# wwPDB EM Validation Summary Report ⓘ

Nov 21, 2022 – 06:35 PM JST

| | | |
|---|---|---|
| PDB ID | : | 7D80 |
| EMDB ID | : | EMD-30611 |
| Title | : | Molecular model of the cryo-EM structure of 70S ribosome in complex with peptide deformylase, trigger factor, and methionine aminopeptidase |
| Authors | : | Akbar, S.; Bhakta, S.; Sengupta, J. |
| Deposited on | : | 2020-10-06 |
| Resolution | : | 4.10 Å(reported) |

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

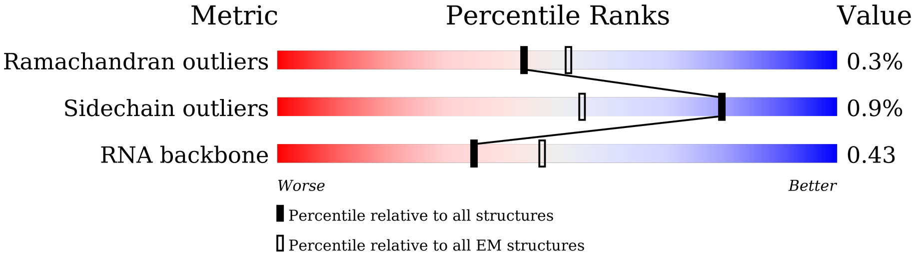
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev43 |
| MolProbity | : | 4.02b-467 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| MapQ | : | 1.9.9 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.31.3 |

# 1 Overall quality at a glance ⓘ

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

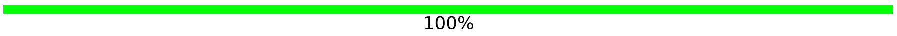
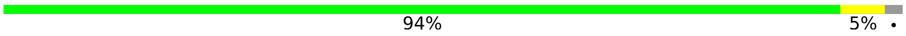
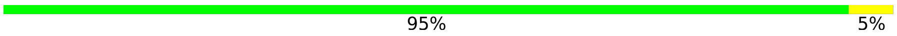
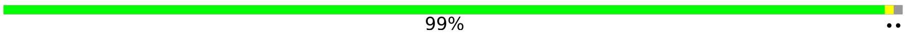
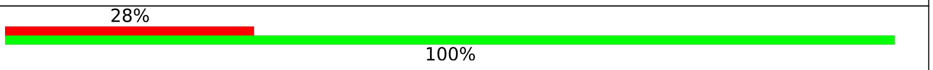
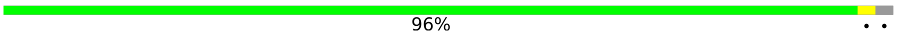
The reported resolution of this entry is 4.10 Å.

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 | 46 |  |
| 2 | 1 | 65 |  |
| 3 | 2 | 38 |  |
| 4 | 3 | 169 |  |
| 5 | 5 | 432 |  |
| 6 | 6 | 57 |  |
| 7 | A | 2903 |  |
| 8 | B | 1539 |  |

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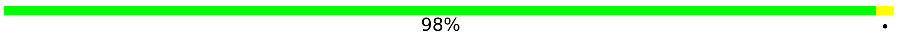
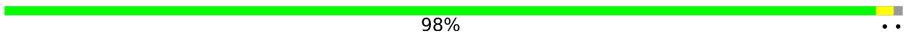
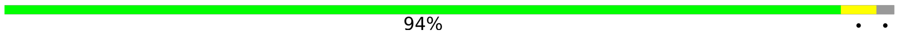
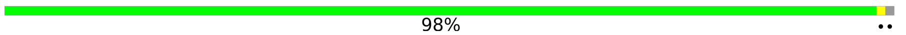
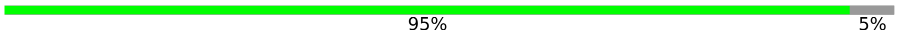
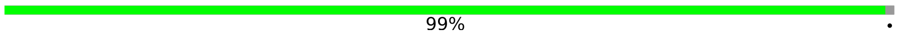
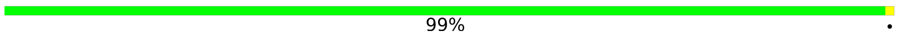
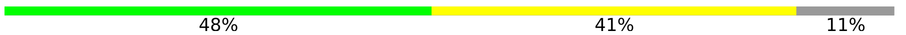
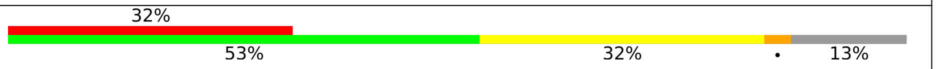
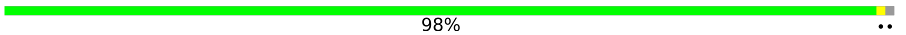
| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 9 | C | 241 |  |
| 10 | D | 233 |  |
| 11 | E | 206 |  |
| 12 | F | 167 |  |
| 13 | G | 135 |  |
| 14 | H | 179 |  |
| 15 | I | 130 |  |
| 16 | J | 130 |  |
| 17 | K | 103 |  |
| 18 | L | 129 |  |
| 19 | M | 124 |  |
| 20 | N | 118 |  |
| 21 | O | 101 |  |
| 22 | P | 89 |  |
| 23 | Q | 82 |  |
| 24 | R | 84 |  |
| 25 | S | 75 |  |
| 26 | T | 92 |  |
| 27 | U | 87 |  |
| 28 | V | 71 |  |
| 29 | W | 100 |  |
| 30 | X | 73 |  |
| 31 | Z | 76 |  |
| 32 | a | 118 |  |
| 33 | b | 273 |  |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 34 | c | 209 | 97% |
| 35 | d | 201 | 100% |
| 36 | e | 179 | 98% |
| 37 | f | 177 | 97% |
| 38 | g | 149 | 32%<br>68% |
| 39 | h | 142 | 10%<br>99% |
| 40 | i | 142 | 99% |
| 41 | j | 123 | 98% |
| 42 | k | 144 | 97% |
| 43 | l | 136 | 97% |
| 44 | m | 127 | 91%<br>6% |
| 45 | n | 117 | 98% |
| 46 | o | 115 | 98% |
| 47 | p | 118 | 99% |
| 48 | q | 103 | 100% |
| 49 | r | 110 | 99% |
| 50 | s | 104 | 93%<br>5% |
| 51 | t | 94 | 100% |
| 52 | u | 85 | 88%<br>12% |
| 53 | v | 78 | 99% |
| 54 | w | 63 | 97% |
| 55 | x | 59 | 98% |
| 56 | y | 77 | 64%<br>27%<br>9% |
| 57 | z | 55 | 87%<br>9% |

# 2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 150808 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 L34.

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

- Molecule 2 is a protein called 50S ribosomal protein L35.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 2 | 1 | 64 | 504 | 323 | 105 | 74 | 2 | 0 | 0 |

- Molecule 3 is a protein called 50S ribosomal protein L36.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 3 | 2 | 38 | 302 | 185 | 65 | 48 | 4 | 0 | 0 |

- Molecule 4 is a protein called Peptide deformylase.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 4 | 3 | 168 | 1346 | 844 | 241 | 255 | 6 | 0 | 0 |

- Molecule 5 is a protein called Trigger factor.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 5 | 5 | 432 | 3386 | 2119 | 582 | 674 | 11 | 0 | 0 |

- Molecule 6 is a protein called 50S ribosomal protein L32.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 6 | 6 | 56 | 444 | 269 | 94 | 80 | 1 | 0 | 0 |

- Molecule 7 is a RNA chain called 23S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 7 | A | 2903 | 62317 | 27801 | 11467 | 20147 | 2902 | 0 | 0 |

- Molecule 8 is a RNA chain called 16S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 8 | B | 1539 | 33015 | 14725 | 6052 | 10699 | 1539 | 0 | 0 |

- Molecule 9 is a protein called 30S ribosomal protein S2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 9 | C | 218 | 1704 | 1081 | 305 | 311 | 7 | 0 | 0 |

- Molecule 10 is a protein called 30S ribosomal protein S3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 10 | D | 206 | 1624 | 1028 | 305 | 288 | 3 | 0 | 0 |

- Molecule 11 is a protein called 30S ribosomal protein S4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 11 | E | 205 | 1643 | 1026 | 315 | 298 | 4 | 0 | 0 |

- Molecule 12 is a protein called 30S ribosomal protein S5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 12 | F | 150 | 1105 | 687 | 211 | 201 | 6 | 0 | 0 |

- Molecule 13 is a protein called 30S ribosomal protein S6, fully modified isoform.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 13 | G | 100 | 817 | 515 | 148 | 148 | 6 | 0 | 0 |

- Molecule 14 is a protein called 30S ribosomal protein S7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 14 | H | 151 | 1181 | 735 | 227 | 215 | 4 | 0 | 0 |

- Molecule 15 is a protein called 30S ribosomal protein S8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 15 | I | 129 | 979 | 616 | 173 | 184 | 6 | 0 | 0 |

- Molecule 16 is a protein called 30S ribosomal protein S9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 16 | J | 127 | 1022 | 634 | 206 | 179 | 3 | 0 | 0 |

- Molecule 17 is a protein called 30S ribosomal protein S10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 17 | K | 98 | 786 | 493 | 150 | 142 | 1 | 0 | 0 |

- Molecule 18 is a protein called 30S ribosomal protein S11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 18 | L | 117 | 877 | 540 | 174 | 160 | 3 | 0 | 0 |

- Molecule 19 is a protein called 30S ribosomal protein S12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 19 | M | 123 | 955 | 590 | 196 | 165 | 4 | 0 | 0 |

- Molecule 20 is a protein called 30S ribosomal protein S13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 20 | N | 114 | 883 | 546 | 178 | 156 | 3 | 0 | 0 |

- Molecule 21 is a protein called 30S ribosomal protein S14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 21 | O | 96 | 774 | 483 | 160 | 128 | 3 | 0 | 0 |

- Molecule 22 is a protein called 30S ribosomal protein S15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 22 | P | 88 | 710 | 437 | 143 | 129 | 1 | 0 | 0 |

- Molecule 23 is a protein called 30S ribosomal protein S16.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 23 | Q | 82 | 649 | 406 | 128 | 114 | 1 | 0 | 0 |

- Molecule 24 is a protein called 30S ribosomal protein S17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 24 | R | 80 | 648 | 411 | 121 | 113 | 3 | 0 | 0 |

- Molecule 25 is a protein called 30S ribosomal protein S18.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 25 | S | 55 | 455 | 288 | 86 | 81 | 0 | 0 |

- Molecule 26 is a protein called 30S ribosomal protein S19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 26 | T | 79 | 637 | 408 | 120 | 107 | 2 | 0 | 0 |

- Molecule 27 is a protein called 30S ribosomal protein S20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 27 | U | 85 | 665 | 411 | 137 | 114 | 3 | 0 | 0 |

- Molecule 28 is a protein called 30S ribosomal protein S21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 28 | V | 51 | 425 | 265 | 86 | 73 | 1 | 0 | 0 |

- Molecule 29 is a protein called 50S ribosomal protein L23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 29 | W | 96 | 764 | 484 | 142 | 136 | 2 | 0 | 0 |

- Molecule 30 is a RNA chain called E-site tRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 30 | X | 65 | 1392 | 621 | 258 | 449 | 64 | 0 | 0 |

- Molecule 31 is a RNA chain called A-site tRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 31 | Z | 66 | 1406 | 629 | 255 | 457 | 65 | 0 | 0 |

- Molecule 32 is a RNA chain called 5S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 32 | a | 118 | 2529 | 1126 | 464 | 821 | 118 | 0 | 0 |

- Molecule 33 is a protein called 50S ribosomal protein L2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 33 | b | 271 | 2082 | 1288 | 423 | 364 | 7 | 0 | 0 |

- Molecule 34 is a protein called 50S ribosomal protein L3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 34 | c | 209 | 1565 | 979 | 288 | 294 | 4 | 0 | 0 |

- Molecule 35 is a protein called 50S ribosomal protein L4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 35 | d | 201 | Total<br>1552 | C<br>974 | N<br>283 | O<br>290 | S<br>5 | 0 | 0 |

- Molecule 36 is a protein called 50S ribosomal protein L5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 36 | e | 177 | Total<br>1410 | C<br>899 | N<br>249 | O<br>256 | S<br>6 | 0 | 0 |

- Molecule 37 is a protein called 50S ribosomal protein L6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 37 | f | 176 | Total<br>1323 | C<br>832 | N<br>243 | O<br>246 | S<br>2 | 0 | 0 |

- Molecule 38 is a protein called 50S ribosomal protein L9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 38 | g | 47 | Total<br>359 | C<br>233 | N<br>62 | O<br>63 | S<br>1 | 0 | 0 |

- Molecule 39 is a protein called 50S ribosomal protein L11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 39 | h | 141 | Total<br>1032 | C<br>651 | N<br>179 | O<br>196 | S<br>6 | 0 | 0 |

- Molecule 40 is a protein called 50S ribosomal protein L13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 40 | i | 142 | Total<br>1129 | C<br>714 | N<br>212 | O<br>199 | S<br>4 | 0 | 0 |

- Molecule 41 is a protein called 50S ribosomal protein L14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 41 | j | 122 | Total<br>938 | C<br>587 | N<br>180 | O<br>165 | S<br>6 | 0 | 0 |

- Molecule 42 is a protein called 50S ribosomal protein L15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 42 | k | 143 | 1045 | 649 | 206 | 189 | 1 | 0 | 0 |

- Molecule 43 is a protein called 50S ribosomal protein L16.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 43 | l | 136 | 1074 | 686 | 205 | 177 | 6 | 0 | 0 |

- Molecule 44 is a protein called 50S ribosomal protein L17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 44 | m | 120 | 960 | 593 | 196 | 166 | 5 | 0 | 0 |

- Molecule 45 is a protein called 50S ribosomal protein L18.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 45 | n | 116 | 892 | 552 | 178 | 162 | 0 | 0 |

- Molecule 46 is a protein called 50S ribosomal protein L19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 46 | o | 114 | 917 | 574 | 179 | 163 | 1 | 0 | 0 |

- Molecule 47 is a protein called 50S ribosomal protein L20.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 47 | p | 117 | 947 | 604 | 192 | 151 | 0 | 0 |

- Molecule 48 is a protein called 50S ribosomal protein L21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 48 | q | 103 | 816 | 516 | 153 | 145 | 2 | 0 | 0 |

- Molecule 49 is a protein called 50S ribosomal protein L22.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 49 | r | 110 | 857 | 532 | 166 | 156 | 3 | 0 | 0 |

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

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 50 | s | 102 | 779 | 492 | 146 | 141 | 0 | 0 |

- Molecule 51 is a protein called 50S ribosomal protein L25.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 51 | t | 94 | 753 | 479 | 137 | 134 | 3 | 0 | 0 |

- Molecule 52 is a protein called 50S ribosomal protein L27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 52 | u | 75 | 569 | 353 | 113 | 102 | 1 | 0 | 0 |

- Molecule 53 is a protein called 50S ribosomal protein L28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 53 | v | 77 | 625 | 388 | 129 | 106 | 2 | 0 | 0 |

- Molecule 54 is a protein called 50S ribosomal protein L29.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 54 | w | 63 | 509 | 313 | 99 | 95 | 2 | 0 | 0 |

- Molecule 55 is a protein called 50S ribosomal protein L30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 55 | x | 58 | 449 | 281 | 87 | 79 | 2 | 0 | 0 |

- Molecule 56 is a RNA chain called P-site tRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 56 | y | 70 | 1496 | 665 | 267 | 494 | 70 | 0 | 0 |

- Molecule 57 is a protein called 50S ribosomal protein L33.

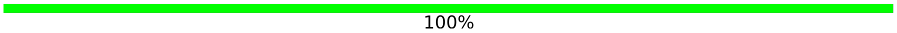
| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 57 | z | 50 | 409 | 263 | 75 | 71 | 0 | 0 |

# 3 Residue-property plots ⓘ

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 L34

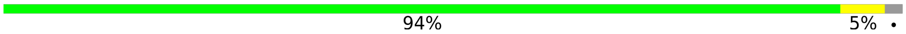
Chain 0:

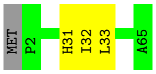


There are no outlier residues recorded for this chain.

- Molecule 2: 50S ribosomal protein L35

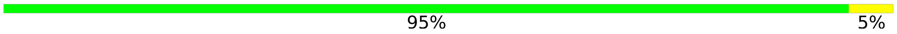
Chain 1:

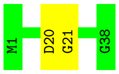




- Molecule 3: 50S ribosomal protein L36

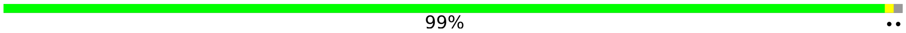
Chain 2:

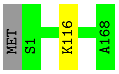




- Molecule 4: Peptide deformylase

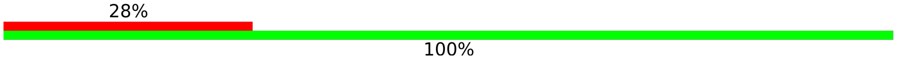
Chain 3:

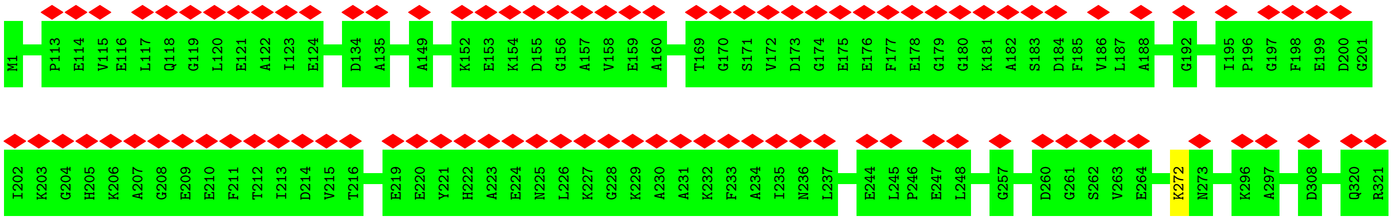


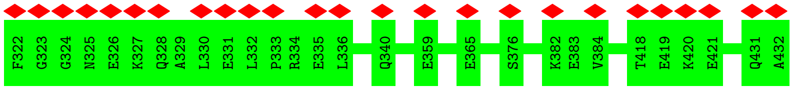


- Molecule 5: Trigger factor

Chain 5:

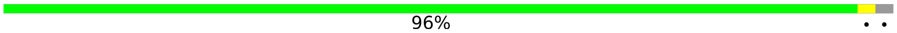


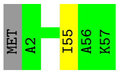




- Molecule 6: 50S ribosomal protein L32

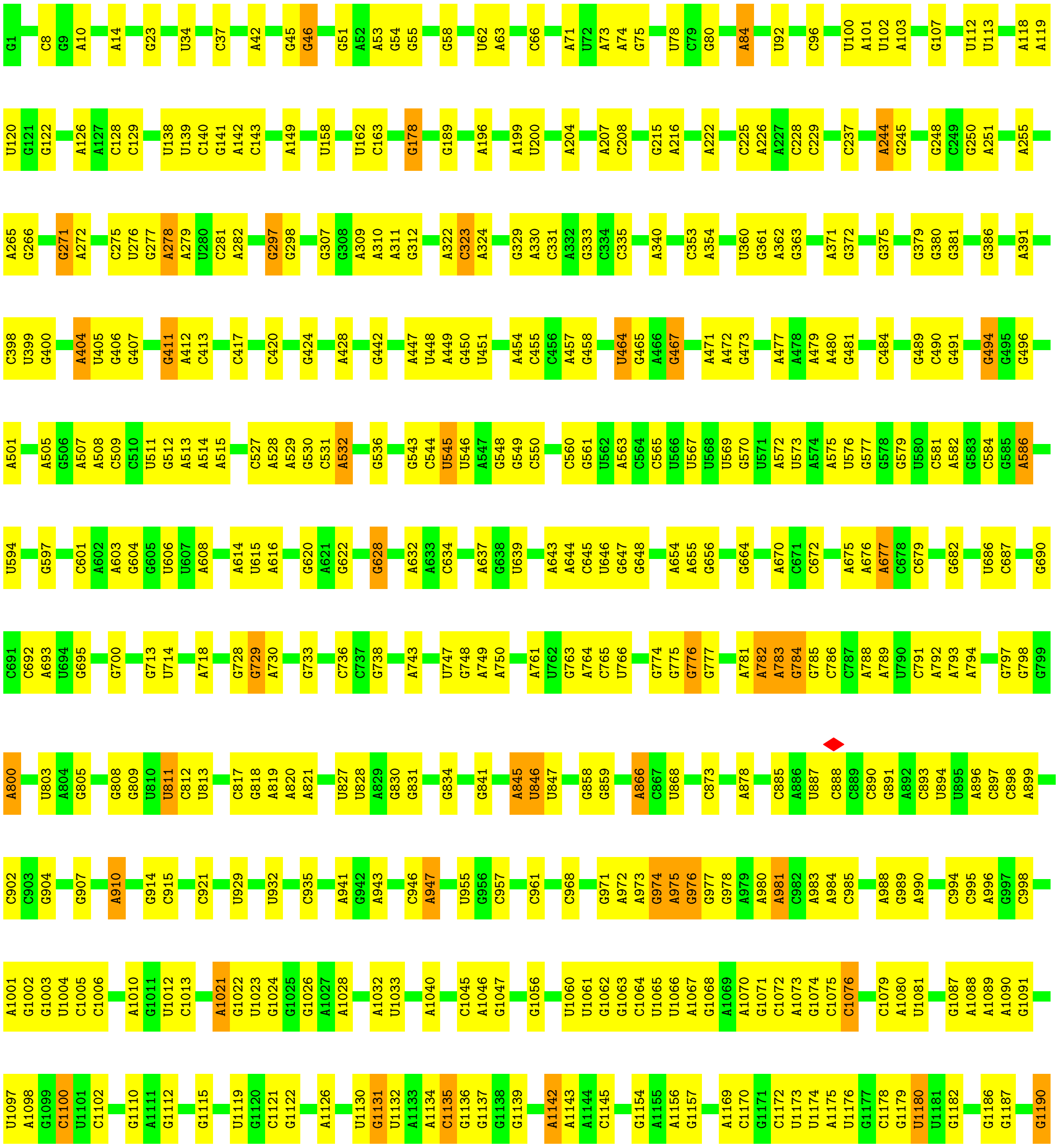
Chain 6:

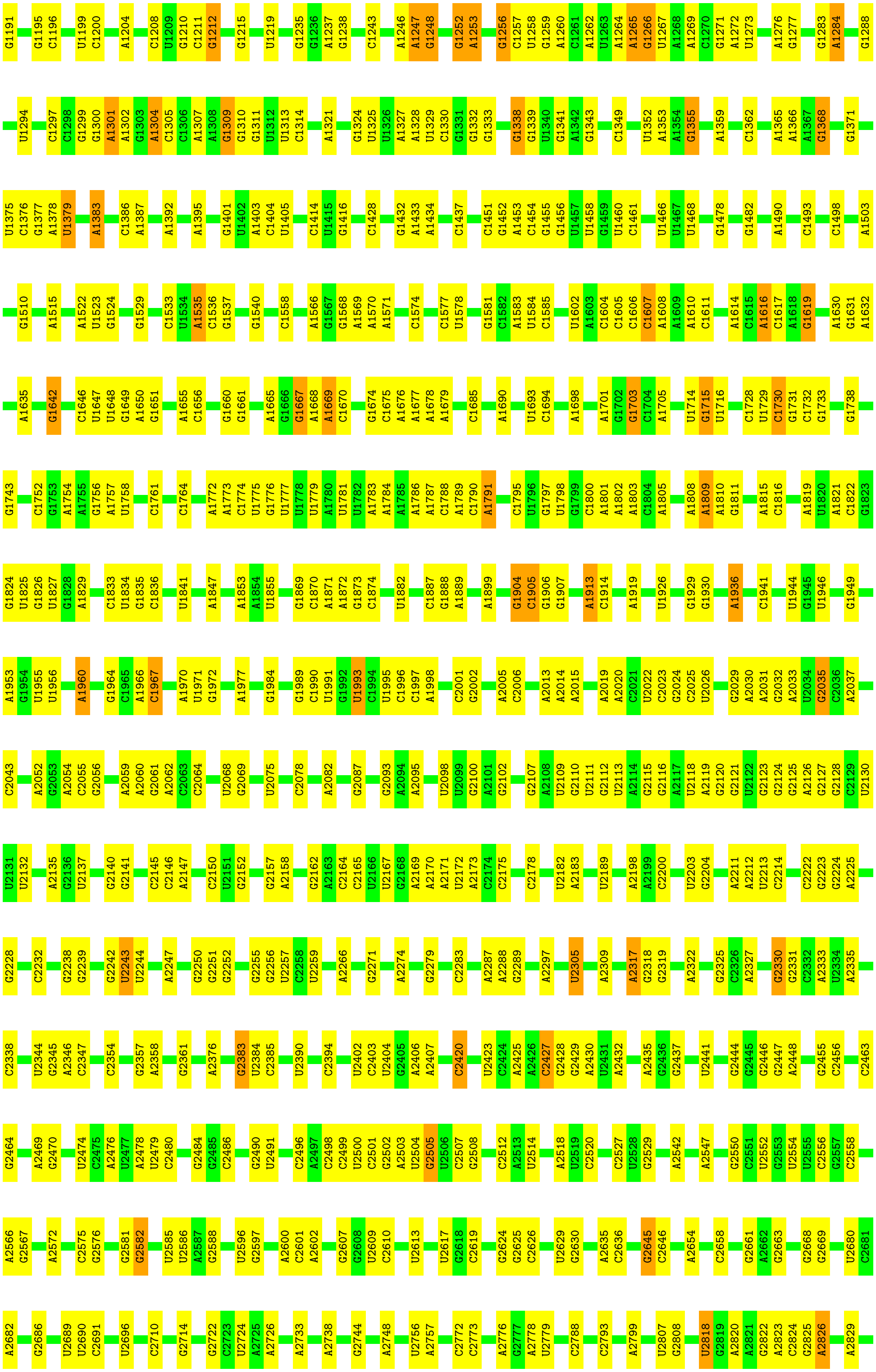




- Molecule 7: 23S ribosomal RNA

Chain A:

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G1212
G1215
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G1235
G1236
A1237
G1238
C1243
A1246
A1247
G1248
G1252
A1253
G1256
C1257
U1258
G1259
A1260
C1261
A1262
U1263
A1264
A1265
G1266
U1267
A1268
A1269
C1270
G1271
A1272
U1273
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G1277
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A1284
G1288
U1294
C1297
C1298
G1299
G1300
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A1302
G1303
A1304
C1305
C1306
A1307
A1308
G1309
G1310
G1311
U1312
U1313
C1314
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G1371
U1375
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U1415
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G1456
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G1459
U1460
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U1523
G1524
G1529
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U1534
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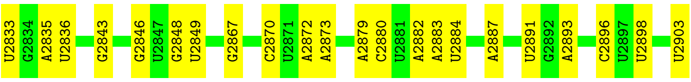
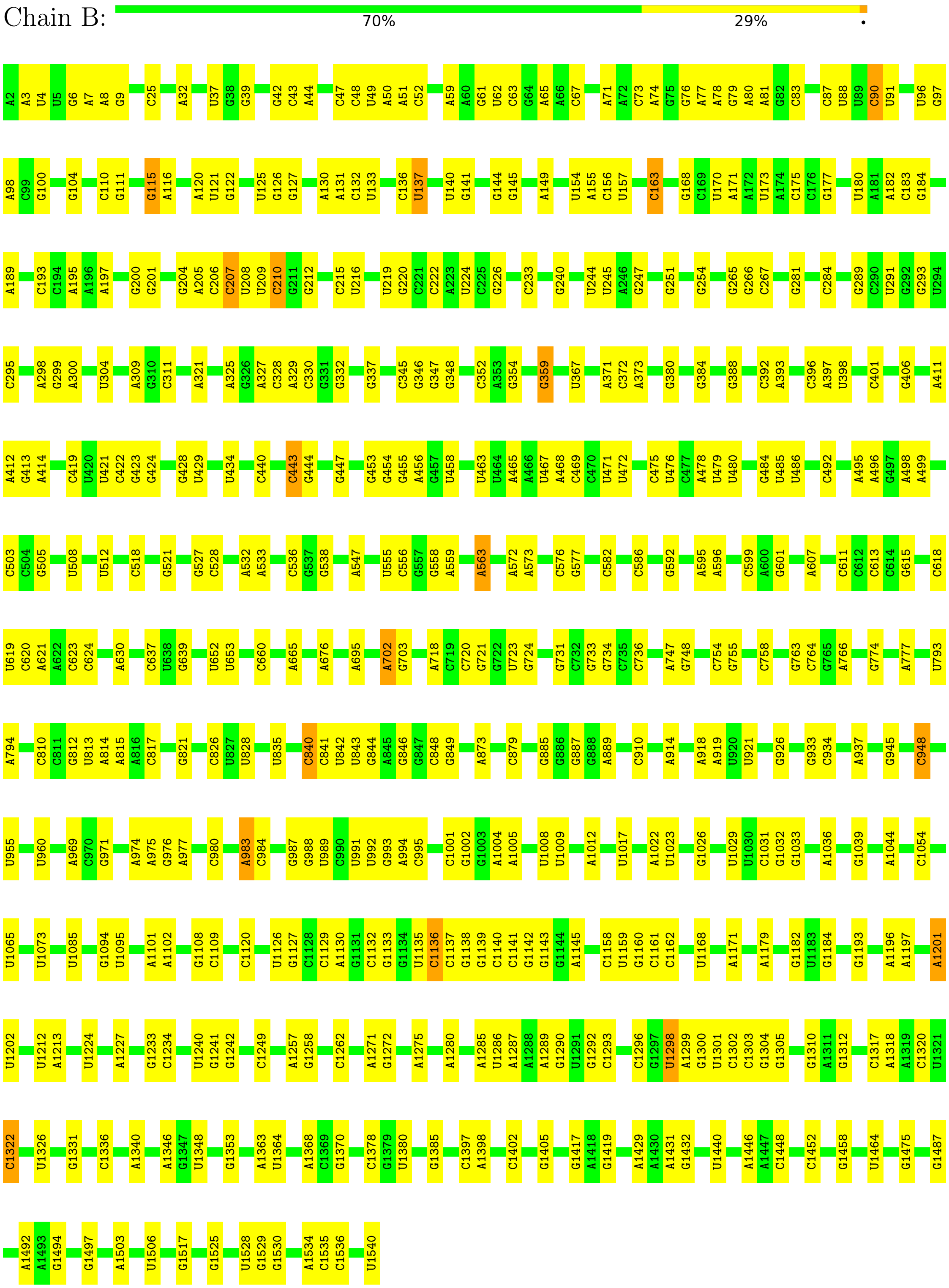


- Molecule 8: 16S ribosomal RNA



- Molecule 9: 30S ribosomal protein S2

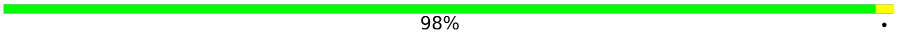
Chain C:

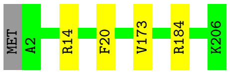
- Molecule 10: 30S ribosomal protein S3

Chain D:

- Molecule 11: 30S ribosomal protein S4

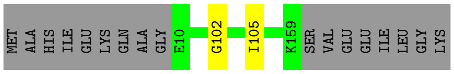
Chain E:





- Molecule 12: 30S ribosomal protein S5

Chain F:

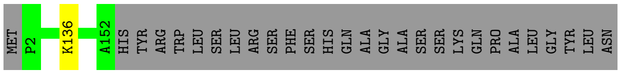


- Molecule 13: 30S ribosomal protein S6, fully modified isoform

Chain G:

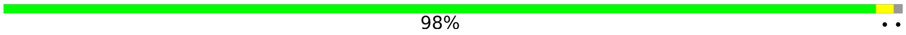
- Molecule 14: 30S ribosomal protein S7

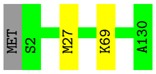
Chain H:



- Molecule 15: 30S ribosomal protein S8

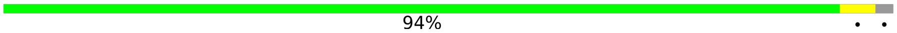
Chain I:

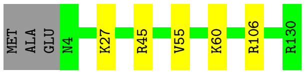




- Molecule 16: 30S ribosomal protein S9

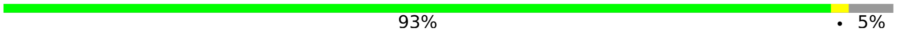
Chain J:

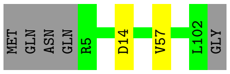




- Molecule 17: 30S ribosomal protein S10

Chain K:



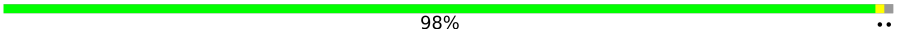


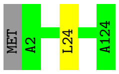
- Molecule 18: 30S ribosomal protein S11

Chain L:

- Molecule 19: 30S ribosomal protein S12

Chain M:



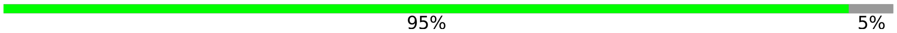


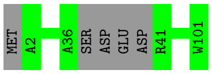
- Molecule 20: 30S ribosomal protein S13

Chain N:

- Molecule 21: 30S ribosomal protein S14

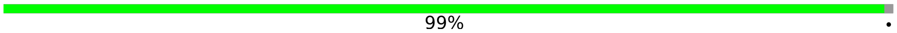
Chain O:

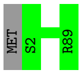




- Molecule 22: 30S ribosomal protein S15

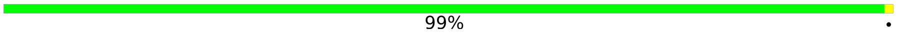
Chain P:

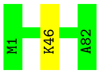




- Molecule 23: 30S ribosomal protein S16

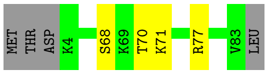
Chain Q:





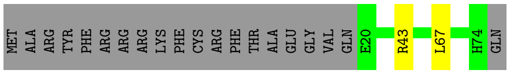
- Molecule 24: 30S ribosomal protein S17

Chain R:



- Molecule 25: 30S ribosomal protein S18

Chain S:

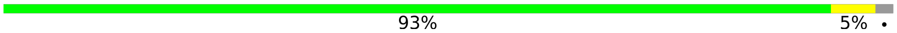


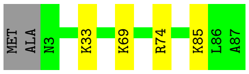
- Molecule 26: 30S ribosomal protein S19

Chain T:

- Molecule 27: 30S ribosomal protein S20

Chain U:



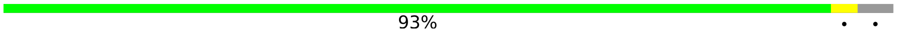


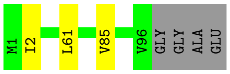
- Molecule 28: 30S ribosomal protein S21

Chain V:

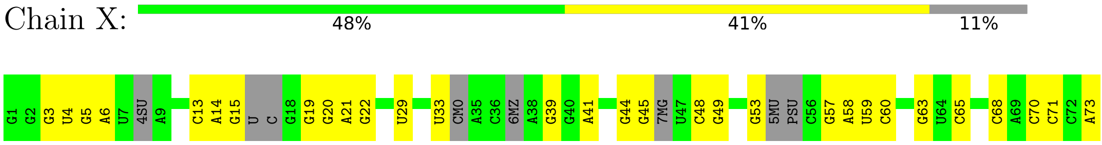
- Molecule 29: 50S ribosomal protein L23

Chain W:

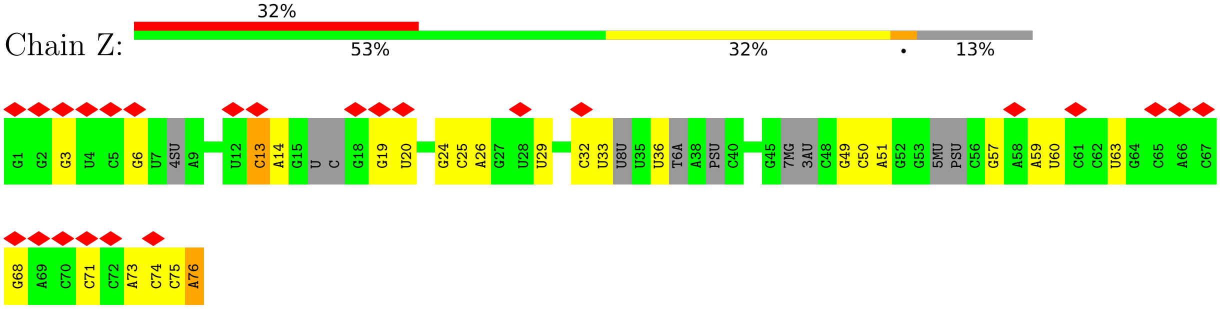




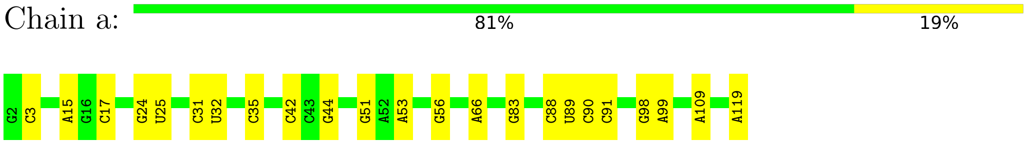
- Molecule 30: E-site tRNA



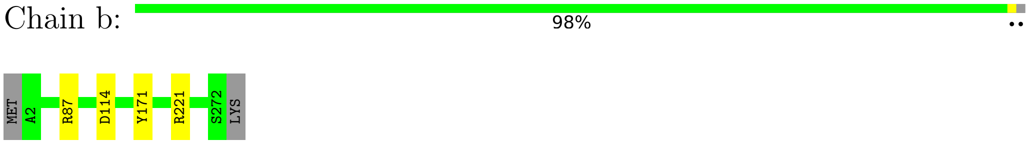
- Molecule 31: A-site tRNA



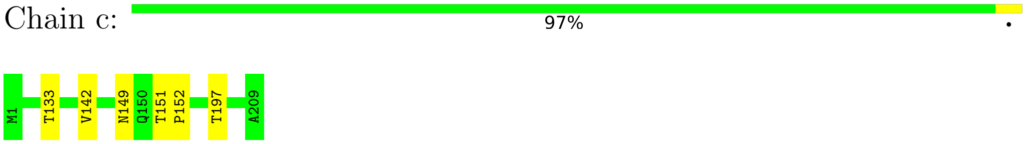
- Molecule 32: 5S ribosomal RNA



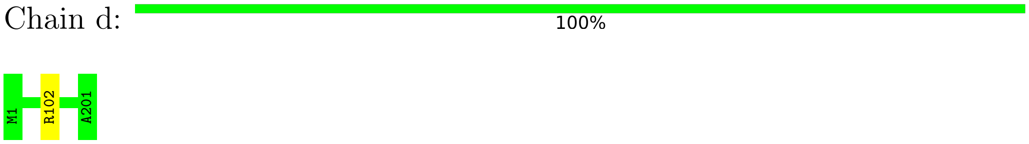
- Molecule 33: 50S ribosomal protein L2



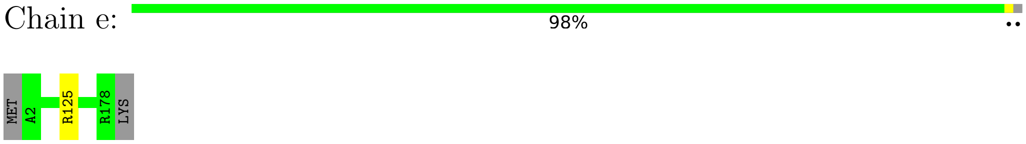
- Molecule 34: 50S ribosomal protein L3



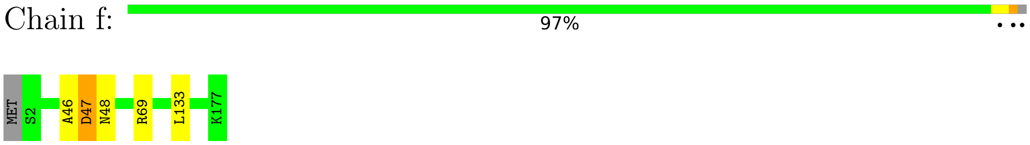
- Molecule 35: 50S ribosomal protein L4



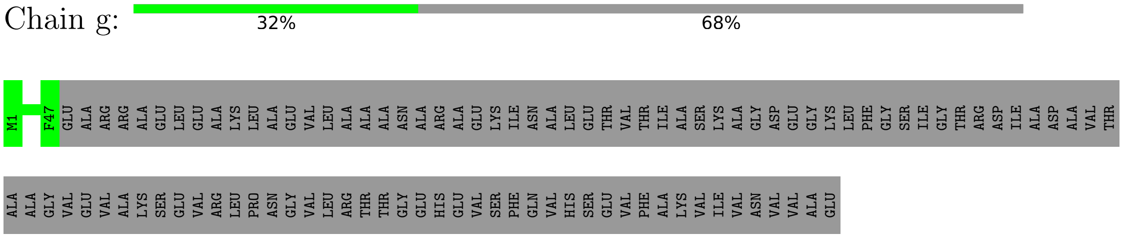
- Molecule 36: 50S ribosomal protein L5



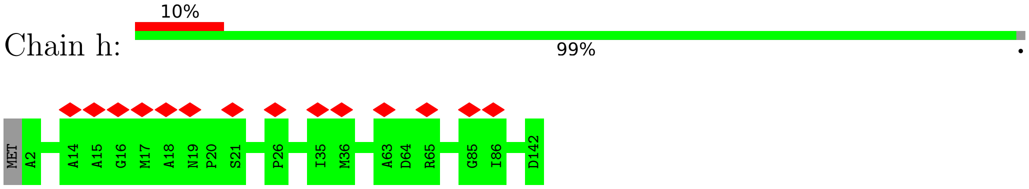
- Molecule 37: 50S ribosomal protein L6



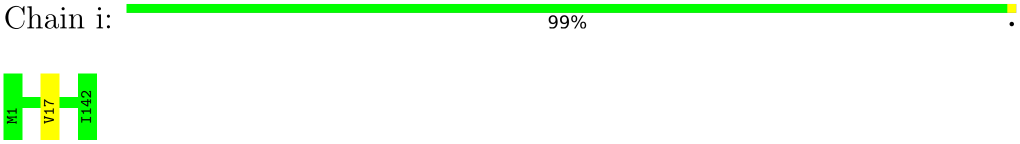
- Molecule 38: 50S ribosomal protein L9



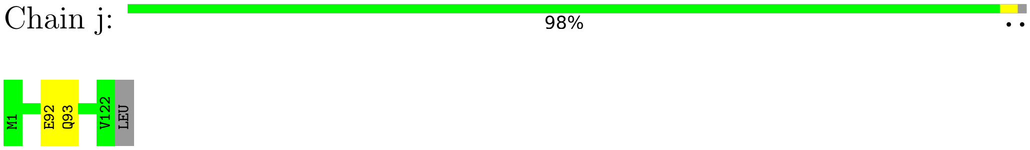
- Molecule 39: 50S ribosomal protein L11



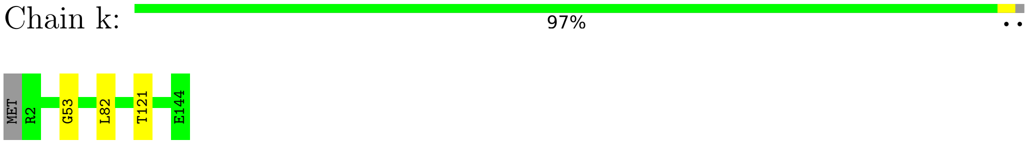
- Molecule 40: 50S ribosomal protein L13



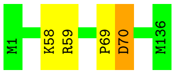
- Molecule 41: 50S ribosomal protein L14



- Molecule 42: 50S ribosomal protein L15

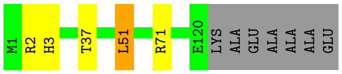


- Molecule 43: 50S ribosomal protein L16

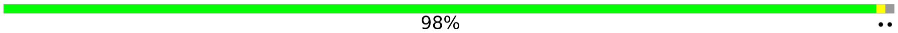


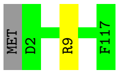
- Molecule 44: 50S ribosomal protein L17

Chain m:

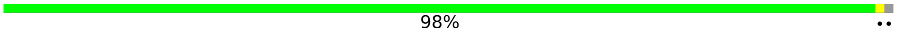



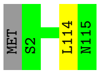
- Molecule 45: 50S ribosomal protein L18

Chain n:


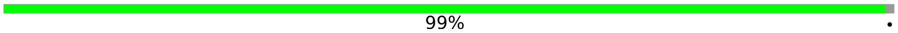


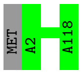
- Molecule 46: 50S ribosomal protein L19

Chain o:




- Molecule 47: 50S ribosomal protein L20

Chain p:


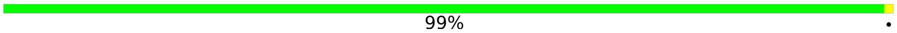


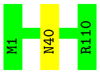
- Molecule 48: 50S ribosomal protein L21

Chain q:

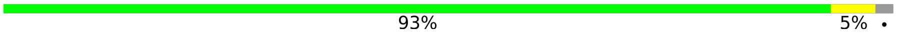

There are no outlier residues recorded for this chain.

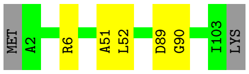
- Molecule 49: 50S ribosomal protein L22

Chain r:




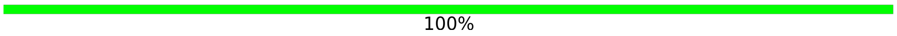
- Molecule 50: 50S ribosomal protein L24

Chain s:




- Molecule 51: 50S ribosomal protein L25

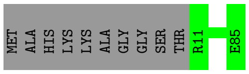
Chain t:



There are no outlier residues recorded for this chain.

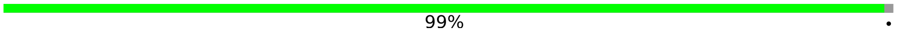
- Molecule 52: 50S ribosomal protein L27

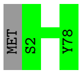
Chain u:



- Molecule 53: 50S ribosomal protein L28

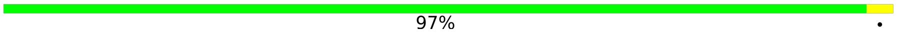
Chain v:

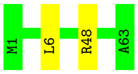




- Molecule 54: 50S ribosomal protein L29

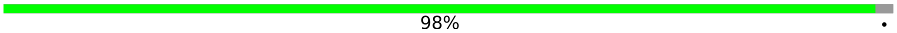
Chain w:

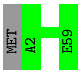




- Molecule 55: 50S ribosomal protein L30

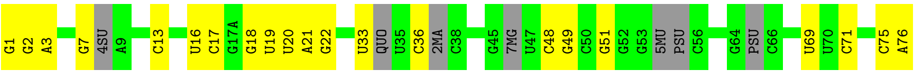
Chain x:





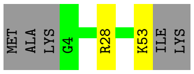
- Molecule 56: P-site tRNA

Chain y:



- Molecule 57: 50S ribosomal protein L33

Chain z:



# 4 Experimental information ⓘ

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, C1 | Depositor |
| Number of particles used | 54875 | 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 ($e^-/\text{Å}^2$) | 32.57 | Depositor |
| Minimum defocus (nm) | Not provided | |
| Maximum defocus (nm) | Not provided | |
| Magnification | Not provided | |
| Image detector | FEI FALCON III (4k x 4k) | Depositor |
| Maximum map value | 0.093 | Depositor |
| Minimum map value | -0.024 | Depositor |
| Average map value | 0.001 | Depositor |
| Map value standard deviation | 0.007 | Depositor |
| Recommended contour level | 0.005 | Depositor |
| Map size (Å) | 441.6, 441.6, 441.6 | wwPDB |
| Map dimensions | 320, 320, 320 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.38, 1.38, 1.38 | 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 | 0.72 | 0/380 | 0.69 | 0/498 |
| 2 | 1 | 0.66 | 0/513 | 0.76 | 0/676 |
| 3 | 2 | 0.63 | 0/303 | 0.64 | 0/397 |
| 4 | 3 | 0.30 | 0/1361 | 0.61 | 0/1830 |
| 5 | 5 | 0.30 | 0/3426 | 0.58 | 0/4605 |
| 6 | 6 | 0.63 | 0/450 | 0.68 | 0/599 |
| 7 | A | 1.54 | 229/69796 (0.3%) | 1.28 | 438/108888 (0.4%) |
| 8 | B | 0.76 | 0/36966 | 1.07 | 76/57666 (0.1%) |
| 9 | C | 0.38 | 0/1735 | 0.58 | 1/2338 (0.0%) |
| 10 | D | 0.33 | 0/1651 | 0.58 | 0/2225 |
| 11 | E | 0.33 | 0/1665 | 0.57 | 0/2227 |
| 12 | F | 0.40 | 0/1118 | 0.63 | 0/1504 |
| 13 | G | 0.35 | 0/835 | 0.63 | 1/1128 (0.1%) |
| 14 | H | 0.29 | 0/1195 | 0.52 | 0/1602 |
| 15 | I | 0.39 | 0/989 | 0.57 | 0/1326 |
| 16 | J | 0.29 | 0/1034 | 0.56 | 0/1375 |
| 17 | K | 0.30 | 0/796 | 0.61 | 0/1077 |
| 18 | L | 0.36 | 0/893 | 0.58 | 0/1205 |
| 19 | M | 0.41 | 0/969 | 0.64 | 0/1300 |
| 20 | N | 0.29 | 0/892 | 0.62 | 1/1193 (0.1%) |
| 21 | O | 0.30 | 0/785 | 0.56 | 0/1043 |
| 22 | P | 0.37 | 0/718 | 0.58 | 0/959 |
| 23 | Q | 0.37 | 0/659 | 0.63 | 0/884 |
| 24 | R | 0.38 | 0/657 | 0.61 | 0/881 |
| 25 | S | 0.35 | 0/462 | 0.59 | 1/621 (0.2%) |
| 26 | T | 0.30 | 0/652 | 0.54 | 0/877 |
| 27 | U | 0.32 | 0/671 | 0.56 | 0/888 |
| 28 | V | 0.38 | 0/430 | 0.77 | 1/570 (0.2%) |
| 29 | W | 0.67 | 0/771 | 0.70 | 0/1031 |
| 30 | X | 0.39 | 0/1551 | 1.04 | 0/2404 |
| 31 | Z | 0.44 | 1/1565 (0.1%) | 1.01 | 5/2421 (0.2%) |
| 32 | a | 1.10 | 0/2828 | 1.09 | 5/4410 (0.1%) |
| 33 | b | 0.71 | 0/2121 | 0.67 | 0/2852 |
| 34 | c | 0.70 | 0/1586 | 0.67 | 0/2134 |

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | #\|Z\| >5 | RMSZ | #\|Z\| >5 |
| 35 | d | 0.70 | 0/1571 | 0.63 | 0/2113 |
| 36 | e | 0.37 | 0/1434 | 0.58 | 0/1926 |
| 37 | f | 0.48 | 0/1343 | 0.59 | 1/1816 (0.1%) |
| 38 | g | 0.44 | 0/364 | 0.66 | 0/490 |
| 39 | h | 0.32 | 0/1046 | 0.61 | 0/1410 |
| 40 | i | 0.75 | 0/1152 | 0.64 | 0/1551 |
| 41 | j | 0.67 | 0/947 | 0.70 | 0/1268 |
| 42 | k | 0.63 | 0/1054 | 0.73 | 0/1403 |
| 43 | l | 0.63 | 0/1093 | 0.69 | 1/1460 (0.1%) |
| 44 | m | 0.69 | 0/973 | 0.78 | 1/1301 (0.1%) |
| 45 | n | 0.48 | 0/902 | 0.56 | 0/1209 |
| 46 | o | 0.67 | 0/929 | 0.65 | 1/1242 (0.1%) |
| 47 | p | 0.85 | 0/960 | 0.65 | 0/1278 |
| 48 | q | 0.72 | 0/829 | 0.67 | 0/1107 |
| 49 | r | 0.71 | 0/864 | 0.64 | 0/1156 |
| 50 | s | 0.60 | 0/787 | 0.62 | 0/1051 |
| 51 | t | 0.57 | 0/766 | 0.57 | 0/1025 |
| 52 | u | 0.66 | 0/576 | 0.60 | 0/762 |
| 53 | v | 0.69 | 0/635 | 0.63 | 0/848 |
| 54 | w | 0.59 | 0/510 | 0.66 | 1/677 (0.1%) |
| 55 | x | 0.63 | 0/453 | 0.69 | 0/605 |
| 56 | y | 0.51 | 1/1664 (0.1%) | 1.02 | 2/2577 (0.1%) |
| 57 | z | 0.47 | 0/416 | 0.54 | 0/554 |
| All | All | 1.12 | 231/163691 (0.1%) | 1.08 | 536/244463 (0.2%) |

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 |
|---|---|---|---|
| 2 | 1 | 0 | 1 |
| 3 | 2 | 0 | 1 |
| 9 | C | 0 | 1 |
| 11 | E | 0 | 2 |
| 12 | F | 0 | 2 |
| 13 | G | 0 | 1 |
| 16 | J | 0 | 2 |
| 17 | K | 0 | 1 |
| 19 | M | 0 | 1 |
| 20 | N | 0 | 1 |
| 23 | Q | 0 | 1 |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|---|---|---|---|
| 24 | R | 0 | 2 |
| 28 | V | 0 | 2 |
| 29 | W | 0 | 1 |
| 34 | c | 0 | 1 |
| 37 | f | 0 | 2 |
| 41 | j | 0 | 1 |
| 42 | k | 0 | 1 |
| 43 | l | 0 | 1 |
| 50 | s | 0 | 3 |
| All | All | 0 | 28 |

The worst 5 of 231 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 56 | y | 1 | G | OP3-P | -10.67 | 1.48 | 1.61 |
| 7 | A | 783 | A | N9-C4 | -8.57 | 1.32 | 1.37 |
| 7 | A | 1142 | A | N9-C4 | -8.35 | 1.32 | 1.37 |
| 7 | A | 984 | A | N9-C4 | -8.20 | 1.32 | 1.37 |
| 7 | A | 447 | A | N9-C4 | -8.01 | 1.33 | 1.37 |

The worst 5 of 536 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 7 | A | 761 | A | N1-C6-N6 | 11.81 | 125.69 | 118.60 |
| 7 | A | 545 | U | C2-N1-C1' | 11.52 | 131.53 | 117.70 |
| 7 | A | 761 | A | C5-N7-C8 | -11.09 | 98.35 | 103.90 |
| 7 | A | 545 | U | N3-C2-O2 | -10.48 | 114.86 | 122.20 |
| 7 | A | 545 | U | N1-C2-O2 | 10.40 | 130.08 | 122.80 |

There are no chirality outliers.

5 of 28 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 2 | 1 | 31 | HIS | Peptide |
| 3 | 2 | 20 | ASP | Peptide |
| 9 | C | 84 | ALA | Peptide |
| 11 | E | 173 | VAL | Peptide |
| 11 | E | 20 | PHE | Peptide |

## 5.2 Too-close contacts ⓘ

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

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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 | 44/46 (96%) | 41 (93%) | 3 (7%) | 0 | 100 | 100 |
| 2 | 1 | 62/65 (95%) | 51 (82%) | 9 (14%) | 2 (3%) | 4 | 30 |
| 3 | 2 | 36/38 (95%) | 30 (83%) | 5 (14%) | 1 (3%) | 5 | 32 |
| 4 | 3 | 166/169 (98%) | 145 (87%) | 21 (13%) | 0 | 100 | 100 |
| 5 | 5 | 430/432 (100%) | 387 (90%) | 43 (10%) | 0 | 100 | 100 |
| 6 | 6 | 54/57 (95%) | 45 (83%) | 8 (15%) | 1 (2%) | 8 | 39 |
| 9 | C | 216/241 (90%) | 178 (82%) | 38 (18%) | 0 | 100 | 100 |
| 10 | D | 204/233 (88%) | 176 (86%) | 28 (14%) | 0 | 100 | 100 |
| 11 | E | 203/206 (98%) | 179 (88%) | 24 (12%) | 0 | 100 | 100 |
| 12 | F | 148/167 (89%) | 114 (77%) | 34 (23%) | 0 | 100 | 100 |
| 13 | G | 98/135 (73%) | 84 (86%) | 14 (14%) | 0 | 100 | 100 |
| 14 | H | 149/179 (83%) | 138 (93%) | 11 (7%) | 0 | 100 | 100 |
| 15 | I | 127/130 (98%) | 119 (94%) | 8 (6%) | 0 | 100 | 100 |
| 16 | J | 125/130 (96%) | 111 (89%) | 14 (11%) | 0 | 100 | 100 |
| 17 | K | 96/103 (93%) | 84 (88%) | 12 (12%) | 0 | 100 | 100 |
| 18 | L | 115/129 (89%) | 92 (80%) | 23 (20%) | 0 | 100 | 100 |
| 19 | M | 121/124 (98%) | 95 (78%) | 26 (22%) | 0 | 100 | 100 |
| 20 | N | 112/118 (95%) | 97 (87%) | 13 (12%) | 2 (2%) | 8 | 40 |
| 21 | O | 92/101 (91%) | 81 (88%) | 11 (12%) | 0 | 100 | 100 |
| 22 | P | 86/89 (97%) | 78 (91%) | 8 (9%) | 0 | 100 | 100 |
| 23 | Q | 80/82 (98%) | 66 (82%) | 14 (18%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 24 | R | 78/84 (93%) | 58 (74%) | 19 (24%) | 1 (1%) | 12 | 47 |
| 25 | S | 53/75 (71%) | 51 (96%) | 2 (4%) | 0 | 100 | 100 |
| 26 | T | 77/92 (84%) | 69 (90%) | 8 (10%) | 0 | 100 | 100 |
| 27 | U | 83/87 (95%) | 78 (94%) | 4 (5%) | 1 (1%) | 13 | 48 |
| 28 | V | 49/71 (69%) | 37 (76%) | 12 (24%) | 0 | 100 | 100 |
| 29 | W | 94/100 (94%) | 80 (85%) | 14 (15%) | 0 | 100 | 100 |
| 33 | b | 269/273 (98%) | 230 (86%) | 39 (14%) | 0 | 100 | 100 |
| 34 | c | 207/209 (99%) | 187 (90%) | 18 (9%) | 2 (1%) | 15 | 52 |
| 35 | d | 199/201 (99%) | 185 (93%) | 14 (7%) | 0 | 100 | 100 |
| 36 | e | 175/179 (98%) | 153 (87%) | 22 (13%) | 0 | 100 | 100 |
| 37 | f | 174/177 (98%) | 159 (91%) | 13 (8%) | 2 (1%) | 14 | 50 |
| 38 | g | 45/149 (30%) | 34 (76%) | 11 (24%) | 0 | 100 | 100 |
| 39 | h | 139/142 (98%) | 115 (83%) | 24 (17%) | 0 | 100 | 100 |
| 40 | i | 140/142 (99%) | 126 (90%) | 14 (10%) | 0 | 100 | 100 |
| 41 | j | 120/123 (98%) | 89 (74%) | 30 (25%) | 1 (1%) | 19 | 58 |
| 42 | k | 141/144 (98%) | 121 (86%) | 19 (14%) | 1 (1%) | 22 | 60 |
| 43 | l | 134/136 (98%) | 118 (88%) | 13 (10%) | 3 (2%) | 6 | 37 |
| 44 | m | 118/127 (93%) | 99 (84%) | 17 (14%) | 2 (2%) | 9 | 42 |
| 45 | n | 114/117 (97%) | 103 (90%) | 11 (10%) | 0 | 100 | 100 |
| 46 | o | 112/115 (97%) | 97 (87%) | 15 (13%) | 0 | 100 | 100 |
| 47 | p | 115/118 (98%) | 109 (95%) | 6 (5%) | 0 | 100 | 100 |
| 48 | q | 101/103 (98%) | 85 (84%) | 16 (16%) | 0 | 100 | 100 |
| 49 | r | 108/110 (98%) | 99 (92%) | 9 (8%) | 0 | 100 | 100 |
| 50 | s | 100/104 (96%) | 81 (81%) | 17 (17%) | 2 (2%) | 7 | 39 |
| 51 | t | 92/94 (98%) | 87 (95%) | 5 (5%) | 0 | 100 | 100 |
| 52 | u | 73/85 (86%) | 62 (85%) | 11 (15%) | 0 | 100 | 100 |
| 53 | v | 75/78 (96%) | 64 (85%) | 11 (15%) | 0 | 100 | 100 |
| 54 | w | 61/63 (97%) | 54 (88%) | 7 (12%) | 0 | 100 | 100 |
| 55 | x | 56/59 (95%) | 51 (91%) | 5 (9%) | 0 | 100 | 100 |
| 57 | z | 48/55 (87%) | 42 (88%) | 6 (12%) | 0 | 100 | 100 |
| All | All | 6114/6586 (93%) | 5314 (87%) | 779 (13%) | 21 (0%) | 44 | 75 |

5 of 21 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | 1 | 32 | ILE |
| 20 | N | 67 | GLY |
| 37 | f | 48 | ASN |
| 2 | 1 | 33 | LEU |
| 3 | 2 | 21 | GLY |

### 5.3.2 Protein sidechains ⓘ

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 | 38/38 (100%) | 38 (100%) | 0 | 100 | 100 |
| 2 | 1 | 51/52 (98%) | 51 (100%) | 0 | 100 | 100 |
| 3 | 2 | 34/34 (100%) | 34 (100%) | 0 | 100 | 100 |
| 4 | 3 | 148/149 (99%) | 147 (99%) | 1 (1%) | 84 | 90 |
| 5 | 5 | 359/359 (100%) | 358 (100%) | 1 (0%) | 92 | 95 |
| 6 | 6 | 47/48 (98%) | 47 (100%) | 0 | 100 | 100 |
| 9 | C | 180/199 (90%) | 179 (99%) | 1 (1%) | 86 | 92 |
| 10 | D | 170/190 (90%) | 170 (100%) | 0 | 100 | 100 |
| 11 | E | 172/173 (99%) | 170 (99%) | 2 (1%) | 71 | 83 |
| 12 | F | 113/126 (90%) | 113 (100%) | 0 | 100 | 100 |
| 13 | G | 87/116 (75%) | 85 (98%) | 2 (2%) | 50 | 70 |
| 14 | H | 124/147 (84%) | 123 (99%) | 1 (1%) | 81 | 88 |
| 15 | I | 104/105 (99%) | 102 (98%) | 2 (2%) | 57 | 75 |
| 16 | J | 105/107 (98%) | 102 (97%) | 3 (3%) | 42 | 64 |
| 17 | K | 86/90 (96%) | 85 (99%) | 1 (1%) | 71 | 83 |
| 18 | L | 90/99 (91%) | 88 (98%) | 2 (2%) | 52 | 71 |
| 19 | M | 103/104 (99%) | 103 (100%) | 0 | 100 | 100 |
| 20 | N | 92/96 (96%) | 89 (97%) | 3 (3%) | 38 | 62 |
| 21 | O | 79/84 (94%) | 79 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 22 | P | 75/77 (97%) | 75 (100%) | 0 | 100 | 100 |
| 23 | Q | 65/65 (100%) | 65 (100%) | 0 | 100 | 100 |
| 24 | R | 74/78 (95%) | 73 (99%) | 1 (1%) | 67 | 80 |
| 25 | S | 48/65 (74%) | 47 (98%) | 1 (2%) | 53 | 72 |
| 26 | T | 70/79 (89%) | 70 (100%) | 0 | 100 | 100 |
| 27 | U | 65/66 (98%) | 62 (95%) | 3 (5%) | 27 | 54 |
| 28 | V | 44/61 (72%) | 43 (98%) | 1 (2%) | 50 | 70 |
| 29 | W | 83/84 (99%) | 81 (98%) | 2 (2%) | 49 | 69 |
| 33 | b | 216/218 (99%) | 212 (98%) | 4 (2%) | 57 | 75 |
| 34 | c | 164/164 (100%) | 161 (98%) | 3 (2%) | 59 | 77 |
| 35 | d | 165/165 (100%) | 164 (99%) | 1 (1%) | 86 | 92 |
| 36 | e | 148/150 (99%) | 147 (99%) | 1 (1%) | 84 | 90 |
| 37 | f | 137/138 (99%) | 136 (99%) | 1 (1%) | 84 | 90 |
| 38 | g | 38/114 (33%) | 38 (100%) | 0 | 100 | 100 |
| 39 | h | 109/110 (99%) | 109 (100%) | 0 | 100 | 100 |
| 40 | i | 116/116 (100%) | 115 (99%) | 1 (1%) | 78 | 87 |
| 41 | j | 103/104 (99%) | 103 (100%) | 0 | 100 | 100 |
| 42 | k | 102/103 (99%) | 101 (99%) | 1 (1%) | 76 | 85 |
| 43 | l | 109/109 (100%) | 109 (100%) | 0 | 100 | 100 |
| 44 | m | 100/103 (97%) | 97 (97%) | 3 (3%) | 41 | 64 |
| 45 | n | 86/87 (99%) | 85 (99%) | 1 (1%) | 71 | 83 |
| 46 | o | 99/100 (99%) | 99 (100%) | 0 | 100 | 100 |
| 47 | p | 89/90 (99%) | 89 (100%) | 0 | 100 | 100 |
| 48 | q | 84/84 (100%) | 84 (100%) | 0 | 100 | 100 |
| 49 | r | 93/93 (100%) | 92 (99%) | 1 (1%) | 73 | 84 |
| 50 | s | 83/85 (98%) | 83 (100%) | 0 | 100 | 100 |
| 51 | t | 78/78 (100%) | 78 (100%) | 0 | 100 | 100 |
| 52 | u | 56/63 (89%) | 56 (100%) | 0 | 100 | 100 |
| 53 | v | 67/68 (98%) | 67 (100%) | 0 | 100 | 100 |
| 54 | w | 55/55 (100%) | 54 (98%) | 1 (2%) | 59 | 77 |
| 55 | x | 48/49 (98%) | 48 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 57 | z | 45/49 (92%) | 43 (96%) | 2 (4%) | 28 | 55 |
| All | All | 5096/5386 (95%) | 5049 (99%) | 47 (1%) | 79 | 87 |

5 of 47 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 33 | b | 114 | ASP |
| 36 | e | 125 | ARG |
| 33 | b | 171 | TYR |
| 34 | c | 142 | VAL |
| 40 | i | 17 | VAL |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 34 | c | 130 | GLN |
| 37 | f | 143 | GLN |
| 51 | t | 49 | ASN |
| 35 | d | 9 | GLN |
| 37 | f | 88 | GLN |

### 5.3.3 RNA ⓘ

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|---|---|---|---|---|
| 30 | X | 58/73 (79%) | 30 (51%) | 0 |
| 31 | Z | 58/76 (76%) | 24 (41%) | 1 (1%) |
| 32 | a | 117/118 (99%) | 21 (17%) | 0 |
| 56 | y | 63/77 (81%) | 19 (30%) | 0 |
| 7 | A | 2902/2903 (99%) | 740 (25%) | 13 (0%) |
| 8 | B | 1538/1539 (99%) | 426 (27%) | 3 (0%) |
| All | All | 4736/4786 (98%) | 1260 (26%) | 17 (0%) |

5 of 1260 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 7 | A | 10 | A |
| 7 | A | 14 | A |
| 7 | A | 23 | G |
| 7 | A | 34 | U |
| 7 | A | 42 | A |

5 of 17 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 8 | B | 428 | G |
| 31 | Z | 13 | C |
| 7 | A | 1730 | C |
| 7 | A | 1904 | G |
| 7 | A | 1913 | A |

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

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

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

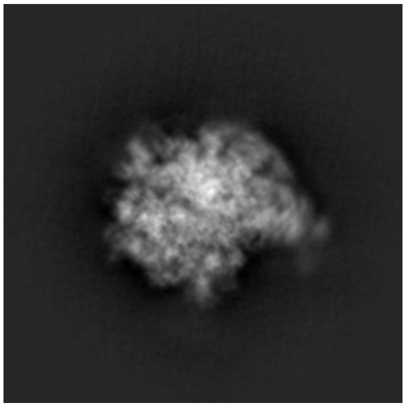
# 6 Map visualisation

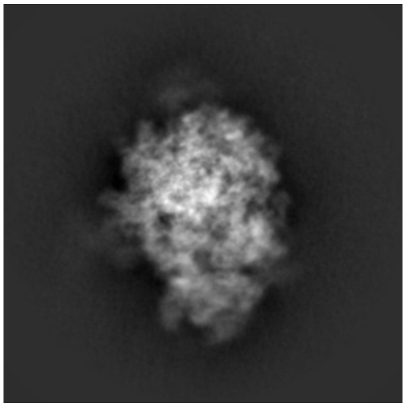
This section contains visualisations of the EMDB entry EMD-30611. These allow visual inspection of the internal detail of the map and identification of artifacts.

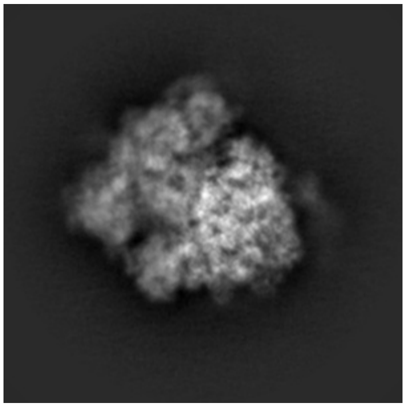
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

## 6.1 Orthogonal projections

### 6.1.1 Primary map


X

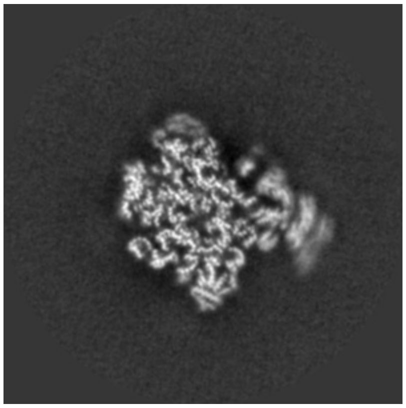

Y

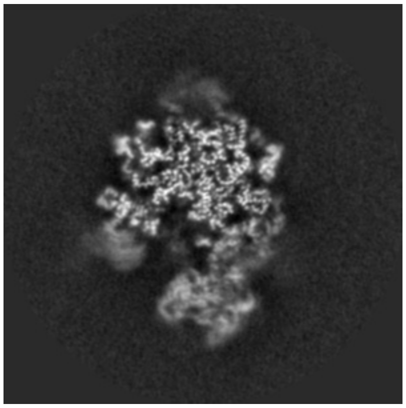

Z

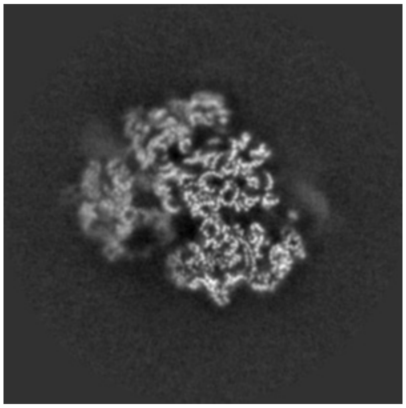
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices

### 6.2.1 Primary map


X Index: 160

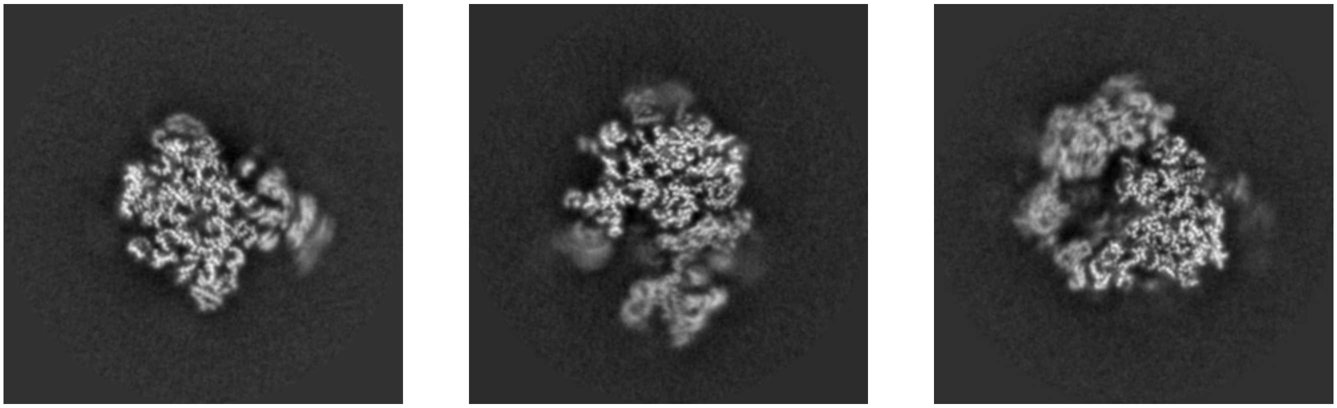

Y Index: 160


Z Index: 160

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

## 6.3 Largest variance slices

### 6.3.1 Primary map



X Index: 161 Y Index: 165 Z Index: 147

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

## 6.4 Orthogonal surface views

### 6.4.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

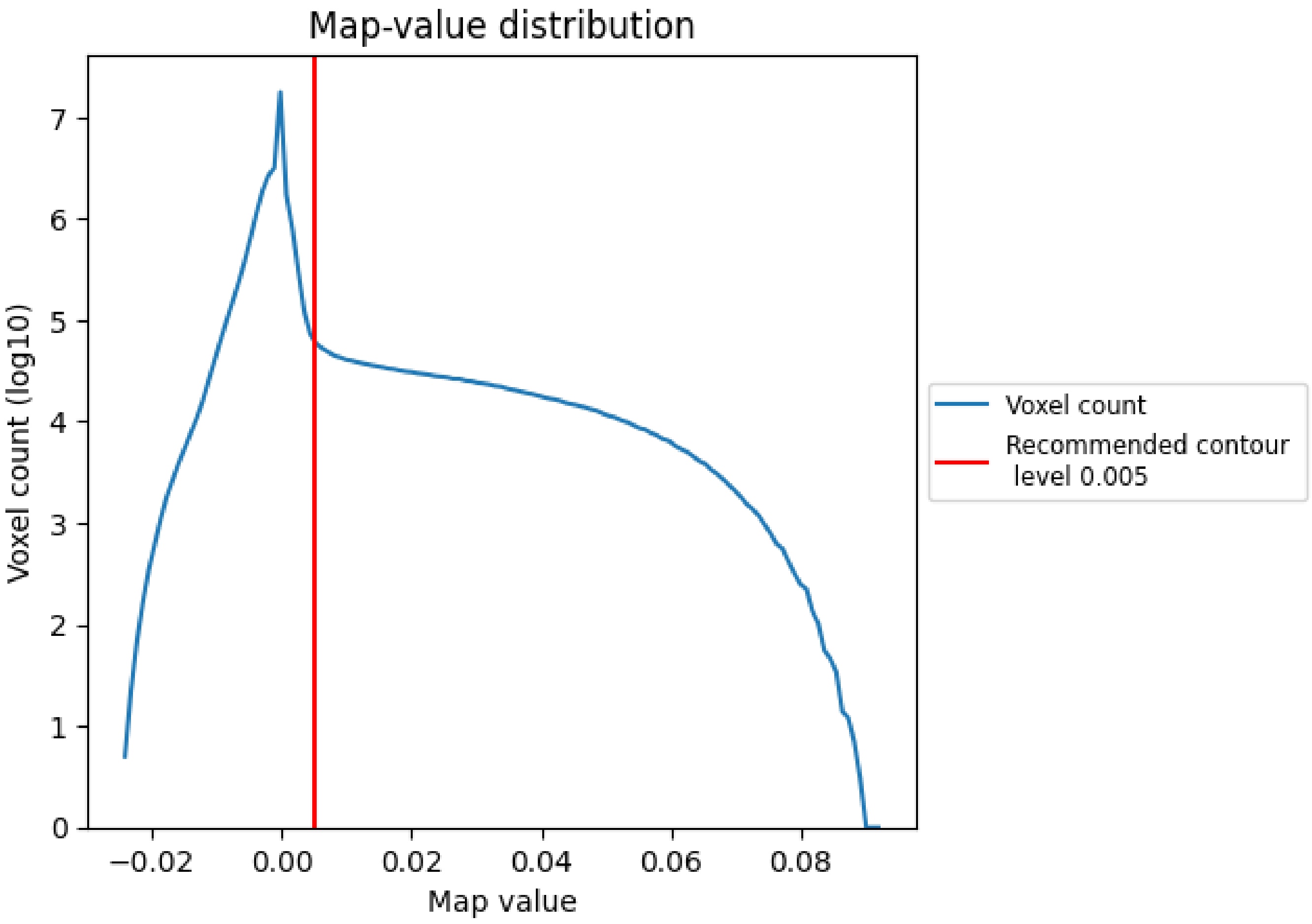
## 6.5 Mask visualisation ⓘ

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

# 7 Map analysis ⓘ

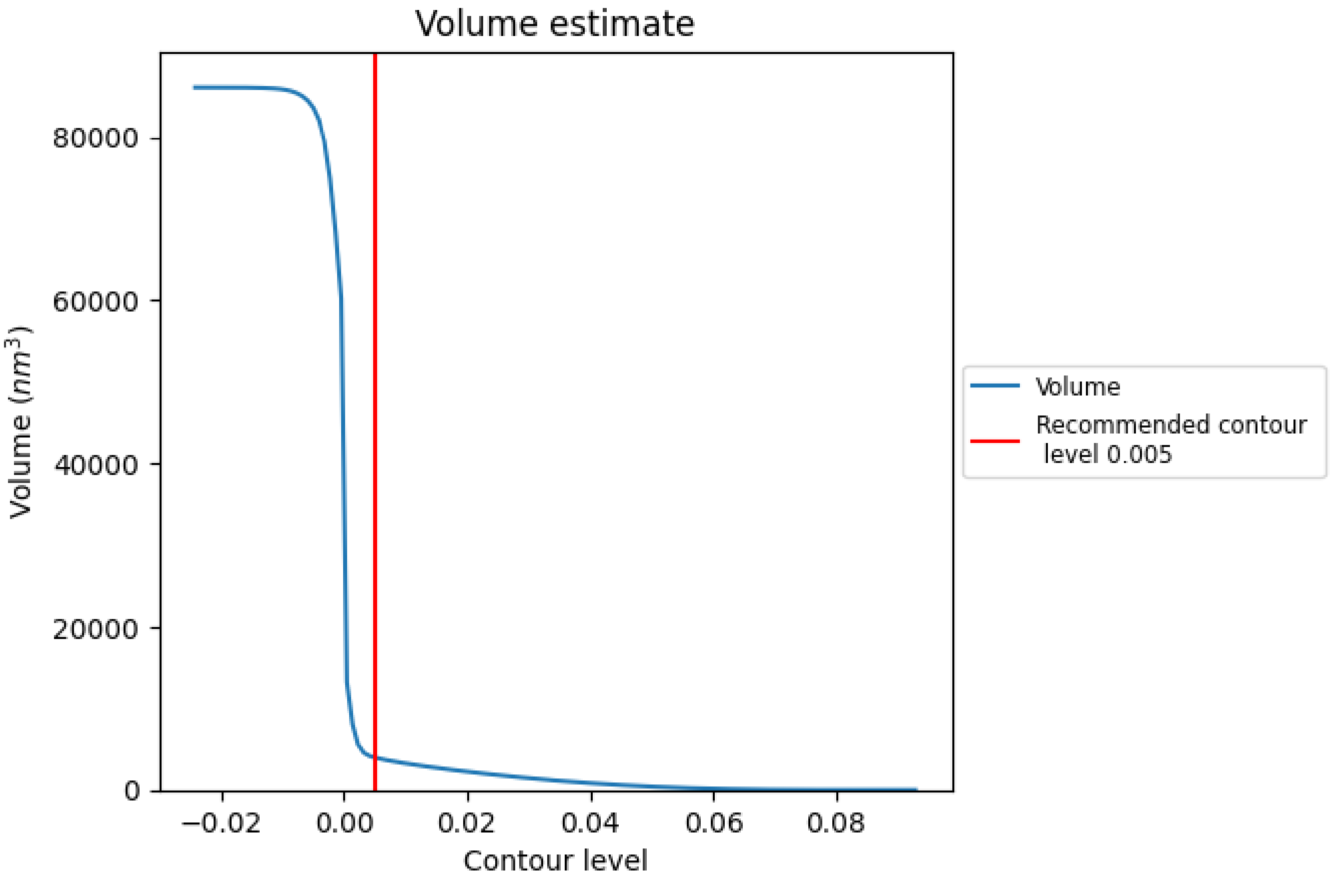
This section contains the results of statistical analysis of the map.

## 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.

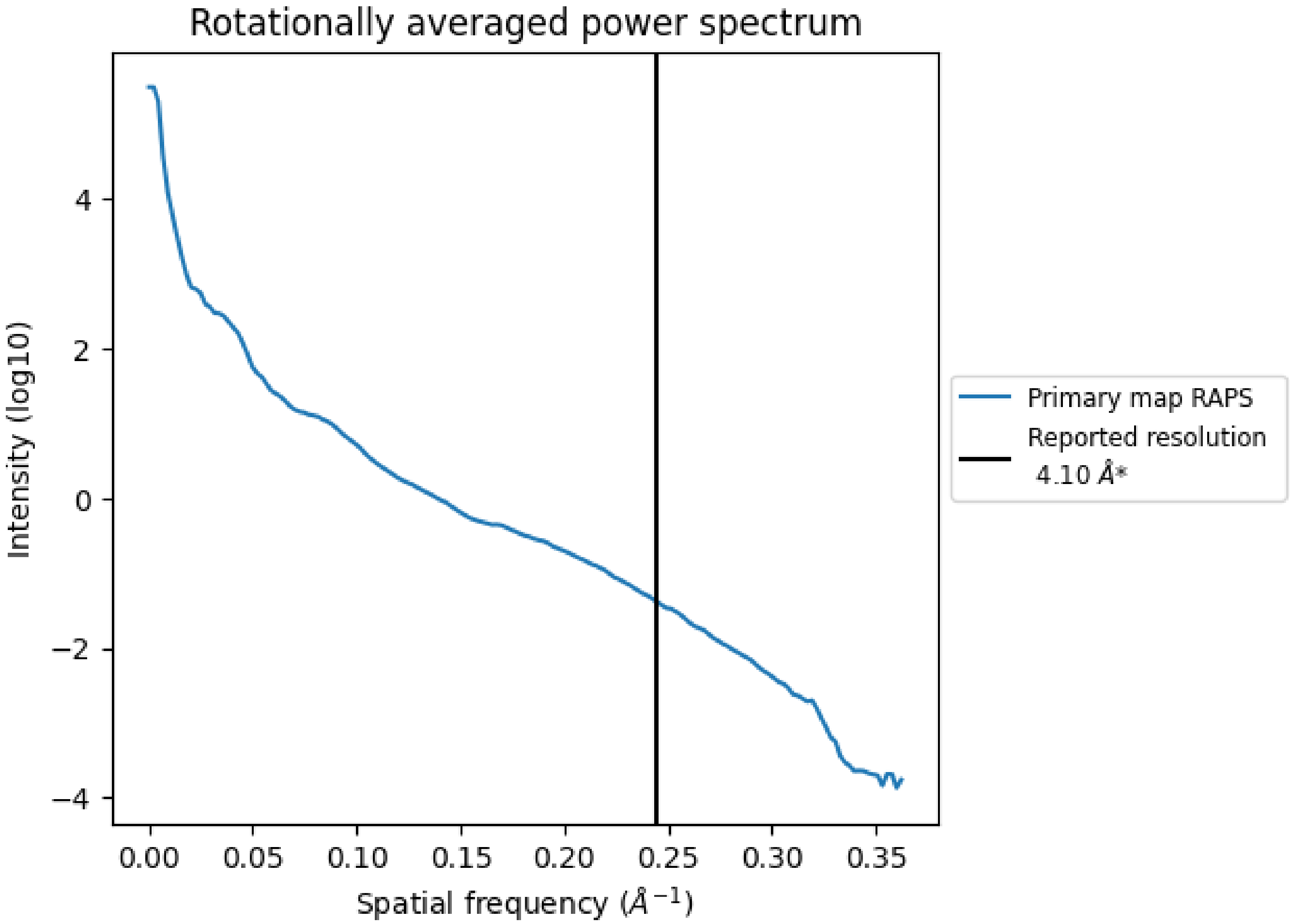
## 7.2 Volume estimate ⓘ



The volume at the recommended contour level is 3991 nm$^3$; this corresponds to an approximate mass of 3605 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 ⓘ

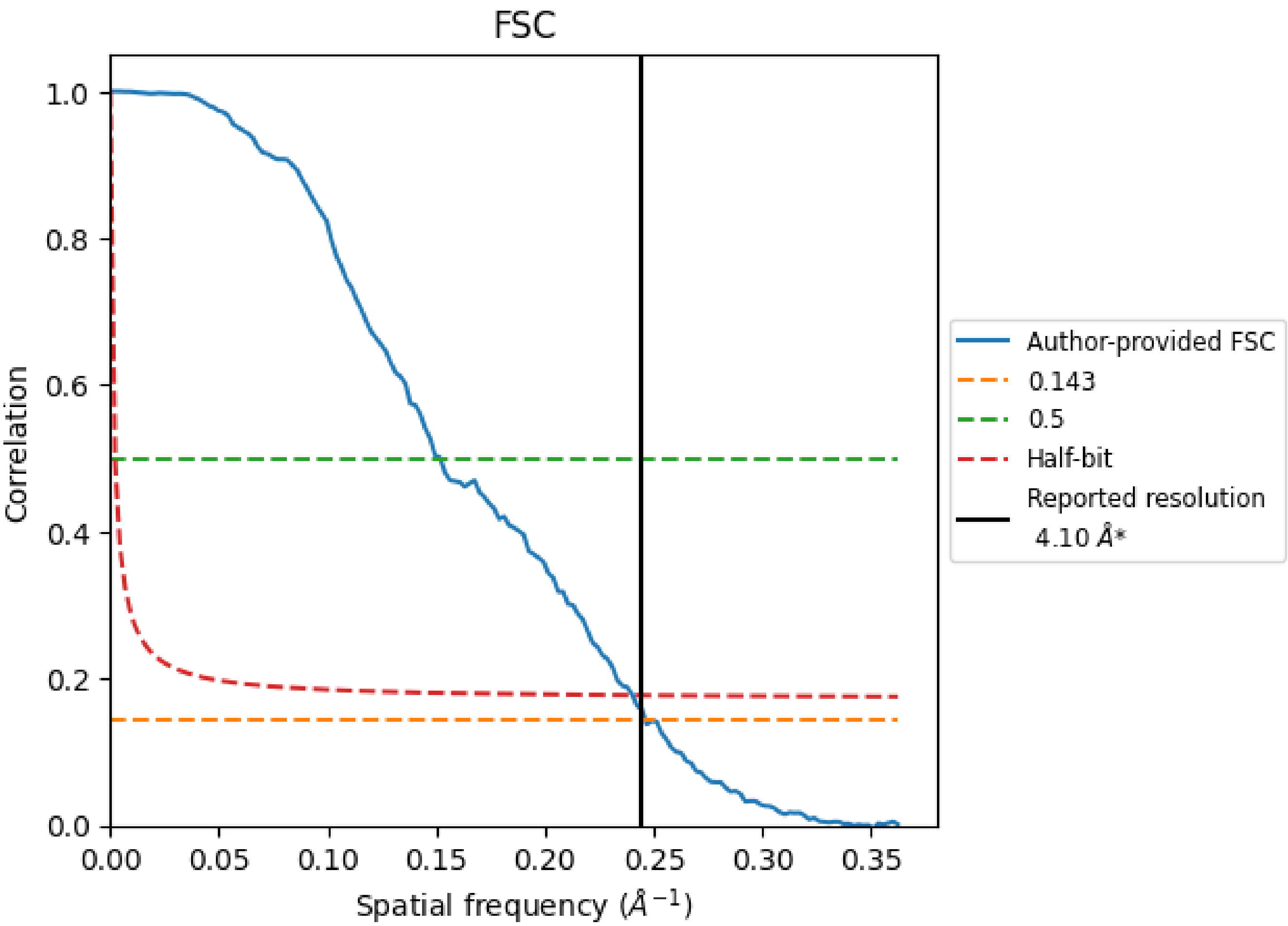


*Reported resolution corresponds to spatial frequency of 0.244 Å$^{-1}$

# 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 0.244 $\AA^{-1}$

## 8.2 Resolution estimates (i)

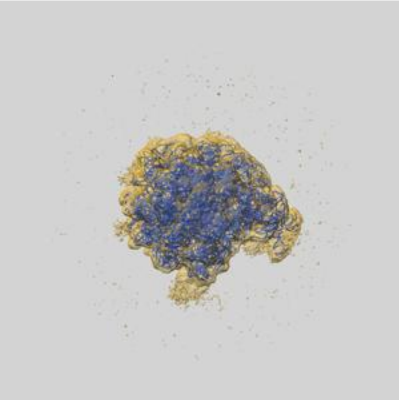
| **Resolution estimate (Å)** | **Estimation criterion (FSC cut-off)** | | |
|---|---|---|---|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 4.10 | - | - |
| Author-provided FSC curve | 4.06 | 6.59 | 4.16 |
| Unmasked-calculated* | - | - | - |

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

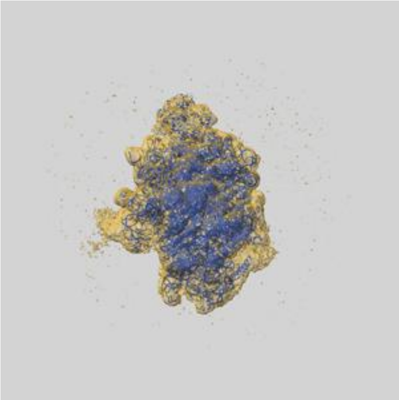
# 9 Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-30611 and PDB model 7D80. Per-residue inclusion information can be found in section 3 on page 14.

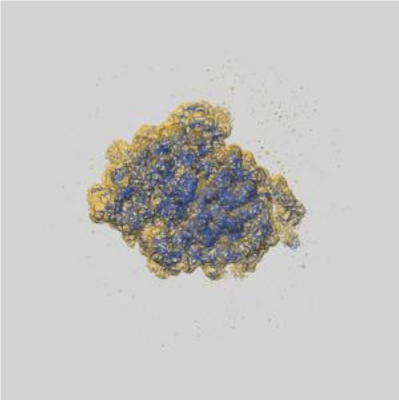
## 9.1 Map-model overlay ⓘ



X



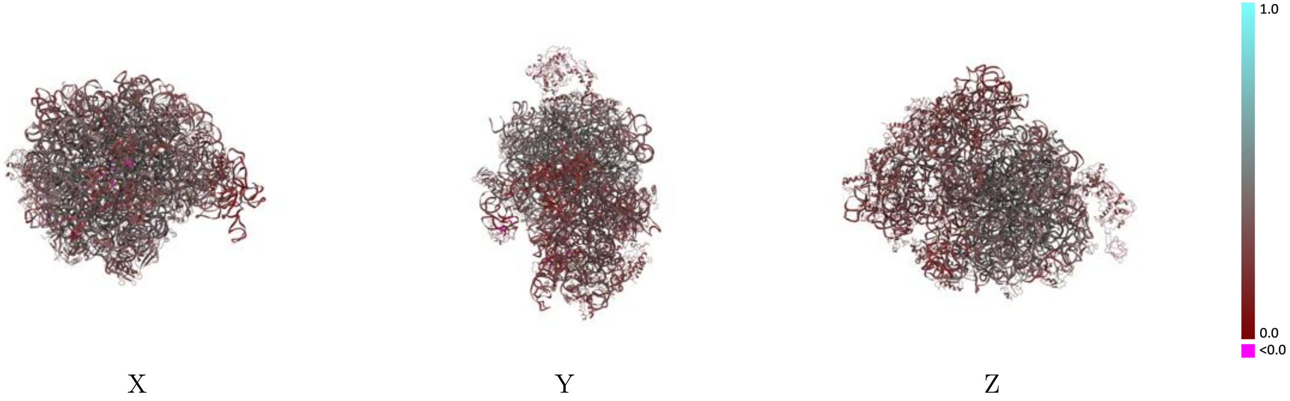
Y



Z

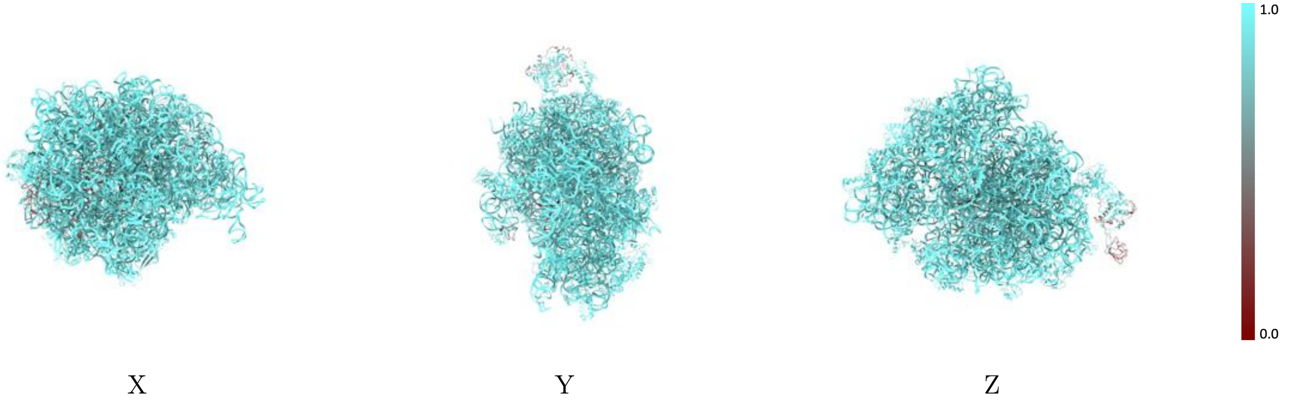
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 9.2 Q-score mapped to coordinate model ⓘ



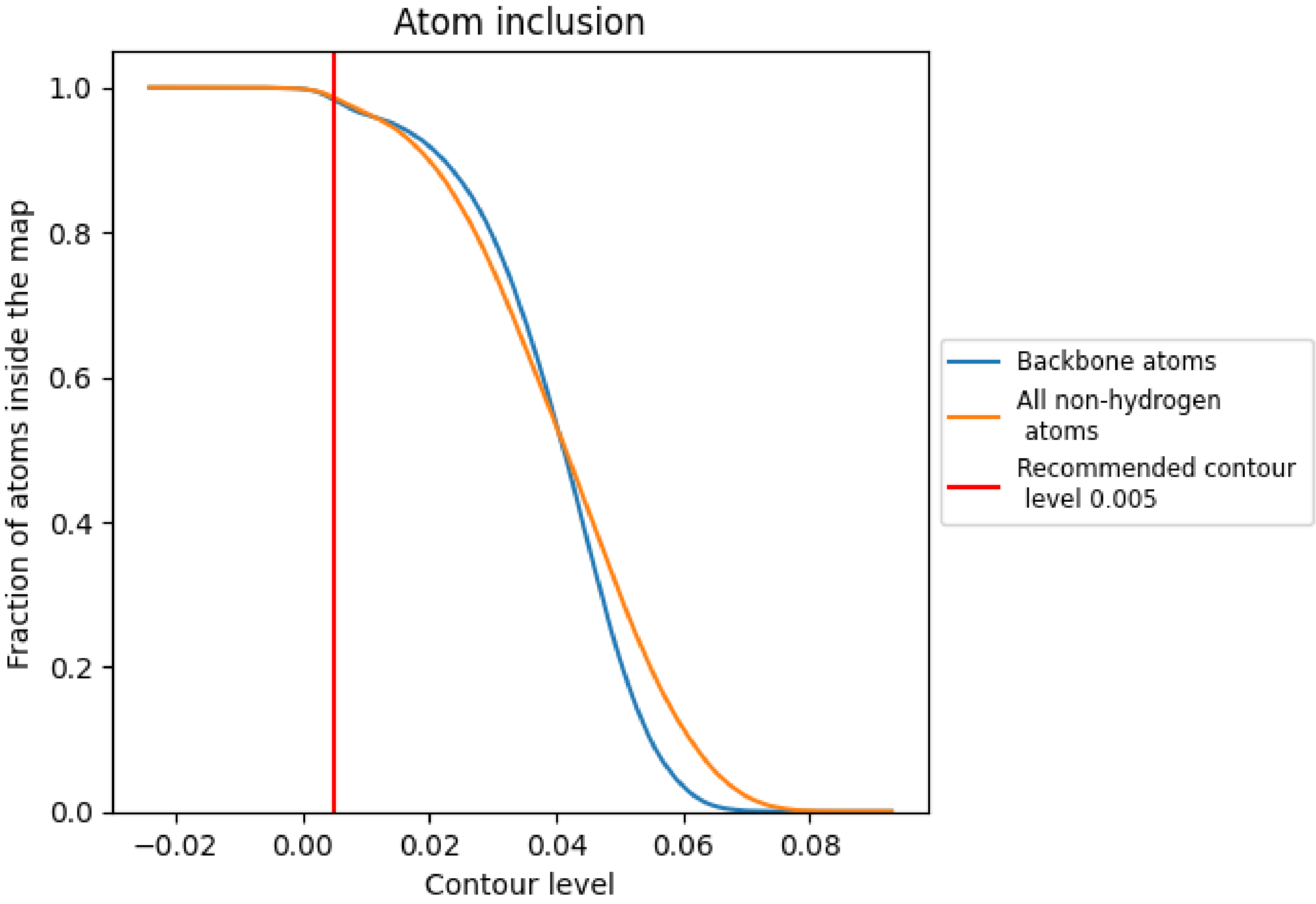
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 ⓘ



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 (0.005).

## 9.4 Atom inclusion ⓘ



At the recommended contour level, 98% of all backbone atoms, 99% 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 (0.005) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|---|---|---|
| All | 0.9859 | 0.3390 |
| 0 | 0.9746 | 0.3790 |
| 1 | 0.9939 | 0.3960 |
| 2 | 1.0000 | 0.3610 |
| 3 | 0.9894 | 0.2710 |
| 5 | 0.6749 | 0.2400 |
| 6 | 1.0000 | 0.3920 |
| A | 0.9993 | 0.3870 |
| B | 1.0000 | 0.3000 |
| C | 1.0000 | 0.2690 |
| D | 0.9981 | 0.2850 |
| E | 1.0000 | 0.2120 |
| F | 0.9982 | 0.3040 |
| G | 0.9937 | 0.2860 |
| H | 0.9991 | 0.2410 |
| I | 0.9990 | 0.2790 |
| J | 1.0000 | 0.2260 |
| K | 0.9974 | 0.2560 |
| L | 0.9965 | 0.2910 |
| M | 0.9935 | 0.2620 |
| N | 0.9976 | 0.2210 |
| O | 1.0000 | 0.2350 |
| P | 0.9956 | 0.2560 |
| Q | 0.9984 | 0.2510 |
| R | 1.0000 | 0.2680 |
| S | 1.0000 | 0.3140 |
| T | 0.9984 | 0.2050 |
| U | 0.9969 | 0.2250 |
| V | 0.9926 | 0.2600 |
| W | 0.9947 | 0.3610 |
| X | 0.9978 | 0.2180 |
| Z | 0.5284 | 0.2640 |
| a | 1.0000 | 0.3520 |
| b | 0.9911 | 0.4030 |
| c | 0.9941 | 0.4000 |

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| Chain | Atom inclusion | Q-score |
|---|---|---|
| d | 🟦 0.9974 | 🟫 0.3740 |
| e | 🟦 0.9993 | 🟫 0.2550 |
| f | 🟦 1.0000 | 🟫 0.3330 |
| g | 🟦 1.0000 | 🟫 0.3360 |
| h | 🟦 0.8796 | 🟫 0.1720 |
| i | 🟦 0.9964 | 🟫 0.3910 |
| j | 🟦 0.9912 | 🟫 0.4010 |
| k | 🟦 0.9951 | 🟫 0.3920 |
| l | 🟦 0.9971 | 🟫 0.3940 |
| m | 🟦 0.9978 | 🟫 0.3800 |
| n | 🟦 1.0000 | 🟫 0.3220 |
| o | 🟦 0.9932 | 🟫 0.3830 |
| p | 🟦 0.9989 | 🟫 0.3670 |
| q | 🟦 0.9962 | 🟫 0.4020 |
| r | 🟦 0.9916 | 🟫 0.3850 |
| s | 🟦 0.9961 | 🟫 0.3580 |
| t | 🟦 1.0000 | 🟫 0.3620 |
| u | 🟦 0.9982 | 🟫 0.4010 |
| v | 🟦 0.9967 | 🟫 0.3730 |
| w | 🟦 1.0000 | 🟫 0.2840 |
| x | 🟦 0.9954 | 🟫 0.3850 |
| y | 🟦 0.9699 | 🟫 0.2890 |
| z | 🟦 0.9875 | 🟫 0.3580 |