



wwPDB EM Validation Summary Report ⓘ

Oct 14, 2024 – 09:26 PM EDT

PDB ID : 8UQP
EMDB ID : EMD-42477
Title : Escherichia coli transcription-translation coupled complex class B (TTC-B) containing RfaH bound to ops signal, mRNA with a 24 nt long spacer, and fMet-tRNAs in E-site and P-site of the ribosome
Authors : Molodtsov, V.; Wang, C.; Ebright, R.H.
Deposited on : 2023-10-24
Resolution : 3.80 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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

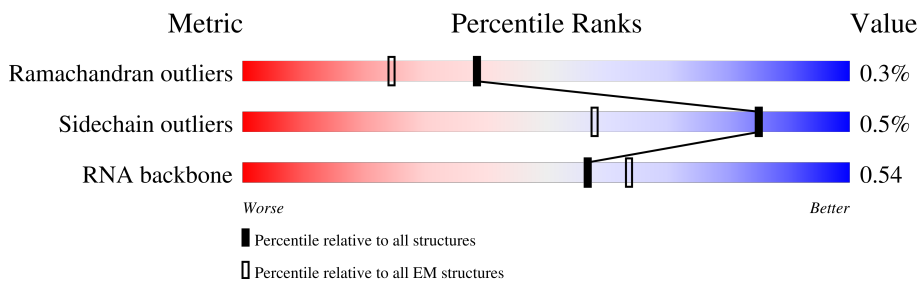
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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 | 207382 | 16835 |
| Sidechain outliers | 206894 | 16415 |
| RNA backbone | 6643 | 2191 |

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 $\leq 5\%$. 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 | 103 | |
| 2 | 1 | 110 | |
| 3 | 2 | 100 | |
| 4 | 3 | 104 | |
| 5 | 4 | 94 | |
| 6 | 5 | 38 | |
| 7 | 6 | 38 | |
| 8 | 7 | 41 | |

Continued on next page...

Continued from previous page...

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 9 | 9 | 165 | 5% 84% 10% |
| 10 | A | 76 | 51% 47% |
| 10 | B | 76 | 51% 47% |
| 11 | AA | 1342 | 98% |
| 12 | AB | 162 | 89% 8% |
| 13 | AC | 329 | 67% 33% |
| 13 | AD | 329 | 6% 66% 34% |
| 14 | AE | 1407 | 93% 5% |
| 15 | AF | 91 | 32% 90% 10% |
| 16 | C | 75 | 84% 12% |
| 17 | D | 1542 | 79% 20% |
| 18 | E | 87 | 99% |
| 19 | F | 71 | 99% |
| 20 | G | 241 | 90% 7% |
| 21 | H | 557 | 11% 45% 54% |
| 22 | I | 233 | 87% 11% |
| 23 | J | 206 | 98% |
| 24 | K | 167 | 91% 7% |
| 25 | L | 135 | 74% 23% |
| 26 | M | 179 | 83% 16% |
| 27 | N | 130 | 98% |
| 28 | O | 130 | 94% |
| 29 | P | 103 | 93% |
| 30 | Q | 129 | 88% 9% |
| 31 | R | 124 | 98% |

Continued on next page...

Continued from previous page...

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 32 | S | 101 | 98% |
| 33 | T | 89 | 98% |
| 34 | U | 82 | 98% |
| 35 | V | 84 | 94% 5% |
| 36 | W | 92 | 87% 10% |
| 37 | X | 118 | 95% |
| 38 | Y | 142 | 20% 98% |
| 39 | Z | 121 | 25% 75% |
| 40 | a | 2904 | 80% 19% |
| 41 | b | 85 | 89% 11% |
| 42 | c | 78 | 96% |
| 43 | d | 120 | 88% 12% |
| 44 | e | 63 | 95% |
| 45 | f | 59 | 97% |
| 46 | g | 70 | 93% 6% |
| 47 | h | 273 | 98% |
| 48 | i | 57 | 96% |
| 49 | j | 209 | 99% |
| 50 | k | 55 | 95% 5% |
| 51 | l | 201 | 99% |
| 52 | m | 46 | 100% |
| 53 | n | 179 | 97% |
| 54 | o | 65 | 94% 5% |
| 55 | p | 177 | 98% |
| 56 | q | 38 | 100% |

Continued on next page...

Continued from previous page...

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 57 | r | 149 | 9% 100% |
| 58 | s | 142 | 97% |
| 59 | t | 123 | 97% |
| 60 | u | 144 | 98% |
| 61 | v | 136 | 99% |
| 62 | w | 127 | 89% 5% 6% |
| 63 | x | 117 | 99% |
| 64 | y | 115 | 97% |
| 65 | z | 118 | 97% |

2 Entry composition [i](#)

There are 67 unique types of molecules in this entry. The entry contains 276039 atoms, of which 98639 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 Ribosomal protein L21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 1 | 0 | 103 | 1655 | 516 | 839 | 153 | 145 | 2 | 0 | 0 |

- Molecule 2 is a protein called 50S ribosomal protein L22.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 2 | 1 | 110 | 1779 | 532 | 922 | 166 | 156 | 3 | 0 | 0 |

- Molecule 3 is a protein called 50S ribosomal protein L23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 3 | 2 | 94 | 1557 | 470 | 811 | 140 | 134 | 2 | 0 | 0 |

- Molecule 4 is a protein called 50S ribosomal protein L24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|
| | | | Total | C | H | N | O | | |
| 4 | 3 | 103 | 1632 | 498 | 844 | 148 | 142 | 0 | 0 |

- Molecule 5 is a protein called 50S ribosomal protein L25.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 5 | 4 | 94 | 1533 | 479 | 780 | 137 | 134 | 3 | 0 | 0 |

- Molecule 6 is a DNA chain called NT DNA ops.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| | | | Total | C | N | O | P | | |
| 6 | 5 | 35 | 726 | 342 | 141 | 208 | 35 | 0 | 0 |

- Molecule 7 is a DNA chain called T DNA ops.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| | | | Total | C | N | O | P | | |
| 7 | 6 | 35 | 703 | 336 | 117 | 215 | 35 | 0 | 0 |

- Molecule 8 is a RNA chain called mRNA with 24 nt long spacer.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| | | | Total | C | N | O | P | | |
| 8 | 7 | 37 | 772 | 345 | 110 | 280 | 37 | 0 | 0 |

- Molecule 9 is a protein called 50S ribosomal protein L10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 9 | 9 | 148 | 1117 | 705 | 196 | 209 | 7 | 0 | 0 |

- Molecule 10 is a RNA chain called E-site and P-site fMet-tRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | P |
| 10 | A | 76 | 2446 | 723 | 826 | 295 | 527 | 75 | 0 | 0 |
| 10 | B | 76 | 2434 | 723 | 814 | 295 | 527 | 75 | 0 | 0 |

- Molecule 11 is a protein called DNA-directed RNA polymerase subunit beta.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| | | | Total | C | N | O | S | | |
| 11 | AA | 1316 | 10381 | 6514 | 1810 | 2014 | 43 | 0 | 0 |

- Molecule 12 is a protein called Transcription antitermination protein RfaH.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 12 | AB | 161 | 1286 | 828 | 222 | 232 | 4 | 0 | 0 |

- Molecule 13 is a protein called DNA-directed RNA polymerase subunit alpha.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 13 | AC | 221 | 1698 | 1060 | 299 | 333 | 6 | 0 | 0 |

Continued on next page...

Continued from previous page...

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 13 | AD | 218 | 1677 | 1048 | 297 | 326 | 6 | 0 | 0 |

- Molecule 14 is a protein called DNA-directed RNA polymerase subunit beta'.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| | | | Total | C | N | O | S | | |
| 14 | AE | 1337 | 10404 | 6535 | 1856 | 1963 | 50 | 0 | 0 |

- Molecule 15 is a protein called DNA-directed RNA polymerase subunit omega.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 15 | AF | 82 | 650 | 396 | 122 | 131 | 1 | 0 | 0 |

- Molecule 16 is a protein called 30S ribosomal protein S18.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---|---------|-------|
| | | | Total | C | H | N | O | S | | |
| 16 | C | 66 | 1103 | 344 | 559 | 102 | 97 | 1 | 0 | 0 |

- Molecule 17 is a RNA chain called 16S rRNA.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|------|-------|------|---------|-------|
| | | | Total | C | H | N | O | P | | |
| 17 | D | 1524 | 49126 | 14585 | 16423 | 6003 | 10591 | 1524 | 0 | 0 |

- Molecule 18 is a protein called 30S ribosomal protein S20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 18 | E | 86 | 1388 | 414 | 719 | 138 | 114 | 3 | 0 | 0 |

- Molecule 19 is a protein called 30S ribosomal protein S21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 19 | F | 70 | 1218 | 366 | 629 | 125 | 97 | 1 | 0 | 0 |

- Molecule 20 is a protein called 30S ribosomal protein S2.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| | | | Total | C | H | N | O | S | | |
| 20 | G | 225 | 3545 | 1113 | 1785 | 316 | 323 | 8 | 0 | 0 |

- Molecule 21 is a protein called 30S ribosomal protein S1.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| | | | Total | C | H | N | O | S | | |
| 21 | H | 259 | 3184 | 1073 | 1454 | 305 | 349 | 3 | 0 | 0 |

- Molecule 22 is a protein called 30S ribosomal protein S3.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| | | | Total | C | H | N | O | S | | |
| 22 | I | 208 | 3346 | 1036 | 1710 | 307 | 290 | 3 | 0 | 0 |

- Molecule 23 is a protein called 30S ribosomal protein S4.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| | | | Total | C | H | N | O | S | | |
| 23 | J | 205 | 3350 | 1026 | 1707 | 315 | 298 | 4 | 0 | 0 |

- Molecule 24 is a protein called 30S ribosomal protein S5.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| | | | Total | C | H | N | O | S | | |
| 24 | K | 156 | 2348 | 717 | 1196 | 217 | 212 | 6 | 0 | 0 |

- Molecule 25 is a protein called 30S ribosomal protein S6.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---|---------|-------|
| | | | Total | C | H | N | O | S | | |
| 25 | L | 104 | 1694 | 536 | 846 | 153 | 152 | 7 | 0 | 0 |

- Molecule 26 is a protein called 30S ribosomal protein S7.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| | | | Total | C | H | N | O | S | | |
| 26 | M | 151 | 2416 | 735 | 1235 | 227 | 215 | 4 | 0 | 0 |

- Molecule 27 is a protein called 30S ribosomal protein S8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| 27 | N | 129 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2010 | 616 | 1031 | 173 | 184 | 6 | | |

- Molecule 28 is a protein called 30S ribosomal protein S9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| 28 | O | 127 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2092 | 634 | 1070 | 206 | 179 | 3 | | |

- Molecule 29 is a protein called 30S ribosomal protein S10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| 29 | P | 99 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1621 | 495 | 831 | 151 | 143 | 1 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| 30 | Q | 117 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1764 | 540 | 887 | 174 | 160 | 3 | | |

- Molecule 31 is a protein called 30S ribosomal protein S12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| 31 | R | 121 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1940 | 580 | 1001 | 194 | 161 | 4 | | |

- Molecule 32 is a protein called 30S ribosomal protein S14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| 32 | S | 100 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1649 | 499 | 844 | 164 | 139 | 3 | | |

- Molecule 33 is a protein called 30S ribosomal protein S15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| 33 | T | 88 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1448 | 439 | 734 | 144 | 130 | 1 | | |

- Molecule 34 is a protein called 30S ribosomal protein S16.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| 34 | U | 82 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1315 | 406 | 666 | 128 | 114 | 1 | | |

- Molecule 35 is a protein called 30S ribosomal protein S17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| 35 | V | 80 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1339 | 411 | 691 | 121 | 113 | 3 | | |

- Molecule 36 is a protein called 30S ribosomal protein S19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| 36 | W | 83 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1351 | 424 | 688 | 126 | 111 | 2 | | |

- Molecule 37 is a protein called 30S ribosomal protein S13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| 37 | X | 116 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1864 | 558 | 964 | 181 | 158 | 3 | | |

- Molecule 38 is a protein called 50S ribosomal protein L11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 38 | Y | 141 | Total | C | N | O | S | 0 | 0 |
| | | | 1032 | 651 | 179 | 196 | 6 | | |

- Molecule 39 is a protein called 50S ribosomal protein L7/L12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 39 | Z | 30 | Total | C | N | O | S | 0 | 0 |
| | | | 227 | 144 | 33 | 47 | 3 | | |

- Molecule 40 is a RNA chain called 23S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-------|-------|-------|-------|---------|-------|---|
| 40 | a | 2880 | Total | C | H | N | O | P | 0 | 0 |
| | | | 92918 | 27587 | 31077 | 11398 | 19976 | 2880 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|--------------|
| a | 887 | A | U | conflict | GB 937521852 |

- Molecule 41 is a protein called 50S ribosomal protein L27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 41 | b | 76 | 1181 | 360 | 599 | 117 | 104 | 1 | 0 | 0 |

- Molecule 42 is a protein called 50S ribosomal protein L28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 42 | c | 77 | 1277 | 388 | 652 | 129 | 106 | 2 | 0 | 0 |

- Molecule 43 is a RNA chain called 5S rRNA.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|-----|---------|-------|
| | | | Total | C | H | N | O | P | | |
| 43 | d | 120 | 3870 | 1144 | 1301 | 468 | 837 | 120 | 0 | 0 |

- Molecule 44 is a protein called 50S ribosomal protein L29.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 44 | e | 62 | 1032 | 308 | 531 | 98 | 94 | 1 | 0 | 0 |

- Molecule 45 is a protein called 50S ribosomal protein L30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 45 | f | 58 | 936 | 281 | 488 | 87 | 78 | 2 | 0 | 0 |

- Molecule 46 is a protein called 50S ribosomal protein L31.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 46 | g | 66 | 1042 | 323 | 520 | 99 | 94 | 6 | 0 | 0 |

- Molecule 47 is a protein called 50S ribosomal protein L2.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| | | | Total | C | H | N | O | S | | |
| 47 | h | 271 | 4236 | 1288 | 2154 | 423 | 364 | 7 | 0 | 0 |

- Molecule 48 is a protein called 50S ribosomal protein L32.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|----|---|---------|-------|
| | | | Total | C | H | N | O | S | | |
| 48 | i | 56 | 903 | 269 | 459 | 94 | 80 | 1 | 0 | 0 |

- Molecule 49 is a protein called 50S ribosomal protein L3.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| | | | Total | C | H | N | O | S | | |
| 49 | j | 209 | 3182 | 979 | 1617 | 288 | 294 | 4 | 0 | 0 |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|
| | | | Total | C | H | N | O | | |
| 50 | k | 52 | 890 | 275 | 464 | 78 | 73 | 0 | 0 |

- Molecule 51 is a protein called 50S ribosomal protein L4.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| | | | Total | C | H | N | O | S | | |
| 51 | l | 201 | 3171 | 974 | 1619 | 283 | 290 | 5 | 0 | 0 |

- Molecule 52 is a protein called 50S ribosomal protein L34.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|----|---|---------|-------|
| | | | Total | C | H | N | O | S | | |
| 52 | m | 46 | 795 | 228 | 418 | 90 | 57 | 2 | 0 | 0 |

- Molecule 53 is a protein called 50S ribosomal protein L5.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| | | | Total | C | H | N | O | S | | |
| 53 | n | 177 | 2853 | 899 | 1443 | 249 | 256 | 6 | 0 | 0 |

- Molecule 54 is a protein called 50S ribosomal protein L35.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|---|
| 54 | o | 64 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1076 | 323 | 572 | 105 | 74 | 2 | | |

- Molecule 55 is a protein called 50S ribosomal protein L6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| 55 | p | 175 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2671 | 826 | 1358 | 241 | 244 | 2 | | |

- Molecule 56 is a protein called 50S ribosomal protein L36.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|---|
| 56 | q | 38 | Total | C | H | N | O | S | 0 | 0 |
| | | | 645 | 185 | 343 | 65 | 48 | 4 | | |

- Molecule 57 is a protein called 50S ribosomal protein L9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| 57 | r | 149 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2259 | 699 | 1148 | 197 | 214 | 1 | | |

- Molecule 58 is a protein called 50S ribosomal protein L13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| 58 | s | 142 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2291 | 714 | 1162 | 212 | 199 | 4 | | |

- Molecule 59 is a protein called 50S ribosomal protein L14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| 59 | t | 123 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1969 | 593 | 1023 | 181 | 166 | 6 | | |

- Molecule 60 is a protein called 50S ribosomal protein L15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| 60 | u | 144 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2182 | 654 | 1129 | 207 | 190 | 2 | | |

- Molecule 61 is a protein called 50S ribosomal protein L16.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| 61 | v | 136 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2231 | 686 | 1157 | 205 | 177 | 6 | | |

- Molecule 62 is a protein called 50S ribosomal protein L17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| 62 | w | 119 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1945 | 588 | 994 | 195 | 163 | 5 | | |

- Molecule 63 is a protein called 50S ribosomal protein L18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| 63 | x | 116 | Total | C | H | N | O | | 0 | 0 |
| | | | 1815 | 552 | 923 | 178 | 162 | | | |

- Molecule 64 is a protein called 50S ribosomal protein L19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| 64 | y | 114 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1879 | 574 | 962 | 179 | 163 | 1 | | |

- Molecule 65 is a protein called 50S ribosomal protein L20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| 65 | z | 117 | Total | C | H | N | O | | 0 | 0 |
| | | | 1967 | 604 | 1020 | 192 | 151 | | | |

- Molecule 66 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| 66 | AE | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |

- Molecule 67 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| 67 | AE | 2 | Total | Zn | 0 |
| | | | 2 | 2 | |

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: Ribosomal protein L21

Chain 0:  100%

There are no outlier residues recorded for this chain.

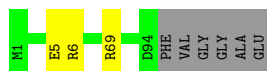
- Molecule 2: 50S ribosomal protein L22

Chain 1:  100%

There are no outlier residues recorded for this chain.

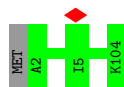
- Molecule 3: 50S ribosomal protein L23

Chain 2:  91% 6%



- Molecule 4: 50S ribosomal protein L24

Chain 3:  99%



- Molecule 5: 50S ribosomal protein L25

Chain 4:  98%



- Molecule 6: NT DNA ops

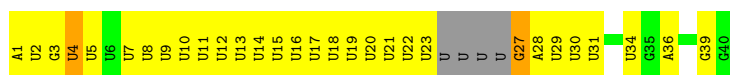
Chain 5:  5% 58% 34% 8%



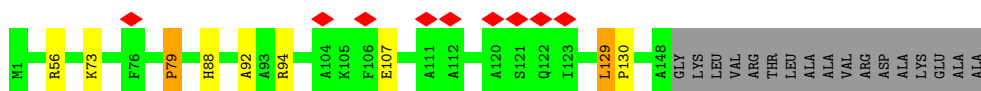
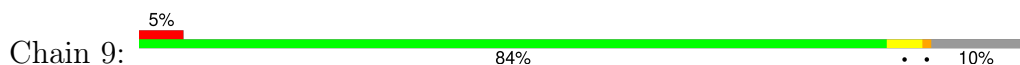
• Molecule 7: T DNA ops



• Molecule 8: mRNA with 24 nt long spacer



• Molecule 9: 50S ribosomal protein L10



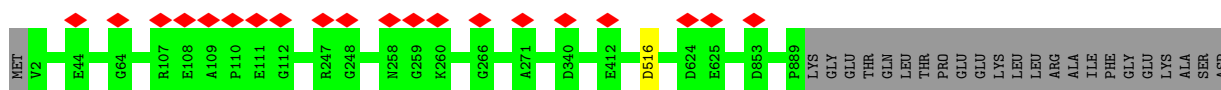
• Molecule 10: E-site and P-site fMet-tRNA

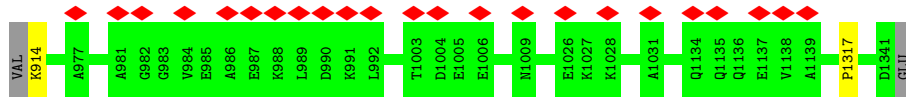


• Molecule 10: E-site and P-site fMet-tRNA

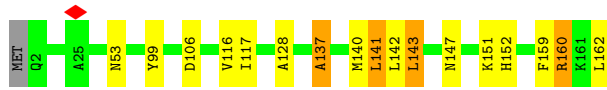


• Molecule 11: DNA-directed RNA polymerase subunit beta

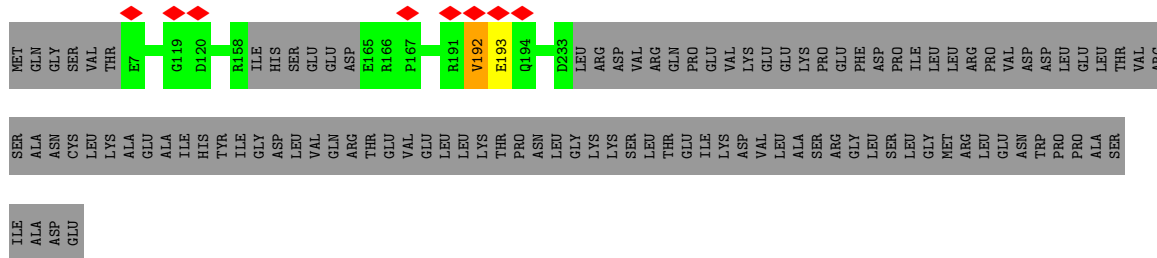




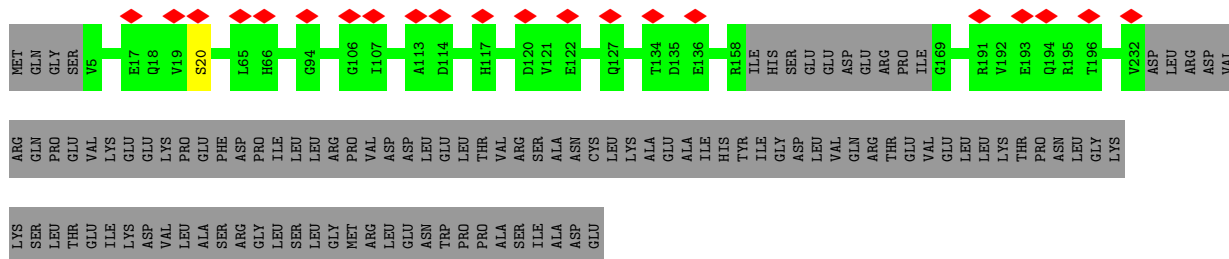
• Molecule 12: Transcription antitermination protein RfaH



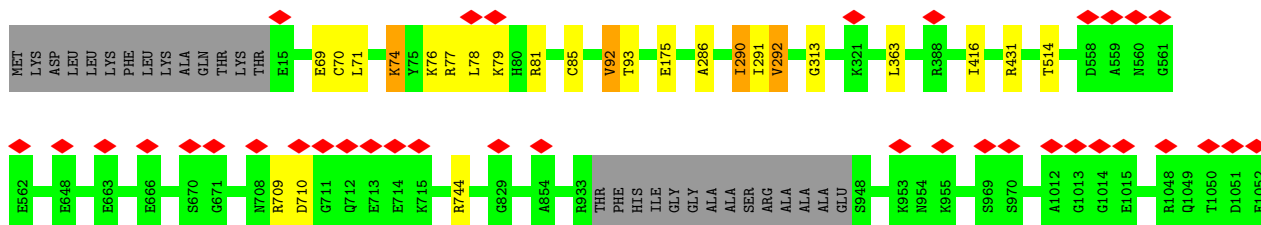
• Molecule 13: DNA-directed RNA polymerase subunit alpha

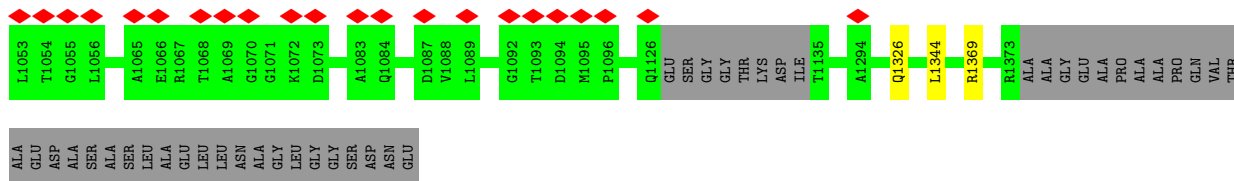


• Molecule 13: DNA-directed RNA polymerase subunit alpha

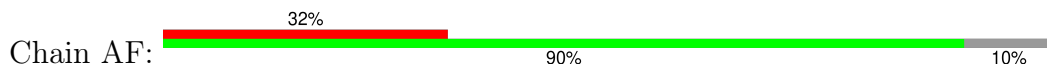


• Molecule 14: DNA-directed RNA polymerase subunit beta'

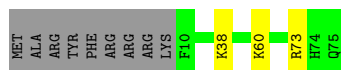
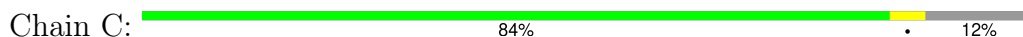




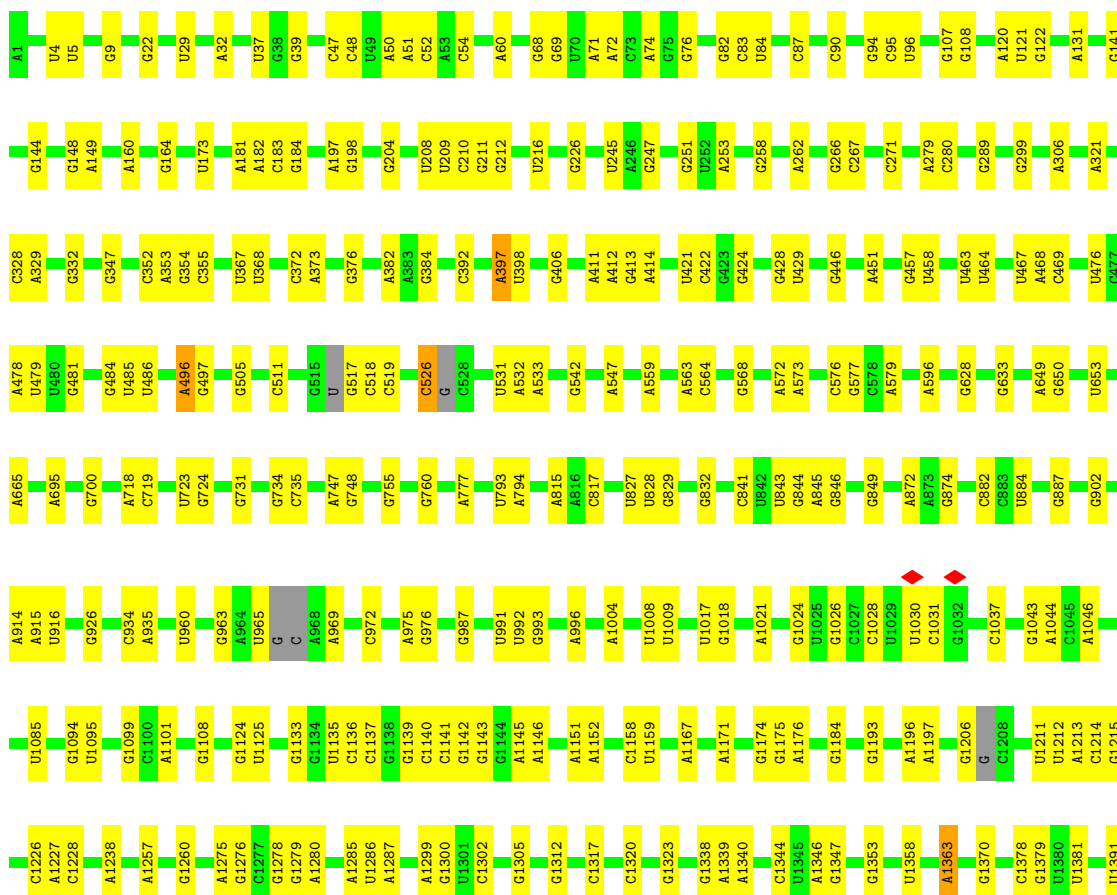
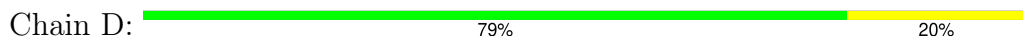
- Molecule 15: DNA-directed RNA polymerase subunit omega



- Molecule 16: 30S ribosomal protein S18




- Molecule 17: 16S rRNA



GLU
LYS
ASP
ALA
ILE
ALA
THR
VAL
ASN
LYS
GLN
GLU
ASP
ALA
ASN
PHE
SER
ASN
ASN
ALA
MET
ALA
GLU
GLU
ALA
PHE
LYS
LYS
GLY
GLU

- Molecule 22: 30S ribosomal protein S3

Chain I:  87% 11%

MET
G2
F29
R72
M134
E166
W167
Y168
G209
GLY
MET
ALA
ALA
VAL
GLU
GLN
PRO
GLU
GLU
LYS
PRO
ALA
ALA
GLN
PRO
LYS
LYS
GLN
GLN
ARG
LYS
GLY
ARG
LYS

- Molecule 23: 30S ribosomal protein S4

Chain J:  98%

MET
A2
R47
F72
F182
R206

- Molecule 24: 30S ribosomal protein S5

Chain K:  91% 7%


MET
ALA
HIS
ILE
GLU
LYS
GLN
ALA
GLY
E10
R45
M71
N77
N78
L165
GLY
LYS

- Molecule 25: 30S ribosomal protein S6

Chain L:  74% 23%

M1
W42
R45
V96
M102
K104
ALA
LYS
ASP
GLU
ARG
GLU
ARG
ARG
ARG
ASP
ASP
PHE
GLN
ALA
ASN
GLU
THR
ALA
ASP
ASP
ALA
GLU
ALA
GLY
GLY
ASP
SER
GLU
GLU
GLU
GLU
GLU

- Molecule 26: 30S ribosomal protein S7

Chain M:  83% 16%

MET
F2
R3
R4
L47
K56
A152
HIS
TYR
ARG
TRP
LEU
SER
LEU
ARG
SER
PHE
SER
SER
HIS
GLN
ALA
GLY
ALA
SER
SER
LYS
GLN
PRO
ALA
LEU
LEU
GLY
TYR
LEU
ASN

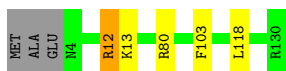
- Molecule 27: 30S ribosomal protein S8

Chain N:  98%

MET
S2
M27
A130

- Molecule 28: 30S ribosomal protein S9

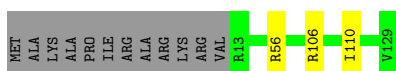
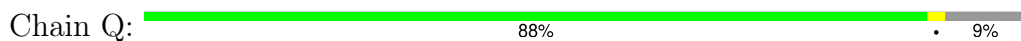
Chain O:  94%



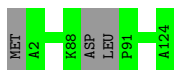
- Molecule 29: 30S ribosomal protein S10



- Molecule 30: 30S ribosomal protein S11



- Molecule 31: 30S ribosomal protein S12



- Molecule 32: 30S ribosomal protein S14



- Molecule 33: 30S ribosomal protein S15

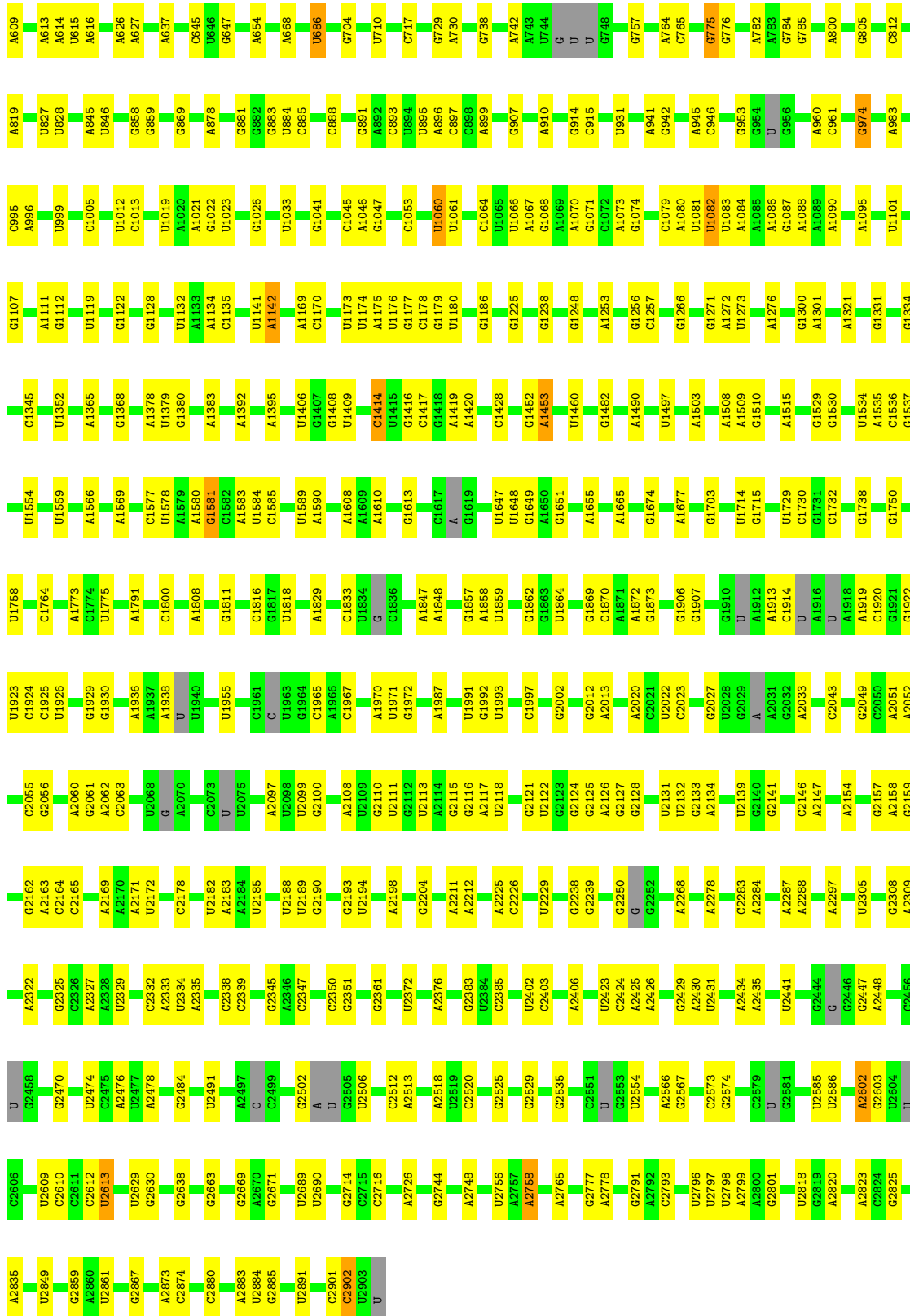


- Molecule 34: 30S ribosomal protein S16

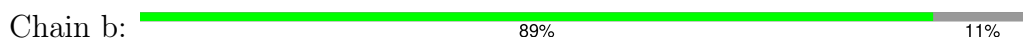


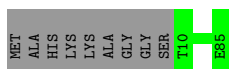
- Molecule 35: 30S ribosomal protein S17





• Molecule 41: 50S ribosomal protein L27





- Molecule 42: 50S ribosomal protein L28

Chain c: 96%



- Molecule 43: 5S rRNA

Chain d: 88% 12%



- Molecule 44: 50S ribosomal protein L29

Chain e: 95%



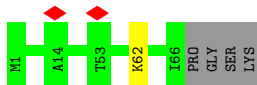
- Molecule 45: 50S ribosomal protein L30

Chain f: 97%



- Molecule 46: 50S ribosomal protein L31

Chain g: 93% 6%



- Molecule 47: 50S ribosomal protein L2

Chain h: 98%



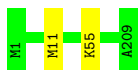
- Molecule 48: 50S ribosomal protein L32

Chain i: 96%



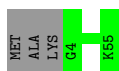
- Molecule 49: 50S ribosomal protein L3

Chain j: 99%



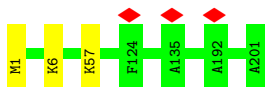
- Molecule 50: 50S ribosomal protein L33

Chain k: 95% 5%



- Molecule 51: 50S ribosomal protein L4

Chain l: 99%



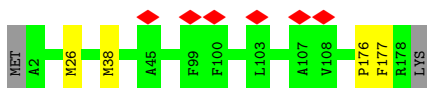
- Molecule 52: 50S ribosomal protein L34

Chain m: 100%

There are no outlier residues recorded for this chain.

- Molecule 53: 50S ribosomal protein L5

Chain n: 97%



- Molecule 54: 50S ribosomal protein L35

Chain o: 94% 5%



- Molecule 55: 50S ribosomal protein L6

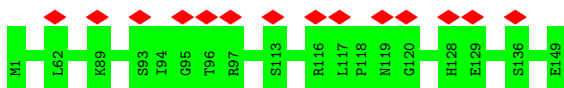
Chain p: 98%



- Molecule 56: 50S ribosomal protein L36



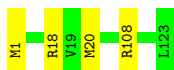
- Molecule 57: 50S ribosomal protein L9



- Molecule 58: 50S ribosomal protein L13



- Molecule 59: 50S ribosomal protein L14



- Molecule 60: 50S ribosomal protein L15



- Molecule 61: 50S ribosomal protein L16

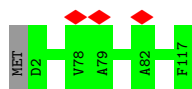


- Molecule 62: 50S ribosomal protein L17

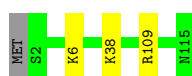




- Molecule 63: 50S ribosomal protein L18



- Molecule 64: 50S ribosomal protein L19



- Molecule 65: 50S ribosomal protein L20



4 Experimental information i

| Property | Value | Source |
|--------------------------------------|---|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 49622 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI TALOS ARCTICA | Depositor |
| Voltage (kV) | 200 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 28 | Depositor |
| Minimum defocus (nm) | 1250 | Depositor |
| Maximum defocus (nm) | 2500 | Depositor |
| Magnification | Not provided | |
| Image detector | GATAN K2 SUMMIT (4k x 4k) | Depositor |
| Maximum map value | 0.034 | Depositor |
| Minimum map value | -0.007 | Depositor |
| Average map value | 0.000 | Depositor |
| Map value standard deviation | 0.002 | Depositor |
| Recommended contour level | 0.0037 | Depositor |
| Map size (Å) | 531.968, 531.968, 531.968 | wwPDB |
| Map dimensions | 512, 512, 512 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.039, 1.039, 1.039 | Depositor |

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

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 | 0.47 | 0/829 | 0.60 | 0/1107 |
| 2 | 1 | 0.58 | 0/864 | 0.69 | 0/1156 |
| 3 | 2 | 0.67 | 1/752 (0.1%) | 0.72 | 1/1005 (0.1%) |
| 4 | 3 | 0.41 | 0/796 | 0.55 | 0/1062 |
| 5 | 4 | 0.65 | 2/766 (0.3%) | 0.69 | 0/1025 |
| 6 | 5 | 1.14 | 11/816 (1.3%) | 1.12 | 2/1259 (0.2%) |
| 7 | 6 | 1.11 | 8/783 (1.0%) | 1.10 | 0/1203 |
| 8 | 7 | 0.53 | 2/856 (0.2%) | 0.89 | 4/1326 (0.3%) |
| 9 | 9 | 0.36 | 0/1131 | 0.66 | 2/1524 (0.1%) |
| 10 | A | 0.55 | 1/1810 (0.1%) | 1.26 | 12/2821 (0.4%) |
| 10 | B | 0.55 | 1/1810 (0.1%) | 1.26 | 11/2821 (0.4%) |
| 11 | AA | 0.42 | 0/10547 | 0.61 | 1/14232 (0.0%) |
| 12 | AB | 0.42 | 0/1317 | 0.85 | 5/1786 (0.3%) |
| 13 | AC | 0.41 | 0/1718 | 0.62 | 0/2328 |
| 13 | AD | 0.36 | 0/1696 | 0.62 | 0/2298 |
| 14 | AE | 0.42 | 0/10561 | 0.63 | 3/14258 (0.0%) |
| 15 | AF | 0.33 | 0/652 | 0.57 | 0/879 |
| 16 | C | 0.70 | 0/553 | 0.92 | 4/743 (0.5%) |
| 17 | D | 0.59 | 14/36610 (0.0%) | 1.03 | 67/57091 (0.1%) |
| 18 | E | 0.57 | 0/675 | 0.71 | 0/895 |
| 19 | F | 0.62 | 0/597 | 0.59 | 0/792 |
| 20 | G | 0.66 | 2/1791 (0.1%) | 0.83 | 7/2413 (0.3%) |
| 21 | H | 0.43 | 0/1746 | 0.70 | 0/2382 |
| 22 | I | 0.62 | 2/1663 (0.1%) | 0.70 | 4/2241 (0.2%) |
| 23 | J | 0.54 | 2/1665 (0.1%) | 0.59 | 0/2227 |
| 24 | K | 0.69 | 1/1165 (0.1%) | 0.86 | 4/1568 (0.3%) |
| 25 | L | 0.79 | 3/867 (0.3%) | 0.82 | 3/1171 (0.3%) |
| 26 | M | 0.54 | 0/1195 | 0.70 | 2/1602 (0.1%) |
| 27 | N | 0.52 | 0/989 | 0.63 | 1/1326 (0.1%) |
| 28 | O | 0.67 | 4/1034 (0.4%) | 0.82 | 4/1375 (0.3%) |
| 29 | P | 0.52 | 0/800 | 0.70 | 2/1082 (0.2%) |
| 30 | Q | 0.71 | 1/893 (0.1%) | 0.82 | 4/1205 (0.3%) |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|------------------|-------------|-------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 31 | R | 0.56 | 0/952 | 0.65 | 0/1274 |
| 32 | S | 0.63 | 1/817 (0.1%) | 0.64 | 0/1088 |
| 33 | T | 0.56 | 0/722 | 0.72 | 1/964 (0.1%) |
| 34 | U | 0.45 | 0/659 | 0.65 | 1/884 (0.1%) |
| 35 | V | 0.56 | 0/657 | 0.70 | 0/881 |
| 36 | W | 0.56 | 1/680 (0.1%) | 0.69 | 3/915 (0.3%) |
| 37 | X | 0.48 | 0/909 | 0.72 | 1/1215 (0.1%) |
| 38 | Y | 0.42 | 1/1046 (0.1%) | 0.57 | 2/1410 (0.1%) |
| 39 | Z | 0.23 | 0/227 | 0.37 | 0/304 |
| 40 | a | 0.61 | 14/69247 (0.0%) | 1.03 | 130/107985 (0.1%) |
| 41 | b | 0.47 | 0/589 | 0.57 | 0/779 |
| 42 | c | 0.56 | 1/635 (0.2%) | 0.66 | 1/848 (0.1%) |
| 43 | d | 0.50 | 0/2872 | 0.95 | 0/4478 |
| 44 | e | 0.81 | 2/502 (0.4%) | 0.66 | 0/667 |
| 45 | f | 0.53 | 0/452 | 0.72 | 2/605 (0.3%) |
| 46 | g | 0.50 | 1/531 (0.2%) | 0.67 | 1/709 (0.1%) |
| 47 | h | 0.53 | 2/2121 (0.1%) | 0.67 | 6/2852 (0.2%) |
| 48 | i | 0.42 | 0/450 | 0.65 | 1/599 (0.2%) |
| 49 | j | 0.53 | 0/1586 | 0.64 | 2/2134 (0.1%) |
| 50 | k | 0.51 | 0/433 | 0.68 | 0/576 |
| 51 | l | 0.54 | 1/1571 (0.1%) | 0.64 | 1/2113 (0.0%) |
| 52 | m | 0.43 | 0/380 | 0.60 | 0/498 |
| 53 | n | 0.51 | 0/1434 | 0.68 | 2/1926 (0.1%) |
| 54 | o | 0.51 | 0/513 | 0.85 | 1/676 (0.1%) |
| 55 | p | 0.50 | 0/1333 | 0.68 | 3/1805 (0.2%) |
| 56 | q | 0.46 | 0/303 | 0.61 | 0/397 |
| 57 | r | 0.34 | 0/1122 | 0.52 | 0/1515 |
| 58 | s | 0.83 | 5/1152 (0.4%) | 0.81 | 4/1551 (0.3%) |
| 59 | t | 0.55 | 1/955 (0.1%) | 0.89 | 5/1279 (0.4%) |
| 60 | u | 0.47 | 1/1062 (0.1%) | 0.63 | 0/1413 |
| 61 | v | 0.61 | 1/1093 (0.1%) | 0.75 | 1/1460 (0.1%) |
| 62 | w | 0.90 | 5/964 (0.5%) | 0.95 | 9/1289 (0.7%) |
| 63 | x | 0.41 | 0/902 | 0.57 | 0/1209 |
| 64 | y | 0.46 | 0/929 | 0.59 | 1/1242 (0.1%) |
| 65 | z | 0.63 | 1/960 (0.1%) | 0.60 | 0/1278 |
| All | All | 0.58 | 93/190707 (0.0%) | 0.92 | 321/281021 (0.1%) |

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 |
|-----|-------|---------------------|---------------------|
| 9 | 9 | 0 | 3 |
| 12 | AB | 0 | 10 |
| 13 | AC | 0 | 1 |
| 13 | AD | 0 | 1 |
| 14 | AE | 0 | 4 |
| 20 | G | 0 | 1 |
| 21 | H | 0 | 5 |
| 22 | I | 0 | 1 |
| 24 | K | 0 | 2 |
| 28 | O | 0 | 1 |
| 37 | X | 0 | 1 |
| 38 | Y | 0 | 1 |
| 53 | n | 0 | 1 |
| 54 | o | 0 | 1 |
| 58 | s | 0 | 1 |
| 60 | u | 0 | 2 |
| All | All | 0 | 36 |

The worst 5 of 93 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|--------|--------|-------------|----------|
| 62 | w | 35 | LYS | CE-NZ | -15.20 | 1.11 | 1.49 |
| 25 | L | 42 | TRP | CB-CG | -12.37 | 1.27 | 1.50 |
| 3 | 2 | 5 | GLU | CG-CD | -11.55 | 1.34 | 1.51 |
| 44 | e | 46 | VAL | CB-CG1 | -11.28 | 1.29 | 1.52 |
| 62 | w | 42 | LYS | CD-CE | -10.80 | 1.24 | 1.51 |

The worst 5 of 321 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|----------|-------|-------------|----------|
| 40 | a | 1019 | U | C5-C4-O4 | 30.70 | 144.32 | 125.90 |
| 40 | a | 1141 | U | C5-C4-O4 | 29.59 | 143.65 | 125.90 |
| 17 | D | 37 | U | C5-C4-O4 | 29.43 | 143.56 | 125.90 |
| 17 | D | 1358 | U | C5-C4-O4 | 29.22 | 143.43 | 125.90 |
| 17 | D | 827 | U | C5-C4-O4 | 28.61 | 143.07 | 125.90 |

There are no chirality outliers.

5 of 36 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 9 | 9 | 107 | GLU | Peptide |
| 9 | 9 | 79 | PRO | Peptide |

Continued on next page...

Continued from previous page...

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 9 | 9 | 92 | ALA | Peptide |
| 12 | AB | 106 | ASP | Peptide |
| 12 | AB | 116 | VAL | 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 | 101/103 (98%) | 97 (96%) | 4 (4%) | 0 | 100 | 100 |
| 2 | 1 | 108/110 (98%) | 107 (99%) | 1 (1%) | 0 | 100 | 100 |
| 3 | 2 | 92/100 (92%) | 87 (95%) | 5 (5%) | 0 | 100 | 100 |
| 4 | 3 | 101/104 (97%) | 98 (97%) | 3 (3%) | 0 | 100 | 100 |
| 5 | 4 | 92/94 (98%) | 89 (97%) | 3 (3%) | 0 | 100 | 100 |
| 9 | 9 | 146/165 (88%) | 101 (69%) | 42 (29%) | 3 (2%) | 5 | 32 |
| 11 | AA | 1312/1342 (98%) | 1198 (91%) | 113 (9%) | 1 (0%) | 48 | 79 |
| 12 | AB | 159/162 (98%) | 111 (70%) | 43 (27%) | 5 (3%) | 3 | 25 |
| 13 | AC | 217/329 (66%) | 203 (94%) | 12 (6%) | 2 (1%) | 14 | 45 |
| 13 | AD | 214/329 (65%) | 198 (92%) | 16 (8%) | 0 | 100 | 100 |
| 14 | AE | 1331/1407 (95%) | 1213 (91%) | 112 (8%) | 6 (0%) | 25 | 58 |
| 15 | AF | 80/91 (88%) | 77 (96%) | 3 (4%) | 0 | 100 | 100 |
| 16 | C | 64/75 (85%) | 63 (98%) | 1 (2%) | 0 | 100 | 100 |
| 18 | E | 84/87 (97%) | 83 (99%) | 1 (1%) | 0 | 100 | 100 |
| 19 | F | 68/71 (96%) | 68 (100%) | 0 | 0 | 100 | 100 |
| 20 | G | 223/241 (92%) | 212 (95%) | 10 (4%) | 1 (0%) | 30 | 63 |

Continued on next page...

Continued from previous page...

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 21 | H | 255/557 (46%) | 182 (71%) | 66 (26%) | 7 (3%) | 4 | 27 |
| 22 | I | 206/233 (88%) | 193 (94%) | 13 (6%) | 0 | 100 | 100 |
| 23 | J | 203/206 (98%) | 201 (99%) | 2 (1%) | 0 | 100 | 100 |
| 24 | K | 154/167 (92%) | 145 (94%) | 8 (5%) | 1 (1%) | 22 | 55 |
| 25 | L | 102/135 (76%) | 97 (95%) | 4 (4%) | 1 (1%) | 13 | 44 |
| 26 | M | 149/179 (83%) | 140 (94%) | 8 (5%) | 1 (1%) | 19 | 52 |
| 27 | N | 127/130 (98%) | 123 (97%) | 4 (3%) | 0 | 100 | 100 |
| 28 | O | 125/130 (96%) | 116 (93%) | 8 (6%) | 1 (1%) | 16 | 49 |
| 29 | P | 97/103 (94%) | 89 (92%) | 8 (8%) | 0 | 100 | 100 |
| 30 | Q | 115/129 (89%) | 107 (93%) | 8 (7%) | 0 | 100 | 100 |
| 31 | R | 117/124 (94%) | 112 (96%) | 5 (4%) | 0 | 100 | 100 |
| 32 | S | 98/101 (97%) | 97 (99%) | 1 (1%) | 0 | 100 | 100 |
| 33 | T | 86/89 (97%) | 83 (96%) | 3 (4%) | 0 | 100 | 100 |
| 34 | U | 80/82 (98%) | 76 (95%) | 4 (5%) | 0 | 100 | 100 |
| 35 | V | 78/84 (93%) | 74 (95%) | 4 (5%) | 0 | 100 | 100 |
| 36 | W | 81/92 (88%) | 80 (99%) | 1 (1%) | 0 | 100 | 100 |
| 37 | X | 114/118 (97%) | 103 (90%) | 9 (8%) | 2 (2%) | 7 | 34 |
| 38 | Y | 139/142 (98%) | 101 (73%) | 38 (27%) | 0 | 100 | 100 |
| 39 | Z | 28/121 (23%) | 22 (79%) | 6 (21%) | 0 | 100 | 100 |
| 41 | b | 74/85 (87%) | 73 (99%) | 1 (1%) | 0 | 100 | 100 |
| 42 | c | 75/78 (96%) | 72 (96%) | 3 (4%) | 0 | 100 | 100 |
| 44 | e | 60/63 (95%) | 57 (95%) | 3 (5%) | 0 | 100 | 100 |
| 45 | f | 56/59 (95%) | 52 (93%) | 4 (7%) | 0 | 100 | 100 |
| 46 | g | 64/70 (91%) | 62 (97%) | 2 (3%) | 0 | 100 | 100 |
| 47 | h | 269/273 (98%) | 255 (95%) | 14 (5%) | 0 | 100 | 100 |
| 48 | i | 54/57 (95%) | 49 (91%) | 5 (9%) | 0 | 100 | 100 |
| 49 | j | 207/209 (99%) | 198 (96%) | 9 (4%) | 0 | 100 | 100 |
| 50 | k | 50/55 (91%) | 50 (100%) | 0 | 0 | 100 | 100 |
| 51 | l | 199/201 (99%) | 188 (94%) | 11 (6%) | 0 | 100 | 100 |
| 52 | m | 44/46 (96%) | 43 (98%) | 1 (2%) | 0 | 100 | 100 |
| 53 | n | 175/179 (98%) | 161 (92%) | 13 (7%) | 1 (1%) | 22 | 55 |

Continued on next page...

Continued from previous page...

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|------------------|------------|----------|----------|-------------|-----|
| 54 | o | 62/65 (95%) | 57 (92%) | 4 (6%) | 1 (2%) | 8 | 36 |
| 55 | p | 173/177 (98%) | 162 (94%) | 11 (6%) | 0 | 100 | 100 |
| 56 | q | 36/38 (95%) | 35 (97%) | 1 (3%) | 0 | 100 | 100 |
| 57 | r | 147/149 (99%) | 139 (95%) | 8 (5%) | 0 | 100 | 100 |
| 58 | s | 140/142 (99%) | 133 (95%) | 7 (5%) | 0 | 100 | 100 |
| 59 | t | 121/123 (98%) | 114 (94%) | 7 (6%) | 0 | 100 | 100 |
| 60 | u | 142/144 (99%) | 134 (94%) | 8 (6%) | 0 | 100 | 100 |
| 61 | v | 134/136 (98%) | 129 (96%) | 5 (4%) | 0 | 100 | 100 |
| 62 | w | 117/127 (92%) | 112 (96%) | 5 (4%) | 0 | 100 | 100 |
| 63 | x | 114/117 (97%) | 107 (94%) | 7 (6%) | 0 | 100 | 100 |
| 64 | y | 112/115 (97%) | 105 (94%) | 7 (6%) | 0 | 100 | 100 |
| 65 | z | 115/118 (98%) | 111 (96%) | 4 (4%) | 0 | 100 | 100 |
| All | All | 9486/10558 (90%) | 8744 (92%) | 709 (8%) | 33 (0%) | 38 | 69 |

5 of 33 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 12 | AB | 141 | LEU |
| 12 | AB | 152 | HIS |
| 20 | G | 127 | ASP |
| 21 | H | 304 | VAL |
| 26 | M | 56 | LYS |

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 | 84/84 (100%) | 84 (100%) | 0 | 100 | 100 |
| 2 | 1 | 93/93 (100%) | 93 (100%) | 0 | 100 | 100 |
| 3 | 2 | 81/84 (96%) | 80 (99%) | 1 (1%) | 67 | 77 |
| 4 | 3 | 84/85 (99%) | 84 (100%) | 0 | 100 | 100 |

Continued on next page...

Continued from previous page...

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-----------------|-------------|----------|-------------|-----|
| 5 | 4 | 78/78 (100%) | 78 (100%) | 0 | 100 | 100 |
| 9 | 9 | 112/123 (91%) | 109 (97%) | 3 (3%) | 40 | 60 |
| 11 | AA | 1135/1157 (98%) | 1134 (100%) | 1 (0%) | 92 | 95 |
| 12 | AB | 141/142 (99%) | 140 (99%) | 1 (1%) | 81 | 86 |
| 13 | AC | 186/286 (65%) | 186 (100%) | 0 | 100 | 100 |
| 13 | AD | 185/286 (65%) | 185 (100%) | 0 | 100 | 100 |
| 14 | AE | 1122/1168 (96%) | 1103 (98%) | 19 (2%) | 56 | 72 |
| 15 | AF | 70/75 (93%) | 70 (100%) | 0 | 100 | 100 |
| 16 | C | 57/65 (88%) | 57 (100%) | 0 | 100 | 100 |
| 18 | E | 65/66 (98%) | 65 (100%) | 0 | 100 | 100 |
| 19 | F | 60/61 (98%) | 60 (100%) | 0 | 100 | 100 |
| 20 | G | 187/199 (94%) | 186 (100%) | 1 (0%) | 86 | 90 |
| 21 | H | 137/461 (30%) | 137 (100%) | 0 | 100 | 100 |
| 22 | I | 171/190 (90%) | 170 (99%) | 1 (1%) | 84 | 88 |
| 23 | J | 172/173 (99%) | 171 (99%) | 1 (1%) | 84 | 88 |
| 24 | K | 119/126 (94%) | 119 (100%) | 0 | 100 | 100 |
| 25 | L | 91/116 (78%) | 91 (100%) | 0 | 100 | 100 |
| 26 | M | 124/147 (84%) | 124 (100%) | 0 | 100 | 100 |
| 27 | N | 104/105 (99%) | 104 (100%) | 0 | 100 | 100 |
| 28 | O | 105/107 (98%) | 104 (99%) | 1 (1%) | 73 | 80 |
| 29 | P | 86/90 (96%) | 85 (99%) | 1 (1%) | 67 | 77 |
| 30 | Q | 90/99 (91%) | 90 (100%) | 0 | 100 | 100 |
| 31 | R | 101/104 (97%) | 101 (100%) | 0 | 100 | 100 |
| 32 | S | 83/84 (99%) | 83 (100%) | 0 | 100 | 100 |
| 33 | T | 76/77 (99%) | 76 (100%) | 0 | 100 | 100 |
| 34 | U | 65/65 (100%) | 64 (98%) | 1 (2%) | 60 | 74 |
| 35 | V | 74/78 (95%) | 73 (99%) | 1 (1%) | 62 | 75 |
| 36 | W | 72/79 (91%) | 72 (100%) | 0 | 100 | 100 |
| 37 | X | 94/96 (98%) | 94 (100%) | 0 | 100 | 100 |
| 38 | Y | 109/110 (99%) | 108 (99%) | 1 (1%) | 75 | 82 |
| 39 | Z | 26/85 (31%) | 26 (100%) | 0 | 100 | 100 |

Continued on next page...

Continued from previous page...

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-----------------|-------------|----------|-------------|-----|
| 41 | b | 58/63 (92%) | 58 (100%) | 0 | 100 | 100 |
| 42 | c | 67/68 (98%) | 67 (100%) | 0 | 100 | 100 |
| 44 | e | 54/55 (98%) | 54 (100%) | 0 | 100 | 100 |
| 45 | f | 48/49 (98%) | 48 (100%) | 0 | 100 | 100 |
| 46 | g | 59/62 (95%) | 59 (100%) | 0 | 100 | 100 |
| 47 | h | 216/218 (99%) | 216 (100%) | 0 | 100 | 100 |
| 48 | i | 47/48 (98%) | 47 (100%) | 0 | 100 | 100 |
| 49 | j | 164/164 (100%) | 164 (100%) | 0 | 100 | 100 |
| 50 | k | 47/49 (96%) | 47 (100%) | 0 | 100 | 100 |
| 51 | l | 165/165 (100%) | 164 (99%) | 1 (1%) | 84 | 88 |
| 52 | m | 38/38 (100%) | 38 (100%) | 0 | 100 | 100 |
| 53 | n | 148/150 (99%) | 148 (100%) | 0 | 100 | 100 |
| 54 | o | 51/52 (98%) | 51 (100%) | 0 | 100 | 100 |
| 55 | p | 136/138 (99%) | 136 (100%) | 0 | 100 | 100 |
| 56 | q | 34/34 (100%) | 34 (100%) | 0 | 100 | 100 |
| 57 | r | 114/114 (100%) | 114 (100%) | 0 | 100 | 100 |
| 58 | s | 116/116 (100%) | 115 (99%) | 1 (1%) | 75 | 82 |
| 59 | t | 104/104 (100%) | 103 (99%) | 1 (1%) | 73 | 80 |
| 60 | u | 103/103 (100%) | 103 (100%) | 0 | 100 | 100 |
| 61 | v | 109/109 (100%) | 109 (100%) | 0 | 100 | 100 |
| 62 | w | 99/103 (96%) | 98 (99%) | 1 (1%) | 73 | 80 |
| 63 | x | 86/87 (99%) | 86 (100%) | 0 | 100 | 100 |
| 64 | y | 99/100 (99%) | 97 (98%) | 2 (2%) | 50 | 68 |
| 65 | z | 89/90 (99%) | 88 (99%) | 1 (1%) | 70 | 79 |
| All | All | 7890/8723 (90%) | 7850 (100%) | 40 (0%) | 85 | 90 |

5 of 40 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 28 | O | 12 | ARG |
| 59 | t | 108 | ARG |
| 29 | P | 5 | ARG |
| 38 | Y | 44 | LYS |
| 64 | y | 6 | LYS |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 52 | m | 29 | GLN |
| 54 | o | 24 | HIS |
| 63 | x | 19 | GLN |
| 14 | AE | 805 | GLN |
| 14 | AE | 777 | HIS |

5.3.3 RNA [i](#)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 10 | A | 75/76 (98%) | 29 (38%) | 8 (10%) |
| 10 | B | 75/76 (98%) | 29 (38%) | 8 (10%) |
| 17 | D | 1514/1542 (98%) | 290 (19%) | 20 (1%) |
| 40 | a | 2859/2904 (98%) | 507 (17%) | 0 |
| 43 | d | 119/120 (99%) | 15 (12%) | 0 |
| 8 | 7 | 36/41 (87%) | 26 (72%) | 5 (13%) |
| All | All | 4678/4759 (98%) | 896 (19%) | 41 (0%) |

5 of 896 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 8 | 7 | 3 | G |
| 8 | 7 | 4 | U |
| 8 | 7 | 5 | U |
| 8 | 7 | 7 | U |
| 8 | 7 | 8 | U |

5 of 41 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 17 | D | 517 | G |
| 17 | D | 1213 | A |
| 17 | D | 991 | U |
| 17 | D | 1196 | A |
| 17 | D | 1447 | 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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

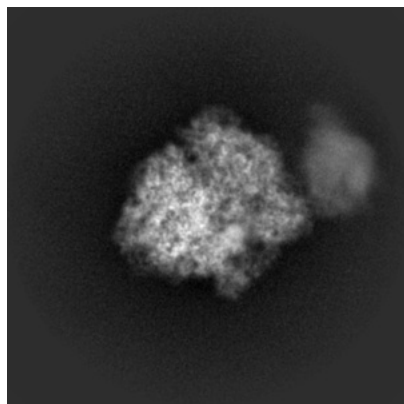
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42477. These allow visual inspection of the internal detail of the map and identification of artifacts.

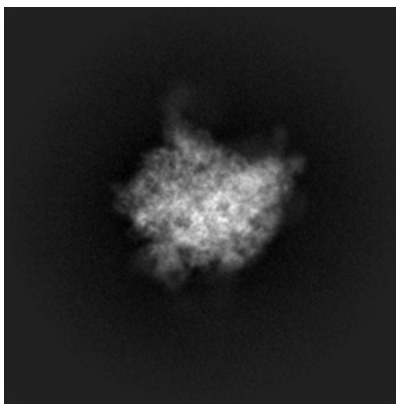
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

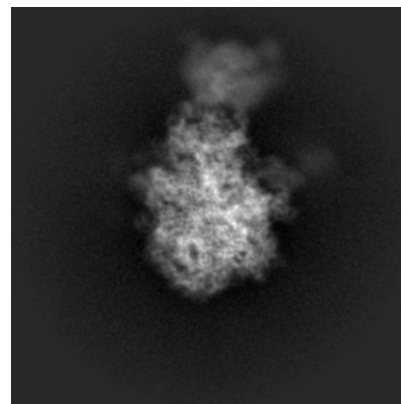
6.1.1 Primary map



X

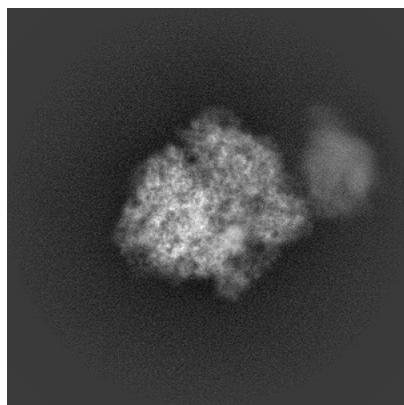


Y

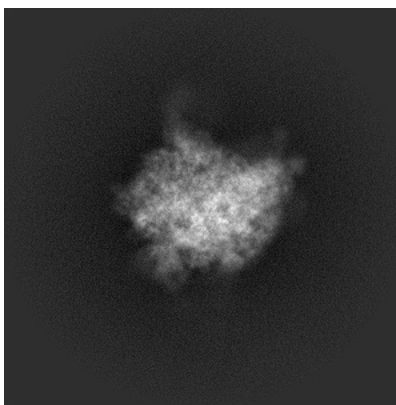


Z

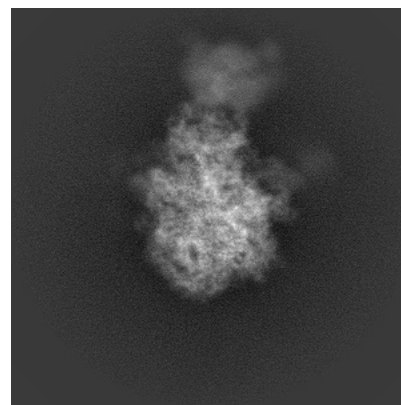
6.1.2 Raw map



X



Y

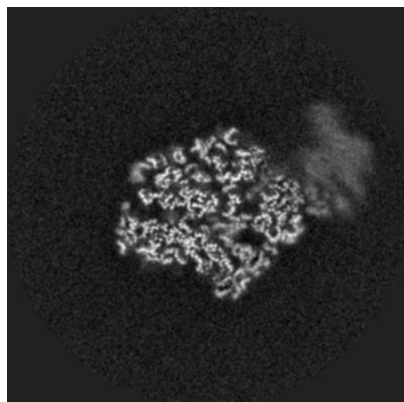


Z

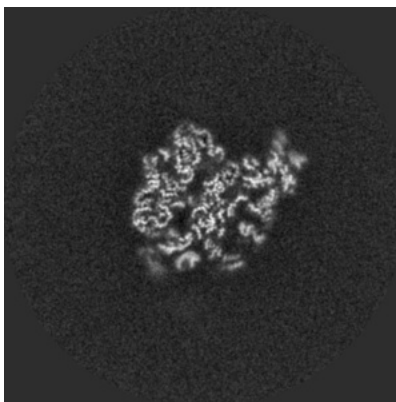
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

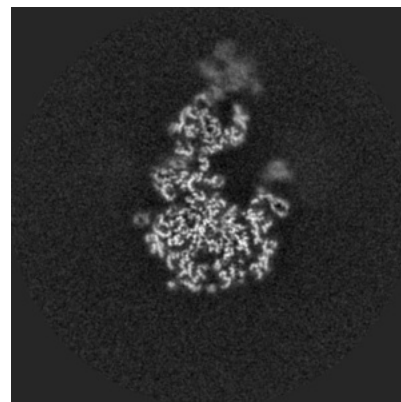
6.2.1 Primary map



X Index: 256

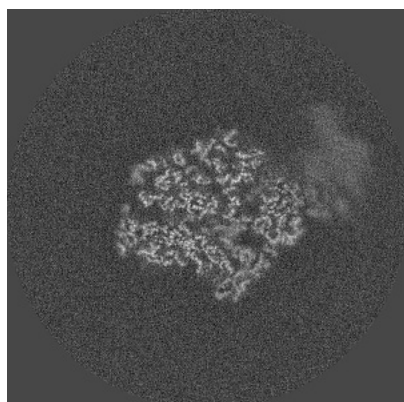


Y Index: 256

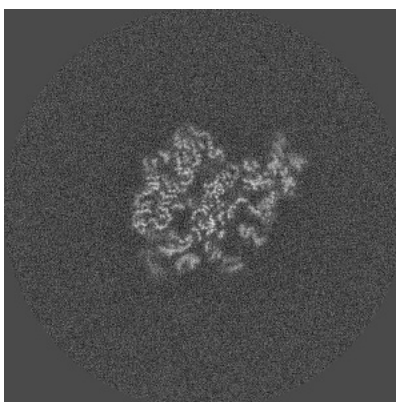


Z Index: 256

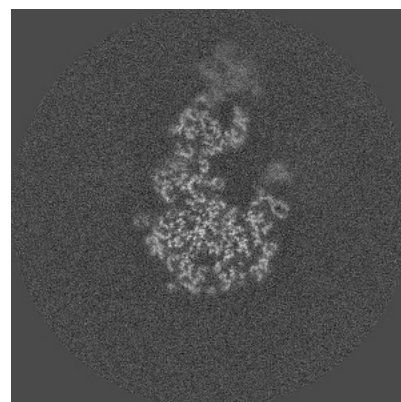
6.2.2 Raw map



X Index: 256



Y Index: 256

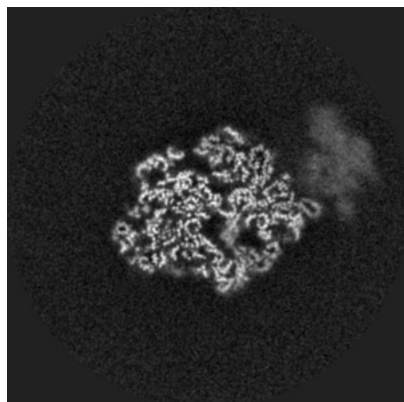


Z Index: 256

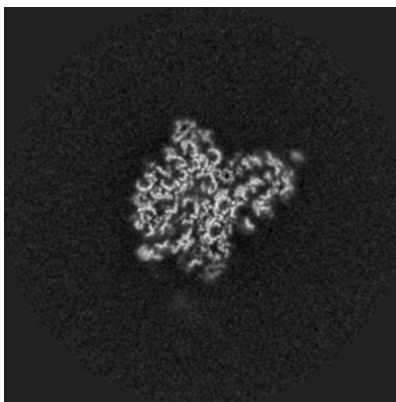
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

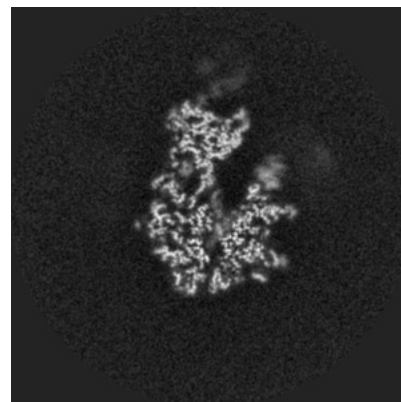
6.3.1 Primary map



X Index: 248

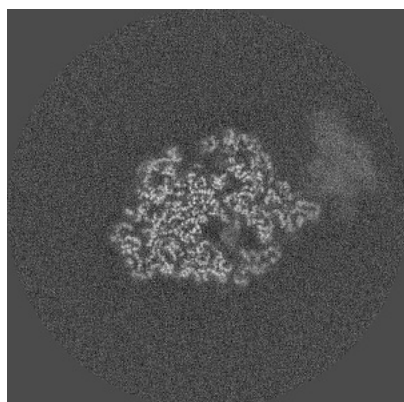


Y Index: 248

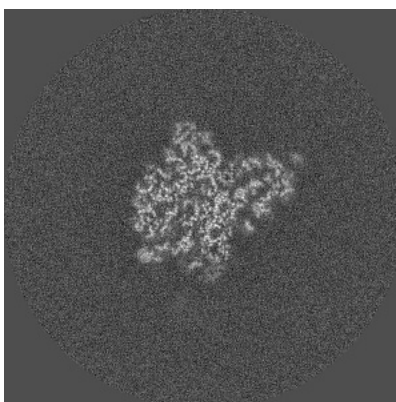


Z Index: 242

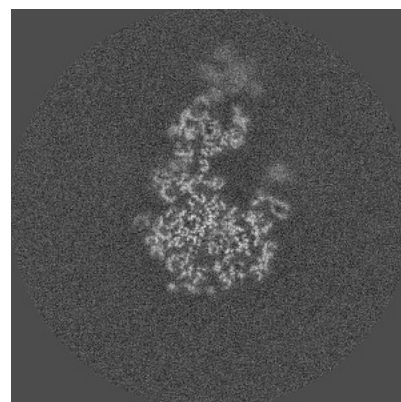
6.3.2 Raw map



X Index: 242



Y Index: 248



Z Index: 257

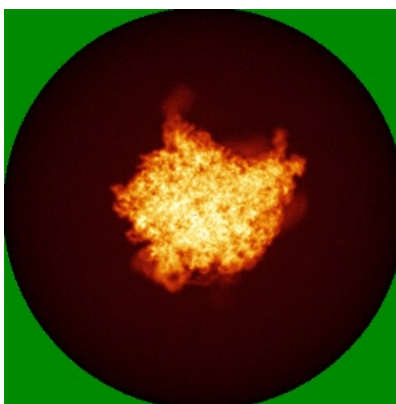
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

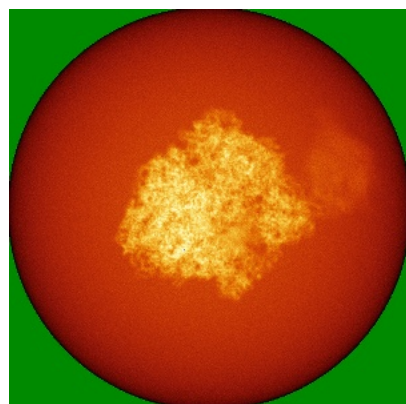


Y

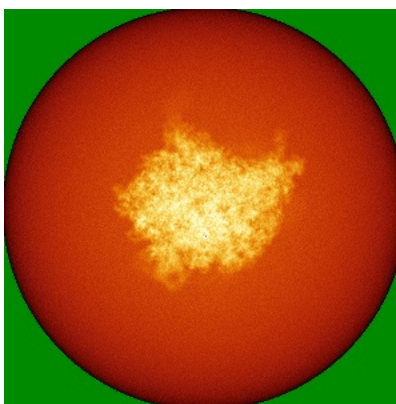


Z

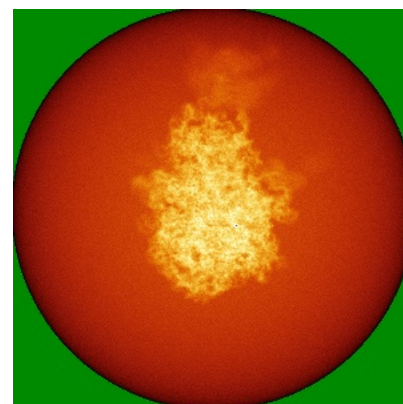
6.4.2 Raw map



X



Y

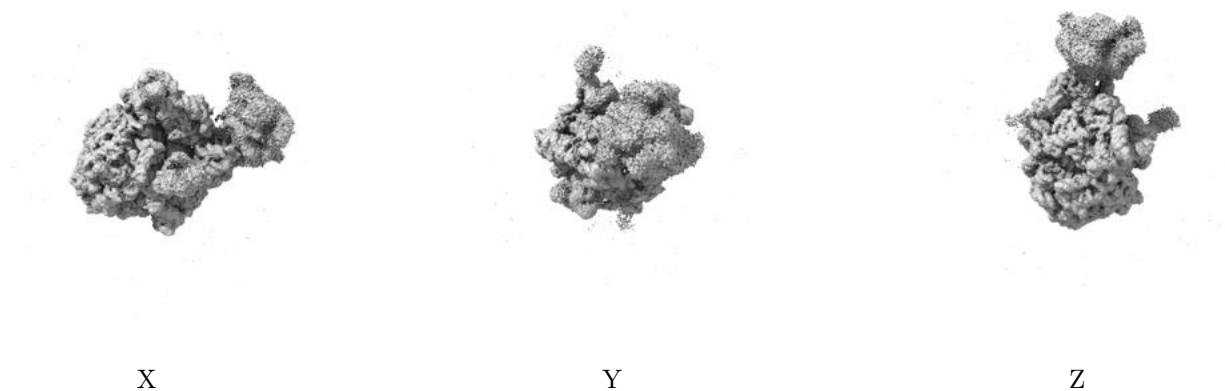


Z

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

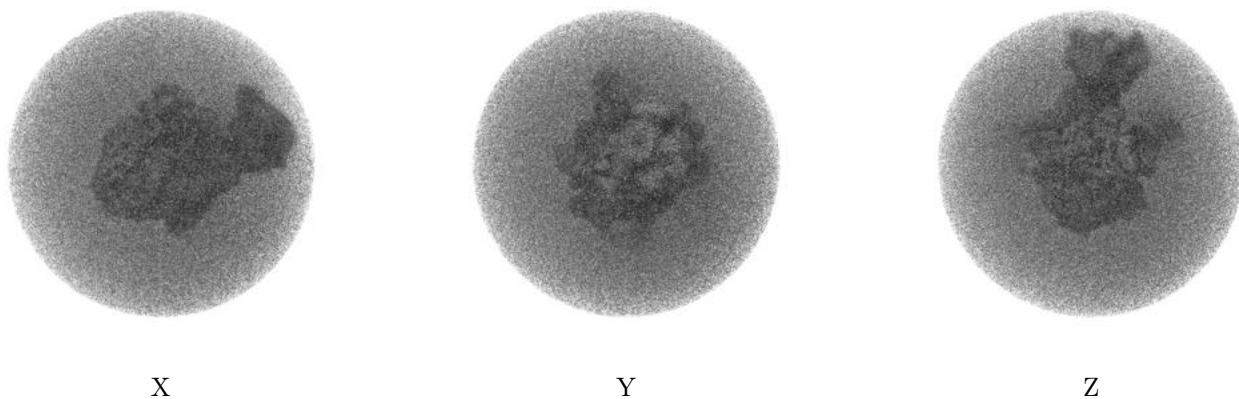
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0037. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

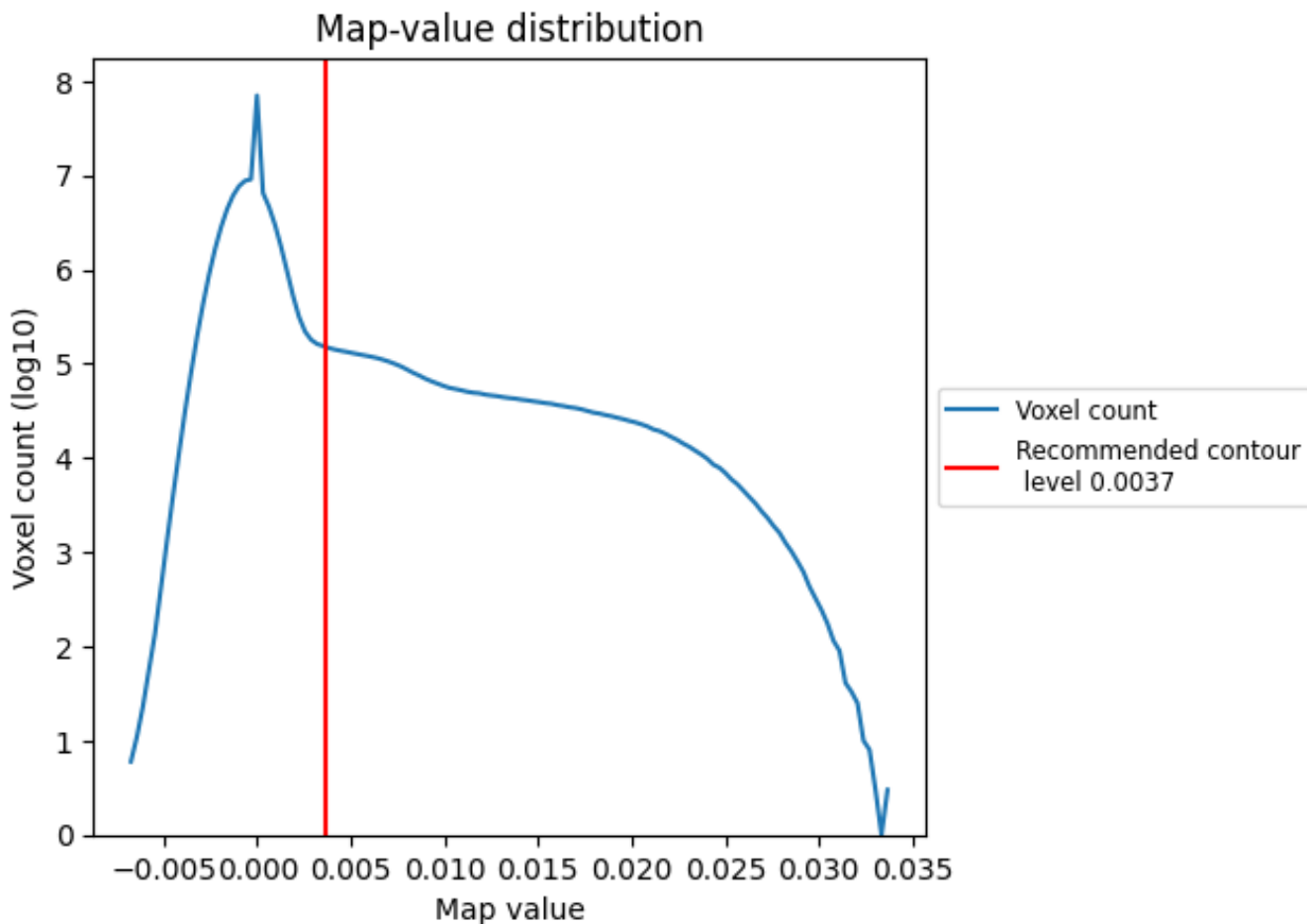
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

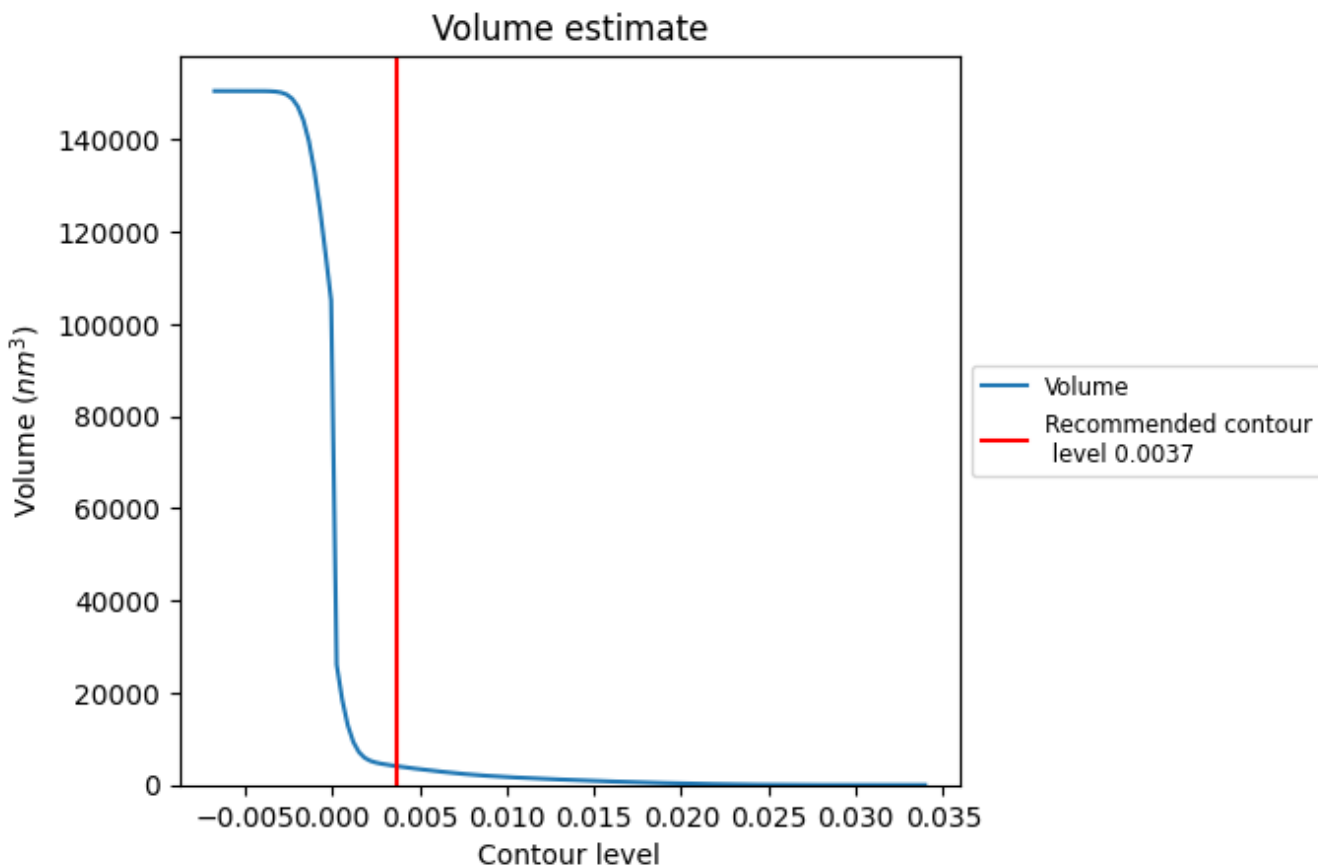
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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.

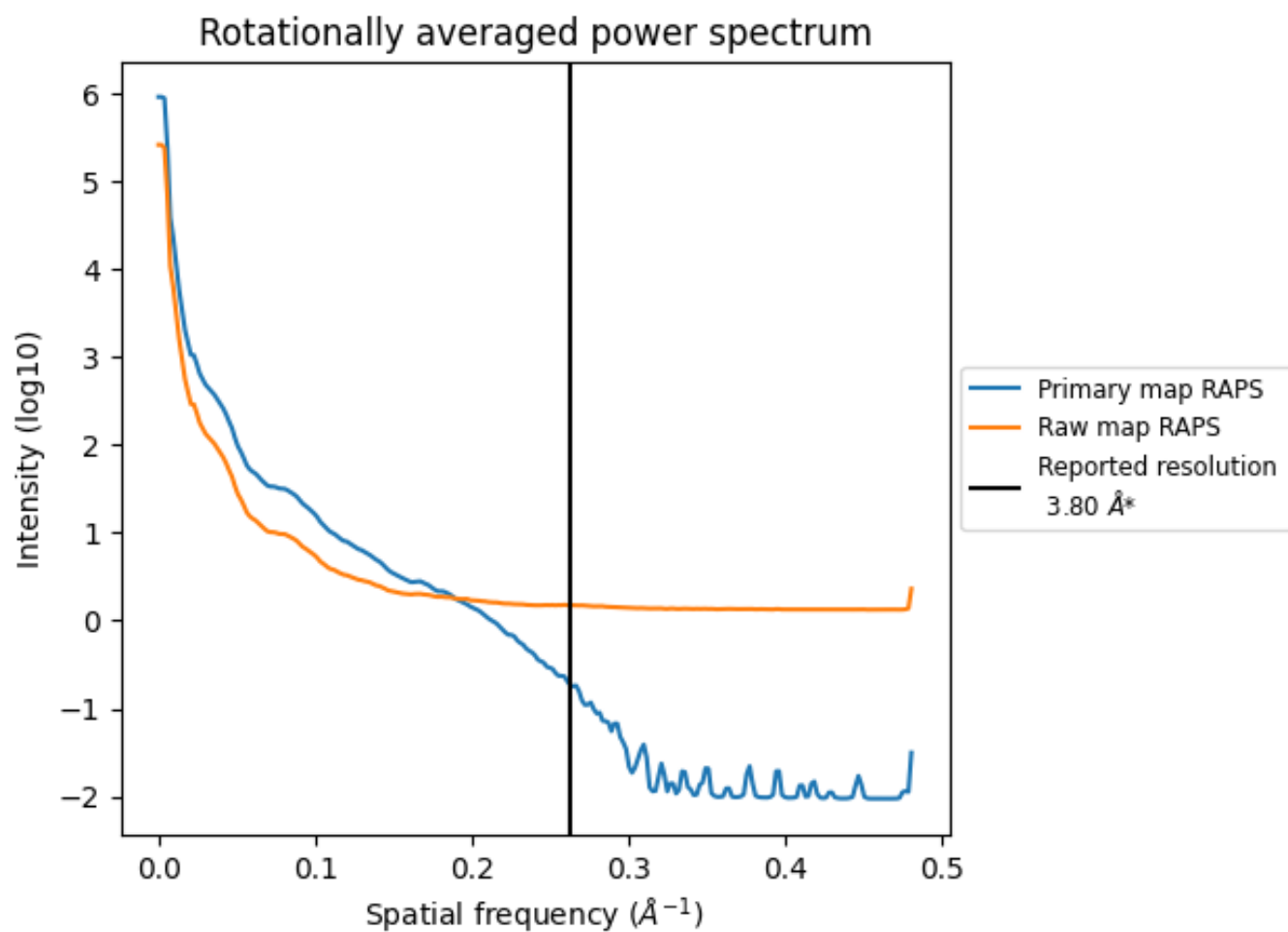
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 4079 nm³; this corresponds to an approximate mass of 3685 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

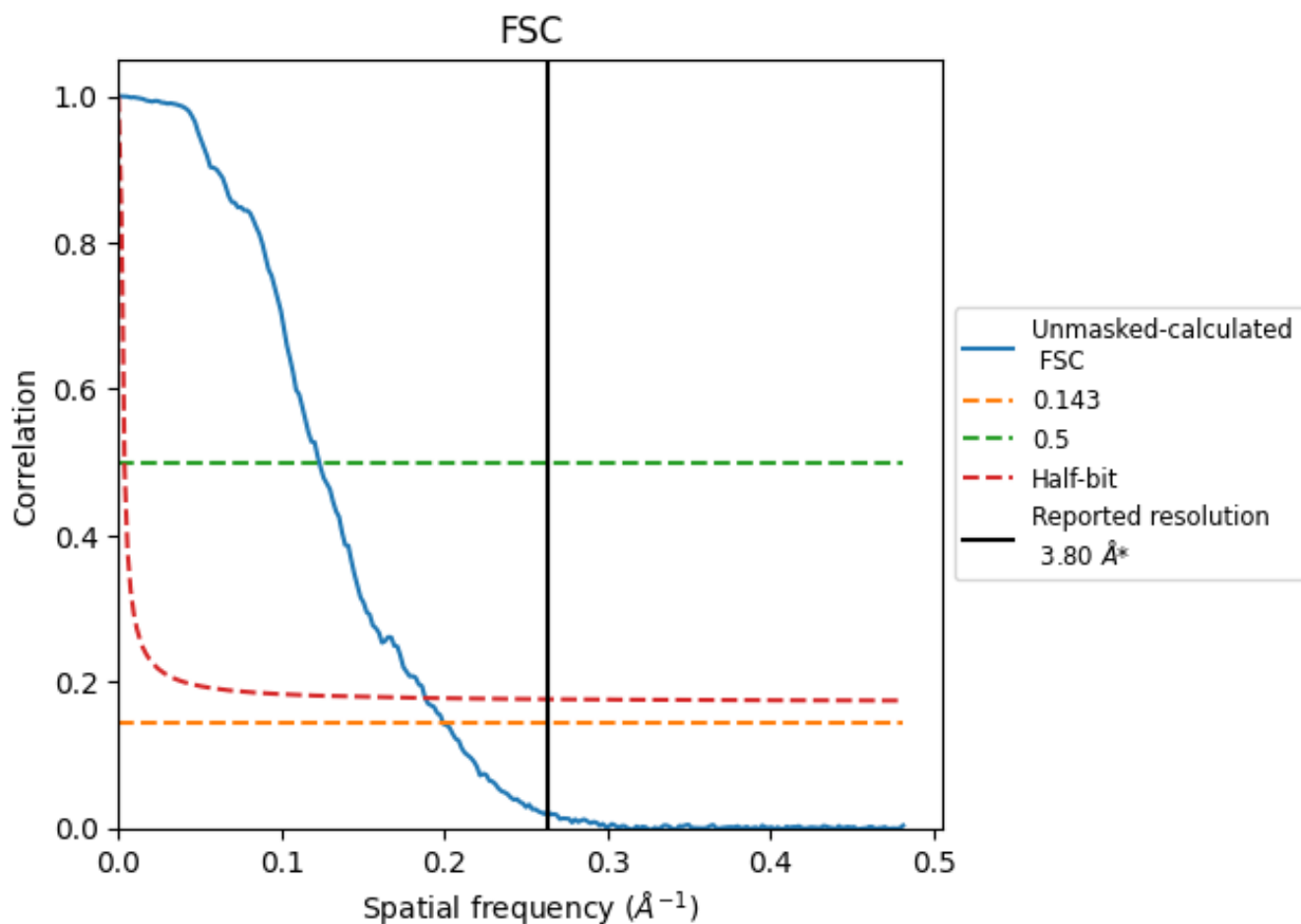


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8 Fourier-Shell correlation [i](#)

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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8.2 Resolution estimates [i](#)

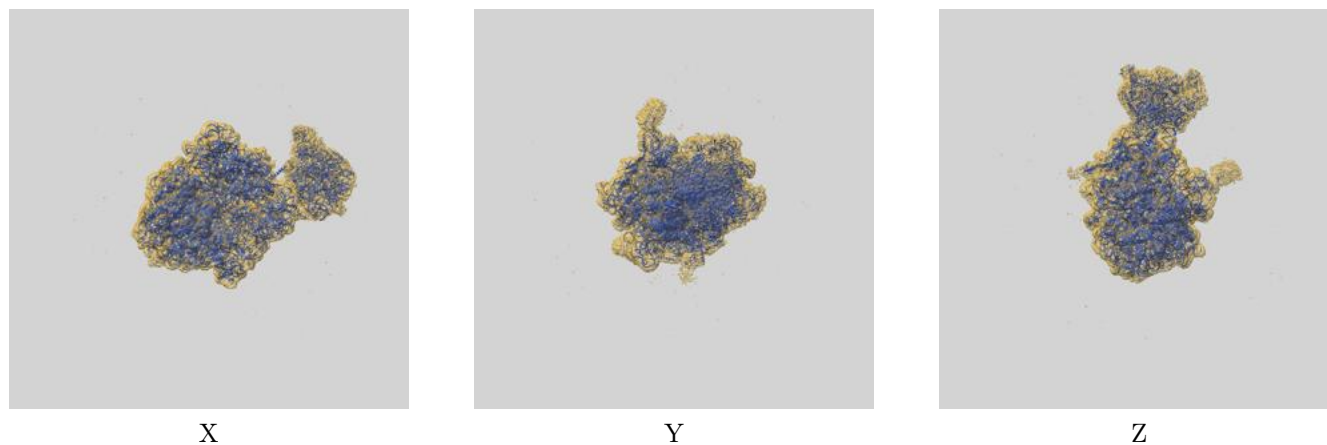
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---------------------------|------------------------------------|------|----------|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 3.80 | - | - |
| Author-provided FSC curve | - | - | - |
| Unmasked-calculated* | 5.02 | 8.12 | 5.31 |

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.02 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

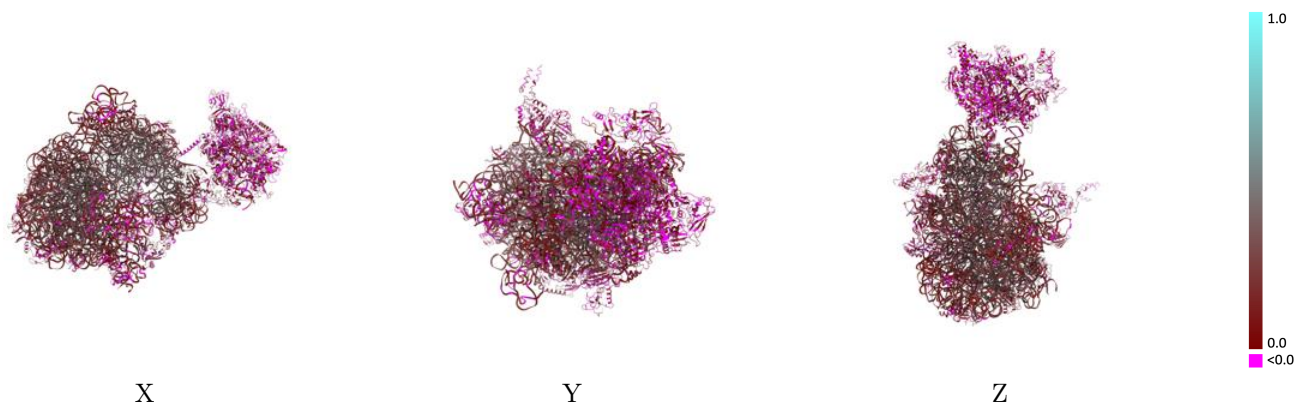
This section contains information regarding the fit between EMDB map EMD-42477 and PDB model 8UQP. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



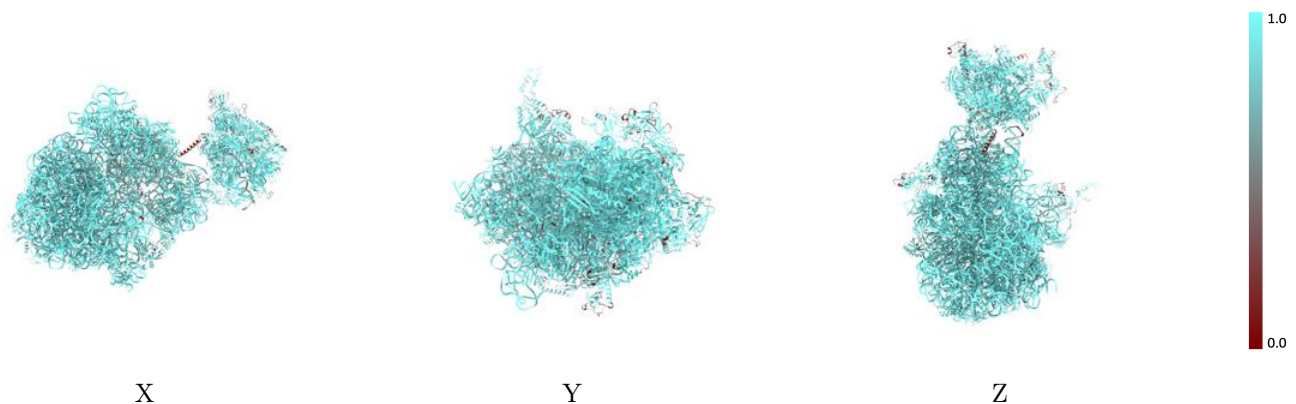
The images above show the 3D surface view of the map at the recommended contour level 0.0037 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



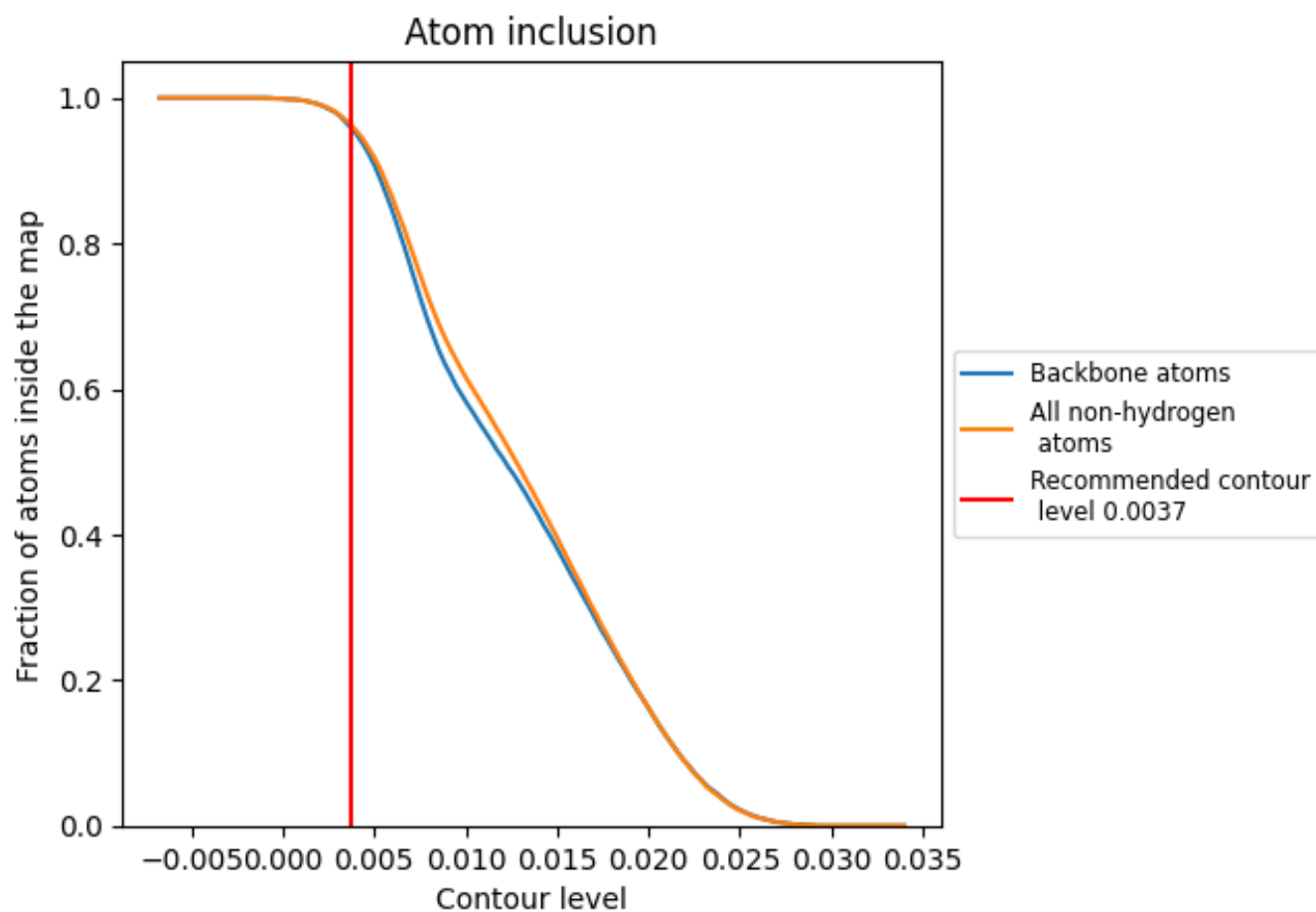
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (0.0037).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% 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 (0.0037) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| All |  0.9640 |  0.1970 |
| 0 |  0.9620 |  0.1700 |
| 1 |  0.9580 |  0.2760 |
| 2 |  0.9490 |  0.1540 |
| 3 |  0.9550 |  0.1090 |
| 4 |  0.9730 |  0.1470 |
| 5 |  0.9020 |  0.0740 |
| 6 |  0.8790 |  0.1000 |
| 7 |  0.9260 |  0.1100 |
| 9 |  0.9120 |  0.0720 |
| A |  0.9880 |  0.1760 |
| AA |  0.9380 |  0.0470 |
| AB |  0.9750 |  0.1520 |
| AC |  0.9330 |  0.0440 |
| AD |  0.8380 |  0.0120 |
| AE |  0.9330 |  0.0610 |
| AF |  0.5600 |  0.0210 |
| B |  0.9200 |  0.0920 |
| C |  0.9730 |  0.1770 |
| D |  0.9940 |  0.2680 |
| E |  0.9790 |  0.1620 |
| F |  0.9590 |  0.2180 |
| G |  0.9560 |  0.2080 |
| H |  0.7420 |  0.0610 |
| I |  0.9620 |  0.2700 |
| J |  0.9800 |  0.2420 |
| K |  0.9830 |  0.3380 |
| L |  0.9540 |  0.1120 |
| M |  0.9650 |  0.1790 |
| N |  0.9710 |  0.2650 |
| O |  0.9720 |  0.1620 |
| P |  0.9600 |  0.2040 |
| Q |  0.9580 |  0.1750 |
| R |  0.9890 |  0.3460 |
| S |  0.9730 |  0.1960 |



Continued on next page...

Continued from previous page...

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| T |  0.9710 |  0.2030 |
| U |  0.9670 |  0.1880 |
| V |  0.9650 |  0.2250 |
| W |  0.9120 |  0.1020 |
| X |  0.9370 |  0.1280 |
| Y |  0.7780 |  0.0690 |
| Z |  0.8850 |  0.0720 |
| a |  0.9920 |  0.2390 |
| b |  0.9470 |  0.1440 |
| c |  0.9530 |  0.1960 |
| d |  0.9860 |  0.1490 |
| e |  0.9450 |  0.1240 |
| f |  0.9660 |  0.1780 |
| g |  0.9370 |  0.0700 |
| h |  0.9680 |  0.2090 |
| i |  0.9700 |  0.2910 |
| j |  0.9770 |  0.2520 |
| k |  0.9710 |  0.1310 |
| l |  0.9260 |  0.1280 |
| m |  0.9800 |  0.2970 |
| n |  0.9310 |  0.1110 |
| o |  0.9470 |  0.1670 |
| p |  0.9680 |  0.1270 |
| q |  0.9560 |  0.1680 |
| r |  0.8130 |  0.0960 |
| s |  0.9670 |  0.2210 |
| t |  0.9590 |  0.2830 |
| u |  0.9530 |  0.1440 |
| v |  0.9710 |  0.2290 |
| w |  0.9720 |  0.2430 |
| x |  0.9490 |  0.0410 |
| y |  0.9620 |  0.2170 |
| z |  0.9710 |  0.2310 |