



wwPDB EM Validation Summary Report ⓘ

Oct 14, 2024 – 04:45 PM EDT

PDB ID : 8TPU
EMDB ID : EMD-41485
Title : Subtomogram averaged consensus structure of the malarial 80S ribosome in Plasmodium falciparum-infected human erythrocytes
Authors : Anton, L.; Cheng, W.; Zhu, X.; Ho, C.M.
Deposited on : 2023-08-05
Resolution : 4.10 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

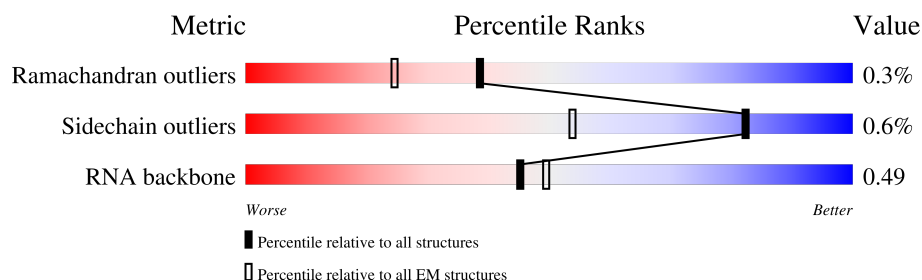
1 Overall quality at a glance

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 | 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 | S1 | 133 | |
| 2 | S2 | 105 | |
| 3 | S3 | 107 | |
| 4 | S4 | 82 | |
| 5 | S5 | 58 | |
| 6 | S6 | 43 | |
| 7 | S7 | 74 | |
| 8 | SA | 2087 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 9 | SB | 262 | |
| 10 | SC | 263 | |
| 11 | SD | 221 | |
| 12 | SE | 189 | |
| 13 | SF | 261 | |
| 14 | SG | 272 | |
| 15 | SH | 306 | |
| 16 | SI | 195 | |
| 17 | SJ | 194 | |
| 18 | SK | 130 | |
| 19 | SL | 218 | |
| 20 | SM | 144 | |
| 21 | SN | 118 | |
| 22 | SO | 137 | |
| 23 | SP | 151 | |
| 24 | SQ | 145 | |
| 25 | SR | 141 | |
| 26 | SS | 156 | |
| 27 | ST | 54 | |
| 28 | SU | 151 | |
| 29 | SV | 161 | |
| 30 | SW | 137 | |
| 31 | SX | 145 | |
| 32 | SY | 170 | |
| 33 | SZ | 82 | |

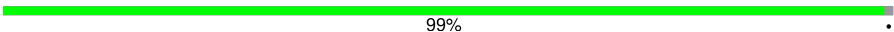



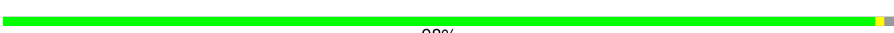










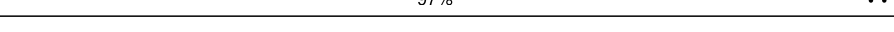
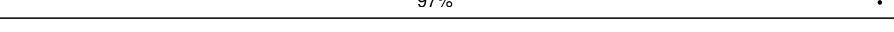
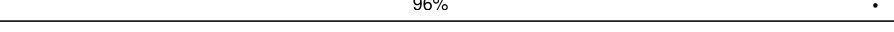
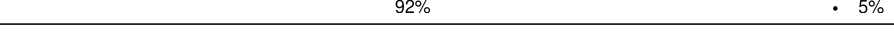


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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 34 | AA | 3788 | |
| 35 | AC | 159 | |
| 36 | AB | 119 | |
| 37 | AL | 215 | |
| 38 | A1 | 146 | |
| 39 | A2 | 126 | |
| 40 | A4 | 67 | |
| 41 | A6 | 107 | |
| 42 | A7 | 120 | |
| 43 | AN | 165 | |
| 44 | A8 | 130 | |
| 45 | A9 | 139 | |
| 46 | Aa | 149 | |
| 47 | Ab | 112 | |
| 48 | Ad | 87 | |
| 49 | Ae | 51 | |
| 50 | Af | 128 | |
| 51 | AP | 203 | |
| 52 | Ah | 95 | |
| 53 | Ai | 103 | |
| 54 | AI | 221 | |
| 55 | AJ | 283 | |
| 56 | Ac | 92 | |
| 57 | AK | 202 | |
| 58 | AM | 139 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 59 | AS | 187 |  99% |
| 60 | AO | 148 |  99% |
| 61 | AQ | 219 |  84% 14% |
| 62 | AR | 294 |  85% 14% |
| 63 | AW | 173 |  98% |
| 64 | AY | 190 |  53% 47% |
| 65 | AT | 182 |  99% |
| 66 | AZ | 126 |  95% |
| 67 | A3 | 124 |  95% |
| 68 | A5 | 257 |  86% 13% |
| 69 | AD | 260 |  94% 5% |
| 70 | AE | 386 |  98% |
| 71 | AF | 411 |  94% 5% |
| 72 | AG | 173 |  71% 28% |
| 73 | AU | 184 |  97% |
| 74 | AH | 190 |  97% |
| 75 | AV | 162 |  96% |
| 76 | Ag | 39 |  92% 5% |
| 77 | AX | 139 |  70% 30% |
| 78 | A0 | 162 |  38% 62% |
| 79 | S8 | 323 |  24% 98% |

2 Entry composition

There are 79 unique types of molecules in this entry. The entry contains 195395 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 40S ribosomal protein S24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 1 | S1 | 120 | Total | C | N | O | S | 0 | 0 |
| | | | 985 | 632 | 189 | 162 | 2 | | |

- Molecule 2 is a protein called 40S ribosomal protein S25.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 2 | S2 | 41 | Total | C | N | O | 0 | 0 |
| | | | 320 | 208 | 56 | 56 | | |

- Molecule 3 is a protein called 40S ribosomal protein S26.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 3 | S3 | 95 | Total | C | N | O | S | 0 | 0 |
| | | | 781 | 478 | 169 | 128 | 6 | | |

- Molecule 4 is a protein called 40S ribosomal protein S27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 4 | S4 | 76 | Total | C | N | O | S | 0 | 0 |
| | | | 586 | 368 | 102 | 107 | 9 | | |

- Molecule 5 is a protein called 60S ribosomal protein L41.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 5 | S5 | 58 | Total | C | N | O | 0 | 0 |
| | | | 458 | 285 | 93 | 80 | | |

- Molecule 6 is a protein called Small ribosomal subunit protein eS30.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 6 | S6 | 43 | Total | C | N | O | 0 | 0 |
| | | | 346 | 213 | 75 | 58 | | |

- Molecule 7 is a RNA chain called 60S ribosomal protein L24, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 7 | S7 | 74 | Total | C | N | O | P | 0 | 0 |
| | | | 1571 | 702 | 275 | 521 | 73 | | |

- Molecule 8 is a RNA chain called 18S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|-------|
| 8 | SA | 1608 | Total | C | N | O | P | 0 | 0 |
| | | | 34208 | 15346 | 6106 | 11170 | 1586 | | |

- Molecule 9 is a protein called 40S ribosomal protein S3a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 9 | SB | 210 | Total | C | N | O | S | 0 | 0 |
| | | | 1713 | 1097 | 301 | 303 | 12 | | |

- Molecule 10 is a protein called 40S ribosomal protein SA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 10 | SC | 195 | Total | C | N | O | S | 0 | 0 |
| | | | 1538 | 990 | 266 | 273 | 9 | | |

- Molecule 11 is a protein called 40S ribosomal protein S3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 11 | SD | 157 | Total | C | N | O | S | 0 | 0 |
| | | | 1228 | 782 | 225 | 214 | 7 | | |

- Molecule 12 is a protein called 40S ribosomal protein S9, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 12 | SE | 185 | Total | C | N | O | S | 0 | 0 |
| | | | 1514 | 962 | 290 | 260 | 2 | | |

- Molecule 13 is a protein called 40S ribosomal protein S4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 13 | SF | 257 | Total | C | N | O | S | 0 | 0 |
| | | | 2061 | 1320 | 377 | 356 | 8 | | |

- Molecule 14 is a protein called 40S ribosomal protein S5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 14 | SG | 224 | Total | C | N | O | S | 0 | 0 |
| | | | 1757 | 1132 | 307 | 309 | 9 | | |

- Molecule 15 is a protein called 40S ribosomal protein S6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 15 | SH | 204 | Total | C | N | O | S | 0 | 0 |
| | | | 1651 | 1046 | 316 | 283 | 6 | | |

- Molecule 16 is a protein called 40S ribosomal protein S5, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 16 | SI | 180 | Total | C | N | O | S | 0 | 0 |
| | | | 1424 | 893 | 263 | 258 | 10 | | |

- Molecule 17 is a protein called 40S ribosomal protein S7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 17 | SJ | 188 | Total | C | N | O | S | 0 | 0 |
| | | | 1528 | 982 | 264 | 278 | 4 | | |

- Molecule 18 is a protein called 40S ribosomal protein S15A, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 18 | SK | 129 | Total | C | N | O | S | 0 | 0 |
| | | | 1037 | 665 | 189 | 178 | 5 | | |

- Molecule 19 is a protein called 40S ribosomal protein S8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 19 | SL | 171 | Total | C | N | O | S | 0 | 0 |
| | | | 1383 | 872 | 264 | 243 | 4 | | |

- Molecule 20 is a protein called 40S ribosomal protein S16.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 20 | SM | 138 | Total | C | N | O | S | 0 | 0 |
| | | | 1098 | 704 | 200 | 193 | 1 | | |

- Molecule 21 is a protein called 40S ribosomal protein S20e, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 21 | SN | 98 | Total | C | N | O | S | 0 | 0 |
| | | | 772 | 484 | 135 | 148 | 5 | | |

- Molecule 22 is a protein called 40S ribosomal protein S10, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 22 | SO | 79 | Total | C | N | O | S | 0 | 0 |
| | | | 686 | 450 | 116 | 118 | 2 | | |

- Molecule 23 is a protein called 40S ribosomal protein S11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 23 | SP | 127 | Total | C | N | O | S | 0 | 0 |
| | | | 954 | 591 | 184 | 176 | 3 | | |

- Molecule 24 is a protein called 40S ribosomal protein S23, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 24 | SQ | 144 | Total | C | N | O | S | 0 | 0 |
| | | | 1129 | 712 | 222 | 193 | 2 | | |

- Molecule 25 is a protein called 40S ribosomal protein S12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 25 | SR | 98 | Total | C | N | O | S | 0 | 0 |
| | | | 746 | 474 | 123 | 145 | 4 | | |

- Molecule 26 is a protein called 40S ribosomal protein S18, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 26 | SS | 128 | Total | C | N | O | S | 0 | 0 |
| | | | 1046 | 657 | 205 | 180 | 4 | | |

- Molecule 27 is a protein called 40S ribosomal protein S29, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 27 | ST | 48 | Total | C | N | O | S | 0 | 0 |
| | | | 405 | 252 | 85 | 64 | 4 | | |

- Molecule 28 is a protein called 40S ribosomal protein S15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 28 | SU | 149 | Total | C | N | O | S | 0 | 0 |
| | | | 1202 | 769 | 220 | 210 | 3 | | |

- Molecule 29 is a protein called 40S ribosomal protein S11, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 29 | SV | 146 | Total | C | N | O | S | 0 | 0 |
| | | | 1206 | 772 | 227 | 200 | 7 | | |

- Molecule 30 is a protein called 40S ribosomal protein S17, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 30 | SW | 95 | Total | C | N | O | S | 0 | 0 |
| | | | 785 | 498 | 149 | 135 | 3 | | |

- Molecule 31 is a protein called 40S ribosomal protein S19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 31 | SX | 96 | Total | C | N | O | S | 0 | 0 |
| | | | 776 | 497 | 137 | 138 | 4 | | |

- Molecule 32 is a protein called 40S ribosomal protein S19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 32 | SY | 154 | Total | C | N | O | S | 0 | 0 |
| | | | 1266 | 811 | 239 | 214 | 2 | | |

- Molecule 33 is a protein called 40S ribosomal protein S21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 33 | SZ | 72 | Total | C | N | O | S | 0 | 0 |
| | | | 557 | 346 | 102 | 105 | 4 | | |

- Molecule 34 is a RNA chain called 28S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|-------|------|---------|-------|
| 34 | AA | 3193 | Total | C | N | O | P | 0 | 0 |
| | | | 67884 | 30446 | 12054 | 22223 | 3161 | | |

- Molecule 35 is a RNA chain called 5.8S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|------|-----|---------|-------|
| 35 | AC | 151 | Total | C | N | O | P | 0 | 0 |
| | | | 3215 | 1444 | 589 | 1034 | 148 | | |

- Molecule 36 is a RNA chain called 5S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 36 | AB | 118 | Total | C | N | O | P | 0 | 0 |
| | | | 2522 | 1128 | 461 | 816 | 117 | | |

- Molecule 37 is a protein called 60S ribosomal protein L13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 37 | AL | 211 | Total | C | N | O | S | 0 | 0 |
| | | | 1761 | 1119 | 349 | 290 | 3 | | |

- Molecule 38 is a protein called 60S ribosomal protein L27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 38 | A1 | 140 | Total | C | N | O | S | 0 | 0 |
| | | | 1134 | 736 | 204 | 191 | 3 | | |

- Molecule 39 is a protein called 60S ribosomal protein L28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 39 | A2 | 104 | Total | C | N | O | S | 0 | 0 |
| | | | 828 | 529 | 150 | 146 | 3 | | |

- Molecule 40 is a protein called 60S ribosomal protein L29.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 40 | A4 | 66 | Total | C | N | O | S | 0 | 0 |
| | | | 555 | 347 | 116 | 90 | 2 | | |

- Molecule 41 is a protein called 60S ribosomal protein L30e, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 41 | A6 | 97 | Total | C | N | O | S | 0 | 0 |
| | | | 732 | 458 | 131 | 136 | 7 | | |

- Molecule 42 is a protein called 60S ribosomal protein L31.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 42 | A7 | 96 | Total | C | N | O | S | 0 | 0 |
| | | | 793 | 508 | 151 | 129 | 5 | | |

- Molecule 43 is a protein called 60S ribosomal protein L14, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 43 | AN | 147 | Total | C | N | O | S | 0 | 0 |
| | | | 1210 | 787 | 212 | 205 | 6 | | |

- Molecule 44 is a protein called 60S ribosomal protein L32.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 44 | A8 | 124 | Total | C | N | O | S | 0 | 0 |
| | | | 1029 | 655 | 205 | 162 | 7 | | |

- Molecule 45 is a protein called 60S ribosomal protein L35ae, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 45 | A9 | 102 | Total | C | N | O | S | 0 | 0 |
| | | | 840 | 541 | 162 | 134 | 3 | | |

- Molecule 46 is a protein called 60S ribosomal protein L34.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 46 | Aa | 105 | Total | C | N | O | S | 0 | 0 |
| | | | 854 | 528 | 183 | 137 | 6 | | |

- Molecule 47 is a protein called 60S ribosomal protein L36.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 47 | Ab | 95 | Total | C | N | O | S | 0 | 0 |
| | | | 756 | 477 | 150 | 129 | | | |

- Molecule 48 is a protein called 60S ribosomal protein L38.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 48 | Ad | 72 | Total | C | N | O | S | 0 | 0 |
| | | | 603 | 395 | 107 | 99 | 2 | | |

- Molecule 49 is a protein called 60S ribosomal protein L39.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 49 | Ae | 43 | Total | C | N | O | S | 0 | 0 |
| | | | 388 | 243 | 92 | 52 | 1 | | |

- Molecule 50 is a protein called Ubiquitin-60S ribosomal protein L40.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 50 | Af | 51 | Total | C | N | O | S | 0 | 0 |
| | | | 413 | 255 | 87 | 66 | 5 | | |

- Molecule 51 is a protein called Ribosomal protein L15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 51 | AP | 202 | Total | C | N | O | S | 0 | 0 |
| | | | 1682 | 1064 | 349 | 265 | 4 | | |

- Molecule 52 is a protein called Large ribosomal subunit protein eL43.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 52 | Ah | 84 | Total | C | N | O | S | 0 | 0 |
| | | | 653 | 414 | 126 | 106 | 7 | | |

- Molecule 53 is a protein called Large ribosomal subunit protein eL42.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 53 | Ai | 94 | Total | C | N | O | S | 0 | 0 |
| | | | 769 | 484 | 150 | 126 | 9 | | |

- Molecule 54 is a protein called 60S ribosomal protein L6, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 54 | AI | 207 | Total | C | N | O | S | 0 | 0 |
| | | | 1685 | 1096 | 298 | 286 | 5 | | |

- Molecule 55 is a protein called 60S ribosomal protein L7a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 55 | AJ | 222 | Total | C | N | O | S | 0 | 0 |
| | | | 1813 | 1174 | 323 | 309 | 7 | | |

- Molecule 56 is a protein called Ribosomal protein L37.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 56 | Ac | 89 | Total | C | N | O | S | 0 | 0 |
| | | | 709 | 441 | 150 | 113 | 5 | | |

- Molecule 57 is a protein called 60S ribosomal protein L13, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 57 | AK | 201 | Total | C | N | O | S | 0 | 0 |
| | | | 1659 | 1064 | 311 | 276 | 8 | | |

- Molecule 58 is a protein called 60S ribosomal protein L23, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 58 | AM | 132 | Total | C | N | O | S | 0 | 0 |
| | | | 996 | 631 | 179 | 178 | 8 | | |

- Molecule 59 is a protein called 60S ribosomal protein L18-2, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 59 | AS | 186 | Total | C | N | O | S | 0 | 0 |
| | | | 1503 | 958 | 299 | 241 | 5 | | |

- Molecule 60 is a protein called 60S ribosomal protein L27a, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 60 | AO | 147 | Total | C | N | O | S | 0 | 0 |
| | | | 1172 | 747 | 232 | 189 | 4 | | |

- Molecule 61 is a protein called 60S ribosomal protein L10, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 61 | AQ | 189 | Total | C | N | O | S | 0 | 0 |
| | | | 1544 | 984 | 291 | 261 | 8 | | |

- Molecule 62 is a protein called 60S ribosomal protein L5, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 62 | AR | 252 | Total | C | N | O | S | 0 | 0 |
| | | | 2049 | 1301 | 385 | 357 | 6 | | |

- Molecule 63 is a protein called 60S ribosomal protein L17, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 63 | AW | 170 | Total | C | N | O | S | 0 | 0 |
| | | | 1319 | 824 | 266 | 222 | 7 | | |

- Molecule 64 is a protein called 60S ribosomal protein L23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 64 | AY | 101 | Total | C | N | O | S | 0 | 0 |
| | | | 796 | 502 | 144 | 144 | 6 | | |

- Molecule 65 is a protein called 60S ribosomal protein L19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 65 | AT | 181 | Total | C | N | O | S | 0 | 0 |
| | | | 1509 | 952 | 309 | 244 | 4 | | |

- Molecule 66 is a protein called 60S ribosomal protein L26, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 66 | AZ | 121 | Total | C | N | O | S | 0 | 0 |
| | | | 1000 | 626 | 206 | 165 | 3 | | |

- Molecule 67 is a protein called 60S ribosomal protein L35, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 67 | A3 | 119 | Total | C | N | O | S | 0 | 0 |
| | | | 994 | 635 | 194 | 163 | 2 | | |

- Molecule 68 is a protein called 60S ribosomal protein L7, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 68 | A5 | 223 | Total | C | N | O | S | 0 | 0 |
| | | | 1879 | 1211 | 357 | 306 | 5 | | |

- Molecule 69 is a protein called 60S ribosomal protein L2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 69 | AD | 247 | Total | C | N | O | S | 0 | 0 |
| | | | 1866 | 1166 | 374 | 317 | 9 | | |

- Molecule 70 is a protein called 60S ribosomal protein L3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 70 | AE | 380 | Total | C | N | O | S | 0 | 0 |
| | | | 3061 | 1948 | 575 | 521 | 17 | | |

- Molecule 71 is a protein called 60S ribosomal protein L4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 71 | AF | 390 | Total | C | N | O | S | 0 | 0 |
| | | | 3094 | 1962 | 594 | 527 | 11 | | |

- Molecule 72 is a protein called 60S ribosomal protein L11a, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 72 | AG | 124 | Total | C | N | O | S | 0 | 0 |
| | | | 1010 | 636 | 197 | 171 | 6 | | |

- Molecule 73 is a protein called 60S ribosomal protein L18a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 73 | AU | 180 | Total | C | N | O | S | 0 | 0 |
| | | | 1497 | 946 | 289 | 255 | 7 | | |

- Molecule 74 is a protein called 60S ribosomal protein L6, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 74 | AH | 185 | Total | C | N | O | S | 0 | 0 |
| | | | 1475 | 950 | 264 | 255 | 6 | | |

- Molecule 75 is a protein called 60S ribosomal protein L21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 75 | AV | 155 | Total | C | N | O | S | 0 | 0 |
| | | | 1275 | 814 | 241 | 214 | 6 | | |

- Molecule 76 is a protein called 60S ribosomal protein L41.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 76 | Ag | 37 | Total | C | N | O | S | 0 | 0 |
| | | | 343 | 210 | 86 | 45 | 2 | | |

- Molecule 77 is a protein called 60S ribosomal protein L22, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 77 | AX | 97 | Total | C | N | O | S | 0 | 0 |
| | | | 824 | 548 | 135 | 139 | 2 | | |

- Molecule 78 is a protein called 60S ribosomal protein L24, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 78 | A0 | 62 | Total | C | N | O | S | 0 | 0 |
| | | | 521 | 336 | 97 | 87 | 1 | | |

- Molecule 79 is a protein called Receptor for activated c kinase.

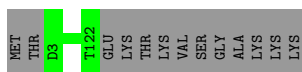
| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 79 | S8 | 317 | Total | C | N | O | S | 0 | 0 |
| | | | 2464 | 1557 | 419 | 478 | 10 | | |

3 Residue-property plots [i](#)

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

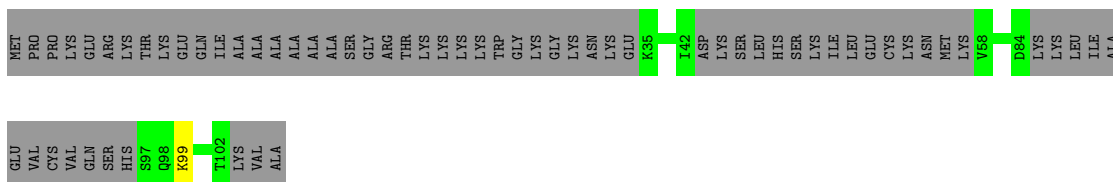
- Molecule 1: 40S ribosomal protein S24

Chain S1: 



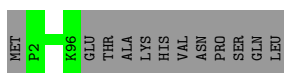
- Molecule 2: 40S ribosomal protein S25

Chain S2: 



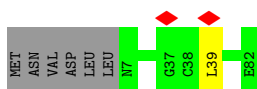
- Molecule 3: 40S ribosomal protein S26

Chain S3: 



- Molecule 4: 40S ribosomal protein S27

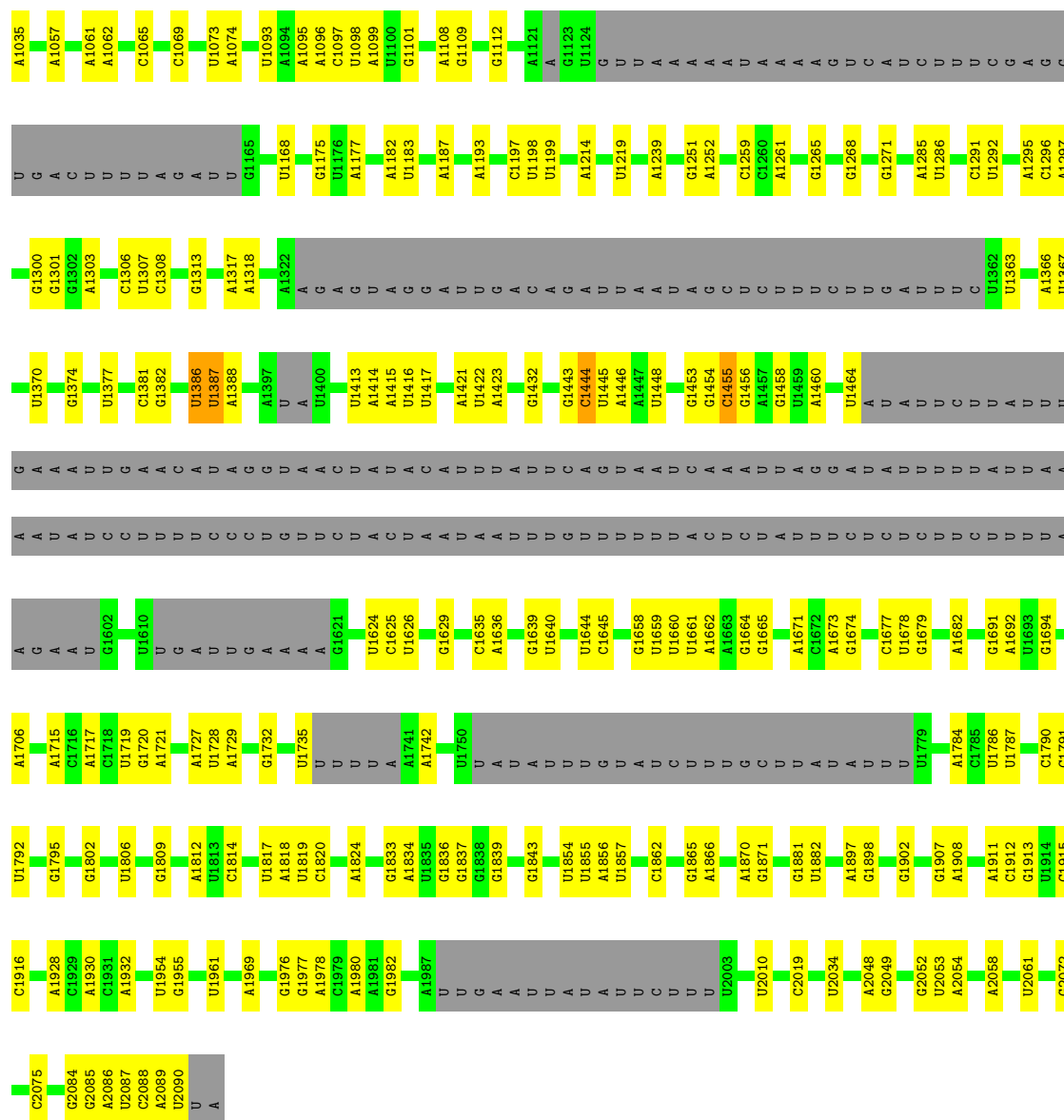
Chain S4: 



- Molecule 5: 60S ribosomal protein L41

Chain S5: 



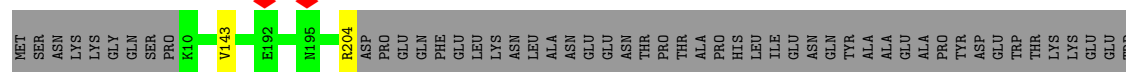


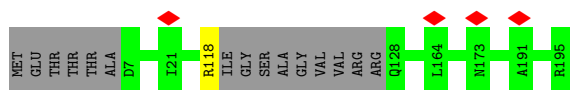
- Molecule 9: 40S ribosomal protein S3a

Chain SB: 79% identity, 20% similarity

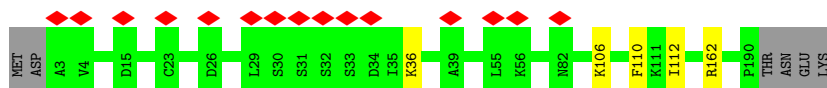
- Molecule 10: 40S ribosomal protein SA

Chain SC: 73% identity, 26% similarity





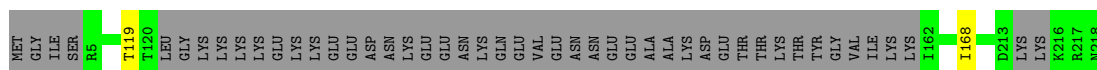
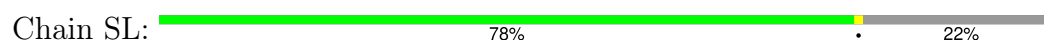
- Molecule 17: 40S ribosomal protein S7



- Molecule 18: 40S ribosomal protein S15A, putative



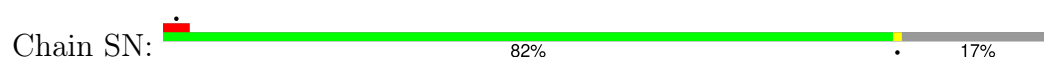
- Molecule 19: 40S ribosomal protein S8



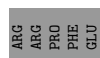
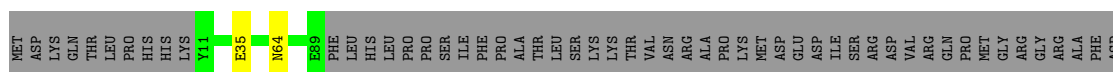
- Molecule 20: 40S ribosomal protein S16



- Molecule 21: 40S ribosomal protein S20e, putative

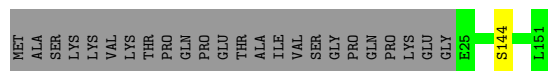


- Molecule 22: 40S ribosomal protein S10, putative



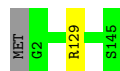
- Molecule 23: 40S ribosomal protein S11

Chain SP:  83% 16%



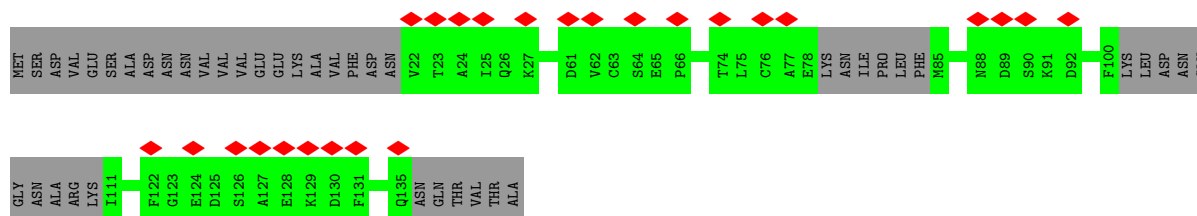
- Molecule 24: 40S ribosomal protein S23, putative

Chain SQ:  99%




- Molecule 25: 40S ribosomal protein S12

Chain SR:  18% 70% 30%



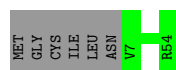
- Molecule 26: 40S ribosomal protein S18, putative

Chain SS:  80% 18%



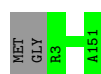
- Molecule 27: 40S ribosomal protein S29, putative

Chain ST:  89% 11%



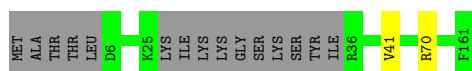
- Molecule 28: 40S ribosomal protein S15

Chain SU:  99%



- Molecule 29: 40S ribosomal protein S11, putative

Chain SV:  89% 9%



- Molecule 30: 40S ribosomal protein S17, putative

Chain SW: 68% 31%



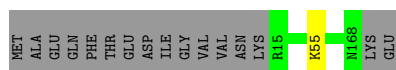
- Molecule 31: 40S ribosomal protein S19

Chain SX: 66% 34%



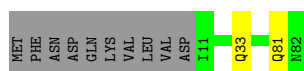
- Molecule 32: 40S ribosomal protein S19

Chain SY: 90% 9%



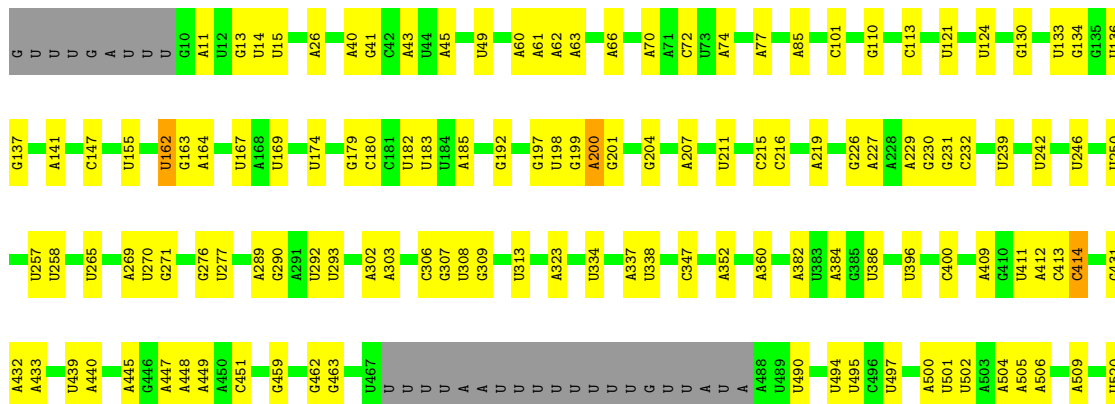
- Molecule 33: 40S ribosomal protein S21

Chain SZ: 85% 12%



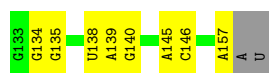
- Molecule 34: 28S ribosomal RNA

Chain AA: 63% 21% 16%









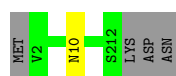
- Molecule 36: 5S ribosomal RNA

Chain AB: 83% 16%



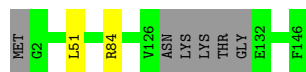
- Molecule 37: 60S ribosomal protein L13

Chain AL: 98%



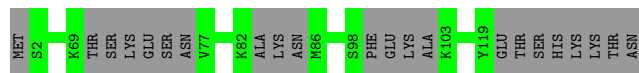
- Molecule 38: 60S ribosomal protein L27

Chain A1: 95%



- Molecule 39: 60S ribosomal protein L28

Chain A2: 83% 17%



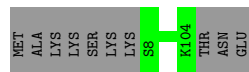
- Molecule 40: 60S ribosomal protein L29

Chain A4: 99%



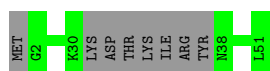
- Molecule 41: 60S ribosomal protein L30e, putative

Chain A6: 91% 9%



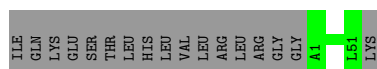
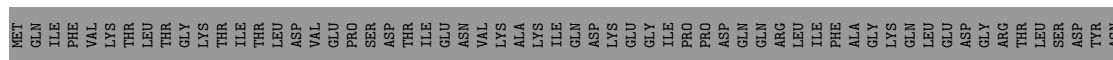
- Molecule 42: 60S ribosomal protein L31

Chain A7: 80% 20%



- Molecule 50: Ubiquitin-60S ribosomal protein L40

Chain Af: 40% 60%



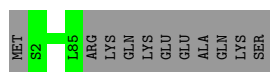
- Molecule 51: Ribosomal protein L15

Chain AP: 98%



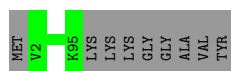
- Molecule 52: Large ribosomal subunit protein eL43

Chain Ah: 88% 12%



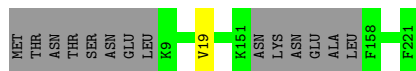
- Molecule 53: Large ribosomal subunit protein eL42

Chain Ai: 91% 9%



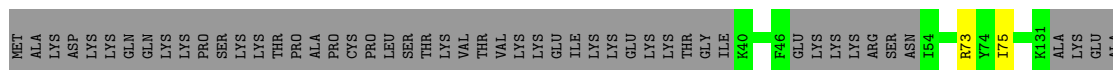
- Molecule 54: 60S ribosomal protein L6, putative

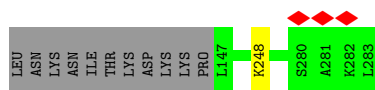
Chain AI: 93% 6%



- Molecule 55: 60S ribosomal protein L7a

Chain AJ: 77% 22%





- Molecule 56: Ribosomal protein L37

Chain Ac: 95%



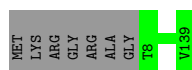
- Molecule 57: 60S ribosomal protein L13, putative

Chain AK: 100%



- Molecule 58: 60S ribosomal protein L23, putative

Chain AM: 95%



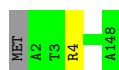
- Molecule 59: 60S ribosomal protein L18-2, putative

Chain AS: 99%



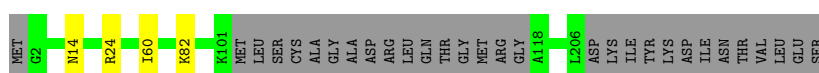
- Molecule 60: 60S ribosomal protein L27a, putative

Chain AO: 99%



- Molecule 61: 60S ribosomal protein L10, putative

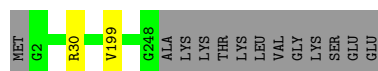
Chain AQ: 84%



- Molecule 62: 60S ribosomal protein L5, putative

Chain AR: 85%

Chain AD:  94% • 5%



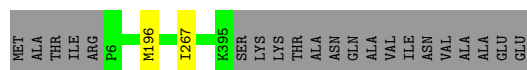
- Molecule 70: 60S ribosomal protein L3

Chain AE:  98% ••



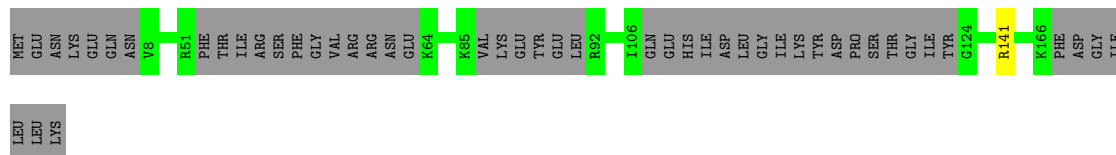
- Molecule 71: 60S ribosomal protein L4

Chain AF:  94% 5%



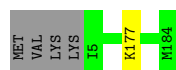
- Molecule 72: 60S ribosomal protein L11a, putative

Chain AG:  71% • 28%



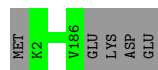
- Molecule 73: 60S ribosomal protein L18a

Chain AU:  97% ••



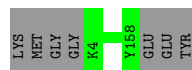
- Molecule 74: 60S ribosomal protein L6, putative

Chain AH:  97% •



- Molecule 75: 60S ribosomal protein L21

Chain AV:  96% •



-

- | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|
| MET | VAL | ALA | LYS | LYS | ASP | SER | THR | LYS | VAL | SER | LYS | LYS | LEU | LYS | LYS | THR | LYS | GLY | I40 | Q136 | LEU | ASN | ASN |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | SER | GLN | LYS | THR | THR | W8 | KG7 | K69 | TS9 | LYS | ILE | GLU | THR | THR | CLN | ARG | ARG | ARG | ARG | LYS | LYS | THR | THR | ILE | VAL | VAL | GLN | LYS | ALA | VAL | VAL | GLY | GLY | LEU | THR | VAL | GLU | ASP | ARG | ASN | ILE | ARG | ALA | LYS | ALA | THR | VAL | VAL | CLN | SER | ILE | GLU | ALA | ALA | LYS | PHE | GLY | THR |
|-----|-----|-----|-----|-----|-----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| LYS | GLU | LYS | GLU | ASP | LYS | LYS | THR | LYS | LYS | ASP | ASP | LYS | LYS | LYS | ASN | LEU | VAL | HIS | PHE | GLN | GLN | LYS | LYS | ASP | PHE | THR | LYS | LYS | SER | LYS | MET | LEU | ASN | MET | ALA | LYS | SER | LYS | MET | HIS | LYS | MET | MET | LYS | LYS |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

- [illegible]

4 Experimental information

| Property | Value | Source |
|--------------------------------------|--|-----------|
| EM reconstruction method | SUBTOMOGRAM AVERAGING | Depositor |
| Imposed symmetry | 3D CRYSTAL, $a=500.24002$ Å, $b=500.24002$ Å, $c=500.24002$ Å, $\alpha=90.0^\circ$, $\beta=90.0^\circ$, $\gamma=90.0^\circ$, space group=C1 | Depositor |
| Number of subtomograms used | 120226 | 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 ($e^-/\text{\AA}^2$) | 120 | Depositor |
| Minimum defocus (nm) | 2800 | Depositor |
| Maximum defocus (nm) | 3200 | Depositor |
| Magnification | Not provided | |
| Image detector | GATAN K3 (6k x 4k) | Depositor |
| Maximum map value | 1.159 | Depositor |
| Minimum map value | -0.276 | Depositor |
| Average map value | 0.009 | Depositor |
| Map value standard deviation | 0.075 | Depositor |
| Recommended contour level | 0.16 | Depositor |
| Map size (Å) | 500.24002, 500.24002, 500.24002 | wwPDB |
| Map dimensions | 296, 296, 296 | wwPDB |
| Map angles ($^\circ$) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.69, 1.69, 1.69 | 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 | S1 | 0.26 | 0/998 | 0.53 | 0/1321 |
| 2 | S2 | 0.24 | 0/323 | 0.46 | 0/435 |
| 3 | S3 | 0.26 | 0/793 | 0.60 | 0/1055 |
| 4 | S4 | 0.26 | 0/597 | 0.58 | 1/801 (0.1%) |
| 5 | S5 | 0.29 | 0/460 | 0.74 | 1/609 (0.2%) |
| 6 | S6 | 0.23 | 0/349 | 0.55 | 0/458 |
| 7 | S7 | 0.24 | 0/1754 | 0.85 | 1/2732 (0.0%) |
| 8 | SA | 0.28 | 0/38276 | 0.84 | 30/59598 (0.1%) |
| 9 | SB | 0.27 | 0/1737 | 0.52 | 0/2321 |
| 10 | SC | 0.26 | 0/1569 | 0.50 | 0/2129 |
| 11 | SD | 0.25 | 0/1240 | 0.55 | 1/1652 (0.1%) |
| 12 | SE | 0.25 | 0/1538 | 0.55 | 0/2055 |
| 13 | SF | 0.27 | 0/2097 | 0.55 | 1/2819 (0.0%) |
| 14 | SG | 0.28 | 0/1799 | 0.53 | 0/2429 |
| 15 | SH | 0.25 | 0/1668 | 0.56 | 0/2214 |
| 16 | SI | 0.25 | 0/1443 | 0.50 | 0/1936 |
| 17 | SJ | 0.25 | 0/1544 | 0.54 | 0/2064 |
| 18 | SK | 0.29 | 0/1054 | 0.57 | 0/1411 |
| 19 | SL | 0.26 | 0/1407 | 0.55 | 0/1879 |
| 20 | SM | 0.25 | 0/1113 | 0.54 | 0/1487 |
| 21 | SN | 0.24 | 0/780 | 0.56 | 0/1053 |
| 22 | SO | 0.27 | 0/705 | 0.51 | 0/950 |
| 23 | SP | 0.25 | 0/966 | 0.58 | 0/1295 |
| 24 | SQ | 0.27 | 0/1149 | 0.55 | 0/1532 |
| 25 | SR | 0.24 | 0/754 | 0.44 | 0/1013 |
| 26 | SS | 0.25 | 0/1062 | 0.59 | 0/1425 |
| 27 | ST | 0.24 | 0/412 | 0.54 | 0/544 |
| 28 | SU | 0.27 | 0/1223 | 0.52 | 0/1634 |
| 29 | SV | 0.27 | 0/1233 | 0.53 | 0/1645 |
| 30 | SW | 0.25 | 0/792 | 0.61 | 0/1053 |
| 31 | SX | 0.25 | 0/787 | 0.54 | 0/1050 |
| 32 | SY | 0.25 | 0/1294 | 0.52 | 0/1742 |
| 33 | SZ | 0.25 | 0/565 | 0.52 | 0/758 |
| 34 | AA | 0.36 | 0/75947 | 0.85 | 47/118255 (0.0%) |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|---------|-------------|---------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 35 | AC | 0.37 | 0/3599 | 0.84 | 0/5603 |
| 36 | AB | 0.33 | 0/2823 | 0.79 | 0/4400 |
| 37 | AL | 0.27 | 0/1793 | 0.54 | 0/2387 |
| 38 | A1 | 0.27 | 0/1151 | 0.55 | 1/1531 (0.1%) |
| 39 | A2 | 0.26 | 0/837 | 0.45 | 0/1112 |
| 40 | A4 | 0.26 | 0/564 | 0.46 | 0/737 |
| 41 | A6 | 0.27 | 0/740 | 0.54 | 0/990 |
| 42 | A7 | 0.28 | 0/805 | 0.53 | 0/1073 |
| 43 | AN | 0.37 | 0/1226 | 0.61 | 0/1632 |
| 44 | A8 | 0.28 | 0/1046 | 0.59 | 1/1389 (0.1%) |
| 45 | A9 | 0.31 | 0/860 | 0.58 | 0/1155 |
| 46 | Aa | 0.29 | 0/867 | 0.61 | 0/1156 |
| 47 | Ab | 0.26 | 0/762 | 0.55 | 0/1008 |
| 48 | Ad | 0.27 | 0/611 | 0.54 | 0/812 |
| 49 | Ae | 0.26 | 0/396 | 0.61 | 0/521 |
| 50 | Af | 0.27 | 0/418 | 0.58 | 0/556 |
| 51 | AP | 0.29 | 0/1720 | 0.58 | 0/2299 |
| 52 | Ah | 0.29 | 0/662 | 0.56 | 0/880 |
| 53 | Ai | 0.27 | 0/779 | 0.52 | 0/1021 |
| 54 | AI | 0.26 | 0/1708 | 0.48 | 0/2274 |
| 55 | AJ | 0.25 | 0/1840 | 0.49 | 0/2456 |
| 56 | Ac | 0.27 | 0/722 | 0.61 | 0/951 |
| 57 | AK | 0.28 | 0/1689 | 0.50 | 0/2260 |
| 58 | AM | 0.27 | 0/1012 | 0.52 | 0/1363 |
| 59 | AS | 0.28 | 0/1531 | 0.57 | 0/2040 |
| 60 | AO | 0.28 | 0/1199 | 0.52 | 0/1597 |
| 61 | AQ | 0.29 | 0/1579 | 0.53 | 0/2113 |
| 62 | AR | 0.27 | 0/2078 | 0.51 | 0/2776 |
| 63 | AW | 0.28 | 0/1244 | 0.56 | 0/1663 |
| 64 | AY | 0.27 | 0/805 | 0.49 | 0/1074 |
| 65 | AT | 0.27 | 0/1525 | 0.54 | 0/2016 |
| 66 | AZ | 0.26 | 0/1012 | 0.60 | 0/1339 |
| 67 | A3 | 0.26 | 0/1004 | 0.51 | 0/1329 |
| 68 | A5 | 0.29 | 0/1917 | 0.55 | 0/2562 |
| 69 | AD | 0.28 | 0/1901 | 0.56 | 0/2544 |
| 70 | AE | 0.28 | 0/3129 | 0.54 | 0/4195 |
| 71 | AF | 0.28 | 0/3144 | 0.52 | 1/4205 (0.0%) |
| 72 | AG | 0.27 | 0/1020 | 0.57 | 0/1349 |
| 73 | AU | 0.28 | 0/1527 | 0.55 | 0/2043 |
| 74 | AH | 0.28 | 0/1500 | 0.56 | 0/2025 |
| 75 | AV | 0.29 | 0/1300 | 0.52 | 0/1732 |
| 76 | Ag | 0.25 | 0/348 | 0.69 | 0/448 |
| 77 | AX | 0.28 | 0/841 | 0.52 | 0/1125 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|-------------|-------------|------------------|
| | | RMSZ | $\# Z > 5$ | RMSZ | $\# Z > 5$ |
| 78 | A0 | 0.27 | 0/533 | 0.53 | 0/711 |
| 79 | S8 | 0.25 | 0/2520 | 0.50 | 0/3428 |
| All | All | 0.31 | 0/209715 | 0.74 | 85/307234 (0.0%) |

There are no bond length outliers.

The worst 5 of 85 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|-----------|-------|-------------|----------|
| 8 | SA | 1444 | C | C2-N1-C1' | 9.62 | 129.38 | 118.80 |
| 34 | AA | 594 | C | C2-N1-C1' | 9.61 | 129.37 | 118.80 |
| 8 | SA | 415 | C | N3-C2-O2 | -8.93 | 115.65 | 121.90 |
| 34 | AA | 3382 | U | C2-N1-C1' | 8.92 | 128.41 | 117.70 |
| 8 | SA | 1635 | C | N1-C2-O2 | 7.98 | 123.69 | 118.90 |

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 1 | S1 | 118/133 (89%) | 112 (95%) | 6 (5%) | 0 | 100 | 100 |
| 2 | S2 | 35/105 (33%) | 33 (94%) | 2 (6%) | 0 | 100 | 100 |
| 3 | S3 | 93/107 (87%) | 84 (90%) | 9 (10%) | 0 | 100 | 100 |
| 4 | S4 | 74/82 (90%) | 60 (81%) | 14 (19%) | 0 | 100 | 100 |
| 5 | S5 | 56/58 (97%) | 49 (88%) | 5 (9%) | 2 (4%) | 3 | 23 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 6 | S6 | 41/43 (95%) | 35 (85%) | 6 (15%) | 0 | 100 | 100 |
| 9 | SB | 208/262 (79%) | 196 (94%) | 10 (5%) | 2 (1%) | 13 | 48 |
| 10 | SC | 193/263 (73%) | 179 (93%) | 13 (7%) | 1 (0%) | 25 | 62 |
| 11 | SD | 149/221 (67%) | 143 (96%) | 6 (4%) | 0 | 100 | 100 |
| 12 | SE | 183/189 (97%) | 171 (93%) | 12 (7%) | 0 | 100 | 100 |
| 13 | SF | 255/261 (98%) | 235 (92%) | 19 (8%) | 1 (0%) | 30 | 67 |
| 14 | SG | 222/272 (82%) | 209 (94%) | 13 (6%) | 0 | 100 | 100 |
| 15 | SH | 200/306 (65%) | 187 (94%) | 12 (6%) | 1 (0%) | 25 | 62 |
| 16 | SI | 176/195 (90%) | 163 (93%) | 13 (7%) | 0 | 100 | 100 |
| 17 | SJ | 186/194 (96%) | 168 (90%) | 16 (9%) | 2 (1%) | 12 | 46 |
| 18 | SK | 127/130 (98%) | 114 (90%) | 13 (10%) | 0 | 100 | 100 |
| 19 | SL | 165/218 (76%) | 147 (89%) | 16 (10%) | 2 (1%) | 11 | 44 |
| 20 | SM | 136/144 (94%) | 128 (94%) | 7 (5%) | 1 (1%) | 19 | 56 |
| 21 | SN | 96/118 (81%) | 90 (94%) | 6 (6%) | 0 | 100 | 100 |
| 22 | SO | 77/137 (56%) | 71 (92%) | 5 (6%) | 1 (1%) | 10 | 42 |
| 23 | SP | 125/151 (83%) | 118 (94%) | 6 (5%) | 1 (1%) | 16 | 53 |
| 24 | SQ | 142/145 (98%) | 132 (93%) | 10 (7%) | 0 | 100 | 100 |
| 25 | SR | 92/141 (65%) | 86 (94%) | 6 (6%) | 0 | 100 | 100 |
| 26 | SS | 126/156 (81%) | 99 (79%) | 24 (19%) | 3 (2%) | 5 | 30 |
| 27 | ST | 46/54 (85%) | 44 (96%) | 2 (4%) | 0 | 100 | 100 |
| 28 | SU | 147/151 (97%) | 141 (96%) | 6 (4%) | 0 | 100 | 100 |
| 29 | SV | 142/161 (88%) | 131 (92%) | 10 (7%) | 1 (1%) | 19 | 56 |
| 30 | SW | 91/137 (66%) | 82 (90%) | 7 (8%) | 2 (2%) | 5 | 32 |
| 31 | SX | 92/145 (63%) | 83 (90%) | 9 (10%) | 0 | 100 | 100 |
| 32 | SY | 152/170 (89%) | 147 (97%) | 5 (3%) | 0 | 100 | 100 |
| 33 | SZ | 70/82 (85%) | 65 (93%) | 4 (6%) | 1 (1%) | 9 | 40 |
| 37 | AL | 209/215 (97%) | 200 (96%) | 9 (4%) | 0 | 100 | 100 |
| 38 | A1 | 136/146 (93%) | 123 (90%) | 13 (10%) | 0 | 100 | 100 |
| 39 | A2 | 96/126 (76%) | 93 (97%) | 3 (3%) | 0 | 100 | 100 |
| 40 | A4 | 64/67 (96%) | 58 (91%) | 6 (9%) | 0 | 100 | 100 |
| 41 | A6 | 95/107 (89%) | 89 (94%) | 6 (6%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 42 | A7 | 92/120 (77%) | 92 (100%) | 0 | 0 | 100 | 100 |
| 43 | AN | 145/165 (88%) | 134 (92%) | 10 (7%) | 1 (1%) | 19 | 56 |
| 44 | A8 | 122/130 (94%) | 100 (82%) | 22 (18%) | 0 | 100 | 100 |
| 45 | A9 | 100/139 (72%) | 87 (87%) | 13 (13%) | 0 | 100 | 100 |
| 46 | Aa | 103/149 (69%) | 95 (92%) | 8 (8%) | 0 | 100 | 100 |
| 47 | Ab | 91/112 (81%) | 85 (93%) | 6 (7%) | 0 | 100 | 100 |
| 48 | Ad | 68/87 (78%) | 66 (97%) | 2 (3%) | 0 | 100 | 100 |
| 49 | Ae | 39/51 (76%) | 39 (100%) | 0 | 0 | 100 | 100 |
| 50 | Af | 49/128 (38%) | 42 (86%) | 7 (14%) | 0 | 100 | 100 |
| 51 | AP | 200/203 (98%) | 179 (90%) | 17 (8%) | 4 (2%) | 6 | 34 |
| 52 | Ah | 82/95 (86%) | 76 (93%) | 6 (7%) | 0 | 100 | 100 |
| 53 | Ai | 92/103 (89%) | 84 (91%) | 8 (9%) | 0 | 100 | 100 |
| 54 | AI | 203/221 (92%) | 190 (94%) | 12 (6%) | 1 (0%) | 25 | 62 |
| 55 | AJ | 216/283 (76%) | 208 (96%) | 7 (3%) | 1 (0%) | 25 | 62 |
| 56 | Ac | 87/92 (95%) | 72 (83%) | 15 (17%) | 0 | 100 | 100 |
| 57 | AK | 199/202 (98%) | 193 (97%) | 6 (3%) | 0 | 100 | 100 |
| 58 | AM | 130/139 (94%) | 122 (94%) | 8 (6%) | 0 | 100 | 100 |
| 59 | AS | 184/187 (98%) | 174 (95%) | 10 (5%) | 0 | 100 | 100 |
| 60 | AO | 145/148 (98%) | 131 (90%) | 14 (10%) | 0 | 100 | 100 |
| 61 | AQ | 185/219 (84%) | 166 (90%) | 16 (9%) | 3 (2%) | 8 | 39 |
| 62 | AR | 244/294 (83%) | 231 (95%) | 13 (5%) | 0 | 100 | 100 |
| 63 | AW | 149/173 (86%) | 139 (93%) | 10 (7%) | 0 | 100 | 100 |
| 64 | AY | 99/190 (52%) | 95 (96%) | 4 (4%) | 0 | 100 | 100 |
| 65 | AT | 179/182 (98%) | 175 (98%) | 4 (2%) | 0 | 100 | 100 |
| 66 | AZ | 119/126 (94%) | 114 (96%) | 5 (4%) | 0 | 100 | 100 |
| 67 | A3 | 117/124 (94%) | 105 (90%) | 12 (10%) | 0 | 100 | 100 |
| 68 | A5 | 221/257 (86%) | 206 (93%) | 15 (7%) | 0 | 100 | 100 |
| 69 | AD | 245/260 (94%) | 230 (94%) | 14 (6%) | 1 (0%) | 30 | 67 |
| 70 | AE | 378/386 (98%) | 361 (96%) | 17 (4%) | 0 | 100 | 100 |
| 71 | AF | 388/411 (94%) | 362 (93%) | 25 (6%) | 1 (0%) | 37 | 71 |
| 72 | AG | 116/173 (67%) | 110 (95%) | 6 (5%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-------------------|------------|----------|----------|-------------|-----|
| 73 | AU | 178/184 (97%) | 172 (97%) | 6 (3%) | 0 | 100 | 100 |
| 74 | AH | 183/190 (96%) | 172 (94%) | 11 (6%) | 0 | 100 | 100 |
| 75 | AV | 153/162 (94%) | 143 (94%) | 10 (6%) | 0 | 100 | 100 |
| 76 | Ag | 35/39 (90%) | 29 (83%) | 6 (17%) | 0 | 100 | 100 |
| 77 | AX | 95/139 (68%) | 88 (93%) | 7 (7%) | 0 | 100 | 100 |
| 78 | A0 | 60/162 (37%) | 57 (95%) | 3 (5%) | 0 | 100 | 100 |
| 79 | S8 | 315/323 (98%) | 300 (95%) | 15 (5%) | 0 | 100 | 100 |
| All | All | 10421/12340 (84%) | 9689 (93%) | 699 (7%) | 33 (0%) | 38 | 71 |

5 of 33 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 15 | SH | 148 | ASP |
| 17 | SJ | 112 | ILE |
| 20 | SM | 41 | GLU |
| 29 | SV | 41 | VAL |
| 30 | SW | 4 | VAL |

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 | S1 | 104/115 (90%) | 104 (100%) | 0 | 100 | 100 |
| 2 | S2 | 35/88 (40%) | 34 (97%) | 1 (3%) | 37 | 58 |
| 3 | S3 | 87/98 (89%) | 87 (100%) | 0 | 100 | 100 |
| 4 | S4 | 70/76 (92%) | 70 (100%) | 0 | 100 | 100 |
| 5 | S5 | 47/47 (100%) | 43 (92%) | 4 (8%) | 8 | 30 |
| 6 | S6 | 36/36 (100%) | 36 (100%) | 0 | 100 | 100 |
| 9 | SB | 195/238 (82%) | 195 (100%) | 0 | 100 | 100 |
| 10 | SC | 167/227 (74%) | 166 (99%) | 1 (1%) | 84 | 88 |
| 11 | SD | 132/188 (70%) | 130 (98%) | 2 (2%) | 60 | 75 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|---------------|------------|----------|-------------|-----|
| 12 | SE | 161/167 (96%) | 161 (100%) | 0 | 100 | 100 |
| 13 | SF | 233/237 (98%) | 233 (100%) | 0 | 100 | 100 |
| 14 | SG | 191/222 (86%) | 191 (100%) | 0 | 100 | 100 |
| 15 | SH | 182/279 (65%) | 181 (100%) | 1 (0%) | 86 | 90 |
| 16 | SI | 154/165 (93%) | 153 (99%) | 1 (1%) | 84 | 88 |
| 17 | SJ | 177/183 (97%) | 174 (98%) | 3 (2%) | 56 | 72 |
| 18 | SK | 115/116 (99%) | 115 (100%) | 0 | 100 | 100 |
| 19 | SL | 151/193 (78%) | 151 (100%) | 0 | 100 | 100 |
| 20 | SM | 116/122 (95%) | 116 (100%) | 0 | 100 | 100 |
| 21 | SN | 91/109 (84%) | 90 (99%) | 1 (1%) | 70 | 80 |
| 22 | SO | 76/129 (59%) | 75 (99%) | 1 (1%) | 65 | 77 |
| 23 | SP | 99/119 (83%) | 99 (100%) | 0 | 100 | 100 |
| 24 | SQ | 120/121 (99%) | 119 (99%) | 1 (1%) | 79 | 84 |
| 25 | SR | 83/121 (69%) | 83 (100%) | 0 | 100 | 100 |
| 26 | SS | 114/136 (84%) | 114 (100%) | 0 | 100 | 100 |
| 27 | ST | 43/48 (90%) | 43 (100%) | 0 | 100 | 100 |
| 28 | SU | 132/133 (99%) | 132 (100%) | 0 | 100 | 100 |
| 29 | SV | 131/144 (91%) | 130 (99%) | 1 (1%) | 79 | 84 |
| 30 | SW | 86/127 (68%) | 86 (100%) | 0 | 100 | 100 |
| 31 | SX | 88/130 (68%) | 88 (100%) | 0 | 100 | 100 |
| 32 | SY | 137/151 (91%) | 136 (99%) | 1 (1%) | 81 | 86 |
| 33 | SZ | 60/70 (86%) | 59 (98%) | 1 (2%) | 56 | 72 |
| 37 | AL | 190/194 (98%) | 189 (100%) | 1 (0%) | 86 | 90 |
| 38 | A1 | 127/132 (96%) | 126 (99%) | 1 (1%) | 79 | 84 |
| 39 | A2 | 97/117 (83%) | 97 (100%) | 0 | 100 | 100 |
| 40 | A4 | 60/61 (98%) | 60 (100%) | 0 | 100 | 100 |
| 41 | A6 | 82/91 (90%) | 82 (100%) | 0 | 100 | 100 |
| 42 | A7 | 90/112 (80%) | 90 (100%) | 0 | 100 | 100 |
| 43 | AN | 136/152 (90%) | 125 (92%) | 11 (8%) | 9 | 31 |
| 44 | A8 | 113/119 (95%) | 112 (99%) | 1 (1%) | 75 | 83 |
| 45 | A9 | 90/127 (71%) | 90 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|------------|----------|-------------|-----|
| 46 | Aa | 89/128 (70%) | 89 (100%) | 0 | 100 | 100 |
| 47 | Ab | 82/97 (84%) | 81 (99%) | 1 (1%) | 67 | 79 |
| 48 | Ad | 69/83 (83%) | 69 (100%) | 0 | 100 | 100 |
| 49 | Ae | 40/48 (83%) | 40 (100%) | 0 | 100 | 100 |
| 50 | Af | 45/114 (40%) | 45 (100%) | 0 | 100 | 100 |
| 51 | AP | 177/178 (99%) | 177 (100%) | 0 | 100 | 100 |
| 52 | Ah | 70/80 (88%) | 70 (100%) | 0 | 100 | 100 |
| 53 | Ai | 86/92 (94%) | 86 (100%) | 0 | 100 | 100 |
| 54 | AI | 189/203 (93%) | 189 (100%) | 0 | 100 | 100 |
| 55 | AJ | 204/260 (78%) | 202 (99%) | 2 (1%) | 73 | 81 |
| 56 | Ac | 74/77 (96%) | 72 (97%) | 2 (3%) | 40 | 61 |
| 57 | AK | 181/182 (100%) | 181 (100%) | 0 | 100 | 100 |
| 58 | AM | 106/110 (96%) | 106 (100%) | 0 | 100 | 100 |
| 59 | AS | 158/159 (99%) | 158 (100%) | 0 | 100 | 100 |
| 60 | AO | 121/122 (99%) | 120 (99%) | 1 (1%) | 79 | 84 |
| 61 | AQ | 165/190 (87%) | 164 (99%) | 1 (1%) | 84 | 88 |
| 62 | AR | 215/254 (85%) | 214 (100%) | 1 (0%) | 86 | 90 |
| 63 | AW | 128/131 (98%) | 127 (99%) | 1 (1%) | 79 | 84 |
| 64 | AY | 90/177 (51%) | 90 (100%) | 0 | 100 | 100 |
| 65 | AT | 162/163 (99%) | 162 (100%) | 0 | 100 | 100 |
| 66 | AZ | 111/115 (96%) | 110 (99%) | 1 (1%) | 75 | 83 |
| 67 | A3 | 110/115 (96%) | 109 (99%) | 1 (1%) | 75 | 83 |
| 68 | A5 | 201/231 (87%) | 200 (100%) | 1 (0%) | 86 | 90 |
| 69 | AD | 191/202 (95%) | 190 (100%) | 1 (0%) | 86 | 90 |
| 70 | AE | 335/340 (98%) | 333 (99%) | 2 (1%) | 84 | 88 |
| 71 | AF | 336/352 (96%) | 336 (100%) | 0 | 100 | 100 |
| 72 | AG | 110/155 (71%) | 109 (99%) | 1 (1%) | 75 | 83 |
| 73 | AU | 162/166 (98%) | 161 (99%) | 1 (1%) | 84 | 88 |
| 74 | AH | 168/173 (97%) | 168 (100%) | 0 | 100 | 100 |
| 75 | AV | 140/145 (97%) | 140 (100%) | 0 | 100 | 100 |
| 76 | Ag | 34/35 (97%) | 33 (97%) | 1 (3%) | 37 | 58 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|------------------|------------|----------|-------------|-----|
| 77 | AX | 92/131 (70%) | 92 (100%) | 0 | 100 | 100 |
| 78 | A0 | 53/146 (36%) | 52 (98%) | 1 (2%) | 52 | 69 |
| 79 | S8 | 281/287 (98%) | 281 (100%) | 0 | 100 | 100 |
| All | All | 9373/10881 (86%) | 9321 (99%) | 52 (1%) | 82 | 88 |

5 of 52 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 43 | AN | 15 | SER |
| 55 | AJ | 248 | LYS |
| 73 | AU | 177 | LYS |
| 43 | AN | 16 | LYS |
| 44 | A8 | 79 | LYS |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 51 | AP | 195 | GLN |
| 78 | A0 | 49 | GLN |
| 61 | AQ | 14 | ASN |
| 70 | AE | 342 | GLN |
| 57 | AK | 28 | ASN |

5.3.3 RNA ⓘ

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 34 | AA | 3164/3788 (83%) | 747 (23%) | 71 (2%) |
| 35 | AC | 148/159 (93%) | 37 (25%) | 5 (3%) |
| 36 | AB | 117/119 (98%) | 18 (15%) | 3 (2%) |
| 7 | S7 | 73/74 (98%) | 19 (26%) | 1 (1%) |
| 8 | SA | 1587/2087 (76%) | 366 (23%) | 27 (1%) |
| All | All | 5089/6227 (81%) | 1187 (23%) | 107 (2%) |

5 of 1187 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 7 | S7 | 8 | U |
| 7 | S7 | 10 | G |
| 7 | S7 | 16 | U |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 7 | S7 | 17 | U |
| 7 | S7 | 18 | G |

5 of 107 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 34 | AA | 821 | C |
| 34 | AA | 1736 | A |
| 35 | AC | 35 | A |
| 34 | AA | 888 | A |
| 34 | AA | 1224 | 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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 63 | AW | 1 |

All chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1 | AW | 154:ASN | C | 197:UNK | N | 32.78 |

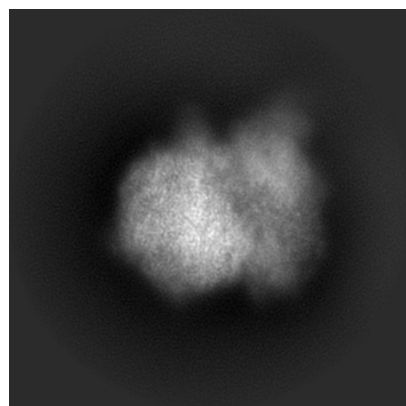
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41485. These allow visual inspection of the internal detail of the map and identification of artifacts.

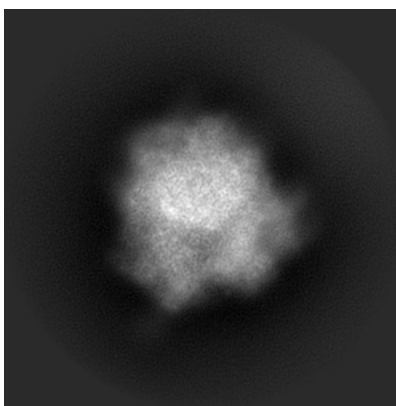
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

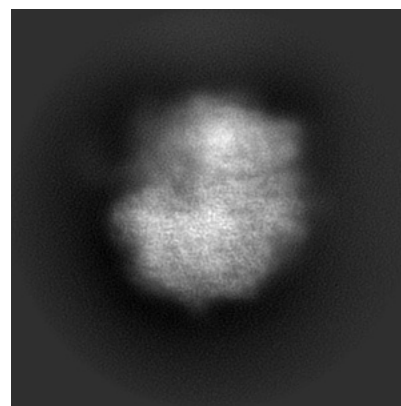
6.1.1 Primary map



X

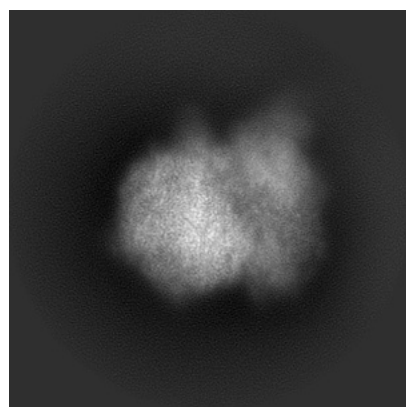


Y

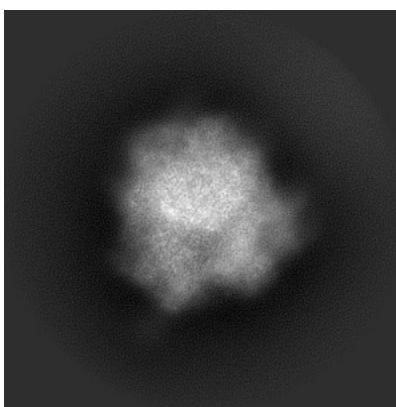


Z

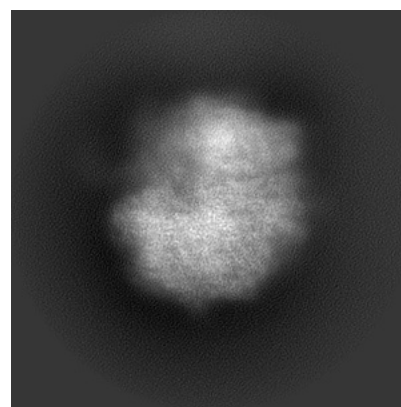
6.1.2 Raw map



X



Y

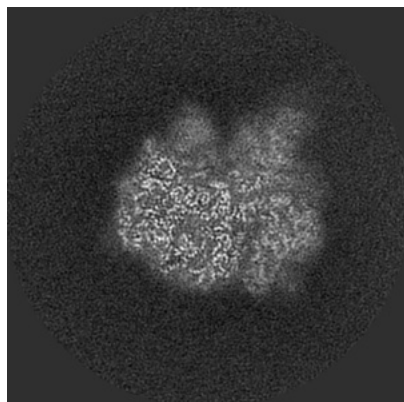


Z

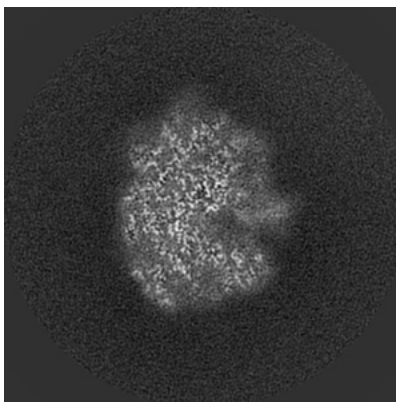
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

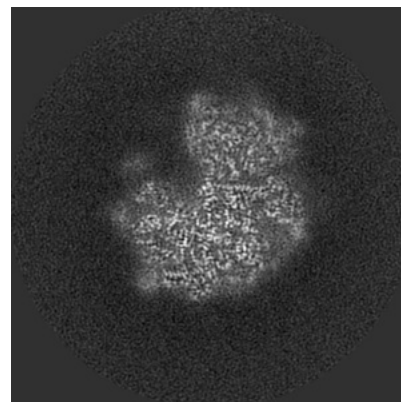
6.2.1 Primary map



X Index: 148

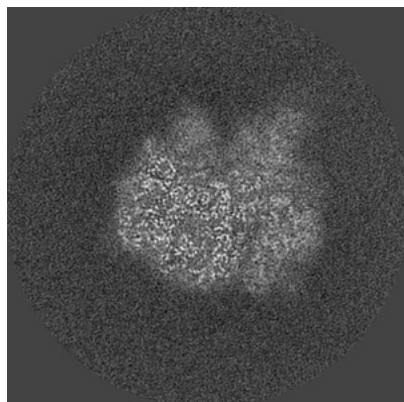


Y Index: 148

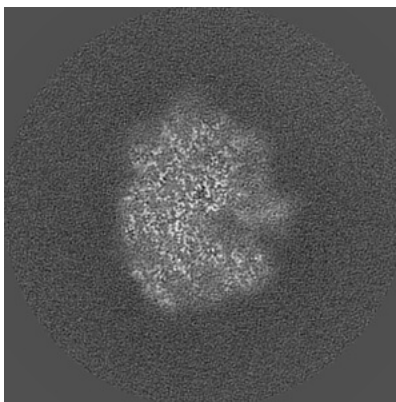


Z Index: 148

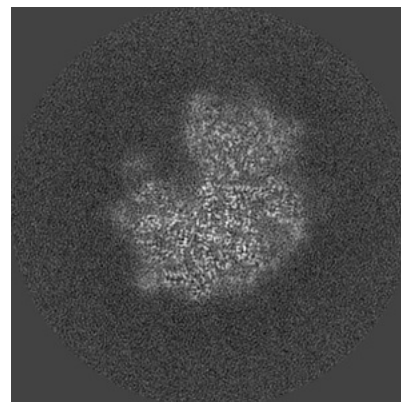
6.2.2 Raw map



X Index: 148



Y Index: 148

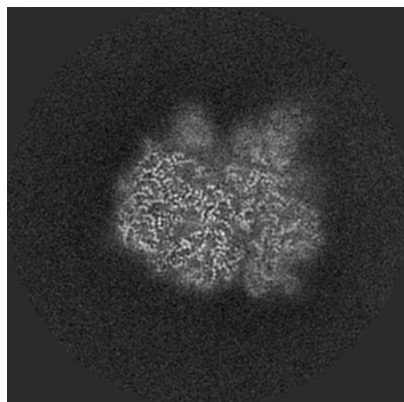


Z Index: 148

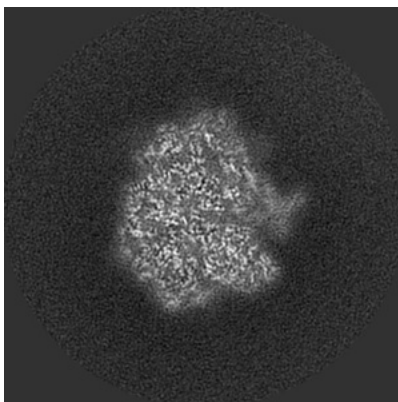
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

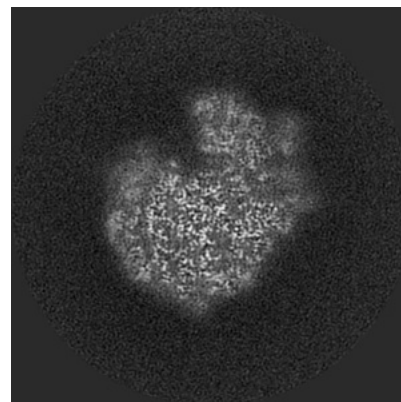
6.3.1 Primary map



X Index: 150

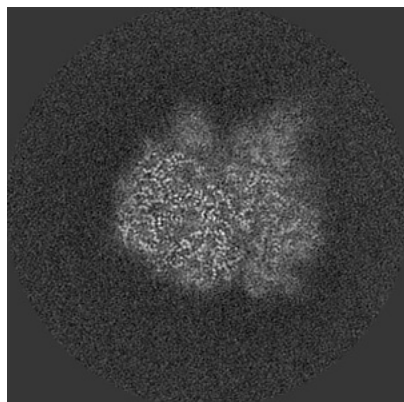


Y Index: 139

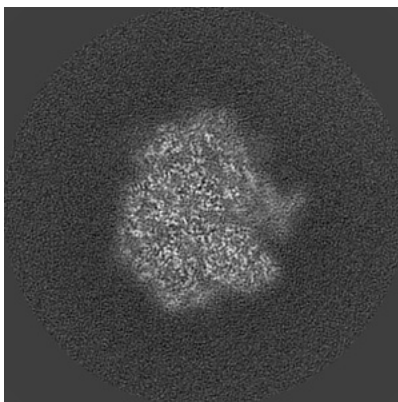


Z Index: 127

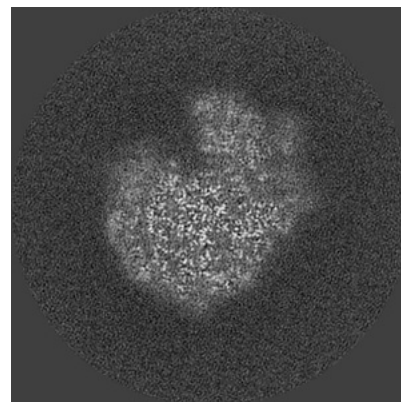
6.3.2 Raw map



X Index: 150



Y Index: 139

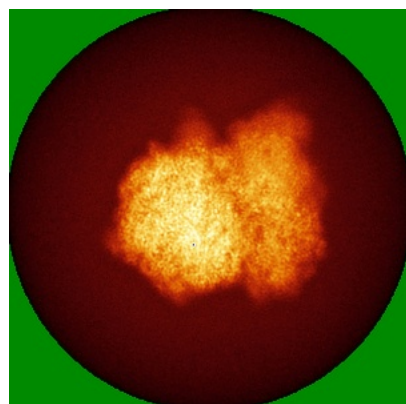


Z Index: 127

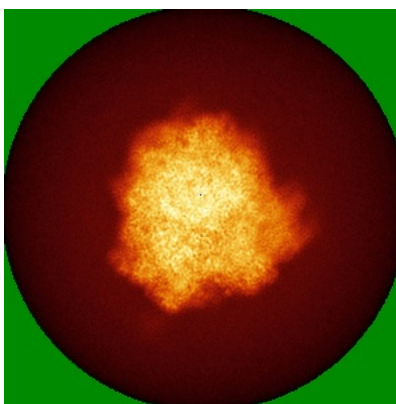
The images above show the largest variance slices of the map in three orthogonal directions.

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

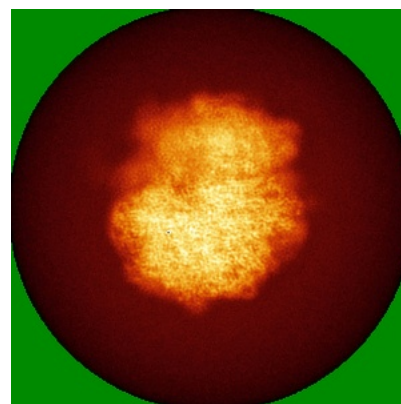
6.4.1 Primary map



X

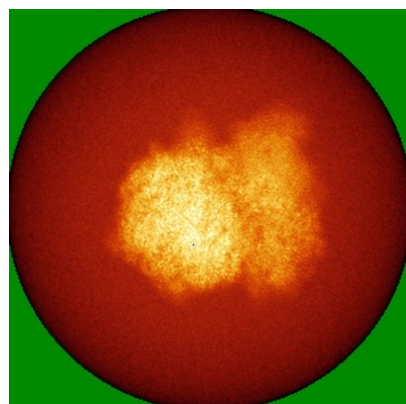


Y

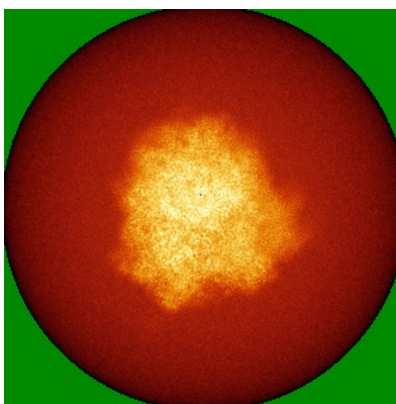


Z

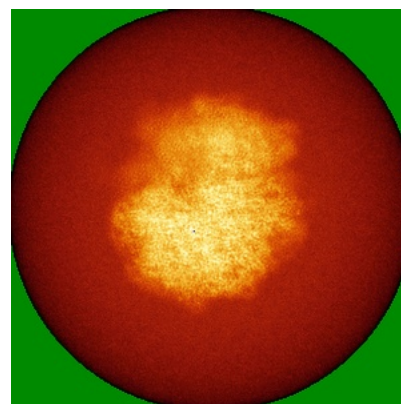
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



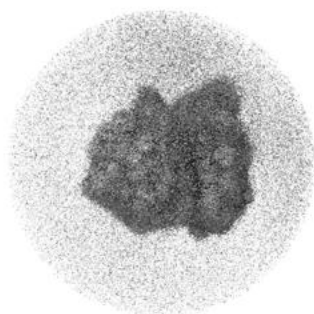
Y



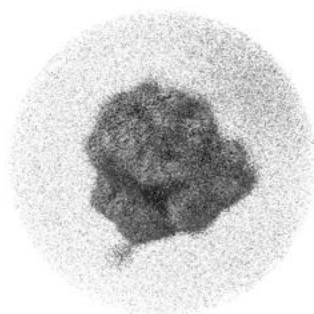
Z

The images above show the 3D surface view of the map at the recommended contour level 0.16. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

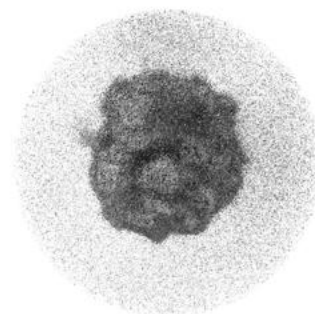
6.5.2 Raw map



X



Y



Z

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

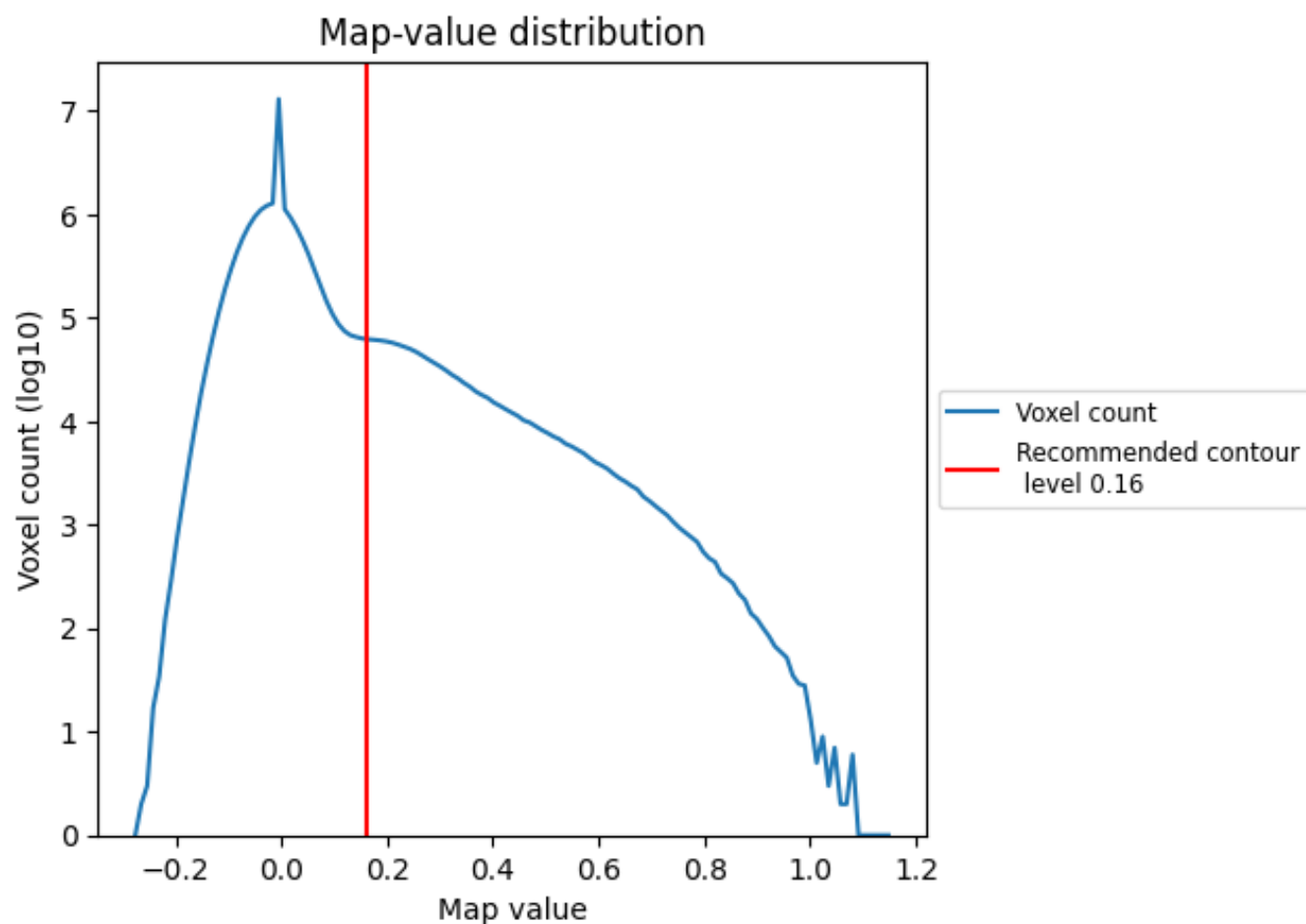
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

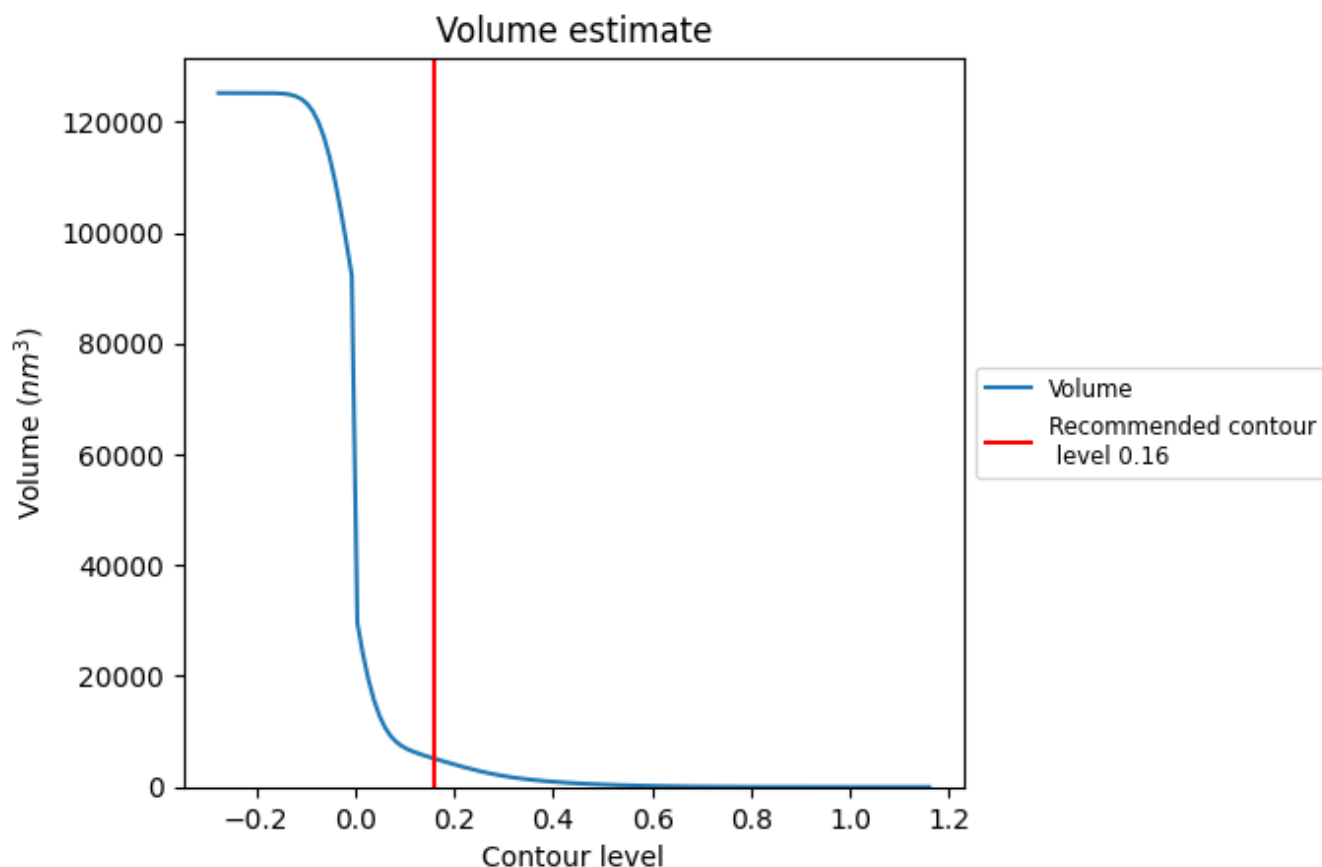
This section contains the results of statistical analysis of the map.

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.

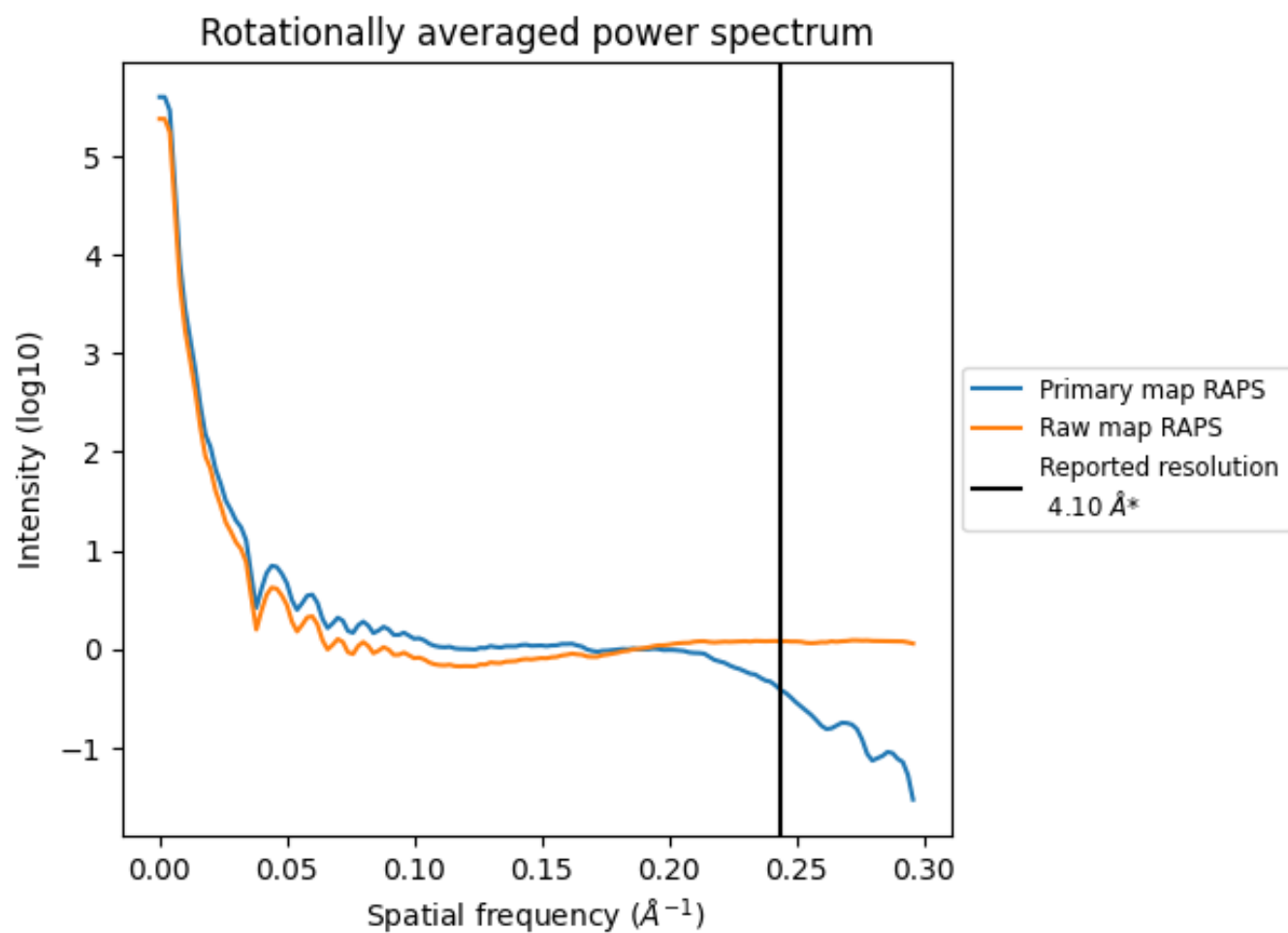
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5103 nm^3 ; this corresponds to an approximate mass of 4610 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 ⓘ

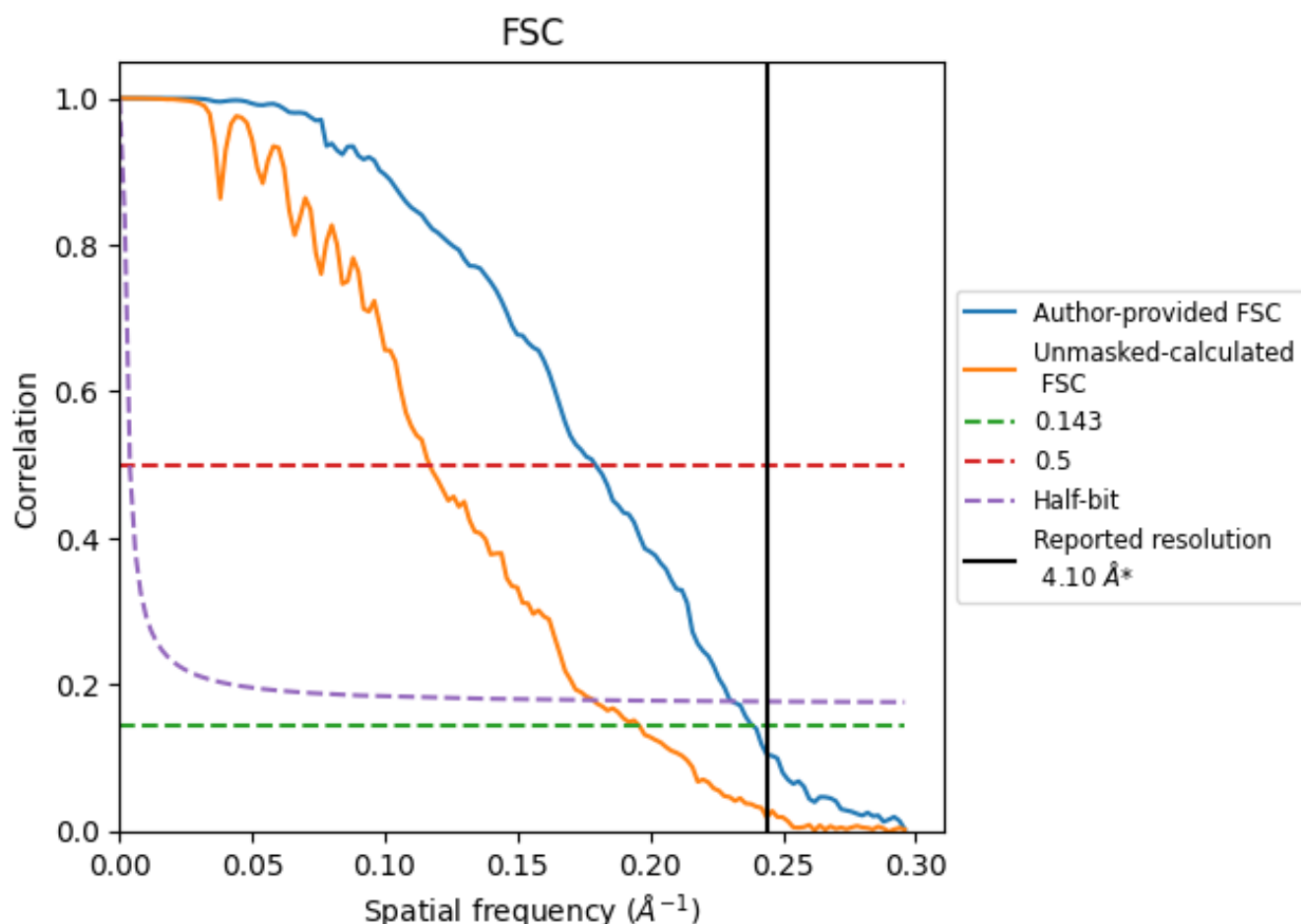


*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

8 Fourier-Shell correlation [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 0.244 \AA^{-1}

8.2 Resolution estimates [i](#)

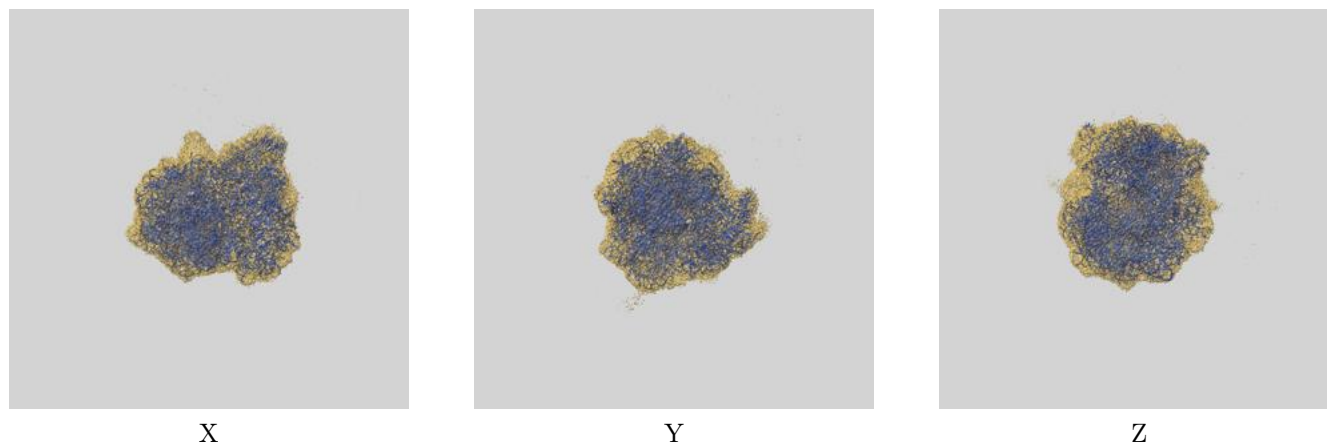
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---------------------------|------------------------------------|------|----------|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 4.10 | - | - |
| Author-provided FSC curve | 4.19 | 5.58 | 4.33 |
| Unmasked-calculated* | 5.10 | 8.55 | 5.60 |

*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 5.10 differs from the reported value 4.1 by more than 10 %

9 Map-model fit [i](#)

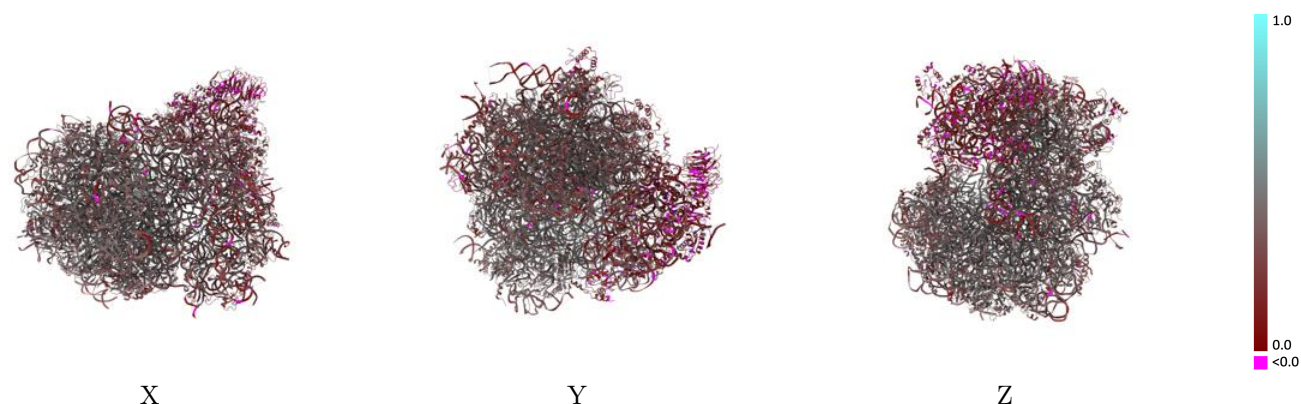
This section contains information regarding the fit between EMDB map EMD-41485 and PDB model 8TPU. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)



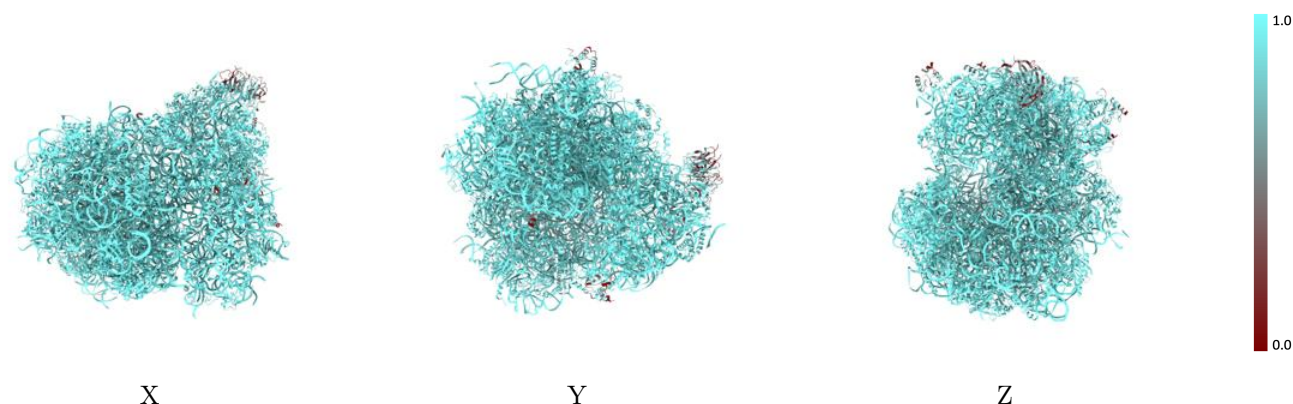
The images above show the 3D surface view of the map at the recommended contour level 0.16 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



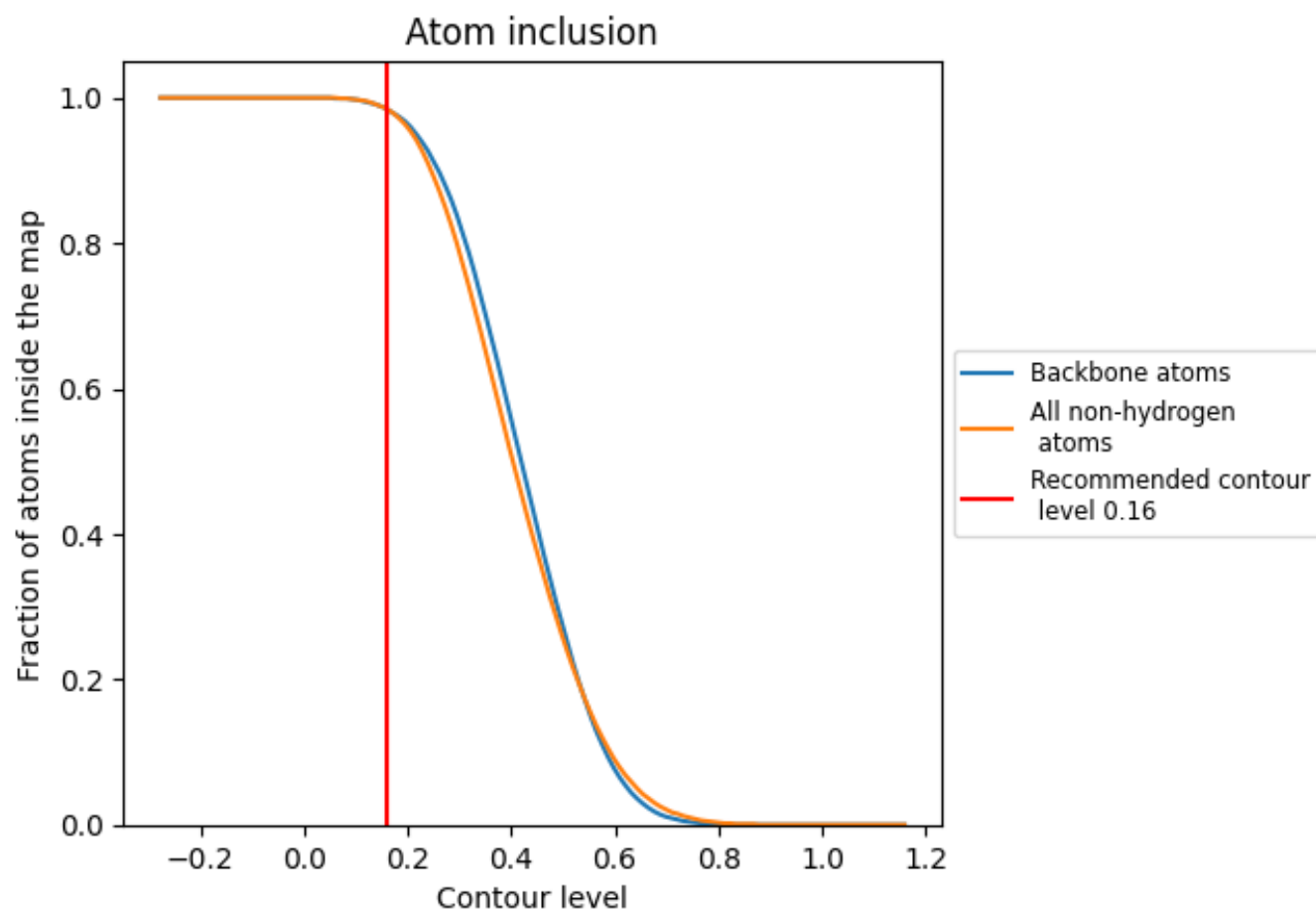
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.16).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.16) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| All |  0.9850 |  0.3590 |
| A0 |  0.9980 |  0.4070 |
| A1 |  0.9870 |  0.3780 |
| A2 |  0.9960 |  0.4000 |
| A3 |  0.9940 |  0.3950 |
| A4 |  0.9890 |  0.3650 |
| A5 |  0.9920 |  0.4090 |
| A6 |  0.9900 |  0.3970 |
| A7 |  0.9960 |  0.4210 |
| A8 |  0.9980 |  0.4200 |
| A9 |  1.0000 |  0.4430 |
| AA |  0.9980 |  0.3920 |
| AB |  1.0000 |  0.3920 |
| AC |  1.0000 |  0.4030 |
| AD |  0.9960 |  0.4270 |
| AE |  0.9910 |  0.4150 |
| AF |  0.9930 |  0.4050 |
| AG |  0.9940 |  0.3640 |
| AH |  0.9920 |  0.3960 |
| AI |  0.9880 |  0.3900 |
| AJ |  0.9550 |  0.3580 |
| AK |  0.9940 |  0.4050 |
| AL |  0.9910 |  0.4040 |
| AM |  0.9910 |  0.4130 |
| AN |  0.9950 |  0.3930 |
| AO |  0.9960 |  0.4280 |
| AP |  0.9990 |  0.4220 |
| AQ |  0.9940 |  0.4030 |
| AR |  0.9840 |  0.3740 |
| AS |  0.9980 |  0.4160 |
| AT |  0.9600 |  0.3700 |
| AU |  0.9970 |  0.4200 |
| AV |  0.9900 |  0.4150 |
| AW |  0.9960 |  0.4270 |
| AX |  0.9740 |  0.3410 |








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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| AY |  0.9950 |  0.4090 |
| AZ |  0.9990 |  0.4010 |
| Aa |  0.9990 |  0.4220 |
| Ab |  0.9990 |  0.3920 |
| Ac |  1.0000 |  0.4310 |
| Ad |  0.9920 |  0.3810 |
| Ae |  1.0000 |  0.4300 |
| Af |  1.0000 |  0.4200 |
| Ag |  1.0000 |  0.3880 |
| Ah |  0.9950 |  0.4230 |
| Ai |  0.9960 |  0.4240 |
| S1 |  0.9880 |  0.2920 |
| S2 |  0.9720 |  0.1910 |
| S3 |  0.9930 |  0.3700 |
| S4 |  0.9640 |  0.3320 |
| S5 |  0.9710 |  0.2180 |
| S6 |  1.0000 |  0.3050 |
| S7 |  0.9840 |  0.1760 |
| S8 |  0.6360 |  0.1440 |
| SA |  0.9930 |  0.3110 |
| SB |  0.9830 |  0.3440 |
| SC |  0.9580 |  0.3090 |
| SD |  0.9810 |  0.2400 |
| SE |  0.9350 |  0.3160 |
| SF |  0.9810 |  0.3450 |
| SG |  0.9840 |  0.3490 |
| SH |  0.9750 |  0.2790 |
| SI |  0.9500 |  0.1480 |
| SJ |  0.8530 |  0.2900 |
| SK |  0.9960 |  0.3700 |
| SL |  0.9910 |  0.3660 |
| SM |  0.9700 |  0.1840 |
| SN |  0.9130 |  0.2260 |
| SO |  0.9840 |  0.2530 |
| SP |  0.9860 |  0.3560 |
| SQ |  0.9960 |  0.3690 |
| SR |  0.6680 |  0.1710 |
| SS |  0.9750 |  0.1940 |
| ST |  0.9970 |  0.2640 |
| SU |  0.9940 |  0.3580 |
| SV |  0.9920 |  0.4070 |
| SW |  0.9610 |  0.2440 |

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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| SX |  0.9250 |  0.1830 |
| SY |  0.9760 |  0.1850 |
| SZ |  0.9710 |  0.3450 |