# wwPDB EM Validation Summary Report

Jul 8, 2024 – 04:37 pm BST

| | | |
|---|---|---|
| PDB ID | : | 7QV2 |
| EMDB ID | : | EMD-14158 |
| Title | : | Bacillus subtilis collided disome (Collided 70S) |
| Authors | : | Filbeck, S.; Pfeffer, S. |
| Deposited on | : | 2022-01-19 |
| Resolution | : | 3.50 Å(reported) |

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

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

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

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

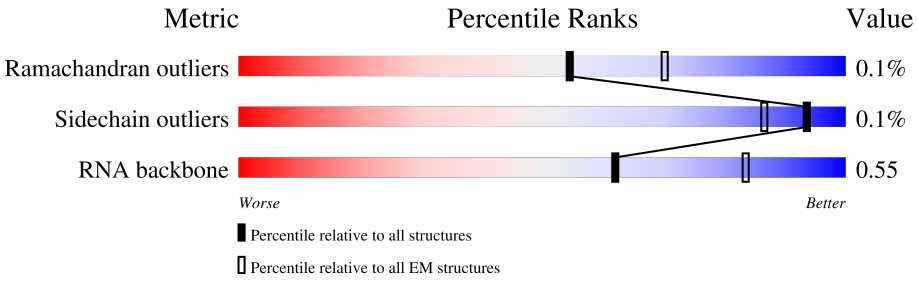
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev92 |
| MolProbity | : | 4.02b-467 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| MapQ | : | 1.9.13 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.37.1 |

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.50 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 | 0 | 59 | 92% 8% |
| 2 | 1 | 49 | 8% 98% |
| 3 | 2 | 44 | 100% |
| 4 | 3 | 66 | 97% |
| 5 | 4 | 37 | 100% |
| 6 | 6 | 66 | 82% 82% 18% |
| 7 | A | 29 | 48% 48% 38% 14% |
| 8 | B | 112 | 5% 74% 26% |

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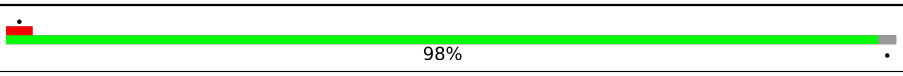
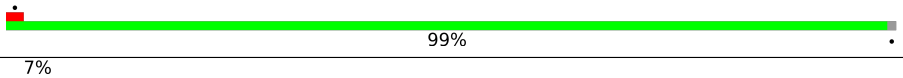
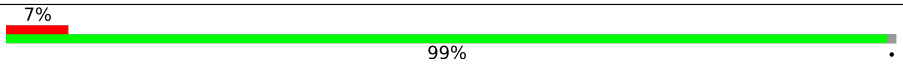
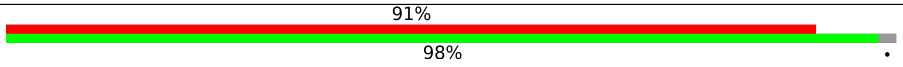
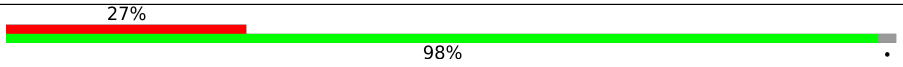
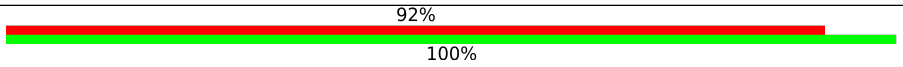
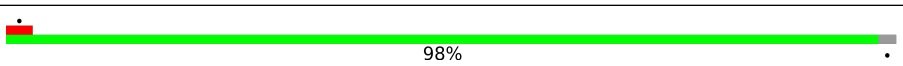
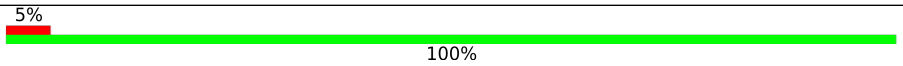
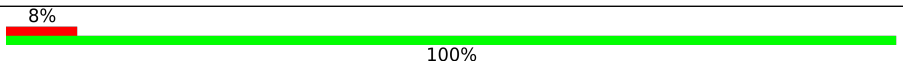
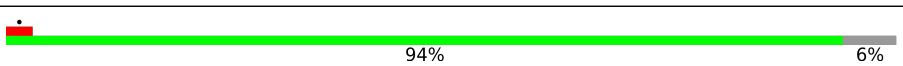
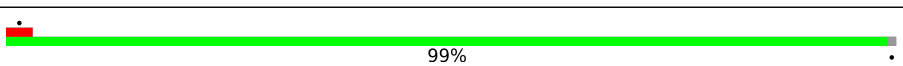
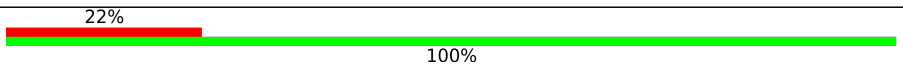
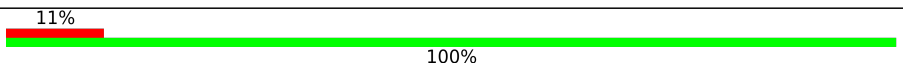
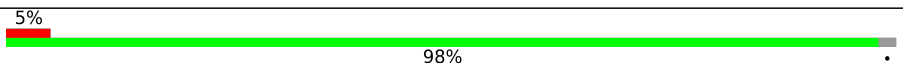
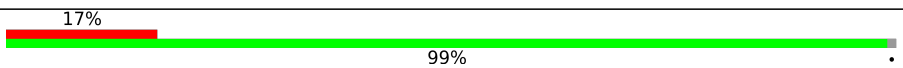
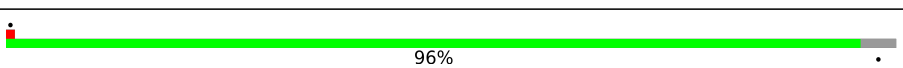
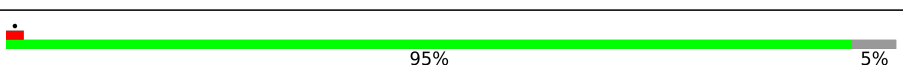
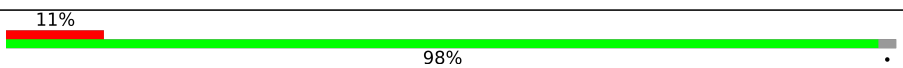
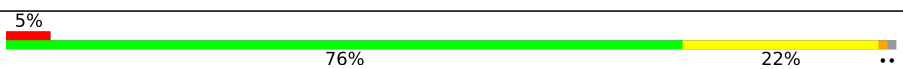
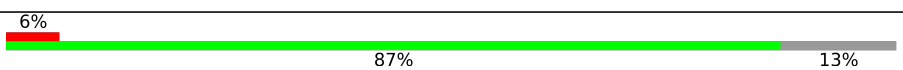
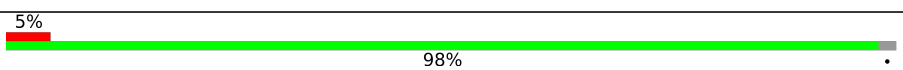
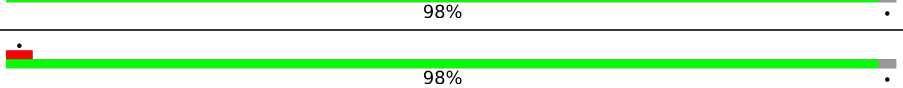
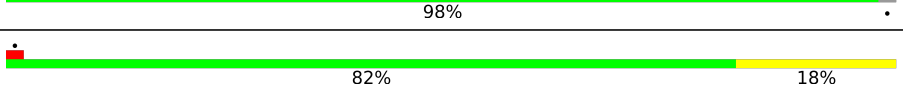
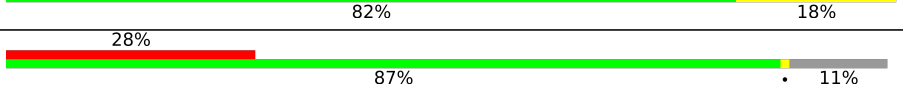
| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 9 | C | 277 |   |
| 10 | D | 209 |   |
| 11 | E | 207 |   |
| 12 | F | 179 |   |
| 13 | G | 179 |   |
| 14 | H | 77 |   |
| 15 | I | 24 |   |
| 16 | J | 145 |   |
| 17 | K | 122 |   |
| 18 | L | 146 |   |
| 19 | M | 144 |   |
| 20 | N | 120 |   |
| 21 | O | 120 |   |
| 22 | P | 115 |   |
| 23 | Q | 119 |   |
| 24 | R | 102 |   |
| 25 | S | 113 |   |
| 26 | T | 95 |   |
| 27 | U | 103 |   |
| 28 | V | 2928 |   |
| 29 | W | 94 |   |
| 30 | Y | 66 |   |
| 31 | Z | 59 |   |
| 32 | a | 1545 |   |
| 33 | b | 246 |   |

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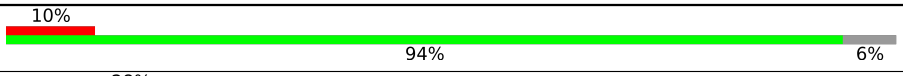
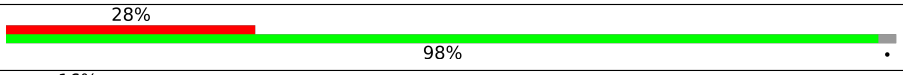
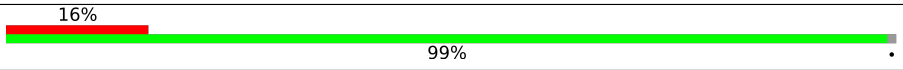
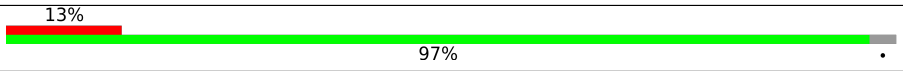
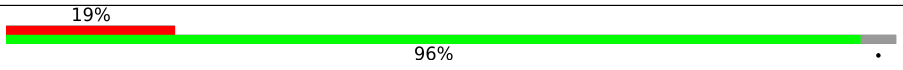
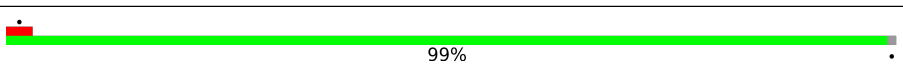
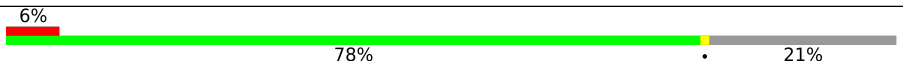
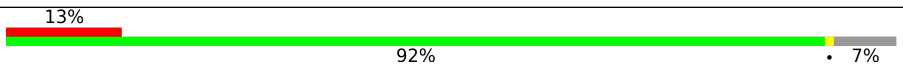
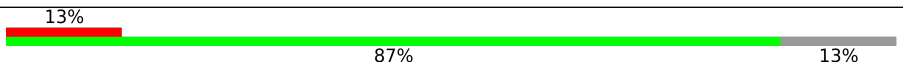
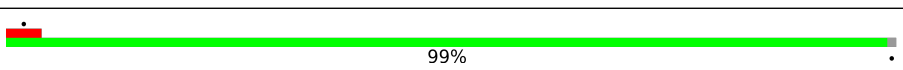
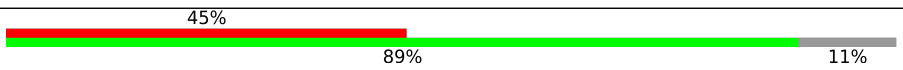
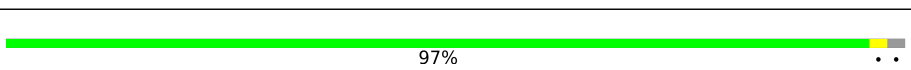
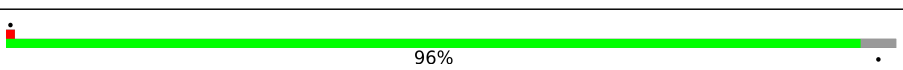
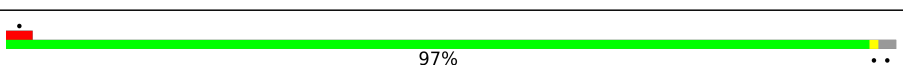
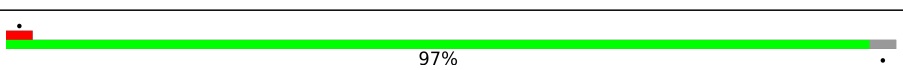
| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 34 | c | 218 |   |
| 35 | d | 200 |   |
| 36 | e | 166 |   |
| 37 | f | 95 |   |
| 38 | g | 156 |   |
| 39 | h | 132 |   |
| 40 | i | 130 |   |
| 41 | j | 102 |   |
| 42 | k | 131 |   |
| 43 | l | 138 |   |
| 44 | m | 121 |   |
| 45 | n | 61 |   |
| 46 | o | 89 |   |
| 47 | p | 90 |   |
| 48 | q | 87 |   |
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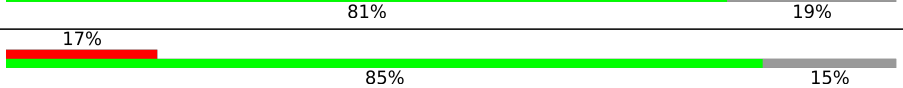
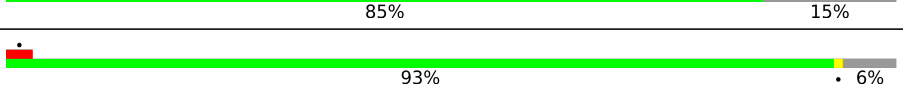
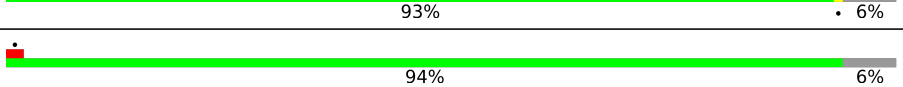
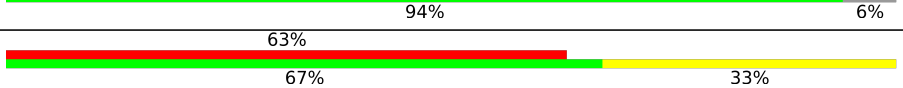
| 50 | s | 92 |   |
| 51 | t | 88 |   |
| 52 | u | 62 |   |
| 53 | x | 76 |   |

# 2 Entry composition (i)

There are 53 unique types of molecules in this entry. The entry contains 142856 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 50S ribosomal protein L32.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 1 | 0 | 54 | 426 | 262 | 86 | 71 | 7 | 0 | 0 |

- Molecule 2 is a protein called 50S ribosomal protein L33 1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 2 | 1 | 48 | 401 | 244 | 80 | 73 | 4 | 0 | 0 |

- Molecule 3 is a protein called 50S ribosomal protein L34.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 3 | 2 | 44 | 368 | 222 | 89 | 55 | 2 | 0 | 0 |

- Molecule 4 is a protein called 50S ribosomal protein L35.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 4 | 3 | 64 | 512 | 321 | 107 | 82 | 2 | 0 | 0 |

- Molecule 5 is a protein called 50S ribosomal protein L36.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 5 | 4 | 37 | 297 | 186 | 60 | 46 | 5 | 0 | 0 |

- Molecule 6 is a protein called 50S ribosomal protein L31.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 6 | 6 | 54 | 413 | 257 | 73 | 78 | 5 | 0 | 0 |

- Molecule 7 is a RNA chain called mRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 7 | A | 29 | Total | C | N | O | P | 0 | 0 |
| | | | 630 | 282 | 124 | 195 | 29 | | |

- Molecule 8 is a RNA chain called 5S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 8 | B | 112 | Total | C | N | O | P | 0 | 0 |
| | | | 2392 | 1068 | 435 | 778 | 111 | | |

- Molecule 9 is a protein called 50S ribosomal protein L2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 9 | C | 272 | Total | C | N | O | S | 0 | 0 |
| | | | 2083 | 1296 | 408 | 373 | 6 | | |

- Molecule 10 is a protein called 50S ribosomal protein L3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 10 | D | 206 | Total | C | N | O | S | 0 | 0 |
| | | | 1569 | 985 | 289 | 290 | 5 | | |

- Molecule 11 is a protein called 50S ribosomal protein L4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 11 | E | 205 | Total | C | N | O | S | 0 | 0 |
| | | | 1561 | 980 | 289 | 290 | 2 | | |

- Molecule 12 is a protein called 50S ribosomal protein L5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 12 | F | 176 | Total | C | N | O | S | 0 | 0 |
| | | | 1386 | 882 | 241 | 256 | 7 | | |

- Molecule 13 is a protein called 50S ribosomal protein L6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 13 | G | 175 | Total | C | N | O | S | 0 | 0 |
| | | | 1342 | 835 | 248 | 257 | 2 | | |

- Molecule 14 is a RNA chain called A/P-site tRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 14 | H | 77 | Total | C | N | O | P | 0 | 0 |
| | | | 1643 | 731 | 290 | 545 | 77 | | |

- Molecule 15 is a protein called Nascent chain.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 15 | I | 24 | Total | C | N | O | 0 | 0 |
| | | | 121 | 72 | 24 | 25 | | |

- Molecule 16 is a protein called 50S ribosomal protein L13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 16 | J | 142 | Total | C | N | O | S | 0 | 0 |
| | | | 1124 | 710 | 206 | 203 | 5 | | |

- Molecule 17 is a protein called 50S ribosomal protein L14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 17 | K | 122 | Total | C | N | O | S | 0 | 0 |
| | | | 921 | 571 | 173 | 173 | 4 | | |

- Molecule 18 is a protein called 50S ribosomal protein L15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 18 | L | 146 | Total | C | N | O | S | 0 | 0 |
| | | | 1082 | 671 | 207 | 202 | 2 | | |

- Molecule 19 is a protein called 50S ribosomal protein L16.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 19 | M | 135 | Total | C | N | O | S | 0 | 0 |
| | | | 1076 | 690 | 205 | 176 | 5 | | |

- Molecule 20 is a protein called 50S ribosomal protein L17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 20 | N | 119 | Total | C | N | O | S | 0 | 0 |
| | | | 954 | 583 | 186 | 181 | 4 | | |

- Molecule 21 is a protein called 50S ribosomal protein L18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 21 | O | 120 | Total | C | N | O | S | 0 | 0 |
| | | | 913 | 564 | 176 | 172 | 1 | | |

- Molecule 22 is a protein called 50S ribosomal protein L19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 22 | P | 115 | Total | C | N | O | S | 0 | 0 |
| | | | 945 | 600 | 185 | 159 | 1 | | |

- Molecule 23 is a protein called 50S ribosomal protein L20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 23 | Q | 117 | Total | C | N | O | S | 0 | 0 |
| | | | 940 | 591 | 189 | 156 | 4 | | |

- Molecule 24 is a protein called 50S ribosomal protein L21.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 24 | R | 101 | Total | C | N | O | 0 | 0 |
| | | | 787 | 501 | 139 | 147 | | |

- Molecule 25 is a protein called 50S ribosomal protein L22.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 25 | S | 109 | Total | C | N | O | S | 0 | 0 |
| | | | 842 | 525 | 164 | 150 | 3 | | |

- Molecule 26 is a protein called 50S ribosomal protein L23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 26 | T | 90 | Total | C | N | O | S | 0 | 0 |
| | | | 725 | 452 | 134 | 136 | 3 | | |

- Molecule 27 is a protein called 50S ribosomal protein L24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 27 | U | 101 | Total | C | N | O | S | 0 | 0 |
| | | | 762 | 478 | 142 | 138 | 4 | | |

- Molecule 28 is a RNA chain called 23S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 28 | V | 2887 | Total | C | N | O | P | 0 | 0 |
| | | | 61999 | 27661 | 11460 | 19994 | 2884 | | |

There are 6 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| V | 243 | G | A | conflict | GB 1491848961 |
| V | 325 | A | - | insertion | GB 1491848961 |
| V | 326 | A | - | insertion | GB 1491848961 |
| V | 327 | G | - | insertion | GB 1491848961 |
| V | 328 | G | - | insertion | GB 1491848961 |
| V | 640 | U | C | conflict | GB 1491848961 |

- Molecule 29 is a protein called 50S ribosomal protein L27.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 29 | W | 82 | Total | C | N | O | 0 | 0 |
| | | | 630 | 390 | 123 | 117 | | |

- Molecule 30 is a protein called 50S ribosomal protein L29.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 30 | Y | 65 | Total | C | N | O | S | 0 | 0 |
| | | | 530 | 328 | 102 | 98 | 2 | | |

- Molecule 31 is a protein called 50S ribosomal protein L30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 31 | Z | 58 | Total | C | N | O | S | 0 | 0 |
| | | | 456 | 281 | 89 | 85 | 1 | | |

- Molecule 32 is a RNA chain called 16S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 32 | a | 1545 | Total | C | N | O | P | 0 | 0 |
| | | | 33138 | 14778 | 6072 | 10743 | 1545 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| a | 1541 | G | - | insertion | GB 225184640 |

- Molecule 33 is a protein called 30S ribosomal protein S2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 33 | b | 218 | Total | C | N | O | S | 0 | 0 |
| | | | 1757 | 1119 | 309 | 323 | 6 | | |

- Molecule 34 is a protein called 30S ribosomal protein S3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 34 | c | 206 | Total | C | N | O | S | 0 | 0 |
| | | | 1619 | 1011 | 304 | 301 | 3 | | |

- Molecule 35 is a protein called 30S ribosomal protein S4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 35 | d | 195 | Total | C | N | O | S | 0 | 0 |
| | | | 1569 | 991 | 291 | 285 | 2 | | |

- Molecule 36 is a protein called 30S ribosomal protein S5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 36 | e | 164 | Total | C | N | O | S | 0 | 0 |
| | | | 1219 | 767 | 225 | 225 | 2 | | |

- Molecule 37 is a protein called 30S ribosomal protein S6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 37 | f | 92 | Total | C | N | O | S | 0 | 0 |
| | | | 755 | 476 | 132 | 146 | 1 | | |

- Molecule 38 is a protein called 30S ribosomal protein S7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 38 | g | 149 | Total | C | N | O | S | 0 | 0 |
| | | | 1181 | 740 | 220 | 215 | 6 | | |

- Molecule 39 is a protein called 30S ribosomal protein S8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 39 | h | 131 | Total | C | N | O | S | 0 | 0 |
| | | | 1037 | 655 | 191 | 188 | 3 | | |

- Molecule 40 is a protein called 30S ribosomal protein S9.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 40 | i | 103 | Total | C | N | O | 0 | 0 |
| | | | 784 | 485 | 151 | 148 | | |

- Molecule 41 is a protein called 30S ribosomal protein S10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 41 | j | 95 | Total | C | N | O | S | 0 | 0 |
| | | | 761 | 479 | 139 | 141 | 2 | | |

- Molecule 42 is a protein called 30S ribosomal protein S11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 42 | k | 114 | Total | C | N | O | S | 0 | 0 |
| | | | 839 | 516 | 164 | 157 | 2 | | |

- Molecule 43 is a protein called 30S ribosomal protein S12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 43 | l | 136 | Total | C | N | O | S | 0 | 0 |
| | | | 1052 | 653 | 211 | 186 | 2 | | |

- Molecule 44 is a protein called 30S ribosomal protein S13.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 44 | m | 108 | Total | C | N | O | 0 | 0 |
| | | | 868 | 534 | 176 | 158 | | |

- Molecule 45 is a protein called 30S ribosomal protein S14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 45 | n | 60 | Total | C | N | O | S | 0 | 0 |
| | | | 498 | 317 | 98 | 78 | 5 | | |

- Molecule 46 is a protein called 30S ribosomal protein S15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 46 | o | 85 | Total | C | N | O | S | 0 | 0 |
| | | | 710 | 436 | 144 | 129 | 1 | | |

- Molecule 47 is a protein called 30S ribosomal protein S16.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 47 | p | 88 | Total | C | N | O | S | 0 | 0 |
| | | | 695 | 441 | 128 | 124 | 2 | | |

- Molecule 48 is a protein called 30S ribosomal protein S17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 48 | q | 84 | Total | C | N | O | S | 0 | 0 |
| | | | 691 | 435 | 128 | 126 | 2 | | |

- Molecule 49 is a protein called 30S ribosomal protein S18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 49 | r | 64 | Total | C | N | O | S | 0 | 0 |
| | | | 518 | 332 | 96 | 88 | 2 | | |

- Molecule 50 is a protein called 30S ribosomal protein S19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 50 | s | 78 | Total | C | N | O | S | 0 | 0 |
| | | | 633 | 409 | 112 | 110 | 2 | | |

- Molecule 51 is a protein called 30S ribosomal protein S20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 51 | t | 83 | Total | C | N | O | S | 0 | 0 |
| | | | 637 | 390 | 130 | 116 | 1 | | |

- Molecule 52 is a protein called 50S ribosomal protein L28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 52 | u | 58 | Total | C | N | O | S | 0 | 0 |
| | | | 444 | 275 | 92 | 75 | 2 | | |

- Molecule 53 is a RNA chain called P/E-site tRNA.

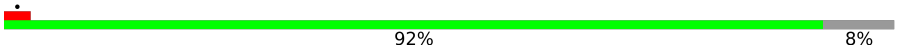
| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 53 | x | 76 | Total | C | N | O | P | 0 | 0 |
| | | | 1621 | 721 | 285 | 539 | 76 | | |

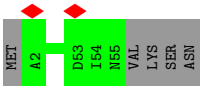
# 3 Residue-property plots (i)

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: 50S ribosomal protein L32

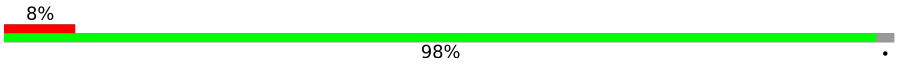
Chain 0:

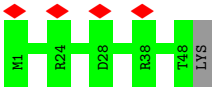



• Molecule 2: 50S ribosomal protein L33 1

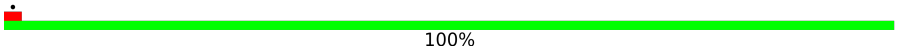
Chain 1:

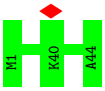



• Molecule 3: 50S ribosomal protein L34

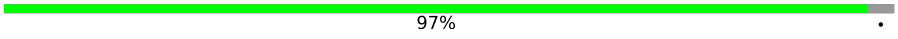
Chain 2:




• Molecule 4: 50S ribosomal protein L35

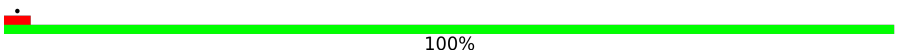
Chain 3:





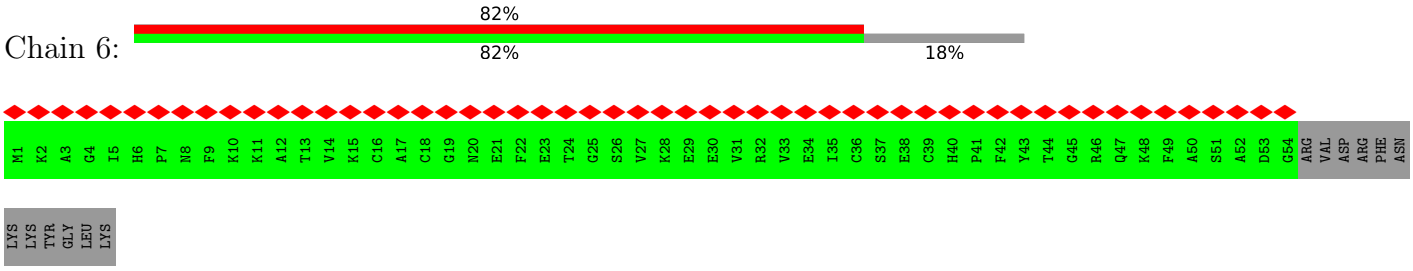
• Molecule 5: 50S ribosomal protein L36

Chain 4:



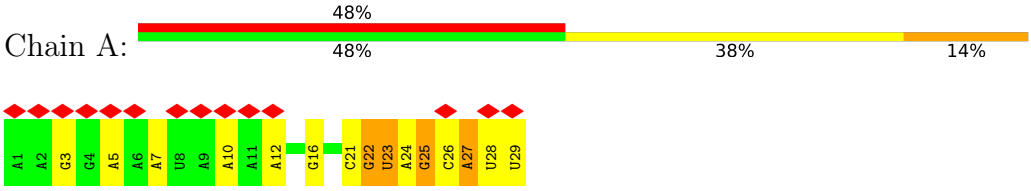

• Molecule 6: 50S ribosomal protein L31

Chain 6:



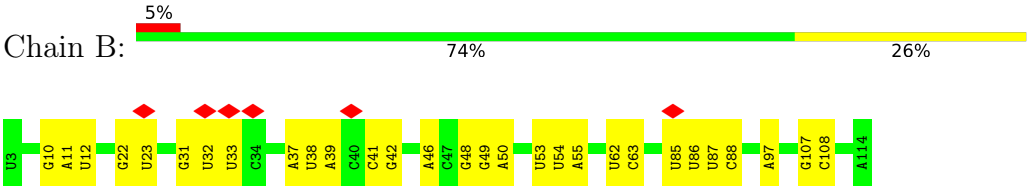

• Molecule 7: mRNA

Chain A:



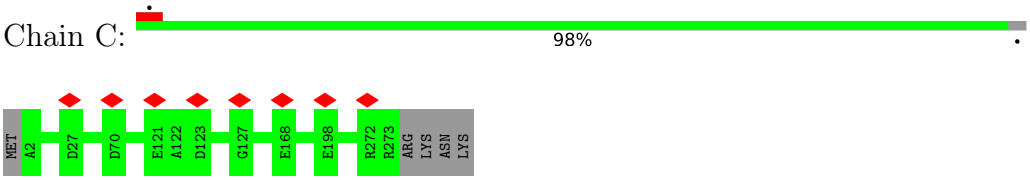

• Molecule 8: 5S ribosomal RNA

Chain B:



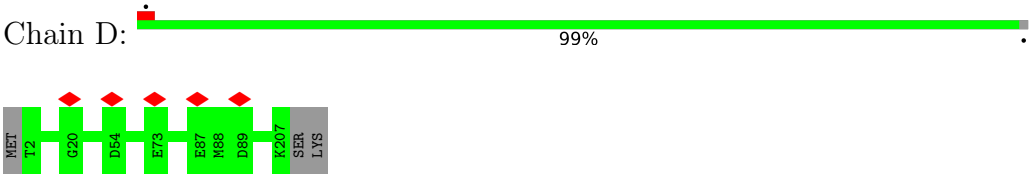

• Molecule 9: 50S ribosomal protein L2

Chain C:



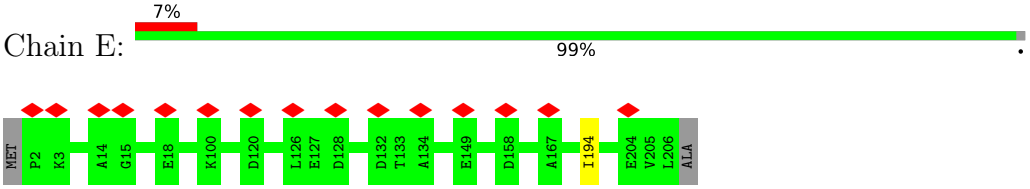

• Molecule 10: 50S ribosomal protein L3

Chain D:



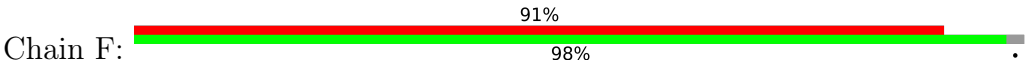

• Molecule 11: 50S ribosomal protein L4

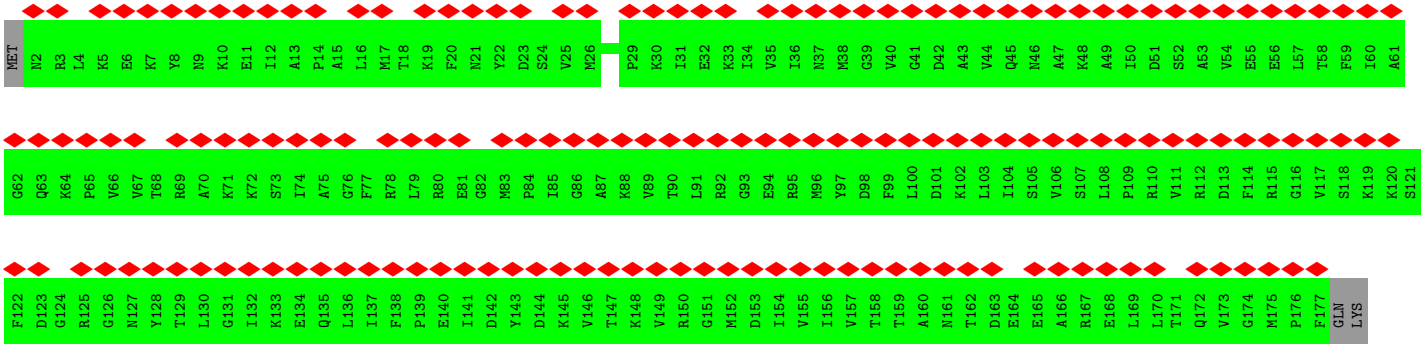
Chain E:




• Molecule 12: 50S ribosomal protein L5

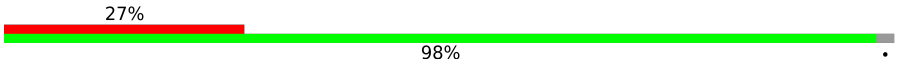
Chain F:

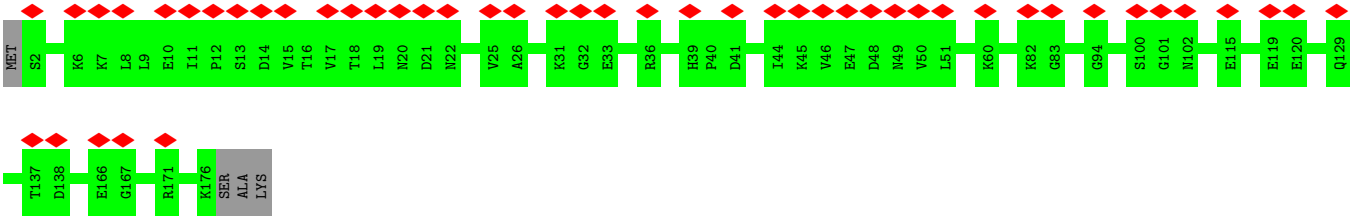





• Molecule 13: 50S ribosomal protein L6

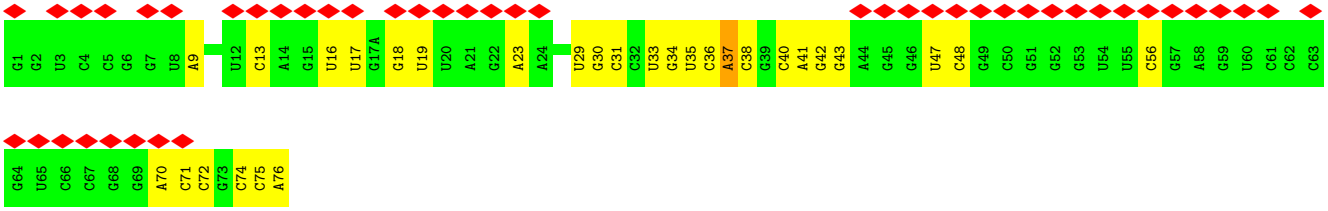
Chain G:



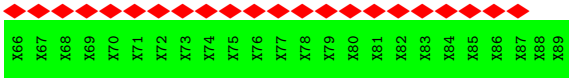

• Molecule 14: A/P-site tRNA

Chain H:

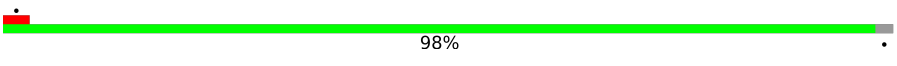

• Molecule 15: Nascent chain

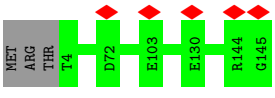
Chain I:


• Molecule 16: 50S ribosomal protein L13

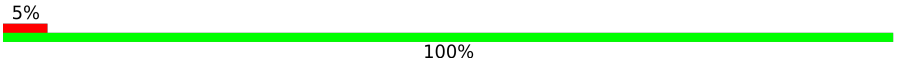
Chain J:

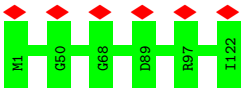



• Molecule 17: 50S ribosomal protein L14

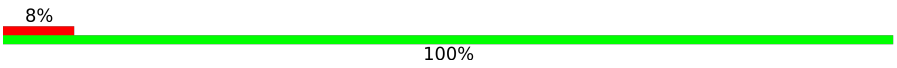
Chain K:

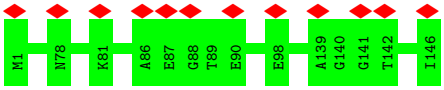



• Molecule 18: 50S ribosomal protein L15

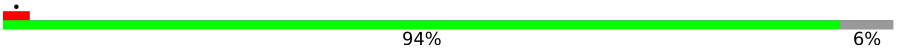
Chain L:

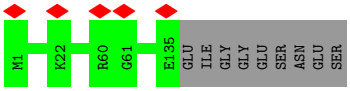



• Molecule 19: 50S ribosomal protein L16

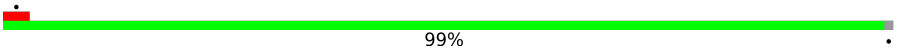
Chain M:

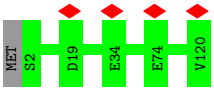



• Molecule 20: 50S ribosomal protein L17

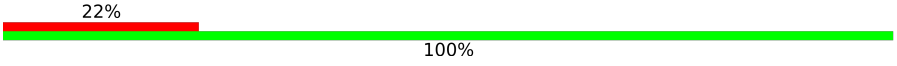
Chain N:

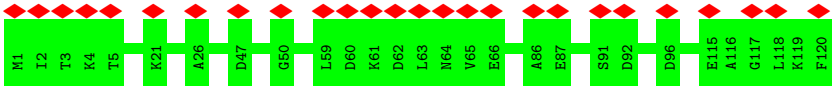



• Molecule 21: 50S ribosomal protein L18

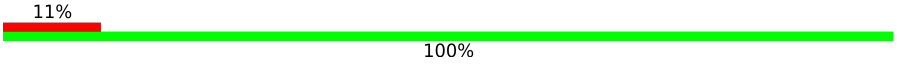
Chain O:

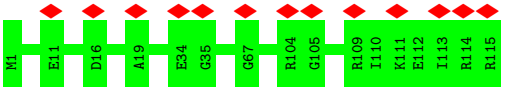



• Molecule 22: 50S ribosomal protein L19

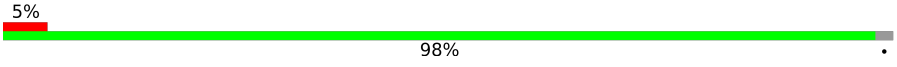
Chain P:

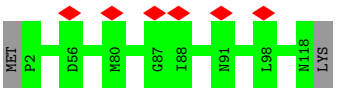



• Molecule 23: 50S ribosomal protein L20

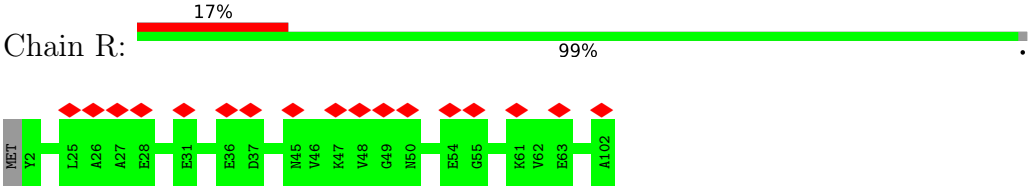
Chain Q:



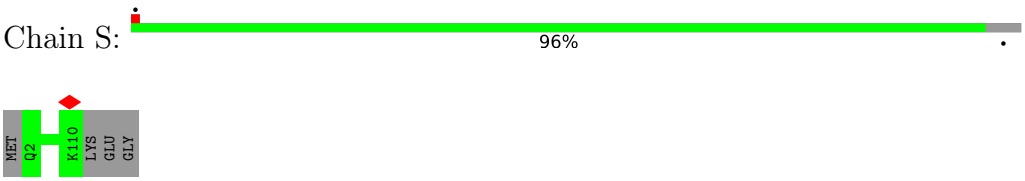
• Molecule 24: 50S ribosomal protein L21

Chain R:



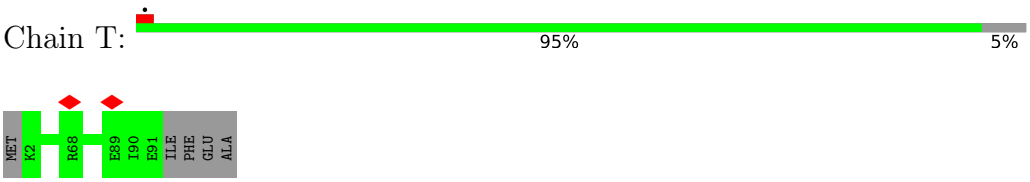

• Molecule 25: 50S ribosomal protein L22

Chain S:



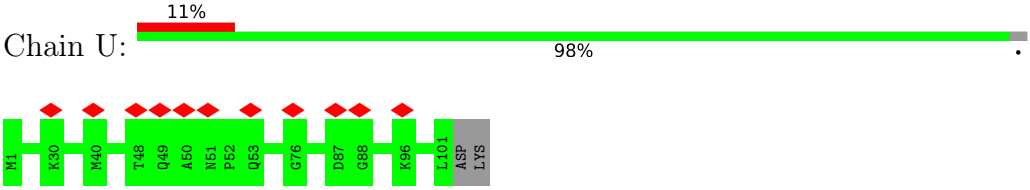

• Molecule 26: 50S ribosomal protein L23

Chain T:



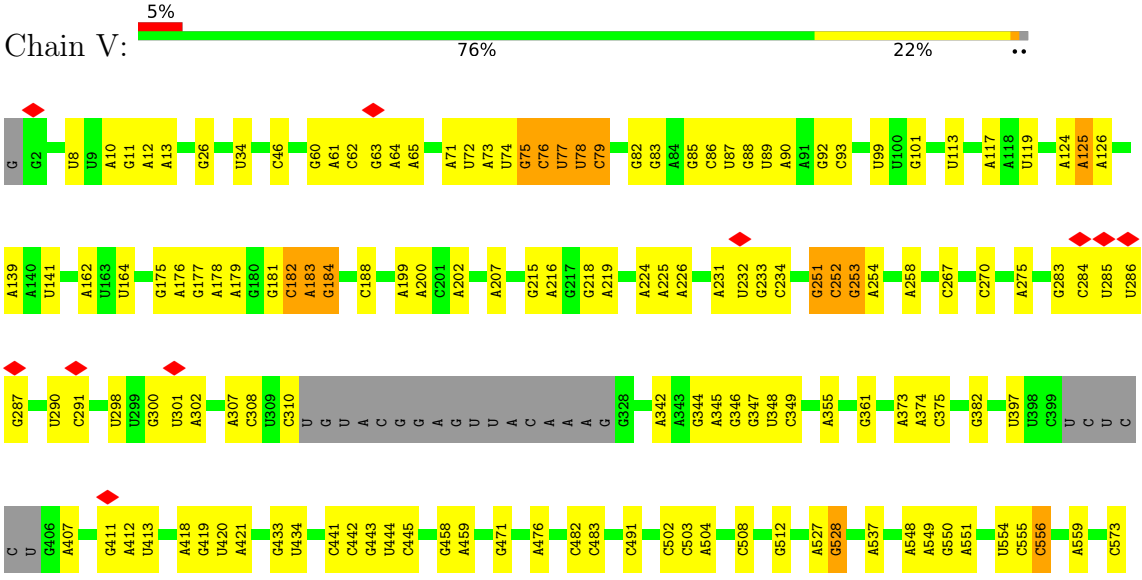

• Molecule 27: 50S ribosomal protein L24

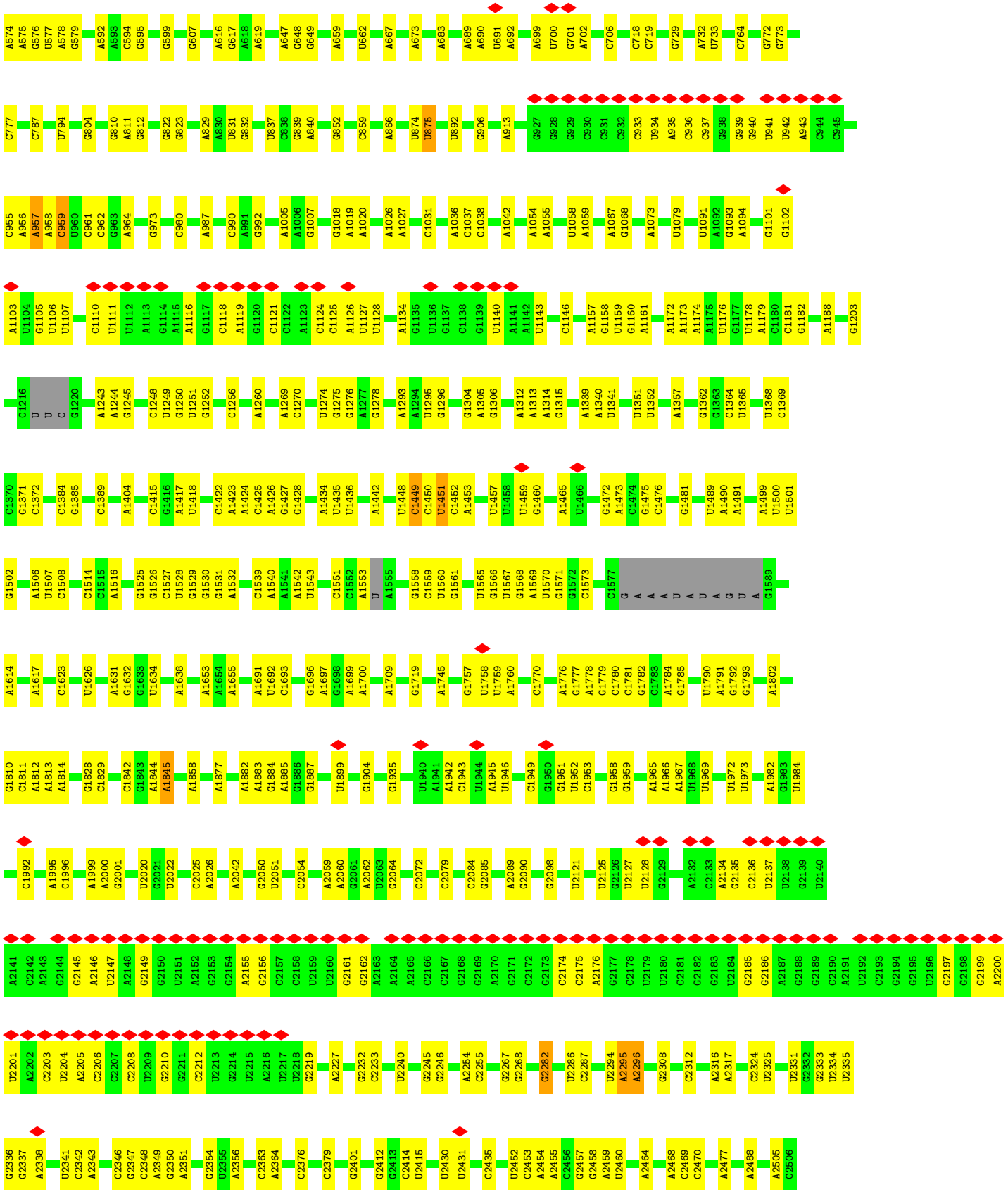
Chain U:




• Molecule 28: 23S ribosomal RNA

Chain V:

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C777 C787 U794 G804 G810 A811 G812 G822 G823 A829 A830 U831 G832 U837 C838 G839 A840 G852 C859 A866 U874 U875 U892 G906 A913 G927 G928 G929 C930 C931 C932 C933 U934 A935 C936 C937 G938 G939 G940 U941 U942 A943 C944 C945
C955 A956 A957 A958 C959 U960 C961 C962 G963 A964 G973 C980 A987 C990 A991 G992 A1005 A1006 G1007 G1018 A1019 A1020 A1026 A1027 C1031 A1036 C1037 C1038 A1042 A1054 A1055 U1058 A1059 A1067 G1068 A1073 U1079 U1091 A1092 G1093 A1094 G1101 G1102
A1103 U1104 G1105 U1106 U1107 C1110 U1111 U1112 A1113 G1114 A1115 A1116 G1117 C1118 A1119 G1120 C1121 C1122 A1123 C1124 C1125 A1126 U1127 U1128 A1134 G1135 U1136 G1137 C1138 G1139 U1140 A1141 A1142 U1143 C1146 A1157 G1158 U1159 G1160 A1161 A1172 A1173 A1174 A1175 U1176 G1177 U1178 A1179 C1180 C1181 G1182 A1188 G1203
C1216 U U U C G1220 A1243 A1244 G1245 C1248 U1249 G1250 U1251 G1252 C1256 A1260 A1269 C1270 U1274 G1275 G1276 A1277 G1278 A1293 A1294 U1295 G1296 G1304 A1305 G1306 A1312 A1313 A1314 G1315 A1339 A1340 U1341 U1351 U1352 A1357 G1362 G1363 C1364 U1365 U1368 C1369
C1370 G1371 C1372 C1384 G1385 C1389 A1404 C1415 G1416 A1417 U1418 C1422 A1423 A1424 C1425 A1426 G1427 G1428 A1434 U1435 U1436 A1442 U1448 C1449 C1450 U1451 C1452 A1453 U1457 U1458 U1459 G1460 A1465 U1466 G1472 A1473 C1474 G1475 C1476 G1481 U1489 A1490 A1491 A1499 U1500 U1501
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C1992 A1995 C1996 A1999 A2000 G2001 U2020 G2021 U2022 C2025 A2026 A2042 G2050 U2051 C2054 A2059 A2060 G2061 A2062 U2063 G2064 C2072 C2079 C2084 G2085 A2089 G2090 G2098 U2121 U2125 G2126 U2127 U2128 G2129 A2132 C2133 A2134 G2135 C2136 U2137 U2138 G2139 U2140
A2141 C2142 A2143 G2144 G2145 A2146 U2147 A2148 G2149 G2150 U2151 A2152 G2153 G2154 A2155 G2156 C2157 C2158 U2159 U2160 G2161 G2162 A2163 A2164 A2165 C2166 C2167 G2168 G2169 A2170 G2171 C2172 G2173 C2174 C2175 A2176 G2177 C2178 U2179 U2180 C2181 G2182 G2183 U2184 G2185 G2186 A2187 G2188 G2189 C2190 A2191 U2192 C2193 G2194 G2195 U2196 G2197 G2198 G2199 A2200
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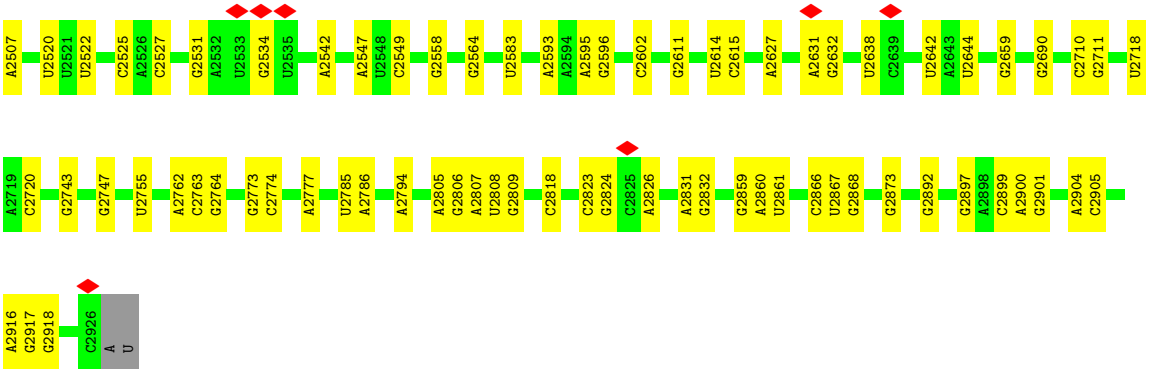
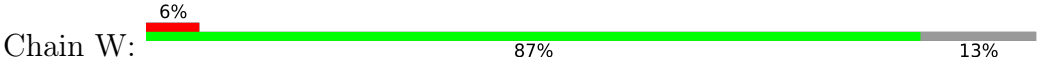
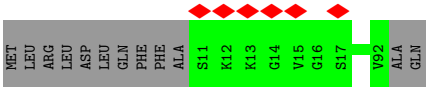
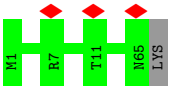



• Molecule 29: 50S ribosomal protein L27



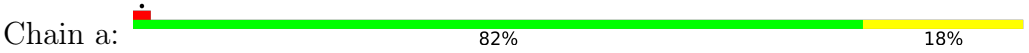

• Molecule 30: 50S ribosomal protein L29

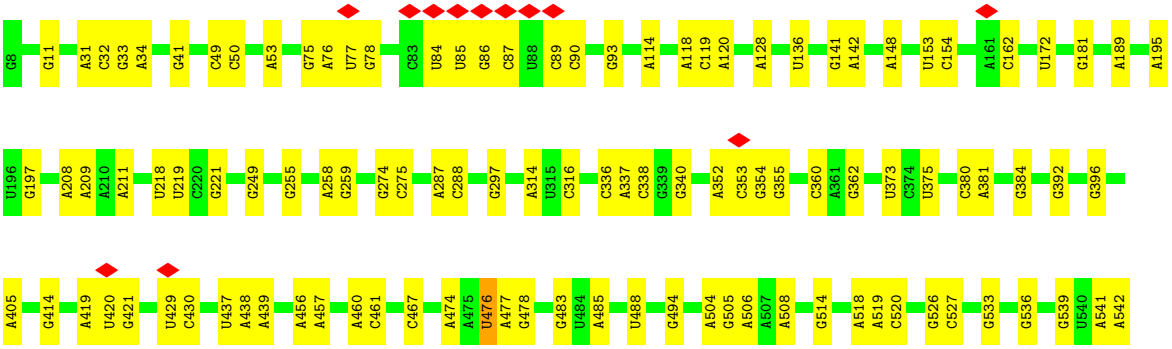



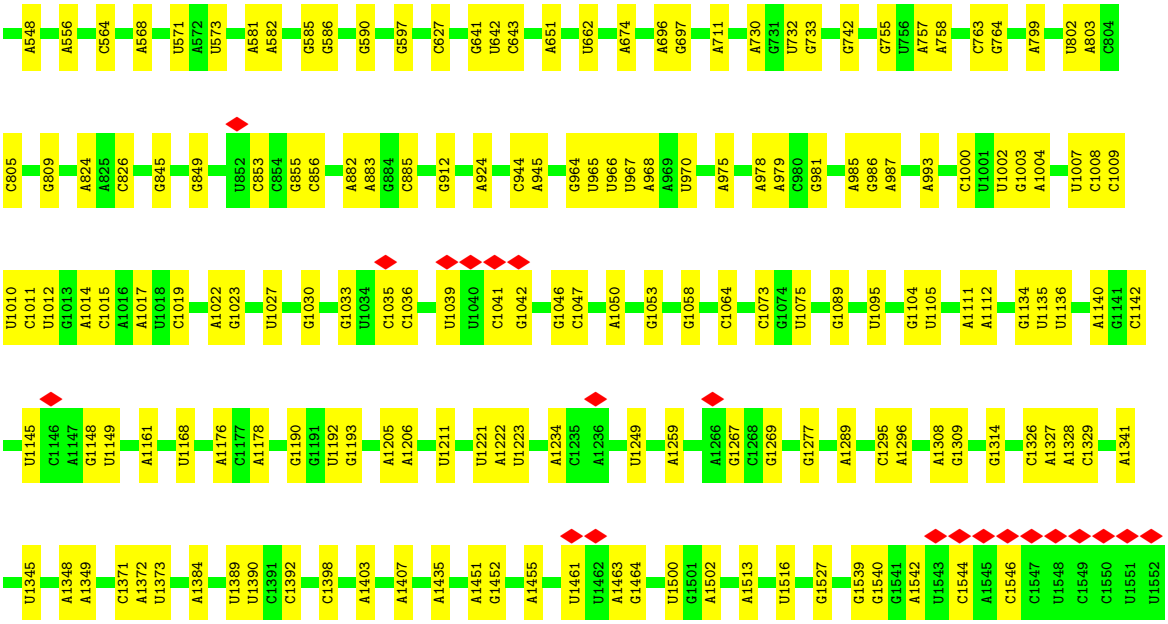

• Molecule 31: 50S ribosomal protein L30



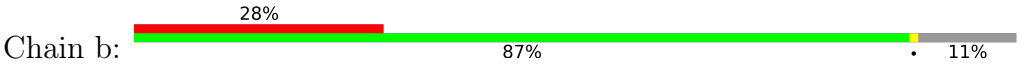
• Molecule 32: 16S ribosomal RNA

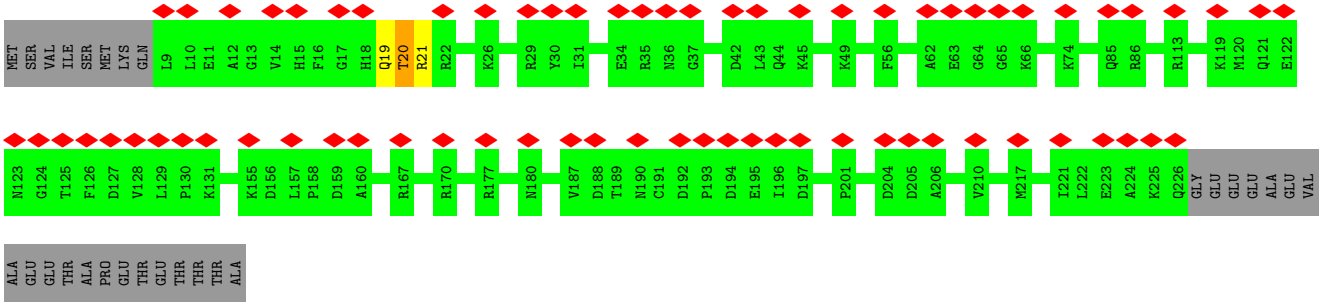


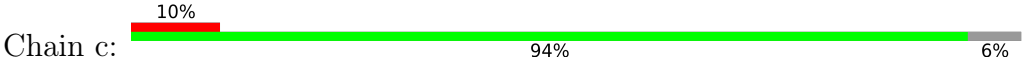


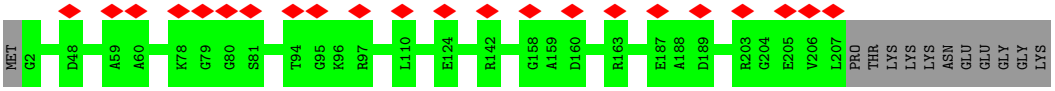

- Molecule 33: 30S ribosomal protein S2



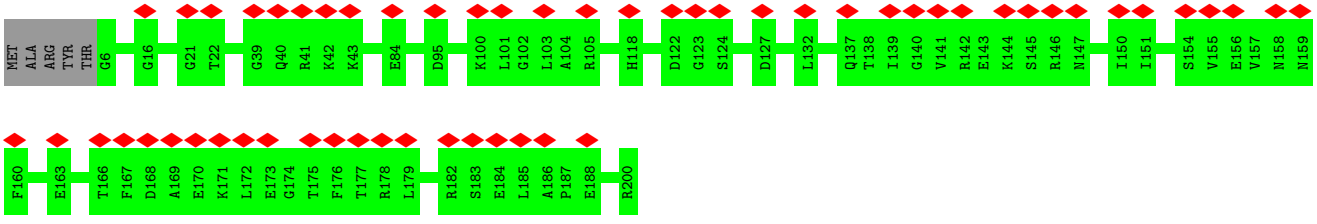




- Molecule 34: 30S ribosomal protein S3



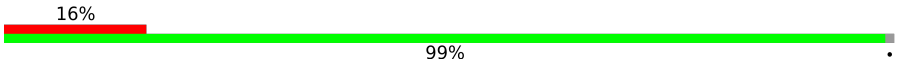



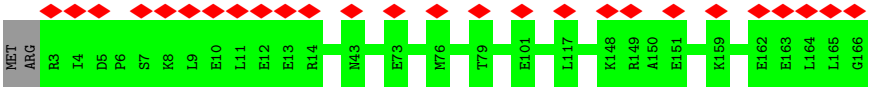

- Molecule 35: 30S ribosomal protein S4

• Molecule 36: 30S ribosomal protein S5

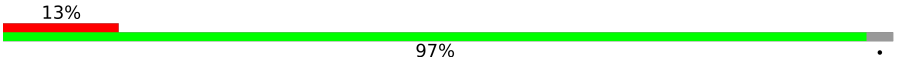
Chain e:

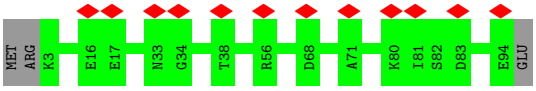



• Molecule 37: 30S ribosomal protein S6

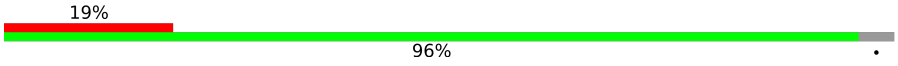
Chain f:

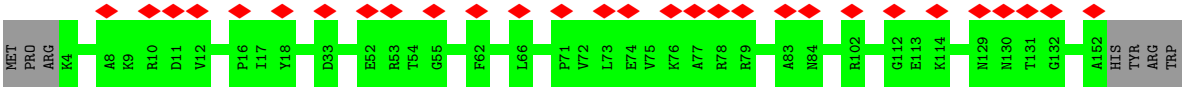



• Molecule 38: 30S ribosomal protein S7

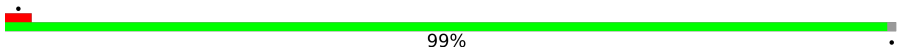
Chain g:

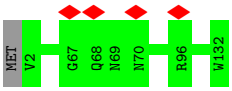



• Molecule 39: 30S ribosomal protein S8

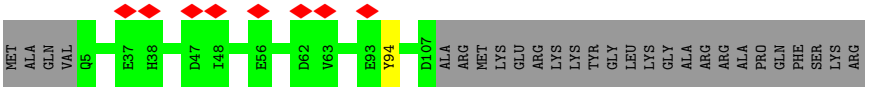
Chain h:



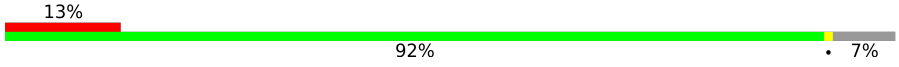

• Molecule 40: 30S ribosomal protein S9

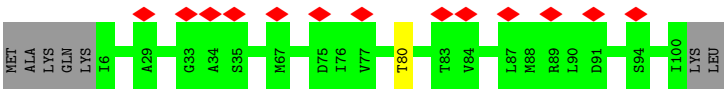
Chain i:


• Molecule 41: 30S ribosomal protein S10

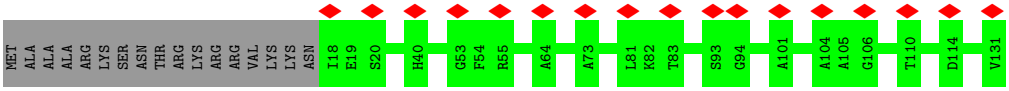
Chain j:



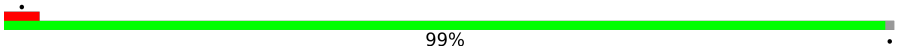

• Molecule 42: 30S ribosomal protein S11

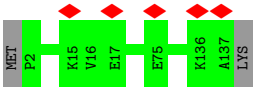
Chain k:




• Molecule 43: 30S ribosomal protein S12

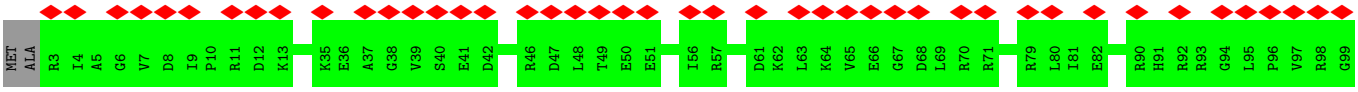
Chain l:

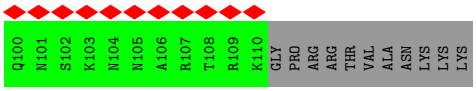



• Molecule 44: 30S ribosomal protein S13

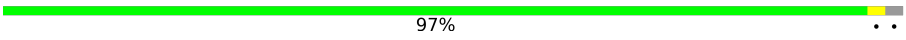
Chain m:

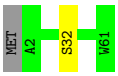




• Molecule 45: 30S ribosomal protein S14

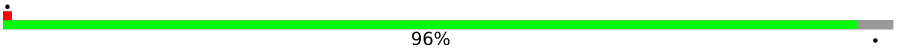
Chain n:

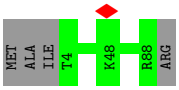



• Molecule 46: 30S ribosomal protein S15

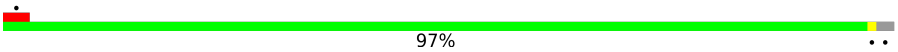
Chain o:

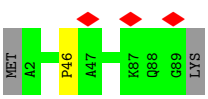



• Molecule 47: 30S ribosomal protein S16

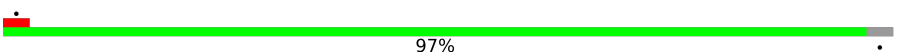
Chain p:

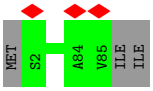



• Molecule 48: 30S ribosomal protein S17

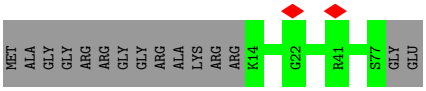
Chain q:





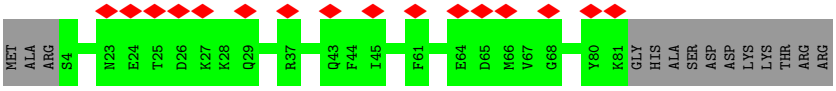

• Molecule 49: 30S ribosomal protein S18

Chain r:

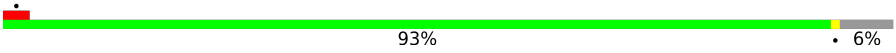

• Molecule 50: 30S ribosomal protein S19

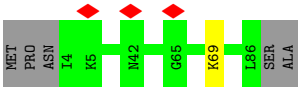
Chain s:


• Molecule 51: 30S ribosomal protein S20

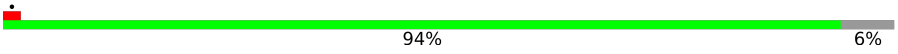
Chain t:

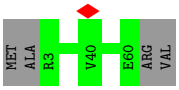



• Molecule 52: 50S ribosomal protein L28

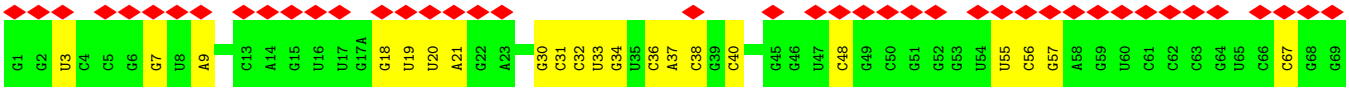
Chain u:

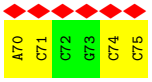



• Molecule 53: P/E-site tRNA

Chain x:

# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 27833 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/Å^2$) | 46.5 | Depositor |
| Minimum defocus (nm) | 750 | Depositor |
| Maximum defocus (nm) | 2000 | Depositor |
| Magnification | Not provided | |
| Image detector | GATAN K3 BIOQUANTUM (6k x 4k) | Depositor |
| Maximum map value | 43.238 | Depositor |
| Minimum map value | -15.141 | Depositor |
| Average map value | -0.028 | Depositor |
| Map value standard deviation | 1.347 | Depositor |
| Recommended contour level | 5.0 | Depositor |
| Map size (Å) | 590.64, 590.64, 590.64 | wwPDB |
| Map dimensions | 368, 368, 368 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.605, 1.605, 1.605 | Depositor |

# 5 Model quality

## 5.1 Standard geometry

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

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | #$\|Z\|>5$ | RMSZ | #$\|Z\|>5$ |
| 1 | 0 | 0.26 | 0/433 | 0.40 | 0/574 |
| 2 | 1 | 0.25 | 0/406 | 0.40 | 0/540 |
| 3 | 2 | 0.25 | 0/371 | 0.42 | 0/483 |
| 4 | 3 | 0.25 | 0/519 | 0.44 | 0/680 |
| 5 | 4 | 0.26 | 0/300 | 0.38 | 0/393 |
| 6 | 6 | 0.26 | 0/421 | 0.40 | 0/562 |
| 7 | A | 0.49 | 0/708 | 1.09 | 5/1103 (0.5%) |
| 8 | B | 0.17 | 0/2675 | 0.74 | 0/4170 |
| 9 | C | 0.25 | 0/2120 | 0.42 | 0/2845 |
| 10 | D | 0.29 | 0/1591 | 0.46 | 0/2132 |
| 11 | E | 0.24 | 0/1580 | 0.40 | 0/2132 |
| 12 | F | 0.25 | 0/1405 | 0.42 | 0/1887 |
| 13 | G | 0.23 | 0/1360 | 0.41 | 0/1832 |
| 14 | H | 0.21 | 0/1834 | 0.83 | 1/2858 (0.0%) |
| 16 | J | 0.24 | 0/1147 | 0.41 | 0/1542 |
| 17 | K | 0.26 | 0/928 | 0.44 | 0/1245 |
| 18 | L | 0.26 | 0/1094 | 0.44 | 0/1457 |
| 19 | M | 0.25 | 0/1099 | 0.41 | 0/1468 |
| 20 | N | 0.24 | 0/961 | 0.42 | 0/1284 |
| 21 | O | 0.24 | 0/922 | 0.41 | 0/1236 |
| 22 | P | 0.25 | 0/958 | 0.44 | 0/1279 |
| 23 | Q | 0.24 | 0/952 | 0.39 | 0/1266 |
| 24 | R | 0.26 | 0/798 | 0.46 | 0/1070 |
| 25 | S | 0.24 | 0/851 | 0.43 | 0/1146 |
| 26 | T | 0.25 | 0/731 | 0.42 | 0/974 |
| 27 | U | 0.26 | 0/772 | 0.42 | 0/1032 |
| 28 | V | 0.22 | 0/69445 | 0.76 | 38/108336 (0.0%) |
| 29 | W | 0.30 | 0/638 | 0.50 | 0/847 |
| 30 | Y | 0.24 | 0/531 | 0.37 | 0/707 |
| 31 | Z | 0.23 | 0/458 | 0.44 | 0/613 |
| 32 | a | 0.20 | 0/37100 | 0.73 | 2/57875 (0.0%) |
| 33 | b | 0.25 | 0/1782 | 0.41 | 0/2392 |
| 34 | c | 0.24 | 0/1641 | 0.43 | 0/2208 |
| 35 | d | 0.25 | 0/1599 | 0.39 | 0/2147 |

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | #\|Z\| >5 | RMSZ | #\|Z\| >5 |
| 36 | e | 0.25 | 0/1231 | 0.44 | 0/1655 |
| 37 | f | 0.24 | 0/766 | 0.40 | 0/1031 |
| 38 | g | 0.23 | 0/1196 | 0.38 | 0/1604 |
| 39 | h | 0.24 | 0/1049 | 0.43 | 0/1407 |
| 40 | i | 0.24 | 0/794 | 0.41 | 0/1074 |
| 41 | j | 0.24 | 0/773 | 0.41 | 0/1044 |
| 42 | k | 0.24 | 0/853 | 0.45 | 0/1153 |
| 43 | l | 0.24 | 0/1069 | 0.42 | 0/1435 |
| 44 | m | 0.23 | 0/873 | 0.42 | 0/1166 |
| 45 | n | 0.26 | 0/508 | 0.41 | 0/672 |
| 46 | o | 0.23 | 0/718 | 0.38 | 0/960 |
| 47 | p | 0.25 | 0/708 | 0.40 | 0/950 |
| 48 | q | 0.24 | 0/699 | 0.43 | 0/933 |
| 49 | r | 0.24 | 0/526 | 0.41 | 0/705 |
| 50 | s | 0.24 | 0/649 | 0.40 | 0/872 |
| 51 | t | 0.23 | 0/639 | 0.38 | 0/852 |
| 52 | u | 0.23 | 0/448 | 0.44 | 0/596 |
| 53 | x | 0.18 | 0/1809 | 0.74 | 0/2819 |
| All | All | 0.22 | 0/155438 | 0.69 | 46/233243 (0.0%) |

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|---|---|---|---|
| 33 | b | 0 | 1 |

There are no bond length outliers.

The worst 5 of 46 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 7 | A | 21 | C | P-O3'-C3' | -12.16 | 105.11 | 119.70 |
| 28 | V | 181 | G | P-O3'-C3' | -9.75 | 108.00 | 119.70 |
| 28 | V | 76 | C | P-O3'-C3' | -9.67 | 108.10 | 119.70 |
| 7 | A | 27 | A | P-O3'-C3' | -8.82 | 109.12 | 119.70 |
| 28 | V | 1842 | C | P-O3'-C3' | -8.76 | 109.19 | 119.70 |

There are no chirality outliers.

All (1) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 33 | b | 20 | THR | Peptide |

## 5.2 Too-close contacts (i)

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

## 5.3 Torsion angles (i)

### 5.3.1 Protein backbone (i)

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

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 1 | 0 | 52/59 (88%) | 51 (98%) | 1 (2%) | 0 | 100 | 100 |
| 2 | 1 | 46/49 (94%) | 45 (98%) | 1 (2%) | 0 | 100 | 100 |
| 3 | 2 | 42/44 (96%) | 41 (98%) | 1 (2%) | 0 | 100 | 100 |
| 4 | 3 | 62/66 (94%) | 58 (94%) | 4 (6%) | 0 | 100 | 100 |
| 5 | 4 | 35/37 (95%) | 34 (97%) | 1 (3%) | 0 | 100 | 100 |
| 6 | 6 | 52/66 (79%) | 49 (94%) | 3 (6%) | 0 | 100 | 100 |
| 9 | C | 270/277 (98%) | 258 (96%) | 12 (4%) | 0 | 100 | 100 |
| 10 | D | 204/209 (98%) | 198 (97%) | 6 (3%) | 0 | 100 | 100 |
| 11 | E | 203/207 (98%) | 192 (95%) | 11 (5%) | 0 | 100 | 100 |
| 12 | F | 174/179 (97%) | 163 (94%) | 11 (6%) | 0 | 100 | 100 |
| 13 | G | 173/179 (97%) | 170 (98%) | 3 (2%) | 0 | 100 | 100 |
| 16 | J | 140/145 (97%) | 136 (97%) | 4 (3%) | 0 | 100 | 100 |
| 17 | K | 120/122 (98%) | 118 (98%) | 2 (2%) | 0 | 100 | 100 |
| 18 | L | 144/146 (99%) | 142 (99%) | 2 (1%) | 0 | 100 | 100 |
| 19 | M | 133/144 (92%) | 128 (96%) | 5 (4%) | 0 | 100 | 100 |
| 20 | N | 117/120 (98%) | 112 (96%) | 5 (4%) | 0 | 100 | 100 |
| 21 | O | 118/120 (98%) | 116 (98%) | 2 (2%) | 0 | 100 | 100 |
| 22 | P | 113/115 (98%) | 108 (96%) | 5 (4%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 23 | Q | 115/119 (97%) | 107 (93%) | 8 (7%) | 0 | 100 | 100 |
| 24 | R | 99/102 (97%) | 90 (91%) | 9 (9%) | 0 | 100 | 100 |
| 25 | S | 107/113 (95%) | 99 (92%) | 8 (8%) | 0 | 100 | 100 |
| 26 | T | 88/95 (93%) | 85 (97%) | 3 (3%) | 0 | 100 | 100 |
| 27 | U | 99/103 (96%) | 93 (94%) | 6 (6%) | 0 | 100 | 100 |
| 29 | W | 80/94 (85%) | 75 (94%) | 5 (6%) | 0 | 100 | 100 |
| 30 | Y | 63/66 (96%) | 62 (98%) | 1 (2%) | 0 | 100 | 100 |
| 31 | Z | 56/59 (95%) | 53 (95%) | 3 (5%) | 0 | 100 | 100 |
| 33 | b | 216/246 (88%) | 195 (90%) | 18 (8%) | 3 (1%) | 11 | 46 |
| 34 | c | 204/218 (94%) | 191 (94%) | 13 (6%) | 0 | 100 | 100 |
| 35 | d | 193/200 (96%) | 188 (97%) | 5 (3%) | 0 | 100 | 100 |
| 36 | e | 162/166 (98%) | 156 (96%) | 6 (4%) | 0 | 100 | 100 |
| 37 | f | 90/95 (95%) | 87 (97%) | 3 (3%) | 0 | 100 | 100 |
| 38 | g | 147/156 (94%) | 146 (99%) | 1 (1%) | 0 | 100 | 100 |
| 39 | h | 129/132 (98%) | 118 (92%) | 11 (8%) | 0 | 100 | 100 |
| 40 | i | 101/130 (78%) | 97 (96%) | 4 (4%) | 0 | 100 | 100 |
| 41 | j | 93/102 (91%) | 85 (91%) | 8 (9%) | 0 | 100 | 100 |
| 42 | k | 112/131 (86%) | 108 (96%) | 4 (4%) | 0 | 100 | 100 |
| 43 | l | 134/138 (97%) | 125 (93%) | 9 (7%) | 0 | 100 | 100 |
| 44 | m | 106/121 (88%) | 98 (92%) | 8 (8%) | 0 | 100 | 100 |
| 45 | n | 58/61 (95%) | 51 (88%) | 6 (10%) | 1 (2%) | 9 | 42 |
| 46 | o | 83/89 (93%) | 83 (100%) | 0 | 0 | 100 | 100 |
| 47 | p | 86/90 (96%) | 79 (92%) | 6 (7%) | 1 (1%) | 13 | 50 |
| 48 | q | 82/87 (94%) | 77 (94%) | 5 (6%) | 0 | 100 | 100 |
| 49 | r | 62/79 (78%) | 58 (94%) | 4 (6%) | 0 | 100 | 100 |
| 50 | s | 76/92 (83%) | 75 (99%) | 1 (1%) | 0 | 100 | 100 |
| 51 | t | 81/88 (92%) | 78 (96%) | 2 (2%) | 1 (1%) | 13 | 50 |
| 52 | u | 56/62 (90%) | 51 (91%) | 5 (9%) | 0 | 100 | 100 |
| All | All | 5176/5518 (94%) | 4929 (95%) | 241 (5%) | 6 (0%) | 54 | 84 |

5 of 6 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 33 | b | 20 | THR |
| 51 | t | 69 | LYS |
| 33 | b | 21 | ARG |
| 47 | p | 46 | PRO |
| 33 | b | 19 | GLN |

### 5.3.2 Protein sidechains (i)

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

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 1 | 0 | 48/53 (91%) | 48 (100%) | 0 | 100 | 100 |
| 2 | 1 | 46/47 (98%) | 46 (100%) | 0 | 100 | 100 |
| 3 | 2 | 39/39 (100%) | 39 (100%) | 0 | 100 | 100 |
| 4 | 3 | 54/56 (96%) | 54 (100%) | 0 | 100 | 100 |
| 5 | 4 | 35/35 (100%) | 35 (100%) | 0 | 100 | 100 |
| 6 | 6 | 44/55 (80%) | 44 (100%) | 0 | 100 | 100 |
| 9 | C | 220/225 (98%) | 220 (100%) | 0 | 100 | 100 |
| 10 | D | 167/170 (98%) | 167 (100%) | 0 | 100 | 100 |
| 11 | E | 169/170 (99%) | 168 (99%) | 1 (1%) | 86 | 94 |
| 12 | F | 151/154 (98%) | 151 (100%) | 0 | 100 | 100 |
| 13 | G | 148/151 (98%) | 148 (100%) | 0 | 100 | 100 |
| 16 | J | 120/123 (98%) | 120 (100%) | 0 | 100 | 100 |
| 17 | K | 101/101 (100%) | 101 (100%) | 0 | 100 | 100 |
| 18 | L | 110/110 (100%) | 110 (100%) | 0 | 100 | 100 |
| 19 | M | 109/116 (94%) | 109 (100%) | 0 | 100 | 100 |
| 20 | N | 99/100 (99%) | 99 (100%) | 0 | 100 | 100 |
| 21 | O | 93/93 (100%) | 93 (100%) | 0 | 100 | 100 |
| 22 | P | 100/100 (100%) | 100 (100%) | 0 | 100 | 100 |
| 23 | Q | 96/98 (98%) | 96 (100%) | 0 | 100 | 100 |
| 24 | R | 83/84 (99%) | 83 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 25 | S | 90/93 (97%) | 90 (100%) | 0 | 100 | 100 |
| 26 | T | 81/85 (95%) | 81 (100%) | 0 | 100 | 100 |
| 27 | U | 85/87 (98%) | 85 (100%) | 0 | 100 | 100 |
| 29 | W | 64/74 (86%) | 64 (100%) | 0 | 100 | 100 |
| 30 | Y | 56/57 (98%) | 56 (100%) | 0 | 100 | 100 |
| 31 | Z | 52/53 (98%) | 52 (100%) | 0 | 100 | 100 |
| 33 | b | 189/212 (89%) | 189 (100%) | 0 | 100 | 100 |
| 34 | c | 168/178 (94%) | 168 (100%) | 0 | 100 | 100 |
| 35 | d | 169/173 (98%) | 169 (100%) | 0 | 100 | 100 |
| 36 | e | 128/130 (98%) | 128 (100%) | 0 | 100 | 100 |
| 37 | f | 81/84 (96%) | 81 (100%) | 0 | 100 | 100 |
| 38 | g | 125/132 (95%) | 125 (100%) | 0 | 100 | 100 |
| 39 | h | 111/112 (99%) | 111 (100%) | 0 | 100 | 100 |
| 40 | i | 81/102 (79%) | 80 (99%) | 1 (1%) | 71 | 87 |
| 41 | j | 86/92 (94%) | 85 (99%) | 1 (1%) | 71 | 87 |
| 42 | k | 86/100 (86%) | 86 (100%) | 0 | 100 | 100 |
| 43 | l | 114/116 (98%) | 114 (100%) | 0 | 100 | 100 |
| 44 | m | 94/104 (90%) | 94 (100%) | 0 | 100 | 100 |
| 45 | n | 53/54 (98%) | 53 (100%) | 0 | 100 | 100 |
| 46 | o | 80/83 (96%) | 80 (100%) | 0 | 100 | 100 |
| 47 | p | 74/76 (97%) | 74 (100%) | 0 | 100 | 100 |
| 48 | q | 77/80 (96%) | 77 (100%) | 0 | 100 | 100 |
| 49 | r | 56/64 (88%) | 56 (100%) | 0 | 100 | 100 |
| 50 | s | 70/81 (86%) | 70 (100%) | 0 | 100 | 100 |
| 51 | t | 66/70 (94%) | 66 (100%) | 0 | 100 | 100 |
| 52 | u | 47/50 (94%) | 47 (100%) | 0 | 100 | 100 |
| All | All | 4415/4622 (96%) | 4412 (100%) | 3 (0%) | 93 | 98 |

All (3) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 11 | E | 194 | ILE |
| 40 | i | 94 | TYR |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 41 | j | 80 | THR |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA (i)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|---|---|---|---|---|
| 14 | H | 76/77 (98%) | 28 (36%) | 4 (5%) |
| 28 | V | 2881/2928 (98%) | 627 (21%) | 57 (1%) |
| 32 | a | 1544/1545 (99%) | 278 (18%) | 0 |
| 53 | x | 75/76 (98%) | 25 (33%) | 0 |
| 7 | A | 28/29 (96%) | 14 (50%) | 5 (17%) |
| 8 | B | 111/112 (99%) | 27 (24%) | 4 (3%) |
| All | All | 4715/4767 (98%) | 999 (21%) | 70 (1%) |

5 of 999 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 7 | A | 3 | G |
| 7 | A | 5 | A |
| 7 | A | 7 | A |
| 7 | A | 10 | A |
| 7 | A | 12 | A |

5 of 70 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 28 | V | 2254 | A |
| 28 | V | 2295 | A |
| 28 | V | 2468 | A |
| 28 | V | 554 | U |
| 28 | V | 549 | A |

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

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

## 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry (i)

There are no ligands in this entry.

## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

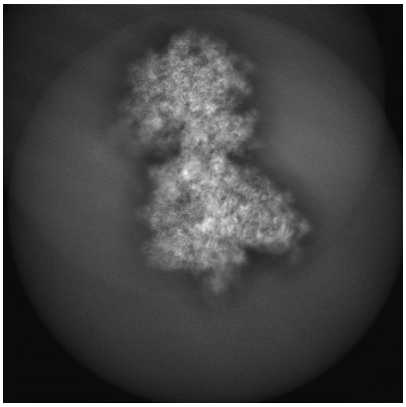
# 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-14158. These allow visual inspection of the internal detail of the map and identification of artifacts.

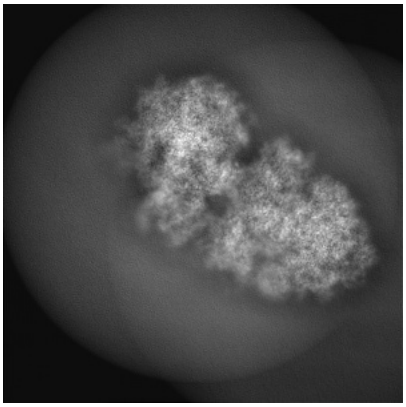
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

## 6.1 Orthogonal projections

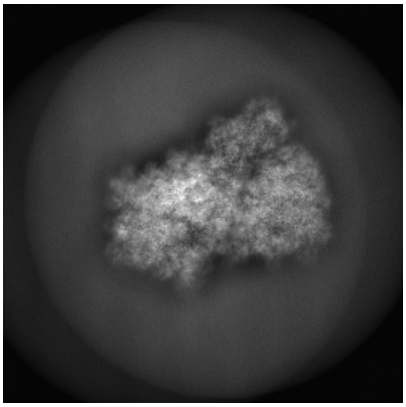
### 6.1.1 Primary map



X



Y

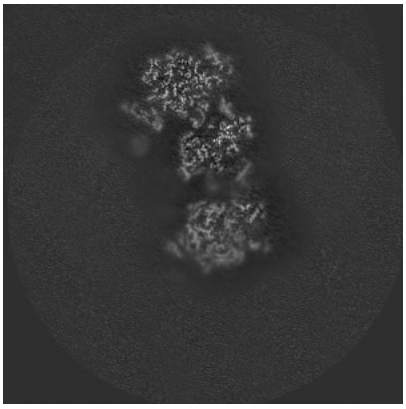


Z

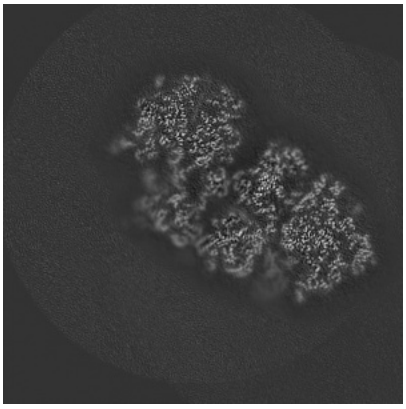
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices

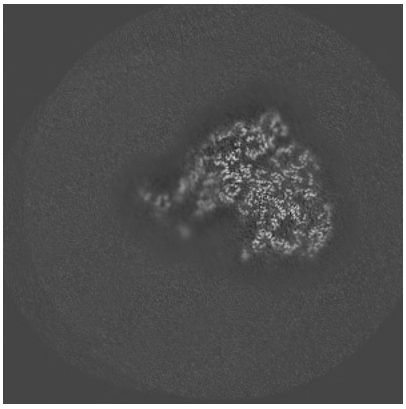
### 6.2.1 Primary map



X Index: 184



Y Index: 184

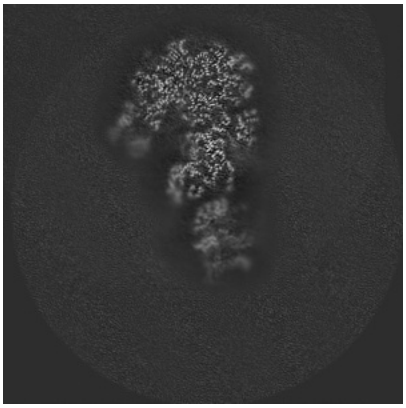


Z Index: 184

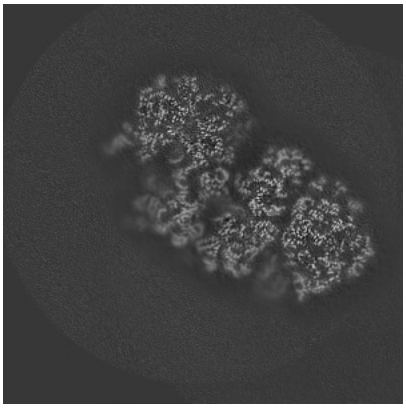
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices (i)

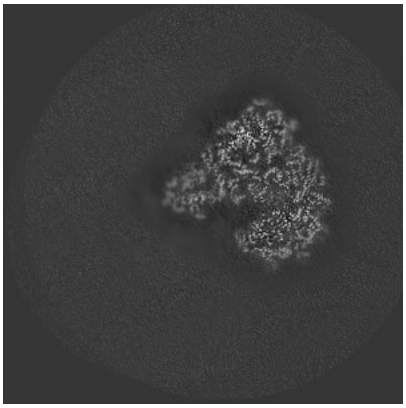
### 6.3.1 Primary map



X Index: 163



Y Index: 187

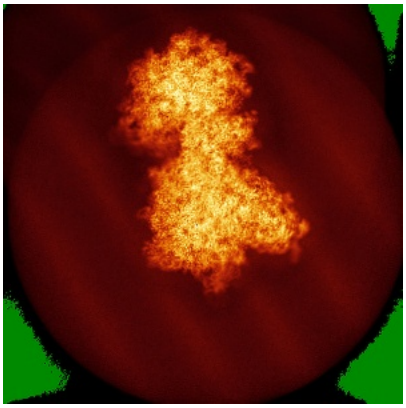


Z Index: 169

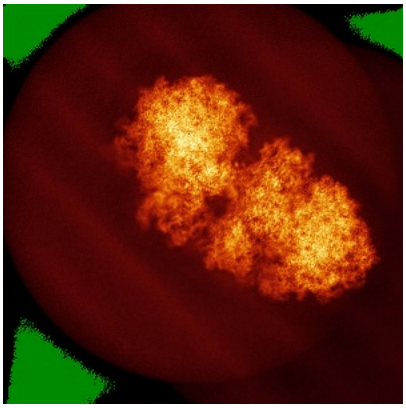
The images above show the largest variance slices of the map in three orthogonal directions.

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

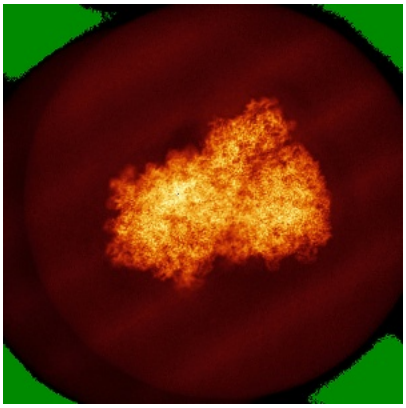
### 6.4.1 Primary map



X



Y



Z

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

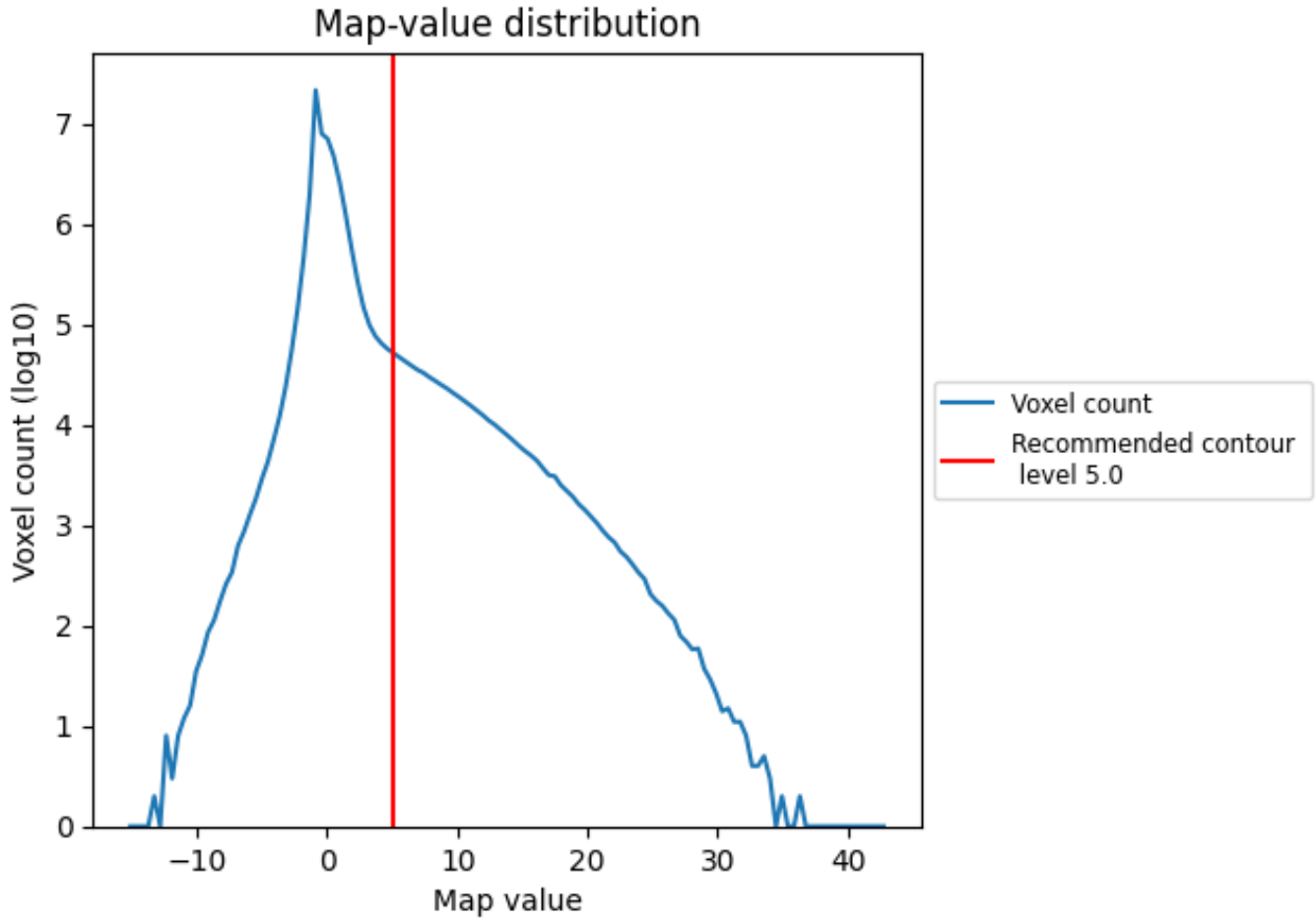
## 6.6 Mask visualisation (i)

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

# 7 Map analysis

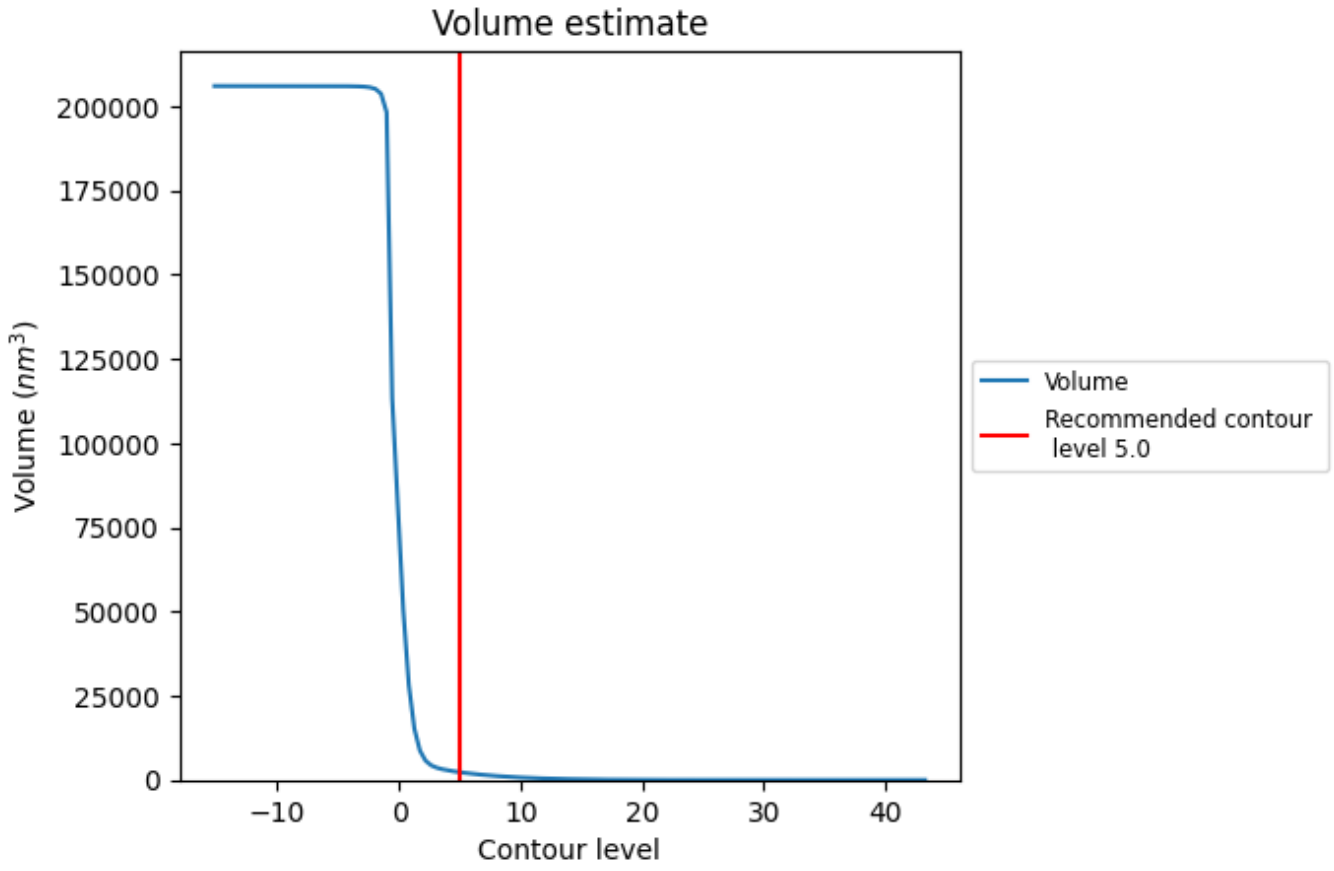
This section contains the results of statistical analysis of the map.

## 7.1 Map-value distribution




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

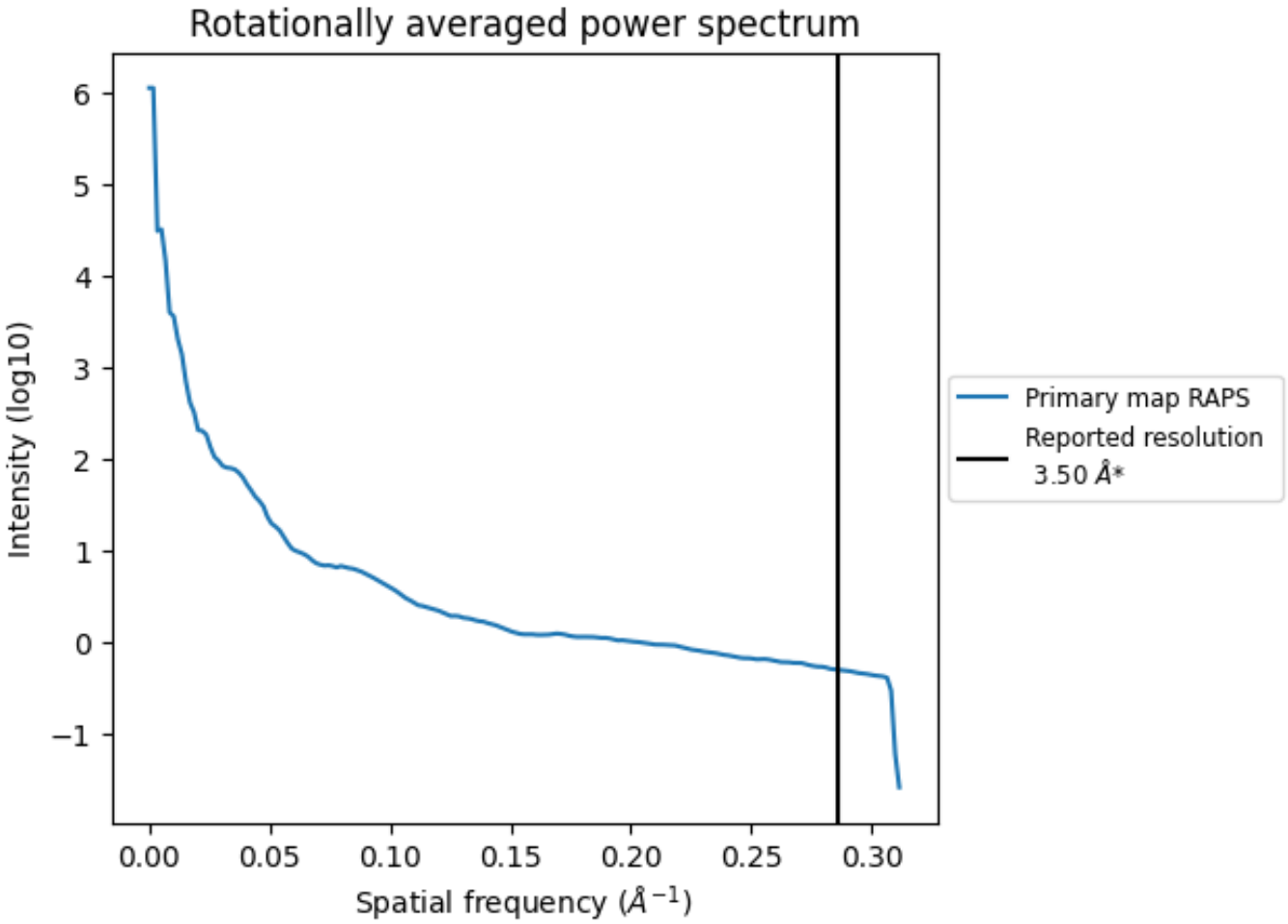
## 7.2 Volume estimate (i)




The volume at the recommended contour level is 2302 $nm^3$; this corresponds to an approximate mass of 2079 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 0.286 $Å^{-1}$

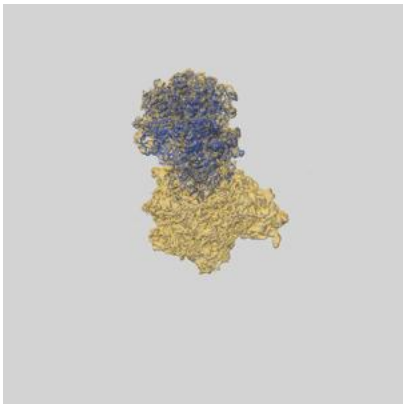
# 8 Fourier-Shell correlation

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

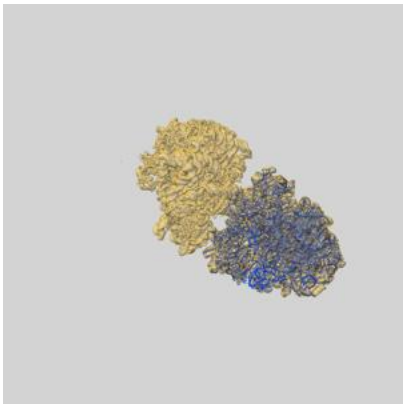
# 9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-14158 and PDB model 7QV2. Per-residue inclusion information can be found in section 3 on page 13.

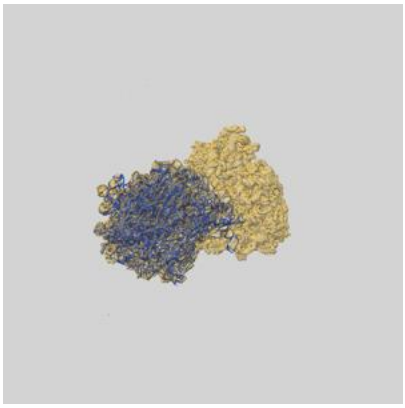
## 9.1 Map-model overlay



X



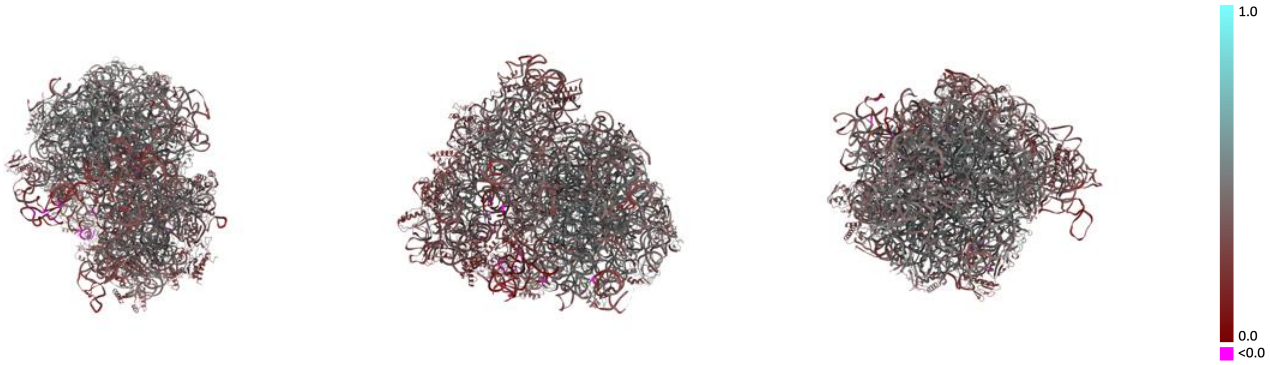
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 5.0 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.

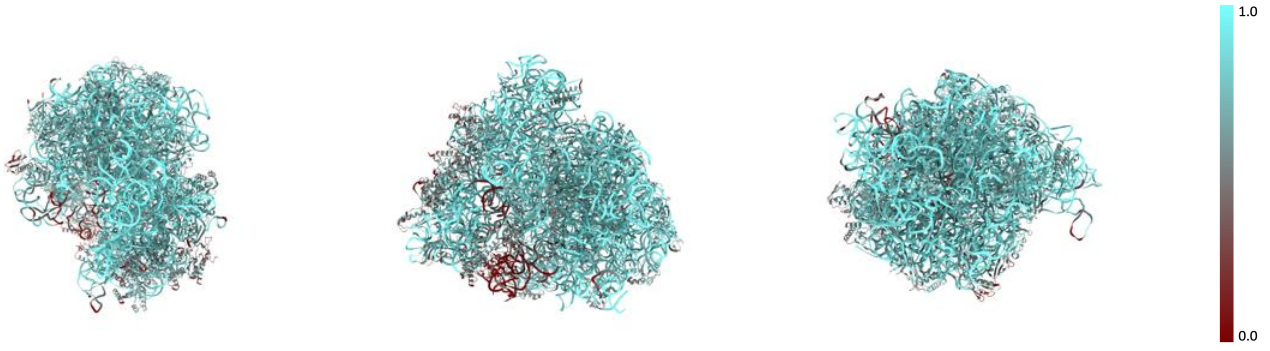
## 9.2 Q-score mapped to coordinate model (i)




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.

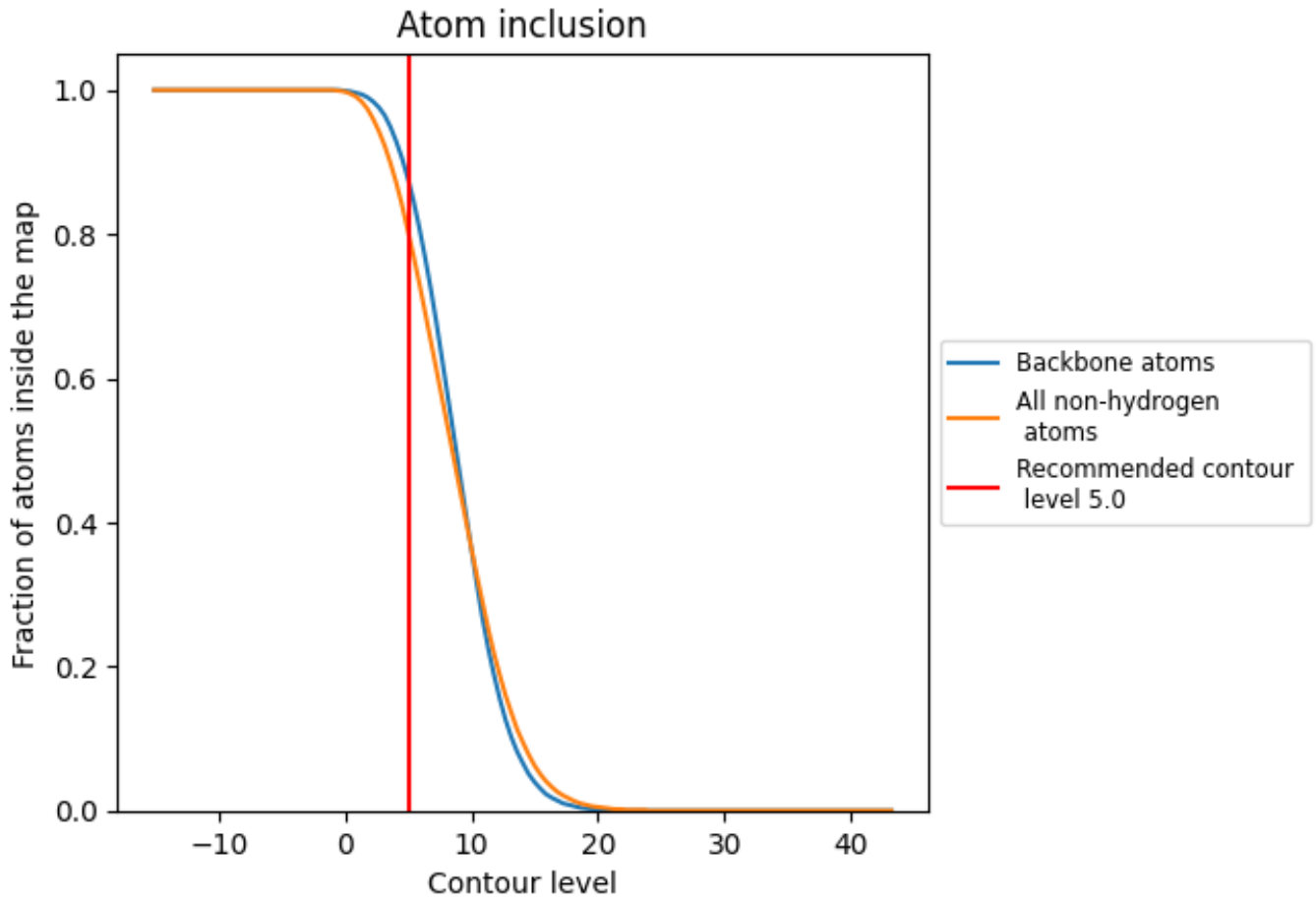
## 9.3 Atom inclusion mapped to coordinate model (i)




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 (5.0).

## 9.4 Atom inclusion (i)




At the recommended contour level, 87% of all backbone atoms, 80% 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 (5.0) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|---|---|---|
| All | 0.8010 | 0.3910 |
| 0 | 0.7800 | 0.4640 |
| 1 | 0.6930 | 0.4110 |
| 2 | 0.8090 | 0.4720 |
| 3 | 0.8100 | 0.5070 |
| 4 | 0.6840 | 0.4120 |
| 6 | 0.0290 | 0.1360 |
| A | 0.4640 | 0.2660 |
| B | 0.8510 | 0.3630 |
| C | 0.7420 | 0.4630 |
| D | 0.7500 | 0.4610 |
| E | 0.6740 | 0.4110 |
| F | 0.1330 | 0.2600 |
| G | 0.5090 | 0.3230 |
| H | 0.3600 | 0.2270 |
| I | 0.1070 | 0.2140 |
| J | 0.7280 | 0.4480 |
| K | 0.6610 | 0.4360 |
| L | 0.6760 | 0.4320 |
| M | 0.7230 | 0.4340 |
| N | 0.7500 | 0.4330 |
| O | 0.5600 | 0.3160 |
| P | 0.6860 | 0.4120 |
| Q | 0.7340 | 0.4250 |
| R | 0.6230 | 0.4130 |
| S | 0.7130 | 0.4500 |
| T | 0.7200 | 0.4200 |
| U | 0.6750 | 0.4180 |
| V | 0.8730 | 0.4170 |
| W | 0.7370 | 0.4550 |
| Y | 0.6910 | 0.3720 |
| Z | 0.7040 | 0.4170 |
| a | 0.9170 | 0.3820 |
| b | 0.4780 | 0.3030 |
| c | 0.6430 | 0.3500 |


*Continued on next page...*

*Continued from previous page...*

| Chain | Atom inclusion | Q-score |
|---|---|---|
| d | 0.5440 | 0.3310 |
| e | 0.6190 | 0.4060 |
| f | 0.6010 | 0.3470 |
| g | 0.5540 | 0.2530 |
| h | 0.7030 | 0.3920 |
| i | 0.6530 | 0.2940 |
| j | 0.6350 | 0.3340 |
| k | 0.6250 | 0.3180 |
| l | 0.7400 | 0.4270 |
| m | 0.3640 | 0.2180 |
| n | 0.7630 | 0.4090 |
| o | 0.7460 | 0.3550 |
| p | 0.7260 | 0.3870 |
| q | 0.6800 | 0.3630 |
| r | 0.6910 | 0.3790 |
| s | 0.5590 | 0.2940 |
| t | 0.6750 | 0.2750 |
| u | 0.7320 | 0.4380 |
| x | 0.3710 | 0.2120 |