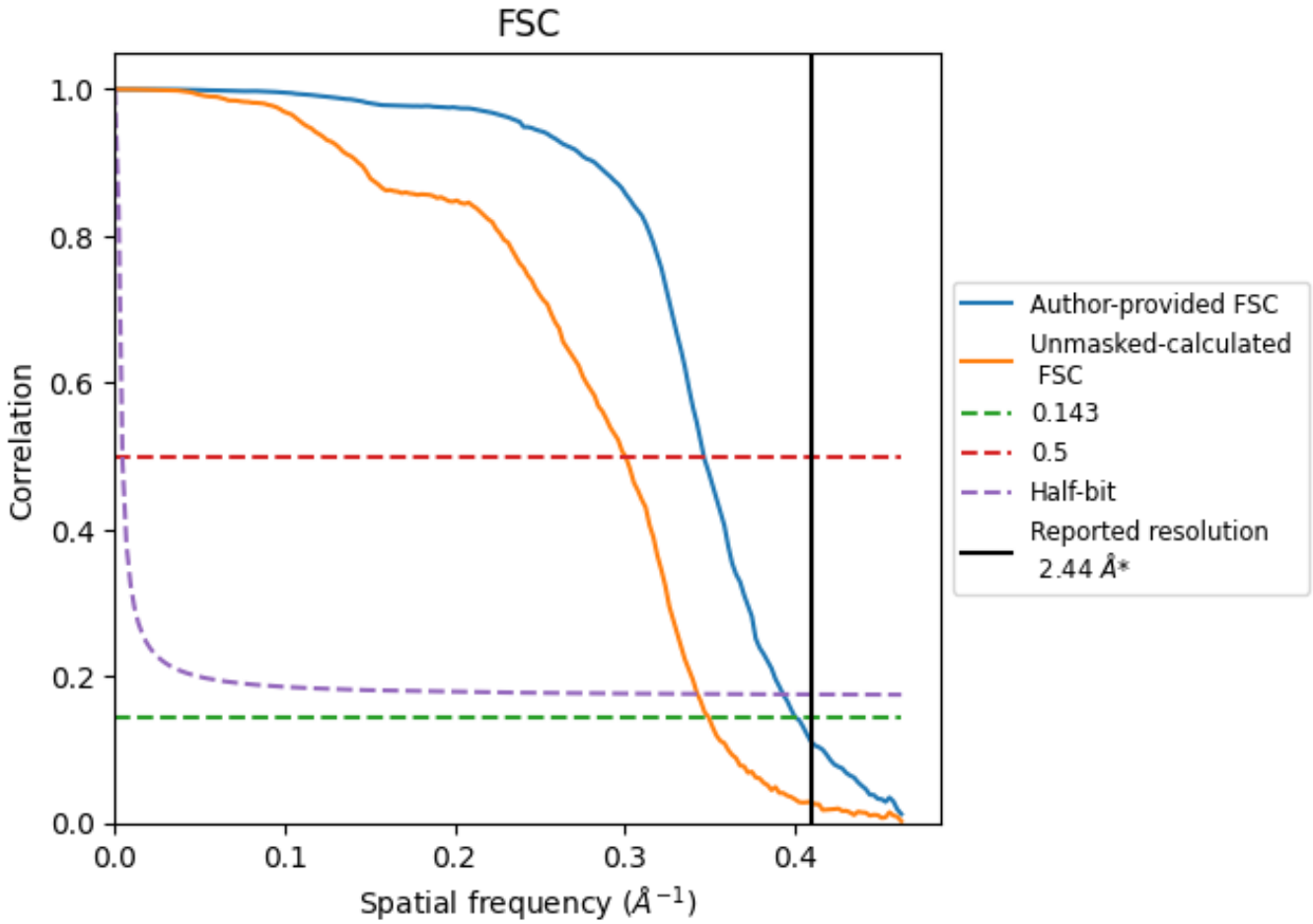



*Reported resolution corresponds to spatial frequency of 0.410 $Å^{-1}$

# 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 0.410 Å$^{-1}$

## 8.2 Resolution estimates (i)

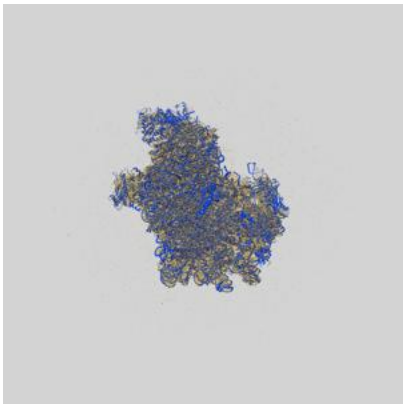
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---|---|---|---|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 2.44 | - | - |
| Author-provided FSC curve | 2.49 | 2.88 | 2.54 |
| Unmasked-calculated* | 2.86 | 3.33 | 2.92 |

*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 2.86 differs from the reported value 2.44 by more than 10 %

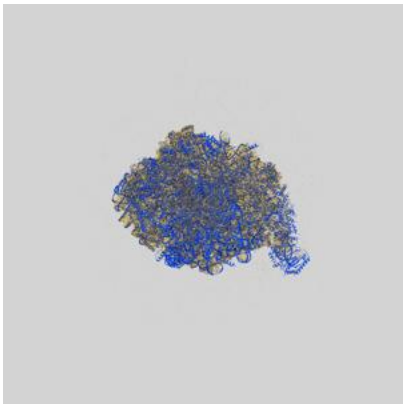
# 9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-26703 and PDB model 7UQZ. Per-residue inclusion information can be found in section 3 on page 18.

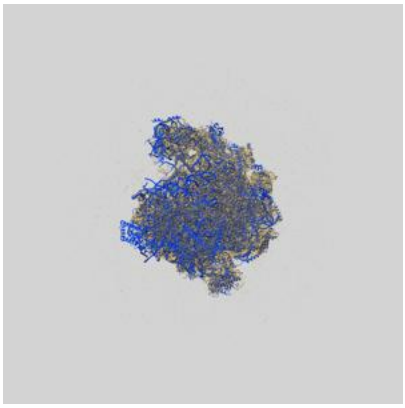
## 9.1 Map-model overlay



X



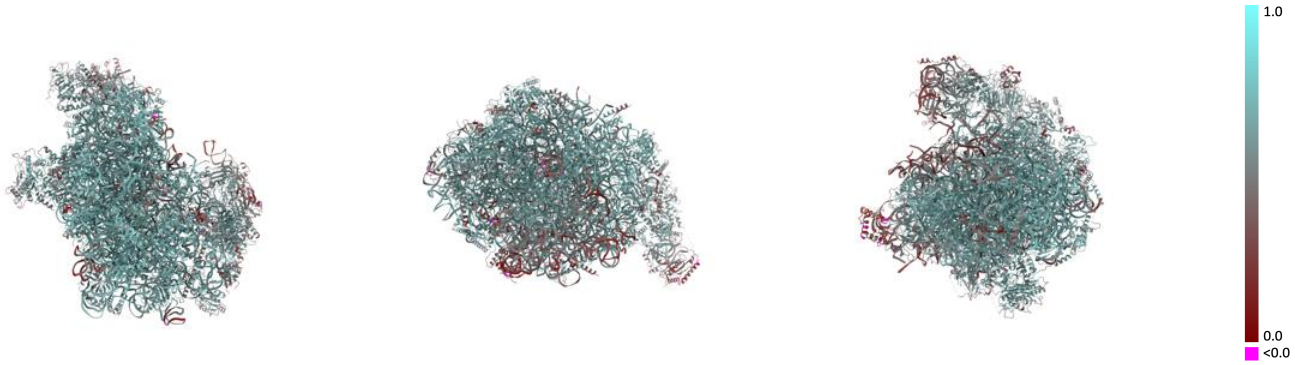
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.032 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.

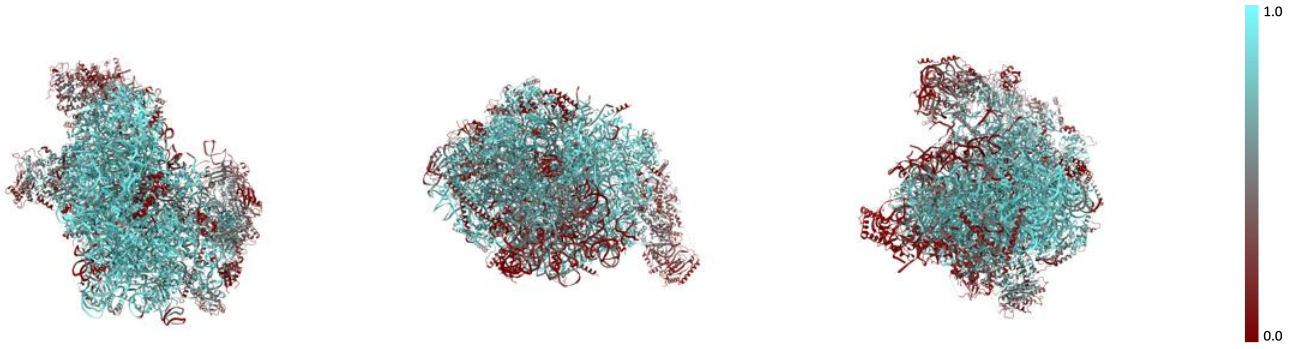
## 9.2 Q-score mapped to coordinate model (i)




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.

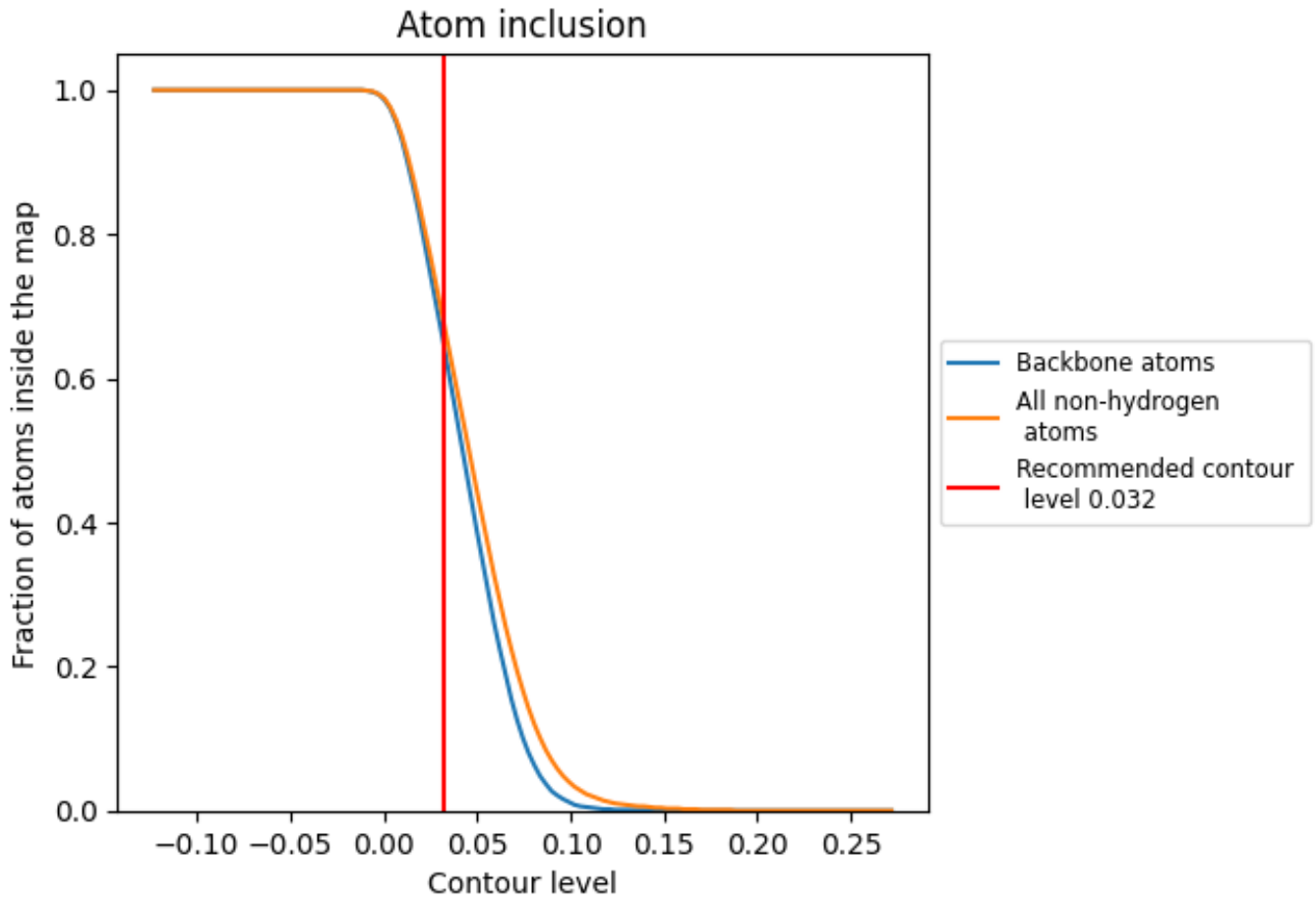
## 9.3 Atom inclusion mapped to coordinate model (i)




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 (0.032).

## 9.4 Atom inclusion (i)




At the recommended contour level, 65% of all backbone atoms, 68% 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 (0.032) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|---|---|---|
| All | 0.6790 | 0.6080 |
| 1 | 0.7760 | 0.6170 |
| 2 | 0.9180 | 0.6710 |
| 3 | 0.2750 | 0.4030 |
| 4 | 0.4660 | 0.5930 |
| 5 | 0.0520 | 0.3360 |
| 6 | 0.2490 | 0.4640 |
| 8 | 0.1660 | 0.4710 |
| 9 | 0.5360 | 0.6130 |
| A | 0.8550 | 0.6970 |
| B | 0.9040 | 0.7000 |
| C | 0.8540 | 0.6800 |
| D | 0.3680 | 0.5160 |
| E | 0.7230 | 0.6440 |
| F | 0.8490 | 0.6750 |
| G | 0.7500 | 0.6430 |
| H | 0.7880 | 0.6510 |
| I | 0.0440 | 0.5310 |
| J | 0.0770 | 0.3090 |
| K | 0.0770 | 0.3900 |
| L | 0.7160 | 0.6260 |
| M | 0.8080 | 0.6580 |
| N | 0.8720 | 0.6950 |
| O | 0.8850 | 0.6920 |
| P | 0.8520 | 0.6820 |
| Q | 0.7320 | 0.6360 |
| R | 0.8430 | 0.6680 |
| S | 0.7270 | 0.6340 |
| T | 0.4390 | 0.5390 |
| U | 0.7120 | 0.6200 |
| V | 0.8350 | 0.6770 |
| W | 0.4690 | 0.5600 |
| X | 0.8420 | 0.6890 |
| Y | 0.8410 | 0.6790 |
| Z | 0.7620 | 0.6440 |

*Continued on next page...*

*Continued from previous page...*

| Chain | Atom inclusion | Q-score |
|---|---|---|
| a | 0.6680 | 0.6190 |
| b | 0.6780 | 0.6160 |
| c | 0.7050 | 0.6280 |
| d | 0.8040 | 0.6670 |
| e | 0.8590 | 0.6870 |
| f | 0.9110 | 0.7000 |
| g | 0.8250 | 0.6700 |
| h | 0.8420 | 0.6770 |
| i | 0.5580 | 0.5970 |
| j | 0.9410 | 0.7150 |
| k | 0.6130 | 0.6140 |
| l | 0.9180 | 0.7140 |
| m | 0.6810 | 0.6290 |
| n | 0.4310 | 0.5790 |
| o | 0.2700 | 0.4650 |
| p | 0.8240 | 0.6720 |
| q | 0.2630 | 0.5370 |
| r | 0.8030 | 0.6670 |
| s | 0.4110 | 0.5190 |
| t | 0.2300 | 0.5060 |
| u | 0.7650 | 0.6370 |
| v | 0.4100 | 0.5520 |
| w | 0.4300 | 0.5420 |
| x | 0.5060 | 0.5540 |
| y | 0.7850 | 0.6510 |
| z | 0.6380 | 0.6200 |